

Negative Training Data

> Q46M54|TFDS_RALEJ HTH -type transcriptional regulator tfdS - *Ralstonia eutropha* (strain JMP134) (*Alcaligenes eutrophus*).
MEFRQLRYFVAAAEEGNVGAAARRLHISQPPVTRQIHAEQHLGVLFFER
SARGVQLTPAGAAFLLEDARRMLELGRTSVDRSRAASRGEIGQLDIGYLG
AIYQTVPALHHAFTQAVPGATLSLALMPKVRQIEALRAGTIHLGVGRFY
QEPGITVEHLHYERLYIAAGSSIARQLRQDPTLLRLKSESLVLFPEGR
SFADEVIALMRRAGVEPRVTAIVEDVNAALGLVAAGAGVTLVPASVAAIR
RPFVRTMEMADASAKVPVSLTYLTDSRVVLRRAFLDVARRGKGQK

> P0A921|PA1_ECOLI Phospholipase A1 - *Escherichia coli*.
MRTLQGWLLPVFMLPMAVYAQEATVKEVHDAPAVRGSIIANMLQEHDNPF
TLYPYDTNYLIYTQTSDLNKEAIASYDWAENARKDEVKFLSLAFPLWRG
ILGPNVSLGASYTQKSWWQLSNSEESSPFRETNYEPQLFLGFATDYRFAG
WTLRDVEMGYNHDSNGRSDPTSRSWNRLYTRLMAENGNWLVVEKWPYVVG
NTDDNPDITKYMGYQLKIGYHLGDAVLSAKGQYNWNTGYGGAELGLSYP
ITKHVRLYTQVYSGYGESLIDYNFNQTRVGVGVMNDLF

> CHEA_SALTY P09384 CHEMOTAXIS PROTEIN CHEA (EC 2.7.3. -). - S
MSMDISDFYQTFDEADELLADMEQHLLDLVPESPAEQLNIAIFRAAHSI
KGGAGTFGFTILQETTHLMENLLDEARRGEMQLNTDIINLFLETKDIME
QLDAYKNSEEPDAAEFYICNALRQLALEAKGETTPAVVETAALSAAIQE
ESVAETESPRDESKLRIVLSRLKANEVDLLEELGNLATLTDVVKGADSL
SATLDGSVAEDDIVAVLCFVIEADQIAFEKVVAAPVEKAQEKTEVAPVAP
PAVVAPAAKSAAEHHAGREKPARERESTSIRVAVEKVDQLINLVGELVI
TQSMLAQRSNELDPVNHGDLITSMGQLQRNARDLQESVMSIRMPMEYVF
SRFPRLVRDLGKGLKQVELTLVGSSTELDKSLIERIIDPLTHLVRNSLD
HGIEMPEKRLEA GKNVGNLILSAEHQGGNICIEVTDDGAGLNRERILAK
AMSQGMVAVNMTDDEVGMLIFAPGFSTAEQVTDVSGRGGMDVVKRNIQ
EMGGHVEIQSKQSGTIRILLPLTLAILDGMSSVRVAGEVFILPLNAVME
SLQPREEDLHPLAGGERVLEVRGEYLPLVELWKFVDVDGAKTEATQGIIV
ILQSAGRRYALLVDQLIGQHVVVKNLESNYRQVPGISAATILGDGSVAL
IVDVSALQGLNREQRMAITAA

> CHEW_ENTAE P21821 PURINE -BINDING CHEMOTAXIS PROTEIN. - ENTE
MAGLATVSKLAGETVQQAFLIFTLGNEEYIGIDILKVQKIRGYDQVTRIAN
TPDFIKGVTNLRGVIVPIIDLVRKYAQQGVSYDENTVVIVLNFQRRVGI
VVDGVSVDVLSLTAEQIRPAPEFAVTMATEYLTGLGALGALLILVDIEKLL
STEEMALVDNVAKSH

> P32557|DSBA_VIBCH Thiol:disulfide interchange protein dsbA - *Vibrio cholerae*.
MKKLFALVATLMLSVSAYAAQFKEGEHYQVLKTPASSSPVNEFFSFYCP
HCNTFEPIIAQLKQQLPEGAKFQKNHVSFMGGNMGQAMSKAYATMIALEV
EDKMVPVMFNRIHTLRKPPKDEQELRQIFLDEGIDAAKFDAAYNGFAVDS
MVRRFDKQFQDSGLTGVPAVVVNNRYLVQGQSVKSLDEYFDLVNYLLTLK

> P05149|GALM_ACICA Aldose 1-epimerase - *Acinetobacter calcoaceticus*.
MKKLAILGVTVYSFAQLANAATLNKSYGTTQNGQKVDLYTMSNNNGVSV
SFISFGGVTQILTPDAQGKQNNIVLGFDDLKGYEVTDTKEGIHFGGLIG
RYANRIGNAKFSLDGKTYNLEKNNGPNSLHSGNPGFDKRVQVKPLVSKG
ETVKASLKLTPNGDQGFPGKLDVEVIYSLSDQNEFKIEYKAKTDQPTVV
NLTNHSYFNLGAGNPNPYGVLDHVVQLNAGRILVTDQNSLPTGEIASVAG
TPFDFRMPKAIVKDIRANNQQLAYGYDQTVWINQKSQKLNLAIVVD
PKSKRTMQVLTTEPSVQMYTADHLLGNIVGANGVLYRQADALALETQHFP
DSPNQPTFPSTRLNPNQTYNSVTVFKEFGVQK

> P14212|HIFA2_HAEIN Major fimbrial subunit - *Haemophilus influenzae*.
MKKTLGSLILLAFAGNVQADINTETSGKVTFFGKVVENTCKVKTEHKNL
SVVLNDVGKNSLSTKVNTAMPTPFTITLQNCDDPTTANGTANKANKVGLYF
YSWKNVDKENNFTLKNEQTTADYATNVNIQLMESNGTKAISVVGKETEDF
MHTNNGVALNQTHPNAHISGSTQLTTGTNELPLHFIAQYYATNKATAG
KVQSSVDFQIAYE

> P22340|SCRY_SALTY Sucrose porin - *Salmonella typhimurium*.
MYRKSTLAMLIALTSAASAHAQTDISTIEARLNALEKRLQEAENRAQTA
ENRAGAAEKVQQLTAQQKNQNSTQEVAQRTARLEKKADDSGFEFHGY

ARSGVIMNDSGASTKSGAYITPAGETGGAIIGRLGNQADTYVEMNLEHKQT
LDNGATTRFKVMVADGQTSYNDWTASTSDLNVRQAFVELGNLPTFAGPFK
GSTLWAGKRFRDRDNFDIHWIDSDVVFLAGTGGGIYDVKWNDGLRSNFSLY
GRNFGDIDSSNSVQNYILTMNHFAGPLQMMVSGLRAKDNDRKDSNGNL
AKGDAANTGVHALLGLHNSFYGLRDGSSKTALLYGHGLGAEVKGIGSDG
ALRPGADTWRIASYGTTPLSENWSVAPAMLAQRSKDRYADGDSYQWATFN
LRLIQAINQNALAYEGSYQYMDLKPEGYNDRQAVNGSFYKLTFAPTFKV
GSIGDFFSRPEIRFYTSWMDWSKLNLYASDDALGSDGFNSGGEWSFGVQ
METWF

> P43822|SYGB_HAEIN Glycyl -tRNA synthetase beta chain - Haemophilus influenzae.

MTTQNFLVEIGTEELPPKALKTLATSFDNVEAELNQAAGLSFDKIEWFAA
PRRLAVKVLNLTQQPSKEIEKRGPAVSAAFDAEGKPTKAAEGWARGCGI
TVEQAERIATDKGEWLIH RAKIEGQPTKNLLNDIVANALAKLP I PKPMRW
ADKTVQFIRPVHTVTMLLGDDELIEGEILGVASARTIRGHRFLGEKEFYIQ
HADQYPQLLREKGSVVADFNERKAEILAKSQAKATALGGVADIEESLLEE
VTSLSVEYPNVLAAKFEEHFLAVPAEALVYTMKGDQKYFPIYDKDGKLLPH
FIFVSNINPEDPTAI IEGNEKVVRPRLTDAEFFFKTDLKQKLVDRLEPRLE
TVLFQQQLGLTKDKTDRIE QLAGEI AKQIGADEAKAKRAGLLSKCDLMTN
MVFEFTDTQGVGMHYARHDGEDEEVAVALNEQYMPRFAGDELPKSLVAS
AVALADKFDTLTGIFGIGQAPKGSADPFALRRAALGALRIIVEKNLPLDL
EDLVKKSAAALFGDKLTNQNVVADVDFMLGRFRAWYQDEGIAVDVIQAVL
ARRPTRPADFDARVRAVSHFRTLDSAEALAAANKRVSNILAKAGAAIGEI
NLTACVEPAEKALAEAVLAL RTEVQPLIAQGDYTTVLDKLANLRAPVDSF
FDNVMVNAEDPALRQNRLAILNTLQGLFLQVADISVLQ

> P0A2S9|RHAS_SALTY HTH -type transcriptional activator rhaS - Salmonella typhimurium.

MTVLHSDVDFPSPKAPVAIEPRLPQAAFPEHHHDFHEIVIVEHGTGIHVF
NGQPYTISGGTVCVFRDHRHLYEHTDNLCLTNVLRSPDAFQFLAGLD Q
LLPQEYQDGYYP SHWRVNVQSVLQQVRLVGLMERAGDGM DAPAVANREILF
MQLLVLLRRSSLMEGATNNDAKLNQLMAWLEDHFAEEVCWEAVAEQFSL
LRTLHRQLKQHTGLTPQRYLNRLRLIKARHLLRHS DHSVTEIAYRCGF
SDSNHSTLFRREFNWSPRDIRQGRDAIIQ

> P62088|PRSX_ECOLI HTH -type transcriptional regulator prsX - Escherichia coli.

MNNTDTLEKII RHQKNKDPAYPFQEHLMLQLCIRANKRMQDNISEFLGAY
GINHSVYMLVTLTFTAESHCLSPSEISQKLOFTRTNI TRITDFLEKTGYV
KRTDSREDRRAKKISLTSEGMFFIQRLTLAQSMYLKEIWGYLTHDEQELF
EVINKKLLAHLDDVSS

> P22541|GUNA_BUTFI Endoglucanase A - Butyrivibrio fibrisolvens.

MVSKKQKFLTVILVIVLAI VIVGGVFGISFVKGRVTFPWQLQNSEAKTEQ
VKEPAKEPKLVIKEKKQDES AKKEQELKKAKEEAEAAVEKETEKTEEEP
VDNLLNDMMLKYYGKLAVEGSHLVDADGHEVLLMGVSTHGINWYPEYASA
ETIKSLRDTWGINVIRLAMYTS DYNGYCVAGKENQEKLKDI IDDAVEAAT
DNDMYVIIDWHTLNDADPNEYKADAIQFFGEMVRKYKDNENVIYEICNEP
NGDTTWNDVRRYAN EVIPVIRNVDAIILVGT PKWATDLDSVLDKPLDFDN
IMYTYHFYAGTHHKAERNALRDALDEGLPVFI SEYGLVDADGDGNLNEKE
ADYWYDMIRKEYGVSSCMWNLSNKDEGSAMINADCKLSDFTEEDLSESA
MWLIDQISQLKHS DLEQGV DWITPENNNR

> P32722|PORD_PSEAE Porin D - Pseudomonas aeruginosa.

MKVMKWSAIALAVSAGSTQFAVADAFVSDQAEA KGFIEDSSLDLLLRNYY
FNRDGGKSGSGDRVDWTQGFLLTYESGFTQGT VGVGVD AFGYLGLKLDGTS
DKTGTGNLPVMNDGKPRDDYSRAGGAVKVRISKTMLKWGEMQPTAPVFAA
GGSRLFPQTATGFQLQSSEFEGLDLEAGHFTEGKEPTTVKSRGELYATYA
GETAKSADYFIGGRYAITDNLSASLYGAELEDIYRQYYLNSNYTIPLASDQ
SLGFDFNIYRTNDEGKAKAGDISNTTWSLAAAYT LDAHTFTLAYQKVHGD
QPFDYIGFGRNGSGAGGDSIFLANSVQYSDFNGPGEKSWQARYDLNLASY
GVPGLTFMVRYINGKDIDGTKMSDNNVGYKNGYGEDGKHHETNLEAKYV
VQSGPAKDL SFRIRQAWHRANADQEGEQNEFRLIVDYPLSIL

> P17052|RURE_PSEOL Rubredoxin -NAD(+) reductase - Pseudomonas oleovorans.

MAIVVVGAGTAGVNAAFWL RQYGYKGEIRIFSRESVAPYQRPPLSKAFLT
SEIAESAVPLKPEGFYTNNTITISLNTPIV SIDVGRKIVSSKDGKEYAYE
KLILATPASARRLTCEGSELSGVCLYLRSMEDAKNLRRLVESASVVVLGG

GVIGLEVASAAVGLGKRVTVIEATPRVMARVVTAAAANLVRARLEAEGIE
FKLNAKLTSIKGRNGHVEQCVCLESGEEIQADLIVVGIGAIPELELATEAA
LEVSNQVVVDDQMCSTSDTSI YAIGDCAMARNPFWGTMVRLETIHNATHA
QIVASSICGTSTPAPT PPRFWSDLKGMALQQLGALKDYDKLVVAINNETL
ELEVLAQKQERLIATETINLPKRQGALAGSIKLPD

> P15713|PHLN_PSEAE Non-hemolytic phospholipase C - *Pseudomonas aeruginosa*.

MISKSRRSFIRLAAGTVGATVATSMLPSSIQAALAI PAHRRHGKLDVEH
VVILMQENRSF DHYFGTLKGVRGFGDRMAIPLPDGQRVVHQKGSKEILP
YHFDSTSTSAQRVDGTPHTWPDAAQQAWNEGRMDKWLPAKTERSLGYYKEQ
DIAFQFAMANAFTICDAYHCSFQGGTNPRLFLWTGTNDPLGQHGGPVTT
NDHDSNGPVEQVGTWTTYPRLQAAGITWRVYQDMADNFSNDPLIGFRQY
RAAAPDSPLIVNGLSTWKLDAKRDVLANSLPQVSWIVAPAKYSEHPGPS
SPIWGAEYTSWV LDALTANPEVWSKTALLVMFDENDGFFDHVAPPAAPSL
NKDGLTRGKTTADATLEWHTKGDIRYRNQPYGLGPRVPMYVISPWSKGGW
VNSQVFDHTSVIRFLEQRFGVMEPNISPWRRAVCGDLTSAFNANPNNEP
FPPELPTDSQADAIVASQIKLPKPKPPAVAAMPKQEMGIRPARALPYELGV
HARYRSGGDALSFTANTGKAGAVFQVFDLLDSENPPKRYTVGARKRLHD
SFQGDASGDYHLE VHGPNGFLRVFRGNLRRDLAERKAPLPEVRIDYEPFLF
GNLRVQLINRGRHPVKLTVKDNVYRQGERRTVNVP PGQRREVRYSLRSSG
NWDYFVSVAQGADSF LRRFSGRMEDGRSGFSDPGMGLGTLTF

> P43827|SYL_HAEIN Leucyl-tRNA synthetase - *Haemophilus influenzae*.

MQEQRPMIEPKVQVQYWAENKVFKAIKDESKEKYCLSMFPYPSGRRLHM
GHVRNYTIGDVISRYQRM LGKNVLPFGWDAFGLPAEGAAIKNKTAPAKW
TYENIAYMKKQLQLLGFQFDWDREIATCKPEYYKWEQWFFTELYKKGLVY
KKTSTVNWC PNDETVLANEQVHEGCCWRC DTPVEQKEIPQWFIKITDYAE
QLLGGLD TLPQWPD MVKTMQRNWI GRSEGVEITFDVANTNEKVAVYTTRP
DTFYGVSYL GIAAAHPLASLAAQNNSELAAFIQEAKNAKVAEADLATMEK
KGMATGLFAIHPLTGDKLP IWVANFVLMHYGTGAVMAVPAHDQRDFEFAQ
KYSLP IKQVIAPLADEEIDLTKQAFVEHGKLVNSDEFDGNFDFGAFNGIA
DKLEKLGVKRQVNYRLRDWGVSRQRYWGAPIPMLTLENGDVVPAPMEDL
PIILPEDVVM DGVKSPINADPNWAKTTFNDAPALKE TDTDFTFMESSWYY
ARYTCPQYQNGMLDAEEANYWLPVDQYIGGIEHATMHLLYFRFFHKLLRD
AGFVTSEEPADKLLCQGMVLADAFYYTSPTNERIWSPTQVTLERDEKGR
IKATDPEGRELVHSGMTKMSKSKNNGIDPQEMVEKYGADTVRLFMMFAS
PAEMTLEWQESGVEGAKRFLGRVWNLVYQYQQNPAKTS LDLTALS AEQKV
LRREVHKTIAKVSDDI GRRQTFNTAIAAVMELMNKLT KASLDSEQDRAVM
AEALS AVVRMLYPITPHICFELWQALGNESAIDTAEWVKADEAMVEDEK
LIVVQVNGKVRGKVT VATDADEDTVKTIAFADENVK FIDNQHIVKVIYV
VGKLLNVVVKP

> P0A7A9|IPYR_ECOLI Inorganic pyrophosphatase - *Escherichia coli*.

MSLLNVPAGKDLPEDIYVIEIPANADPIKYEIDKESGALFVDRFMSTAM
FYPCNYGYNHNTLSLDGDPVDVLPVTPYPLQPGSVIRCRPVGLKMTDEA
GEDAKLVAVPHSKLSKEYDHIKDVNDLPELLKA QIAHFFEHYKDLEKQKW
VKVEGWENAEAAKAEIVASFERAKN

> P06971|FHUA_ECOLI Ferrichrome-iron receptor - *Escherichia coli*.

MARSKTAQPKHSLRKAIVVVATAVSGMSVYAQA AVEPKEDTITVTAAPAP
QESAWGPAATIAARQSATGTKTDTPIQKVPQSI SVVTAEMALHQPKSVK
EALS YTPGVSVGTRGASNTYDHLIIRGFAAEGQSQNNYLNLGLK LQGNFYN
DAVIDPYMLERAEIMRGPVSVLYGKSSPGGLLMVSKRPTTEPLKEVQFK
AGTDSL FQTGFDFSDSLDDDGVYSYRLTGLARSANAQQKGSEEQRYAIAP
AFTWRPDDKTNFTFLSYFQNEPETGYGWL PKEGTVEPLPNGKRLPTDFN
EGAKNNTYSRNEKMGYSFDHEFNDFTVRQNL RFAENKTSQNSVYGYGV
CSDPANAYSQCAALAPADKGHYLARKYVV DDEKLQNF SVDTQL QSKFAT
GDIDHTLLTGVD FMRMRNDINAWFGYDDSVPLLNLYNPVNTDFDFNAKDP
ANS GPYRILNKQKQGTGVYVQDQAQW DKLVTLGGRYDWADQESLNRVAGT
TDKRDDKQFTWRGGVNYLFDNGVTPYFSYSESEFEPSSQVKGDNIFAPSK
GKQYEVGVKYVPEDRPIVVTGAVYNLTKTNNLMADPEGSFFSVEGGEIRA
RGVEIEAKAALSASVNVVGSYTYTDAEYTTDTTYKGNTPAQVPH MASLW
ADYTFDGLSGLTLGTGGRYTGSSYGD PANSFKVGSYTVVDALVRYDLA
RVGMAGSNVALHVNNLFDREYVASC FNITYGCFWGAERQV VATAFRF

> P45375|PHBB_CHRVI Acetoacetyl-CoA reductase - *Chromatium vinosum*
(*Allochromatium vinosum*).

MARIALVTGGIGIGT SICTRLAKDGCTVVANCHPSEAAAAE EWQARAA

EGFDIAVFTADVSSFDDARMVREITEQVGPIDILVNCAGITRDKTFKKM
EQAHEAVINVNLSVFNVTQVWDGMLERGFGRINIINSSVNGQRQFGQ
ANYSAAKAGMHGFTMALAQEGASKGVTVNTISPGYVETAMTLAMNDDVRN
SIIISGIPMRRMAQPNEIAAAIAFLAGDESGYMTGANLPVNGGLFMH
> Q51883|PLAS_PHOLA Plastocyanin - *Phormidium laminosum*.
MKLIAQISRSLSLALFALVLMVGSFVAVMSPAAAETFTVKMGADSGLLQF
EPANVTVHPGDTVKVVNNKLPHPNIFDQKQVPGASKELADKLSHSQLMF
SPGESYEITFSSDFPAGTYTYCAPHRGAGMVGKITVEG
> Q01551|TBUD_BURPI Phenol 2 -monooxygenase - *Burkholderia pickettii*
(*Ralstonia pickettii*) (*Pseudomonas pickettii*).
MTKYNEAYCDVLIVGAGPAGVMAAAHLLSYGTTARPHRVRIFDATKEVNG
SDESTESLSTDVIADALNSGASGPEKDAASTTEDLPMLVTTLQVSDVLHD
TGDDTKIAYRETATEQQVLLADTTANTSSMTNPRSMCEAGCRFHQIYQG
HCFPEYELDSERLSVDGRAQVLEDEHETGQLRLERLGRPEELLELDEEN
SMSVVTNLKAAPYKFLMKDVDFENFPGELSTSGGKTTSISADESAIDAALH
AVWDADDLGAAWHLDEASGLRAVDWNAQWFKSGQPWTPDAAKSLQEGRV
FLAGDARHRHPPLTIGIKNTS IADCYNLTWKLLGVLLGVARADPARTYVA
ERVYIRMRAATDIAVDAEMESLAAKWITVQLTLSRSWISSAKEAERWDAV
LRDSAMSASKPMWTTSDMRASFDAGLMGHGHAHDHVTPTIKEFASSSISR
SISELASTSWWESRGWNGGPFESLMEDARWTGAVESNCRYAAYDRDAPV
LHEHVAVVTRFTSRARTAVLEAAVQQAHVVDVDCWDVGLVEPALDDLDSDAGA
GLHVAHHADQWPAQLDEAVWPRESLSDWRIVTDTSATGEGYQTSPREAPG
DYADLNADNAKAHFNQFAGHKAYGDAADGGGCHGRILVGPVAVRGRHL
HREIPLGEECQRAAQPLFKEV
> P43828|SYM_HAEIN Methionyl -tRNA synthetase - *Haemophilus influenzae*.
MTTQPRKILVTCALPYA NGAIHLGHMLEHIQADIWVRFQMRGNKIHFVC
ADDAHGTPIMLNADKLGITPEELIAKAKADHIRDFAGFNISFDNYHSTHS
EENKQLTAEIYNKLGANGFIKSKVISQLFDPEKNMFLPDRFVKGTCPKCK
AEDQYGDNCEVCASTYSPMDLINPRSAVSGTTPIVKESHEHFFDLPAFEG
MLKEWTRSGSLQSEIANKMQEWFESDLQQWDISRDPYFGFEIPGAKDKF
FYVWLDAPIGYMASFKNL CNREGIDFNEFWAEGSDAELYHFIGKDIVYFH
SLFWPAMLEGSYRKPNTNVFAHGYVTVDGAKMSKSRGTFIQASTYLNHID
PECLRYYYAAKLNDRIEDLDFNLEDFVQRVNTDIVNKLVLNLSRNAGFIA
KRFEGKLADKLEKSLFAEFTAQAEQIAAYYESREYNKTIREIMALTDKA
NKYIDEKAPWVIAKEEGKEAELQAVCSMGIELFRVLMYSYLPVLPKLAER
AETFLQAE LRWDNIHQPLL GHTLAPFKALFSRLEKKQIDAVVEETKALFA
AANKAAEKTEAKPTALSAVEPIAETITIDDFAKLDMRVAKVLKCEAVPES
NKLLRFELDLGDHTRQVFSGIIKAAAYNKPEELEGRFVIMVANLAPRKMKFG
VSEGMILSAGTGGSDLFLLSADSGVTAGMQVK
> P16700|CYSP_ECOLI Thiosulfate -binding protein - *Escherichia coli*.
MAVNLLKKNLALVASLLLAG HVQATELLNSSYDVSRELFAALNPPFEQQ
WAKDNGGDKLTIKQSHAGSSKQALAILQGLKADVVTYNQVTDVQILHDKG
KLIPADWQSRPNSSPFYSTMGFLVRKGNPKNIHDWDLVRSQVDFKLIFF
NPKTSGNARYTYLAAWGAADKADGGDKGKTEQFMTQFLKNVEVFDTGGRG
ATTTFAERGLGDVLISFESEVNNIRKQYEAQGFVVIKPTNILAEFPVAW
VDKNVQANGTEKAAKAYLNWLY SPQAQTIIIDYVYRVNNPEVMDKLDKDF
PQTELFVRVEDKFGSWPEVMKTHFTSGGELDKLLAAGR
> P0AG80|UGPB_ECOLI Glycerol -3-phosphate-binding periplasmic protein -
Escherichia coli.
MKPLHYTASALALGLALMGNAQAVTTIPFWSMEGELGKEVDSLQRFNA
ENPDYKIVPTYKGNIEQNLSAGIAAFRTGNAPAILQVYEVGTATMMAS KA
IKPVYDVFEKAGIQFDESQFVPTVSGYSDSKTGHLSSQPFNSSTPVLYY
NKDAFKKAGLDPEQPPKTWQDLADYAAKLKASGMKCGYASGWQGWIQLEN
FSAWNGLPFASKNNGFDGTDVLEFNKPEQVKHIAMLEEMNKKGDFSYVG
RKDESTKIFYNGDCAMTTASSGSLANIREYAKFNYGVMMPYDADAKDAP
QNAIIGGASLWVMQGDKETYTGVAFLDFLAKPENAAEWHQKTGYLPI T
KAAAYDLTREQGFYEKNPGADTATRQMLNKPPLPFTKGLRLGNMPQIRVIV
DEELESVWTGKKTPOQALDVAVERGNQLLRRFEKSTKS
> Q55806|SYT_SYNY3 Threonyl -tRNA synthetase - *Synechocystis* sp. (strain PCC
6803).
MAKTVVSPDITIALPRTSESEQLKKIRHTTSHVMAMAVQKLFPAQVTTIGP
WTETGFYYDFDVAEPFTEADLKAIKKEMVK IINKLFPVIREEISREEAKQ
RIESIQEPYKLEILDSIHEPITVYHLGDQWDLACAGPHLESTADINPKAI

ALESVAGAYWRGDANKAQLQRIYGTAWETPEQLAEYQRRKEEALKRDHRK
LGKELGLFIFADPVGPLPLWTPKGTIIRTILEDFLKQEIKRGYLPVVT
PHIARVDLFKQSGHWQKYQEDMFPMAESPEEAAQEMGFVLKPMNCPFHI
QIYKSELRSYRDPLRLAEFGTVYRYEQSGE LGGLTRVRGFTVDDSHLFV
TPDQLDEEFLSVVDLILTVFKSLQLKNFKARLSFRDPESDKYIGSDEAWE
KAQGAIIRRAVQELEMDYFEAPGEAAFYGPKLDFIFQDALEREWQLGTVQV
DYNLPERFDLEYIAADGSRQRPVMIHRAPFGSLERLIGILIEEYAGDFPL
WLAPIQVRLAVSDEFLLPFAQSIVQQMQLGLRAEVDTSGDRLGKMIRNA
EKQKIPVMAVIGAKEVEANALNIRTRASGELG EIPVTEVLEKLQATVTNH
DTW

> NRDG_HAEIN P45080 ANAEROBIC RIBONUCLEOSIDE -TRIPHOSPHATE RED
MNYLQYYPTDVINGEGTRCTLFVSGCTHACKGCYNQKSWFSAGVLFDDV
MEQQIINDLKDTRIKRQGLTSLGGDPLHPLNVETLLPFVQRVKRECPDKD
IWWWTGYKLELDKQQRAMLPIYIDVLIDGKFIQEQADPSLVWRGSANQII
HRFKL

> P27032|GUNY_DICD3 Minor endoglucanase Y - *Dickeya dadantii* (strain 3937)
(*Erwinia chrysanthemi* (strain 3937)).

MGKPMWRCWALMLMVFSASATAANGWEIYKSRFMTTDGRIQDTGNKNVS
HTEGQGFAMLMVAHYDDRIAFDNLWNWTQSHLRNNTSGLFYWRYDPSAAN
PVVDKNNASDGDVLIWALLKAGNKWQDNRYLQASDSIQKAIIASNIIQF
AGRTVMLPGAYGFNKNNSYVILNPSYFLFPAWRDFANRSHLQVWRQLIDDS
LSLVGEMRFGQVGLPTDWAALNADGSMAPATAWPSRFSYDAIRIPLYLYW
YDAKTALVPPFQLYWRNYPRLTTPAWVDVLSNTATYNMQGGLLAVRDLT
MGNLDGLSDLPGASEDYSSSLRLLVMLARGK

> P14532|CCPR_PSEAE Cytochrome c551 peroxidase - *Pseudomonas aeruginosa*.

MQSSQLLPLGSLLSFATPLAQADALHDQASALFKPIPEQVTELRGQPIS
EQQRELGKLLFFDPRLSRSHVLSCNTCHNVGTGGADNVPTSVGHGWQKGP
RNSPTVFNAVFNAAQFWDGRAKDLGEQAKGPIQNSVEMHSTPQLVEQTLG
SIPYVDAFRKAFKAGKPVSFDMALAEAYEATLVTDPSPFDLYLKGD
DKALDAQKKGKGLKAFMDSGCSACHNGINLGGQAYFPFGLVKKPDASVLP
GDKGRFAVTKTQSDYVVFRAAPLRNVALTAPYFHSQVWELKDAVAIMGN
AQLGKQLAPDDVENIVAFHLSLGSQKPRVEYPLLPASTETTPRPAE

> P27477|THTR_SYNP7 Putative thiosulfate sulfurtransferase - *Synechococcus*
sp. (strain PCC 7942) (*Anacystis nidulans* R2).

MSVRSRWRPQKAFLAVISLVVAVLLAVPGWLTPAT AASQATVQFVAPTW
AAERLNNKQLKILDVRTNPLAYIEGHLPGAVNIADAAYRGPNGFLPVQIW
DPEKLASLFGRAGVSNNDTVLVYS DGNVDVLGATLVAYLLERSGVQNI AVL
DGGYKGYK DAGLPVTKEYPRYQAARFAPKDNRAFRVDIKQVEQLTGKSTF
VDPRPPALFSGEQVVFIRNGHIPGARNIPWPTFTEANNANESLKNPHKLL
PLSELKAILEAKGVTPDKDVIVTCSTGREASLQYLVL KHLKYPKVRIYE
GSWTEYSASNLPVETGPD RV

> P0A948|RIMJ_ECOLI Ribosomal -protein-alanine acetyltransferase -
Escherichia coli.

MFGYRSNVPKVRLTDRVLVRLVHDRDAWRLADYYAENRHFLKPWEVPRD
ESHCPYSGWQARLGMINEFHKQGSFAFYFLGDFDPEKEIIGVANFSNVVRG
SFHACYLGSYQKQKGLMFEALTAIRYMQRT QHIHRIMANYMPHNK
RSGDLLARLGFKEGYAKDYLLIDGQWRDHVLTALTTPDWTPGR

> P32520|FLAA1_TREHY Flagellar filament outer layer protein flaA1 -
Treponema hyodysenteriae (*Serpulina hyodysenteriae*).

MKKLFVVLTSIFIAASAYGLTNSTLIDFALTGNADNLQAGEGDTNEVVPV
AENLYNDNWWVWLNESARLTENR RNSYVTNVDSKGNNGAWAEGKVLGVRV
HFPLAAWNSYALVKPVYELEMYGGADGTKYTEGKGVIHNVGEIKSISWV
YGRNYLISYFVNLQNEFEGELKSYPMGTVYFNGWRQVRWENREYLPNVRDR
VLVREPLYPRMIPSVKLDLGFYRTKDTKGGDFITYVKDVTLEYDVVVVVD
FEEDIDDEATWQLKTENDRKQAIESARIREQAELRDLEQRRIGDGTAA
DQAAANTGAADTGAQEQAQ

> P28718|G6PI_ZYMMO Glucose -6-phosphate isomerase - *Zymomonas mobilis*.

MARIANKAAIDAANKVQSACSEKTLKQLFEEDSNRLSGLVETAKLRFDF
SKNHLDSQKLTAFKKLLEACDFDARRKALFAGEKINITEDRAVEHMAERG
QGAPASVARAKEYHARMRTLIEAIDAGAFGEVKHLLHIGIGGSALGPKLL
IDALTRESGRYDVAVVSNVDGQALEEVFKKFNPHK TLIIVASKTFTTAET
MLNAESAMEWMMKKGVEDPQGRMIALTANPAKASEMGIDDTRILPFAESI
GGRYLSWSSIGFPAALALGWEGFQQLLEGGAAAMDRHFLEAAPEKNAPILA

AFADQYYSAVRGAQTHGIFAYDERLQLLPFYLLQOLEMESNGKRVLDLGNL
IDHPSAFITWGGVGTDAQHAVFQLLHQGTRLVPIEFIAAIKADDTLNPVH
HKTLTNAFAQGAALMSGRDNKDPARSYPGDRPSTT ILMEELRPAQLGAL
IAFYEHRTFTNGVLLGINSFDQFGVELGKEMAHAIADHPENSDFDPSTKA
LIAAALK

> P0A9A6|FTSZ_ECOLI Cell division protein ftsZ - Escherichia coli.

MFPEMELTNDAVIKVIGVGGGGNAVEHMRERIEGVEFFAVNTDAQALR
KTAVGQTIQIGSGITKGLGAGANPEVGRNAADEDRLRAALEGADMVFI
AAGMGGGTGTGAA PVVAEVAKDLGILTVAVVTKPFNFEGKKRMAFAEQGI
TELSKHVDSLITIPNDKLLKVLGRGISLLDAFGAANDVLKGAVQGI AELI
TRPGLMNVDFADVTRVMSEMGYAMMGSGVASGEDRAEAAAEMAISSPLLE
DIDLSGARGVLVNI TAGFDLRLDEFETVGNTRAFASDNATVVIGTSLDP
DMNDELRVTVVATGIGMDKRPEITLVTKVQVQPPVMDRYQQHGMAPLTQE
QKPVAKVVNDNAPQ TAKEPDYLDIPAFLRKQAD

> P0A705|IF2_ECOLI Translation initiation factor IF -2 - Escherichia coli.

MTDVTIKTLAAERQTSVERLVQQFADAGIRKSADDSVSAQEKQTLIDHLN
QKNSGPKLTLQKRTRSTLNI PGTGGKSKSVQIEVRKKRTFVKRDPQEA
RLAAEEQAQREAEQARREAEESAKREAQQAEREAAEQAKREAAEQAKR
EAAEKDKVSNQDDMTKNAQAEKARREQEAALKRKAEEEEARRKLEEEAR
RVAAEEARRMAENKWTDNAEPTEDSSDYHVTTTSQHARQAEDES DREVEGG
RGRGRNAKAARPKKGNKHAESKADREEARAAVRGGKGGKRGSSSLQQGFQ
KPAQAVNRDVVIGETITV GELANKMAVKGSQVIKAMMKLGAMATINQVID
QETAQLVAEEMGHKVI LRRENELEEAVMSDRDTGAAAEPRAPVVTIMGHV
DHGKTSLLDYIRSTKVASGEAGGITQHIGAYHVETENGMITFLDTPGHAA
FTSMRARGAQATDIVVLVVAADDGVMPQIEAIQHAKAAQVPPVVAVNKI
DKPEADPDRVKNELSQY GILPEEWGGESQFVHVSAKAGTGIDELLDAILL
QAEVLELKA VRKGMASGAVIESFLDKGRGPVATVLRVREGTLHKGDIVLCG
FEYGRV RAMRNELGQEVLEAGPSIPVEILGLSGVPAAGDEVTVVRDEKKA
REVALYRQGKF REVKLARQQSKLENMFANMTEGEVHEVNI VLKADVQGS
VEAISDSLKLSTDEVVKV KIIIGSGVGGITETDATLAAASNAI LVGFNVRA
DASARKVIEAESLDLRY SVIYNLIDEVKAAMSGMLSPELQQIIGLAEV
RDVFKSPKFGA IAGCMVTEGVV KRHNPIRVLRDNVVIYEGELES LRRFKD
DVNEVRNGMECGIGVKNYNDVRTGDVIEVFEIIEIQRTIA

> Q55013|CY550_SYNY3 Cytochrome c-550 - Synechocystis sp. (strain PCC 6803).

MKRFFLVAIASVLF FNTMVGSANAVELTESTRTI PLDEAGGTTTLTARQ
FTNGQKIFVDTCTQCHLQ GKTKTNNNVS LGLADLAGAEPRRDNV LALVEF
LKNPKSYDGEDDYSELHPNISRPDIYPEMRNYTEDDIFDVAGYTLIAPKL
DERWGGTIYF

> O05947|SYT_RICPR Threonyl -tRNA synthetase - Rickettsia prowazekii.

MINISFPDGSVKQFAQNITAFEIVNAISMSLAKAAI VVEINGELKDLSTV
IENDCKLRILTAQDYECLEIIRHDA AHLTAEAVKELFPETQV TIGPAIEN
GYYDFARDKPF SIDL L ANIEAKMQELS KNEKITRELWDRDKAVEFFLS
IGEHYKAKIIAS IPEGEPITLYRQGNFIDL CRGPHSPSTGFVKHF KLMKV
AGAYWRGNSR NEMLQRIYGT AWATKEQLDNYLFMLEEA EKRDHRKIGKEL
DLFHFQEEAQGMVFW HDKGWSIYNTIEQYIRKKIRKNGYIEVKTPV LVDK
SLWEASGHWAKFRCDMFTLETDDKTLALKPMNCPCHVQIFKQGIKSYRDL
PLRMSEFG LCHRNEASGALHGLMRVRS LVQDDAHI FCAEEQITDET VRF
KLLTEVYKDFGFTDIKVKFS DRSEICAGNDEVWDKAENALKTAIEKAGFI
YTLNPGEEAFYGP KIEFVLTDAIGRQWQCGLQMD FVLPERLDANY IAAS
GEKKRPV MLHRAILGSLERFIGILIEEYAGKFP IWLAPVQVAIATITNDL
NDYALEVQKTLIDNGVRTDINISPKIN YKIREFSNQKIPIIAVIGKQEQ
ANKQVTIRKLG TIEQEILSIEQLIAMIKKENS NYL

> P56075|NDK_HELPY Nucleoside diphosphate kinase - Helicobacter pylori
(Campylobacter pylori).

MKQRTLSIIKPDALKKKVVGKIIDRFESNGLEVVAMKRLHLSVKDAENFY
AIHRERPF FDKLIEFMVSGPVVVMVLE GKDAVAKNRDLMGATDPKLAQKG
TIRADFAESIDANAVHGS DSLENAHNEIAFFFAARDL

> NEUA_NEIME_Q57385 ACYLNEURAMINATE CYTIDYLYLTRANSFERASE (EC

MEQNIAVILARQNSKGLPLKNLRKMNGISLLGHTINAAISSKCFDR IIV
STDGGLIAEEAKNFGEVVLRPAELASDTASSISGVIHALETIGSNSGTV
TLLQPTSPLRTGAHIREAFSLFDEKIKGSVVSACPM EHHPLKTL LQINNG
EYAPMRHLSDL EQPQQLPQAFRPNGAIYINDTASLIANNCFFIAPT KLY
IMSHQDSIDIDTELDLQQAENILNHKES

> P15930|FLGI_SALTY Flagellar P -ring protein - Salmonella typhimurium.
MFKALAGIVLALVATLAHAERIRDLTSTVQGVRENLSLIGYGLVVGLDGTGD
QTTQTPFTTQTLNMLSQLGITVPTGTNMQLKNVAAMVMTASYPFFARQG
QTIDVVVSSMGNAKSLRGGTLLMTPLKGVDSQVYALAQGNILVGGAGASA
GGSSVQVNQLNGGRITNGAIIERELPTQFGAGNTINLQLNDEDFMAQQI
TDAINRARGYGSATALDARTVQVRVPSGNSSQVRFLADIQNMEVNVTPQD
AKVVINSRTGSVMMNREVTLDSCAVAQGNLSVTVNRQLNVNQPNTPFGGG
QTVVTPQTQIDLRQSGGSLQSVRSSANLNSVVRALNALGATPMDLMSILQ
SMQSAGCLRAKLEII

> Q55267|HISZ_SYNP7 ATP phosphoribosyltransferase regulatory subunit -
Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
MVHQPAGTRDLLPQDVTQKRWIESRLQQVVFQQWGYQRIITPTLERLDTL
VAGGAVQRSVAIVQVQSDDEESGLGLRPELTASIARAAVTRLAGSSPLRLY
YLANVFRPAFQGDRLQQRELFQAGVELLGVGGTLADAEVLHVLADALAE
GFGQPPLGSHWLVVGEASLTRSLLQFPKDLREKVRQAIQQLDRVTLESL
PLESQLRDRALLHDLRGQPDQVFAKLQQLTLTPLEQTLRDRLAQLVELY
NASAGPQDSPLLLDLSLRSFDYTGIVFEVVYETPTGPWVLAQGGRYDR
LLDVYDPAAGQPGIGFSCNIENLQQVLLAANRLPHRPPAIDQLVIPVDS
EAYGAALAEARLQRQDQLRVELYLDSDRRPEVVQAFARRRRIGRIVWVS
SGSAPQSEAVAVAERATTC

> P07024|USHA_ECOLI Protein ushA [Includes: UDP -sugar hydrolase -
Escherichia coli.

MKLLQRGVALALLTFTLASETALAYEQDKTYKITVLHTNDHHGHFWRNE
YGEYGLAAQKTLVDGIRKEVAAEGGSVLLSSGGDINTGVPESDLQDAEPD
FRGMNLVGYDAMAIGNHEFDNPLTVLRQOEKWKAFPLLSANIYQKSTGER
LFKFPWALFKRQDLKIAVIGLTTDDTAKIGNPEYFTDIEFRKPADEAKLVI
QELQQTEKPDIIIAATHMGHYDNGEHGSNAPGDVEMARALPAGSLAMIVG
GHSQDPVCMMAENKKQVDYVPGTPCKPDQQNGIWIWQAHEWVKYVGRADF
EFRNGEMKMVNYQLIPVNLKKKVTWEDGKSERVLYTPEIAENQOMISLLS
PFQNGKMGKLVYKIDGLQASVLYRKDASGKTEVFLDPNKFSDKGTTSLANL
FAVMSGGGIRDSIEAGDISYKNVLKVPFGNVVVYADMTGKEVIDYLTAV
AQMKPDSGAYPQFANVSFVAKDGKLNLDLKIKGEPVDPKTYRMATLNFNA
TGGDGYPRLDNPKGYVNTGFIDAENVLQKSSPLDVSVEPKGEVSWQ

> P27195|PPCF_ELIMR Prolyl endopeptidase - Elizabethkingia miricola
(Chryseobacterium miricola).

MKYKLSVAVAAFAFAAVSAQNSNSLKYPETKKVNHTDTYFGNQVSDPYR
WLEDDRAEDTKAWVQQEVKFTQDYLAQIPFRGQIKKQLLDIWNYEKISAP
FKKGKTYTYFKN DGLQAQSVLYRKDASGKTEVFLDPNKFSDKGTTSLANL
SFNKKGTLVAYSISEGGSDWNKIIILDAETKKQIDETLLDVKFSGISWL
DEGFFYSSYDKPKDGSVLSGMTDKHKVYFHKLGTKQSQDELIIGGDKFPR
RYLSGYVTEQRYLVVSAANATNGNELYIKDLKNKTDIFIPITGFESNVG
LVDTDGDTLFLHTDKNAPNMRMVKTTIQNPKPETWKDVAIETSEPMRVNS
GGGYFFATYMKDA LSQIKQYDKTGKLVREIKLPGSGTAGGFGGKTEKEL
YYSFTNYITPPTIFKFSIDSGKSEVYQKPKVKFNPENYVSEQVFYTSADG
TKIPMMISNKKGLKDKGNPTILYSYGGFNISLQPAFVSVNNAIWMENGGI
YAVPNIRGGGEYGKKWHDAGTKQQKKNVFNDFIAAGEYLQKNGYTSKDYM
ALSGRSNGLLVGATMTMRPDLAKVAFPGVGVLDMLRYNKFTAGAGWAYD
YGTAEDSKEMFEYL KSYSPVHNKAGTCYPSTMVITSDHDDRVPVPAHSFK
FGAELQAKQACKNPVLRIRIETNAGHGAGRSTEQVVMENADLLSFALYEMG
IKNLK

> CYPB_HAEIN P44499 PEPTIDYL -PROLYL CIS-TRANS ISOMERASE B (EC

MVTLHTNFGDIKIKLDFDKAPVTAENFLNYCKDGFYNNITIFHRVIDGFMI
QGGGMESGMREKATKAPIQNEANNRLSNKRGTIAMARTSDPHSATAQFF I
NVADNDFLNYRSKEMFGREVVQEWGYAVFGEVVEGMDVVDKIKKVKTKGN
GFHQDVPTEDVVITSVIE

> Q01911|TETX_BACFR Tetracycline resistance protein from transposon
Tn4351/Tn4400 - Bacteroides fragilis.

MTMRIDTDKQMNLLSDKNVAIIGGGPVGLTMAKLLQQNGIDVSVYERDND
REARIFGGTLDLHKSGQEQAMKKAGL LQTYDYDLALPMGVNIADKKNILS
TKNVKPENRFDNPEINRNDLRAILLNSLENDTVIWRKLVMLEPGKKKWT
LTFENKPSSETADLVILANGGMSKVRKFVTDTEVEETGTFNIQADIHQPEI
NCPGFFQLCNGNRLMASHQGNLLFANPNNGALHFGISFKTPDEWKNQTQ

VDFQNRNSVVDFFLLKEFSDWDERYKELIHTTLSFVGLATRIFPLEKPKWS
KRPLPITMIGDAAHLMPPFAGQGVNSG LVDALILSDNLADGKFNSEIEAV
KNYEQQMFMYGKEAQEESTQNEIEMFKPDFTFQQLLN
> P22390|BLAC_CITDI Beta-lactamase - *Citrobacter diversus*.
MFKKRGRQTVLIAAVLAFFFTASSPLLARTQGEPTQVQQKLAALEKQSGGR
LGVALINTADRSQILYRGDERFAMCSTSKTMVAAAVLKQSETQHDILQOK
MVIKKADLTNWNVPTEKYVDKEMTLAELSAAT LQYSDNTAMNKLEHLGG
TSNVTAFARSIGDTTFRLDRKEPELNTAIPGDERDTTCPLAMAKSLHKL
LGDALAGAQRALVLEWLKGNNTGGQSIRAGLPEGWVVGDKTGAGDYGTTN
DIAVIWPEDRAPLILVYFTQPPQDAKGRKDILAAAAKIVTEGL
> P28223|CHIA_ALT5 Chitinase A - *Alteromonas* sp. (strain O-7).
MKLNKITSYIGFALLSGGALAAPSTP TLDWQPQQYSFVEVNVNVDGLGSYKQ
LVKAKDVVDISIKWNAWSGSGGDNYKVYFDDLLVNQGSPLPAGTKSGVVQF
PYTKSGRHQLYLELCEGTVCARSAGKEI VIADTDGAHLAPLPMNVDPNNR
NNGTIPGRVTGAYFVEWGIYGRNYDVTKI PAHNLSHILYGFIPICGPNES
LKSIEIGNSWRALQACADSQDYEVVIHDPWAAVQKSMPPGVDKDPPIRGV
YSQLMALKQRYPDLKILPSVGGWTLSD PFHGFNTKANRDTFVASVKQFLK
TWKFDYDGVDDWDFEFGGDPNPDLGDPINDGPAYVALMQELRAMLDELEA
ETGRQYELTSAIGAGYDKIEDVDYQAAQQYMDYIFAMTYDFYGAWNNETG
HQTGIYCGSHLSTDECNGTGVDDNGVPRKGPAYTGDHAIQLLQGGVQPS
KLVMGVAMYGRWEGVLDANAAIPGNPMTAPGNGPLTGSTSEGVWEPGIM
DYKAIANAAGVGGSGVNGYEVGYDEQA QAAYVWNRSNGLITYDSPRSV
IAKQYANTHQLAGLFGWEIDADNGDILNAMYDGLTAGEIPNRAPTIGVS
GPINVTSGQVVNVAQASDLNDPLTYSWVAAPGLALSANNTAAVAVTAP
SVAQQTSYDLTVTVNDGALSTTKTIVVVVNPEGANAAPVVTVPVSDISVNE
GASATVNVSATDEGAALSYSWSPAELSVANGSSATI TAANVTADTTVP
VTVTVSDGVNAVDTTFNVTIKDGAEYPTW DRSTVYVGGDRVIHNSNVFEA
KWWTQGEETADVWKAVTN
> P27603|PHEA_PEST P-protein [Includes: Chorismate mutase - *Pseudomonas*
stutzeri (*Pseudomonas perfectomarina*).
MSEADQLKALRVRIDSLDERILDLISERARCAQEVARVKTASWPKAEEAV
FYRPEREAWVLKHIMELNKGPLDNEEMARLFREIMSSCLALEQPLRVAYL
GPEGTFSSQAALKHFGHVSISKMAAIDEVFREVVAGAVNFGVVPVENST
EGAVNHTLDSFLEHDIVICGEVELRIHHHLLVGETTKTDRITRIYSHAQS
LAQCRKWLDAHYPNVERVAVSSNADAAKRVKSEWNSAAIAGDMAAQLYGL
SKLAEKIEDRPVNSTRFLIIGSQEVPPTGDDKTSIIVSMRNKPGALHELL
MPFHSNGIDLTRIETRPSRSGKWTYVFFIDCMGHHQDPLIKNVLEKIGHE
AVALKVLGSSYPKAVL
> P0A9F9|METR_ECOLI HTH-type transcriptional regulator metR - *Escherichia*
coli.
MIEVKHLKTLQALRNCGSLAAAAATLHQTQSALSHQFSDLEQRLGFRFLV
RKSQPLRFTPQGEILLQLANQVLPQISQALQACNEPQQTRLRIAIECHSC
IQWLTPALENFHKNWPQVEMDFKSGVTFDPQALQOGELDLVMTSDILPR
SGLHYSMPFDYEVRLVLPADHPLAAKTRITPEDLASETLIYPVQRSRLD
VWRHFLQPAGVSPSLKSVDNTHLLIQMVAARMGIAALPHWVVESFERQGL
VVTKTLGEGLWSRLYAAVRDGEQRQPVTEAFIRSARNHACDHLFPVKSAE
RPTYDAPTVRPGSPARL
> P46244|SYT_BUCAP Threonyl-tRNA synthetase - *Buchnera aphidicola* subsp.
Schizaphis graminum.
MPVIRFCDSQQVYKHSVSLREIENKPNIIIRSLIAISVNSFSNFNTL
ITEDSSISFISKDCEALNIIRYSCIQLLNAAKKTWPSCKIGESEITKS
GFYCDIDFENSITEDFFILENNMKTLIKREYFISHQNISFDHAYEMFKK
KSEIYKIHLIKKYINKKNKISLYHENYFDIDMGMQVFNKFKCYFKLQK
IGGIYWKGDHKNMLQRIYGTAWSTKKELDKHSYINELKKRDHRKIGKL
LNLYHMQKESPGMIFWHNNGWIIIFNELEIFVREKLKEYKYKEVKTPLLID
KSIWQKSGHWDNYQDAIFTTSENREYCIKPMNCPGHVQIFNCGLSYRD
LPIRMAEFGSCHRNESSGSLHGLMRIRNFTQDDAHIFCTQEQLRYEINNC
IKMIYDLYSTFNFKKILVKFSTRPKKRIGDESVDQAEKDLSDVLIENNL
KFEHQEGEGAFYGPKIEFVLQDSLDRNWQCGTIQLDFYLPRLRSFYIDE
HNHQKIPIIIHRAILGSIERFIGILIEEFSGKLPWLSPIQVVILSITDS
HINYVKKIVQHFSDINIRVESDLRNEKIGFKIREHTLRQIPYILICGEKE
IKSKKISVRTRNGYNLGIIDIDCFIKKLQKEIFTRSIFYQMEE
> Q00964|VIUA_VIBCH Vibriobactin receptor - *Vibrio cholerae*.

MAVLCPARVSVSAENKKFKLHTLSAMMMGLFTGSAFAYAETQNTSNQEQEMP
VLVVIQEKTRQSIYETSASVEVFDQDTIERTPGATEIDDLQLIPNLVDS
GQSNMPTIRGIDGSGPSVGLASFACTSPRLNMSIDGRSLTYSEIAFGP
RSLWDMQQVEIYLG PQSYIQGRNTSAGAIVMKSNDPTHHFE SAVKAGIGE
SDYSQTAGMISAPIIQDELAFLRSLFDQQRKDSFVDLAAFEFAGDPKKIEM
NSVRGKLLYEPSALDGFKTTLLSHMDSRGPQTENINVAGNEAFRPVYET
ASFTTAWDIIWHLNDLFTFENNLYADFSYDRYTNPNRSGDFNTDGKEFH
IEPLRLRYIALDGSVNTLIGARYYQSSQDDMYIDAASAYPMDGRTKAKSVF
AEVTYALTPSINVNLAGRFFEREQVKRNVSHPRYKLDYDETSVFLPKLDV
AYTPVQGGQTYGIIKAAKGYNASGAGLAFNSMQFTGFRPYEFEQESIWNIEF
YTRHRFHSVSVLNLNFYNDFDSMQMTQTSSGDVFIANLDEASTYGAEI
GSRWYATSSLELFANLGLLKEFKETGTGNTKELPRAPKMSANVGLLYDFG
QGFEFSSNAAYTGSYFSESGNSEKFAIDSYWVANAYLAVFEHGRATLYA
TNLLDSDKTTLYLSTNNTLDQLKQPPRMIGASVQLNF

> P13430|SFAS_ECOL5 S-fimbrial adhesin protein sfaS - *Escherichia coli*
O6:K15:H31 (strain 536 / UPEC).

MKLKAIILATGLINCIASFSAQAVDTTITVTGNVLQRTCNPVGNVDVSLGN
LYVSDFPNAGSGSPWVNFDSLSTGCQNMNTVRATFSGTADGQTYANTGN
AGGIKIEIQDRDGSNASYHNGMFKTLNVQNNNATFNLKARAVSKGQVTPG
NISSVITVTTYA

> P77754|SPY_ECOLI Spheroplast protein Y - *Escherichia coli*.

MRKLTALFVASTLALGAANLHAADTTAAPADAKPMMHHKG KFGPHQDM
MFKDLNLTDAQQQIREIMKGQRDQMKRPPLEERRAMHDIASDTFDKVK
AEAQIAKMEEQKANMLAHMETQNKIYNILTPEQKQFNANFEKRLTERP
AAKGMPATAE

> P11439|TOXA_PSEAE Exotoxin A - *Pseudomonas aeruginosa*.

MHLTPHWIPLVASLGLLAGGSFASAAEEAFDLWNECAKACVLDLKDGVRS
SRMSVDPAIADTNGQVGLHYSMVLE GGNDALKLAIDNALSITSDGLTIRL
EGGVEPNKPVRYESIYTRQARGSWSLNWLVP IGHKPSNIKVF IHELNAGNQ
LSHMSPIYTIEMGDELAKLARDATFFVRAHESNEMQPTLAI SHAGVSVV
MAQAQPRREKRWEWASGKVLCLLDPLDG VYNYLAQQRCNLDDTWEGKIY
RVLAGNPAKHDLDIKPTVISHRLHFPEGGSLAALTAHQACHLPLETFTRH
RQPRGWEQLEQCGYPVQRLVALYLAA RLSWNQVDQVIRNALASPGSGGDL
GEAIREQPEQARLALTLAAAESERFVRQGTGNDEAGAASADVSLTCPVA
AGECAGPADSGDALLERNYPTGAEF LGDGGDISFSTRGTQNWTVRLLQA
HRQLEERGYVFGYHGTFLEAAQSI VFGGVRARSQDLDAIWRGFYIAGDP
ALAYGYAQDQEPDARGRIRNGALLRVYVPRSSLPGFYRTGLTLAAPEAAG
EVERLIGHPLPLRLDAITGPEEEGRL ETILGWPLAERTVVIPSAIPTDP
RNVGGDLDPSSI PDKEQAISALPDYASQPGKPPREDLK

> P13628|PHFS_DESVO Periplasmic [Fe] hydrogenase small subunit -
Desulfovibrio vulgaris (strain Oxamicus Monticello).

MQIVNLTRRGFLKAACVVTGGALISIRMTGKAVAAKQLKDYMMDRINGV
YGADAKFPVRASQDNVQVQKLYAD FLEKPM SHKAEQLLHTHWVDRSKAIE
RMKAQGAYPNPRAKEFEGNTYPYE

> P27217|SCRB_KLEPN Sucrose -6-phosphate hydrolase - *Klebsiella pneumoniae*.

MSLPSRLPAILQAVMQGPQALADSHYPQWHLAPVNGLLNDPNGFCQVAG
RYHLFYQWNPLACDHTYKCGWHWSSADLLHWRHEPIALMPDEEYDRNGCY
SGSAVEFEGALTLCYTGNVKFPDGGRT AWQCLATENADGTFRKLGPVLP
PEGYTGHRDPKVVWRQDGRWYMLGAQDVQQRGKVLFF TASDLREWRLVG
EIAGHDVNGLANAGYMWECPDLFPLADTHLLICCPQGLAREAQRFLNTYP
AVWMAGRFD AERGI FDHGPLHELD SGFEFYAPQTMQADDGRLLVGMWGV
PDGDEMHPTRAQGWIHQMTCVRELEWQAGTLYQRPLRELVALRGEAQGW
CGQTLPLAPMELAFDLS PDSTLGLDFAG ALQLTVNRDGLRLSRRGLQTAE
MHHRYWRGEARRLRIFIDRSSVEIFINDGEGVMSSRFFPGYPGQLIFSGA
TPVAFCRWLLRPCMVE

> P15644|GSPD_KLEPN General secretion pathway protein D - *Klebsiella pneumoniae*.

MIANVIRSFLTLLIFAAALLFRPAAEEFSASFKGTDIQEFINTVSKNL
NKTVIDPSVRGTTITVRSYDMLNEEQYYQFFLS VLDVYGFVINMNGVL
KVVRSKDAKTAAPVVASDAAPGIGDEVVTRVVPLTNVAARDLAPLLRQLN
DNAGVGSVVHYEPSNVLLMTGRAAVIKRLLTIVERVDNAGDRSVVTVPLS
WASAADVVKLVTELNKDTSKSALPGSMVANVADERTNAVLVSGEPNSRQ
RIIAMIKQLDRQQATQGN TKVIYLYKAKASDLVEVLTGISSTMQSEKQAA

KPVAALDKNIIKKAHGQTNALIVTAAPDVMNDLE RVIAQLDIRRPQVLVE
AIIAEVQDADGLNLGIQWANKNAGMTQFTNSGLPISTAIAGANQYNKDG
VSSSLASALSSFNNGIAGFYQGNWAMLLTALSSSTKNDILATPSIVTLDN
MEATFNVGQEVPLTGSQTTSGDNI FNTVERKTVGIKLVKPKQINEGDSV
LLEIEQEVSSVADAASSTSSDLGATFNTRTVNNAVLVGSGETVVVVGLLD
KSVSDTADKVPLLGDIPVIGALFRSTSKKVKRNL MLFIRPTVIRDRDEY
RQASSGQYTAFNDAQSKQRGKENNDAMLNQLLEIYPRQDTAAFRQVSAA
IDAFNLGGNL
> P46445|CYC6_SYNY3 Cytochrome c6 - *Synechocystis* sp. (strain PCC 6803).
MFKLFNQASRIFFGIALPCLIFLGGIFSLGNTALAADLAHGKAIFAGNCA
ACHNGGLNAINPSKTLKMDLEANGKNSVAAIQAQITNGNGAMPGFKGR
SDSDMEDVAAYVLDQAEKGW
> P94845|GLNA_HELPY Glutamine synthetase - *Helicobacter pylori*
(*Campylobacter pylori*).
MIVRTQNSSEKIKEFFEFCKENEVEFVDFRFSDIKGTWNHIAYSFGAL
GMLKEGIPFDASCFFKQWQIEHSDMILTPDLVRYFIDPFSAVSVVVFCD
VYDVYKNQPYEKCPRSIAKKALQHLKDSGLGDVAYFGAENEFFIFDSIK I
KDASNSQYYEVDSEEGEWNDRDRSFENGVNFGHRPGKQGGYMPVPPTDTMM
DIRTEIVKVLNQVLETFFVHHEVAQAQGEVGVKFGDLVEAADNVQKLY
VVKMVAHLNGKTATFMPKPLYGDNGSGMHTHVSVWKNENLFSGETYKGL
SEFALHFLGGVLRHARGLAFTNASTNSYKRLIPGYEAPSIILTYSANR
ASVRIPYGISKNSARFEFRFPDSSSNPYLAFAAILMAGMDGVKNKIDPGE
AMDINLFKLTLEIREKGIKQMPHTLRRSLEEMLADKQYLKESQVFSEEF
IQAYQSLKFNAEVFPWESKPHPFEFITTYSC
> KDSA_HAEIN P45251 2-DEHYDRO-3-DEOXYPHOSPHOCTONATE ALDOLASE
MQNKIVKIGNIDVANDKPFVLFGGMNVLESRDMMAMQVCEAYVKVTEKLG
PYVFKASFDKANRSSIHSYRGPMEGLKIFQELKDTFGVKIITDVHEIY
QCQPVADVVDIIQLPAFLARQTDLVEAMAKTGAVINVKKQFLSPSQMGN
IVEKIEECGNDKIIILCDRGTNFGYDNLIVDMLGFSVMKASKGSPVIFDV
THSLQCRDPFPGAASSGRRRAQVTELARSGLAVGIAGLFLEAHPNPNQAKC
GPSALPLSALEGFVSQMKAIDDLKVSFPELDTSI
> Q04681|PMFA_PROMI Major fimbrial subunit - *Proteus mirabilis*.
MKLSKIALAAALVFGINSVATAENETPAPKVSSTKGEIQLKGEIVNSACG
LAASSSPVIVDFSEIPTSALANLQKAGNIKKDIELQDCDTTVAKTATVSY
TPSVVNAVNKDLASFVSGNASGAGIGLMDAGSKAVKWNATTPVQLINGV
SKIPFVAVVQAESADAKVTPGEFQAVINFQVDYQ
> P23135|CY1_RHORU Cytochrome c1 - *Rhodospirillum rubrum*.
MTTIVKRALVAAGMVLAI GGAA QANEGGVS LHKQDWSWK GIFGRYDQPQL
QRGFQVFLHEVCSTCHGMKRVAYRNL SALGF SEDGIKELAEKEFPAGPDD
NGDMFTRPGTPADHIPSPFANDKAAAAANGGAAPPDLSLLAKARPGGPNY
IYSLLEGYASDSPGEPAEWVWVQVQEKGLEVAFNEAKYFNDYFPGHAISM
PPPLMDDLITYEDGTAATKDQMAQDVVAYLNWAAPEL DARKSLGLKVLL
FLGVL TAML LALKLAIWRDVKH
> P10858|YADA_YERPS Adhesin yadA - *Yersinia pseudotuberculosis*.
MTKDFKISVSAALISALFSSPYAFAEPEPDGNDGIPRLSAVQISP NVDPK
LGVGLYPAPKPI LRQENPKLPPRGPPQPEKKRARLAEAIQPQVLGGLDARA
KGIHSIAIGATAEAAKPAAVAVGAGSIATGVNSVAIGPLSKALGDSAVTY
GASSTAQKDGVAIGARASASDTGVAVGFNSKVDAQNSVA IGHSSHVAADH
GYSIAIGDLSKTDRENSV SIGHESLNRQLTHLAAGTKDNDAVNVAQLKKE
MAETLENARKETLAQSNVDLDAKKHSNSVARTTLETAEHANKKSAEAL
VSAKVYADSNSSHTLKTANSYTDVTVSSSTKKAISESNQYTDHKFSQLDN
RLDKLDRKVDKGLASSAALNSLFQPYGVGKVNFTAGVGGYRSSQALAI
GYRVNESVALKAGVAYAGSSNVMYNASFNIEW
> P00083|CYC2_RHOVI Cytochrome c2 - *Rhodopseudomonas viridis*.
MRKLVFGLFVLAASVAPAAAQDAASGEQVFKQCLVCHSIGPGAKNKVGPV
LNLGFRHSGTIEGFAYS DANKNSGITWTEEVFREYIRDPKAKIPGTKMI
FAGVKDEQKVSLLIAYIKQFNADGSKK
> P09378|RHAR_ECOLI HTH -type transcriptional activator rhaR - *Escherichia coli*.
MAFCNNANLLNVFVRHIANNQLRSLAEVATVAHQKLLKDDFFASDQQAV
AVADRYPQDVFAEHTHDFCELVI VWRGNGLHVLNDRPYRITRGDLFYIHA
DDKHSYASVNDLVLQNIICYPERLKLNLWDQGAIPGFNASAGQPHWRLGS
MGMAQARQVIGQLEHESQHVFPANEMAELLFGQLVMLLNHRHYTSDSLP

PTSSETLLDKLITRLAASLKSPFALDKFCDEASCSEVLRQQF RQQTGMT
INQYLRQVRVCHAQYLLQHSRLLISDISTECGFEDSNYFSVVFRETGMT
PSQWRHLNSQKD

> Q05202|FCUA_YEREN Ferrichrome receptor fcuA - *Yersinia enterocolitica*.

MNQTISSRAPQKRLLAPRLLCVMIGAALGTLSSASSWAAAATDSTAENAKKT
SATAATAKAEDSKTNDTITVVGAQETFRAGGNDLIPTYLDGQVANGGRIG
FLGQQDARNVPFNVIGYTSKMIEDQQANSIADVVKNDASVQNVRGYGNPS
QNYRIRGYNLDGDDISFGGLFGVLPQIVSTSMVERVEVFKGANAFINGI
SPSGSGVGGMINLEPKRAGDTPLTRVTVDYGSASQVGGALDVGRRYGGDD
QFGVRVNVLHREGESAIHDQKERTTAVSTGLDYRGDRARTSLDVGYQKQT
IHMMRTDVAIGGATVIPEPPSSTLNYGQSWVYTDMETTFGMLRSEYDVSQ
NWTVYGSVGA SRNEETGQYGAPMLTNNNGDATISRLYVPYVADSVAGLGG
IRGHFDTGPIITHKVNLGYAANYRRTTKSAWNMSGQEDTNIYNPGVIGFPQT
VMGSDSQDPQLTSQVRASGLSLSDTLSMMDDKVSMLGVRRQEV TIRNFD
SGVPNSAGSLDAMKVTFPIYGIMVKPWEKVS LYANHIEALGPGKSAPYQYN
GKPVVNAGQIPGI IHSKQNEIGVKFDNQRYGGTLALFEITRPTGMVDPAT
NVYGFYGEQRN RGIELNVFGEVFGTRLLASATWLDPKLTKAADSANNNGN
DAVGVANYQLVFGGEYDIPVVEGLTATGTVVRSGSQYANEANTLKLKPWT
RLDLGVRYTMPMKDTSLTWRANIENVTNERYWESVEDSGTYIYQGDPRAL
KLSVSMDF

> P00101|CY551_PSEST Cytochrome c -551 - *Pseudomonas stutzeri* (*Pseudomonas perfectomarina*).

MKKILIPMLALGGA LAMQPALAQDGEALFKSKPCAACHSVDTKMVGPALK
EVAANKAGVEGAADTLALHIKNGSQGVWGPIMPMPNPVTEEEAKILAEWV
LSLK

> P00935|METB_ECOLI Cystathionine gamma -synthase - *Escherichia coli*.

MTRKQATI AVRSGLNDDQYGCVPPIHLSSTYNFTGFNEPRAHDYSRRG
NPTRD VVQRALAELEGGAGAVLTNTGMSAIHLVTTVFLKPGDL LVAPHDC
YGGSYRLFDSLAKRGCYRVLFVDQGDQALRAALAEKPKLVLVESPSNPL
LRVVYDI AKI CHLAREV GAVSVVDNTFLSPALQNPALALGADLVLH SCTKYL
NGHSDVVAGVVI AKDPDVVTELA WANNIGVTGGAFDSYLLLRGLRTLVP
RME LAQRNAQAI V KYLQ TQPLVKKLYHPSLPENQ GHEIAARQQKGF GAML
SFELDGDEQTLRRFLGGLSLFTLAESLGGVESLISHAATMTHAG MAPEAR
AAAGISETLLRISTGIEDGEDLIADLENGFRAANKG

> P74941|SYA_THET8 Alanyl -tRNA synthetase - *Thermus thermophilus* (strain HB8 / ATCC 27634 / DSM 579).

MRTAEI REKFLSFFEGK GHLR LPSFSLI PEDDPSLLFTSAGMAPLKP YFL
GAKPIFGGREWRRTTCQECLRVGDIENVGRTSRHNTYFEMLGNFSFGDY
FKKEAILWAWEFLEHLKLDPGRLWVTVFEDDDEAYE IWRDLVGVPEERI
GRFGEDENYWPGGAI THGPNGPSGPCSEIFYDRGPAYGTPDETGPNTGSG
DRFVEIWNLVFTQYDRQGPIPGPGILKPLPQKNIDTGMGLYRVAAILQDV
EDFYRTDTFFPI IQEVARMSGRPYEGKTSVSHRVIADHVRAVVAALSDGA
TFSNTGRGYVIRRLRRALRHGYLLGLSDPFLHRLAPLVAELLGDFYPEM
RENLP AVEKQIRLEERFLETLEGGLKRLDALLSGLKPGEVLPGKEAFRL
YDTYGFPLDLTVEIAAERGYGVDTGEFQKAMEEQQSRSRAAMAFEREIFK
KGAQVLEELYAERGATEFLGYNALAEAEV LALLAGDQS LLEAGPGTEVQ
VVLDKTPFYAEGGGQIGDFGLLEWPGGRARVETTRKTERGIFLHKARVEE
GVLRVGERVRAVVDPRRRDTERNHTATHLLHAALRAVLGPHVRQAGSLVA
PDRLRFDFTH PEPLKPEELERVELLVNRWIMADFPVTWRYMPLEEARKEG
AMALFGEKYGEVVRVVEGSPLEGLSKELCGGCHVRRRTGEIGAF LIRS
EEAVSAGVRRIEAVTGEEAIRFARGSLNRLKALAEERLEVGEEAAL EERLEK
LLAELKEKEREVESLKARLVQAALGGGGASLEEKGGLRWTVAELPGLDA
KALRQAADDLVARGADVALVLSGGQAVLKLSPKAQGMGLEAGALFRALAE
KAGGRGGGKGA LAQGGGLDPRKAREALPGLLP

> P15452|CY552_HYDTH Cytochrome c -552 - *Hydrogenobacter thermophilus*.

MKKFLLVAVVGLAGITFANEQLAKQKGMACHDLKAKKVGPAYADVAKKY
AGRKDAVDYLAGKIKKGGSGVWGSVMPPPQNVTDAAEQLAQWILSIK

> P0AD60|IVY_ECO57 Inhibitor of vertebrate lysozyme - *Escherichia coli* O157:H7.

MGRISGGMMFKAITTVAALVIATSAMAQDDLTISSLAKGETTKAAFNQM
VQGHKLPAWVMKGGTYTPAQTVTLGDETYQVMSACKPHDCGSQRIAVMWS
EKSNOQTGLFSTIDEKTSQEKL TWLNVNDALSIDGKTVLFAALTGSLENH
PDGFNFK

> P42517|CHMU_ENTAG Monofunctional chorismate mutase - *Enterobacter agglomerans* (*Erwinia herbicola*) (*Pantoea agglomerans*).
MTHFVAIFFSSLFMCSNVFAGSVSSVSLGSLSSALNERMQVMKAVAGYKA
LHHLPIEDLPREQVVLDMMLQNAQQAGLEPHSVEPFVHALMNASKTIQYR
YRADWLSSPDSAVPVRDLTETROQIQQLDTQLLTAISQRLMTGAFSQEDK
EFLMSHLTAPHLSESDKNSLFFASLSRIQRQH

> AMY2_SALTY P26613 CYTOPLA SMIC ALPHA-AMYLASE (EC 3.2.1.1) (1
MKNPTLLQYFHWYYPDGGKLWSELAERADGLNDIGINMVWLPPACKGASG
GYSVGYDITYDLFDLGEFDQKGTIATKYGDKRQLLTAIDALKKNNIAVLLD
VVVNHKMGGADEKERIRVQRVNQDDRTQIDDNIECEGWTRYTFPARAGQY
SNFIWDYHCFSGIDHIENPDEDGIFKIVNDYTDGDGWNQVDDMGNFYDL
MGENIDFRNHAVTEEIKYWARWVMEQTHCDGFRDLDAVKHPIPAWFYKEWIE
HVQAVAPKPLFVIAEYWSHEVDKLTQTYIDQVDGKTMFLDAPLQMKFHEAS
RQGAEYDMRHIFTGTLVEADPFHAVTLVANHDTQPLQALEAPVEPWFKPL
AYALILLRENGVPSVFYDPDLYGASYEDSGENGETCRVDMFVINQLDRLIL
ARQRFAGHIQTLFFDHPNCIAFSRSGTEENPGCVVLSNGDDGEKTLLLG
DNYANKTWRDFSNGRDEYVVTNDQGEATFFCNAGSVSVWVIEDV

> P20862|FANH_ECOLI Protein fanH - *Escherichia coli*.
MIKKVPVLLFFMASISITHASQTATKSLGVSITLSKAQCKINNRAGISGS
FVLPIMISTSGQIISSKKFTTVPIIIDCTAGGNVNQLEITFGDNSSKKIDS
TTWYTTNKDLGLRFSWTKDKTQGFNLGVAHNINKSIWLEGNKKFNASVDV
SPVVIRNTVQGGQYTSALPVTVT FI

> P0A9E0|ARAC_ECOLI Arabinose operon regulatory protein - *Escherichia coli*.
MAEAQNDPLLPYGFNAHLVAGLTPIEANGYLDFFIDRPLGMKGYILNLT
IRGQGVVKNQGREFVCRPGDILLFPPEIHHYGRHPEAREWYHQVYFRP
RAYWHEWLNWPSIFANTGFFRPPDEAHQPHFSDLFGQIINAGQGEGRYSEL
LAINLLEQLLLRMEAINESLHPPMDNRVREACQYISDHLADS NFDIASV
AQHVCLSPSRLSHLFRQQLGISVLSWREDQRISQAKLLSTTRMPIATVG
RNVGFDDQLYFSRVFKKCTGASPSEFRAGCEEKVNDAVKLS

> P37902|GLTI_ECOLI Glutamate/aspartate periplasmic -binding protein -
Escherichia coli.
MQLRKPATAILALALSAGLAQADDAAPAAGSTLDKIAKNGVIVVGHRESS
VPFSYYDNQQKVVGYSDYSNAIVEAVKKLNKPDQVKLIPITSQNRIP
LLQNGTFDFECGSTTNNVERQKQAAFSDTIFVVGTRLLTKKGGDIKDFAN
LKDKAVVVTSGTTEVLLNKLNEEQKMNMRIISAKDHGDSFRTLESRAV
AFMDDALLAGERAKAKKPDNWEIVGKPKSQEAYGCMLRDKDDPQFKKLM
DTIAQVQTSGEAEKWFDFKWFKNPIPPKLNLMNFELSDEMKA LFKEPND
KALN

> P04960|PELE1_ERWCH Pectate lyase E - *Erwinia chrysanthemi*.
MKNTRVRSIGTKSLAAVVTAALMATSAYA AVETDAATTGWATQNGGTTG
GAKAAKAVEVKNISDFKKALNGTDSSAKI IKVTGPIDISGGKAYTSFDDQ
KARSQISIPSNTTIIIGVGSNGKFTNGSLVIKGVKNVILRNLYIETPVDVA
PHYESGDGWNAEWDAVIDNSTNVVDHVTISDGSF TDDKYTTKDGKEYV
QHDGALDIKKGSYVTSYSR FELHDKTILIGHSDSNGSQDSGKLRVTFH
NNVFDRTVTERAPRVRFGSIHAYNNVYLGDKHVSVPYLYSFGGLTSGSIL
SESNSFTLSNLKSIDGKNPECSIVKQFNSKVFSKGSVNGSTTTKLDT
GLTAYKPTLPYKYSAQTMTSSLATSINNNAGYGKL

> P36267|GGT_PSEUA Gamma -glutamyltranspeptidase - *Pseudomonas* sp. (strain
A14).
MKNQTFSKALLATALSCALFNVAASQAPVGAENGMVVTAQHIAASKVGE
VLKSGGNAIDA AVAVGYALAVVYPAAGNIGGGGFMTIQLADGRKTF LDFR
EKAPLAATANMYLDKDGNIK GASTTG YLAVGVPGTVSGMEYAREKEYGTK
TRQQILISPAITLADKGFVLEQGDV DMLWTSTKDFEKDRANS GAI FMNKGQ
PFQFGERLVQKDLARTLRLISAKG TDGFYKGEVADKLVASMKAGGGIITQ
ADLDQYKTRELAPVECDYRGYHVVSAPPPSSGGVVICEIMNILEGYPMKE
LGYHSAQGVHYTIEAMRHAYVDRNSYLGDPDFVKNPLAHL LDKDYAAKIR
AAINPQKAGISQEI KPGVPPHEGSNTTHYSIVDKDGN AVSVTYTLNDWFG
AKVMANGTGVLNDEMDDFTSKVGVPNMYGLIQGEANAIGPGRRPLSSMS
PTIVTKDGKTVMVVGT PGGSR IITA TLLTMLNMIDYGMNLQEAVDAPRFH
QQWMPPESTNIEAFALSPDTQKILESWGQK FAGPQPANHIAAILV GAPS LG
GKPIGKNRFYGAN DRRNTGLALGY

> FUMC_BRAJA P28894 FUMARATE HYDRATASE C (EC 4.2.1.2) (FUMARA
MKRPRGISRGGMDVLMASARTKTARPATRTETDSFGPIEVPSDRYWGAQ

TERSQNFRIGTDRMPISLVHALGIVKLAAAQSNRELGLL DQRRASAIIR
AAREVSTADLDDHFPLVVVWQTGSGTQTNMNLNEVIANRANELLGELGAK
KPVHPNDHVNMSQSSNDSFPTAMHIAASRITADLVPALGELLRALRKE
KEFAKIVKIGRTHQTQDATPLTLGQEFSGYAAQVERGIARLKVAVKELYPL
AQQGTAVGTGLNAKPRFARLFAKHVAGITKLPFTSAANKFEALASNDAYV
LAHGAISSVATGLFKIANDIRLLGSGPRSGLGELILPENEP GSSIMPGKV
NPTQCEAMTMVCCQVFGNHTAITVAGSQGHFELNVYKPVLAYNMLHSIRL
MADAARSFTEHCVSGIRADEKRISSELMQRSLMLVTALAPKIGYDNAAKVA
KTAHANGTTLKEEALRLGFVTADEFDRLVQPEKMTKPG
> Q03011|MRPA_PROMI Major MR/P fimbria protein - *Proteus mirabilis*.
MKLNKLALVLGLGLSVVAGSALAADQGHGTVKFVSGI IDAPCSITPDTEN
QTVPLGQIATAALKDGGRSNSRDFKISLENCTTETYKTQVTTFTGSEATE
VLEGLGIEGIAKNAAVVITDAGGKQIKLGTSPSAAQNLRDGNNDLNFAAY
LQGSASEAAVPGDFTAIAITFALTYQ
> P45605|PHOB_KLEPN Phosphate regulon transcriptional regulatory protein
phoB - *Klebsiella pneumoniae*.
MARRILVVEDEAPIREMVCVFLVLEQNGFQVVEAEDYDSAVNQLNEPWPDLI
LLDWMLPGGSGLQFIKLLKREAMTRDIPVVMLTARGEEDRVRGLETGAD
DYITKPFSPKELVARIKAVMRRISPMAVEEVIEMQGLSLDPSSHRVMTGD
SPLDMGPTEFKLLHFFMTHPERVYSREQLLNHVWGTNVYVEDRTVDVHIR
RLRKALEHSGHDMVQTVRGTGYRFSARF
> P0A0Y4|FBPA_NEIMB Major ferric iron-binding protein - *Neisseria*
meningitidis serogroup B.
MKTSIRYALLAAALTAATPALADITVYNGQHKEAAQAVADAFTRATGIKV
KLNSAKGDQLAGQIKEEGSRSPADVYSEQIPALATLSAANLLEPLPAST
INETRGKGVVAAKDWVALSGRSRVVYDTRKLSEKLEKSVLNYATPK
WKNRIGYAPTSGAFLEQVVAIVKLGEEAAALKWLKGLKEYGKPY AKNSVA
LQAVENGEIDAALINNYWHAFAREKGVQNVHTRLNFVRHRDPGALVTYS
GAAVLKSSQNKDEAKKFVAFSLASKEGQRALTAVRAEYPLNPHVVSTFNLE
PIAKLEAPQVSATTVSEKEHATRLLEQAGMK
> Q06006|NIR_PSECL Copper-containing nitrite reductase - *Pseudomonas*
chlororaphis (*Pseudomonas aureofaciens*).
MSVFRSVLGACVLLGSCASSLALAGGAEGLRVKVDLVAPPLVHPHEQVV
SGPPKVVQFRMSIEEKKMVIDDQGTTLQAMTFNGSMPGPTLVVHEGDYIE
LTLVNPATNSMPHNVDFAATGALGGAGLTQVVPQVEVVLRFKADRSGTF
VYHCAPOGMVPHVWVSGMNGALMVLPRDGLRDPQKLLHYDRVYTIIGESD
LYIPKDKDGHYKDYPDLASSYQDTRAVMRTLTPSHVVFNGRVGALTGANA
LTSKVGESVLFIHQSQRNDRSRPHLIGGHGDWVWTTGKFANPPQRNMETWF
IPGGSAAVALYTFKQPGTYVYLSHNLIEAMELGALAQIKVEGQWDDDLMT
QVKAPGPIVEPKQ
> P0AEE5|DGAL_ECOLI D-galactose-binding periplasmic protein - *Escherichia*
coli.
MNKKVLTLSAVMASMLFGAAHAADTRIGVTIYKYDDNFMSVVRKAIEQD
AKAAPDVQLLNMDSQNDQSKQNDQIDVLLAKGVKALAINLVDPAAGTVI
EKARGQNVVFFNKEPSRKALDSYDKAYVVGTDSDKESGIIQGDLIAKHW
AANQGWDLNKGQIQFVLLKGEPGHPDAEARTTYVIKELNDKGIKTEQLQ
LDTAMWDTAQAKDKMDAWLSGPNANKIEVVIANNMAMGAVEALKAHNK
SSIPVFGVDALPEALALVKSGALAGTVLNDANNQAKATFDLAKNLADGKG
AADGTNWKIDNKVVRV PYVGVDKDNLAEFSSK
> P44715|PTFAH_HAEIN Multiphosphoryl transfer protein - *Haemophilus*
influenzae.
MLELSESNIHLNANAIDKQQAIEMAVSALVQAGNVENGYLQGMLARELQT
STFLNGIAIIPHGTLDRMLVKKTGQVVFQFPQGI EWEGEINIAVYVIGIA
ARSDEHLSLLRQLTHVLSDEDTAAKLAKITDVAEFCAILMGETIDPFEIP
AANISLDVNTQSLTLVAINAGQLQVQSAVENRFISEVINNAALPLGKGL
WVTDSVGVNKNALAFSRAKTI FSHNGKAVKGVITVSAVGDIINPTLVRL
LDDDVQTTLLNGNSTEILTALLGSSSDVETQSVEGAVVGTFTIRNEHGLH
ARPSANLVNEVKKFTSKITMQNLTRESEVVSAKSLMKIVALGVTQGHRLR
FVAEGEDAKQAIESLGKAIANGLGENVSAVPPSEPDTIEIMGDQIHTPAV
TEDDNL PANAEAVFVIKNEQGLHARPSAILVNEVKKYNASVAVQNLDRN
SQLVSAKSLMKIVALGVVKGTRLRFBVATGEEAQQAIDGIGAVIESGLGE
> P13036|FECA_ECOLI Iron(III) dicitrate transport protein fecA -
Escherichia coli.

MTPLRVFRKTTPLVNTIRLSLLPLAGLSFSAFAAQVNIAPGSLDKALNQY
AAHSGFTLSVDASLTRGKQSNGLHGDDYD VESGLQQLLDGSGLQVKPLGNN
SWTLEPAPAPKEDALTVVGDWLDGARENDVFEHAGARDVIRREDFAKTGA
TTMREVLNRI PGVSAPENNGTGSHDLAMNFGIRGLNPRLASRSTVLMDCI
PVPFAPYQGPQLSLAPVSLGNMDAIDVVRGGGAVRYGPQSVGGVVNFVTR
AIPQDFGIEAGVEGQLSPTSSQNNPKETHNLMVGGTADNGFGTALLYSGT
RGSWDREHSATRIDDMLKSKYAPDEVHT FNSLLQYYDGEADMPGGLSRA
DYDADRWQSTRPYDRFWGRRKLASLGYQFQPDSQHKFNIQGFYTQTLRSG
YLEQGKRITLSPRNYWVRGIEPRYSQIFMIGPSAHEVGVGYRYLNESTHE
MRYYTATSSGQLPSGSSPYDRDTRSGTEAHAWYLDKIDIGNWTITPGMR
FEHIESYQNNAITGTHEEVSYNAPLPALNVLYHLTDSWNLYANTEGSFGT
VQYSQIGKAVQSGNVEPEKARTWELGTRYD DGALTAEMGLFLINFNNQYD
SNQTNQDVTARGKTRHTGLETQARYDLGTLTPTLDNVSYASYAYVNAEI
REKGDYGNLVPFSPKHKGTGLVDYKPGNWFNLNSDFQSSQFADNANTV
KESADGSTGRIPGFMLWGARVAYDFGPQADLNLAFGVKNI FDQDYFIRS
YDDNNKGIYAGQPRTLYMQGSLKF

> P35823|SLAP_AERSA S-layer protein - *Aeromonas salmonicida*.

MEFKKTLIAAAIIVGSAAPAFADVVISPNQNTFVTTSLASVTKQPVLDFST
AQQNLTNLFSEVGLKNNGFIVLEIQEGEQFNDAEIRQWLSNGFWRRPFT
GLLVNPNHDHGNFANSGEVNDVRKFFKII SDGTQTLTI VHTIDSNGKRLRLA
LASDVEETINFADAEVELKLNLANQAFKLTSGSQGTVALTAGALWNASYT
ADPVATKPLFKLGLKLFQLSLTNAGKATALVSEGFLKLNIGDANISATD FA
ITNVTTNQTIIQRDKVNLTLTGDVSAFKKDANGNLVNKAGASIGWAAAADG
QSATAVLGAGNMAGGVQNALAAFGLTYVAADNTVPVPAVNFVNAEKAEIQGD
SQATYNYFKDELADLFILTRDGMKFDITTTGTTSANLIHIRDVSNILPTE
GGKIFVTITEYADHAANGRGEQTVLVTRKALSVTLPSGGAVTLKPADVAA
DVGASITAGRQARLVFEVETNQGEVAVKKSNAEGVDIQNGTRGTAPLVD F
TL

> HXKG_ECOLI P46880 GLUCOKINASE (EC 2.7.1.2) (GLUCOSE KINASE)

MTKYALVGDVGGTNARLALCDIASGEISQAKTYSGLDYPSLEAVIRVYLE
EHKVEVKDGCIAIACPIITGDWVAMTNTWAFSIAEMKKNLGFHLEIIND
FTAVSMANPMLKKEHLIQFGGAEPVEGKPIAVYGAGTGLGVAHLVHVDKR
WVSLPGEGGHVDFAFNSEEEAIIILEILRAEIGHVSA EACLSGPGLVNLVYR
AIVKADNRLPENLKPDKITERALADSCTDCRRALSFCVIMGRFGGNLAL
NLGTFGGVFIAGGIVPRFLEFFKSGSFRAAFEDKGRFKEYVHDI PVYLIV
HDNPGLLGSAGHLRQTLGHIL

> P73443|SYK_SYNY3 Lysyl -tRNA synthetase - *Synechocystis* sp. (strain PCC 6803).

MADSHSHSLEEIRATRLEKAEQLRQLGLNPNYAYTWE ITHQAQDLQETYR
DLSNGEEVDLKVAIAGRILARRVMGKLAFFTLQDESGTIQLYLEKQRLTE
HMEPELENAFNLLKKITDVGDILGVTGLKRTEKGEVSVYVQTYAVLTKSL
LPLPDKWHGLTDEKRYRQRYVDLIVNPTVRQTFRRRAQITAAIRRYLDK
QGFIEIETPVLQGESGGAEARPFITHHNTLGMPLYLRIATELHLKRLVVG
GFEKVFELGRIFRNEGVSTRHNPEFTSIEVYQAYVDYN EMMALTEALVT
AAQAVLGLTKITYQGEEIDLTPPWKRITMHEAVQLETGIDFSQFTDLETA
KQAATKAGIGVPEDCPSLGHLLNHAFEQKVEGTLMQPTFIIDFPVEISPL
AKPHRSKPGVLEFELFVYGRELANSELTDPIDQRSRLEAQAAKKAAG
DLEAHSVDEDFLTALEYGMPTGGGLGIGIDRLVMLLTDSPSIRDVIAFPL
LKNQEAGSDG

> P04172|AMCY_METEX Amicyani n-alpha - *Methylobacterium extorquens* (*Protomonas extorquens*).

MRALAFAAALAAFSAATAAALAGALEAVQEAPAGSTEVKIAKMKFQTPEVR
IKAGSAVTWNTTEALPHNVHFKSGPGVEKDVEGPMRLSNQTYSVKFNAPG
TYDYICTPHPFMKGKVVE

> P43763|PROB_HAEIN Glutamate 5-kinase - *Haemophilus influenzae*.

MNKKTI VVKFGTSTLTQGSPLNSPHMMEIVRQIAQLHNDGFRIVIVTSG
ATAAGRHYLNHPQLPPTIASKQLLAAVGQSQLIQAWKLFAYDIHIGQL
LLTRADIEDRERFLNARDTLYALLDNHIIPVINENDAVATAEIKVGDNDN
LSALVAILVQAEQLYLLTDQQLFSDPRKNPEAKLIPVVEQITDHIRSI
AGGSGTNLTGGMMTKIIAADVATRSGETIIAPGNRPVNIADLAYEQNI
GTKFIAHQSDRLESRKQWLFAAPSAGIITIDNGAQNAILEQNKSLLPAGI
INVEGRFSRGEVVKIRTQSGKDIALGMPRYNSDALQLIKGRKSADIENVL
GYEYGAVAMHRDDMI ILS

> P0AGD1|SODC_ECOLI Superoxide dismutase [Cu -Zn] - Escherichia coli.
MKRFLAILALVVATGAQAASEKVMNLVTSQGVGQSIGSVTITETDKGL
EFSFDLALPPGEHGFHIAKAG SCQPATKDGKASAAESAGGHLDPQNTGK
HEGPEGAGHLGDLPALVVNNDGKATDAVIAPRLKSLDEIKDKALMVHVGG
DNMSDQPKPLGGGGERYACGVK

> P51837|RNC_COXBU Ribonuclease III - Coxiella burnetii.
MNHLNKLMLERLGHQFNLELLKIALTHCSSGADNNERLEFLGDSVLGFII
ASELYQRRPQAREGLSRMRASVNGDELAQMSTKLGINEYLQL GVGEQK
SGGKRRRSILADALEAIVGAIYIDAGLETCCRRCVLNHWYGERVDDLSKLS
KKDAKSLLEWQLQARRLPLPTYEVKITGEAHAQTFTVNCYVKGLPHKTEG
VNTTRRRAEQIAAKRFLELLDDGKGDGITERDQ

> P04977|TOX1_BORPE Pertussis toxin subunit 1 - Bordetella pertussis.
MRCTRAIRQTARTGWLTLAILAVTAPVTSPAWADDPATVYR YDSRPE
DVFQNGFTAWGNNDVLDHLTGRSCQVGSNSAFVSTSSRRRYTEVYLEH
RMQEAVEAERAGRGTGHFIGYIYEV RADNNFYGAASSYFEYVDTYGDNAG
RILAGALATYQSEYLAHRRIPPENIRRVTRVYHNGITGETTTTEYSNARY
VSQQTRANPNPYTSRRSVASIVGTLVRMAPVIGACMARQAESSEAMAAWS
ERAGEAMVLVYYESIAYSF

> Q02760|CY1_RHOSH Cytochrome c1 - Rhodobacter sphaeroides
(Rhodopseudomonas sphaeroides).
MIRKLTTLTAATALALSOGAAMAAGGHVEDVPFSEFEGPFGTFDQHQLQRG
LQVYTEVCAACHGMKFPVIRSLSEPGPELQVRAATQFTVTDEETG
EDREGKPTDHFPHSALENAADLSLMAKARAGFHGPMGTGISQLFNGIGGP
EYIYSVLTGFPEEPPKCAEGHEPDGFYNNRAFQNGS VPDTCKDANGVKT
AGSWIAMPPPLMDDLVEYADGHASVHAMAEDVSAFLMWAAEPKLMARKQ
AGFTAVMFLTVLSVLLYLTNKRLWAGVKGKKKTNV

> P44305|RIMI_HAEIN Ribosomal -protein-alanine acetyltransferase -
Haemophilus influenzae.
MSIISQIEACDFERLYEIEQQAHLVPWSFGTLKNNQGERYLNLKLIENNO
IIGFAICQTVLDEATLFNIAILPTYQCGCGFKLLLGKLIQFQLEKGVQTL
WLEVRESNSARFLYEKIGFNEVDIRKNYYPKPSGGRENNAVVMACYL

> GLN1_RHILV P09826 GLUTAMINE SYNTHETASE I (EC 6.3.1.2) (GLUT
MATASEILKQIKENDVKFVLDLRFDRRASLQHVMTDVCVDEDMFADGVM
FDGFSIGGWKAINESDMVLPDTEVHMDPFFAQSTMVIVCDILDVPSGE
AYNRDRRGTAKKAEAYLKASGIGDVFVFGREAEFFVDDVKYKADPYNTG
FKLDSTELPSNDDTDYETGNLGHPRVVKGGYFPVPPVDSAQDMRSEMLTV
LSEMGVVVEKHHHEVAAAQHDTLVRNADELGIKFKMQIYKYVVHQVANAY
GKTATFPKPIFGDNGSGMHVHQS IWKGGKPTFAGDEYAGLSECLFYIG
GIIKHAKAINAFNTPSTNSYKRFVPGYEAPVLLAYSARNRSASCRIPFGS
NPKAKRVEVRFDPDPTANPYLAFAAMLMAGLDGIKNIHPGKAMDKLDLYDL
PPKELKKIPTVCGSLRQALESLDKDRKFLTAGGVFDDQIDAFIELKMAE
VMRFEMTPHPVEYDMYSA

> APT_PSEAE Q04633 PROBABLE ADENINE PHOSPHORIBOSYLTRANSFERASE
MIFDEFTLKSQLRAVPDFPKPGVFRDITPLFQSPRALRMTVDSFVQRYI
EADFSHIGAMDARGFLIGSAVAYALNKPL VLFKQKGLPADVLAEGYQTE
YGEAFLEVHADSLCEGDSVLI FDDLIATGGTLLAAASLVRRLGARVFEEA
AIIDLPELGGSTRLQDAGISTFSLTAFALDER

> Q07408|MSP4_ANAMA Major surface antigen 4 - Anaplasma marginale.
MNYRELFTGGLSAA TVCACSLLVSGAVVASPMSHEVASEGGVMGGSFYVG
AAYSPAFPSVTSFDMRESSKETS YVRGYDKSI ATIDVSV PANFSKSGYTF
AFSKNLITSF DGAVGYS LGGARVELEASYRRFATLADGQYAKSGAESLAA
ITRDANITETNYFVVKIDEITNTSVMLNGCYDVLHTDLPVSPYVCAGIGA
SFVDISKQVTTK LAYRGKVGISYQFTPEISLVAGGFYHGLFDES YKDIPA
HNSVKFSGEAKASVKAHIADYGFNLGARFLFS

> GLN2_RHILP Q02154 GLUTAMINE SYNTHETASE II (EC 6.3 .1.2) (GLU
MTKFKLEYIWL DGYTFV PNLRGKTQIKEFDEFPTLEQLPLWGFDSSTMQ
AEGSSDCVLPVATY PDPARTNGALVMCEVMPDGHAAHASNARATILDDE
DAWFGFEQEYFFYQNGRPLGFPEQGY PAPPYTYGVGYSNVGDVAREIVE
EHLDLCLAAGINHEGINAEVAKGQWEFQIFGKGSKKAADQIWMARYLLQR
LTEKYGIDIEYHCKPLGDTDWNGSGMHCNFSTKYLREVGK EYFEALMAS
SDKNLMDHIAVYGPNDKRLTGKHETAPWNKFSYGVADRGASIRVPHSFI
KNDYKGYLED RRPNSQGDOPYQIVRRF

> LYSR_ECOLI P03030 TRANSCRIPTIONAL ACTIVATOR PROTEIN LYSR. -

MAAVNLRHIEIFHAVMTAGSLTEAAHLLHTSQPTVSRELARFEKVIIGLKL
FERVRGRHLHPTVQGLRLEFEVQRSWYGLDRIVSAAESLREFRQGELSIAC
LPVFSQSFLPQLLQPLFLARYPDVSLNIVPQESPLLEEWLSAQRHDLGLTE
TLHTPAGTERTELLSLDEVCVLPPGHPLAVKVLTPDDFQGENYISLSRT
DSYRQLLDQLFTEHQVKRRMIVETHSAASVCAMVRAGVGISVVNPLTALD
YAASGLVVRFSIAVPFTVSLIRPLHRPSSALVQAQFSGHLQAGLPKLVTS
LDAILSSATTA

> P06191|ALR2_SALTY Alanine racemase, catabolic - *Salmonella typhimurium*.

MTRPIQASLDLQVMKQNLAIVRRAAPEARVWSVVKANAYGHGIERVWSAL
GATDGFAMLNLEEAITLRERGWKGPILMLEGFFHAQDLEAYDTYRLTTCI
HSNWQLKALNARLNAPLDIYVKVNSGMNRLGFQPERAQTVWQQLRAMRN
VGEMTLMSHFAQADHPGEIGEMRRIALATEGLQCAYSLSNSAATLWHPQ
AHYDWRPGIILYGASPSGQWR DIADTGLKPVMTLSSEIIGVQTLASAGER
VGYGGYSVTQEQRIGIVAAGYADGYPRHAPTGTPLVDGIRTRTVGTVS
MDMLAVDLTPCPQAGIGTPVELWGKEIKVDDVASAAGTLGYELLCAVAPR
VPFVTT

> Q55729|SYM_SYNY3 Methionyl -tRNA synthetase - *Synechocystis* sp. (strain PCC 6803).

MLDSSVPTFSVTTPLYVNDVPHLGSAYTTVVAD TLARFKRLQGYDVLMI
TGTDEHGQKIQRTAEAQELDPQTHCDRTVVVKFELWRSNLNLYDRFSRTT
DPRHLAIVKIDFFQVWVDKGDIIYLAQQQGWYCVACEEFKEKRDLLLEDNHCP
LHPNRKAEWRDEENYFFRLSRYQHPLLEELYAQRPEFIQSSRRNEVLNFV
AQGLQDFSISRNVLDWGFPLPNDPNHTIYVWFDALLGYVTALLDEDEEPN
LTNALVKWVWIPINLHLIGKDILRFHAVYWPAMLSA ELAIPAQVFGHGFLT
KDGQKMGKSLGNTVPLDLINRYGEDAFRYYFLKEIEFGKDGDFNEQRFV
NVLNADLANDLGNLLNRTLGMVKKYCQGGPQVMATDLAPDNPLKALGSH
LGEEVSSAYERLSFTDACEAIFTLVRAGNKYIDDMAPWKLKQGSQKEVE
DVLYSVLESIRLSAYLLSPIVPRLSTKIYQQLGFTWDFDQWRSPLEQAE
FNRHQSWGQLGANQNLPPAQPIFTKLELPAEE

> P50176|PHBC_RHIME Poly -beta-hydroxybutyrate polymerase - *Rhizobium meliloti* (*Sinorhizobium meliloti*).

MTAEKAEGATGFAGFDPKSVEPYIVKDPESLAINMARAEEQLGKAASAWL
APREAGEKTDSFAEPVSDMVKTLKSVSEYWLSDPRTLEAQTLLGSSFFD
MWSRTLQRMAGDAVEDPANLQRNDKRFADWDVKNPFFDFIRQAYFVTS
WAERMVRDAEGLDHTRHKAIFYRQIASALSPTNFITTNPQLYRETVAS
SGANLVKGMQMLAEDIAAGRGELRLRQTDTSKFAIGENIAITPGKVIAQN
DVCQVLQYEASTETVLKRPLLCPPWINKFYVLDLNLPEKSFIKWAVDQGG
TVFVISWVNPDERHASKDWEAYAREGIGFALDIEQATGEREVNSIGYCV
GGTLLAATLALHAAEGDERIRSATLFTTQVDFTHAGDLKVFVDDDQIRHL
EANMSATGYLEGSKMASAFNMLRASELIWPFVNNYLKQDPLPFDLLYW
NSDSTRMPAANHSFYLRNCYLENRLSKGEMVLAGRRVSLGDVKIPIYNLA
TKEDHIAPAKSVFLGSSSFGGKVTFVLSGSGHIAGVNPAPSKYQYWTG
GAPKGDIEWTMGKAKETAGSWWPHWQGWVERLDKRRVPARKAGGPLNSIE
EAPGSYVRVA

> P37080|PTRA_KLEPN Sorbose -specific phosphotransferase enzyme IIA component - *Klebsiella pneumoniae*.

MVHAIFCAHQLAGAMLDVCMVYGEVNVSAVAFVPGENAADIINLEKL
VSAHTDEEWVIAVDLQCGSPWNAAGLAMRHPQIRVISGLSLPLALELVD
NQHTLSADDLCQHLQAIASQCCVVWQQPETVEEEF

> P18815|MALE_ENTAE Maltose -binding periplasmic protein - *Enterobacter aerogenes* (*Aerobacter aerogenes*).

MKIKTGARILALSALTTMMFSASALAKIEEGKLVIIWINGDKYNGLAIEVG
KKFEKDTGIKVSVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGAYAQSG
LLAEITPDKAFQDKLYPFTWDVAVRYNGKLIAYPVAVEALSLIYNKDLVPN
PPKTWEEIIPALDKALKAKGKSALMFNLQEPYFTWPLIAADGGYAFKFENG
KYDVKNVGVNDSAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAM
TINGPVAWSNIDKSKVNYGVTLLPTFKGKPSKPFVGVLSAGINAASPNKE
LAKEFLENYLMTPGLEAVNNDKPLGAVAVKSFQEKLEKDPRIAATMANA
QKGEIMPNIPOMSAFWYAVRTAVINAASARQTVDAALKDAQGRITK

> P15320|HLYA_SERMA Hemolysin - *Serratia marcescens*.

MKNNNFRLSAAGKLAALAIILAASAGYAAEIVAANGANGPGVSTAATG
AQVVDIVAPNGNLSHNQYQDFNVNQPGAVLNSREAGLSQLAGQLGANP
NLGGREASVILNEVIGRNPSSLHGGQQEIFGMAADYVLANPNGISCSQSCGF

INTSHSSLVVGNPVLENGVLQGYSTFGNRNTLSLNGTLNAGGVLDLIAPK
IDSRGEVIVQDFKQSNQKVTSAAINAISGLNRVARDGTVQASQOMPTALD
SYLLGSMQAGRINIINTAQSGVKLAGSLNAGDELKVKAYDIRSESRVDD
ASSNKNGGDNYQNYRGGIYVNDRSSQTLRTELKGNISLVADNHAHLT
ATDIRGEDITLQGGKLTLDGQQLKQTQGHDDRWYFSWQYDVTREREQLQ
QAGSTVAASGSAKLISTQEDVKLLGANVSADRALSVAARDVHLAGLVEK
DKSSERGYQRNHTSSLRTGRWSNSDESESLKASELRSEGELTLKAGRNVS
TQGAKVHAQRDLTIDADNQIQVGVQKTANAKAVRDDKTSWGGIGGGDNKN
NSNRREISHASELTSGGTLRLNGQQGVITITGSKARGQKGGEVTTATHGGLR
IDNALSTTVDKIDARTGTAFNITSSSHKADNSYQSSTASELKSDTNLTLV
SHKDADVIGSVASGGELSVESKTGNINVKAAERQQNIDEQKTALTVNGY
AKEAGDKYRAGLRIEHTRDSEKTRTENSASSLSGGSVKLKAEKDVTF
GSKLVADKGDASVSGNKVSFLAADDKTASNTEQTKIGGGFYTTGGIDKLG
SGVEAGYENNKTAQSSKAITSGSDVKGNLTINARDKLTQQAQHSVGGGA
YQENAAGVDHLAAADTASTTTTKTVDGVNIGANVDYSAVTRPVERAVGKA
AKLDATGVINDIGGIGAPNVGLDIGAQGGSSSEKRSSSSQAVVSSVQAGSI
DINAKGEVRDQGTQYQASKGAVNLTADSHRSEAAANRQDEQSRDTRGSAG
VRVYTTTGSDLTVDAKGEGETQRSNSSASQAVTGSIDAANGINNVKKA
IYQGTALNGGRGKTAVNAGGDIRLDQASDKQSESRSGFNVKASAKGGFTA
DSKNFGAGFGGTHNGESSSTAQVGNISGQQGVELKAGRDLTLQGTQV
SQGDVSLSAGNKVALQAESTQTRKESKLSGNIDLAGSSDSKEKTGGNL
SAGGAFDIAKVNESATERQGATIASDGKVTLSANGKGDALHLQGAQVSG
GSAALEAKNGGILL ESAKNEQHKDNWSLGIKANAKGGQTFNKDAGGKVD
NTGKDTHTLGLAGLVGVEQDKTTHANTGITAGDVTLSNGKDTLRLAGARV
DADSVQGVGGDLHVESRDKDVENGKVDVDAGLSHSNDPGSSITSKLSKV
GTPRYAGKVKELEAGVNVKADATTDKYNVSVARRLDPOQDPTGAVSFSKA
EGKVTLPATPAGEKPPQGLWDRGARTVGGAVKDSITGPAGRQGHKLVNAD
VVNNNAVGEQSAIAGKNGVALQVGGQTQLTGGEIRSQQGKVELGGSQV
QDVNGQRYQGGGRVDAAATVGGLLGGAQKQSVAGNVPFASGHASTQQADA
KAGVFSKG

> P0AD64|BLA1_KLEPN Beta-lactamase SHV-1 - *Klebsiella pneumoniae*.

MRYIRLCIISLLATLPLAVHASPPLEQIKLSESQLSGRVGMIEMDL
ASGRTLTAWRADERFPMSTFKVVLGAVLARVDAGDEQLERKIHYRQ
QDLVDYSPVSEKHLADGMTVGECAAAITMSDNANLLLATVGGPAGLTA
FLRQIGDNVTRLDRWETELNEALPGDARDTTTPASMAATLRKLLTSQ
RLSARSQRLLQWVDDRVAGPLIRSVLPAGWFIADKTGAGERGARGI
VALLGPNNKAERIVVIYLRDTPASMAERNQIAGIGAALIEHWQR

> Q05489|LIP_BURGL Lipase - *Burkholderia glumae* (*Pseudomonas glumae*).

MVRSMSRVAARVAALAVMPLAGAAGLTMAASPAVAADTYAATRYPV
ILVHGLAGTDKVFANVVDYWYGIQSDLQSHGAKVYVANLSGFQSDDG
PNRGEQLLAYVKQVLAATGATKVNLIHSGGLTSRYVAAVAPQLVASV
TTIGTPHRGSEFADFVQDVLKTDPTGLSSTVIAAFVNVFGTLVSS
SHNTDQDALAALRTLTTAQTATYNRNFPASAGLGAPGSCQTGAATE
TVGGSQHLLYSWGGTAIQPTSTVLGVTGATDTSTGTLVDVANVTD
PSTLALLATGAVMINRASQNDGLVSRCSLFGQVISTSYHWNHLDE
INQLLGVRGANAEDPVAVIRTHVNRKLGQV

> P73141|SYY_SYNY3 Tyrosyl-tRNA synthetase - *Synechocystis* sp. (strain PCC 6803).

MVNSDPDWLRGTAEIFPHNADSNNPQEHGILTQQDRPLRVKLGIDPT
GTDIHLGHSIPFRKLRAFQDAGHTAVVIIGDFTAQIGDPTGKSEVRK
QLTADQVKRNAESYLAQLKPIILDFDTPGRLEIRYNSEWLSNLDL
NKILELLATMTVQMLAKEGFARFQKENPIFLHEFLYPLMQGYDSV
AVNADVELGGTDQKFNIAGVGRDLQRHFQKTPQFGLLLPILLGTDG
QQKMSKSLNNYVGLQEDALSMYSKLEKTPDRLLEGEYFELLT
NLDAELPENPRECQKLLAKEVTAQFHGVAGIAAQKTAEDIVTQ
GKAGNTDSVPEFSLAEITFPVKLAYLLSASGLCPSSSEGR
RQIKGAVRLDGDRLLEDVNQYADPKMLINKVLQMGKKKFI
RLIS

> P04338|NODA_RHILV Nodulation protein A - *Rhizobium leguminosarum* bv. *viciae*.

MSEVVRWKICWENELEASDHAEADFFCKTYGPTGAFNAKPFETGR
SWGGRARPERRAIAYDSHGVAASHMGLLRRFIKVGTTDLLVAELG
LYGVRPDLEGLGIAHSVRAMFPIRELSVPPFAFGTVRHAMRNHME
RYCRDGTANIMTGLRV RSTLPDAHSDLPATRTEDVLVLPVDRP
MTEWPAGSLIERNGSEL

> GT_HAEIN P44521 GLUTATHIONE S -TRANSFERASE (EC 2.5.1.18). -
MKLYGLIGACSFVPHVALEWVKIRENADYEFEPVTRELIKSPEFLSLNPR
GAVPVLVDGDLVLSQ NQAILHLYLDELYPNSKLFSGKTVRDKAKAARWLAF
FNSDVHKS FVPLFRLPNYAKDNETLAHTIRQQAVEQILDQLAVANEHLES
HIYFGENISVADAYLYIMLNWCKAVKIDFSHLTQLSAFMQRVETDQAVEN
VRKSEELKV
> P06717|ELAP_ECOLI Heat-labile enterotoxin A chain - Escherichia coli.
MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKR SGGLMPRGHNEYFD
RGTQMNNINLYDHARGTQTGFVRYDDGYVSTSLSLRSAHLAQSSILSGYST
YYIYVIATAPNMFVNDVLDVGVSPHPYEQEVSALGGIPYSQIYGWYRVNF
GVIDERLHRNREYRDRYRNLNIAPAEDGYRLAGFPDPHQAWREEPWIHH
APQCGNSRRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDI
YNRIRDEL
> P52276|SYN_SYNY3 Asparagin yl-tRNA synthetase - Synechocystis sp. (strain
PCC 6803).
MNKRRRIIEVLRHGQADDQVMVQGWLRTRKRTLKDFS FVEVNDGSSLANLQV
VLDGSLADYDRLLSQLQTGAALVVEGKLAPSPGKGQRVELKATKLELLGG
ADPGSYPLQKKRHSFEFLRTIGHLRPRNTIGAVMRVRNACATAIHQFFQ
ERGFLLVWHTPIITASDCEGAGDLFKVTTLDLQRPVKNKEGIDYSQ DFFGK
QAYLTVSGQLEAEVMAALAFQNVYTFGPTFRAENSNTSRHLAEFFWVPEM
AFCDLEGDRQWAEFFLKYIFKVVLEKCPEDMEFFDQRIDNTVLATADNII
NNEFAWLTYSEAIKLEKADQKFEYPVAWGVLDQSEHERYLAETVFKRPT
IVTDYPKDIKAFYMRNDDGKTVAAMDILAPKIGEIIIGGSQREERLDILT
QRMQEQGVPEEDLWVYLDLRRYGSVPHAGFGLGFERIVQFMTGMAN IRDV
IPFPRTPMNAEF
> P55875|IF2_STIAU Translation initiation factor IF -2 - Stigmatella
aurantiaca.
MSKKRVHEIAKELKGHGIELDNKEVVTELAGLGYDVKSHSSSLDDDDQATA
AVQKILDKRKPQAAAAPVTAKGFVVRKVGPPPTGSGVYDASQEPSQAASD
VSSPPSEPVHEASGAEAAAASERVPEAAAVQEPVAEAPRAAAASEPAAEAPK
ATAPVAPEPTVEAPKAAAPVAPEPTVEAPKTEAPVAAAPIAEAPTTPPART
EVPVTSGRRAASCRGAAPLPCSGKDLALNSSPQSSAAFCPDARNPGDCD
FPSTSGRWHAWPSRGSGRFAHGAGRPSGWT FARWTSGRPRAASRRTAVQ
RPSGRAGAGASHGLQRRKGFAGAGA QASGQPQNVMTMVGGI PHAPTAPDARA
LRPTATQAVVISRPLIQVRRVTPTTSSAKQYPMAPGKKAIGEVRFEKVVV
DHAGRGRELVDVSKNKDKSPRKRGGPNDSISKQELTDLAWGRVNIPLRG
KKKKPTKKGAKTQITQMAEDKKVIKIQEGISVSDLGQRMGVRTSDI IKKL
MGLGKMATANQVMDADTVELIASDYGWKVDVGVGFEVEDYLPVVARPEDA
RTRPPVVTVMGHVDHGKTSLLDAIRANVASGEAGGITQHIGAYSVTTAR
GDITFLDTPGHEAFTSMRARGANVTDIVILVVAADDGVMPQTIEAIKHAK
AAEVP IVVALNKMDVPGANPDRVKKDLANHELVPPEEWGGETIMVPVSAKQ
KMGIDLLLENVVLAQEVLELTSNPSRPAVGAIIEGELDRGRGPVATVVLVQ
EGTLRVGDVAVTGTDYGRVRAMNNSRGESVKEVLPGYCAEVI GLSGVPSA
GDTINVVADEKAAKQIAEHRGMKERQSELSKVSRETLDQLFAKTKAGGGP
KELRVVIKADVQGSAAEAVKQAVQKLTTHKVKVEVIDTGVGAIITESDVMRA
AASKGVVLGFNVKPESGAESAAKAEGVMLRSFSIIYELIDGVRSSMEELL
EPIRTERKLGRAEVRNTFNVPKLGTIAGAAVL DGVIKRGA FVRLMRENKQ
LFAGKMASLRRFKDDVKEVAQGFECGIGIENFNDLKAGDII EAYEIEETR
QSLT
> Q03961|KPSD1_ECOLI Polysialic acid transport protein kpsD - Escherichia
coli.
MKLFKSIILLIAACHAAQASAAIDINA DPNLTGAAPLTGILNGQQSDTQNM
SGFDNTPPPSPVMSRMFGAQLFNGTSADSGATVGFNPDIILNPGDSIQ
VRLWGAFTFDGALQVDPKGNIFLPNVGPVKVAGVSNSQLNALVTSKVKEV
YQSNVNVYASLLQAPVKVYVTFVVRNPGLYGGVTS DSSLNLYLIKAGGVD
PERGSYVDIVVKRGNRVRSNVNLYDFLLNGKLGLSQFADGDTIIVGPRQH
TFSVQGDVFNKYDFEFRESSIPVTEAL SWARPKPGATHITIMRKQGLQKR
SEYYPISSAPGRMLQNGDTLIVSTDRYAGTIQVRVEGAHSGEHAMVLPYG
STMRAVLEKVRPNMSQMNNAVQLYRPSVAQRQKEMLNLSLQKLEEASLSA
QSSTKEEASLRMQEAQLISRFAKARTVVPKGEVILNESNIDSVLLEDGD
VINIPEKTSLVMVHGEVLF PNAVSWQKGMTTEDYIEKCGGLTQKSGNARI
IVIRQNGAAVNAEDVDSLKPGDEIMVLP KYESKNIEVTRGISTILYQLAV
GAKVILSL

> P37696|GUNA_ACEXY Probable endoglucanase - *Acetobacter xylinus* (*Gluconacetobacter xylinus*).
MSVMAAMGGAQVLSSTGAFADPAPDAVAQQWAIIFRAKYLRPSGRVVDVTGN
GGESHSEGQGYGMLFAASAGDLASFQSMWMMWARTNLQHTNDKLFWSRFLK
GHQPPVPDKNNATDGDLLIALALGRAGK RFQRPDYIQDAMAIYGDVNLNM
TMKAGPYVVLMPGAVGFTKKDSVILNLSYYVMPSSLQAFDLTADPRWRQV
MEDGIRLVSAGRFQWRLPPDWLAVNRATGALSISGWPPRFSDAIRVP
LYFYWAHMLAPNVLADFTRFWNNFGANALPGWVDLTTGARSYPNAPPGYL
AVAECTGLDSAGELPTLDHAPDYISAALTLVYIARAEEETIK
> P0ADU5|YGIW_ECOLI Protein ygiW - *Escherichia coli*.
MKKFAAVIAVMALCSAPVMAAEQGGFSGPSATQSQAGGFQGPNGSVTTVE
SAKSLRDDTWWTLRGNIVERISDDLIVFKDASGTINVDIDHKRWNGVTVT
PKDTVEIQGEVDKDWNSVEIDVKQIRKVN
> P37735|DCTP_RHOCA C4 -dicarboxylate-binding periplasmic protein -
Rhodobacter capsulatus (*Rhodopseudomonas capsulata*).
MLTRRILGALVGATASLALSVPALAEPIVIKFSHVVPDTPKGGKAAKF
EELAEKYTNGAVDVEVYVNSQLYKDKEELEALQLGAVQMLAPSLAKFGPL
GVQDFEVFDLPYIFKDYEALHKVTQGEAGKMLLSKLEAKGITGLAFWDNG
FKIMSANTPLTMPDDFLGLKMRISQSSKVEAEMNALGAVPQVMAFSEVYQ
ALQTGVVDGTENPPSNMFTQKMNEVQKHATVSNHGYLGY AVIVNKQFWDG
LPADVRTGLEKMAESTDYANGIAKEENEKALQAMKDAGTTEFHELTAEE
RAAWEEVLTVPVHDEMAERIGAETIAAVKAATAE
> P0A402|PSAF_SYNEN Photosystem I reaction center subunit III -
Synechococcus elongatus naegeli.
MRRFLALLLVLTWLWLGFTPLASADVAGLVPCKDSPAQKRAAAAVNTTAD
PASGQKRFERY SQALCGEDGLPHLVVDGRLSRAGDFLIPSVLFLYIAGWI
GWVGRAYLIAVRNSGEANEKEIIVDPLAIKCLMTGFAWPLAALKELASG
ELTAKDNEITVSPR
> 26KD_HELPY P21762 26 KD ANTIGEN. - *HELICOBACTER PYLORI* (CAM
MLVTKLAPDFKAPAVLGNNEVDEHFELSKNLGKNGAILFFWPKDFTFVCP
TEIIAFDKRVKDFQEKGFNVIGVSIIDSEQVHFVAKNT PVEKGGIGQVTFP
MVADITKSISRDYDVLFEAAIALRGAFLIDKNMKVRHAVINDLPLGRNAD
EMLRMVDALLHFEEHGEVCPAGWRKGDGKMKATHQGVAEYLKENSIKL
> P42454|RURE_ACIAD Rubredoxin -NAD(+) reductase - *Acinetobacter* sp. (strain
ADP1).
MHPIVIIGSGMAGYTLAREFRKLNPEHELVMICADDAVNYAKPTLSNALS
GNKAPEQI PLGDAEKMSTQLKLQILSETWVKAINPETHELKLEKNGQETI
QPYSKLVAVGANPTRLAIAGDGSDDIHVVNSLIDYRAFRENLAQRQDKR
VVILGAGLIGCEFANDLQHTGHQVTVIDLSRPLGRLLPAHIADAFQKNL
EESGIHFVLSTTVEKVSINDGQDYAVTLANGQTLVADIVLSAIGLQPNI
DLAKHAGVHTSRGILTNSLLETNLEDIYAIGDCAEVNGTLLPYVMPIMQQ
ARALAKTLSGETTHVHY PAMPVAVKTPAAPLTVLPVPVDVDVNWETEFE
DGMLAKAIDNTDLRGFVLLGATAGQRLTLTKLVPDLIPAQL
> P17543|PAPJ_ECOLI Protein papJ - *Escherichia coli*.
MVVNKTTAVLYLIALSLSGFIHTFLRAEERGIYDDVFTADALRHYRINER
GGRTGSLTCSGALLSSPCTLVSNEVPLSLRPENHSAAGAPLMLRLAGCG
DGGALQPGKRGVAMT VSGSLVTGPGSGSALLPDRKLSGCDHLVIHDGDTF
LLCRPDRRQEEMLAARWRKRATQEGEYSDARSNPAMLRLSIKYE
> P31133|POTF_ECOLI Putrescine-binding periplasmic protein - *Escherichia*
coli.
MTALNKKWLSGLVAGALMAVSVGTLAAEQKTLHIYNWSDYIAPDTVANFE
KETGIKVVYDVFDSNEVLEGLMAGSTGFDLVVPSASFLEQLTAG VFQP
LDKSKLPEWKNLDPELLKLVAKHDPDNKFAMPYMWATTGIGYNVDKVKAV
LGENAPVDSWDLILKPENLEKLKSCGVSFLDAPEEVFATVNLNLGKDPNS
TKADDYTG PATDLLLKRPNIRYFHSSQYINDLANGDICAIGWAGDVWQ
ASNRAKEAKNGVNSFSIPKEGAMAFFDVVFAMPADAKNKDEAYQFLNYLL
RPDVVAHISDHVFYANANKAATPLVSAEVRENPGIYPPADVRAKLFT LKV
QDPKIDRVRTRAWTKVKSJK
> P33012|GYRI_ECOLI DNA gyrase inhibitory protein - *Escherichia coli*.
MNYEIKQEEKRTVAGFHLVGPWEQTVKKGFEQLMMWVDSKNIVPKEWVAV
YYDNPDETPAEKLRCDTVVTVPGYFTLPENSEGVILTEITGGQYAVAVAR
VVGDDFAKPWYQFNSLLQDSAYEMLPKPCFEVYLNNGAEDGYWDIEMYV
AVQPKHH

> P09403|PGK_THET8 Phosphoglycerate kinase - *Thermus thermophilus* (strain HB8 / ATCC 27634 / DSM 579).

MRTLLDLDPKGKRVLRVDYNVPVQDGKVDQDETRILESPLTRHLLAGGA
SLVLLSHLGRPKGPDPKYSLAPVGEALRAHLPEARFAPFPFPGSEEARREA
EALRPGEVLLLENVRFEPGEEKNDPELSARYARLGEAFVLDAFGSAHRAH
ASVVGVARLLPAYAGFLMEKEVRALSRLKDPERPYAVVLGGAKVSDKIG
VIESLLPRIDRLIIGGAMAFTFLKALGGEVGRSLVEEDRDLAKDLLGRA
EALGVRVYLPEDVVAERIEAGVETRVFPARAIPVPYMGDLIGPKTREF
ARALEGARTVFWNGPMGVFEVPPFDEGTLAVGQAIAALEGAFTVVGGGDS
VAAVNRLGLKERFGHVSTGGGASLEFLEKGTLPGLEVLEG

> DEOC_ECOLI P00882 DEOXYRIBOSE -PHOSPHATE ALDOLASE (EC 4.1.2.

MTDLKASSLRALKMLDLTTLNDDDTDEKVIALLCHQAKTPVGNTAAICIIYP
RFIPIARKTLKEQGTPEIRIATVTNFPHGNDIDIALAETRAAIAYGADE
VDVVPYRALMAGNEQVGFDLVKACKEACAAANVLLKVI IETGELKDEAL
IRKASEISIKAGADFIKTSTGKAVNATPESARIMMEVIRDMGVEKTVGF
KPAAGVRTAEDAQKYLAIADELFGADWADARHYRFGASSLLASLLKALGH
GDGKSASSY

> P44322|IF1_HAEIN Translation initiation factor IF -1 - *Haemophilus influenzae*.

MAKEDCIEMQGTILETLPNTMFRVELENGHVVTAHISGKMRKNYIRILTG
DKVTVEMTPYDLSKGRIFRSR

> P0A9P4|TRXB_ECOLI Thioredoxin reductase - *Escherichia coli*.

MGTTKHSKLLILGSGPAGYTAAVYAARANLQPVLITGMEKGGQLTTTTEV
ENWPGDPNDLTGPLLMERMHEHATKFETEIIFDHINKVDLQNRPFRLNGD
NGEYTCDALIIATGASARYLGLPSEEAFFKGRGVSACATCDGFFYRNQKVA
VIGGGNTAVEEALYLSNIASEVHLIHRRDGFRAEKILIKRLMDKVENGNI
ILHTNRTLEEVTGDQMGVTVGRLRDTQNSDNI ES LDVAGLFVAIGHSPNT
AIFEGQLELENGYIKVQSGIHGNATQTSIPGVFAAGDVMHDIYRQAITS
GTGMAALDAERYLDGLADAK

> LPSZ_RHIME P31858 LIPOPOLYSACCHARIDE PROCESSING PROTEIN LPS

MKNVGIKKAALQMSRYVLASKQVQRALKLLGLPASRANEVSGIPKPADTS
LSFPGYEAFAALHGEAWQAAGEQKPIILMFGVHPWKRDLARYFSDFRVAY
VRTNTSWTKVQTSFCQFTPQAFVFWGMTEIRAAKNYAIAKSSIPLWRVEDG
FLRSVGLGAQHVLPLSLAVDTTGIYFDPSRPSTLETLISEIGVTENATLI
ERARRCMSMISAFGLSKYNGVDVPLKRLPPSDRRRVLVVGGVEDDASIV
MGCAARYTNNDIVRITQKENPEAEVIYRPHDPVLGGHRKEFSNPRDVANI
CTILSGDYDLGSLDSDVDHVYTITSLLGFEALIRKKVTVFGAPFYSGWG
LTDDRQPTPRRTRKPSLDELFAAAYILYPRYCVGSLGSSAEIEHAIMSLA
LEKNGVPRELAEGVSSALPAEAINVDCVSQTLEGLKSIPS

> P74936|PROB_TREPA Glutamate 5 -kinase - *Treponema pallidum*.

MIRALFAAAKIVIKIGSNTLAQADGTPDEEFLAECARACAALMRDGKQI
VVVSSGAQVAGISALHCLSSPPQGAGLERHESRGPVPGDGASCKQALCAV
GQAEILSRWRSFAAAHQCVGQFLCTKEDFTDSDRAAQVRYTSLFLLERR
VVPILNENDALCCSDVPSVPADRRVSLSPQKRIGDNDLSAFVALLWQAD
LLLLLSDIDGVYDKDKAHTDAQHVPLVTDVSALVGKTSMGSSNVFGTGG
IATKLDAAARLVTRAGIPLVLANGRHLDPILSLMRGDARGTLFVFPVS

> P17266|OMPW_VIBCH Outer membrane protein W - *Vibrio cholerae*.

MKQTCIGLAVLAALSAPVFAHQEGDFIVRAGIASVVPNDSSDKVLNTQS
ELAVNSNTQLGLTLGYMFTDNISFEVLAATPFSHKISTSGGELGSLGDIG
ETKHLPPFTFMVQYFGEANSTFRPYVGAGLNYTTFFDESFNGTGTNAGLS
DLKLDSDWGLAANVGFYMLNDSWFLNASVWYANIETTATYKAGADAKST
DVEINPWVFMIAAGGYKF

> P0A3T3|BCSP_BRUAB 31 kDa immunogenic protein - *Brucella abortus*.

MKFGSKIRRLAVAAVAGAIALGASFAVAQAPTFFRIGTGGTAGTYYPPIGG
LIANAISGAGEKGPVGLVATAVSSNGSVANINAIKSGALESFTQSDVAY
WAYNGTPLYDGKGVEDLRLLATLYPETIHIVARKDANIKSVADLKGKRV
SLDEPGSGTIVDARIVLEAYGLTEDDIKAEHLKPGPAGERLKDGDALDAYF
FVGGYPTGAISELAISNGISLVPISGPEADKILEKYSFFSKDVVPAGAYK
DVAETPTLAVAAQWVTSKQPDDLIYNITKVLWNEDTRKALDAGHAKGKL
IKLDSATSSSLGIPLHPGAERFYEAGVLK

> Q03155|AIDA_ECOLI Adhesin AIDA -I - *Escherichia coli*.

MNKAYSIIWSHSRQAWIVASELARGHGFVLAKNTLLVLAVVSTIGNAFV
NISGTVSSGGTVSSGETQIVYSGRGNSTV NSGGTQIVNNGGKTTATTV

NSSGSQNVGTSGATISTIVNSGGIQRVSSGGVASATNLSGGAQNIYNLGH
ASNTVIFSGGNQTIFFSGGITDSTNISSGGQQRVSSGGVASNTTINSSGAQ
NILSEEGAISTHISSGGNQYISAGANATETIVNSGGFQRVNSGAVATGTV
LSGGTQNVSSGSAISTSVYNSGVQTVFAGATVTDTTVNSGGNQNISSGG
IVSETTVNVSGTQNIYSSGGSALSANIKGSQIV NSEGTAINTLVSDGGYQH
IRNGGIASGTIVNQSGYVNISSGGYAESTIINSGGTLRVLSDDGYARGTIL
NNSGRENVNSGGVSYNAMINTGGNQYIYSDGEATAAIVNTSGFQRINSSG
TAPVQNSVVTTRTVSSAAKPFDAEVYSGGKQTVYLRGIWYSNFLTAVWS
MFPGTASGANVNLGRNLNAFAGNVVGTILNQEGRQYVYSGATATSTVGNN
EGREYVLSGGITDGTVLNSGGLQAVSSGGKASA TVINEGGAQFVYDGGQV
TGTNIKNGGTLIRVDSGASALNIALSSGGNLTSTGATLPELTTMAALSVS
QNHASNIIVLENGLLRVTSGGTATDTTVNSAGRLRIDDDGTINGTTTINA
DGIVAGTNIQNQDNFILNLAENYDFEELSGSGVLVKDNTGIMTYAGTLL
QAQGVNVKNGGIIFDSAVVNADMAVNQAYINISDQATINGSVNNNGSIV
INNSIINGNITNDADLSFGTAKLLSATVNGSLVN NKNIIILNPTKESAGNT
LTVSNYTGTPGSVISLGGVLEGDNSLTDRLVVKGNTSGQSDIVYVNEGDS
GGQTRDGINIISVEGNSDAEFLSKNRVAVAGAYDYTLQKGNESGTDNKGWY
LTSHLPTSDTRQYREPENGSYATNMALANSFLMLDLNERKQFRAMSDNTQP
ESASVWMKITGGISSGKLNQKNTTQFINQLGGDIYKFHAEQLGDFT
LGIMGGYANAKGKTINYTSNKAARNTLDGYSVGVY GTWYQNGENATGLFA
ETWMQYNWFNASVKGDLGEEKYNLNLGLTASAGGGYNLNVHTWTSPEGIT
GEFWLQPHLQAVWVGTPDTHQEDNGTVVQAGKNNIQTAKGIRASWKVK
STLDKDTGRRFRPYIEANWIHNTHFVGVKMSDDSQLLSGRNQGEIKTGI
EGVITQNLVNGGVAYQAGGHGSNAISGALGIKYSF

> P30860|ARTJ_ECOLI Arginine-binding periplasmic protein 2 - *Escherichia coli*.

MKKLVLAALLASFTFGASAAEKINFGVSATYPPFESIGANNEIVGFDIDL
AKALCKQMVAECTFTNHAFDLSLIPSLKFRKYDAVISGMDITPERSKQVSF
TTPYYNSQAVHIAKDKTYKTFADLKGKRIGMENGTHQKYIQDQHPEVKT
VSYDSYQNAFIDLKNGRIDGVFGDTAVVNEWLKTNPQLGVATEKVTDPQY
FGTGLGIAVRPDNKALLEKLNNAAIKADGTYQKISDQWFPQ

> P23537|PTHP_RALEH Phosphocarrier protein HPr - *Ralstonia eutropha* (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (*Cupriavidus necator* (strain ATCC 17699 / H16 / DSM 428 / Stanier 337)).

MLQRDTHIINKLGLHARASAKLTQLAGNFVSQVKMSRNGRQVDA KSIMGV
MMLAAGIGSTVLTETDGPDEQEAMDALLALIANRFGEGE

> P14899|AMY3_DICTH Alpha-amylase 3 - *Dictyoglomus thermophilum*.

MKIKFFIKRTLIFIFILVTFITYIHGYNEPWWYKNAIFYEVFVRSFADSDG
DRVGDNLNGLIDKLDYFKNLNITALWLMPIFSPSVSYHGVDYDYDIHPGY
GTMEDFENLIRKAHEKNIKIILDLVNHTSSRHPWFVSSASS YNSPYRDI
YIWSTEKPEKNSNLWYKKTGYYYALFWSEMPDLNFDNPKVREEVKKIAK
FWIEKVDGFRDLAAKHIDDDSKNIQWWKEFYSLKSIKPDVYLVGEVW
DNEYKIAEYKGLPSNFNPLSDKIMNSSSKSKRLRNYRISRLKRLFGEN
NTDFADAIFLRNHDQVRVTRFFGGSIDKSIILAGSIYLTLAGNTFIYYGEE
IGMEGSKPDEYIREPFKWTDDMKSQYTYWIIIPRYNLPNGIA LDTEEKD
PNSIYNHYKLLERVKCRALNSNGKIERIKTQDRSILAYKLELEDEKIMV
VHNLNRIENTFNFNEIKEKDILYIRNAKTEKNKIILGPYSTVIVKIP

> P31522|PSAA_YERPE pH 6 antigen - *Yersinia pestis*.

MKMKCFAKNALAVTTLMIAACGMANASTVINSKDVSGEVTVKQGNFTFHVD
FAPNTGEIFAGKQPGDVTMTFTLTMGDTAPHGGWRLIPTGDSKGGY MISAD
GDYVGLYSYMSWVGIDNNWYINDDSPKDIKDHLYVKAGTVLKPPTYKFT
GRVEEYVF

> P13415|OMPA1_NEIMC Major outer membrane protein P.IA - *Neisseria meningitidis* serogroup C.

MRKKLTALVLSALPLAAVADVSLYGEIKAGVEGRNIQAQLTEQPQVTNGV
QGNQVKVTKAKSRIRTKISDFGSFIGFSGEDLGEGLKAVWQLEQD VSVA
GGGASQWGNRESFTGLAGEFGTLRAGRANQFDDASQAINPWDSNNDVAS
QLGIFKRHDDMPVSVRYDSPEFSGFSGSVQFVPAQNSKSAYKPAYYTKDT
NNNLTLVPAVVGKPGSDVYYAGLNYKNGGFAGNYAFKYARHANVGRNAFE
LFLIGSATSDEAKGTDPLKNHQVHRLTGGYEEGGLNLALAAQLDLENGD
KAKTKNSTTEIAATASYRFGNAVPRISYAHGFDLIERGKKGENTSYD QII
AGVDYDFSKRTSAIVSGAWLKRNTGIGNYQINAASVGLRHKF

> P26602|UBIC_ECOLI Chorismate--pyruvate lyase - *Escherichia coli*.

MSHPALTQLRALRYCKEIPALDQPQLLDWLLLEDSMTKRFEQQGKTVSVTM
IREGFVEQNEIPEELPLLPKESRYWLREILLCADGEPWLAGRTVVPVSTL
SGPELALQKLGKTPLRGRLFTSSSTLTRDFIEIGRDAGLW GRRSRLRLSGK
PLLLTELFLPASPLY

> P08704|CDGT_KLEOX Cyclomalto-dextrin glucanotransferase - *Klebsiella oxytoca*.

MKRNRFNNTSAAIAISIALNTFFCSMQTIAAEPEETYLDFRKETIYFLFL
DRFSDGDPSNAGFNSATYDPNNLKKYTGDDLRLINKLPYLKSLGVTSI
WITPPIDNVNNTDAAGNTGYHGYWGRDYFRIDEHFGLNDDFKELTSL MHS
PDYNMKLVLDYAPNHSNANDENEFALYRDGVFITDYPTNVAANTGWYHH
NGGVTNWNDFQVKNHNLFNLSDLNQSNTDVIYQYLLDGSKFWIDAGVDI
RIDAIKHMDKSFQKWTSDIYDYSKISIGREGFFFFGEWFGASANTTTGVD
GNAIDYANTSGSALLDFGFRDTLERVLVGRSGNTMKTLSYLIKRTVFT
SDDWQVVFMDNHDMARIGTALRSNATTFGPGNNETGGSQSEAFQKRI DL
GLVATMTVRGIPAIYYGTEHYAANFTSNSFGQVSDPYNREKMPGFDTES
EAFSIIKTLGLDRKSSPAIQNGTYTELWVNDLILVFERRSGNDIVIVALN
RGEANTINVKNIAVPNGVYPSLIGNNSVSVANKRTTLTLMQNEAVIRSQ
SDDAENPTVQSINFTCNNGYTISGQSVYIIGNIPQLGGWDLTKAVKISPT
QYPQWSASLELPSDLNVEWKCVKRNETNPTANVEWQSGANNQFNNDTQ T
TNGSF

> P43817|SYD_HAEIN Aspartyl-tRNA synthetase - *Haemophilus influenzae*.

MMRTHYCGALNRNINIGQDVTLSGWVHRRRDLGGLIFIDMRDRDGIVQVCF
DPKYQDALTAAGLRNEFCIQIKGEVIARPDNQINKMATGEVEVLAKEL
RIYNASDVLPLDFNQNTTEEQRKLYRYLDLRRPEMAQRLKTRAKITSFVR
RFMDDNGFLDIETPMLTKATPEGAR DYLVPSRVHKGKFYALPQSPQLFKQ
LLMMSGFDRYYQIVKCFRDEDLRADRQPEFTQIDVETSFLTAPREIME
RMVHGLWLDITIGVDLKGKFPVMTWQEAAMRRFGSDKPDLRNPLEMVDVADIV
KDVEFKVFNPNPNNGRVAIVRPNAGAEITRKQIDEYTFVGIYGAAGL
AWAKVNDINAGLEGVQSPIAKFLNEDVWKGLAERVNAQTGDIFFGADKW
QTTTDMAMRRLKLRDLGLTRLDEW QPLWVIDFPMFERDEEGNLAAMHH
PFTSPKDFSPQEADPTSAVANAYDMVINGYEVGGGVRIFDPKMQQTV
FRILGIDEEQREKFGFLLDALKFGTTPHAGLAFGLDRLTMLLTGTENIR
DVIAFPKTTAAACLMTEAPSFANPQALEELAISVVKAE

> P00120|CY553_DESVM Cytochrome c -553 - *Desulfovibrio vulgaris* (strain Miyazaki).

MKRILVVMISICAAALAFGVSAAMAADGAALYKSCVGCAGDGSQAMGVGH
AVKGQKADELFKKLGKYGADGSYGGEEKAVMTNLVKRYSDEEMKAMADYMS
KL

> P23608|PHBC_RALEH Poly-beta-hydroxybutyrate polymerase - *Ralstonia eutropha* (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (*Cupriavidus necator* (strain ATCC 17699 / H16 / DSM 428 / Stanier 337)).

MATGKGAASSTQEGKSQPFKVTGPFDPATWLEWSRQWQTEGNGHAAAS
GIPGLDALAGVKIAPAQLGDIQQRVMKDFSSALWQAMAEGKAEATGPLHDR
RFAGDAWRNTNLPYRFAAFYLLNARALTELADAVEADAKTRQIRIFAISQ
WVDAMSPANFLATNPEAQRLLIESGGESLRAGVRNMMEDLTRGKISQDE
SAFEVGRNVAVTEGAVVFENEYFQLLQYKPLTDKVHARPLLMVPPCINKY
YILDLQPESSLRHVVEQGHTVFLVSWRNPDASMAGSTWDDYIEHAAIRA
IEVARDISGQDKINVLGFCVGGTIVSTALAVLAARGEHPAASVTLTLL
DFADTGILDVDFVEGHVQLREATLGGGAGAPCALLRGLLANTFSFLRPN
DLVWNYVVDNYLKGNTVPPFDLLFWNGDATNLPGPWCYLRHTYLNEL
KVPGLTVCGV PVDLASIDVPTYIYGSREDHIVPWTAAAYASTALLANKLR
FVLGASGHIAGVINPPAKNKRSHWTNDALPESPQQWLAGAIEHHGSWWPD
WTAWLAGQAGAKRAAPANYGNARYRAIEPAPGRYVKA

> P43830|SYP_HAEIN Prolyl-tRNA synthetase - *Haemophilus influenzae*.

MRTSQYLFSTLKETPNDAQVVSQMLRAGMIRPMASGLYNWLPTGIRVL
KKVEKVVREEMNKGAIEVLMPPVQPAELWEESSGRWDQYGPPELLRFEDRG
NRNFVLGPTHEEVI TDLVRREVSSYKQLPLNLYQIQTKFRDEVPRFGVM
RSREFIMKDAYSFHTTQESLQATYDVMYQVYSNIFNRLGLDFRAVQADTG
SIGGSASHEFQVLASSGEDDVVSTESDFAANIELAEIAI GERQAPTAE
MCLVDTPNAKTIAELVEQFNLPKIEKTVKTLIVKGADENQPLVALIIRGDH
ELNEIKAQKHPLVADPLEFADETEIKAKIGSGVSLGAVNLNI PAIIDRT
VALMSDFSCGANIDGKHVFNVNWERDVAIPKVFDLRNVVEGDPSPDGKGT
LQIKRGIEVGHIFQLGKKYSEAMKATVQGEDGKPLVMTMGCYIGVTRVV

ASAIEQHHDERGIIWPSDEIAPFTVAIVPMNMHKSEAVQKYAEELYRTLQ
SQGVDFIFDDRKERPGVMFADMELIGVPHMVVIGEKNLDNGEIEYKNRRT
GEKEMISKDKLLSVLNEKLGNL

> HOXF_ALCEU_P22317_NAD-REDUCING_HYDROGENASE_HOXS_ALPHA_SUBUN
MDSRITITILERYRSDRTRLIDILWDVQHEYGHIPDAVLPQLGAGLKLSP
DIRETASFYHFFLDKPSGKYRIYLCNSVIKINGYQAVREALERETGIRF
GETDPNGMFLFDTPCIGLSDQEPAMLIDKVVFTLRPGKITDIIAQLKQ
GRSPAELIANPAGLPSQDIAYVDAMVE_SNRVTKGPVFFRGRDRLRSLLDQC
LLLKPEQVIETIVDSRLRGRGGAGFSTGLKWRLCRDAESEQKYVICNADE
GEPGTFKDRVLLTRAPKKVFGVMVIAAYAIGCRKGIVYLRGEYFYLKDY
ERQLQELREDGLLGRAIGGRAGDFDIRIQMGAGAYICGDESALIESCEG
KRGTPRVKPPFPVQQGYLGKPTSVNNVETFAAVSRIMEEGADWFRAMGTP
DSAGTRLLSVAGDCSKPGIYEVEWGVTLNEVLAMVGARDARAVQISGSPG
ECVSVAKDGERKLAYEDLSCNGAFTIFNCKRDLEIVRDHMQFFVEESCG
ICVPCRAGNVDLHRKVEWVIAGKACQKDLDDMVSWGALVRRTSRCGLGAT
SPKPILTTLEKFPEIYQNKLVREHGPLLPSPFDLDTALGGYEKALKDLEEV
TR

> P50205|PHBB_RHIME_Acetoacetyl-CoA_reductase - Rhizobium_meliloti
(Sinorhizobium_meliloti).

MSRVALVTGGSRGIGAAICVALKAAGYKVAANYAGNDERAKAFEQESGIP
VYKWDVSSYQACVDGIARVEADLGPVDILVNNAGITRDAMFHKMTPEQWG
EVIGTNLTGVFNMTHTPLWSGMRDRGFGRIVNISSINGQKGMQVNYSA
KAGDLGLTKALAQEGAAGKITVNAICPGYIGTEMVRVPEKVLNERIIPQ
IPVGRLGPEEVARCVVFLASDDAGFITGSTISAN_GGQYFA

> P62593|BLAT_ECOLI_Beta-lactamase_TEM - Escherichia_coli.

MSIQHFRVALIPFFAAFLPVPFAHPETLVKVKDAEDQLGARVGYIELDLN
SGKILESFRPEERFPMSTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDL
VEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTITGGPKELTAF
HNMGDHLVTRLDREWFELNEAIPNDERDTPMPAAMATT_LRKLLTGELTLA
SRQQQLDWMEDKLVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPD
GKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKHW

> P52977|LON_CAUCR_ATP-dependent_protease_La - Caulobacter_crescentus
(Caulobacter_vibrioides).

MSELRTLPVPLRDIIVFPVPHMVVPLFVGRDKSVRALEEVMRGDKQILLVT
QKNSADDDPAPGDI FEVGVLATVQLLKLDPDGTVKVLEVEGKARA AVVSFT
DQESYEEAQIGEVESEDDGAGPEAEALSRAVVEQFENYVKNKKVPPEALA
SIPQIAEPGKLADSI AAHL SVKIGDKQNLEIFDVVKRLEKVFALMEGEI
SVLQVEKKIRSVRKRQMEKTQREYYLNEQMKAIQRELGDPPDARDELIDL
EKRIKTKLSKEARTKAESELKLRNMSPSAESTVVRNYLDWLLSIPWG
KAKTKKIDLVESEGILDADHYGLEKVKERILEYLAVQARTNSLKGPI LCL
VGPPGVGKTSLGKSIKATGREFVRMSLGGVRDEAEIRGHRRTYIGSMPG
KVVSQMKKAKTTNAFVLLDEIDKMGSDYRGDPASALLEVLDPSONSTFGD
HYLEVVDYDLSQVMFVTTANSLNMPQPLDRMEIIRIPGYTEDEKLEIAKR
HILPKLAKDHGLKPAEFIVPDKAIRDLIRYYTREAGVRSLEREL GALARK
TVRDLAREKVASITIDDERLAKYAGVKYRYGETDEVQVGI V TGLAWTE
FGGDILTIEAVKMPGKGRMQITGNLKDVMKESIAAANSYVRSRALQFGIK
PPVFEKTDVHIHVPD GATPKDGPSAGIAMALAMVSVLTGPIRKDIAMTG
EITLRGRVTAIGGLKEKLLAALRSVKT V LIPQENEKDLADVPQTVKDGL
EII PVSTVDEV LKHALTGPLTPVEWNEAEEPITTSAKKDDGSDAMLTH

> P37918|TSAT_RICTS_56_kDa_type-specific_antigen - Rickettsia_tsutsugamushi.

MKKIMLIASAMSALS L PFSASAIELGDEGGLECGPYAKGVVGGMITGVE
STRLDPADAGGKQLPLTTSMPFGGTLAAGMTIAPGFRAELGVMYLANVK
AEVESGKTGSDADIRSGADSPMPQRYKLT P P Q P T I M P I S I A D R D L G V D I P
NVPQGGANHLGDNLGANDIRRADDRITWLKNYAGVDY MVPDPNNPQARIV
NPVLLNIPQPPNANPRQAMQPCSILNHDHWRHLVVGITAMSNANKPSVS
PIKVLSEKIVQIYRDVKNPFARVAGIEVPSDPLPNSASVEQIQNKMQELND
ILDEIRDSFDGICIGNAFANQIQLNFRIPQAQQQQGQQQQQAQATAQEA
AAAAAVRVLNNNDQIIKLYKDLV L K R H A G I K K A M E E L A A Q D G G C N G G G D
NKKKRGASEDS DAGGASKGKGKTKETEFDL SMIVGQ VKLYADLFTTES
FSIYAGLGAGLAYTSGKIDGVDIKANTGMVASGALGVAINAAEGVYVDIE
GSYMHSFSKIEEKYSINPLMASFGVRYNF

> P0A2D5|CHEY_SALTY_Chemotaxis_protein_cheY - Salmonella_typhimurium.
MADKELKFLVDDFSTMRIVRNLKELGFNNVEEAEDGVDALNKLQAGG

FGFIISDWNMPNMDGLELLKTIIRADSAMSALPVLMTAEAK KENIIAAAQ
AGASGYVVKPFTAATLEEKLNKIFEKLG

> P69441|KAD_ECOLI Adenylate kinase - *Escherichia coli*.

MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDMRLRAAVKSGSELGKQAK
DIMDAGKLVTDDELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAG
INVDYVLEFDVPELIVDRIVGRRVHAPSGRVYHVKNPPKVEGKDDVTG
EELTTRKDDQEETVRKRLVEYHQMTAPLIGYYSKEAEAGNTKYAKVDGTR
PVAEVRADLEKILG

> P44312|G6PI_HAEIN Glucose -6-phosphate isomerase - *Haemophilus influenzae*.

MKNINPHTHAWKSLEAHKAELSNITIQDLFKQEKNRFFDDYSLTFNNQIL
IDFSKNNINQTTLSHLRQLAQECALDSAKEAMFTGKINRTENRAVLHTA
LRNRTNTPVLDVGKDVMP E VNAVLA KMKDFCQRIISGEWKGYTGKAITDV
VNIGIGSDLGPMVTEALRPYKNHLMHFVSNVDGTHIAETLKKVNPET
TLFLVASKTFTTQETMTNAQSARDWLLKAAKDES AVAKHFAALSTNAKDV
EKFGIDTNNMF EFWDWVGGRYSLWSAIGLSIALSIGFENFEALLNGAHEM
DKHFLSTPIEQNIPTTLALVGLWNTNFLGAQTEAILPYDQYLHRFAAYFQ
QGNMESNGKYVDRDGNVIKN YQTGPIIWGEPGTNGQHAFYQLIHQGTTLI
PCDFIAPAQRHNPLADHNNKLLSNFFAQTEALAFGKTKEEVEAEFVKAGK
SLDDVKNIVPFKVFETGNKPTNSILVQKITPFTL GALI AMYEHKIFVQGVI
FNIFSFDQWGVELGKQLANRILPELTDSEK VASHDSSTNGLINQFKAWR

> P02924|ARAF_ECOLI L-arabinose-binding periplasmic protein - *Escherichia coli*.

MHKFTKALAAIGLAAVMSQSAMAENLKLGLFLVKQPEEPWFQTEWKFADKA
GKDLGFEVIAKIAVPDGEKTLNAIDSLAASGAKGFVICTPDPKLGSAIVAK
ARGYDMKVI AVDDQFVNAK GKPM DTVPLVMM AATKIGERQGOELYKEMQK
RGWDVKESAVMAITANELDTARRRTTGSM DALKAAGFPEKQIYQVPTKSN
DIPGAFDAANSMLVQHPEVKHWLIVGMNDSTVLGGVRATEGQGFK AADII
GIGINGVDAVSELSKAQATGFYGSLLPSPDVHGYKSSEM LYNVWAKDVEP
PKFTEVTDVVLITRDNFKEELEKKGGLGK

> P09169|OMPT_ECOLI Protease 7 - *Escherichia coli*.

MRAKLLGIVLTTPIAISSFASTETLSFTPDNINADISLGLTSGKTKERVY
LAEEGGRKVSQLDWKFNNAAIKGA INWDLMPQISIGAGWTTLGSRRGN
MVDQDWMDSNPGTWT DESRHPDTQLNYAN EFDLNIKGWLLNEPNYRLGL
MAGYQESRYSFTARGGSYIYSSEEGFRDDIGSFNGERAIGYKQRFKMPY
IGLTGSYRYEDFELGGTFKYSGWVESDNDEHYDPGKRIT YRSKVKDQNY
YSVAVNAGYVTPNAKVYVEGAWNRVTNKKGNTSLYDHNNTSDYSKNGA
GIENYNFITTAGLKYTF

> P44420|TYSY_HAEIN Thymidylate synthase - *Haemophilus influenzae*.

MKQYLELCRRIVSEGEVWVANERTGKHCLTVINADLEYDVANNQFPLITTR
KSYWKA AIAEFLGYIRGYDNAADFRALGKTWDANANENAAWLANPHRRG
VDDMGRVYGVQGRWRKPNGETIDQLRKIVNNLTGKIDDRGEILTFNPG
EFDLGLRPCMHTHTFSLVGD TLHLTSYQRS CDVPLGLNFNQIQVFTFLA
LMAQITGKKAGKAYHKIVNAHIYEDQLELMRDVQL KREPFPLPKLEINPD
IKTLEDLETWVTMDDFKVVGYSHEPIKYPFSV

> RFFE_ECOLI P27828 UDP -N-ACETYLGLUCOSAMINE 2 -EPIMERASE (EC 5

MKVLTVFGRPEAIKMAPLVHALAKDPFEAKVCVTAQHREMLDQVLKLF
SIVPDYDLNIMQPGQLTEITCRILEGLKPILAEFKPDVVLVHGDTTTL
ATSLAAFYQRI PVGHVEAGLRTGDLYSPWPEEANRTLTGHLA MYHFSPT E
TSRQNLLENVADSRIFITGNTVIDALLWVRDQVMSSDKLRSELAANYPF
IDPDKMILVTGHRRESFGRGFEEICHALADIATTHQDIQIVYPVHLNPN
VREPVNRI LGHVKNVILIDPQEYLPFVWLMNHAWLILTDSGGIQEEAPSL
GKPVLMRDTTEREAVTAGTVRLVGTDKQRIVEEVTRLLKDENEYQAMS
RAHNYPGDGQACSRILEALKNNRISL

> P19843|NOSD_PEST Copper-binding periplasmic protein - *Pseudomonas stutzeri* (*Pseudomonas perfectomarina*).

MFKAQATFSRYSAAVSLLLLFSGAAQAPQSITTLPLQPDGENRWRLPAG
EYQGQFTIEQPMQLRCEPGAVIQSQGSSLLISAPDVLVEGCTLYEWGS
DLTAMDSAVFILPAAERAQISNNRM RGPFGV FVDGTRDVQVIGNEIDGD
AGVRSQDRGNG IHLFAVSGARVLHNVHVRNARDGIYIDTSNGNHLEGNVIE
DVRYG VHYMFANENSLIDNVTRRTRTGYALMQSRKLTVTGNRSEQDQNYG
ILMNYITYSTITGNFVSDVQRGDTGGDSMISGGEGKALFIYNSLFNTIEN
NHFEEKSSLGIIHLTAGSEDNRISGNAFVGNQQQVKYVASRTQEWSVDGRGN
YWSDYLGWDRNNDGLGDIAYEPNDNVDRLLWLYPQVRLMNSPSIEVLRW

VQRAFPVIKSPGVQDSHPLMKLPTEKLLTEKQEPTS

> P20713|ATSA_KLEAE Arylsulfatase - *Klebsiella aerogenes*.

MNKKAMAAVSMILAGGAHAAQQERPNVIVI IADDMGYSDISPFGEIPT
PNLQAMAEQGMRSQYYS PMSAPARSMLLTGNSNQAGMGMWYDSTI
GKEGYELRLTDRVTTMAERFKDAGYNTLMAGKWHLGFVPGATPKDRGFNH
AFAFMGGGTSHFNDAIPLGT VEAFTYYTRDGERVSLPDDFYSSEAYARQ
MNSWIKATPKEQPVFAWLAFTAPHDPLQAPDEWIKRFRKQYEQGYAEVYR
QRIARLKALGI IHDDTPLPHLELDKEWEALTPEQQKYTAKVMQVYAAMIA
NMDAQIGTLMETLKQTGRDKNTLLVFLTDNGANPAQGFYESTPEFWKQF
DNSYDNVGRKGSFVSYPHWANVSNAPYANYHKTTSAQGGINTDFMISGP
GITRHKIDASTMAVYDVAPT LYEFAGIDPNKSLAKKPVLP MIGVLSAI
SPAKYRSRRAELRG

> P43819|SYFA_HAEIN Phenylalanyl -tRNA synthetase alpha chain - *Haemophilus influenzae*.

MQHLNELVEKAKLAIESIQDKSLTALDEIRVEYFGKKGHFTQLMQELRNV
SAEERPAMGAKINEAKQAALFLNAKKTWEQAELENSKLEKERVVSLPG
RKVETGGLHPVMTINRVTKFF SELGFSVENGEPIESDYNF DALNIPKH
HPARADHDTFWFNPPELLLRQTQSGVQIRTMEKMQPPIRIMAPGRVYRNDY
DQTHTPMFHQIELLYVDKKNFTELKGLLHDFLRAFFEDLQVRFPSYF
PFTEPSAEVDVMGKNGKWLLEVLGCGMVHPNVLNRVGDIPNEYSGFAVGMG
VERLTMRLRYNVTDLRSFFENDLRFLKQFK

> O05542|DHET_GLUOX Alcohol dehydrogenase [a cceptor] - *Gluconobacter oxydans* (*Gluconobacter suboxydans*).

MTSGLLTPIKVTKRLLSCAAALAFSAAVPVAFQAEDTGTAITSSDNGGH
PGDWLSYGRSYSEQRYSPLDQINTENVGKLLKLAWHYDLDTNRGQEGTPLI
VNGVMYATTNWSKMKALDAATGKLLWSYDPKVPGNIA DRGCCDTVSRGAA
YWNGKVYFGTFDGRILALDAKTGKLVSVYTIKPEAQLGHQR SYTVDGAP
RIAKGKVLIGNGGAEFGARGFVSAFDAETGKLDWRFFTVPNPENKPDGAA
SDDILMSKAYPTWNGKNAWKQGGGGTVWDSLVDVPTDLVYLGVGNGSP
WNYKRYSEGKTDNLFSGSIVAINPDTGKYVWHFQETPMDEWDYTSVQQIM
TLDMPVNGEMRHVIVHAPKNGFFYIIDAKTGKFITGKPYTYENWANGLDP
VTGRPNYVPDALWTLTGKPLGIPGELGGHNFAAMAYSPKTKL VYIPAQQ
IPLLYDGQKGGFKAYHDANLGLDMNKIGLFDNDPEHVAKKDFLKV LK
GWTVAWDPEKMAPAFTINHKGPNWGLLATAGNVI FQGLANGEFHAYDAT
NGNDLYSFPQSAI IAPPVITYTANGKQYVAVEVGWGGIY PFLYGGVARTS
GWTVNHSRVIAFSLDGKDSLPPKNELGFTPVKPVPTYDEARQKDG YFMYQ
TFCSACHGDNAISGGVLPDLRWGAPRGRESFYKLVGRGALTAY GMDRFD
TSMTPEQIEDIRNFIVKRANESYDDEVKARENSTGVPNDQFLNVPQSTAD
VPTADHP

> P35811|XYNC_FIBSU Endo -1,4-beta-xylanase C - *Fibrobacter succinogenes* (*Bacteroides succinogenes*).

MKTFSVTKSSVVFAMALGMATAFAQDFCSNAQHSGQKVTITSNQTKIG
DIGYELWDENGHGGSATFYSDGSMDCNITGAKDYLCRAG LSLGSKNTYKE
LGGDMIAEFKLVKSGAQNVGYSYIGIYGWMEGVSGTSPSQLVEYYYIDNTL
ANDMPGSWIGNERKGTITVDGGTYIVYRNRTRTGPAIKNSGNVTFYQYFSV
RTSPRDCGTINI SEHMRQWEKMG LTMGKLYEAKVLGEAGNVNGEVRRGGM
DFPHAKVYVKNKSDPVSSSSSVKSSS TDAPKSSSKNGNVS GKIDACKD
VMGHEGKETRTQGNSSVTGNVGS SPYHYE IWIYQGGNNS MTFYDNGTYK
ASWNGTNDFLARVGFYDEKHTYEELGP IDAYYKWSKQGSAGGNYIGIY
GWTVDPLVEYYYIVDDWFKPGANLLGQRKGEFTVDGDTYEWQNTRVQQP
SIKGTQTFPQYFSVRKSARSCGHIDITAHMKKWEELGMKMGMYEAKVLV
EAGGGSGSFDVTYFKMTDKAHPLAQPEPESSSSEAKVESSSSTVALHAAP
KMELKSGNFQVFDMQGRFLGTVKLDAGASVAQVLKANFKNA GIYMKVQGN
FMQRVAVK

> PROB_THETH_Q60050 GLUTAMATE 5 -KINASE (EC 2.7.2.11) (GAMMA -G

MEFFGLPLRVEEGVLI PRPETEGLVELALGLPLPPAPRIARQVAALREEG
REVVLVSSGAVAAGMRRLLGLKERPKDMPKKQALALGQPLLMAFWQEAFA
PFGLPVAQVLLTAEDLSSRSRYLNAKATLRALLDLGAI PVINENDTVAFE
EIRFGDNDQLSARVAALVEAGL LALLSDVDALYEEDPKKNPQARPIPEVE
SVEAVLAHAGEENPLGSGGMKSKLLAARIAGRVGIPTLLLPGKRPVLLQ
ALSGAPLGTYFHARRRYRGEKAWLFGLLRPKGELVLD RGA VRALKERGAS
LLPAGVKEVRGRFSRGEAVRLLSEEGEEVGVGLANYASEE IARIKGRRSA
EIEAVLGYRYTEEVVHRDHLALKEEA

> P26501|ISOA_PSEUM Isoamylase - Pseudomonas sp. (strain SMP1).
MKCPKILAAALLGCAVLGVPAMPAAHAINSMSLGSYDAQANITFRVYS
SQATRIVLYLYSAGYVQESATYTLSPAGSGVAVTVPVSSIKAAGITGA
VYYGYRAWGNWPYASNWKGKSQAGFVSDVDANGDRFNPNKLLLDPYAQE
VSQDPLNPSNQNGNVFASGASYRTTDSGIYAPKGVVLPSTQSTGKPTR
AQKDDVIYEVHVRGFTQDTSIPAQYRGTYYGAGL KASYLASLGVTAVEF
LPVQETQNDANDVVPNSDANQNYWGYMTENYFSPDRRYAYNKAAGGPTAE
FQAMVQAFHNAGIKVYMDVVYNHTAEGGTWTSDDPTTATIYSWRGLDNTT
YYELTSGNQYFYDNTGIGANFNTYNTVAQNLIIVDSLAYWANTMGVDGFRF
DLASVLGNSCLNGAYTASAPNCPNGGYNFDAADSNVAINRILREFTVRPA
AGGSGLDLFAEPWAIIGGNSYQLGGFPQGWSEWNGLF RDSLRLQAQNELGSM
TIYVTQDANDPFGSSNLFQSSGRSPWNSINFIDVHDGMTLKDVIYSCNGAN
NSQAWPYGNSDGGTSTNYSWDQGMASGTGAAVDQRRRAARTGMFAEMLSAG
TPLMQGGDEYLRTLQCNNNAYNLDSSANWLTYSWTTDQSNFYTFQAQLIA
FRKAHPALRPSSWYSGSQLTWYQPSGAVADSNYWNNTSNYAIAYAINGPS
LGDSNSIYVAYNGWSSSVTFTLPAPPSGTQWYRVTD CDWNDGASTFVAP
GSETLIGGAGTTYQCGQSLLLISK

> P31554|OSTA_ECOLI Organic solvent tolerance protein - Escherichia coli.
MKKRIPTLLATMIATALYSQQGLAADLASQCMLGVPSYDRPLVQGDNDL
PVTINADHAKGDYDDAVFTGSVDIMQGNRSLQADEVQLHQKEAPGQPEP
VRTVDALGNVHYDDNQVILKGPKGWANLNTKDTNVWEGD YQMVGRQGRGK
ADLMKQRGENRYTILDNGSFTSCLPGSDTWSVVGSEI IHDRREQVAEIWN
ARFKVGPVPIFYSPYLQLPVGDKRRSGFLIPNAKYTTTNYFEFYLPHYWN
IAPNMDATITPHYMHRGNIMWENEFYLSQAGAGLMELDYLP SDKVYED
EHPNDSSRRWLFYWNHSGVMDQVWRFNVDTYTKVSDPSYFNDFDNKYGSS
TDGYATQKFSVGYAVQNFNATVSTKQFQVFSEQNTSSYSA EPQLDVNYQ
NDVGFDFTRIYGQAVHFVNTRDDMPEATR VHLEPTINLPLSNWGSINTE
AKLLATHYQQTNLWDYNSRNTTKLDES VNRVMPQFKVDGKMVFERDMEML
APGYTQTLPEPQYLYVPIYRDQSDIYNYDSSLQSDYSGLFRDRTYGGGLD
RIASANQVTTGVTSR IYDDAAVERFNISVQIYYFTESRTGDDNITWEND
DKTGSLVWAGD TYWRISERWGLRGGIYDTRLDNVATSNSS IEYRRDEDR
LVQLNRYASPEYIQATLPKYYSTAEQYKNGISQVGAVASWPIADRWSIV
GAYYYDTNANKQADSM LGVQYSSCCYAIRVGYERKLNWDNDKQHAYVDN
AIGFNIELRGLSSNYGLGTQEMLRSNILPYQNTL

> P18473|TRBC_ECOLI Periplasmic protein trbC - Escherichia coli.
MKLSMKSLAALLMMLNGAVMA SENVNTPENRQFLKQQENLSRQL REKPDH
QLKAWAEKQVLENPLQRSDNHFLDELVRKQOASQDGKPRQGALYFVFSFI
PEEGLKRM LGETRHF GI PATLRGMVNNDLKT TAEAVLSLVKDGATDGVQI
DPTLFSQYGI RTVPALVVFC SQGYDI IRGNLRV GQALEKVAATGDCRQVA
HDLLAGKGD SGK

> P12293|DHM1_PARDE Methanol dehydrogenase subunit 1 - Paracoccus
denitrificans.
MNRNTPKARGASSLAMAVAMGLAVLTTAPATANDQLVELAKDPANWVMTG
RDYNAQNYSEM TDINKENVKQLRPAWSFSTGVLHGHEGTPLVVGD RMFIH
TPFPNTTFALDLNEPGKILWQNKPKQNPTARTVACCDVNRGLAYWPGDD
QVKPLIFRTQLDGHIVAMDAETGETRWIMENS DIKVGSTLTIAPYVIKDL
VLVGSSGAELGVRGYVTAYDVKS GEMRWRAFATGPDEELLLAEDFNAPNP
HYGQKNLGL ETWEGDAWK IGGGTNWGWYAYDPEVDL FYYGSGNPAPWNET
MRPGDNKWTMAIWGREATTGEAKFAYQKTPHDEWDYAGVNVMMMLSEQEDK
QGQMRKLLTHPDRNGIVYTLDR TNGDLI SADKMDDTVN WVKEVQLDTGLP
VRDPEFGTRMDHKARDICPSAMGYHNQGHDSYDPERKVFMLGINHICMDW
EPFMLPYRAGQFFV GATLTMYPGPKATAERAGAGQIKAYDAISGEMKWEK
MERFSVWGGTMATAGGLTFYVTL DGFIKARDSDTGDL LKFKLPSGVIGH
PMTYKHDGRQYVAIMYGVGGWPGVGLVFDLADPTAGLGSVGA FKRLEFT
QMGGGVMMVFLDGESPYSDPNVGEYAPGEPT

> P19487|GUNA_XANCP Major extracellular endoglucanase - Xanthomonas
campestris pv. campestris.
MSIFRTASTLALATALALAAGPAFSYSINNS RQIVDDSGKVVQLKGVNVF
GFETGNHVMHGLWARNWKDMIVQMQLGFNAVRLPFCPATLRSDTMPASI
DYSRNADLQGLTSLQILDK VIAEFNARGMYVLLDHHTPDCAGISELWYTG
SYTEAQWLADLRFVANRYKNVPYVLGLDLKNEPHGAATWGTGNAATDWNK
AAERGSAAVLAVAPKWLIAVEGITDNPVCSTNGGIFWGGNLQPLACTPLN
IPANRLLLAPHVYGPVDFVQSYFNDSNFPNNM PAIWERHFGQFAGTHALL

PHVPTSHANVRFFCAEKEGEEPVVWFGGGFDLTPYYAHEEDCVHWHRRVAR
DACAPFGADVPRYKE WCDRYFHLKHRNEPRGIGGLFFDDLNQWDFDTCF
AFIRAIGDAYIDAYLPIVQRRKHTPFDERQREFQAYRRGRYVEFNLVFDR
GTLFGLQSGGRTESILMSLPPQVRWGYDWKPEPGSEEARLTEYFLADRWD
LAGQP

> P09961|AMY1_DICTH Alpha -amylase 1 - *Dictyoglomus thermophilum*.

MTKSIYFSLGIHNNQPVGNDFVIERAYEMSYKPLINFFFKHPDFPIN VH
FSGFLLLWLEKNHPEYFEKCLKIMAERGQIEFVSGGFYEPILPIIPDKDKV
QQIKKLNKYIYDKFGQTPKGMWLAERVWEPHLVKYIAEAGIEYVVVDDAH
FFSVGLKEEDLFGYYLMEEQGYKLVAVFPISMKLRYLIPFADPEETITYLD
KFASEDKSKIALLFDDGEEKFGLWPDYRTVYEEGWLETFVSKIKENFLLV
TPVNLYTYMQRVKFKGRIYLPASYSREMMEWVLFPEAQKELEELVEKLEK T
ENLWDKFSPYVKGGFWRNFLAKYDESNHMQKMLYVWKKVQDSPNEEVKE
KAMEEVFQGGANDAYWHGIFGGLYLPHLRTAIYEHLIKAENYLENSEIRF
NIFDFDCDGNDEIIVESPFFNLYLSPNHGGSVLEWDFKTKAFNLTNVLTR
RKEAYHSKLSYVTSEAQGKSIHERWTAKEEGLENILFYDNHRRVSFTEKI
FESEPVLEDLWKDSRLEVDSEFYENYDYEINKDENKIRVLFSGVFRGFEL
CKSYILYKDKSFVDVVYEIKNVSETPISLNFGEINLNFAPNHPDYYFL
IGDQKYPLSSFGIEKVNWNKIFSGIGIELECVLDVEASLYRYPIETVLSL
EEGFERVYQGSALIHFYKVDLPGSTWRRTTIRFWVK

> P15321|HLYB_SERMA Hemolysin activator protein - *Serratia marcescens*.

MIKKITALTLLVSTALSAETLPDSHMMQDMSMGESRRALQDSTRE VNQLI
EQRRYQQLKQORLLAEPAPALPQSAQCLPIAGVYLQGVTLTLLSPADLSAL
SGLPEQCISNSDINRLTRELTRLYVQKGYITARVQIVRPNSSQELGLSVT
EGFIEKIEGGDRWVNSRLLFPGLEKPLKLELDQGLDQANRLQSNTTKL
DILPGRQVGGSVIRLRNQHAKPWLITAGTDNYGQKSTGRWLARATATLDS
PFGLSDFVSLNANSTLENPAHRYNRAYTLLYSLPYGAFTFSGFASF SSYE
NHQQLPHNVVKLHGQTQQYGLRSDYVYFRDHDQIDSLSGQLTYKRIDNYF
ESVRLEQVSSPTLTLAELSASHLQILPNGVFSANLSVEQGMFWLGAHRHS
SVHLDSQFTKGLFANLSQRLRLGDATYQLNNLFYGGYSRDPLPGVEWLS
LTDRAVARGFSRSTQSGDNGWYLQNTLSRSFNLGATTLTPRLGADVGRIL
PRQDNQSGWRSSAGISTGATLRYQRALVDLEVSRGWILSNHATPEDPV QVL
ARFSYTF

> P16114|RNS_ECOLI Regulatory protein rns - *Escherichia coli*.

MDFKYTEEKETIKINNIMIHKYTVLYTSNCIMDIYSEEEKITCFNSRLVF
LERGVNISVRMQRQILSEKPYVAFRLNGDMLRHLKDALMIYGMISKIDTN
ACRSMRSRKIMTTEVNKTLLELKNINSHDNSAFISSLIYLISKLENNEKI
IESIYISSVFFSDKVRNLIKDLRKTW LGIADAFNASEITIRKRLES
ENTNFNQILMQLRMSKAALLLENSYQISQISNMIGISSASYFIRIFNKH
YGVTPKQFFTYFKGG

> P0A1Z2|SKP_SALTY Chaperone protein skp - *Salmonella typhimurium*.

MKKWLLAAGLGLAMVTSQAADKIAIVNMGNLFQQVAQKTGVSNTLENEF
KGRAAELOKMETDLQSKMQRLOSMKAGSDRTKLEKDVMSQRQTFAQKAQ A
FEKDRARRSNEERNKLVTRIQTAVKKVANDQSIDLVVDANTVAYNSSDVK
DITADVLKQVK

> IDH_SUNY3 P80046 ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.

MYEKLQPPSVGSKITFVAGKPVVNDPIIPYIRGDGTGVDIWPATELVIN
AAIAKAYGGREENFWFKVYAGDEACELYGTQIFPEDTLTAIKEYGVAIK
GPLTTPVGGGIRSLNVALRQIFDLYTC VRPCRYYPGTPSPHKTPKLDII
VYRENTEDIYLGIEWAEGTEGAKKLIAYLNDELIPPTPALGKKQIRLDSG
IGIKPISKTGSQRLVRRAILHAKRLPKAKQMVTLVHKGNIMKFTEGPFRD
WGYELATTEFRAECVTERESWICGNKESNPDLTIEANAHMIDPGYDTLLE
EKQAVIKQEVEQVLSIWESHGNGQWKEKVMVNDRIADSIFQQIQTRPDE
YSILATMNLNGDYLSDAAAAVVGGGLMG PGANIGDSAAIFEATHGTAPKH
AGLDRINPGSVILSGVMMLEFMGWQEAADLIKKGIGAAIANREVTYDLAR
LMEPKVDKPLKCEFAQAIVSHFDD

> P0AEQ3|GLNH_ECOLI Glutamine -binding periplasmic protein - *Escherichia coli*.

MKSVLKVSLAALTLAFVSSHAADKLVVATDTAFVPPFEFKQGDKYVGF
VDLWAAIAKELKLDYELKPMDFSGIIP ALQTKNVLDLALAGITITDERKKA
IDFSDGYYSKGLLMVMKANNDVKSVDLDGKVVAVKSGTGSVDYAKANI
KTKDLRQFPNIDNAYMELGTNRADAVLHDTPNILYFIKTAGNQFKAVGD
SLEAQQYGIAPFKGSDLRDKVNGALKTLRENGTYNEIYKKWFGTEPK

> P43900|PHEA_HAEIN P-protein [Includes: Chorismate mutase - Haemophilus influenzae.

MALELSDIRQQITQIDRSLLKLLSERHRLAFDVVRSKEISQKSLRDVERE
QQLLQELVQFAENENYQLEAQYITSI FQKIIEDSVLTQQVYLQNKLNQQR
NQNLIHIAFLGKRGYSNLAARNYAARYQKQFVELGCQSFEQVFEKVQTGE
ADFGVLPLENTTSGAINEVYDLLQHTDLSLVGELAYPIKHCVLVNDKTDL
NQIDTLYSHQPVIQQCSQFIHSLDRVHIEYCESSSHAMQLVASLNKPN IA
ALGNEDGGKLYGLSVLKTNIANQENNI TRFIVVAKEPREVSSQIPTKTLL
LMTTSQQAGALVDALLVFKKHQINMTKLESRPIYGKPWEEMFYLEIEANI
HHPDTKQALEELKNYSNYLKLILGCPSEIVKPVSV

> P0A9N4|PFLA_ECOLI Pyruvate formate -lyase 1-activating enzyme - Escherichia coli.

MSVIGRIHSFESCGTVDGPGRIFITFFQGCLM RCLYCHNRDWTWTHGGKE
VTVEDLMKEVVYTRHFMNASGGGV TASGGAILQAEFVRDWFRAKKEGI
HTCLDTNGFVRRYDPVIDELLEVTDLVMLDLKQMNDEIHQNLVGVSNHRT
LEFAKYLANKNVKVVIRYVVVPGWSDDDSAHRLGEFTRDMGNVEKIELL
PYHELKHKWVAMGEEYKLDGVKPKPKETMERVKGILEQYGHKVMF

> P14768|XYNA_PSEFL Endo -1,4-beta-xylanase A - Pseudomonas fluorescens.

MRTAMAKSLGAAFLGAALFAHTLAAQTATCSYNITNEWNTGYTGDITIT
NRGSSAINGWSVNWQYATNRLSSSWNANVSGSNPYSASNLSWNGNIQPGQ
SVSFGFQVKNKNGSAERPSVGGSSICSGSVASSAPASSVPSSIASSSPSS
VASSVISSMASSSPVSSSSVASSTPGSSSGNQCCNWTLYPLCVTTTNG
WGVEDQRSCARSTCAA QPAPFGIVGSGSSTPVSSSSSSLSSSSVSSIR
SSSSSSSSSVATGNGLASLADFP IGVAVAASGGNADIFTSSARQNVRAE
FNQITAENIMKMSYMYSGSNFSFTNSDRLVSWAAQNGQTVHGHALVWHPS
YQLPNWASDSNANFRQDFARHIDTVAHFAGQVKSWDVVNEALFDSADDP
DGRGSANGYRQSVFYRQFGGPEYIDEAFRRARAADPTAELYNDFNTEEN
GAKTTALVNLVQRLNNG VPIDGVGFQMHVMNDYPSIANIRQAMQKIVAL
SPTLKIKITELDVRLLNNPYDGNSSNDYTNRNDCAVSCAGLDRQKARYKEI
VQAYLEVVPPEGRGGITVWGIADPDSWLYTHQNLDPDWPLLFNDNLQPKPA
YQGVVEALSGR

> P0A9B6|E4PD_ECOLI D-erythrose-4-phosphate dehydrogenase - Escherichia coli.

MTVRVAINGFGRIGRNVVRALYESGRRAEIT VVAINELADAAGMAHLLKY
DTSHGRFAWEVRQERDQLFVGDDAIRVLHERSLQSLPWRELGVDDVLDCT
GVYGSREHGEAHIAAGAKKVLFSHPGSNDLDATVVYGVNQDLRAEHRIV
SNASCTTNCIIPVIKLLDDAYGIESGTVTTIHSAMHDQVIDAYHPDLRR
TRAASQSIIPVDTKLAAGITRFFPQFNDRFEAIAVRVPTINVTADLSVT
VKKPVKANEVNLLQKAAQGA FHGIVDYTELP LVSVDFNHDPHSAIVDGT
QTRVSGAHLIKTLVWCDNEWGFANRMLD TTLAMATVAFR

> P44440|RNB_HAEIN Exoribonuclease 2 - Haemophilus influenzae.

MFQDNPLLAQLKQQIHDSKEQVEGVKSTDKAYGFLECDKTYFIAPPSM
KKVMHGDKIKATIEKQGDKEQAEPEALIEPMLTRFIAKVRFNKDKKLQVL
VDHPSINQPIGAQQAKSVKEELQEGDWVANL KTHPLRDDRFFYATINQL
ICRADDELAPWVWTLARHEQSRYPVGAEPYEMLDQKTRENLTALHFVTI
DSESTMDDDALYIEPIAQNSTQTGWKLVAIADPTAYIALDSQIEQEAQ
QRCFTNYLPGFNI PMLPRELSDELCSLIANETRPALVCYIETDLTGNITA
KPHFVSAYVQSKAKLAYNKVSDYLEQADNAWQPEMPETAQQIHWLHQFTK
ARIQWRKTHSLFFKEKPDYAFVLAENGKVQEIK AEYRRIANQIVEEAMII
ANICAAQFLHEQAKTGIFNTHSGFDKFL ENAHNFLMANLANEQNQTALA
ERYSVENLATLNGYQMRHDIEPIESDYLELRLRRYLTFAEFKSELAPHF
GLGLEGYATWTSPIRKYS DMVNHRLIKAVLAKQPYEKPQNDVLARLQEAR
RQNRLVERDIADWLYCRYLADKVASNAEF EAQVQDVMRAGLRVQLLENGA
SLFIPAATLHNNKEEIQLNPDDELALYIKGERTYK IGDMVKVKLTEVKEAT
RSIVGEILQ

> P52111|GLPD_PSEAE Glycerol -3-phosphate dehydrogenase - Pseudomonas aeruginosa.

MSQAHTPSAPLAEVYDVAVVGGINGV GIAADAAGRGLSVFLCEQHDLAQ
HTSSASSKLIHGGLRYLEHYEFRLVREALAEREVLLAKAPHIVKPLRFVL
PHRPHLRPAWMIRAGLFLYDHLGKREKLPASRGLRFTGSSPLKAEI RRGF
EYSDCAVDDARLVVLANAISAREHGAHVHTRTRCVSARRSKGLWHLHLERS
DGSLSYIRARALVNAAGPWVARFIQDDLKQKSPY GIRLIQGSIIIVPKLY
EGEHAYILQNEDRRIVFAIPYLD RFTMIGTTDREYQGDPAKVAISEETA

YLLQVVNAHFQQQLAAADILHSFAGVRPLCDDDESDEPSAITRDYTLSSLA
GNGEPLLVSFVGGKLTTRYKLAESALTQLQFFANLGPWATAKAPLP GGE
MQQSVEALTEQLANRYAWLDRELALRWARTYGTWRVRLLDGVNGEADLGE
HLGGGLYAREVDYLCCKHEWAQDAEDILWRRSKLGLFLSPSQVRLGQYLQ
SEHPHRPRVHAA

> P74368|RNC_SYNY3 Ribonuclease III - *Synechocystis* sp. (strain PCC 6803).

MNHPDFPPIGDPQLKLEALTHRSYCNEHPGTPSYDRLEFLGDAVLGFVVG
RILFERYPHFT EAELTRLSQLVNQNQLAYLARFLHIAPEIRLSQSLARD
DGQSSPSILADVFESELLGAALLDRGLTAVEDFIQELFVPILEQWEKSQDG
RSPKLVPTMDVKSMQQWALAKTKQLPEYELINTSGPPHAQEFTFTVKVA
GKIHGQSGSPKQIATKQAALALKSLGLLQ

> P19926|AGP_ECOLI Glucose -1-phosphatase - *Escherichia coli*.

MNKTLIAAAVAGIVLLASNAQ AQTVPEGYQLQQVLMMSRHNLRAPLANNG
SVLEQSTPNKWPEWDVPGGLTTKGGVLEVYMGHYMREWLAEQGMVKSQE
CPPPYTVYAYANSIQRVATAQFFITGAFPGCDIPVHHQEKMGTMPTFN
PVITDDSAAFSEQAVAAMEKELSKLQLTDSYQLLEKIVNYKDSPACKEKQ
QC SLVDGKNTFSAKYQQEPGVSGPLKVGNSLVD AFTLQY YEGFPMQVAV
GEIKSDQQWKVLSKLNKYQDS LFTSPEVARNVAKPLVSYIDKALVTDRT
SAPKITVLVGHSDNIASLLTALDFKPYQLHDQNERTPIGGKIVFQRWHS
KANRDLMKIEYVYQSAEQLRNADALTLQAPAQRVTLLESGCPIDADGFCP
MDKFDSVLNEAVK

> P0AES9|HDEA_ECOLI Protein hdeA - *Escherichia coli*.

MKKVLGVILGGLLLPVVSNAAQAADNKKPVNSWTCEDFLAVDESFO
PTAVGF AEALNNKDKPEDAVLDVQGIATVTPAIVQACTQDKQANFKDKVK
GEWDKIKKDM

> P73201|SYS_SYNY3 Seryl -tRNA synthetase - *Synechocystis* sp. (strain PCC 6803).

MLDLKQIRENPTAIQNRLNQRGGGASYDLEPILAI AAEQKAKESERTVLQ
SRNEIGKLIGQKIGQGADPKGEEIQTREEGNSLKIQLADLEPQEKDLK
EQLQKLLLELPLNLCETTP IGASEADNIEVKRWGDQYLKAETVGILPHWE
IGEKLGIIIDSERGVKVAQSRFISLMKAGAALERALINFMLERHIGVGYQE
IMPPIVNSDSLLGTGQLPKFAEESFQCRGDDLWLIPTAEVPVTNLYRDE
VLDLEQLPIKHCA YTPCFRREAGSYGRDTKGLIRLHQFNKVELVKLVKPE
ESAAEHQALVADAEAILQALELPYRVVELCTGDLGFGAACYDLEVWLPS
ANTYREISSCSNFHDFQARR ANIRYKEKGGKGTQFVHTLNGSGLAIGRTM
AAILENYEPSSGQVKVPVVLQDFLKR DYL

> FUCI_ECOLI P11552 L-FUCOSE ISOMERASE (EC 5.3.1. -) - ESCHER

MKKISLPKIGIRPVIDGRRMGVRESLEEQTMMNAKATAALLTEKLRHACG
AAVECVISDTCIAGMAEAAAACEEKFSQNVGLTITVTPCWCYGETIDMD
PTRPKAIWGFNGTERPGAVYLAALAAHSQ KGIPAFSIYGHVQDADDTS
IPADVEEKLLRFARAGLAVASMKGKSYLSLGGVSMGIAGSIVDHNFFESW
LGMKVQAVDMTELRRRIDQKIYDEAELEMALAWADKNFRYGEDENNKQYQ
RNAEQSRVLRRESLLMAMCIRDMMQNSKLADIGRVEESLGYNAIAAGFQ
GQRHWTQYPNGDTAEAILNS SFDWNGVREPFVATENDSLNGVAMLMGH
QLTGTAQVFADVRTYWSPEAIERTVGHKLDG LAEHGI IHLINSGS AALDG
SCKQRDSEGNPTMKPHWEISQQEADACLAATEWC PAIHEYFRGGGYSSRF
LTEGGVPFTMTRVNI IKGLGPVLQIAEGWSVELPKDVHDILNKRTNSTWP
TTWFAPRLTGKGPFTDVYSVMANWGANHGVL TIGHVGADFITLASMLRIP
VCMHNVEETKVYRPSAWAAHGMDIEGQDYRACQNYGPLYKR

> P48638|GSHR_ANASP Glutathione reductase - *Anabaena* sp. (strain PCC 7120).

MTFDYDLFVIGAGSGGLAASKRAASYGAKVAIAENDLVGGTCVIRGCVPK
KLMVYGSHPALFEDAAGYGWQVGAELNWEHFITSIDKEVRRLSQLHIS
FLEKAGVELISGRATLVDNHTVEVGERKFTADKILIAVGGRIKPELPGM
EYGITSNIEIFHLKTQPKHIAIIGSGYIGTEFAGIMRGLGSQVTQITRGDK
ILKGFDEDIRTEIQEGM TNHGIRIIPKNVTAIEQVPEGLKISLSGEDQE
PIIADVFLVATGRVNVVDGLGLENAGVDVVDSSIEGPGYSTMNIAIVNEY
SQTSPNIIYAVGDVTDRLNLT PVAIGEGRADFADSEFGNNRREFSHETIAT
AVFSNPQASTVGLTEAEARAKLGDDAVTIYRTRFRPMYHSFTGKQERIMM
KLVVDTKTKDKVLGAHMGVGENAAEIIQGVAVKMGATKKDFDATVGIHPS
SAEEFVTMR

> ALKK_PSEOL Q00594 MEDIUM-CHAIN-FATTY-ACID--COA LIGASE (EC 6

MLGQMMRNQLVIGSLVEHAARYHGAREVVS VETS GEVTRSCWKEVELRAR
KLASALGKMGLTPSDRCATIANNIRHLEVYAVS GAGMVCHTINPRLFI

EQITYVINHAEDKVVLLDDTFLPIIAEIHGSLPKVKAFVLMAHNNSNAS
QMPGLIAYEDLIGQDDNYIWPDVDENEASSLCYTSGTTGNPKGVLYSH R
STVLHSMTTAMPDTLNLNSARDTILPVPVPMFHVNAWGTPYSAAMVGA
KLVLPALDGLASLSKLIASEGVSIALGVVWQGLLAAQAGNGSKSQSLTRV
VGGACAPASMIREFNDIYGVEVIHAWGMTELSPFGTANTPLAHHVDLSPD
EKLSLRKRSQGRPPYGVELKIVNDEGIRLPEDGRSKGNLMARGHWVIKDYF
HSDPGSTLSDGWSTGDVATIDSDGFMTICDRAKDIKSGGEWISTVELE
SIAIAHPHIVDAAVIAARHEKWDERPLLIIVKSPNSELTSGEVCNYFADK
VARWQIPDAAIFVEELPRNGTGKILKNRLREKYGDILLRSSSSVCE
> P24059|CY552_BRAJA Cytochrome c -552 - Bradyrhizobium japonicum.
MHLHLRGICLVAVASSSSSALAADAGHGADLAKRWCASCHVVANGQAVA
SADVPSFASVARRPDFSSEKLAFFLLDPHPKMPSFPLSRT EAGDIAAYIG
SLRP
> P08506|DACC_ECOLI Penicillin-binding protein 6 - Escherichia coli.
MTQYSSLLRGLAAGSAFLFLFAPTAFAAEQTV EAPSVDARAWILMDYASG
KVLAEAGNADEKLDPASLTKIMTSYVVGQALKADKIKLTDMMVTVGKDAWAT
GNPALRGSSVMFLKPGDQVSVADLNKGVIIQSGNDACIALADYVAGSQES
FIGLMNGYAKKLGTLNTT FQTVHGLDAPGQFSTARDMALLGKALIHDPVE
EYAIHKEKEFTFNKIRQPNRNRLLWSSNLNVDGMKTGTAGAGYNLVA
SA TQGDMLRISVVLGAKTDRIRFNESEKLLTWGFRFFETVTPIKPDATFVTQ
RVWFGDKSEVNLGAGEAGSVTI PRGQLKNLKASYTLTEPQLTAPLKKGV
VGTIDFQLNGKSIEQRPLIVMENVEEGGFFGRVWDFVMMKFHQWFGSWFS

> P0AED0|USPA_ECOLI Universal stress protein A - Escherichia coli.
MAYKHILIAVDLSPESKVLVEKAVSMARPYNAKVS LIHVDVNYSDLYTGL
IDVNLGDMQKRI SEETHHALTELSTNAGYPITETLSGSGDLGQVLVDAIK
KYDMDLVVCGHHQDFWSKLMSSARQLINTVHVDMLIVPLRDEEE
> P0AFI5|PBP7_ECOLI Penicillin-binding protein 7 - Escherichia coli.
MLIMPKFRVSLFSLALMLAVPFAPQAVAKTAAATTASQPEIASGSAMIVD
LNTNKVIYSNHPDLVRPIASISKLMTAMVVDARLPLDEKLVKVDISQTPE
MKGVYSRVRLNSEISRKDMLLLALMSENRAAASLAHHYPGGYKAFIKAM
NAKAKSLGMNTRFVEPTGLSVHNVSTARDLTKLLIASKQYPLIGQLSTT
REDMATFSNPTYTLPFRNTNHLVYRDWNWNIQLTKTGFTNAAGH CLVMRTV
INNKPVALVMDAFGKYTHFADASRLRTWIETGKVMVPVAAAALSYKKQKA
AQMAAAGQTAQND
> P24228|PBP4_ECOLI Penicillin-binding protein 4 - Escherichia coli.
MRFSRFIIGLTSCIAFSVQAANVDEYITQLPAGANLALMVQKVGASAPAI
DYHSQQMALPASTQK VITALAALIQLGPDFRFTTTLETKGNVENGVKGD
LVARFGADPTLK RQDIRNMVATLKKSGVNQIDGNVLIDT SIFASHDKAPG
WPWDMTQCFSAPAAAIVDRNCFVSLSYAPKPGDMAFIRVASIYPVTM
FSQVRTLPRGSAAEQYCELDVVPGLNRFLLTGCLPQRSEPLPLAFVQD
GASYAGAILKDELKQAGITWSGTLRQTQVNEPGTVVASKQSAPLHDLK
IMLKKSDNMIADTVFRMIGHARFNVPGTWRAGSDAVRQILRQQAGVDIGN
TIIADGSGLSRHNLIAPATMMQVLQYIAQHDNELNFI SMLPLAGYDGSLO
YRAGLHQAGVDGKVS AKTGS LQGVYNLAGFITTASGQRMAFVQYLSGYAV
EPADQRNRRIPVRFESRLYKDIYQNN
> P06111|OMPV_VIBCH Outer membrane protein ompV - Vibrio cholerae.
MKKIALFITASLIAGNALAAQTYIRNGNIYTHEGQWAAEVGAFGSTDLLK
DQDKSYGALLNFGYHGDFNA DLSGLNYRFFGNTGDIVNLGTYLTGSGVA
YDQDSANSVKGMDKRKATVDLGLNADIALGDGTVSTYFQHDILNENKGYK
TGVNYFHIIDLGVADLVPPFAGISYQSSDYNNYYFGVKDKEATAQRKAYHA
GGDFSYNLGYKLVYPINDRWEITQTSAYTRLGSDIAHSPIVDSANQWLVG
ATVAYHF
> P45523|FKBA_ECOLI FKBP-type peptidyl-prolyl cis-trans isomerase fkpA -
Escherichia coli.
MKS LFKVTLATMAVALHAPITFAAEAAKPATAADSKAAFKNDDQKSAY
ALGASLGRYMENS LKEQEKLGIKLKDQLIAGVQDAFADKSKLSDQEIEQ
TLQAFEARVKSSAQAKMEKDAADNEAKGKEYREKFAKEKGVKTSSTGLVY
QVVEAGKGEAPKSDTVVVVNYKGTLLIDGKEFDNSYTRGEPLSFRLDGVIP
GWTEGLKNIKKGGKIKLVIPPELAYG KAGVPGIPPNSTLVFDVELLDVVKP
APKADAKPEADAKAADS AKK
> P19449|BCSA1_ACEXY Cellulose synthase catalytic subunit [UDP -forming] -
Acetobacter xylinus (Gluconacetobacter xylinus).

MSEVQSPVPAESRLDRFSNKILSLRGANYIVGALGLCALIAATTVTLSIN
EQLIVALVCVLFVFFIVGRGKSRRTQIFLEVLVSALVS LRYLTWRLTETLDF
DTWIQGGGLGVTLLMAELYALYMLFLSYFQTIQPLHRAPLPLPDNVDDWPT
VDIFIPITYDEQLSIVRLTVLALGIDWPPDKVNVYI LDDGVRPEFEQFAK
DCGALYIGRVDSSHAKAGNLNHAIKRTSGDYILILDCDHIPTRAFLOIAM
GWMVADRKIALMQTPHHFYSPDPFQRNLAVGYRTPPEGNLFYQVIQDGN
FWDATFFCGSCAILRREAIESIGGFAVETVTEDAHTA LRMQRRGWSTAYL
RIPVASGLATERLTHIGQRMWRWARGMIQIFRVDNPMPLGGGLKLGQRLCY
LSAMTSFFFAPRVIIFLASPLAFLFFGQNI IAASPLAVLAYAIPMHFHSI
ATAAKVKNKGRYSFWESEVYETTMALFLVRVTIITLMPFSKGFVNVEKGG
VLEEEEFDLGATYPNIIFAGIMTLGLLIGLFELTFHFNLQLAGIAKRAYLL
NCIWAMISLIILLAAIAVGRETKQVRYNHRVEAHPVT VYEAPVAGQPNT
YHNATPGMTQDVSMGGVAVHMPWPDVSTGPVKTRIHAVLDGEEIDIPATM
LRCKNGKAVFTWDDNDLTERDIVRFVFGRAAWLQWNNYEDDRPLRSLW
SLLSIKALFRKKGKMMANSRPRKPLALPVERREPTTIQSGQTQEGKIS
RAAS

> CHEZ_SALTY P07800 CHEMOTAXIS PROTEIN CHEZ. - SALMONELLA TYP

MMQPSIKPADEGSAGDIIARIGS LTRMLRDSLRELGLDQAI AEAEEAIPD
ARDRLDYVVQMTAQAAERALSVEASQPHQDAMEKEAKALTQRWDEWFND
PIELSDARELVTDRQFLRDVPGHTSF'TNAQLLDIMMAQDFQDLTGQVIK
RMDMVIQEIERQLLMVLENIPEQSARPKRENESLLNGPQVDTSKAGVVA
SQDQVDDLLDSLGF

> P0AG82|PSTS_ECOLI Phosphate -binding periplasmic protein - Escherichia coli.

MKVMRTTVATVVAATLSMSAFSVFAEASLTGAGATFPAPVYAKWADTYQK
ETGNKVNYQGIGSSGGVQKQIIANTVDFGASDAPLSDEKLAQEGLFQFP
TIGGVVLAVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLNPLGLK
PSQNI AVVRRADSGSTSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGK
GNDGIAAFVQRLPGAIGYVEYAYAKQNNLAYTKL ISADGKPVSPTEENFA
NAAKGADWSKTFAQDLTNQKGEDAWPITSTTFILIHKDKKPEQGEVLK
FFDWAYKTGAKQANDLDYASLPDSVVEQVRAAWKTNIKDSSGKPLY

> P27755|PRU_MYXXA Protein U - Myxococcus xanthus.

MNAIKTAVA AVTAAASLVAFSPAEAAATATANLNV TANVGGACSIGSGAGG
GTLNFGTYDPVVVNSALGVDLFGTGSLSVQCTLLSTAVI TLGQGLYP AAG
STAAVPLRRMRNAASTDYLSYFLYMDVTRLI AWGNTSGTGLPFLGLGLPV
PVQVYGTVP RQNVPSGTYNDTVVATITF

> P0C1A8|PMEA_ERWCH Pectinesterase A - Erwinia chrysanthemi.

MLKTI SGTLALSIIAASVHQQAATTYN AVVSKSSSDGKTFKTIADAIA
SAPAGSTPFVILIKNGVYNERLTI TRNLLKGESRNGAVIAAATAAGTL
KSDGSKWGTAGSSTITISAKDFSAQSLTIRNDFDFPANQAKSDSDSSKIK
DTQAVALYVTKSGDRAYFKDVS LVGYQDTLYVSGGRSFFSDCRISGTVDF
IFGDGTALFNCDLVSRYRADVKSGNVSGYLTAPSTNINQKYGLVITNSR
VIRESDSVPKASYGLRPHPTTTTFSDGRYADPNAIGQTVFLNTSMDNHI
YGWDKMSGKDKNGNTIWFNPEDSRFFEYKSYGAGAAVSKDRRQLTDAQAA
EYTQSKVLGDWTP TLP

> P0AFM2|PROX_ECOLI Glycine betaine -binding periplasmic protein - Escherichia coli.

MRHSVLFATAFATLISQTFAADLPKGITVNPVQSTITEETFQTL LVSR
ALEKLG YTVNKPSEVDY NVGYTSLASGDATFTAVNWTPLHDNMYEAAGGD
KKFYREGVFN GAAQGYLIDKKTADQYKITNIAQLKDPKIAKLFDTNGDG
KADLTGCNPGWGCEGAINHQ LAAYELTNTVTHNQGN YAAMMADTISRYKE
GKPVFYTTWTPYVWSNELKPGKDVVWLQVPFSALPGDKNADTKLPNGANY
GFPVSTMHIVANKAWAEKNPAAAKLFAIMQLPVADINAQNAIMHDGKASE
GDIQGHVDGWIKAHQQQFDGWVNEALAAQK

> P14775|DHM2_METEX Methanol dehydrogenase subunit 2 - Methylobacterium extorquens (Protomonas extorquens).

MKTTLIAAAI VALSGLAAPALAYDGTCKCAAGNCWEPKPGFPEKIAGSKY
DPKHDPKELNKQADS IKQMEERNKKRVENFKKTGKFEYDVAKISAN

> P37921|FIMA1_SALTY Type -1 fimbrial protein, A chain - Salmonella typhimurium.

MKHKLMSTIASLMFVAGAAVAADPTPVSVSGGTIHFEGKLVNAA CAVST
KSADQTVTLGQYRTASFTAIGNTTAQVPSIVLND CDPKVAANA AVAFSG
QADNTNP NLLAVSSADNSTTATGVGIEILDNTSSPLKPDGATFSAKQSLV

EGTNTLRFTARYKATAAAATTPGQANADATFIMKYE
> P13717|NUCA_SERMA Nuclease - *Serratia marcescens*.
MRFNNKMLALAALLFAAQASADTLESIDNCAVGCPTGGSSNVSVIRHAYT
LNNNSTTKFANWVAYHITKDTPASGKTRNWKTDPALNPADTLAPADYTGA
NAALKVDRGHQAPLASLAGVSDWESLNYLSNITPQKSDLNQGAWARLEDQ
ERKLI DRADISSVYTVTGPLYERDMGKLPGTQKAHTIPSAWVKVIFINNS
PAVNHYAAFLDQNTPKGADFCQFRVTVDEIEKRTGLIIWAGLPDDVQAS
LKSKPGVLPPELMGCKN
> P32099|LPLA_ECOLI Lipoate-protein ligase A - *Escherichia coli*.
MSTLRLLLISDSYDPWFNLAVEECIFRQMPATQRVLFLWRNADTVVIGRAQ
NPWKECNTRMEEDNVRLARRSSGGGAVFHDLGNTCFTFMAGKPEYDKTI
STSIVLNALNALGVSAAEASGRNDLVVKTVVEGDRKVSAYSRET KD RGFHH
GTLNLLNADLSRLANYLNPDKKLAAGKITSVRSRVTNL TELLPGITHEQV
CEAITEAFFAHYGERVEAEIISPKNTPDLPN FAETFARQSSWEWNFGQAP
AFSHLLDERFTWGGVELHFDVEKGHITRAQVFTDSLNPAPLEALAGRLQG
CLYRADMLQQECEALLVDFPEQEKELELSAWMAGAVR
> P56154|PGK_HELPHY Phosphoglycerate kinase - *Helicobacter pylori*
(*Campylobacter pylori*).
MLAKMSFMQNVKNIQEVEVSHKRVLIRVDFNVPLDENL NITDDTRIRESL
PTIQYCIDNKADIIIVSHLGRPKGVEEKLSLKPFLKRRLERLLNHEVVFS
QNI VQLKQALNENAPTRIFLLENIRFLRGEENENDENLAKDLASLCDVFN
DAFGTSHRKHASTYGTAKFAPIKVS GFLKKEIDSFYQAFNHPLRPLLLI
VGGAKVSSKLTLLKNILDIDKLI IAGAMSNTFLKALGYDVQDSSVEDAL
INDALELLQSAKEKKVKVYLPIDAVTTDDILNPKHIKISPVQDIEPKHKI
ADIGPASLKL FSEVIESAPTILWNGPLGVHEKQEFARGTTFLAHKIADTY
AFSLIGGGDTIDAINRAGEKDNMSFISTGGGASLELLEGGKILPCFEVLDK
RH
> P04164|CY552_THETH Cytochrome c -552 (Fragment) - *Thermus thermophilus*.
QADGAKIYAQCAGCHQQNGQIGPFAFPPLAGHVAEILAKEGGREYLILVL
LYGLQQQIEVKGMKYNVMSSFAQLKDEEIAAVL NHIATAWGDAAKVKGF
KPF TAAEVKLLRAKKLTPQQVLAERKKLGLK
> Q55210|CY550_SYNP2 Cytochrome c -550 - *Synechococcus* sp. (strain PCC 7002)
(*Agmenellum quadruplicatum*).
MNKILGIDPLKKFIFGISAFVLLFWQLNVGAANATALREVDRTVNLNETE
TVVLSDQQVAKGERIFINTCSTCHNSGRTKSNPNVTL SLVDLEGAEP RRD
NILAMVDYLNKPTS YDVELDLSQLHPNTVRADIWSSMRNLNEEDLQNVSG
YVLVQAQVRGVAVWGGGKTVN
> HMC6_DESVH P33393 52.7 KD PROTEIN IN HMC OPERON (ORF 6). -
MPEGKFCNRKPVNTEEDLKALLGDKGAQYYKEMEELEVDQEALWANIEK
TCQSRKTWLEICAHCGMCADSCFLYRVNDRDPKQVPAYKI QSTLGEIIR
RKGKVD TQFMLHAMEVAWSQ CTCCNRCGQYCPHGIDMGVMFSYLRGLLYS
QGFVPWELKIGSGMHRVYGAQMDVTTEDWVETCEWMAEEQQEWPGL EIP
VDVENADIMYVLNAREPKHYPEDVAEAAILFHIAGENWTVPSEGWEQ TSL
AMFAGDWAACKMQVERVYAAIERLKPKCVVGTECGHAHRASAIEGPYWAG
YEDGKTPAPWLHYVEWVAMALRTGKIKIDPEKRIKEPVTLQDSCNYIRNH
GLAKCTREIMSYIADDFREMT PNREHNYCCGGGGFNGIGKFRKQRNKAL
QTKRDQILATGAKLVVAPCHNCWDAIRDLEEEYRIGIRWSFLKPLIIKMA
I IPEHLRPEEE
> FABB_HAEIN P43710 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE
MRRTVITGFGI ISSIGNNKEEVLASLKAGKSGIEVVPEFVEMNMRSHVAG
TIKLN PSEHIDRKVFRFMGDAAYAYLSMREAI EDAGLTEDQVSNDR TGL
VIGAGTGS AHNQLVACDAVRGPRGVKAIGPYAVTKTMAS SVSACLATPYK
IRGVNYSMS SACATS AH CIGHAVELIQLGKQDVVFAGGAEELSWECATEF
DAMGAVSTKYNETPEKASRAYDANRDGFVIAGGGAVVVVEELEHALARGA
KIYAEIVGYGATSDGYDMVAPS GEGAERC MKQAMATVDTPIDYINVHGTS
TPVGDVKELGAIKNVFGDKIPAISS TKSMTGHSLGAAGAHEAIYTLMLD
NDFIAPSINIETLDEAAEGCNIVTETKENAGLQTVMSNSFGFGGTNATLI
FKRYNG
> HPRT_HAEIN P45078 HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE (E
MKKHHVDVLI SENDVHARIAELGAQITK FYQEKQIDNLVVVGLLRG SFMF
MADIVRQINLPVEIEFMTTSSYGTGMTNHDVRI TKDLGD IKGKHLVIV
EDIIDTGYTLEKVRDILNLREPASLTICTLLDKP SRREVEVPVEWVGFEI
PDEFVVG YGIDY AQRRHNLGYIGKVVLEE

> P07254|CHIA_SERMA Chitinase A - *Serratia marcescens*.

MRKFNKPLLALLIGSTLCSAAQAAAPGKPTIAWGNTKFAIVEVDQAATAY
NNLVKVKNAADVSVSNLWNGDAGTTAKILLNGKEAWSGPSTGSSGTANF
KVNKGGRYQMQUALCNADGCTASDATEIVVADTDGSHLAPLKEPLLEKNK
PYKQNSGKVVGSYFVEWGVYGRNFTVDKIPAQNLTHLLYGFIPICGGNGI
NDSLKEIEGSFQALQRSCQGREDFKVS IHDPFAALQKAQKGVTAWDDPYK
GNFGQLMALKQAHDPDLKILPSIGGWTLSDPFFFFMGDKVKRDRFVGSVKEF
LQTWKKFFDGVDI DWEFPGGKGANPNLGS PQDGETYVLLMKELRAMLDQLS
AETGRKYELTS AISAGKDKIDKVAYNVAQNSMDHIFLMSYDFYGFDFLKN
LGHQTALNAPAWKPD TAYTTVNGVNALLAQGVKPGKVVVG TAMYGRGWG
VNGYQNNIPFTGTATGFVKGTWKNIGVDYRQIAGQFMSGEWQYTYDATAE
APYVFKPSTGDLITGFDDARSVQAKGKYVLDKQLGGLFSWEIDADNGDILN
SMNASLGN SAGVQ

> P56118|RNC_HELPY Ribonuclease III - *Helicobacter pylori* (*Campylobacter pylori*).

MKNKRSQNS PYITPNSSYTTLEKALGYSFKDKRLLLEQAL THKSCKLALNN
ERLEFLGDAVLGLVIGELLYHKFYQYDEGKLSKLRAS IVSAHGFTKLAKA
IALQDYLRVSSSEEISNGREKPSILSSAFEALMAGVYLEAGLAKVQKIMQ
NLLNRAYKRDLDEHLFMDYKTALQELTQAQFCVIPTYQLLKEKGPDDHKE
FEMALYIQDKMYATAK GKSKKEAEQQCAYQALQKLEAK

> Q56268|LEU3_THIFE 3-isopropylmalate dehydrogenase - *Thiobacillus ferrooxidans* (*Acidithiobacillus ferrooxidans*).

MKKIAIFAGDGIGPEIVAAARQVLD AVDQAAHLGLRCTEGLVGG AALDAS
DDPLPAASLQLAMAADAVILGAVGGPRWDAYPPAKRPEQGLLRLRKLGLDL
YANLRPAQIFPQLLDASPLRPELV RDVDILVVRELTGDIYFGQPRGLEVI
DGKRRGFNTMVYDEDEIRRIAHVAFRAAQGRRKQLCSVDKANVLETTRLW
REVVTEVARDYPDVR LSHMYVDNAAMQLIRAPAQFDVLLTGMMFGDILSD
EASQLTGSIGMLPSASLGEGRAMYEP IHGSAPDIAGQDKANPLATILSVA
MMLRHSLSNAEPWAQRVEAAVQRVLDQGLRTADIAAPGTPVIGTKAMGAAV
VNALNLKD

> P43902|TYRA_HAEIN T-protein [Includes: Chorismate mutase - *Haemophilus influenzae*].

MSFMEALKDLRSEIDSLDRELIQLFAKRLELVSQVGKVKHQHGLPIYAPE
REIAMLQARRLEAEKAGISADLIEDVLRRFMRESYANENQFGFKTINSDI
HKIVIVGGYKGLGGLFARYLRASGYPISILDREDWAVAESILANADVIV
SVPINLTLETIERLKP YLTENMLLADLTSVKREPLAKMLEVHTGAVLGLH
PMFGADIASMAKQVVVRC DG RFPERYEWLLEQIQIWKAKIYQTNATEHDH
NMTYIQALRHFS TFANGLHLSKQPINLANLLALSSPIYRLELAMIGRLF
QDAELYADIIMDKSEN LAVIETLKQTYDEALTFFENNDRQGFIDAFHKVR
DWFGDYSEQFLKESRQLLQ QANDLKQG

> P43834|SYV_HAEIN Valyl-tRNA synthetase - *Haemophilus influenzae*.

MTQKFEMADRNFNSAVEQALYQRWEESG YFKPSENENAPSYCIAIPPPNV
TGSLHMGHAFQQTLM DTLIRFNRMEGHNTLWQTGTDHAGIATQM VVERKI
AAEEGKTRHDYGREAFINKIWDWKAYSGGTISQQMRRLGNSIDWERERFT
MDDGLSNAVKEVFVRLHEEGLIYRGKRLVNWDPK LHTAISDLEVENKESK
GSLWHFRYPLANDAKTADGKDYLVA TTRPETMLGDTAVAVHPEDERYQS
LIGKTVVLP LANREIPIIADEYVDREFGT GVVKITPAHDFNDYEVGKRHN
LPMVNVLTNLNANIRDEAEIIGTDGKPLAGYEATIPADYRGLERFAARKKI
VADFEALGLLDEIKPHDLKVPYGD RGGVPIEPMLTDQWYVSVKPLADVAI
KAVEDGEIQFV PKQYENLYFSWMRDIQDWCSRQLWWGHRI PAWYDAEGN
VYVARNEEEVRSKYNLDS AVELKQDEVDLDTWFSSGLWTFSTLGWPEQTK
ELKMFHPTDVLITGFDI IFFWVARMIMFTM HFVKDENGKPVVPFKTVYVT
GLIRDEQQQKMSKSKGNVLDPIDMIDGISLEDLLEKRTGNMMQPQLAEKI
AKATRKEFAEGIAAHGTDALRFTLAALASNGRDINWDMKRLEGYRNFNCNK
LWNASRFVLTNEKLDLSQGEIEFSLADRWIQSEFNRTVETFRSSLSQYRF
DLCANAIYEFTWQFCDWYLELTKPVFANGNAAQIRAASQTLVHVLEKLL
RLAHPLIPFITEE IHWQKVKGFV GITADSIML QPFPQVEESGDFPEAEAEI
EWLKEVIVAVRNIRAESNIAPSKGLDLLFRNLSAENAKILEKQTALLKAM
AKLDNVQV LATNETAPLAVAKLVGNAELLVPMAGFINKEAELARLTKEIE
KYQNEVKRIENKLSNEAFVAKAPEAVIAKEREKQAEYQSGLEKIQEYKAI
IEAL

> Q07703|METC_BORAV Cystathionine beta-lyase - *Bordetella avium*.

MSDTS AKHIDTLLQHLGSAPFNPDTGAAPVNLPSVRASTVRFQSLAKLED

AQRRKAAGERASTYGRMGMDTHAALEQVFAELEGGTHCYLASSGLAGISM
VFLSLLSAGEHALVADCAYGVPVHELHEAVLSRLGIDVTFDAKADLASLV
RPTTRLIFAEAPGSLLEFEMLDMPALARFAKQHDLLILATDNTWGSYIYRP
LTLGAQVSVIAGTKYVGGHSDLMLGAVVTNDEAIAKRLNRTQYALGYSVS
ADDAWLALRGVRTM PVRMAQHARHALEVCEFLQNRPEVVRLYHPAWPADP
GHALWQRDCSGSNGMLAVQLGLSPQAARDFVNALTLFGIGFSWGGFESLV
QLVTPGELARHQYWQGGSDALVRLHIGLESPADLIADLAQALDRAA
> P0A9X9|CSPA_ECOLI Cold shock protein cspA - Escherichia coli.
MSGKMTGIVKWFNADKGGFITPDDGSKDVFVHFSAIQNDGYKSLDEGQK
VSFTIESGAKGPAAGNVTSL

> P11797|CHIB_SERMA Chitinase B - Serratia marcescens.
MSTRKAVIGYFIPTNQINNYTETDTSVVPFVSNITPAKAKQLTHINFS
FLDINSNLECAWDPATNDAKARDVNVNRLTALKAHNPSLRIMFSIGGWYYS
NDLGVSHANYVNAVKTTPAARTKFAQSCVRIMKDYGFDGVDIDWEYPQAAE
VDGFIAALQEIRTLNQQTIADGRQALPYQLTI AGAGGAFFLSRYYSKLA
QIVAPLDYINLMTYDLAGPWEKITHNQAAALFGDAAGPTFYNALREANLW
SWEELTRAFPSPFSLTVDAAVQQHLMMEGVPSAKIVMGVFPFYGRAFKGVS
GGNGGQYSSHSHTPGEDPYPNADYWLVGCDCEVRDKDPRIASRQLEQMLQ
GNYGYQRLWNDKTKTPYLYHAQNGLFVYDDEAFKFKYKAKYIKQQQLGGV
MFWHLGQDNRNGDLLAALDRYFNAADYDDSQLDM GTGLRYTGVGPGNLP
MTAPAYVPGTTYAQGALVSYQGYVWQTKWGYITSAPGSDSAWLKVGRLA
> P37060|NANH_VIBCH Sialidase - Vibrio cholerae.

MRFKNVKKTALMLAMFGMATSSNAALFDYNATGDTEFDSPAKQGWMDNT
NNGSGVLTNADGMPAWLVQIGIGRAQWTYSLSTNQHAQASSFGWRMTTEM
KVLSSGMITNYYANGTQRVLPPIISLDSSGNLVVEFEGQ TGRTVLATGTAA
TEYHKFELVFLPGSNPSASFYFDGKLRDNIQPTASKQNMIVWNGSSNT
DGVAAYRDIKFEIQGDVIFRGPDRIPSI VASSVTPGVVTAFAEKRVGGGD
PGALSNTNDIITRTRSDGGITWDTLNLTEQINVSDEFDFSDPRPIYDPS
SNTVLVSYARWPTDAAQNGDRIKPWPMPNGIFYSVYDVASGNWQAPIDVTD
QVKERSFQIAGWGGSELYRRNTSLNSQQDWQSNAKIRIV DGAANQIQVAD
GSRKYVVTLSIDESGGLVANLNGVSAPI ILQSEHAKVHSFHDYELQYSAL
NHTTTLFVDGQQITTWAGEVSEQENNIQFGNADAQIDGRLHVQKIVLTQQG
HNLVEFDADFYLAAQQTPEVEKDLEKLGWTKIKTGNTMSLYGNASVNPQPGH
GITLTRQQNISGSQNGRLIYPAIVLDRFFLNVMSIYSDDGGSNWQTGSTL
PIPFWRKSSSILETLEPSEADMVELQNGDLLLTARLDFNQ IVNGVNYSPR
QQFLSKDGGITWSLLEANNANVFSNISTGTVDASITRFEQSDGSHFLLFT
NPQGNPAGTNGRQNLGLWFSFDEGVTWKGPIQLVNGASAYSIDIYQLDSEN
AIVIVETDNSNMRILRMPITLLKQKLTLSQN

> AMPL_RICPR P27888 CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEU
MLNINFVNEESSTNQGLIVFIDEQLKLNLIALDQQHYELISKTIQNK L
QFSGNYGQITVVPVSVIKSCAVKYLIIVGLGNVEKLTAKIEELGGKILQH
ATCAKIATIGLKI INRINRFTSPTFTSLIASGAFLASYRFHKYKTTLKEV
EKFAVESIEILTNDNSEAMKLFVKKLIAEAVFFTRDISNEPSNIKTPOV
YAERIVEILEPLGVNIDVIGEHDIKNLGMGALLGVGQGSQNESKLVVMEY
KGGSRDDSTLALVGKGVIFDTGGISLKPSSNMHLMRYDMAGSAAVVGTTII
ALASQKVPVNVVGVVGLVENMQSGNAQRPGDVVVTMSGQTAEVLNTDAEG
RLVLADTVVYVQEKFNPKCVIDVATLTGAITVALGSTYAGCFSSNNDELAD
KLKAGEAVNEKLRMPLHDDYDAMINSDIADIANIGNVPGAAGSCTAAH
FIKRFIKDGVDAWHLDIAGVANSNNASALCPKGAVGYGVRLLEKFIKEYN

> P00131|CYC3_DESVH Cytochrome c3 - Desulfovibrio vulgaris (strain
Hildenborough / ATCC 29579 / NCIMB 8303).

MRKLFCCGVLALAVAFALPVVAAPKAPADGLKMEATKQPVVFNHSTHKS
KCGDCHHPVNGKEDYRKCGTAGCHDSMDKDKSAKGYHYVMHDKNTKFKS
CVGCHVEVAGADAAKKDLTGCKKSKCHE

> P54737|PKN5_MYXXA Serine/threonine -protein kinase pkn5 - Myxococcus
xanthus.

MPLKVIGPYRVLETLGSGGAGTVYRALDRRTTDEVALKLLSAGPARDARA
ARRLAREFDTLVDLSHPNVVVFESGVHQVPPYLAMELIEGLTLRHYLDL
SSGDRQTPPGSHTPRSPLSVLRTADDDFGPLSRFSDSMDDSEDSFPDGT
FGLEAFAEEAPSEDESFASSASPHVIGSDDSLEGFDLPPMPRPAEPE
EEPGRVVREEDLNRPERMGRKLDAMLQICEALAYIIGH GLVHRDLKPSNI
MVDDDRQVRLMDFGLAKFLADDAATEAGKLVGTYYRMAPEQILGEPLDG

RADLYSLGVILYELLSGRPPFDKTPHELWRQVLETEPPPVLALNLHGDP
QLARVAHRLIRKEPDDRFQTAEEVYEALSE
> MASY_ECOLI P08997 MALATE SYNTHASE A (EC 4.1.3.2) (MSA). - E
MTEQATTTDELAFTRPYGEQEKQILTAEAVEFLTELVTHTFPQRNKLL AA
RIQQQQDIDNGTLPDFISETASIRDADWKIRGIPADLEDRRVEITGPVER
KMVINALNANVKVFMADFEDSLAPDWNKVIDGQINLRDAVNGTISYTNEA
GKIYQLKPNPAVLICRVRGLHLPEKHVTWRGEAIPGSLDFALYFFHNYQ
ALLAKGSGPYFYLPKTQSWQEAAWWSEVFSYAEDRFNLPRGTIKATLLIE
TLPVAFQMDEILHALRDHIVGLNCGRWDYIFSYIKTLKNYPDRVLPDRQ A
VTMDKPFNLNAYSRLLIKTCHKRGAFAMGGMAAFIPSKDEEHNNQVLNKVK
ADKSLEANNHGDGTWIAHPGLADTAMAVFNDILGSRKNQLEVMREQDAPI
TADQLLAPCDGERTEEGMRANIRVAVQYIEAWISGNGCVPFIYGLMEDAAT
AEISRTSIWQWIHHQKTLNKGKPVTKALFRQMLGEEEMKVIASELGEERFS
QGRFDDAARLMEQITTSDELIDFLTLPGYRLLA
> P11073|PELC_ERWCH Pectate lyase C - *Erwinia chrysanthemi*.
MKSLITPITAGLLALSQPLLAATDTGGYAATAGGNVTGAVSKTATSMQD
IVNIIDAARLDANGKVKGGAYPLVITYTGNEDSLINAAAANICGQWSKD
PRGVEIKEFTKGITIIIGANGSSANFGIWKSSSDVVVQNMRIQYLPGGAK
DGMIRVDDSPNVVDHNELFANHECDGTPDNDDTFESAVDIKASNTV
TVSYNYIHHGVKGLDGGSSSDTGRNITYHHNYNDVNARLPLQRGGLVH
AYNNLYTNIITGSGLVNRQNGQALIEENNWFKAINPVTSTRYDGNKFGTWVL
KGNMITKPADFSTYSITWTADTKPVNADSWTSTGTFTPTVAYNYSVPSAQ
CVKDKLPGYAGVGKNLATLTSTACK
> P33225|TORA_ECOLI Trimethylamine -N-oxide reductase 1 - *Escherichia coli*.
MNNNDLFQASRRRFLAQLGGLTVAGMLGPSLLTPRRATAAQAAATDAVISK
EGILTGSHWGAIIRATVKDGRFVAAKPFELDKYPSKMIAGLPDHVHNAARI
RYPMVRVDWLRKRHLSDTSQRGDNRFVRVSWDEALDMFYEELERVQKTHG
PSALLTASGWQSTGMFHNASGMLAKAIALHGNSVGTGGDYSTGAAQVILP
RVVSGMEVVEAQEIEVLSIDPVVSTHEYLGREHVKHIAVNPQTDVPLQLA
LAHTLYSENLYDKNFLANYCVGFQFLPYLLGEKDGQPKDAAWAEKLTGI
DAETIRGLARQMAANRTQIIAGWCVQRMQHGEQWAWMIVVLAAMLGQIGL
PGGGFGFGWHYNGAGTPGRKGVILSGFSGSTSIPPVHDNSDYKGSSTIP
IARFIDAILEPGKVINWNGKSVKLPPLKMCIFAGTNPFRHQINRIIEG
LRKLETVIAIDNQWTSCTRFADIVLPATTQFERNDLDQYGNHNRGIIAM
KQVVPQFEARNDFDIFRELCRRFNREEAFTEGLDEMGLKRIWQEGVQQ
GKGRGVHLPAFDDFWNNKEYVEFDHPQMFVRHQAFREDPDLEPLGTPSGL
IEIYSKTIADMNYYDCQGHMWFEEKIERSHGGPGSQKYPHLQLSVHPDFR
LHSQLCESETLRQYTVAGKEPVFINPQDASARGIRNGDVVRVFNARGQV
LAGAVVSDRYAPGVARIEGAWYDPDKGGEFGALCKYGNPNVLTIDIGTS
QLAQATSAAHTTLVEIEKYNVTVEQVTAFAFNGPVEMVAQCEYVPASQVKS
> P74917|CY552_THIFE Cytochrome c -552 - *Thiobacillus ferrooxidans*
(*Acidithiobacillus ferrooxidans*).
MTTYLSQDRLRNKENDTMTYQHSKMYQSRTFLLFSALLLVAGQASAAVGS
ADAPAPYRVSSDCMVCHG MTGRDITLYPIVPRLAGQHKSYPMEALQKAYKDH
SRADQNGEIMWPVAQALDSAKITALADYFNAQKPPMQSSGIKHAGAKEG
KAIFNQGVTEQIPACMECHGSDGQAGFPRLAGQRYGYIIQQLTIFYHN
GTRVNTLMNQIAKNITVAQMKDVAAYLSSL
> P43856|APT_HAEIN Adenine phosphoribosyltransferase - *Haemophilus*
influenzae.
MTTQLDLIKSS IKSIPNYPKEGIIFRDITLLEVPAAFKATIDLIVEQYR
DKGITKVLGTESRGIIFGAPVALALGLPFELVRKPKKLPRETISQSYQLE
YGQDTLEMHVDAISEGDNVLIIDDLLATGGTVEATVKLVQRLGGAVKHAA
FVINLPELGGEKRLNNLGVDCTLVNFEGH
> P18539|AMPC_SERMA Beta -lactamase - *Serratia marcescens*.
MTKMNRCAALIAALILPTAHAAQQQ DIDAVIQPLMKKYGVPGMAIAVSV
GKQQIYPYGVASKQTGKPIEQTLFEVGSLSKFTATLAVYAQQQSKLSF
KDPASHYLPDVRGSAFDGVSLLNLATHTSGLPLFVPDDVTNNAQLMAYYR
AWQPKHPAGSYRVSNLIGMLGMIAAKSLDQPFQIAMEQGMPLALGMSH
TYVQVPAQMANYAQGYSKDDKPVVRVNPGLDAESYGIKSNARDLIRYLD
ANLQQVQKVASVARWRPRRTSVITSAG AFTQDLMWENYPYPVKLSRLIEGN
NAGMIMNGTPATAITPPQPELRAGWYNKTGSTGGFSTYAVFIPAKNIAVE
MLANKWFPNDDRVEAAYHIIQALEKR

> P0ABW5|SFMA_ECOLI Sfm fimbrial protein, A chain - Escherichia coli.
MKLRFISSALAAALFAATGSYAAVVDGGTIHFEGELVNAACSVNTDSADQ
VVTLGQYRTDIFNAVGNSTALIPFTIQLNDCD PVVAANA AVAFSGQADAI
NDNLLAIASSTNTTATGVGIEILDNTSAILKPDGNSFSTNQNLIPGTV
LHFSARYKGTGTSASAGQANADATFIMRYE

> P56071|SYT_HELPY Threonyl -tRNA synthetase - Helicobacter pylori
(Campylobacter pylori).
MSAELIAVYKDEQIIDLES AKVLGLSDGIKALNGTEPIYFDDSPLELEVI
RHSCAHLAQLSKA LYPDAKFFVGPVVEEGFYDFKTSSKI SEEDLPKIE
AKMKEFAKLKLAIKTETLTREQALERFKGDELKHAVMSKIGGDAFGVYQQ
GEFEDLCKGPHLPNTRFLNHFKLTKLAGAYLGGDENNEMLIRIYGIAFAT
KEGLKDYLFQIEEAKKRDRHKLGLVGLFSFDDEIGAGLPLWLPKGARLR
KRIEDLLSQALLLRGYEPVKGPEILKSDVWKISGHYDNYKENMYFTTIDE
QEYGIKPMNCVGHK VYQSALHSYRDLPLRFYEGVVHRHEKSGVLHGLL
RVREFTQDDAHI FCSFEIQSEVSAILDFTHKIMQAFDFSYEMELSTRPA
KSIGDDKVWEKATNALKEALKEHRIDYKIDEGGGAFYGPKIDIKITDALK
RKWQCCTIQVDMNLPERFKLAFTNEYNHAEQPVMIHRAILGSFERFIAIL
SEHFGGNFPFFVAPTQIALIPINEEHHVFALKLKEALKKRDFVEVLDKN
DSLKKVRLAEKQKIP MILVLGNEEVETEILSIRDREKQDQYKMPLEKFL
NMVESKMQEVSF

> P00282|AZUR_PSEAE Azurin - Pseudomonas aeruginosa.
MLRKLAAVSLLSLLSAPLLAAECSVDIQNDQM QFNNTNAITVDKSKQFT
VNL SHPGNLPKNVMGHNWVLSTAADMQGVVTDGMASGLDKDYLPDDSRV
IAHTKLI GSKEKDSVTFDVSKLKEGEQYMFCTFPGHSALMKGTLTLK

> P0C0V0|DEGP_ECOLI Protease do - Escherichia coli.
MKKTTLALSALALSGLALSPLSATAAETSSATTAQQMPSLAPMLEKVMP
SVVSINVEGSTTVNTPRMPRNFQQFFGDDSPFCQEGSPFQSSPFCQGGQG
GNGGGQQQKFMALGSGVIIDADKGYVVTNNHVVDNATVIKVLSDGRKFD
AKMVGKDRSDIALIQIQNPKNLTAIKMADSDALRVGDYTVAI GNPFGLG
ETVTSGIVSALGRSGLNAENYENFIQTDAAINRGNSSGALVNLNGELIGI
NTAILAPDGGNIGIGFAIPSNMVKNLTSQMVEYGVKRGELGIMGTELNS
ELAKAMKVDAQRGAFVSQVLPNSSAAKAGIKAGDVITSLNGKPISSFAAL
RAQVGTMPVGSKLTLLGLLRDGKQVNVNLELQSSQNQVDSSIFNGIEGA
EMSNKGDQGVVNNVKTGT PAAQIGLKKGDVIIGANQQAVKNIAELRKV
LDSKPSVLALNIQRGDSTIYLLMQ

> Q55690|SYGB_SYNY3 Glycyl -tRNA synthetase beta chain - Synechocystis sp.
(strain PCC 6803).
MPLQTFLFEIGTEELPADFVRSAITQWQGLIPPGLAAEFLQ PESVEIYGT
PRRLAVLIKGLPECPDRLEEIKGPPASAAFKDGQPTPAALGF AKKQGVN
PEDFEIRSTPKGDFIFVNKQLQGQASRDLLPKLALS WLKAL DGRRFMRWG
DGDWRFP RPIRWLVCLLDDQVLP LQIDNGSTTLVGDRLSRGHRILHPADV
SLEHGQNYLAQLKTAGVVVDPQERRAMIEQQIT TQAAATLEGEAIIYEDLL
DEVEQLVEYPTAVL GKFDQEFLSLPREVTTTVMVTHQRYFPVVDKDGRL
PHFITIANGDP SKGDI IAAGN GRVIRARLADAKFFYQADCDDSLDSYLPQ
LETVT FQEELGTM RDKVD RIMEMAAA IADQLGVTEQQRGEID STAM LCKA
DLVTQM VYEFPELQ GIMGEK YALVSGESA AAVAQ GIVEHYLPRHQDDDL PQ
GLPGQVVMADRDLT LVSIFGLGLLPTGSSDPFALRRANAVINVAWAAS
LEINLLELLTQGC RDFVT SHPKT SPLQALKTFFLQRLQTL LQDEQ GIDY
DLVNAV LGNGETNCDEAQSRLH DRLLADLQDV KERAQYLQELRDNGHLDA
IYPTVNRSAKLASKGTLPTDQLDPRPVIQAPQLVQDSEKAVYQ ALLAIYP
KAVEVQESRDYETLVN ALHELAPTVAEFFDGPDSVLVMAENDEL RQNR LN
LLGLIRNYALILGDFGAI VKGI

> Q57142|C554_NITEU Cytochrome c -554 - Nitrosomonas europaea.
MKIMIACGLVAAALFTLTSGQSLAADAPFEGRKKCSSCHKAQAQSWKDTA
HAKAMESLKNVKEAKQKAKLDPKDYTDKDCV GCHVDGFGQKGGYTI
ESPKPMLTGV GCSCHGPRNFRGDHRKSGQAF EKSGKTPRKDLAKKGG
DFHFEERC SACHLNYEGSPWKGAKAPYTPFTPEVDAKYTFKFDEMVKEVK
AMHEHYKLEGVFEGEPKFKFHDEFQASAKPAKKGK

> P32966|UVRP_PSEFL UvrABC system protein C - Pseudomonas fluorescens.
MTDFPDP S AFLSTCSGRPGVYRMFSDTRLLYV GKAKNLKSR LASYFRKT
GLAPKTAALVGRIAQIETTITANETEALLLEQT LIKEWRPPYNI LLRDDK
SYPYVFLSDGEFPFRESIHRGAKKQKGYF GPYPSAGAIRESL SLLQKTFM
VRQCEDSY YKNRTRPCLQYQIKRCKAPCVGLVEAEVYAEDVRHSVMFLEG

RSNALTDELSAGMEQAASSTLDFEKAELRDQISLLRRVQDQOSMEGGSGD
VDVVAAFVNPVGGACVHLISVVRGGRVLSKNFFPQVGIIEEVAEVMASFLG
QYFLSSPERDLPSSELIVNVVHEDFPALIAAIQELRGRELSISHRVRGTRA
RWQQLAVTNAEQALSARLANRQHVAARFEALAEVLNLDPEPQRLECYDIS
HSSGEATVASCVVFGPEGPLKSDYRRYNIIEGVTAGDDYAAMHQALTRRFS
KLKDGEGKLPDILLVDGGKQQLSMARDVLNELAVPDLILLGVAKGATRKT
GFETLYLNDAAHEFTLKGDSPALHLIQQIRDEAHRFAITGHRARRGKTRR
TSTLEDVAGVGPKRRRDLKHFGLQELSRASIEEIAKAPGISKKLAELI
YANLHSE
> P20861|FANG_ECOLI Protein fanG - Escherichia coli.
MKKLYKAITVICILMSNLQSAQGATKSVQVPIRTEVKIPTCQLEIDSSID
FSFVKIEDIISRATSKEANLNFRCDAHVDNVRIMFVPGSNRTSSDKRVM
HSGTTGLGYSLQWSRASSGYSIDIGFNTQYQWSDSDAYQNLISGKLRKLPV
SFPGESLSKEGKVSSTINIEVTYD
> Q52369|CYC4_PEST Cytochrome c4 - Pseudomonas stutzeri (Pseudomonas
perfectomarinā).
MNKVLVLSLLTLGITGMAHAAGDAEAGQGKVAVCGACHVDGNSPAPNFP
KLAGQGGERYLLKQLQDIKAGSTPGAPEGVGRKVLEMTGMLDPLSDQDLED
IAAYFSSQKGSVGYADPALAKQGEKLEFRGGKLDQGMFACTG CHAPNGVGN
DLAGFPKLGQHAAYTAKQLTDFREGNRTNDGDTMIMRGVAAKLSNKDIE
ALSSYIQGLH
> P45069|FTSZ_HAEIN Cell division protein ftsZ - Haemophilus influenzae.
MLYPEYPEYDNFNEGALIKVVGVGGGGNAVNHMVMNMVKQEMGGTFVG
ESSLTSEEHGRIVFYAVNTDAQALRKSQVQOTVQIGGETTKGLGAGANPN
IGRKAEDDQDEIRKMLEGADMVFIAGMGGGTGTGAAPVVAKIAKELGI
LTVAVVTKPFTEFGKRMQFAELGIKDLISQYVDSMIIIPNQIQKVLKPN
AKLIDAFAAANDVLRNSVMGISMITSPLINVDFAVVRTVMSVQGGQAMI
GFGSAVGEPEGAGRAEEAARLAVRNDLLEKIDLSNAQGILVNITAGMDLVF
EEFNIIGETIGSFASEEATVVVGTSLVPEMSDEIRVTIVATGLGEIAGNE
PIQVVRQGLS TQNIIEGGRVNIPELHRRRESVEVSRTASEEYQRPLDKPI
TDRLEAFKKNFFNPAQREEN
> P0ABZ6|SURA_ECOLI Chaperone surA - Escherichia coli.
MKNWKTLLGLIAMIANSTFAAPQVVDKVAAVVNNGVVLESVDVGLMQSVK
LNAAQARQQLPDDATLRHQIMERLIMDQIILQMGQKMGVKISDEQLDQAI
ANIAKQNNMTLDQMSRLAYDGLNYNTYRNQIRKEM IISEVRNNEVRRRI
TILPQEVESLAQQVGNQNDASTELNLSHILIPLENPTSDQVNEAESQAR
AIVDQARNGADFGKLAIAHSADQQALNGGQMGWGRIQELPGIFAQALSTA
KKGDIVGPIRSVGFHILKVNDRGESKNI SVTEVHARHILLKPSPIMTD
EQARVKLEQIAADIKSGKTTFAAAAKEFSQDQPGSANQGGDLGWATPDI
PAFRDALTRLNKGQMSAPVHSSFGWHLIELLDTRNVD KTDAAQKDRAYRM
LMNRKFSEEAASWMEQQRASAYVKILSN
> P52663|BLAN_ENTCL Imipenem -hydrolyzing beta -lactamase - Enterobacter
cloacae.
MSLNVKQSRIALIFSSCLISISFFSQANTKGIDEIKNLETDFNGRIGVYA
LDTGSGKSFYSRANERFPLCSSFKGLAAAVLKGSDNRLNQLVNYNT
RSLEFHSPITTKYKDNMSLGDMAAAALQYS DNGATNIILERYIGGPEGM
TKFMRSIGDEDFRLDRWELDLNTAIPGDERDTSTPAAVAKSLKTLALGNI
LSEHEKETYQTWLGNTTGAARIRASVPSDWVVGDKTGSCGAYGTANDYA
VVWPKNRAPLIISVYTTKNEKEAKHEDKVI AEASRIAIDNLK
> P13063|PHSS_DESBA Periplasmic [NiFeSe] hydrogenase small subunit -
Desulfovibrio baculatus (Desulfomicrobium baculatus).
MSLSRREFVKLCSAGVAGLGISQIYHPGIVHAMTEGAKKAPVIWVQGGC
TGCSVSLNNAVHPRIKEILLDVISLEFHPTVMASEGEMALAHMYEIAEF
NGNFFLLVEGAIPTAKEGRYCVGETLDAKGGHHEVTMMELIRDLAPKSL
ATVAVGTCSAYGGIPAAEGNVTGSKSVRDFFADEKIEKLLVNVPGCPPHP
DWMVGTLVAAWVSHVLPTEH PLPELDDDGRPLFFGDNIHENCPLYDKYD
NSEFAETFTKPGCKAELGCKGPSTYADCAKRRWNNGINWCVENAVCIGCV
EPDFPDGKSPFYVAE
> P0C1A4|PELE2_ERWCH Pectate lyase E - Erwinia chrysanthemi.
MNSRMSVSTQKTTGRSALGTKSALAAIATMMVSVASAASLQTTKAT
EAASTGWATQSGGTTGGAKASSKIYAVKSISEFKAALNGTDSSPK IIQV
TGAIIDISGGKAYTSFDDQKARSQISIPSNTTIIGIGNKGF TNGSLVVKG
VSNVILRNLYIETPVDVAPHYEEGDGWAEDAVIDSTDHVVDHVTIS

DGSFTDDKYTTKNGEKYVQHDGSLDIKRGSDYVTVSNSRFELHDKTILIG
HSDNNGSQDAGKLRVTFHNNLFDRVGERTPRVRFSGSVHAYNNVYVGDVNH
KAYRYQYSFGIGTSGSLLSENAFTIDNMKKISGRDKESVVKAFNG KIF
SDKGSIINGASYNLNGCGFGFSAYSAKIPYKYSAQTTITSLAGSISSNAG
YGKL

> Q07740|NODB_AZOCA Chitoooligosaccharide deacetylase - Azorhizobium
caulinodans.

MSVLGQAARITQNQSSIIYITFDDGPHPSVTPAVCEILREHSALTAFFQIG
RFTKEYPSISRQCQLDGHAIIGNHTFDHPNLQDRAGEEVEYQISSAQKCLE
HICGRGFVRHFRA PYGAWSTQILNVVNIKIGLRPVSWPVDPRDWEAPRIEN
LINEILDNARPSIIILLHDGCPPDEAAMWDVRRGGAQTALALRYVVPALQ
ARGFALQPLP

> P31697|FIMC_ECOLI Chaperone protein fimC - Escherichia coli.

MSNKNVNVNRKSQEITFCLLAGILMFAMMMVAGRAEAGVALGATRVIYPAG
QKQEQLAVTNNDENSTYLIQSWVENADGVKDRFIVTPPLFA MKGKKENT
LRILDATNNQLPQDRESLFWMNVKAIPSMDSKSLTENTLQLAIISRIKLY
YRPAKLALPPDQAAEKLRFRRSANSLTLINPTPYLLTVTELNAGTRVLEN
ALVPPMGESTVKLPSDAGSNITYRTINDYGALTPKMTGVME

> P25394|FMF7_ECOLI F107 fimbrial protein - Escherichia coli.

MKRLVFIISFVALSMTAGSAMAQQGDVKFFGNVSATTCNLTP QISGTVGDT
IQLGTVPSPGTSEIPFALKASSNVGCASLSTKTADITWSGQLTEKGFA
NQGGVANDSYVALKTVNGKTQGGQEVKASNSTVSFDASKATTEGFKFTAQL
KGGQTPGDFQGAAYAVTYK

> ARGJ_NEIGO P38434 GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.3

MAVNLTEKTAEQLPDIDGIALYTAQAGVKKPGHTDLTLIAVAAGSTVGAV
FTTNRFCAPVHIAKSHLFDEEDGVRALVINTGNANAGTGAQGRIDALAVC
AAAARQIGCKPNQVMPFSTGVILEPLPADKIIAALPKMQPAFWNEAARAI
MTTDTVPKASREGKVGQDHTVRATGIAKSGMIHPNMATMLGFIATDAK
VSQFVLQMLTQIEADETFNTITVDGDTSTNDSFVI IATGKNSQSEIDNIA
DPRYQLKELLCSLAEQAIVRDGEGATKFITVRVENAKTCDEARQAA
YAAARSPLVKTAFASDPNLGKRLAAIGYADVADLDTDLVEMYLDDILVA
EHGGRAASYTEAQQQAVMSKDEITVRIKLRHGQAAATVYTCDLSHGYVSI
NADYRS

> P45356|HXUB2_HAEIN Heme/hemopexin utilization protein B - Haemophilus
influenzae.

MKMRPRYSVIASAVSLGFVLSKSVMALGQPDTGSLNRELEQRQIQSEAKP
SGELFNQNTANSPYTAQYKQGLKF PLTQVQILDRNNQEVVTDLAHILKNY
VGKEVSLSDLNLANEISEFYRHNNYLVAKAILPPQEIEQGTVKILLKLG
NVGEIRLQNHSLSNKFVSRLSNTTNTSEFILKDELEKFALTINDVPGV
NAGLQLSAGKKVGEANLLIKINDAKRFSSYVSDNQNKYTGRYRLAAGT
KVSNLNGWGDELKLDLMSNQANLKNARIDYSSLIDGYSTRFGVTANYLD
YKLGGNFKSLQSQGHSHTLGAYLL HPTIRTPNFRLSTKVSFNHQNLTDKQ
QAVYVVKQRKINSLTAGIDGSWNLIKDGTTFYFSLSTLFGNLANQTSEKKH
NAVENFQPKSHFTVYNYRLSHEQIILPKSFAFNIGINGQFADKTLESSQKM
LLGGLSGVRGHQAGAASVDEGHLIQTEFKHYLPVFSQSVLVSSLFYDYGL
GKYKNSQFLEQGVKNSVKLQSVGAGLSLSDAGSYAINVSAKPLDNNIN
NADKHQFWLSMIKTF

> P29957|AMY_PSEHA Alpha-amylase - Pseudoalteromonas haloplanktis
(Alteromonas haloplanktis).

MKLNKIITTAGLSLGLLLPSIATATPPTTFVHLFEWNWQDVAQECEQYLGP
KGYAAVQVSPNEHITGSQWWTRYQPVSYELQSRGGNRAQFIDMVNRCSA
AGVDIYVDTLINHMAAGSGTGTAGNSFGNKSFPPIYSPQDFHESCTINNSD
YGNDRYRVQNCVELVGLAD LDTASNYVQNTIAAYINDLQAIGVKGRFDAS
KHVAASDIQSLMAKVNQSPVVFQVEIDQGGAEVAVGASEYLSLSTGLVTEFKYS
TELGNTFRNGSLAWLSNFEGEGWGFMPSSSAVVFDNHDNQRGHGGAGNVI
TFEDGRLYDLANVFLAYPYGYPKVMSSYDFHGDTFDAGGNVNPVHNNGNL
ECFASNWKCEHRWSYIAGGVDFRNNADNWAATNWNNDNTNNQISFGRGSS
GHMAINKEDSTLTATVQTD MASGQYCNVVKGELSADAKSCSGEVI TVNSD
GTINLNIGAWDAMAIHKNAKLNTSSASSTESDWQRTVIFINAQTQSGQDM
FIRGGIDHAYANANLGRNCQTSNFECAMP IRHNNLKNVTSPWKANDNYL
DWYGIENGQSSEAEASATDWTNTNVWPAGWGAEKTVNTDGFVTPLNWIGE
HYWMLDVMDCSKAVNGWFEKAFIKNGQGWETAIAQDNAPYTSTNHMAQ
CGKINKFEFNNSGVVIRSF

> P24093|FMDR_ECOLI Dr hemagglutinin structural subunit - Escherichia coli.
MKKLAIMAAASMVFAVSSAHAGFTPSGTTGTTKLTVTTEECQVRVGDLTVA
KTRGQLTDAAPIGPVTVQALGCDARQVALKADTDNFEQKFFLISDNNRD
KLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQTNTPPGNYT
LTLTGGYWAK

> P43859|XGPT_HAEIN Xanthine phosphoribosyltransferase - Haemophilus
influenzae.
MSEKYVVTWDMFQMHARRLSERLLPASQWKGIIVSRGGLFPAAVLAREL
GLRHIE TVCIASYHDHNNQGELQVLHAAQVPNGGEGFIVVDDLVDVTGNTA
RAIRQMYPNKAFVTVFAKPAEALVDDYVIDIPQNTWIEQPWDLGLTFVP
PLSRK

> AMPR_CITDI P52658 TRANSCRIPTIO NAL ACTIVATOR PROTEIN AMPR. -
MRSNLP LNALRAFEASARHLSFTRAALELCVTQAASVQVRILEDR LN RV
LFRKRLPRGLEMTDEA QALFAVLTDAFGQIDTIFRQFEGGEYREVLTVAAV
GTFAVGWLLPRIEQFRQAHPFVELRLRTNNNVNLA AEGLDFAIRFGNGL
WPATHNEMLF EAPLTVLCTPETAQRLRRPADLLQENLRSYRVDEWDNWF
AAAGVTAERINGAVFDSRLMV ETVIHTGGAALVPAVMFARELAAGQLVR
PFDIEIQMGYWLTHLKS KPMTPAMEIFRDWIVKMA

> P06129|BTUB_ECOLI Vitamin B12 transporter btuB - Escherichia coli.
MIKKASLLTACSVTAFSAWAQDTSPTLVV TANRFEQPRSTVLAPTTVVT
RQDIDRWQSTSVNDVLRRLPGVDITQNGGSGQLSSIFIRGTNASHVLVLI
DGVRLNLAGVSGSADLSQFP IALVQRVEYIRGPRSAVYGS DAIGGVNII
TTRDEPGTEISAGWGSNSYQNYDVSTQQQLGDKTRVTL LGDYAHTHG YDV
VAYGNTGTQAQTDNDGFLSKTLYGALEHNFTDAWSGFVRGYDNRTNYD
AYYSPGSPLLDTRKLYSQSWDAGLR YNGELIKSQLITSYSHSKDYNYPH
YGRYDSSATLDEM KQYTVQWANNVIVGHGSIGAGVDWQKQTTTPGTGYVE
DGYDQRNTGIYLTGLQQV GDFTFEGAARSDDNSQFGRHGTWQTSAGWEFI
EGYRFIASYGTSYKAPNLGQLYGFYGNPNLDPEKSKQWEGAFEGLTAGVN
WRISGVRNDVSDLDIYDDHTLKYNEGKARIKGEVEATANFDTGPLTHTVS
YDYVDARNAITDTPLLRRAKQQVKYQLDWQLYDFDWGIT YQYLTRYDKD
YSSYPYQTVKMGGVSLWDLAVAYPVTSHLTVRGKIANLFDKDYETVYGYQ
TAGREYTLSGSYTF

> P0AE22|APHA_ECOLI Class B acid phosphatase - Escherichia coli.
MRKITQAI SAVCLLFALNSSAVALASSP SPLNPGTNVARLAEQAPIHWVS
VAQIENSLAGRPM AVGFDDIDTVLFS SPGFWRGKKTFSPESEDYLKNPV
FWEKMNGWDEF S IPKEVARQLIDMHVRRGDAIFFVTGRSPTKTETVSKT
LADNFHIPATNMN PVI FAGDKPGQNTKSQWLQDKNIRIFYGSDSN DITAA
RDVGARGIRILRASNSTYKPLPQAGAFGEEVIVNSEY

> P69059|MIP_LEGPN Outer membrane protein MIP - Legionella pneumophila.
MKMKLVTA AVMGLAMSTAMAATDATSLATDKDKLSYSIGADLGKNFKNQG
IDVNPEAMAKGMQDAMSGAQLALTEQQMKDVLNKFQKDLMAKRTAEFNKK
ADENKVKGEAFLTENKNKPGVVVLP SGLQYKVINAGNG VKPGKSDTVTVE
YTGRLIDGT VFDSTEKTGKPATFQVSQVIPGWTEALQLMPAGSTWEIYVP
SGLAYGPRSVGGPIGPNETLIFKIHLISVKKSS

> Q59516|DHGY_METEX Glycerate dehydrogenase - Methylobacterium extorquens
(Protomonas extorquens).
MTKKVFLDRESLDATVREFNFPHEYKEYESTWTPEEIVERLQGA EIAMI
NKVPMRADTLKQLPDLKLI AVAATGTDVVDKAAAKAQGITV VNI RN YAFN
TVPEHV VGLMFA LRRAIVPYANSVRRGDWNKSKQFCYFDYPIYDIAGSTL
GIIGYGALGKSI AKRAEALGMKVLAFDVFQDGLVDLETILTQSDVITLH
VPLTPDTKNMIGAEQLKKMKRSAILINTARGGLVDEAALLQALKDGTIGG
AGFDVVAQEP PKDGNILCDADLPNLIVTPHVAWASKEAMQILADQLVDNV
EAFVAGKPNVVEA

> P49433|G3P1_SYNY3 Glyceraldehyde -3-phosphate dehydrogenase 1 -
Synechocystis sp. (strain PCC 6803).
MLKIGINGFGRIGRLVARIAMANPQVTLV GINDLV PASNLAYLFKYDSTH
GSYGGTVVAKEEGIVIDDQFI PCFSQRNPAQLPWGDLGADYVVESTGLFT
TYATAENHLKAGAKRVIISAPSKDPEKIPTFVVGVNHLNYNADTDK IVSN
ASCTTNCLAPIAKI LDDNFGIVEGLMTTVHAMTATQPTVDGSPKKDFRGG
RGAAQNIIPSS TGAAKAAALVLPQLKGLTGMAFRVPTPNVSVDLTFKT
EKATSYEEICAAMKTA AEGELKGILGYTADDVVSMDFRTPR SSI FDAGA
GIGLNSNFFKVVS WYDNEWGYSCRVIDLMLTMSKDG LV

> P18956|GGT_ECOLI Gamma -glutamyltranspeptidase - Escherichia coli.

MIKPTFLRRVAIAALLSGSCFSAAAAPPAPPVSYGVEEDVFHPVRAKQGM
VASVDATATQVGVLDILKEGGNAVDAAVAVGYALAVTHPQAGNLGGGGFML
IRSKNGNTTAIDFREMAPAKATRDMFLDDQGNPDSKSLTSHLASGTPGT
VAGFSLALDKYGTMPLNKVVQPAFKLARDGFIVNDALADDLKYGSEVLP
NHENSKAIFWKEGEPLKKGDTLVQANLAKSLEMIAENGPDF YKGTIAEQ
IAQEMQKNGGLITKEDLAAYKAVERTPISGDYRGYQVYSMPPPSSGGIHI
VQILNILENFMKKYGFSGADAMQIMAEAEKYAYADRSEYLGDPDFVKVP
WQALTNKAYAKSIADQIDINKAKPSSEIRPGKLAPYESNQTHYSVVDKD
GNAVAVTYTLNFTFGTGIVAGESGILLNNQMDDFSAKPGVFNVYGLVGGD
ANAVGPNKRPLSSMPTIVVKDGTWLVGTSPGGSRITTVLQ MVVNSID
YGLNVAEATNAPRFHHQWLPDELRLVEKGFSPDTLKLLEAKGQKVALKEAM
GSTQSIMVGPDPGELYGASDPRSVDLDTAGY

> P43927|SELB_HAEIN Selenocysteine -specific elongation factor - Haemophilus influenzae.

MIIVTSGHVDHGKTALLKALTGTSTAHLPEEKRRGMTIDLGYAYLPLENK
VLGFIDVPGHEKFLSNMLAGLGGVHYA MLIVAADEGVAVQTKHEHLAILRQ
LQFHEIIVVITKADRTNSAQIESLIQTIKQDYSFLRNANYFVTS AETGQG
ISELRHYLANLAELADTQKPFYAI DRVFSVKGAGTVVGTAFSGTVKVN
DEIYLSTGQKIRIKAIHAQNTSSEQGIAGQRLALNLNADLDRTPMKRGDW
LLQNEPLPPTDRISVQILAEVPLNESQPVHIYHGASRTTGKLTLLQGKNA
AKNDRTLAEIILDSPLFLAFGDKLILRS GDTKTLIAGARVLEINSPKRHK
RTEVRLNFLANLALAENASQRIALTLQHNATTARQLMWTEQLTSLQLDKA
LAERDAVRYQDWCFNPNYVQEKTOQILTALNIYHEQHNDQLGVSKARLYR
MATLNQPENLIHFFIDEMLDDGRLQQTRGWIHLPEHKIQFNTEEKSRWTD
VLNEFEKANGQAIWVRDMANALAI DESIMRNFMYKAGKLYLTPIVKDRF
FLTETLYAYARLIKQIAEEKGKVSVNEVR DKLNFGRKLTVQLMEYFDRMG
FLRRKGNHDHILRDKNVFDL

> P0A9L7|PPIC_ECO57 Peptidyl -prolyl cis-trans isomerase C - Escherichia coli O157:H7.

MAKTAAALHILVKEEKLALDLLEQIKNGADFGKLAKKHSICPSGKRGDDL
GEFRQGMVPAFDKVVVFSCPVLEPTGPLHTQFGYHIIKVLRYN

> P54263|SYN_THET8 Asparaginyl -tRNA synthetase - Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579).

MRVFIDEIARHVDQVELRGWLYQRRSKGKIHFLLIRLDGTGFLQATVVQG
EVPEAVFREADHLRQETALRVWGRVREDRRAPGGFELAVRDLQVVS RPQG
EYPIGPKEHGIDFLMDHRHLWLRHRRPFVAMRIRDELERAIHEFFGERGF
LRFDAPILTPSAVEGTTELFLEVELFDGEK AYLSQSGQLYAEAGALAFKAV
YTFGPTFRAERSKTRRHLLLEFWMVEPEVAFMTHEENMALQEELVSFLVAR
VLERRSRELEMLGRDPKALEPAAEGHYPRPTYKEAVALVNRIAQEDPEVP
PLPYGEDFGAPHEAALSRRFDRPVFVERYPARIKAFYMEPDPELVLN
DDLPAPEGYGEIIGGSQRIHDLELLRRKIQEFGLPEEVYDWYLDLRRFGS
VPHSGFGLGLERTVAWICGLAHVREAI PFP RMYTRMRP

> P15922|PEHX_ERWCH Exo -poly-alpha-D-galacturonosidase - Erwinia chrysanthemi.

MKVITFSRRSALASIVATCLMSTPALAATAQAPQKLQIPTLSYDDHSVML
VWDTPEDTSNITDYQIYQNGQLIGLASQNNDKNSPAKPYISAFYKSDAAN
FHHRIVLQNAKVDGLKAGTDYQFTVTRTVYADGTTSDNSNTVTTTTTAVPK
VINITQYGAKGDGTT LNTSAIQKAIDACPTGCRIDVPAGVFKTGALWLKS
DMTLNLLQGATLLGSDNAADYPDAYKIYSYVSQVRPASLLNAIDKNSSAV
GTFKNIRIVGKGIIDGNGWKRSDAKDELGNTLPQYVKS DNSKVS KDGIL
AKNQVAAAVATGMDTKTAYSQRRSSLVTLRGVQNAVYIADVTIRNPANHGI
MFLESENVVENSVIHQTFNANNGDGVFEFGNSQNMVFNVSVDTGDD SINP
AAGMGQDAQKQEPSQN AWLFNFFRHHGHGAVVLGSHTGAGIVDVL AENNV
ITQNDVGLRAKSAPAIGGGAHGIVFRNSAMKNLAKQAVIVTLSYADNNGT
IDYTPAKVPARFYDFTVKNVTVDSTGNSNPAIEITGSSKDIWHSQFIFS
NMKLSGVSPSTISDLSDSQFNLLTFSNLRSGSSPWKFGTVKNVTVDGKTV
TP

> P43820|SYFB_HAEIN Phenylalanyl -tRNA synthetase beta chain - Haemophilus influenzae.

MKFSEQWVREWVNPVAVSTEQLCEQITMLGLEVDGVEAVAGTFNGVVVGEV
VECAQHPDADKLRVTKVNVGGDRLLDIVCGAPNCRQGLKVACATEGAVLP
GDFKIKKTKLRGQPSGMLCSFSELGIDVEADGIIELPLDAPIGTDLREY
LALDDNAIEISLTPNRADCLSIAGIAREIGVVNKQLVNLQHFEEAAPATIS

DKVQIDLQAPEACPRYLRLVIKVNKAPSP MWMQEKLRRCGIRSIDPIV
DITNYILLEFGQPMHAFDAAKVTQPVQVRFakegeELVLLDGSTAKLQSN
TLLIADQNGPLAMAGIFGGAASGVNSETKDVILESAFFAPLAIAGRARQY
GLHTDASHRFERGVDFELARKAMERATALLLEICGGEAGEICEASSETHL
PKVNTVQLRRSKLDALLGHHIETGSVTEIFHRLGFDVITYANDIWTVTSAS
WRFDIEIEEDLIEEVARIYGYNSIPNNAFLAH LCMREHKESDLDLARIKT
ALVDADYQEAITYSFVDPKIQSLLHHPQEALVLPNPISVEMSAMRVSLIS
GLLGAVLYNQNRQQSRVRLFETGLRFVPDANAEEFVGRQEFVLSAVITGTA
KSEHWAGKAESVDFFDLKGDLSEVLSLTEGGHRVRFVAKQFDALHPGQSA
AIELDQGEIGFIGAIHPSISQKLGLNGKTFVFEILWNAIAARNVVQAKEI
SKFFANRRDLALVVADSVAPAGELIAACKQAGGE KLVQVNLFDVYQGVGVA
EGYKSLAISLTVQDNEKTLEDEEINAVISAVLAEVKQRFNAELRD

> P43816|SYC_HAEIN CysteinyI -tRNA synthetase - Haemophilus influenzae.

MLKIFNTLTREKEIFKPIHENKVGMYVCGVTVYDLCHIGHGRTFVCFDVI
ARYLRSGLGYDLTYVRNITDVDDKIIKRALENKETCDQLVDRMVQEMYKDF
DALNVLRPDFEPRATHHIP EIIIEIVEKLIKRGHAYVADNGDVMFVDESFK
EYGLKSRQDLEQLQAGARIEINEIKKNPMDFVLWKMSKENEPSWASPWGA
GRPGWHIECSAMNCKQLGEYFDIHGGGSDLMFPHHENEIAQSCCAHGGQY
VNYWIHSGMIMVDKEKMSKSLGNFFTIRDVNLHYNAAEVRYFLLTAHYRS
QLNYSEENLNLAQGALERLYTALRGTDQSAVAFGGENFVATFREAMDDEF
NTPNALSVLFEMAREINKLK TEDVEKANGLAARLRELGAILGLLQOPEK
FLQAGSNDDEVAKIEALIKQRNEARTAKDWSAADSARNELTAMGIVLEDG
PNGTTWRKQ

> ACEA_ECOLI P05313 ISOCITRATE LYASE (EC 4.1.3.1) (ISOCITRASE

MKTRTQOIEELQKEWTQPRWEGITRYPYSAEDVVKLRGSVNPECTLAQLGA
AKMWRLHLHGESKKGYSINSLGALTGGQALQQAAGIEAVYLSGWQVAADAN
LAASMPDQSLYPANVPVVERINNTFRADQIQWSAGIEPGDPRYVDY
FLPIVADAEAGFGGVLNFAELMKAMIEAGAAVHFEDQLASVKKCGHMG
KVLVPTQEAIQKLVAAARLAADVTVPTLLVARTDADAADLITSDCDPYDS
EFITGERTSEGFFRTHAGIEQAISRGLAYAPYADLVWCETSTPDLELARR
FAQAIHAKYPGKLLAYNCSPSFWQKNLDDKTIASFQQQLSDMGYKFQFI
TLAGIHSMWFNMFDLANAYAQQEGMKHYVEKVQQPEFAAAKDGTYTFVSHQ
QEVGTGYFDKVTIIQGGTSSVTALTGSTEESSQF

> Q56143|SOXS_SALTY Regulatory protein soxS - Salmonella typhimurium.

MSHQQIIQTLIEWIDEHIDQPLNIDVVAKKSGYSKWWLQRMFRVTVHTQL
GEYIRQRLLLAABELRTTERPIFDIAMDLGYVSQQTFSRVFRREFDRTP
SDYRHRL

> HOXY_ALCEU P22319 NAD-REDUCING HYDROGENASE HOXS DELTA SUBUN

MRAPHKDEIASHELPAATPMDPALAANREGKIKVATIGLCGCWGCTLSFLD
MDERLLPLLEKVTLLRSSLTDIKRIPERCAIGFVEGGVSSEENIETLEHF
RENCILISVGACAVWGGVPAMRNVFELKDCLAEAYVNSATAVPGAKAVV
PFHPDIPRITTKVYPCHEVVKMDYFIPGCPPD GDAlFKVLDDLvNGRPF
LPSSINRYD

> P36649|CUEO_ECOLI Blue copper oxidase cueO - Escherichia coli.

MQRDFLKYVALGVASALPLWSRAVFAAERPTLPIDLLTTDARNRIQL
TIGAGQSTFGGKTATTWGYNGLLGPVAVKLQRGKAVTVDIYNQLTEETTL
HWHGLEVPGEVGGPQGIIPGGKRSVTLNVDQPAATCWFHPHQHGTGR
QVAMGLAGLVVIEDDEILKLMPLPKQWGI DDVPVIVQDKKFSADGQIDYQL
DVMTAAVWGFWDLLTNGAIYPQHAAPRGWLRRLRLNGCNARSLNFATSD
NRPLYVIASDGGLLPEPVKSELVLMGERFEVLVEVNDKPFDLVTLVP
SQMGMAIAPFDKPHVMRIQPIAISASGALPDTLSSLPALPSLEGLTVRK
LQLSMDPMLDMMGMQMLMEKYGDQAMAGMDHSQMMGHMGHNMNMNHGG
KFDFHHANKINGQAFDMNKPMFAAAKQYERWVISGVGDMLLHPFHIHGT
QFRILSENGKPPAAHRAGWKDVKVEGNVSEVLVKFNHDAPKEHAYMAHC
HLEHEDTGMMLGFTV

> P17989|GUB_FIBSU Beta -glucanase - Fibrobacter succinogenes (Bacteroides succinogenes).

MNIKKTAVKSALAVAAAAAALTTNVSADKDFSGAELYTLEEVQYKGFARM
KMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIIITGK
AGAQTSEKHHAVSPAADQAFHTYGLEWTPNYVVRWTVDGQEVKTEGGQV
SNLTGTQGLRFNLWSESAAWVQGFDESKLPLFQFINWVKVYKYPGQGE
GGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILA
LTRKGQESFNGQVPRDDEPAPQSSSSAPASSSSVPASSSSVPASSSSAFV

PPSSSATNAIHGMRTTPAVAKEHRNLVNAKGAKVNPNGHKRYRVNFEH
> P18317|UREE_KLEAE Urease accessory protein ureE - *Klebsiella aerogenes*.

MLYLTQRLEIPAAATASVTLPIDVRVKSrvkvtlndgrdaglllprglll
RGGDVLSNEEGTEFVQVIAADEEVSVVRCDDPFMLAKACYHLGNRHVPLQ
IMPGEELRYHHDHVLDDMLRQFGLTVTFGQLPFEPEAGA YASESHGHHHAH
HDHHAHSH

> P09166|AERA_AERTR Aerolysin - *Aeromonas trota*.
MKALKITGLSLIIISATLAAQTNAAEPIYDPQLRFLSLGEDVCGTDYRPIN
REEAQSVRNNIVAMMGQWQISGLANNWVILGPGYNGEIKPGKASTTWCYP
TRPATAEIPVLPFAFNIPDGDAVDVQWRMVHDSANFIKPVSYLAHYLGYAW
VGGDHSQFVGGDDMDVIQEGDDWVLRGNDGGKC DGYRCNEKSSIRVSNFAY
TLDPGSFVSHGDDVTQSERTLVHTVVGWATNISDTPQSGYDVTNLNYTTMSNW
SKTNTYGLSEKVTSTKNKFKWPLVGETEVSIEIAANQSWASQNGGAVTTAL
SQSVRPVVPARSVPVKIELYKANISYPYEFKADMSYDLTFNGFLRWGGN
AWHHPEDRPTLSHTFAIGPFKDKASSIRYQWDKRYLPGEMKWWDNWAI
QQNGLATMQDSLARVLRPVRASITGDFRAESQF AGNIEIGTPVPLGSDSK
VRRTRSVDGANTGLKLDIPLDAQELAEFGFENVTLVSVTPARN

> Q04710|XYLSI_PSEPU XylDLEGF operon transcriptional activator 1 -
Pseudomonas putida.

MDFRLLNEKSQIFVHAEPIYAVSDYVNQYVGTHTSIRLPKGRPAGRLHHRI
FGGLDLCRISYGGSVRVISPGLETCHYLQIILKGHCLWRDHGQEHYFAPG
ELLLLNPDDQADLYSEDCEKFIVKLPSVVLDRACSENNWHKPREGIRFA
ARHNLQQLDGFINLLGLVCDEAEHTKSMPRVQEHYAGI IASKLLEMLGSN
VSREIFSKGNPSFERVVQFIEENLKRNISLERLAELAMMSPRSLYNLFK
HAGTTPKNYIRNRKLESIRACLNDPSANVRSITEIALDYGFLHLGRFAEN
YRSFAGELPSDTLRQCKKEVA

> P05825|FEPA_ECOLI Ferrienterobactin receptor - *Escherichia coli*.

MNKKIHSALLVNLGIYGVAQAQEPDTPVSHDDTIVVTAAEQNLQAPGV
STITADEIRKNPVARVDVSKIIRTMPGVNLTGNSTSGQRGNRQIDIRGMG
PENTLILIDGKPVSSRNSVRQGWGERDTRGDTSWVPEMERIEVLRGP
AAARYNGAAGGVVNIITKKGSGEWHGSDAYFNAPEHKEEGATKRTNFS
LTGPLGDEFSFRLYGNLDKTQ ADAWDINQGHQSARAGTYATTLPAGREGV
INKDINGVVRWDFAPLQSLLEAGYSRQGNLYAGDTQNTNSDSYTRSKYG
DETNRLYRQNYALTWNGGWDNGVTTSNWVQYEHTRNSRIPEGLAGGTEGK
FNEKATQDFVDIDLDDVMLHSEVNLPIDFLVNQTLTLGTEWNQORMKDL
SNTQALTGTNTGGAIDGVSTTDRSPYSKAEIFSLFAENMELTDSTIVTP
GLRFDHHSIVGNNSPALNISQ GLGDDFTLKMGIARAYKAPSLYQTNPNY
ILYSKQGQCYASAGGCYLGNDLKAETSINKEIGLEFKRDGWLAVGTWF
RNDYRNKIEAGYVAVGQNAVGTDLQWQNDVNPKAVVEGLEGLNVPVSETV
MWTNNITYMLKSENKTGDRLSIIPYTLNSTLSWQAREDLSMQTTFTWY
GKQQPKKYNKQPAVGPETKEISPYSIVGLSATWDVTKNVS LTGGVDNL
FDKRLWRAGNAQTGDLAGANYI AGAGAYTYNEPGRTWYMSVNTHF

> CYAA_HAEIN P40134 ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROP

MECNLAQAKQWVSALDQRRFERALQSGDAFQHVLAIVPLLLHLNHPQLP
GYVIHAPSGIASFLASDYQKKWLTNEYGIHYADHKPSTLKSAVNFHEVFP
PILGVYVMGFSFGSISQTSSSDLDTWICVRDGLSLDEYTLTQKAKRISEW
AMQFNVEINFYLMDDQQR FRNEHYADPLTIENSGSAQYMLLLDEFYRSAVR
LAGKPLLWLHLWVENEKDYKEVARLITEGEIDPNDWVDFGGLGQFSANE
YFGASLWHLKYGIDSPYKSVLKILLEAYSKEYPNTCLIARTFKRDLLAG
NTNPDHFFDPYIAILAKVTQYLTALSEFKRLDFVHRCFYVKATEDFARYQ
ANNWRIRYMEILAQEWGWSAETVKHLNKRPFWKIKAVKENHDNIMKFLML
SYRNLFVEFARKHHIHSSV VPQDINILSRKLYTAFEELPGKVSLLNTQISH
NLSEAHLTFVEVRGNKHKFDGWYLNQPIHHIMFSKERVIEYGESLNKLV
SWAYFNHLLTEKTELSIFSKNVTLSLQRFVTNLRQSFSTIAKQPKNSD
LLNQCEIRSLFIAINLTTDPTSKVEEVLGTGISSRDLFSFGSLEQSLVGS
IDFTYRNWVNEIRTLHFEGQNAILLALKVLSNKIYRGNRPDSIQVYCYSE
RYRQDLRQLVMGLVNRVCS IQVGDIIQQPCQTSRLRVAGKNWQLFFEDRGI
SLQEIGNESVCNEAESAVDFDEVLTQPIEDGETNQESRRYPPEMDFASE
GFLQFFFEDNSDHSFNVIILDESNHLEIYRHCDGEKDEKREINQLYQNA
KQEGDKNPYNIQHNFNYPQFYQLQNGKNGISIVPFKFRQMNK

> P27033|GUNC_PSEFL Endoglucanase C - *Pseudomonas fluorescens*.

MGHVTSPSKRYPAF KRAGSILGVSIALAAFSNVAAGCEYVVTNSWGS
FTAAIRITNSTSSVINGWVSWQYNSNRVTNLWNPNLGSGNPYSASNLW

> P07294|TRAM2_ECOLI Protein traM - Escherichia coli.
MAKVQAYVSDEIVYKINKIVERERRAEGAKSTDVFSFSSISTMLELGLRVY
EAQMERKESAFNQAEFNKVLLECAVKTQSTVAKILGIESLSPHVSNGN PKF
EYANMVEDIRDKVSSEMERFFPENDEE

> P24702|SODC_ACTPL Superoxide dismutase [Cu -Zn] - Actinobacillus
pleuropneumoniae (Haemophilus pleuropneumoniae).
MKLTNLALAFITLFGASAVAFAHADHDHKKADNSSVEKLVVQVQQLDLPVKG
NKDVGTVETITESAYGLVFTPHLHGLAQGLHGFHIIHQNPSCPEKEDGKLV
AGLGAGGHWDPKETKQHGYPWSDNAHLGDLPALFVEHDGGSATNPVLAAPRL
KKLDEVKGHSLMIHEGGDNHSDHPAPLGGGGPRMACGVK

> P48982|BGAL_XANMN Beta -galactosidase - Xanthomonas manihotis.
MLRFTTLAPLVLALALPAAAATPESWPTFGTQGTQFVRDGPYQLLSGA
IHFQRI PRAYWKDRLQKARALGLNTVETVYFVWNLVPEQQGFDFSGNNDV
AAFVKEAAAQGLNVLIRPGPYACAWEAGGYPAWLFGKGNIRVRSRDRPF
LAASQAYLDALAKVQVPLLNHNGGPI IAVQVENEYGSYADDHAYMADNRA
MYVKAGFDKALLFTSDGADMLANGTLPDTLAVVNFAPGEAKSAFDKLIK
RDPQPRMVGEYWAGWFDHWGKPHAATDARQQAEFEWILRQGH SANLYMF
IGGTSFGFMNGANFQNNPSDHYAPQTTSDYDAILDEAGHPTPKFALMRD
AIARVTGVQPPALPAPI TTTTLPATPLRESASLWDNLPTPIAIDTPQPM
QFGQDYGYILYRTTITGPRKGPLYLGVDVRDVARVYVDQRPVGSVERRLQ
VSLEVEIPAGQHTLDVLVENSGRINYGTRMADGRAGLVDVPLLDSSQQLTG
WQAFPLPMRTPDSIRGWTGKAVQGPAPFHRGTLRIGTPTDITYLDMRAFGK
FAWANGVNLGRHWNIGPQTALYLRPSSARVTTTRWWSSTWTMLHPSVRG

> CAIB_ECOLI P31572 L-CARNITINE DEHYDRATASE (EC 4.2.1.89) (L -
MDHLMPKFGPLAGLRVVFSGIEIAGPFAGQMFAEWGAEVIWIENVAWAD
TIRVQPNYPQLSRRLHALSLNIFKDEGREAFKLKMETTDIFIEASKGPA
FARRGITDEVLWQHNPKLVIHLSGFGQYGTTEEYTNLPAYNTIAQAFSGY
LIQNGDVMQMPAFPYTADYFSGLTATTAALAALHKVRETGKGESIDIAM
YEVMLRGMQYFMMDYFNGGEMCPRMSKGDPPYAGCGLYKCADGYIVMEL
VGITQIEECFKDGLAHLGLTPEIPEGTQLIHRIECPYGPLVEEKLDLAWL
ATHTIAEVKERFAELNIAKAVLTVPELESNPQYVARESITQWQTM DGRT
CKGPNIMPKFKNNPQGIWRGMP SHGMDTAAILKNIGYSENDIQELVSKGL
AKVED

> MURF_ECOLI P11880 UDP -N-ACETYLMURAMOYLALANY L-D-GLUTAMYL-2,6
MISVTLSQLTDIINGELQGADITLDAVTTDTRKLT PGCLFVALKGERFDA
HDFADQAKAGGAGALLVSRPLDIDLPLQLIVKDRALFAGELAAVWRQVPA
RVVALTGSSGKTSVKEMTAAILSQCGNTLYTAGNLNNDIGVPMTLRLTP
EYDYAVIELGANHQGEIAWTVSLTRPEALVNNLAAAHLEGFGLAGVAK
AKGEIFSGLPENGLAIMNADNNDWLNWQSVIGSRK VWRFSNAANSDFTA
TNIHVTSHGTEFTLQPTGSDVLLPLPGRHNIANALAAAALSMSVGATL
DAIKAGLANLKA VPGRLFPQLAENQLLDDSYNANVGSMTAAVQVLAEM
PGYRVLVVGDMaelGAESEACHVQVGEAAKAAGIDRVLSVGKQSHAISTA
SGVGEHFADKTALITRLKLLIAEQQVITILVKGSRSAAMEEVVRLQENG
TC

> P0A8X2|YCEI_ECOLI Protein yceI - Escherichia coli.
MKKSLGLTFASLMFSAGSAVAADYKIDKEGQHAFVNFRIQHLGYSWLYG
TFKDFDGTFTFDEKNPAADKVNVTINTSVDTNHAERDKHLRSADFLNTA
KYPQATFTSTSVKKGDELDTGDLTLNGVTKPVTLEAKLIGQGDDPWGG
KRAGFEAEGKIKLKD FNIKTDLGPASQEVDLIISVEGVQQK

> P36936|PEPE_SALTY Peptidase E - Salmonella typhimurium.
MELLLSNSTLPGKAWLEHALPLIANQLNGRRSAVFIPFAGVTQWDEYT
DKTAEVLAPLGVNVTGIHRVADPLAAIEKAEI IIVGGNTFQLLKESRER
GLLAPMADRVRGALYIGWSAGANLACPTIRTTNDMPIVDPNGFDALDLF
PLQINPHFTNALPEGHKGETREQRIRELLVVAPELTVIGLPEGNWIQVSN
GQAVLGGPNTTWVFKAGEEAVALEAGHRF

> P45482|FTSZ_ANASP Cell division protein ftsZ - Anabaena sp. (strain PCC
7120).
MTLDNNQELTYRNSQSLGQPGFSLAVNSSNPFNHSGLNFGQNNDSKKISV
ENNRIGEIVPGRVANIKVIGVGGGGNAVNRMIESDVSVEFWFSINTDAQ
ALTLGAPSRLQIGQKLRGLGAGGNPAIGQKAAEESRDEIATALEGADL
VFITAGMGGGTGTGAAPIVA EVAKEMG ALT VGVVTRPFVFEGRRTSQAE
QGIEGLKSRVDTLIIIPNNKLEVIPEQTPVQEA FRYADDVLRQGVQGIS
DIITIPGLVNVDFADVRAVMADAGSALMGIGVSSGKSRAREAAIAAISSP

LLECSIEGARGVFNITGGSDLTLEHVNAAAETIYEVVDPNANIIIFGAVI
DDRLOGEVTRITVIATGFTGEIQAAPQONANARVVSAPPKRTPTQTPLTN
SPAPTPEPKEKSGLDIPDFLQRRRPPKN
> P27830|RFFG_ECOLI dTDP -glucose 4,6-dehydratase - Escherichia coli.
MRKILITGGAGFIGSALVRYIINETSDAVVVVVKLTYAGNLMSLAPVAQS
ERFAFEKVDICDRAELARVFTEHQPCVMHLAAESHVDRSIDGPAAFIET
NIVGTYTLLAARAYWNALTEDKKSARFRFHISTDEVYGLHSTDDFFTE
TTPYAPSSPYSASKASSDHLVRAWLRTYGLPTL ITNCSNNYGPYHFPEKL
IPLMILNALAGKSLPVYNGGQQIRDWLYVEDHARALYCVATTGKVGETYN
IGGHNERKNLDVETICELLEELAPNKPVGVAHYRDLITFVADRPGHDLR
YAI DASKIARELGLWPQETFESGMRKTVQWYLANESWWKQVQDGSYQGER
LGLKG
> P23598|PRTF_ERWCH Proteases secretion protein prtF - Erwinia chrysanthemi.
MRRKAVLLTVVLSLSSGSAQAMGLLDAWELALRNDAQLRAAGFERDAGQE
EVAIGRAGLLPSLQYTYGANYSHSKVTQRDRTLNNTTKRDYDNYVSTLTL
RQPLLDYAAWARYQQGVTRKLMADQRFDRSQDLMVRLYQSWSEALLAQE
KLMLLDAQRRAYQEQALNRRLLAAGEGTQTDLRETEARYTVTEAQRIEQ
EDTLDAAMTDLENMMSPLQIQDLSPLALDTPDNVTENRSLSQWRELTV
RHNAKLAVQRENVDYSRYEIERNRAGHLPTLDLVASTRNSLSESEYNYNQ
KYDTQTVGLQVRVPLYSGGAVSASMRQAAAEYQSSQAELDNQRQTFAEL
RRQFNLCANGAAKIRAWQMSVAAAEEAIRATRQSVAGGERINLDVLMAEQ
EWYNARRELTEVKYRWLQAWLNLRYSYTAGTLNEQDMMQLAAWFQSAFVINK
TGINAATGNKTN
> ASRC_SALTY P26476 ANAEROBIC SULFITE REDU CTASE SUBUNIT C (EC
MSIDIDI IKARAKNEYRLSKVRGEAMISVRIPGGILPAHLLTVARDIAET
WNGNQIHLTTRQK LAMP G IRYEDI DN VNAALEPFLREIEIELCDVQVEDT
KAGYLAIGGRNIVACQGNRICQKANTD TTGLSRRLEKLVYPSPYHLKTVI
VGCPNDCAKAS MADLGIIGVAKMRFTADRCIGCGACVKACSHHAVGCLAL
KNGKAVKEESACIGCGEVLACPTLAWQRKPD QLWQVRLGGRTSKKSGAL
GKLFNLNVTEDVIKQVIVNLYEFEKEMLGGKPIYLHMGHLIDKGGYLRFK
ERVLRGVQLNPEAMVAERIYWAEDSVARMHLKPAGH
> NHAR_ECOLI P10087 TRANSCRIPTIONAL ACTIVATOR PROTEIN NHAR. -
MSMSHINYNHLYYFWHVYKEGSVVGAAEALYLTPTITGQIRALEDALQA
KLFKRKGRGLEPSELGELVYRYADKMF TLSQEMLD IVNYRKESNLLFDVG
VADALSKRLVSSVLNAAVVEGEPIHLRCFESTHEMLLEQLSQHKLEMIIS
DCPIDSTQQEGLFSVRIGECGVSFWCTNPPPEKFPFACLEERRLLIPGRR
SMLGRKLLNWFNSQGLNVEILGEFDDAALMKAFGAMHNAIFVAPTLYAYD
FYADKTVVEIGRVENVMEEYHAI FAERMIQHPAVQRICNTDYSALFSPAV
R
> P28904|TREC_ECOLI Trehalose -6-phosphate hydrolase - Escherichia coli.
MTHLPHWQNGVIYQIYPKSFQDTTGS GTDLRGVIQHL DYLHKLGVDAI
WLTFFYVSPQVDNGYDVANYTAIDPTYGLDDDFDELVTQAKSRGIRIILD
MVFNHTSTQHAWFREALNKESPYRQFYIWRDGEPEP PPNWRSKFGGSAW
RWAHAESEQY YLHLFAPEQADLNWENPAVRAELKKVCFWADRGV DGLRLD
VVNLISKDRFPED LDGDGRRFYTDGPRAHEFLHEMNRDVF TPRGLMTVG
EMSSTSLEHCQRYAALTGSELSMTFNFHHLKVDYPGGEKWT LAKPDFVAL
KTLFRHWQQGMHNVAWNALFWCNHDQPRIVSRFGDEGEYRVPAKMLAMV
LHGMQGTPIYIQGEEIGMTNPHFTRITDYRDVESLNMFAELRNDGRDADE
LLAILASKSRDNSRTPMQWSNGDNAGFTAGEPWIGLDNYQQINVEAALA
DDSSVFYTYQKLI AL RKQEA I LTWGN YQDLLPNSPVLWCYRREWKGQTL L
VIANLSREIQPWQAGQMRGNWQLVMHNYEEASPPQCAMNLRPF EAVWWLQ
K
> P56126|SYK_HELPY Lysyl -tRNA synthetase - Helicobacter pylori
(Campylobacter pylori).
MFSNQYIQQRIRHKANS LREEGKNPYQNGLKRSLTNAAFLEKYAYVKGLEE
PKDKEKCESIVGRVKLLRLMGKACFIKVE DESTILQVYVSQNELNDEFKS
LKKHLEVGDIVLVKGFPPFATKTGELS IHALEFHILSKTIVPLPEKFHGLS
DIELRYRQRYLDLIVNPSVKDVFKKRS LIVSSVRKFFEMEGFLEVETPMM
HIPPGANARPFITYHNALEVERYLRIAPELYLKR LI VGGFEAVFEINRN
FRNEGMDHSHNPEFTMIEFYWAYHTYEDLIELSKR LFDYLLKTLNLD SKI
IYNDEVDFNQTSVISYLDAL ETIGGISKD ILEKEDRLLAYLLEQGIKVE
PNLTYGKLLAEAFDHFVEHQ LINPTFVTQYPIEISPLARRNDSNPNIADR
FELFIAGKEIANGFSELNDPLDQLERFKNQVAEKEKGDEEAQYMD EYVW

ALAHGMPPTAGQGIGIDRLVMLLTGAKSIKDVILFPAMRPVKNDNFVSE
E
> P15412|RUBR_DESVM Rubredoxin - Desulfovibrio vulgaris (strain Miyazaki).
MKKYVCTVCGYEYDPAEGDPDNGVKPGTAFEDVPADWVCPICGAPKSEFE
PA
> P0ADA1|TESA_ECOLI Acyl-CoA thioesterase I - Escherichia coli.
MMNFNNVFRWHLPFLFLVLLTFRAAAADTLLILGDSLSAGYRMSASA
ALLNDKWQSKTSVNVNASISGDTSQQGLARLPALLKQHQP
RWWLVLEVELGGND
GLRGFQPQQTEQTLRQILQDVKAANAEP
LLMQIRLPANYGR RYNEAFSAI
YPKLAKEFDVPLLPFFMEEVYLK
PQWQDDGIHPNRDAQPF
IADWMAKQL
QPLVNHDS
> SYN_HAEIN P43829 ASPARAGINYL-TRNA SYNTHETASE (EC 6.1.1.22)
MNYIQLQRFNMSKVASIVDVLQGKVAIGETVTVRGWVRTRRDSKAGLSFL
AVYDGSCFDPIQAIINNDIENYSEILRLTTGCSVIVTGKVVESPAEQQA
VELQAEKVEVTGFVEDPDTYPM AAKRHSIEYLRVAHLRPR
TNIIGAVAR
VRHCLSQAHRFFHEQGFYVATPLITASDTEGAGEMFRVSTLDLENLPR
SENGKVDVFSQDFFGKESFLT
VSGQLNGETYACALSKIYTFGPTFRAENS
N
TTRHLAEFWMVEPEVAFATLADNAKLAEDMLKYVFR
AVLAERKDDLQFFE
KHVDKDVITRLENFVNSDFAQIDYTD
AIDVLLKSGKKEFPVSWGIDLSS
EHERFLAEYFKSPVVVKNYPKD
IKAFYMRLNDEKTVAAAMDV
LAPGIGE
IIGGSQREERLEVLDKRMEEMGLN
PDDYWWYRDLRKYGSVPHSGFGLGFE
RLIVYVTGVQNI
RDVIPPAPRANANF
> P09790|IGA_NEIGO IgA-specific serine endopeptidase - Neisseria
gonorrhoeae.
MKAKRFKINAI
SLSIFLAYALTPYSEALV
RDDVDYQIFRDF
AENKGGKFF
VGATDLSVK
NKRGNIGNAL
SNVPMIDFSV
ADV
NKR
IATVVD
PQYAVSVK
HAKAEVHTFY
YQGYNHNDV
ADKENEYRV
VEQNNYEP
HKAWGASNL
GRLE
DYNMARFNK
FVTEVAPI
A
PTDAGGLD
TYKDKNRF
SSFVRI
GAGRQLV
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KGVYHQE
GNEKGYD
LRDLSQAY
RYAIA
AGTPYK
DINIDQ
TMNTEGL
IGF
GN
HNKQYSA
EELKQALS
QDAL
TNYGVL
GDSGSP
LFAFDK
QKNQW
VFLGTY
DY
WAGYGGK
SWQEWNI
YKKEFAD
KIKQHD
NAGTVK
NGEHHW
KTGTN
SHIG
STAVRLAN
NEG
DANNGQ
NVTFED
NGTLV
LNQNI
NQGAG
GLFFK
GDYTV
KG
ANNDITW
LGAGI
DVADG
KKVW
QVKNP
NGDRL
AKIGK
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EINGT
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> P21413|FM98_ECOLI Fimbrial protein 987P - Escherichia coli.
MRMKKSALT
LAVLSSLFSGYSLA
PAENNTSQANL
DFTGKVTASLCQ
VDT
SNLSQTID
LGELST
SALKAT
GKGP
AKSFA
VN
LINC
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LNS
IKY
TI
AG
NN
NTGSDTK
YLVP
ASND
TSAS
GV
GVY
IQD
NNA
QAVE
IGTE
KTV
PV
VS
NG
GLA
LSDQSI
PLQAY
IGTT
TGN
PDT
NGG
VTAG
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MT
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SAG
TP
> P04127|PAPA_ECOLI Pap fimbrial major pilin protein - Escherichia coli.
MIKSVIAGAVAMAVSFGVNNAAPTIPQGQKVT
FNGTVVDAPCSISQKS
ADQSIDFGQLSKSFLEAGGVSKPMDLDIELV
NCDITAFKGGNGAKKGTVK

LAFTGPIVNGHSDELDTNGGTGTAIVVQGAGKNVVFDDGSEGDANTLKDGE
NVLHYTAVVKKSSAVGAAVTEGAFSAVANFNLTYYQ
> METC_HAEIN P44527 CYSTATHIONINE BETA-LYASE (EC 4.4.1.8) (CB
MQTKYDLSTMFIIHSGRQKRFSQGSVNPVLQRASSLLFDSIEDKKHATQRR
AKGELFYGRRGTLTHFALQDLMCEMEGGAGCYLYPCGTAAVTNSILSFVK
TGDHVLMSGAAEPTQYFCNIVLKKMQIDITYYDPLIGEDIATLIQPNTK
VLFLEAPSSITMEIPDIPTIVKAARKVNPVIMIDNTWSAGVLFKALEH
DIDISIQAGTKYLVGHSDIMIGTA VANARTWDQLREHSYLMGQMVADDSA
YTTARGIRTLGVRKQHQESSIKVAKWLSEQPEVKTVYHPALPSCPGEHF
FLRDFSGSSGLFSFELTQRLTSEQVSKFMDHFQLFAMAYSWGGEFSLILC
NQPEEIAHIRPNIKRNLTGSLIRVHIGFENVDELIADLKAGFERIA
> AMPD_ECOLI P13016 AMPD PROTEIN. - ESCHERICHIA COLI.
MLLEQGWLVGARRVPSPHYDCRPDDE TPTLLVVHNSLPPGEGFPWIDA
LFTGTIDPQAHFFAEIAHLRVSACHLIRRDGEIVQYVFPDKRAWHAGVS
QYQGREERCNDFSIGIELEGTDTLAYTDAQYQQLAAVTRALIDCYPDIANK
MTGHCDIAPDRKTDGPAFDWARFRVLVSKETT
> P42673|PCP_PSEFL Pyrrolidone -carboxylate peptidase - Pseudomonas
fluorescens.
MRIVLLTGFPEFPDQD PVNPSWEAVRQLDGVQLGSDVKIVARRLPCAFATA
GECLETRLIDELHPAMVIATGLGPRSDISVERVAINDARIPDNLGEP
IDTAVVADGPAAFPTLPIKAMKAVREAGIAASVSQTAGTFVCNQVFYL
LQHALAGSGVRSGFIVHPFLPEQVAGSQRPSMALDAMVAGLQAAVLTAWH
TPVDVKEAGGQVS
> P39187|YTFJ_ECOLI Protein ytfJ - Escherichia coli.
MTRLKILALTCLLPMMAHAHQFETGQRVPPIGITDRGELVLDKQDQFSYK
TWNASQLVGKVRVLQHIAGRTSAKEKNATLIEAIKSAKLPKPHDRYQTTTTIV
NTDDAIPGSGMFRSSLESNKKLYPWSQFIVDSNGVALGAWQLDEESSAV
VVLDDKGRVQWAKDGALTPPEEVQQVMDLLQKLLK
> P0A940|YAE_T_ECOLI Outer membrane protein assembly factor yaeT -
Escherichia coli.
MAMKLLIASLLFSATVYGAEGFVVKDIHFEGLRVAVGAALLSMPVRT
GDTVNDEDISNTIRALFATGNFEDVRVLRDGTLLVQVKERPTIASITFS
GNKSVKDDMLKQNLASGVRVGESLDRTTIADIEKGLEDFYYSVGKYSAS
VKAVVTPPLRNRVLDKLVFQEGVSAEIQQINIVGNHAFITDELISHFQLR
DEVFPWWNVVGDREYQKQKLAGDLETLSYLDLDRGYA RFNIDSTQVSLTPD
KKGIYVTVNITEGDQYKLSGVEVSGNLAGHSAEIEQLTKIEPGELYNGTK
VTKMEDDIKLLGRYGYAYPRVQSMPEINDADKTVKLRVNVDAAGNRFYVR
KIRFEGNDSKDAVLRREMRQMEGAWLGSDDLVDQGERLNRLGFFETVDT
DTQRVPGSPDQVDVVYKVKERNKTSFNFGIGYGTESGVSFQAGVQDNLW
GTGYAVGINGTKNDYQTYAELSVTNPYFTVDGVSLGG RLFYNDQADDAD
LSDYTNKSYGTDVTLGFPINEYNSLRAGLGYVHNSLSNMQPQVAMWRYLY
SMGEHPSTSDQDNSFKTDDFTFNYGWTYNKLDGRYFPTDGSRVNLTGKVT
IPGSDNEYKVTLDATYVPIDDDHKVVVLGRTRWGYDGLGKEMPFYE
NRYAGGSSTVRGFSNTIGPKAVYFPHQASNYDPDYDECATQDGAKDLC
KSDDAVGGNAMAVASLEFITPTPFISDKYANSVRTSFF WDMGTVWDTNWD
SSQYSGYPDYSNIRMSAGIALQWMSPLGPLVFSYAQPFKKYDGDKAE
QFQFNIGTW
> P01559|HST1_ECOLI Heat -stable enterotoxin ST-IA/ST-P - Escherichia coli.
MKKLMIAIFISVLSFSPFSQSTESLDSSEKITLETKKCDVVKNNSEKKS
ENMNNTFYCCELCNPACAGCY
> P31884|MBHS_WOLSU Quinone -reactive Ni/Fe-hydrogenase small chain -
Wolinella succinogenes.
MLEEKGIERRDFMKWAGAMTAMLSLPATFTPLTAKAAELADRLPVIWLHM
AECTGCSESLLRDTPGIDSLIFDYISLEYHETVMAAAGWQAEHNLEHAI
EKYKGRYVLMVEGGIPAGSSEFYLTVGPHGTTGAEHARHASANAAAIKFAI
GSCSSFGGVQAARPNPTNAQPLSKVTNKPVINVPGCCPPSEKN IVGNVLHF
ILFGTLPSVDAFNREPMWAYGLRIHDLCEERRGRFDAGEFVQEFVDEGAKKG
YCLYKVGCKGPYTFNNSKLRFNQHTSWPVQAGHGCIGCSEPDFWDTMGP
FEFPVANRLYATAFDGLGADKTADKIGITLLAATAVGVAAHAVLSMMVKD
KENN
> P43825|SYK_HAEIN Lysyl -tRNA synthetase - Haemophilus influenzae.
MSEQEVKELDLNGEMLVRREKL AALRAKGNFNPKNFRDALAQDLHNQYD
AEDGEILKEKIEVQVAGRIMTRRAMGKATFITIQDMSGKIQLYVARDNL

PEGVYKDDVGTWDLGDIVGIGKTLFKTKTDELTVKTTTEVQLLTKALRPLP
DKFHGLTDQEVRYRQRYLDLISNEESRRTFIIRSKVVAGIREYFISKGFM
EVETPMLQVPIPGGASARPFVTHHNALDVMYLRIAPELYLKRLVVGGER
VFELNRNFRNEGVSVRHNPEFTMLEYYQAYADYHDLMDNTEELLRKLAI
ILGTTIVKYGDLEDFGKPFERITLHDATIKYGADKGIKEDLYDFDRAK
ATAERLGIEVQKSWGLGSIVNAIFEEVAEHHLIQPTFLNGSPAETSPLAR
RNDENPEVTDRELFIFGGREIGNGFSELNDAEDQNERFDAQVAAKEAGDD
EAMFKDEDFVVALEHGLPPTAGEGLGIDRLAMLYANAPSIRDVILFPAMR
QK

> P05827|ILVY_ECOLI HTH-type transcriptional regulator ilvY - Escherichia coli.

MDLRDLKTLFHLAESRHFGRSARAMHVSPTLSRQIQRLLEEDLGQPLFVR
DNRTVTLTEAGEELRVFAQQTLLQYQQLRHTIDQQGPSLSGELHIFCSVT
AAYSHLPPILDRFRAEHPSVEIKLTTGDAADAMEKVVTEADLAIAGKPE
TLPGAVAFSMLLENLAVVLIAPALPCPVRNQVSVEKPDWSTVPFI MADQGP
VRRRIELWFRNKISNPMIYATVGGHEAMVSMVALGCGVALLPEVVLNS
PEPVRNRVMILERSDEKTPFELGVCAQKRLHEPLIEAFWKILPNHK

> P37648|YHJY_ECOLI Protein yhjJ - Escherichia coli.

MQGTKIRLLAGGLMMATAGYVQADALQPDPAWQQGTLNSGLQWQVLTTP
QRPSDRVEIRLLVNTGSLAESTQQSGYSHAIPRIALTQSGGLDAAQ ARSL
WQQGIDPKRPMPPVIVSYDTTLFNLSLPNNRNDLLKEALSILANATGKLT
ITPETINHALQSQDMVATWPAADTKEGWRYRLKGSTLLGHDPADPLKQPV
EAEKIKDFYQKWYTPDAMTLLVGVNDARSVVDQINKTFGELKGRKRETPA
PVPTLSPLRAEAVSIMTDAVRQDRLSIMWDPWQPIRESAALLRYWRADL
AREALFWHVQQALSASNSKDIGLGFDCRVLYLRAQCAINIESPNDKL NSN
LNLVARELAKVRDKGLPEEEFNALVAQKLELQKLFAYARADTDILMGQ
RMRSLQNVVDIAPEQYQKLRQDFLNSLTVEMLNQDLRQQLSNDMALILL
QPKGEPEFNMKALQAVWDQIMAPSTAAATTSVATDDVHPEVTDIPPAQ

> P0A283|PTGA_SALTY Glucose-specific phosphotransferase enzyme IIA component - Salmonella typhimurium.

MGLFDKLSLVSDDKKDTGTIEIVAPLSGEIVNIEDVPDVFVFAEKIVGDG
IAIKPTGNKMPVAVDGTIGKIFETNHAFSIESDSGIELFVHFGIDTVELK
GEGFKRIAEQGVRKVGDPVIEFDLPLLEEKAKSTLTPVVISNMDEIKEL
IKLSGSVTVGETPVIRIKK

> P11312|FMF3_ECOLI F17 fimbrial protein - Escherichia coli.

MQKIQFILGILAAASSSATL AYDGGKITFNGKVVDQTCVTTESKNLTVKL
PTVSANSLASSGKVVLTPFTTILLEGCNTPAVTGAQNVNAYFEPNANTDY
TTGNLTNTASSGASNVQIQLLNADGVKAIKLGQAAAAQSVDTVAINDANV
TLRYNAQYYATGVATAGDVTSTVNYTIAVQ

> P44443|RNE_HAEIN Ribonuclease E - Haemophilus influenzae.

MKRMLINATQKEELRVALVDGQRLFDLDIESP GHEQKANIYKGIKTRVE
PSLEAAFVDYGAERHGFPLKEIAREYFPDDYVFQGRPNIRDILVEGQEV
IVQVNKEERGNKGAALTTFFVSLAGSYLVMPNNPRAGGISRRIEGDERTE
LKEALSSLDVDPDGLIVRTAGVGKSPPEELQWDLKVLHHEAIIKQASQS
RPAPFLIHQESDVIVRAIRDYLRDIDIGEILIDSPKIFEKAKEHIKLVPRD
FINRVKLYQGEVPLFSHYQIESQIESAFQREVR LPSGGSIDVIDTEALTA
IDINSARSTRGGDIEETALNTNLEAADEIARQLRLRDLGGLVVIDFIDMT
PIRHQREVENRIRDVPRDRARIQISRISRFGLLEMSRQLSPSLGESSH
HICPRCQGTGKVRDNESLSLSILRLLLEEEALKENTKQVHTIVPVQIASYL
LNEKRKAISNIEKRHNVDIIVAPNEAMETPHFSVFRLRDGEVNELSYNL
AKIHCAQDENTEESLLSRNVETTAVIEQPAVESA VVALSISEAAPTVER
KSNEPSLLAKIIAKIKGLFATKSEENKPKNNRTRSNPNRNQRRSQDRRSS
RRRSENNETERTEEQVRNVRERNQRRPRRNLVEESIAESAVNSTPVFEA
KEERTEPVTQRRQRDLRKRVRVEDNETVVENNFSTTEKMPVDVITVQN
NDEKPVHQNQRSERQERQRTPHLRAANNQRRRDQEPKSPMPLFAAVV
SPELASGKAWIDYSTVNLKPNHFLSVDELLEQEK TKKGFITPAMGIVVE
EKSPDVKALDFITQPANESVQKKVQESLDRLSSYKPKQEVVESIDPAINV
DEPETLEKVSKEFVRTYEFNGRLGTISSVPHTKAEMTLAKANDEMPEDFPI
RAWQDSRYFFYKGAAGHHCAISHVYSEPTRTKSE

> P35636|SCR_ZYMMO Sucrose-6-phosphate hydrolase - Zymomonas mobilis.

MESPSYKNLIKAEDAQKAGKRLLSSEWYPGF HVTPLTGMMNDPNGLIFF
KGEYHLFYQYPPFAPVWGPMPHWGHAKSRDLVHWETLPVALAPGDSFDRDG
CFSGCAVDNNGVLTLIYTGHIIVLSNDSLDAIREVQCMATSIDGIHFQKEG

IVLEKAPMPQVAHFRDPRVWKENNHWFVVGVRTDDEKHHQIGHVALYRS
ENLKDWFIVKTLGLDGNSQLPLGKRAFWECPDFSLGNRSVLMFSPQGLK
ASGYKRNRLFQNGYILGKWQAPQFTPETSFOEL DYGHDYFAAQRFEAKDG
RQILIAWFDMWENQKPSQRDQWAGCMTLPRKLDLIDNKIVMTPVREMEIL
RQSEKIESVVTLSAEHPFTMDSPLQEIELEIFDLEKSSAYQAGLALRCNG
KGQETLLYIDRSQNRILDRNRSGQNVKIRSCPLPNTSKVRLHIFLDRS
SIEIFVGGDDQTQGLYSISSRIFPDKDSLKGRLLFAIEGYAVFDSFKRWTLO
DANLAAFSSDAC

> P43928|RF3_HAEIN Peptide chain release factor 3 - Haemophilus influenzae.

MSYPLEEVNKRRTFAIISHPDAGKTTITEKVLLYGNAIQTAGSVKKGKSA
AHAKSDWMEMEKQRGISITTSVMQFPYNDCLVNLDDTPGHEDFSEDYRT
LTAVDSCMLVIDSAKVEERTIKLMEVTRLRDTPIIITFMNKLDRDIRDPI
ELLDEVENVLKIRCAPITWPIGCGKLFKGVYHLAKDETYLYQSGQGST IQ
AVRVVVKGLNNPELDVAVGDDLAQQRLREELVQVQASNEFEQDAFIKGELE
PVFFGTALGNFVDFLDGLTQWAPKQSRQADTRTVESAEEKFSGFVFK
IQANMDPKHRDRVAFMRVVSQKYEKGMKLVKRVIRIGKDVVISDALTFMAGD
RAHAEEAYAGDI IGLHNHGTIQIGDTFTQGETLKFITGIPNFAPELFRIR
LKDPLKQKQLLGLVQLSEEGAVQVFRPLNNDLIVGAVGVLFQFDVVVS R
LKTEYNVEAIYENVVATARWVECADEKKFEEFKRNEQNLALDGGDNLT
YIAPTMMVNLNAQERYPDVVVFKTREH

> P13720|PAPG_ECOLI Fimbrial adhesin papG - Escherichia coli.

MKKWFPAFLFLSLSGNDALAGWHNVMFYAFNDYLTNAGNVKVIDQPQL
YIPWNTGSATATYYS CSGPEFASGVYFQEYLAWMVVPHVYTNEGFNIFL
DVQSKYGWSME NENDKDFYFFVNGYEWDTWTNNGARICFYPGNMKQLNKK
FNDLVFRVLLPVDLPKGHYNFPVRYIRGIQHYYDLWQDHYKMPYDQIKQ
LPATNTLMLSFDNVGGCQPSTQVLNIDHGSIVIDRANGNIASQTLISYCD
VPVSVKISLLRNTPIYNNKFSVGLGNGWDSIISLDGVEQSEELRWYT
AGSKTVKIESRLYGEEGKRKPGELSGSMTMVLSP

> P13734|AGAR_ALTAT Beta -agarase - Alteromonas atlantica (Pseudomonas atlantica).

MLKVIPWLLVTSLSVAIPTIYIHAATTEVVVNLNVKHSVEGKSEFERKNHIK
LHSTLNDNDWQGEEDKLKYMMEELDVYFGRDNGGTVWVNFQAIEDPANIG
YADPQNI IARGQAQRETNWQNKSAHLHQYDGRGDLMIGGQPRAYHLGNTS
PCCGGSAAWQAKGGDAVGDFLGQYVNEFFRSAGDPVTKGHLAPVYFEVL NE
PLYQVTDAPHELGLLEQPIPPIDIFTFHNDVADAFRQHNTHIKIGGFTVAF
PIFEQREFARWEERMKLFIDTSGSHMDVYSTHFYDLEDDNRFKGSRLEAT
LDMIDQYSLALGETKPHVISEYGGRRNRPENAPWSALRDWWFLKTASPM
LMQFLSRPDSVLTSIPFVPIKALWGTAADGTPYNWRLRQQKEAPNETGE
NWWFTEMVKFYQLWSDVKGTRVDTFSTNSDFLIDSYVQNDKAYVLISNL T
EQAEKIVVHKYGA PASSQPTTRIKHLYLKGAAPRLMKQVMRQISKSRLL
LKRLW

> P46025|OPP23_HAEIN Outer membrane protein P2 - Haemophilus influenzae.

MKKTAAALIVGAFAAANAAVVYNNEGTNVELGGRLSIITEQSNSTVDD
QEQQHGALRNAGSRFHKATHNFGDGFYAQGYLETRLVSDYPSSSDHFG
GITTKYAYVTLGNKAFGEVCLK RAKTIADGITS AEDKEYGVLLNNKKIPT
NGNTVGYTYKIGDGLDGLVGLGANYLLAQS RVPGGPSPFPRKQGEVYQQI
SNGVQVGAKEYDANNI IAGIAFGRTNYKTAGADFPYGDVFLGRKEQVEGV
LSTLGYRFSDLGLLVSLDSGYAKTKYTTTDS SSGSQITNPAYDEKR SF
VSPGFQYELMEDTNVYGNFKYERTSVNQKNTREQAVLFGVDHKLHKQVL
TYIEGAYARTKTNDKGKTEKTGK EKS VGVGLRVYF

> P24930|RUS2_THIFE Rusticyanin - Thiobacillus ferrooxidans (Acidithiobacillus ferrooxidans).

MYTQNTMKNWYVTVGAAAALAAATVGMGTAMAGTLDTTWEATLPQVKAM
LEKDTGKVS GDTVYSGKTVHVVA AAVLPGFPPSFEVHDKKNPTLEIPA
GATVDVTFINTNKGFGHSFDITKKGPPYAVMPVIDPIVAGTGFSPVP KDG
KFGYTDFTWHP TAGTYYYVCQIPGHAATGMFGKIVVK

> P24305|OMP32_COMAC Outer membrane porin protein 32 - Comamonas acidovorans (Pseudomonas acidovorans) (Delftia acidovorans).

MKKSIALAVLAASGAAMAQSSVTLFGIVDTNVAYVNKDAAGDSRYGLGT
SGASTSRLGLRGTEDLGGGLKAGFWLEGEIFGDDGNA SGFNFKRRSTVSL
SGNFGEVRLGRDLVPTSQKLTSYDLFSATGIGPFMGFRNWAAGQGADDNG
IRANNLISYYPNFGGFNAGFGYAFDEKQTI GTADSVGRYIGGYVAYDNG
PLSASLGLAQQTAVGGLATDRDEITLGASYNFGVAKLSGLLQQT KFKRD

IGGDIKTNSYMLGASAPVGGVGEVKLQYALYDQKAIDSKAHQITLGYVHN
LSKRTALYGNLAFLNKNDASTLGLQAKGVYAGGVQAGE SQTGVQVGIRHA
F

> P02930|TOLC_ECOLI Outer membrane protein tolC - *Escherichia coli*.

MKKLLPILIGLSLSGFSSLSQAENLMQVYQQARLSNPELRKSAADRDAAF
EKINEARSPLLPQLGLGADYTYNNGYRDANGINSNATSASLQLTQSIFDM
SKWRALTLEKAAGIQDVTYQTDQQTLLINTATAYFNVLNAIDVLSYTQA
QKEAIYRQLDQTTQRFNVGLVAITDVQNARAQYDTVLANEVTARNNLDNA
VEQLRQITGNYYPELAALNVENFKTDKQPVNALLKEAEKRNLSLLQARL
SQDLAREQIRQAQDGHLPDLTASTGISDTSYSGSKTRGAAGTQYDDSN
MGQNKVGLSFSPLPIYQGGMVNSQVKQAQYNFVGASEQLESABRSVQTVR
SSFNNINASSINAYKQAVVSAQSSLDAMEAGYSVGTTRTIVDVLDATTT
LYNAKQELANARYNYLINQLN IKSALGTLNEQDLLALNNALSKEPVSTNPE
NVAPQTPEQNAIADGYAPDSPAPVVQQTSAARTTTSNGHNPFRN

> P73456|FTSZ_SYNY3 Cell division protein ftsZ - *Synechocystis* sp. (strain PCC 6803).

MTLNNDLPLNNGFTGSGLNDGTEGLDDLFSISSIVDNEPLEALVETPTFA
SPSPNLKRDQIVPSNIAKIKVIGVGGGCNAVNRMIASGVTGIDF WAIN
DSQALNTNAPDCIQIGKLRGLGAGGNPAIGQKAAEESRDEIARSLEG
TDLVFITAGMGGGTGTGAAPIVAFAVAKEMGCLTVGIVTRPFTFEGRRRAK
QAEEGINALQSRVDTLIVIPNNLLSVIPAETPLQEAQFRVADDILRQGVQ
GISDIIIIIPGLNVNDFADVRAVMADAGSALMGIGVSGKSRAKEAATAAI
SSPLESSIQGAKGVVFNVTGGTDLTLHEVNVAEEIIYEVVDADAN IIFG
AVIDDRLQEMRITVIATGFNGEKEKPKQAKTSSKPVLSGPPAGVETVPST
TTPEDPLGEIPMAPELDIPDFLQKRRFR

> P52682|BLAN_SERMA Carbapenem-hydrolyzing beta-lactamase Sme-1 - *Serratia marcescens*.

MSNKVNFKTSFLFSVCLALSFAFNAHANKSDAAAKQIKKLEEDFDGRIGV
FAIDTQSGNTFGYRSDFRPLCSSFKGFLAA AVLERVQQKLDINQVKY
ESRDLEYHSPITTYKYKSGMGLGDMASAALQYSDNGATNIIEMERFLGGPE
GMTKFMRSIGDNEFRDLRWELELNNTAIPGDKRDTSTPKAVANSLNKLALG
NVLNAKVKAIIYQNLKGNNTGDARIRASVPADWVVGDKTGSCGAIGTAND
YAVIWPKNRAPLIVSIYTTTRKSKDDKHSDKTIAEASRIAIQAID

> P39186|NAPB_RALEH Diheme cytochrome c napB - *Ralstonia eutropha* (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (*Cupriavidus necator* (strain ATCC 17699 / H16 / DSM 428 / Stanier 337)).

MKPSRSWASLLAVCAVLLAALAMQAIFFPAPARAQGLVDMRGPTAIANE
PRAPLLYPTENKDIRRTRNYTMQPPTIPHKIDGYQLDKDFNRCMFCHART
RTEETQAIIPVSIITHYMDRDNVLDVSPRRYFCTQCHVPQADTKPLIGNN
FVDVDTILKRRPGAKGAAK

> P45600|CYSB_KLEPN HTH-type transcriptional regulator cysB - *Klebsiella pneumoniae*.

MKLQQLRYIIVEVNNHNLNVSSTAEGLYTSQPGISKQVRMLEDELGIQIFA
RSGKHLTQVTPAGQEIIRIAREVLSKVDIAIKSVAGEHTWPKGSLYVATT
HTQARYALPGVIKGFIERYPVSLMHMQGSPTQIAEAVSKGNADFIAIATE
ALHLYDDLVMPLCYHWNRSIVVTPEHPLATKGSVSIIELAQYPLVTTYTFG
FTGRSELDTAFNRAGLTPRIVFTATDADVIKTYVRLGLGVGVIASMAVDP
VSDPDLVKLDANGIFSHSTTKIGFRRTFLRSYMYDFIQRFAPHLTRDVV
DTAVALRSNEDIEAMFKDIKLPEK

> P56000|SYV_HELPY Valyl-tRNA synthetase - *Helicobacter pylori* (*Campylobacter pylori*).

MIMKQEPPTYQPEIEKKIYEICSHRGYFEIDGNEAIQEKNRFCMMPP
PNVTGVLHIGHALTLSLQDILARYKRMDGYKTLYQPGLDHAGIATQNVVE
KQLLSQGIKEDLGREEFIKKVWEWKEKSGGAILEQMKRLGVSAAFSRTR
FTMDKGLQRAVKLAFWKWYEKGLIIQDNMNVNCTKDGALSDIE VEYEEER
KGALYYIRYYLENQKDYLVVATTRPETLFGDSALMVNPNDEYKHLVQOK
AILPLIHRTIPIIADEHVEMEFGTGCVKVTPGHDFNDYEVGKRHHLETIK
IFDEKGILNAHCGEFENLERLEARDKVVERLKENALLEKIEEHTHQVGHC
YRCHNVVEPYVSKQWFVKPEIAQSSIEKIQOGLARFYPSNWINNYNAWMR
ELRPWCISRQLFWGHQIPVFTCENNHQFVSLDTPLSCTCKSETL EQDKD
VLDTWFSSGLWAFSTLWGWQEKSGLFNESDLKDFYPNTTLITGFDILFFW
VARMLFCSESLGELPFKDIYLHALVRDEKGEKMSKSGNVIDPLEMIEK
YGADSLRFTLANLCATGRDIKLS'THLENNKNFANKLFNAASYLKLKQES

FKDKERLNEYQTPLGRYAKSRLNSATKEARNALDNYRFNDATTLRYRFLW
GEFCDWFIEFSKVENEAIDELGSLKEALKLLHPMPFISESLYHK LSNT
ELENTESEMVPYPKDLAQDEKLEHEFEVIKDCIVSLRRLKIMLETPPIV
LKEASVGLREAIENTERLQTYAQKLARLEKVSVISSKPLKSVSDVGEFCQ
TYANLENLDLSPLVARLKKQLEKLEKEKLLKLNHNENFVKNAPKSVLEKA
KESLKTLLKESKIKQELDLLEQP
> P15488|FMS3_ECOLI CS3 fimbrial subunit A - *Escherichia coli*.
MLKIKYLLIGLSLSAMSSYSLAAAGPTLTKELALNVLSPAALDATWAPQD
NLTLNNTGVSNTLVGVLTLSNTSIDTVSIASNTVSDTSKNGTVTFAHETN
NSASFATTISTDNANITLTKNAGNTIVKTTNGSQLPTNPLPKFITTEGNE
HLVSGNYRANITITSTIK
> Q06530|DHSU_CHRVI Sulfide dehydrogenase [flavocytochrome c] flavoprotein
chain - *Chromatium vinosum* (*Allochromatium vinosum*).
MTLNRDFIKTSGAAVAAVGILGFPHLAFGAGRKVVVGGGTGGATAAKY
IKLADPSIEVTLIEPNTDYYTCYLSNEVIGGDRKLESIKHGYDGLRAHGI
QVVHDSATGIDPKKLVKTAGGAIEFGYDRCVVAPGIELIYDKIEGYSEEA
AAKLPHAWKAGEQTAILRKQLEDMADGGTVVIAPPAAPFRCPGPPYERAS
QVAYYLKAHKPKSKVIIIL DSSQTFQSKQSQFSKQWERLYGFGTENAMIEWH
PGPDSAVVVKVDGEMMVETAFGDEFKADVNLIPPQRAGKIAQIAGLTND
AGWCPVDIKTFESSIHKGIHVIGDACIANPMPKSGYSANSQGVAAAAV
ALLKGEPEGTPSYLNTCYSILAPAYGISVAAIYRPNADGSAIESVPDSGG
VTPVDAPDWLREVEVQYAYSWYNNIVHDTFG
> P26509|PGLR2_PCECC Endo -polygalacturonase - *Pectobacterium carotovorum*
subsp. *carotovorum* (*Erwinia carotovora* subsp. *carotovora*).
MEYQSGKRVLSSLGLIGLFSASAWASDRTVSEPKTPSSCTTLKADSST
ATSTIQKALNNCDQKAVRLSAGSTSVFLSGPLSLPSGVSLLIDKGVTLR
AVNNAKSFENAPSSCGVVDKNGKGCDAFITAVSTTNSGIYGPGTIDGQGG
VKLQDKKVSWWELAADAKVKKLQNTPRLIQINKSKNFTLYNVSLINSPN
FHVVFSDGDFGFTAWKTIKTPSTARNTDGDIPMSSKNITIAYSNIATGDD
NVAIKAYKGRAETRNISILHNDFGTGHGMSIGSETMGVYVNVTVDDLMNG
TTNGLRIKSDKSAAGVNVGVRYSNVVMKNVAKPIVIDTVYEKKEGSNVPD
WSDITFKDVTSETKGVVVLNGENAKKPIEVTMKNVKLTSdstwQIKNVNV
KK
> P12608|IRPA_SYNP7 Iron-regulated protein A - *Synechococcus* sp. (strain
PCC 7942) (*Anacystis nidulans* R2).
MIVTGSQVRQGLNTWFLPLRRTAIGLGCAGVATLFSACGQTQALITNQT
IQGFVDQVVVPSYVSVAAAGATQLEQALQTYQQAPTAANLEAARQAWRVAR
DRWEQTECFAFGPADSEGFDMGTWPI DRQGLKTAQAQVVEQREDSRKG
FHAIEELLFAATEPTLSDRQHLVILATDLTKQAQGLVTRWQQASDQPAYR
SVLLSAGSTDSAYPTLNAAGTEIVQGLVDSLSEVASEKIGGPLETQEPDR
FESFVSRNTLSDLRNNWTGAWNVYRGQRSDGVAAGSLQQRLQQHPVIAQ
QLDQQFATARQALWAIPEPIETNLASPRGKVAVLTAQTAAVSDTLERQ
VLPLVQ
> P29492|TCPN_VIBCH TCP pilus virulence regulat ory protein - *Vibrio*
cholerae.
MIGKKSFTNVYRMSKFDTYIFNNLYINDYKMFWDISGIAKLIDKNCLVS
YEINSSSIILLKNSIQRFSLTSLSDENINVSVITISDSFIRSLKSYILG
DLMIRNLYSENKDLLWNCEHNDAVLSEVVNGFREINYSDEFKLVFFSG
FFSKVEKKYNSIFITDDLAMEKISCLVKS DITRNWRWADICGELRTNRM
ILKKELESRGVKFRELINSIR ISYSISLMKTGEFKIKQIAYQSGFASVSY
FSTVFKSTMNVAPSEYLFMLTGVAEK
> P23536|PT1_RALEH Phosphoenolpyruvate -protein phosphotransferase -
Ralstonia eutropha (strain ATCC 17699 / H16 / DSM 428 / Stanier 337)
(*Cupriavidus necator* (strain ATCC 17699 / H16 / DSM 428 / Stanier 337)).
MPFALHGI PVSRGVAIGRAHLLAPAALDVSHYLVDEQQLDAEVERLRAAR
AAVRAELAAALKRDLPRDAPEELGAFLDVHAMILDDEALAREPEALIRGRR
YNAEWALTTREELMRQFDEIEDEYLRERKTDIRQVVERILKALAGAPVL
VPAPVPALAADGEAATGVIVVAHDIAPADMLQFRHTVVFHGFVTDMGGRTS
HTAIVARSLDIPAAVGVQASASELIRQDDWIIDGDAGLVIV DPTAIILEE
YRHRQSERALEKKRLQRLRHTPAVTL DGLEIDLLANIEMAEDAGAALAAG
AVGVGLFRSEFLFMNRRDELPGEDEQFQAYRGAVDAMHGLPVTIRTIDIG
ADKPLDARGDEFETALNPALGLRAIRWSLSEPGMFLTQLRALLRASAFGP
VRLLVPMLAHASEIDQTLALIAKAKRQLDERGEAYDPGMKVGAMIEIPAA

VLLLPLFLRKMDFLSIGTNDLIQYTLAIDRADNAVAHLFDPL HPAVLQLV
ARTIREANRAGVPVAVCGEMAGDPSMTRLLLGMLGREFSMHPAQLLRVKQ
EILHAHCERLEPLVDQVLQAFDPEEQAAALRQLARP
> P96197|LEU3_AZOVI 3-isopropylmalate dehydrogenase - *Azotobacter vinelandii*.
MSKQILVLPDGGIGPEIMAEAVKVLQLANEKYQLGFVLYDELGGAAVDK
YGVPLADETLERARRRCHPARRRRRSEMGR HRPGHPPGARPAENPFATGP
VRQPAPGVLYPQLAEASTLRPEVVAGLDLILVRELTGGIYFGAPRESRL
ANGERMAYDTLPYSESEIRRIAKVGFDMARVRGKCLCSVDKANVLASSQL
WRAVVEEVAKDYPDVLVLSHMYVDNAAMQLVRAPKQFDVIVTDNMFGDILS
DEASMLTGSIGMLPSASLDADNKGMYEPCHGSRRPDIAGKGIANPLATIL
SVSMMLRYSFGQVEAANAIEQAVSKVLDQGL RTGDIWSEGCRKVGTAEMG
DAVVAALATL
> P43832|SYR_HAEIN Arginyl-tRNA synthetase - *Haemophilus influenzae*.
MNIQSILSDKIKQAMILAGADQSCDALIRQSGKPQFGDYQANGIMAAAKK
LGLNPREFAQKVLNDLQLSDIAEKLEIAGPGFINIFLNPTWLTTEISAAL
SHKNLGIQATNKQTVVIDYSSPNVAKEMHVGHRLRSTIIGDAVARTLEFLG
HNVIRANHVGDWGTQFGMLIAYLEKMONEHASEMELQDLEAFYREAKKHY
DEDEVFAEKARNYVVKLQSGDEYCRMTWKRLVDITMQQNQHNYARLNVTL
TEKDVMGESLYNPLMPSIVKDLKKQGLAVENDGALVVYLDLDFKKNKDGPM
GVIVQKKDGGFLYTTTDIAAAKYRYETLKANRALVFSDFRQSQHMQQAWL
ITRKAGYVPDSFSLHKNFGMMLGKDGKPFKTRTGGTVKLADLLDEAIER
ATVLINEKNTNLSNDEKEAVIEAVGIGAVKYADLSKNRTTDYVFDWDNML
SFEANTAPYMQYAYTRIRSIFNKTDINSTALLAAPTIKDDKERTLAIKL
LQFEEAVQTVGKEGTPHVLCAYLLEYLAGIFSSFYEHCPILNAEDESIKLS
RLKLALLTEKTLKQGLTLLGIKTVEKM
> CATA_PROMI_P42321 CATALASE (EC 1.11.1.6). - *PROTEUS MIRABIL*
MEKKKLTTAAGAPVVDN NNVITAGPRGPMLLQDVWFLEKLAHFDREVIPE
RRMHAKGSGAFGTFTVTHDITKYTRAKIFSEVGGKTEMFARFSTVAGERG
AADAERDIRGFALKFYTEEGNWDVMGNTPVFYLRDPLKFPDLNHIVKRD
PRTNMRNMAYKWDFFSHLPESLHQLTIDMSDRGLPLSYRFVHGFSGHTYS
FINKDNERFWKHFHRCQQGKIKNLMDEAEALVGKDRESSQRDLFEAIER
GDYPRWKLQIQIMPEKEA STVPYNPFDLTKVWPHADYPLMDVGYFELNRN
PDNYFSDVEQAAFSPANIVPGISFSPDKMLQGRLFSYGDHRYRLGVNHH
QIPVNAPKPCPFHNYHRDGAMRVDGNSGNGITYEPNSGGVFQEQPDFKEPP
LSIEGAADHWNHREDEDYFSQPRALYELLSDDDEHQRMFARIAGELSQASK
ETQQRQIDLFTKVHPEYGAGVEKAIKVLEGKDAK
> P06996|OMP_C_ECOLI Outer membrane protein C - *Escherichia coli*.
MKVKVLSLLVLPALLVAGAANAEEVYNKDGKLDLYGKVDGLHYFSDNKDV
DGDQTYMRLGFKGETQVTDQLTGYGQWEYQIQGNSAENENNSWTRVAFAG
LKFQDVGVSFDYGRNYGVVYDVTSWTDVLPFEGGDTYGSDFMQRGNGFA
TYRNTDFFLVDGLNFAVQYQKNGNPSGEGFTSGVTNNGRDALRQNGDG
VGSITYDYEGFGIGGAISSSK RTDAQNTAAYIGNGDRAETYTGGLKYDA
NNIYLAAQYTQTYNATRVGSLGWANKAQNFEEVAQYQFDFGLRPSLAYLQ
SKGKNLGRGYDDEDILKYVDVGATYYFNKNMSTYVDYKINLLDDNQFTRD
AGINTDNIVALGLVYQF
> P06972|FHUB_ECOLI Ferrichrome transport system permease protein fhuB -
Escherichia coli.
MSKRIALFPALLLALL VIVATALTWMNFSQALPRSQAQAASPDIDVIE
QMIFHYSLLPRLAISLLVGAGLGLVGLVLFQQVLRNPLAEPTTLGVATGAQ
LGITVTTLWAI PGAMASQFAAQAGACVVGLIVFGVWAGKRLSPVTLILAG
LVVSLYCGAINQLLVI FHHDLQLSMFLWSTGTLTQTDWGGVERLWPQLLG
GVMLTLLLLRPLTLMGLDDGVARNLGLALSARLAALS LAIVISALLVNA
VGIIGFIGLFPALLAKM LGARRLLPRLMLASLIGALILWLSAQIILWLTR
VWMEVSTGSVTALIGAPLLLWLLPRLRSISAPDMKVNDRVAAERQHVLA
FALAGGVLLMVAVVALSFGGRDAHGTWASGALLEDLMPWRWPRIMAALFA
GVMLAVAGCIIQRLTGNPMASPEVLGISSGAAFGVVLMLFLVPGNAFGWL
LPAGSLGAAVTLIIMIAAGRGGFSPHRMLLAGMALSTAFMLLMMLQAS
GDPRMAQVLTWISGSTYN ATDAQVVRTGIVMVILLAITPLCRRWLTILPL
GGDTARAVGMALTPTRIALLLLAACLTATATMTIGPLSFVGLMAPHIARM
MGFRRTMPHIVISALVGGLLLVFADWCGRMVLFPPFQIPAGLLSTFIGAPY
FIYLLRKQSR
> P09489|PRTS_SERMA Extracellular serine protease - *Serratia marcescens*.

MILNKRLKLAYCVFLGCYGLSIHSSLAAAYQDPGRLGA PDSWKTAEFNRQW
GLEAISAEFAYARGTYGKGITIGVIDNAILSHSEFSGKLTRLDNNGSYNFS
YDKQDNMSFGDHGTHVAGIAAAKRDGAGMHGVAFDADIIGTKLNDYGNRN
GREELIQSAARVINNSWGIAPDIRRDAKGDI IWLPNGRPDYVAVFKSEVI
AEMMRSSVVEWGSEQPVPTGGHSAMSTLLRAARHGKLVFSAGNYNNYN
IPEAQKSLPYAFPVDLVNLYLIVTNLSDENQLSVSSTSC GQTASYCVSAPG
SDIYSTVGRLESNTGGAVNREAYNKGELSLNPGYGNKSGTSMAAPHVTGV
AAVLMQRFPYMSADQISAVIKTTATDLGVAGIDNLFVGWGRVNLRDAINGP
KMFITKEDIPOEYVPGSYSEKQFVVNIPGLGNIVEPGTPVERRCTSSEC
SFDSWSNDISGHGGLTKTGAGTLALLGNNTYRGDTWVKQGVLAIDGVSAS
NVYIENSGLTSSEGTGAFRAARSGSVAPGNIGITLHVL HDAIFDRGSQY
NVEVADNGRSDKIAARRAFLNGGSVNVSLERSQNLLSQNEAQSLLGNKYT
ILTTTDGVTGRFENANPSYFPVKVALDYRGNDVGLGITRTRDASFDLAST
ENEKAVARAVETLNATEPVTETAKRSVAIPAAEEANLLQSDGGEAQAVNE
EASIVAGHPYIESFLGFTSARELQQATRQLSGQIHADMASAQINESRYLR
DTATERLRQAEGRRATDIKADDNGAWAKLLGWSGHASGN DNATGYQTST
YGVLLGLDSEFGDGRGLGMMTGYTRTSLDGGYQSDAHS DNYHLGLYGDKR
FGALALRAGGTYTWHRIDTSRSVNYGAQSDREKAKYNARTGQLFIESGYD
WTSDAVNLEPFANLAYTHYRNEEINEQGGAAALRGDKQSQSATASTLGLR
ADTEWQTDVVAIALRGELGWQHGYGKLERKTQLMFKRTDAAFDVNSVPVS
RDGAILKAGVDVSNKNAVLSLGYGGQLSSNHQDNSVNAAGL TWRP
> P44529|IPYR_HAEIN Inorganic pyrophosphatase - Haemophilus influenzae.
MADFNQILTPGDVDAGI INVVNEIPEGSCHKIEWNRKVAAFQLDRVEPAI
FAKPTNYGFIPQTLDEDELDVLLITRQPLATGVFLEAKVIGVMKFVDD
GEVDDKIVCVPADDRDTGNAYNSLADLPANLIKQIEFHFNKYKALKKPGS
TKVTHWGDVEEAKVIRESIKRWNER
> P20379|SODC_CAUCR Superoxide dismutase [Cu -Zn] - Caulobacter crescentus
(Caulobacter vibrioides).
MIRLSAAAALGLAAALAASPALAQTSAVAVKAGDGKDGAVTVTEAPHG
VLLKLELKLTPGWHAHAFHEKGCCTPDFKSAGAHVHTAATTVHGLLNP
DANDSGDLNPIFAAADGAATAEIIYSPLVSLKAGGRPALLDADGSSIVVH
ANPDDHKTQPIGGAGARVACGVK
> P18668|EFTU_SYNP6 Elongation factor Tu - Synechococcus sp. (strain ATCC
27144 / PCC 6301 / SAUG 1402/1) (Anacystis nidulans).
MARAKFERTKPHANIGTIGHVDHGKTLTAAITTVLAKAGMAKARAYADI
DAAPEEKARGITINTAHVEYETGNRHYAHVDCPGHADYVKNMITGAAQMD
GAILVVSAADGMPQPTREHILLAKQVGVNIVVFLNKEDMVDDAELLELV
ELEVEVLDSSYDFPGDDIPIVAGSALQALEAIQGGASGQKGDNPWVDKIL
KLMEVVDAYIPTPEREVDPRPFLMAVEDVFTITGRGTVAATGRIERGSVKVG
ETIEIVGLRDRSTTVTGVMFQKTLDEGLAGDNVGLLLRGIQKTDIERG
MVLAKPGSITPHTKFESEVYVLKKEEGGRHTPFFPGYRPPQFYVRTTDDVTG
AISDFTADDGSAEMVIPGDRIKMTVELINPIAIEQGMRFIREGGRTIG
AGVVSKILQ
> P0AG78|SUBI_ECOLI Sulfate-binding protein - Escherichia coli.
MNKGVGLTFLLAATSVMAKDIQLLNVSYPDTPRELYEQYNKAFSAHWKQQ
TGDNVVIRQSHGGSGKQATSVINGIEADVVTLALAYDVDAIAERGRIDKE
WIKRRLPDNSAPYTSITVFLVRKGNPKQIHDWND LIKPGVSVITPNPKSSG
GARWNYLAAGYALHNNNDQAKAQDFVRALYKNVEVLDSGARGSTNTFV
ERGIGDVLIAWENEALLAANELGKDKFEIVTPSESILAEPTVSVVDKVV
KKGTEVAEAYLYLSPGQEI AAKNYRPRDAEVAKKYENAFPKLKL
TIDEEFGGWTAKQKEHFANGGTFDQISKR
> P13507|AMT4_PSEST Glucan 1,4 -alpha-maltotetraohydrolase - Pseudomonas
stutzeri (Pseudomonas perfectomarina).
MSHILRAAVLAAMLLPLPSMADQAGKSPNAVRYHGGDEIILQGFHWNVVR
EAPNDWYNILRQQAATIAADGFSAIWMPVPWRDFSSWSGSKSGGEGYF
WHDFNKNGRYGSDAQLRQAASALGGAGVKVLYDVVPHNMNRGYPDKKEINL
PAGQGFWRNDCADPNYPNDCDDGDRFIGGDADLNTGHQPQVYGMFRD EFT
NLRSQYGAGGFRDFVIRGYAPERVNSWMTDSADNSFCVGEVWKGPSSEYPN
WDRNTASWQQI IKDWSDRACKPVDFALKERMQNGSIADWKHGLNGNPD
PRWREVAVTFVDNHDGTGSPGQNGGQHHWALQDGLIRQAYAYILTSPTGTP
VVYWSHMYDWGYGDFIRQLIQVRRRAAGVRADSAISFHSGYSGLVATVSGS
QQTLVVALNSDLNPGQVVASGSFSEAVNASNGQVRVWRSRGTGSGGGEPA
LVSVSFRCDNGATQMGDSVYAVGNVSQLGNWSPAAALRLTDTSGYPTWKG

SIALPAGQNEEWKCLIRNEANATQVRWQGGANNSLTPSEGATTVGRL
> P39049|ALXM_PHOS4 Alginate lyase - Photobacterium sp. (strain ATCC 433367).
MIKSNLVISSLAIVSSMSYAGVEFSNPSGQLGEPANYTQFANILSASELQ
ISDPNGKKGKEYFALDNDFTGIV NDNFYVDKQSQUALVFKMANDHLRNEL
RVQKNFRITDLPDHFYTYANVEILHPLQSMANSTSKQNEITFLQVHNKGL
DDQGTHNVPHPLLRVVWKENNQGVKGFHFWAITKNNAVICKGSFGKKNKDK
EMCRADVAYSIDLGPAPTDKGTDFITITVGNKTLAIDVNGQRKVEKNIDY
WRHLLSYFKAGVYNQFTQGESEAHFNQLRYQVNTF
> P96142|SYV_THETH Valyl -tRNA synthetase - Thermus thermophilus.
MDLPKAYDPKSVPEPKWAEKWAKNPFVANPKSGKPPFVIFMPPPNVTGSLH
MGHALDNSLQDALIRYKRMRFGEAVWLPDGTDHAGIATQVVVERLLKKEGK
TRHDLGREKFLERFWQWKEESGGTILKQLKRLGASADWSREAFMDEKRS
RAVRYAFSRYHEGLAYRAPRLVNWCPRCETTLSDELVEETEPTPGKLYTL
RYEVEGGGFIEIATVRPETVFADQAI VHPEDERYRHLGKRARIPLTEV
WIPILADPAVEKDFGTGALKVTPAHDPLDYEIGERHGLKPVSVINLEGRM
EGERVPEALRGLDRFEARRKAVELFREAGHLVKEEDYTIALATCSRCTP
IEYAIFFQWLLMRPLAEVVLKGLRRGDIAFVPERWKKVNMWLENVVDW
NISRQLWGWGHQIPAWYCEDCQAVNVRPERYLEDPDTSCEACGSPRLKRDE
DVFDTWFFSALPLSTLWPEETEDLKA FYPGDVLTGYDILFLWVSRME
VSGYHFMGERPFKTVLLHGLVLDKQKMSKSGNVIDPLEMVERYGADA
LRFALIYLATGGQDIRLDRWLEMARNFANKLYNAARFVLLSREGFQAKE
DTPTLADRFMRSLRSGVEEITALYEALDLAQAAREVYELVWSEFCDWYL
EAAKPALKAGNAHTLRTLEEVLAVLLKLLHPMPFLTSELYQALTGKEEL
ALEAWPEPGGRDEEAERAFEALKQAVTAV RALKAEAGLPPAQEVRVYLEG
ETAPVEENLEVFRLSRADLLPERPAKALVKAMPVVTARMPLEGLLDVVEE
WRRRQEKRLKELLALAERSQRKLASPGFREKAPKEVVEAEEARLKENLEQ
AERIREALSQIG
> P50199|GNO_GLUOX Gluconate 5 -dehydrogenase - Gluconobacter oxydans
(Gluconobacter suboxydans).
MSPDLFSLSGARALVTGASRG IGLTLAKGLARYGAEVVNLGRNAESLDS
AQSGFEAEGLKASTAVFDVTDQDAVIDGVAAIERDMGPIDILINNAGIQR
RAPLEEF SRKDWDDL MSTNVNAVFFVVGQAVARHMI PRGRGKIVNICSVQS
ELARPGIAPYTATKGAVNLTGKMATDWGRHGLQINGLAPGYFATEMTER
LVADEEFTDWLCKRT PAGRWGQVEELVGA AVFLSSRASFFVNGQVLMVDG
GITVSL
> P17835|FM3_BORPE Serotype 3 fimbrial subunit - Bordetella pertussis.
MSKFSYPALRAALILAASPVLPALANDGTIVITGSISDQTCVIEEPSTLN
HIKVVQLPKISKNALRNDGDTAGATPFDIKLEKCPQALGALKLYFEPGIT
TNYDTGDLIAYKQTYNASGNLSTVSSATKAKGVEFRLANLNGQHIRMG
TDKTTQAAQFTTGKVTNGSKSYTLRYLASVYVKKPKEDVDAQITSYVG FS
VVYP
> O84686|EFTS_CHLTR Elongation factor Ts - Chlamydia trachomatis.
MSDFSMETLKNLRQQTGVGLTKCKEALHAKGNLEDAVVYLRKLG LASAG
KKEHRETKEGVIAARVDERGAALVEVNVETDFVANNNVFRFVTSLLSDL
LDHELSDVDALALVMSQEPSLSVEELKAVTMQTVGENIRISRAFYTPVN
SGQSVGIYSHGNKAVAI AFLSGSENQEA LAKDIAMHIVASQPQFLSKES
VPQEVLEREREVSSQVAGKPQEVVEKITQGKFRAFFQEACLLAQAFIKD
PEVTIQGLIDRAAKASGEPLKVEHFVFWKMGA
> P16481|PTHP_KLEPN Phosphocarrier protein HPr - Klebsiella pneumoniae.
MFQQEVTITAPNGLHTRPAAQFVKEAKGFTSEITVTSNGKSASAKSLFKL
QTLGLTQGTVVTL SAEGEDEQKAVEHL VKLMAELE
> P31101|HCP_DESVH Hydroxylamine reductase - Desulfovibrio vulgaris (strain
Hildenborough / ATCC 29579 / NCIMB 8303).
MFCFQCQETAKNTGCTVKGMCCKPEETANLQDLLIFVLRGIAIYGEKLKE
LGQPDFRSDDFVLQGLFATITNANWDDARFEAMISEGLARRDKLRNAFLA
VYKAKNGKDFSEPLPEAATWTGDSTAF AEKAKSVGILATENEDVRSRLREL
LIIGLKGVAAYAEHAAVLFGRKTEIDEFMLEALASTTKDLSVDEMVALVM
KAGGMAVTTMALDEANTTTYGNPEITQVNIGVGKNPGILISGHDLKDMA
ELLKQTEGTGDVYTHGEMPLPANYYP AFKKYPHFVGNVGGSWWQQNPEFE
SFNGPILLTTNCLVPLKENTYLDRLYTTGVVGYEGAKHIADRPAGGAKD
FSALIAQAKKCPPVEIETGSIVGGFAH HQVLALADKVVEAVKSGAIKRF
VVMAGCDGRQKRSRYTEVAENLPKDTVILTACAKYRYNKNLNGDIGGI

PRVLDAGQCNDSSYSLAVIALKLKEVFLGDDINDLPVSYDIAWYEQKAVAV
LLALLFLGVKGIKIRGLPTLPAFLSPNVAKVLVENFNKIPKIGTVQDDIAAMM
AGK

> FES_ECOLI P13039 ENTEROCHELIN ESTERASE. - ESCHERICHIA COLI.

MFEVTFWWRDPQGS EEYSTIKRVVYITGVTDHHQNSQPQSMQRIAGTNV
WQWTTQLNANWRGSYCFIPTERDDIFSVSPDRLELREGWRKLLPQAIAD
PLNLQSWKGGGRGHAVSALEMPQAPLQPGWDCQAPEIPAKEIIWKSERLK
KSRRVWIFTTGDATAEERPLAVLLDGEFWAQSMVPVPLTSLTHRQQLPP
AVYVLIDAIDTTHRAHELPCNADFWLAVQQEELLPLVKAIAPFSDRADRTV
VAGQSFGLSALYAG LHWPERFGCVLSQSGSYWWPHRGGQQEGVLEKLLK
AGEVSAEGLRIVLEAGIREPMIMRANQALYAQLHPKESIFWRQVDGGHD
ALCWRGGLMQGLIDLWQPLFHDRS

> P77849|KDSA_CHLTR 2 -dehydro-3-deoxyphosphooctonate aldolase - Chlamydia trachomatis.

MFPENKMLLIAGPCVIEDNSVFETARRLKEIVAPYASSVHWIFKSSYDKA
NRSSVHNRYRGPGLKGLQTLAKIKEELDVEILTDVHSPDEAREAAKVCDI
IQVPAFLCRQTDLLVLTAGETQAIVNIKKGQFLSPWEMQGPIDKVLSTGNN
KIILTERGCSFGYNNLVSDMRSIEVLRRFVFPVVFVFDGTHSVQLPGALHSQ
SGGQTEFIPVLRSAIAAGVQGLFIETHPNPSSALSDAASMLSLKDLERL
LPAWVQLFTYIQEMDAVSV

> P04042|CHEB_SALTY Chemotaxis response regulator protein-glutamate methylesterase - Salmonella typhimurium.

MSKIRVLSVDDSSALMRQIMTEIINSHSDMEMVATAPDPLVARDLIKKFNP
DVLTLDVEMPRMDGLDFLEKLMRLRPMVVMVSSLTGKGSEVTLRALELG
AIDFVTKPQLGIREGMLAYSEMIAEKVRTAARARIAAHKPMAPTTLKAG
PLLSSEKLIAGASTGGTEAIRHVLPPLSS PAVIITQHMPPGFTRSF
ERLNKLCQISVKEAEDGERVLPGHAYIAPGDKHMEIARSGANYQIKIHDG
PPVNRHRPSVDVLFHSAKHAGRNAVGVILTGMGNDGAAGMLAMYQAGAW
TIAQNEASCVVFGMPREAINMGGVSEVVDLSQVSQMLAKISAGQAIRI

> P15319|PAPD_ECOLI Chaperone protein papD - Escherichia coli.

MIRKKILMAAIPLEVISGADAA VSLDRTRAVFDGSEKSMTLDISNDNKQL
PYLAQAWIENENQEKIITGPVIATPPVQRLEPGAKSMVRLSTTPDISKLP
QDRESLFYFNLEIPRSEKANVLQIALQTKIKLFYRPAAIKTRPNEVWQ
DQLILNKVSGGYRIENPTPYVTVIGLGGSEKQAEEGEFETVMLSPRSEQ
TVKSANYNTPYLSYINDYGGRPVLSFICNGSRCSVKKEK

> P37726|PORF_PSEFL Outer membrane porin F - Pseudomonas fluorescens.

MKLKNTLGFAGISIAATSFGALAQGGAVEGELFYKKQYNDVSKHIEDG
FNPGARIGYFLTDDLSLNSYDKTNHTRSNDGTGSQKIGGDTSSLTAQYH
FGQAGVDSLRYVEGGFGHQSRGNVKADGHSGRDQSTLAIAGAGVKYYFT
NNVYARAGVEADYALDNGKWDYSALVGLGVNFGGNAGAAAPAPTAPAPE
PTPEPEAPVAQVVRVE LDVKFDFDKSVKPNVSYGDVKNLADFMAQYPATN
VEVAGHTDSIGPDAYNQKLSQRRADRVKQVLVKDGVAPSRITAVGYGESR
PVADNATEAGRAVNRREASVEAQAQ

> P43821|SYGA_HAEIN Glycyl-tRNA synthetase alpha chain - Haemophilus influenzae.

MSTKFNKVFQGMILALQEQYWANQGCTIVQPFDMVEVGAGTSHPMALRAL
GPEPMAFAYVQ PSRRPTDGRYGENPNRLQHYYQFQVVIKPSPDNIQELYL
GSLEMLGFDPTKNDIRFVEDNWENPTLGAWGLGWEVWLNMEVTVQFTYFQ
QVGGLECKPVTGEVTYGLERLAMYIQGVDSVYDLVWSDGPLGKTTYGDVF
HQNEVEQSTYNFEHANTDFLFYCFDQYEKEAQELLALEKPLPLPAYERIL
KAAHSFNLLDARKAISVTERQRYILRIRALTKGVAEAYASREALGFPGC
KK

> P0A6P1|EFTS_ECOLI Elongation factor Ts - Escherichia coli.

MAEITASLVKELRERTGAGMMDCCKALTEANGDIELAIENMRKSGAIKAA
KKAGNVAADGVIKTKIDGNYGIIILEVNCQTFVAKDAGQAFADKVLDA
VAGKITDVEVLKAQFEEERVALVAKIGENINIRRVAALEGDVLGYSYQHG
RIGVLVAAKGADEELVKHIAHVAAASKPEFIKPEDVSAEVEVEKEYQVQLD
IAMQSGPKPEIAEKMVEGRMKKFTGEVSLTGQPFVMEPSKTVGQLLKEHN
AEVTGFIRFEVGEIEKVETDFAAEVAAMSKQS

> P46739|NFAA_ECOLI Nonfimbrial adhesin 1 - Escherichia coli.

MKAKKYENQIYNENGRRCQRHGRRLAIADANGLNTVNAGDGKNLGTATAT
ITTLQSCSVLDLNLVTPNATVNRAGMLANREITKFSVSGKDCPSDTYAVWF
KEIDGEGQGVAGQTTVTKNFYLMKMTSADGTASVGDINIGTKSGKLSGQL

VGGKFDGKITVAYDSATAPADVYTYDLMAAVYVQ
> FDHD_WOLSU P28181 FDHD PROTEIN. - WOLINELLA SUCCINOGENES.
MRHTDRFVKKVIERIGDQRVLAEEEDVVIKEERISLYLNGTKLMSMMSL
PSDQDAHAVGFLMSEGVIEKIEDLKSQVQISSDGSSVYVEALINHENITNL
FKEKTLTSGCCVGVGTGNLEGNVLRKFIATPMQISLERIWEGMEEFEMSSH
LFHETGCVHKASLLEDGSKITAEDIGRHNAIDKVMGKARLGRIDTEKAV
LVSGLRSLMEMVVKAVMHNIPMIVSRAAATFLGIKTAQELGVTLVGFARG
EKMNIYTHSGRVDLRACKRKRGVTLHAPNQSSSLLR
> P61316|LOLA_ECOLI Outer-membrane lipoprotein carrier protein -
Escherichia coli.
MKKIAITCALLSSLVSWADAASDLKSRLDKVSSPHASFTQKVTDGSG
AAVQEGQGDLDWVKRPNLFWNHTQPDSEILVSDGKTLWFYNPFFVEQATAT
WLKDATGNTPFMLIARNQSSDWQYNIKQNGDDFVLTPKASNGNLKQFTI
NVGRDGTIHFQSAVEQDDQRSSYQLKSQONGAVDAAKFTTTPPQGVTVDD
QRK
> P25910|BLAB_BACFR Beta-lactamase type II - Bacteroides fragilis.
MKTVFILISMLFPVAVMAQKSVKISDDISITQLSDKVYTYVSLAEIEGWG
MVPSNGMIVINNHOAALLDTPINDAQTEMLVNWVTDLSLHAKVTTFIPNH
HGDCIGGLGYLQRKGVQSYANQMTIDLAKKGLPVPEHGFTDSLTVSLDG
MPLQCYLLGGGHATDNIVVWLPTENILFGGCMKLDNQATSIGNISDADVT
AWPKTLDKVKAKFPFASARYVVPGHGDYGGTEL IEHTKQIVNQYIESTSKP
> P70865|SYA_BARBA Alanyl-tRNA synthetase - Bartonella bacilliformis.
MNSVNNIRSTFLDYFHRNGHEVLSSSPLVPRNDPTLMFTNAGMVDKKNV
TGLEKHSYNRATTAQKCVRAGGKHNDLDNVGYTARHHTFFEMLGNFSFSN
YFKEEAIFYAWNLLTKEFCLSKDKLLVTVYHDDVAAGLWRKISGLSEEK
IIRIATNDNFWMGM DTGPCGPCSEIFYDHGDKIWGGPPGSADEDGDRFIE
IWNLVFMQYEQLSKEKRIELPQPSIDTGMGLERIAAVLQGVHDNYDIDLF
RTLIIHASQEIIGVKATGDFFASHRVIADHLRSSAFLIADGIMPSNEGRGY
VLRIRRRARRHALLGSKDLLMWRVLPVLI SEMGQAYPELVRAESLISE
ILKLEETRFRKTLERGLGLLNEASTHLEEGDYFNGEVAFKLYDITYGFPLD
LTQDALRRRGISVDV DAFDKAMKRQKAEARANWSGSGDCVTEVWFSIRD
QVGATEFLGYETEKAEGIITALIRDGEVVDHIDLQKAMIVVNQTPFYGE
SGGQVGDSGIISGANFIFEVHDTQKKGDNVFIHIGEIKTGQAKKHDCVEL
IVDSARRRKIRANHSATHLLHESLRQTLGSHVVQKGSFVSPDRLRFDFSH
PKSISSEELKKIEDLANDIVLQNSKVTRLM AIDDAIAEGAMALFGEKYG
DEVRVISMGNNEQTG SKKWSIELCGGTHVQRTGDIGLIHI ISETSVAA
GVRRIEALTATAARLYLHGQDRRVYEIAGLLKTPADVQERVQTLLDERR
KLEKELNDSRKKIALNGGSSVNSQGDITINGISFMGGVVSNI LPKDLKAL
VDSGKKKIGSGVVAFISVSEDGKGSVAVGVTDLTDLTLNAVDLVRIISVT
LGGQGGGRRDMAQAGGSEGGKADEALVALKDSLKG
> P50203|PHAB_ACISR Acetoacetyl-CoA reductase - Acinetobacter sp. (strain
RA3849).
MSEQKVALVTGALGGIGSEICRQLVTAGYKIIATVVPREEDREKQWLQSE
GFQDSDFRVFLTDLNNHEAATAAIQEATAAEGRVDVLVNNAGITRDATFK
KMSYEQWSQVIDTNLKTFTVTQPVFNKMLEQKSGRIVNISSVNLKGGQF
GQANYSASKAGIIGFTKALAQEGARSNICVNVVAPGYTATPMVTAMREDV
IKSIEAQIPLQRLAAPAEIAAAVMYLVSEHGAYVTGETLSINGGLYMH
> P0A1F0|DDLA_SALTY D-alanine--D-alanine ligase A - Salmonella typhimurium.
MAKLRVGI VFGGKSAEHEVSLQSAKNIVDAIDKTRFDVLLGIDKAGQWH
VNDAENYLQNADDPAHIALRPSAISLAQVPGKHQHQLINAQNGQPLPTVD
VIFPIVHGTLEDGSLQGMRLRVANLPFVG SDVLSAACMDKDVAKRLLRD
AGLNIAPFITLTRNRHAFSFAEVESRLGLPLFVKPANQSSVGVSKVAN
EAQYQQAVALAFEFDHKVVEQGIKGREIECAVLGNDNPQASTCGEIVLN
SEFYAYDTKYIDDNGAQVVVPAQIPSEVNDKIRAIQAYQTLGCAGMAR
VDVFLTADNEVVINEINTLPGFTNISMYPKLWQASGLGYTDLISRLIELA
LERHTANNALKTTM
> P18190|MBHS_AZUCH Uptake hydrogenase small subunit - Azotobacter
chroococcum mcd 1.
MSQLETXYDVMRRQGITRRSFLKYCSLTGRPCLGPTFAPQIAHAMETRPP
TPVVWLHGLECTCCSESFIRSGDPLVKDVVLSMISLDYDDTLMPPRHQGT
VEETMRKYKGEYLLAVEGNPPLNEDGMFCIVGGKPFLLDQLKHAAKDAKAV
IANGSCASWGCVQAAKPNPTQAVPIHKVITDK PMIKVPGCPPIAEVMTGV
ITYMLTFFGKLELDRQGRPKMFYQRIHDKSYRRPHFDAGQFVEHWDDG

ARKGYCLYKVGCKGPTSYNACSTVRWNEGTSFPFIQAGHGCI GCSEDFWD
KGSFYERLTTIPQFGIEKNADQIGPRRRRSGAAIAAAHVTAIKRLQNK
GDQA

> P21982|FLAA_SPIAU Flagellar filament outer layer protein - Spirochaeta
aurantia.

MKRFFAILGAALFVNGSFAFAEQATLIDFSKLVGEGNTGLHAPTTIDYSR
QAGSAYS AEDKAAMKISLAIPSWEI ELASSSQTVENQTL SLVTAAPVKQD
AARYGGETVMGVRIHFPSFGINSFAVIKPPFTIPAYATLGDATAQNAVAG
GQFDGFGVLKNVGVIKSIQINILGRNYLNRLSLLLEDQNGDEREIVMGYL
NFDGWKSLQWNNPNYQTEVRNRDLQIVPLYPRSAPLIKLKGIKIHRDG SQ
EGGDIVSYIKDIKVIYDQAVVDRNSDVDEAIWGILRQREEQYRNFELAK
LGNLQVLRSLKLEKKMAKEADFDQAAPAAAAARAPATN

> P0AA19|OMPR_SALTY Transcriptional regulatory protein ompR - Salmonella
typhimurium.

MQENYKILVVDDMRLRALLERYLTEQGFQVRSVANAEQMDRLLTRESFH
LMVLDLMLPGEDGLSICRRLRSQSNPMPIIMVTAKGEEVDRIVGLIIGAD
DYIPKPFNPRELLARIRAVLRRQANELPGAPSQEEAVIAFGKFKLNLGTR
EMFREDEPMLPTSGEFAVLKALVSHPREPLSRDKLMLNARGREYSAMERS
IDVQISRLRRMVEEDPAHPRYIQTWVGLGYVFPVDPGSKA

> P27002|SYFB_THETH Phenylalanyl -tRNA synthetase beta chain - Thermus
thermophilus.

MRVFFSWLKAYVPELESPEVLEERLAGLGFETDRIERVFPPIRGVVFARV
LEAHPPIPGTRLKRLVLDAGRTVEVVS GAENARKGIGVALALPGTELPGLG
QKVGERVEIQVRSFGMALSPRELVGGEYGGGLLEFPEDALPPGTPLSEAW
PEEVVLDLEVTNRPDALGLLGLARDLHALGYALVEPEAALKAEALPLPF
ALKVEDPEGAPHFTLGYAFGLRVAPSLWMQRALFAAGMRPINNVVDVTN
YVMLERAQPMHAFDLRFVGEIAVRRAREGERLKTLDGVERTLHPEDLVI
AGWRGEESFPLGLAGVMGGAESEVREDTEAIALEVACFDVPSIRKTARRH
GLRTEASHRFERGLDGTQVPAQRRLSLLQALAGARVAEALLEAGSPKP
PEAIPFRPEYANRVDLGTSYPEAEQIAILKRLGCRVEGEGPTYRVTPPSHR
LDRLEEDLVEEVARIQGYETIPLALPAFFPAPDNRGVEAPYRKEQRLRE
VLSGLGFQEVYTYSFMDPEDARRFRLDPPRLLLLNPLAPEKAALRTHLFP
GLVRVLKENLDLDRPERALLFEVGRVFREREETHLAGLLFGEGVGLPWAK
ERLSGYFLKGYLEALFARLGLAFRVEAQAFPFLHPGVSGRVLVEGEEVG
FLGALHPEIAQELLEPPVHLFELRLPLPKPLAFQDPSRHPAAFRDLAVV
VPAPTPYGEVEALVREAAGPYLESALFDLYQGPPLEPGHKS LAFHLRFR
HPKRTL RDEEVEEAVSRVAEALRARGFGLRGLDTP

> P40120|OPGD_ECOLI Glucans biosynthesis protein D - Escherichia coli.

MDRRRFIKGSMAA VCGTSGIASLFSQA AFAADSDIADGQTQRFDFSIL
QSM AHDLAQTAWRGAPRPLPDTLATMTPQAYNSIQYDAEKSLWHNVENRQ
LDAQFFHMGMGFRRRVRMFSVDPATHLAREIHF RP E LFKYNDAGVDTKQL
EGQSDLG FAGFRVFKAPELARRDVVSFLGASYFRAVD DTYQYGLSARGLA
IDTYTDSKEEFPDFTAFWFDTVKPGATFTFTVYALLDSASITGAYKFTIHC
EKSQVIMDVENHLYARKDIKQLGIAPMTSMFSCGTNERMCDTIHPQIHD
SDRLSMWRNGEWICRPLNNPQKLFNAYTDNNPKGFGLLQLDRDFSHYQ
DIMGWYNKRPSLWVEPRNKWGKGTIGLMEIPTTGETLDNIVCFWQPEKAV
KAGDEF AFQYRLYWSAQPPVHCPLARVMATRTGMGGFSEGWAPGEHYPEK
WARRFAVDFVGGDLKAAAPKGI EPVITLSSGEAKQIEILYIEPIDGYRIQ
FDWYPTSDSTDPVDMRMYLRCQGD A ISETWLYQYFPPAPDKRQYVDDRVM
S

> ISPA_HAEIN P45204 GERANYLTRANSTRANSFERASE (EC 2.5.1.10) (FA

MGHFSEELQVQTRINRFLEAQFEGIESHNAPLLEAMKYALLLGG KRVRP
FLVYATGQMLGAEKQTLDYAAAAIEAIIHAYSLIHDDLPAMDDDLNRRGHP
TCHI QFDEATAI LAGDALQSFAFEILTKTPNISTEQKLALI QILAQGAGV
QGMCLGQSLDLISEHKQISLSELELIHRNKTGALLIAALKLGFICSPHFT
DKRLEQSLTQYAEAI GLAFQVQDDILDIEGDSAEIGKQV GADL DL DKSTY
PKLLGLSGAKQKAQDLYQSALSELEKIPFDTTVRALAEFII TRKS

> P41255|SYK_THETH Lysyl -tRNA synthetase - Thermus thermophilus.

MNDQTRQRLNLEALVEAGFAPYPYRFPKTHSAEAILKAKRGAPPESEWP
EEEVAVAGRLVALRRMGKVTFAHLLEDTGRIQLYFQRDLTPKYELLK KLD
VGDILGVRGHPFTTKTGEVTVKVL DWTPLVKSLHPLPKWHGLRDKEVRY
RQRYLDLIVNPEVREVFRRRSEIVRYIRRF EAKGFLE VETPILQPTTGG
AEARPFKTYHNALDHEFYLRISLELYLKRLLVGGYEKVF E IGRNFRNEGI

LRQIVLNCGEEPSVVANTVKGGDGNYGYNAAATEEYGNMIDMGILDPTKVT
RSALQYAASVAGLMITTECMVTDLPKSDAPDLGAAGGMGGMGGMM
> P69828|PTKA_ECOLI Galactitol -specific phosphotransferase enzyme IIA
component - *Escherichia coli*.
MTNLFVRSGISFVDRSEVLTHIGNEMLAKGVVHDTWPQALIAREAEFPTG
IMLEQHAIAIPHCEAIAHAKSSAIYLLRPTNKVHFQQADDDNDVAVSLVIA
LIVENPQQQLKLLRCLFLGKLLQPPDIVETLITLPETQLKEYFTKYVLDSE

> P60720|LIPB_ECOLI Lipoyltransferase - *Escherichia coli*.
MYQDKILVRQLGLQPYPISQAMHEFTDTRDDSTLDEIWLVEHYPVFTQG
QAGKAEHILMPGDIPIVQSDRGGQVYHGPQGQVMYVLLNLKRRKLGVRE
LVTLLLEQTVVNTLAEELGIEAHPRADAPGVYVGEKKICSLGLRIRRGCSFH
GLALNVNMDLSPFLRINPCGYAGMEMAKISQWKPEATTNNIAPRLLENIL
ALLNNPDFEYITA

> P45483|FTSZ_BORBU Cell division protein ftsZ - *Borrelia burgdorferi* (Lyme
disease spirochete).
MKDYNMIDSHTRRFDDSTTNPTILKVIAGGGGSNAVNRMIEYGV RDVEFI
VANTDLQALQTSIAPIKIALGAKVTAGLGAGGKPEIGQAAAEEDIDVIRN
HLSGADMVFITAGMGGGTGTGAAPVIAQVAKELGILTVGVVTKPFKEG
KKLRLAEQGINNLRKSVDTLIIIPNQKLLTVVDKRTTIKDAFKRADDVLR
MGVQGIAGLIEHGEVNI DFADVKSIMQGGDALMGIGYKGENRAVDAA
TSAISNPLLEEVRIEGSKGLLVNVTGGDDFSLLELEEIMGIITVSV DDEA
TVIYGHAINSNLEDEIYVTVVATGFASKKQKEISSTPENNTLSSKEFDL
MSGNQAPSGSYEQDSSFAAKSKNVNYFDDIDVPTFLRNLNKKSSD D
> Q01578|GNL_ZYMMO Gluconolactonase - *Zymomonas mobilis*.
MTTGRMSRRECLSAAMVPIAAMTATATITGSAQAANKNMNGSTIGKITK
FSPRLDAILDVSTPIEVIASDIQWSEGPVWVKNGNFLLFS DPPANIMRKW
TPDAGVSI FLKPSGHAEP IAGQFREPGSNGMKVGPDKGIWVADSGTRAI
MKVDPVTRQRSVVVDNYKGRFNSPNDLFFSKSGAVYFTDPPYG LTNLDE
SDIKEMNYNGVFRLSPDGRDLIEAGLSRPNGLALS PDETKLYVSNSDRA
SPNIWVYSLDSNGLPTSR TLLRNFRKEYFDQGLAGLPDGMNIDKQGNLFA
SAPGGIYIFAPDGECLGLISGNPGQPLSNCCFGEKQTLFISASHNVVRV
RTKTFG

> P25718|AMY1_ECOLI Alpha -amylase - *Escherichia coli*.
MKLAACFLTLLPGFAVAASWTS PGFPAFSEQGTGT FVSHAQLPKGTRPLT
LNFDDQQCWQPADAIKLNQMLSLQPCNS TFPQWR LFRDGEYTLQIDTRSGT
PTLMISIQNAEPVASLVRECPKWDGLPLTV DVSATFPEGAAVRDYYSQQ
IAIVKNGQIMLQPAATSNGLLLLERAETDTSAPFDWHNATVYFVLTDRFE
NGDPSNDQSYGRHKDGM AEIGTFHGGDLRGLTNKLDY LQQLG VNALWISA
PFEQIHGWVGGGTGDFPHYAYHGYTQDWTNLDAN MGNEADLRTLVD SA
HQRGIRILFDVVMNHTGYATLADMQEYQFGALYLSGDEVKKS LGERWSDW
KPAAGQTWHSFN DYINFSDKTGWKWWGKNWIRTDIGDYDNPGFDDLTMS
LAF L PDIKTESTTASGLPVFYKNKMDTHAKAIDGYTPRDY LTHWLSQWVR
DYGIDGFRVDTAKHVELPAWQQLKTEASAALREWKANPDKALDDKPFWM
TGEAWGHGVMQSDYYRHGFDAMINFDYQEQA AKAVDC LAQMDTTWQQMAE
KLQGFNVLSYLSHDTRLFR EGGDKAAELLLLAPGAVQIF YGDESSRPF
PTGSDPLQGT RSDMNWQDVSGKSAASVAHWQKISQFRARHPAIGAGKQTT
LLLKQGYGFVREHGDDKVLVWVAGQQ

> P07941|PAC_KLUCI Penicillin G acylase - *Kluyvera citrophila* (*Kluyvera
cryocrescens*).
MKNRNRMI VNGIVTSLICSSLSALA ASPPTEVKIVRDEYGMPHIYADD
YRLFYGYGYVVAQDR L FQMEMARRSTQGT VSEVLGKAFVSFDKDIRQNYW
PDSIRAQIASLSAEDKSILQGYADGMNAWIDKVNASPKLLPQQFSTFGF
KPKHWE PFDVAMIFVGTMANRFS DSTSEIDNLALLTAVKDKYGNDEGMAV
FNQLKWL VNPAPT TIAARESSYPLKFDLQNTQTAALLVPRYDQPAPMLD
RPAKGTD GALLAVTAIKNRETIAAQFA NGLAGYPTTSNMWVIGK NKA
QDAKAIMVNGPQFGWYAPAYTYGIGLHGAGYDVTGNTPFAYPGLVFGHNG
TISWGSTAGFGDDVDIFA EKLSAEKPGYYQHNGEWVKLSRKETIAVKDG
QPETFTVWR TLDGNVIKTDTRTQTAYAKARAWAGKEVASLLAWTHQMKAK
NWPEWTQQA AKQALTINWYYADVNGNIGYVHTGAYPDRQPGHDPRLPVPD
GKWDWKGLLSFDLNPKVYNPQSGYIANW NNSPQKDY PASDLFAFLWGGAD
RVTEIDTILDKQPRFTADQAWDVIRQTS LRDLRLFLPALKDATANLAEN
DPRRQLVDK LASWDGENLVNDDGKTYQQPGSAILNAWLTSMLKRTVVA AV

PAPFGKWYSASGYETTQDGP TGSLNISVGAKILYEALQGDKSPIQAVDL
FGGKPEQEVLAAALDDAWQTL SKRYGNDVTGWKTPAMALTFRANFFGV
QAAAKEARHQAEYQNRGTENDMIVFSPTS GNRPVLAWDVVAPGQSGFIAP
DGKADKHYDDQLKMYESFGRKSLWLPQDQVDEHKESQEVLQVQR
> P26648|SUF1_ECOLI Protein suf1 - Escherichia coli.
MSLSRRQFIQASGIALCAGAVPLKASAAGQQPLPVPPLLESRRGQPLFM
TVQRAHWSFTPGTRASVWGINGRYLGPTIRVWVGDDVKLIYSNRLTENVS
MTVAGLQVPGPLMGGPARMMSPNADWAPVLPVIRQ NAATLWYHANTPNRTA
QQVYNGLAGMWLVEDEVSKSLPIPNHYGVDDFPVVIQDKRLDNFGTPEYN
EPGSGGFVGD TLLVNGVQSPYVEVSRGWVRLRLLNASNRRYQLQMNDR
PLHVISGDQGFPLPAPVSVKQLSLAPGERREILVDMNSGDEVSITCGEAS
IVDRIRGFFEPSSILVSTLVLTTLRPTGLLPLVTDLSLPMRLLPTEIMAGSP
IRSRDISLGD DPGINGQLWDVNRIDVTAQQGTWER WTVRADEPQAFHIEG
VMFQIRNVNGAMPFPEDRGWKDTVWVDGQVELLVYFGQPSWAHFPFYFNS
QTLEMADRG SIGQLLVNPVP
> P0ADV1|YHBN_ECOLI Protein yhbN - Escherichia coli.
MKFKTNKLSLNLVLAASSLLAASIPAFAVTGD TDQPIHIESDQQSLDMQGN
VVFTTGNVIVTQGTIKINADKVVVTRPGGEGQKEVIDGYKPFATFYQM
NGKPVVEGHASQMH YELAKDFVVL TGNAYLQQVDSNIKGDKITYLVEQKM
QAFSDKGRVTTVLVPSQLQDKNNKGQTPAQKKN
> P33770|HEMF_RHOS4 Coproporphyrinogen III oxidase, anaerobic 1 -
Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158).
MTNIALQLSLGLFDARVPRYTSYPAAPVFSGAVGADFQAQA IEALDPAVP
ISVYVHVPFCERLCWFCACRTQGTQTLAPVEAYVGTLLQELVQHLPA
GVKAGRLHWGGGTPTILSPELIHKLAQAIKAVIPFAEDYEFVSVEIDPMV
DEPKIRALSEEEMNRASIGIQDFTDIVQNAIGREQPFENTKACVETLRRY
GVHSLNTDLVYGLPHQNRESLAATIDKVLSLRPDRVAIFGYAHVPWMAKR
QKLIDETVLPDIERHELANLAARLFTEGGFERIGIDHFALP DDSMAVAA
RSRKLRRNFQGYTDDTCPTLLGIGASSISKFEQGYLQNTAATAAYIKSIE
EGRLPGYRGHRMTEEDYLHGRAIEMIMCDFL DLPALRARFGEPAETMVP
RIAEEAAEKFTPFVTV DADGMSIAKEGRALARM IARLFDAYETPEARYSQ
AS
> P14489|BLP2_PSEAE Beta -lactamase PSE-2 - Pseudomonas aeruginosa.
MKTFAAYVIIACLSS TALAGSITE NTSWNKEFSAEAVNGVFLCKSSSKS
CATNDLARASKEYLPASTFKI PNAIIGLETGVIKNEHQVFKWDGKPRAMK
QWERDLTLRGAIQVSAVPVFQQIAREVGEVRM QKYLKFKFSYGNQNISGGI
DKFWLEGQLRISAVNQVEFLESYLNLKLSASKENQLIVKEALVTEAAPEY
LVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNMIDIDNESKLPLR
KSIPTKIMESEGIIG
> P0A1N4|FLHE_SALTY Flagellar protein flhE - Salmonella typhimurium.
MRKWLALLFLPLTVQAAGEGAWQDSGMGVTLN YRGVSASSPLSARQPV
GVMTLVAWRYELNGPTPAGLRVRLCSQSRCVELDGGSGTTHGFAHVP
PLRFVVEVPGGGRLIPALKVRSNQVIVNYR
> P06202|OPPA_SALTY Periplasmic oligopeptide -binding protein - Salmonella
typhimurium.
MSNITKKS LIAAGILTALIAASAATAADVPA GVLADKQTLVRNNGSEVQ
SLDPHKIEGVPE SNVSRDLFEGLLISDVEGHPSPGVAEKWENKDFKVVTF
HLRENAKWS DGT PVT AHDFVYSWQRLADPNTASPYASYLQYGHIANIDDI
IAGKKPATDLGKALDDHTFEVTLSEVPYFYKLLVHPSVSPVPSAVEK
FGDKWTQ PANIVTNGAYKLNWVNER IVLERNPQYWDNAKTVINQVTYL
PISSEVTDVNRYSGEIDMTYNNMPIELFQK LKKEIPNEVRVDPYLCTYY
YEINNQKAPFNDVVRV TALKLALDRDIIVNKVKNQGDLPAYS YTPPYTDG
AKLVEPEWFKWSQQKRNEEAKLLAEAGFTADKPLTFD LLYNTSDLHKKL
AIAVASIWKKNLGVNVLENQEWKTFLDTRHQGTFDVARAGWCADYNEPT
SFLNTMLS DSSNNTAHYKSPAFDKLIAD TLKVADDTQRSELYAKAEQQLD
KDSAIVPVYYVYVNR LVKPVWGGYTGK DPLDNIYVKNLYI IKH
> MOXR_PARDE P29901 MOXR PROTEIN. - PARACOCCUS DENITRIFICANS.
MDSNISDWHARFRDAEAAALNGVV LGQARTIRLLLSALCRGHVLLAGDVG
TGKTLLRAMARALGGPYGRVEGTVDLLPTDLIYSTHIAEDGRPRIEPGP
VLEQGEDMAVFFFNEINRARPQVHA LLLRLMAERSLSAFRREYRPHLQV
FADR NQIERDET FELPAAARDRFLMEI AVDAPAAPEDRVALAFEPFRHDT
TALIAE VGGILPYRGLNGLAAGVQSGTHAS PALRRYVFDLCEALRNPAS
AGLALLEGADAARLIRGGVSPRGMQHLVRAARACAWLEGREAVLPQDVRAV

LAPVMAHRIFLSPAYEPRREALVLPALIDAAFATIPVPA
> Q09064|UREE_HELPY Urease accessory protein ureE - *Helicobacter pylori*
(*Campylobacter pylori*).
MI IERLVGNLRDLNPLDFSVHDVLEWFETRKKIARFKTRQGKDIAIRLK
DAPKLGSLQGDILFKEEKEIIAVNILDSEVIHIQAKSVAEVAKICYEIGN
RHAALYYGESQFEFKTPFEKPTLALLEKLGVQNRVLSKLDKERLTVSM
PHSEPNFKVSLASDFKVVVK
> P29930|COBO_PSEDE Cob (I)yrinic acid a,c-diamide adenosyltransferase -
Pseudomonas denitrificans.
MSDETTVGGGEAPAEKDDARHAMKMAKKAAREKIMATKTDEKGLIIVNTG
KKGKSTAGFGMIFRHHAGMPCAVVQFIKAMATGERELIEKHFGDVCQ
FYTLGEGFTWETQDRARDVAMAWEKAKELIRDERNMSVLLDEINIAL
RYDYIDVAEVVRFLEKKEKPHMTHVVLT GRNAKEDLIEVADLVTEMLIKH
PFRSGIKAQQGVEF
> P10332|MOMPA_CHLPS Major outer membrane porin - *Chlamydia psittaci*
(*Chlamydomydia psittaci*).
MKKLLKSALLFAATGSALSQALPVGNPAPESLLIDGTMWEGASGDPCDP
CATWCDAISIRAGYGGDYVDFRVLKVDVNKTFSGMAATPTQATGNASNTN
QPEANGRPNIAYGRHMQDAE WFSNAAFALALNIWDRFDIFCTLGASNGYFK
SSSAFNLVGLIGFSAATSSSTSTELPMQLPNVIGITQGVVEFYDTSFWSV
GARGALWECGCATLGAEFQYASQSNPKIEVLNVTSSPAQFVIHKPRGYKGA
SSNFPLPITAGTTEATDTKSATIKYHEWQVGLALSRLNMLVPYIGVNWS
RATFDADTIRIAQPKLKSEILNITWNPSSLGSTTTLPNNGGKDVLSV
QIASIQINKMKSRAKCGVAVG ATLIDADKWSITGEARLINERAAHMNAQF
RF
> P0AEB2|DACA_ECOLI Penicillin-binding protein 5 - *Escherichia coli*.
MNTIF SARIMKRLALTTALCTAFISAHADDLNIMIPGVPQIDAESYI
LIDYNSGKVLAEQNADVRRDPASLTKMMTSYVIGQAMKAGFKETDLVTI
GNDAWATGNPVFKGSSLMFLKPGMQVPSQLIRGINLQSGNDACVAMADF
AAGSQDAFVGLMNSYVNALGLKNTHFQTVHGLDADGQYSSARDMALIGQA
LIRDVPNEYSIYKEKEFTFNGIRQLNRNGLLWDNSLNVGDKTGTGDKAG
YNLVSATEGQMRLLISAVMGGRTFKGREAESKLLTWGFRFFETVNPVKV
GKEFASEPVWFGSDRASLGVDKDVYLTIPRGRMKDLKASYVLNSELHA
PLQKNQVVGTFINFLDQGTIEQRPLVVLQEIPEGNFFGKI IDYIKLMFHH
WFG
> P29725|BMP_TREPA Basic membrane protein - *Treponema pallidum*.
MGRIYVALLCVAGMGFAHAQSALQPIAEVNLFRREPVTLGQIKARISAI
EKEMGKLLSTAERRQFMDSLIDEKLFQAQAEKAGIQVDAEVNQYFNGML
SQQIGRAVTEAEFANYVKEKQNISLDQFMKQONGMTMAEYKFKLKTQVST
QRYVAQKKADEFRLKGPEDSQIRSYEELNKQAFFRP DTVKLFLLISVPKG
SGPAAAKAKAQEFVKKLKSSGVKATADIKSKANGAQAGYSAGEIYLGKTA
VTATQLGLTMEALLEIFGMGVGAVSDVNETANDYQCFIVLKKEEAKILTL
SDLVEPKTVSLEYEFIKNLLTSQIQKALEDAIREVSAELRKSQTYKVFL
ADAELGKVLWD
> P0ABE7|C562_ECOLI Soluble cytochrome b562 - *Escherichia coli*.
MRKSLAILAVSS LVFSSASFAADLEDNMETLNDNLKVIKADNAAQVKD
ALTKMRAALDAQKATPPKLEDKSPDPEMKDFRHGFDILVQGIDDALKL
ANEGKVKEAQAAAEQLKTTNRNAYHQYR
> P19247|VVHA_VIBVU Cytolysin - *Vibrio vulnificus*.
MKKMTLFTLSLLATAVQVGAQEYVPIVEKPIYITSSKIKCVLHTSGDFNA
TRDWCNAGASIDVRVNVAVQMRVQSATS DGFTPD AK IVRFTVDADKPGTG
IHLVNELQQDHSWFQSWANRRTYIGPFASSYDLWVKPVSGYTPKKARDLP
QENKNYQHRDITYGSIGINGKVGAEVNDGPKVGGVEVSGSFTYNYSKTL
VFDTKDYRINRSSLSDFDISFEREFGEDELRRQELGCYFTAAHWGSGW
VFDKTKFNPISYSNFKPNYDVLVEAPVSETGVTD FEMGVKLNRYRARGTV
LPSALFSVYGSAGSSTNSSTVKQRIRIDWNHPLFEAE AHVTLQSLSNNDL
CLDVYGENGDKTVAGGSVNGWSCHGSWNQVWGLDKEERYRSRVASDRCLT
VNADKTLTVEQCGANLAQKWYWEGDKLISRYVDGNNTRYLLNIVGGRNVQ
VTPENEANQARWKPTLQQVKL
> Q47898|ASPG_ELIMR N(4) -(Beta-N-acetylglucosaminyl)-L-asparaginase -
Elizabethkingia miricola (*Chryseobacterium miricola*).
MRIIYKQQTMMNNRRDFIKKLGIIATAAIAINPLEAKNLLDTSEPKTTNKP
IVLSTWNFGLHANVEAWKVLKSGGKALDAVEKGVRLVEDDPTERSVGYGG

RPDRDGRVTLDACIMDENYNIQSVACMEHIKNPISVARAVMEKTPHVMLV
GDGALEFALSQGFKKENLLTAESEKEWKEWLKTSQYKPIVNIENHDTIGM
IALDAQGNLSGACTVSGMAYKMHGRVGDSPPIIAGLFDVNEIGAAT ATGH
GEEVIRTVGTHLVVVELMNQGRTPQQACKEAVERIVKIVNRRGKNLKDIOV
GFIALNKKGEYGAYCIQDGFNFVAVHDQKGNRLETPGFALK

> P41258|SYK_CAMJE Lysyl -tRNA synthetase - *Campylobacter jejuni*.

MFDNILEQQRIEKAKELKLNGLINYPHFLEKEMSLKTFKDKFSYILEQVE
KRDESVNAVAVAGRLKLLRIAGKSIIFANIEDEDNLQIYFSKDS VGEELYT
ILKKNLEVGDIVLVKGFPPVTKTGEFSLHASEVKLATKAIIVPLPEKYHGL
TDIEQRYRKRYVDMIMNVEVRKDFLVRKVVSLIRHFFENKGFLEVETPM
MHPIAGGANAKPFVTFHNSLGVFRFLRIAPELYLKRLLIVGGFEAVFEINR
CFRNEGMDLTHNPEFTTIEFYWAYHNYKDLMDLTEELFALLLDKLNGLKT
IEFDGKMINFSKPFERITYKDALCKYGGDRDLIEDKEKILTKL KADGFE
ANEKLELGHQLAELFDNYVEEKLINPTFVIDFPISISPLSRRSDEDSQIA
ERFELFICGRELANGFNELNDPLDQYERFLKQIEAKNAGDEEACEMDEDF
VNALGYGMPPTAGQIGIDRLVMLLTNKKSIIRDVILFPAMRPLKSELKEK
E

> P43886|CYSE_HAEIN Serine acetyltransferase - *Haemophilus influenzae*.

MTLDVWQHIRQEAKELAENEPML ASFFHSTILKHQNLGGALSYLELLANKLA
NPIMPALSLREIIEEAYQSNPSIIDCAACDIQAVRHRDPAVELWSTPLLY
LKGFHAIQSYRITHYLNQNRKSLALYLQNQISVAFDVDIHPAAKIGHGI
MFDHATGIVVGETSVIENDVSILQGVTLGGTGKESGDRHPKVREGVMIGA
GAKILGNIEVGKYAKIGANSVVLNPVPEYATAAGVPARIVSQDKAAKPAF
DMNQYFIGIDGMLNLI

> P00811|AMPC_ECOLI Beta -lactamase - *Escherichia coli*.

MFKTTLCALLITASCSTFAAPQQINDIVHRTITPLIEQQKIPGMAVAVIY
QGKPYFYFTWGYADIACKQPVTTQTLFELGVSVKTFGTGLGGDAIARGEIK
LSDPTTKYWPPELTAKQWNGITLLHLATYTAGGLPLQVPDEVKSSDLLRF
YQNWQPAWAPTEKRYANSSIGLFGALAVKPSGLSFEQAMQTRVFPQLKL
NHTWINVPPAEKKNYAWGYREGKAVHVSFGALDAEAYGVKSTIEDMARWV
QSNLKLPLDINEKTLQGGIQLAQSRYWQTGDMYQGLGWEMLDWPNPDSII
NGSDNKIALAARPVKAITPPTPAVRASVWHKTGATGGFGSYVAFIPEKEL
GIVMLANKNYPNPARVDAAWQILNALQ

> P22751|PELX_ERWCH Pectate disaccharide -lyase - *Erwinia chrysanthemi*.

MKYAASGLLSVALNSLLLSNQRFATQDVAPVWRGIAFGQSTDVNFATN
VLPEKVGVDVNTINGKKLTVNDKADLSAPITIESRGGKIANTHDGLTFFY
TQLPANVNFLLQSDVTVEQFGPESDAKPNQEGAGLLVRDILGVPRQEPL
KEGYEEFPAASNVMNAIMTQDKKSKTEVKMQLISRNGVTQPWGNTNAEI
TRTSYQEKINLEQPTFRKLKERTNDGFIYAYAPKGSQWVSKTVKGADL
VTHQDKDHYYVGVFFASRNAKITISNASLTTSPANTKPSAPFKAETTAPLL
QVASSSLSTSDTYPVQARVNYNGTVEVFQNGKSLGKQPVRAGDDFSLTT
RLTQQKSDFKLVYIPSEGEDKTAKETSFSVEKITLADARNLYVSPGKAG
NDGSKNAPLDIKTAINALPGGGTLWMDGDYSATVIPVSATQRKGMKMTLM
PVGKKAIVFHGLQLNASYWKVKGIEITEKSFRIEGSHNQIERLLAHHCNT
GIQVSSSDNVGRPLWASHNLIILNSESNSHQHPSKDKADGFVAVKMRVGEEN
VIRGAFSHDNVDDGFDLNFKIEDGPNGAVMIENSISLNNTSNGFKLGEG
QPVAVHQVKNSIAIGNHMDGFSDFNPNFALQVSNNIALDNVRFNFIFRPS
YYGYEKQGIKNNVSLRTQPGKYDDAVVGRDLASNYFIRIIRSTVVRK
SRRRITNPSRCQRSSAGMKKAACNWWIFCRRSNRHKTRHRNRYPSTPA

> DHSS_SYN1 P14776 SOLUBLE HYDROGENASE, SMALL SUBUNIT (EC 1).

MQDKAMLMPGTPVPESVLLSLGKHPIGHRSGEFSQIMAAMTAGIKWLH
QTQNEVLILAASGTGAMEAGIINFLSAGDRVVVGCNGKFGDRWGEVCDAY
GLTTERISAPWQPLNPDFFKAVLDGHRQKPSKAVIVTHSETSTGVINDL
EAINRHVKAHGQALIIVDAVTSLGAVSVPIDEWGLDVVSGSGSQKGYMIPP
GLAFVSVSPKAWWAYKATLTKFYLDLGYRKAADKHTTPTPPVNLFFA
LKTALEMMQAEGLAIFQRHQRLMQATRAAMKALNPLAADCASPAIT
AVAPQVEAENIRSLMKKRFDIALAGGQDHLKQIFRIGHLGFVGDRIIL
AAVSALEAVLAEELGTYNFTPGAGVAAASRVLSTA

> P06960|OTC2_ECOLI Ornithine carbamoyltransferase chain F - *Escherichia coli*.

MSDLYKKHFLKLLDFTPAQFTSLTLTAAQLKADKNGKEVQKLTGKNIAL
IFEKSDSTRTRCSFEVAADFQGARVTYLGPSSQIGHKESIKDTARVLGRM
YDGIQYRGGHGEVETLAQYAGVPVWNGLTNEFHPTQLLADLMTMQEHL

GKAFNEMTLVYAGDARNMGNMGMLEAAAALTGLDLRLLAPKACWPPEESLVA
ECSALAEKHGGKITLTEDVAAGVKGADFIYTDVWVSMGEAKE KWAERIAL
LRGYQVNAQMMALTDNPNVKFLHCLPAFHDDQTTLGKQMAKEFDLHGGME
VTDEVFESAASIVFDQAENRMHTIKAVMMATLGE

> P0A8N3|SYK1_ECOLI Lysyl -tRNA synthetase - Escherichia coli.

MSEQHAQGADAVVDLNNELKTRREKLANLREQGIAFPNDFRRDHTSDQLH
AEFDGKENELEEALNIEVAVAGRMTRRIMGKASFVTLQDVGGRILY VA
RDDLPEGVYNEQFKKWDLDGILGAKGLFKTKTGELS IHCTELRLLTKAL
RPLPDKFHGLQDQEARYRQRYLDLISNDESRNTFKVRSQILSGIRQFMVN
RGFMEVETPMQVIPGGAAARPFITHHNALDLDMYLRIAPELYLKRLVVG
GFERVFEINRNNEGIVSRHNPEFTMMELYMAYADYKDLIELTESLFR
LAQDILGKTEVTVYGDVTLDFGKPFKELTMREAIKKYRPEPDMADLDFD S
AKAIAESIGIHVEKSWGLGRIVTEIFEEVAEAHLIQPTFITTEYPAEVSPL
ARRNDVNPEITDRFEFFIGGREIGNGFSELNDAEDQAQRFLDQVAAKDAG
DDEAMFYDEYVTALEHGLPPTAGLGIGIDRMVMLFTNSHTIRDVILFPA
MRPVK

> P21163|PNGF_ELIMR Peptide -N(4)-(N-acetyl-beta-D-glucosaminyl)asparagine
amidase F - Elizabethkingia miricola (Chryseobacterium miricola).

MRKLLIFSISAYLMAGIVSCKGVDSATPVTEDRALNAVNPADNTVNIK
TFDKVKNFAFGDGLSQAEGTFTFPADVTTVKTIKMFIKNECPNKTCDEWD
RYANVYVKNKTTGSEWYEIGRFITPYWVGTEKLPRGLEIDVDFKSLLSGN
TELKIYTETWLAKGREYSVDFDIVYGPDYKYSAVVPIQYNKSSIDGVP
YGKAHTLGLKKNIQLPTNTEKAYLRRTISGWGHAKPYDAGSRGCAEWCFR
THTIAINNANTFQHQLGALGCSANPINNQSPGNWAPDRAGWCPGMAVPTR
IDVLNNSLTGSTFSYEYKQSWTNNGTNGDAFYAISSFVIKSNTPISAP
VVTN

> P0AFK0|PMB_A_ECOLI Protein pmbA - Escherichia coli.

MALAMKVISQVEAQRKILEEAVSTALELASGKSDGAEVAVSKTTGISVST
RYGEVENISFNSDGLGITVYHQNRKGSASSTDLSPQAIARTVQAALDIA
RYTSPDPCAGVADKELLAFDAPDLDFHPAEVSPDEAIELAARAEQAALQ
ADKRITNTEGGSFNSHYGVKVFNGSHGMLQGYCSTRHLSLSCVIAEENG
MERDYAYTIGRAMSDLQTPPEWVGADCARRTLRSLSPRKLSTMKAPVIFAN
EVATGLFGHLVGA IAGGSVYRKSTFLDLSLQILPDWLTIEEHPHLLKG
LASTPFDSEGVRTERRDI IKDGILTQWLLTSYSARKLGLKSTGHAGGIHN
WRIAGQGLSFEQMLKEMGTGLVVTELMGQGVSAITGDYSRGAAGFWVENG
EIQYPVSEITIAGNLKDMWRNIVTVGNDIETRSNIQCGSVLLPEMKIAGQ

> P29822|LACE_AGRD Lactose -binding protein - Agrobacterium radiobacter.

MDYSRLLKRSVSAALTAALLCSTAAFAAGEV TIWCWDPNPNVAIMKEAAE
RYTAKHPDFTFNIVDFAKADVEQKLQTGLASGMTDTLDPDIVLIEDYGAQK
YLQSFPGSFAALTDKIDFSGFAKYKVDLMTLEGQVYGVPPFDSGVTGLYYR
TDYLEQAGFKPEDMQNLTWDRFIEIGKEVKAKTGHEMMALDANDGGLIRI
MMQSGGQWYFNEDGSLNITGNAALKAALETQARIVNERVAKPTSGSNDGI
RALTSGDVASVLRGVWITGTVKSQPDQAGKWA LTAIPKLNIEGATAASNL
GGSSWVLEASA EKDEAIDFLNEIYAKDLDFYQKILTERGAVGSLLAART
GEAYQKPDFFGGQTVWQNFADWLQVPAVNYGIFTNELDTAVTANFPAL
VKGTPVDEVLKAIEDQAAGQIQ

> P56194|SYH_THET8 Histidyl -tRNA synthetase - Thermus thermophilus (strain
HB8 / ATCC 27634 / DSM 579).

MTARAVRGTKDLFGKELRMHQIRIVATARKVLEAAGALELVTPIFEETQVF
EKGVGAATDIVRKEMFTFQDRGGRSLTLRPEGTAAMVRAYLEHGMKVWPQ
PVRLWMAGPMPFRAERPQKGRYRQFHQVNYEALGSENPI LDAAEVVLLYEC
LKELGLRRLKVKLSSVGDPEDRARYNAYLREVLSPHREALSEDSKERLEL
NPMRILDSKSERDQALLKELGVRPMLDFLGEEARAHLEVERHLERLSVP
YELEPALVRGLDYVRTAFEVHHEEIGAQSALGGGGRYDGLSELLGGPRV
PGVGFAGVERVALALEAEGFGLPEEKGPDLYLIPLTEEAVAEAFYLAEA
LRPRLRAEYALAPRKPAKGLEEALKRGAAGFAGFLGEDELRAAGEVTLKRLA
TGEQVRLSREEVPGYLLQALG

> P44584|PNP_HAEIN Polyribonucleotide nucleotidyltransferase - Haemophilus
influenzae.

MNPVVKQFKYGQHTVTLTETGAIARQATAAVMASMDDTTVEVTVVAKKDVK
EGQDFFPLTVNYQERTYAAGKIPGGFFKREGRPSEGETLIARLIDRPIRP
LFPEGFFNEIQVATVVSVPNQISPDLVAMIGASAALTLGVPFNGPIGA

ARVGFIDNQFVLNPTMAEQKQSRDLVAVAGTDKAVLMVESEADILTEEQM
LAAVVFVGHQQQQVVVEAIKEFAKEAGKPRWDVWVAPQNTDLINKVKAIAE
ARLGDAYRITEKQLRYEQIDAIAKADVIAQITAEDDEEXSEGKIVDIFTALE
SQIVRGRI IAGEPRIDGRTVDTVRALDICTGVLPRTGSAIFTRGETQAL
AVATLGTERRDAQI IDELTGERQDHFHFNFPYVSVGETGMIGSPKRREI
GHGRLAKRGVAAVMPSLAEFFPYVVRVSEITESNGSSSMASVCGASLALM
DAGVPIKAAVAGIAMGLVKEEEKFVVLSDILGDEDHLGDMDFKVAGTREG
VTALQMDIKIEGITPEIMQIALNQAKSARMHILGVMEQAI PAPRADISDY
APRIYTMKIDPKKIKDVIKGGATIRSLTEETGTSIDIDDDGTVKIAAVD
SNAAKNVMGRIEIEVAEVEAGVIYKGVTRLADFGAFVAIVGNKEGLVHI
SQIAEERVEKVSVDYLQVQVEVNVKVEIDRQGRIRLTMKDLAPKQETEIN
QEDSVEEQE

> P74132|HEMN_SYNY3 Oxygen-independent coproporphyrinogen III oxidase -
Synechocystis sp. (strain PCC 6803).

MTTTFPTVEFSAELLNKYNQGI PRYTSYPPATELNKEFDPSDFQTAINLG
NYKKTPLSLYCHIFPCKACYFCGCNTIITQHKAQVDPYLKAVAKQIALV
APLVDQQRPVQQLHWGGGTPNYLTLEQAEFLFNTITDAFLAENAEISIE
INPCYVDKDYIFALRQLGFNRISFGIQDFNSQVQAVNRIQ PEAMLFQVM
DWIRQANFDSVNVLDIYGLPHQNLATFRETLRKTAQLNPDRIAVFNFAVY
PWLKPVQKKMPESALPPAEELKIMQATIADLTEQGYVFIGMDHFAKPD
ELAIARRRGELHRNFQGYTTQPESDLLGFGITSISMLQDVYAQNKHTLKA
FYNALDREVMPIEKGFKLSQDDLIIRRTVIKELMCQFKLSAQELESKYNLG
FDCDFNDYFAKELSALDVLEADGLLRRLGDLVTPRGRILI RNIAAVFD
TYLQNKSKQQMFSRAI

> P07102|PPA_ECOLI Periplasmic appA protein [Includes: Phosphoanhydride
phosphohydrolase - Escherichia coli.

MKAILIPFLSLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQL
MQDVTTPDAWPTWPVKLGWLT PRGGELIAYLGHYQRQLVADGLLAKKGC
QSGQVAIIADVDERTKRTG EAFAGLAPDCAITVHTQADTSSPDLFNL
KTGVCQALDNANVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLC
LKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQQAQG
MPEPGWGRITDSSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTA
LTPHPPQKQAYGVTLPVSVLFIAGHDTNLANLGGALELNWTLPGQPDNTP
PGGELVFERWRRLSDNSQWI QVSLVFQTLQQMRDKTPLSLNTPPGEVKLT
LAGCEERNAQGMCSLAGFTQIVNEARIPACSL

> P69795|PTQB_ECOLI N,N'-diacetylchitobiose-specific phosphotransferase
enzyme IIB component - Escherichia coli.

MEKKHIYLFCSAGMSTSLVSKMRAQAEKYEVPVIEAFPETLAGEKGN
ADVLLGPGQIAYMLPEIQRLLPNKPEV IDSLLYGKVDGLGVLKAAVA
KKAAN

> Q3J164|CYC2_RHOS4 Cytochrome c2 - Rhodobacter sphaeroides (strain ATCC
17023 / 2.4.1 / NCIB 8253 / DSM 158).

MKFQVKALAAIAAFAALPALAQEGDPEAGAKAFNQCQTCHVIVDDSGTTI
AGRNAKTGPNLYGVVGRTAGTQADFKGYGEGMKEAGAKGLAWDEEHFVQY
VQDPTKFLKEYTG DAKAKGKMTFKLKEADAHNIWAYLQQVAVRP

> NADA_SALTY P24519 QUINOLINATE SYNTHETASE A. - SALMONELLA TY

MSVMFDPQAAIYFPFPKPTPLNDEKQFYREKIKRLLKERNVAVMVAHYT
DPEIQQLAEETGGCISDSLEMARFGTKHAASTLLVAGVRFMGETAKILSP
EKTILMPTLAAECSLDLGCPIDEFSAFCDAHPDRTVVVYANTSAAVKARA
DWVVTSSIAVELIEHLDSLGEKIIWAPDRHLGNVYVQKQTGADVLCWQGAC
IVHDEFKQTALTRLKKIYPDAALLVHPESPQIVEMADAVGSTSOLIKAA
KTLPHRQLIVATDRGIFYKMQQAVPEKELLEAPTAGEGATCRSCAHC
PMM AMNGLKAI AEGLEQGGARMKYRLMRRYARAHYCRSTGCWILRLHFGRKDG
NLWGREWIFLVRTTY

> NODA_BRAEL P50326 NODULATION PROTEIN A (EC 2.3.1.-). - BRAD

MNIAVSPSAEEPSARTQVQVSLRWESELQADHAELADFFRKSYPGTGAF
NAQPFEGIRSWAGARPEMRVIGYDAHGVAAHIGLLRRFIKIGVDLLVAE
LGLYAVRPDLEGLGISHSMRVMYPALQELGVFPFGFTVRPALEKHLTRLV
GRRGLATLMPGIRVRSQTADVYPNLSPIRIEDVLVVVFPVGRSMGEWPAG
TIIDRNGPEL

> P68588|PSAE_YERPE Protein psaE - Yersinia pestis.

MSHCVVNLKLESVLIIGDSRYALSKNEVLLLECLYLRAGDVISHDELLTT
CWPDRVVSPTSPLVAIKHIRDVFRKITRSEVIKTYKNEGYSYQKDSVLI

IDDGSTEKESHSAAYTRKEKPDIPKLVGLQILSHLNSTFFIAIMMVIII
IFFMVGGNDIVSFIDSDTNSVIIITNVTTKMNGPTAGLPKVKNSMIFKDDF
GLVIICDQSECKQQ
> CH10_ECOLI P05380 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN
MNIRPLHDRVIVKRKEVETKSAGGIVLTGSAAAKSTRGEVLAVGNRILE
NGEVKPLDVKVGDIVIFNDGYGVKSEKIDNEEVLIMSESDILAIVEA
> P33136|OPGG_ECOLI Glucans biosynthesis protein G - Escherichia coli.
MMKMRWLSAAVMLTLYTSSSWAFSIDDVAKQA QSLAGKGYETPKSNLPSV
FRDMKYADYQQIQFNHDKAYWNNLKTPEFKLEFYHQGMFYDTPVKINEVTA
TAVKRIKYSPTYFTFGDVQHDKDTVKDLGFAGFKVLYPINSKDKNDEIVS
MLGASYFRVIGAGQVYGLSARGLAIDTALPSGEEFPRFKEFWIERPKPTD
KRLTIYALLDSPRATGAYKFFVMPGRDTPVVDVQSKIYLRDKVKGKLGAVPL
TSMFLFGPNQSPANNYRPELHDSNGLSIHAGN GEWIWRPLNNPKHLAVS
SFSMENPQGFGLLQRGRDFSRFEDLDDRYDLRPSAWVTPKGEWGKGSVEL
VEIPTNDETNDNIVAYWTPDQLPEPGKEMNFKYTITFSRDEDKHLAPDNA
WVQQTRRSTGDVKQSNLIRQPDGTIAFVVDFTGAEMKKLPEDTPVTAQTS
IGDNGEIVESTVRYNPVTKGWRLVMRVKVKDAKKTTEMRAALVNADQTL
ETWSYQLPANE
> P0A9P0|DLDH_ECOLI Di hydrolypoyl dehydrogenase - Escherichia coli.
MSTEIKTQVVVLGAGPAGYSAAFRCADLGLLETIVIVERYNTLGGVCLNVGC
IPSKALLHVAKVIEEAKALAEHGIVFGEPKTDIDKIRTWKEKVINQLTGG
LAGMAKGRKVKVNVGLGKFTGANTLEVEGENGKTVINFDNAIIAAGSRPI
QLPFI PHEDPRIWSDTALELKEVPERLLVMGGGIIGLEMGTVYHALGSQ
IDVVEMFDQVIPAADKDIVKVFTKRI SKKFNLMLETKVTAVEAKEDGIYV
TMEGKKAPAEPQRYDAVLVAIGRVPNGKNLDAGKAGVEVDDRGFIRVDKQ
LRTNVPHIFAIGDIVGQPM LAHKGVHEGHVAAEVIAGKKHYFDPKVI PSI
AYTEPEVAWVGLTEKEAKEKGISYETATFPWAASGRAIASDCADGMTKLI
FDKESHVRVIGGAI VGTNGGELLGEIGLAIEMGCDAEDIALTIHAHPTLHE
SVGLAAEVFEGSITDL PNPKAKKK
> P31075|PSRA_WOLSU Polysulfide reductase chain A - Wolinella succinogenes.
METTMTRRDFLKSAGAAGAAGLVWSQTIPGTLGALEKQEIKGSAKFVPSI
CEMCTSSCTIEARVEGDKGVFIRGNPKDKSRGGKVCARGGSGFNQLYDPQ
RLVKPIMRVGERGEGKWEVSWDEAYTFIAKKLDEIKQKHGAHTVAFTAR
SGWNKTWFHHLAQAYGSPNIFGHESTCPLAYNMAGRDFVGGSMNRDFAKA
KYI INMGHNVFEGIVISYVRQYMEA IENGAKVVTLEPRLSVMAQKASEWH
AIKPGHDLPFVLFMHTLIFENLYDKKFVQKYCTGFEEELKASIEPCTPEK
MALECDIPADTIKRLAREFAKAAPKAI FDFGHRVTFTPQELELRRAMMV
NALVGNIERDGGMYFGKNASFYNQFLGEEDPKAKGLKKPKTPAYPKVEVP
RIDRIGEKDG EFFLANKGEGIVSLVPKATLNELPGVPCKIHGWFIVRNNP
VMTQTNADTVIKALKSMDLVVCVDIQVSDTAWFADVLLPDTTYLERDEEF
TAGGGKNPSFGIGRQKVVEPLGDAKPGWKIAKELSEKMGLGEYFPWKDIE
DYRLQOVDGDLDLLAKLKKDGSASFGVPLMLQEKKSVAEFVKKFPGAASK
VNEEGLIDFPKKIQLFSPKLEEVSGKGLGYEPFKYKEEDEL YFVQGKTP
VRSNSHTGNVP WLNLM EYDAIWIHPKTASKLGIKNGDAIELYNKFSQK
SKALITEGVREDTLFGYFGFGHVS KDLKRAYGKGVNSNALMPSFTSPNSG
MDLHVFGVKVKA
> P0AFK9|POTD_ECOLI Spermidine/putrescine -binding periplasmic protein -
Escherichia coli.
MKKWSRHLAAGALALGMSAAHADDNNTLYFYNWTEYVPPGLLEQFTKET
GIKVIYSTYE SNETMYAKLKYKDGAYDLVVPSTYYVDKMRKEGMIQKID
KSKLTNFSNLD PMLNKPFPDPNDYSIPYIWGATAIGVNGDAVDPKSVTS
WADLWKPEYKGSLLTDDAREVFQMLRKLGYSGNTTDPKEIEAAYNELK
KLMPNVA AFNSDN PANPYMEGEVNLGMIWNGSAFVARQAGTPIDVWVWPK
GGIFWMDSLAIPANAKNKEGALKLINFLLRPDVAKQVAETIGYPTPNLAA
RKLSP EVANDK TLYPDAETIKNGEWQNDVGAASSIYEEYYQKLKAGR
> P44323|IF2_HAEIN Translation initiation factor IF -2 - Haemophilus
influenzae.
MTEDVKADAPKLSIQRRTKTVSSSTTTGGKSKEVQVEVRKKRTVKTDIA
QQEEAKLKAQQEAEAKKIAEQKAAEEKARLEAEKAKAETAKPVKSAVDSK
AKSVESEKEKRKAGEAELRRKAEELARQKAEEQARR AVEEAKRYAEADD
DNESSSEDYSDYNLSSRYALEAEDEEDRRNENRGRGKNKVAKAKGGRDD
ENSKNSKNERESNRKNQKDAKFGKGNKGGKGAALQQAFTKPAQVVKSDVV
IGETITVAELANKMAVKATEI IKMMMKMGEMVTINQVIDQETAQLVAEEL

GHKVILRNENELEEAFLGDRDVAEKVTRAPVVTIMGHVDHGKTSLLDYI
RKAKVAAGEAGGITQHIGAYHVEMDDGKMITFLDTPG HAAFTSMRARGAK
ATDIVVLVVAADDGMPQTIEAIQHAAGAAPLVAVNKIDKPEANLDRV
EQELLQHDVISEKFGGDVQFVPSAKKGTGVDDLLDAILLQSEVLELTAV
KDGMAAGVIVIESYLDKGRGPVATILVQSGTLRKGDIVLCGFYGRVRAMR
DENGKEVDEAGPSIPVELLGLSGVPAAGDEATVVRDEKKAREVALYRQ GK
FREVKLARQQKAKLENMFSNMSEGDVAELNVIVKADVQ GSVEAIVQALNE
LSTNEVKVKGVSQGGITETDATALATASNAIIVGFNVRADATARRVIEA
ENIDLRYYSIIYELLNEIKAAMSGMLEPEFKQEIIGLAEVRDVFRHPKFG
AIAGCMVTEGVKRNPIRVLRDNVVFEGELESRRFKDDVSEVRNGME
CGIGVKNYNDVKVGDQIEVFEVVEVKRSI

> FTSZ_HELPY P56097 CELL DIVISION PROTEIN FTSZ. - HELICOBACTE

MVHQSEMENYNIGQASIEEVSDPAYKGAKIVVIGVGGGSMIKHLVEYG
VHQDVTPIATNTDQHLKNNPAPVKILLGKESTGGLGAGGIPDGRKAAE
ESANEIKEAIKDAKLVIIISTGLGGGTGTGATPTIVKIAKEVGALTIAIVT
KPFKYEGNQKRKRAEEGLKELEQSSDSILVIPNDKILLTMKKNASTTECY
REVDDVLVRAVSGISTIIITKPGNINVDFADLKSALGFKGFALMGIGEATG
EESAKLAVQNAIQSPLLDDASIEGAKSIVFFEHHPDYPMMAYSQACDFI
QDQAHQDQVDFKQHTSDNIPIDHVRVTIIATGAERNSSGGASLESIAATPS
QPVVVKQTRKVGNGEYLKIPTEEELSIPITMTRIQQD

> P13627|CY1_PARDE Cytochrome c1 - Paracoccus denitrificans.

MTLRNASLTAVALTVALAGGAVAQDASTAPGTTAPAGSSYHTNEAAPAA
ADTAPAAEADEPAEEAEAGEAEVTEEPAAETPAEPAADEPAATEEP
DAEAEPAAEEAQTTEEAPAEPAEPAEPAEPAEPAADAPAEAAAAEE
APAEPEAAEEPAEPEATEEEAPAEAAAAEEAPAEVVEDEAAADHGD
AAAQEAGDASHAAHIEDISFSFEGPFGKFDQHQLQRLQVYTEVCSACHG
LRYVPLRLTADDEGGPQLPEDQVRAAANFDITDPETEEDRPRVPTDHFPT
VSGEGMGPDLSLMAKARAGFHGPGYGTGLSQLFNGIGGPEYIHAVLTGYDG
EKEEAGAVLYHNAAFAGNWIQMAAPLSDQVYEDGTPATVDQMATDVA
AFLMWTAEPKMMDRKQVGFVSVIFLIVLAALLYLTNKKLWQPIKHPKPE

> P33781|FMS5_ECOLI CS5 fimbrial subunit - Escherichia coli.

MKKNLLITSVLAMATVSGSVLAAVTNGQLTFNWQGVVPSAPVTQSSW AFV
NGLDIPFTPGTEQLNITLDSNKDITARSVKPYDFFIVPVSGNVTPGAPVT
RDTSANINSVNAFLSSVPVSNFVGNKQLTLSTAVEAAKGEVAITLNGQA
LKVGSASPTVTVASNKKESHISIDMNAKAAAADVAEGAAINFVAPVTF
VDI

> P44336|SERC_HAEIN Phosphoserine aminotransferase - Haemophilus influenzae.

MSQVFNFSAAGPAMIFPEV LQKAQNELINWLNQGVSVMEVSHRGKYFMELV
TQAEKDLREVYNIPDNYRTLFLQGGARGQFATIPMNLIGKKGKALYLNSG
HWSATAAKEARNFAEIDEITIVENGEQTRITDLDFSHIADQYDYVHYCPN
ETISGVEIFDVPNVGNAVLVADMSSNILSRQIDISKFGVIYAGAQNKLG
AGITLVIIRDLDIGNARKETPSIWNATORDADSMINTPPTFAWYLCSLV
FKHLKEIGGLEIIEKRNALKAQTLYDYIDS SKLYRNVVAKENRSTMNVTF
ITGNPELDAKFVAESTAAGLQALKGHKVLGGMRASIYNAMSQNGVEALIS
FMKKFETENLPQ

> KAD_HELPY P56104 ADENYLATE KINASE (EC 2.7.4.3) (ATP -AMP TRA

MKQLFLIIGAPGSGKTTDAELIAKNNSETIAHFSTGDLLRAESAKKTERG
LLIEKFTSQGELVPLEIVVETILSAIKSSGKGIILIDGYPRVSEQMQ ALD
KELNAQNEVILKSVIEVEVSENTAKERVLGRSRGADDNEKVFHNRMRVFL
DPLGEIQNFYKKNKVKYKAIDGERSIEEIVGEMQYIILSFGN

> P24040|NIRS_PSEST Nitrite reductase - Pseudomonas stutzeri (Pseudomonas
perfectomarina).

MSNVGKPILAGLIAGLSLLGLAVAQAAPEMTAEKEASKQIYFERCAGC
HGVLKRGATGNLEPHW SKTEADGKKTEGGTLNLGTRKLENI IAYGTEGG
MVNYDDILTKEEINMMARYIQHTPDIPEFSLQDMKDSWNLIVPEKRV
KQMNKINLQNVFAVTLRDAGKLALIDGDTHKIWKVLESYAVHISRMSAS
GRYVYTTGRDGLTTIIDLWPEEPMTVATVRFSGDMRSVDVSKFEGYEDKY
LIGGTYWPPQYSIVDGLTLEPIKVVSTRGQTVDGEYHPEPRVASIVASHI
KPEWVVNVKETGQIILVD YTDLKNLKTITTESAKFLHDGGWDYSKRYFMV
AANASNKVAAVDTKTGKLAALIDTAKI PHPGRGANFVHPQFGPVWSTGHL
GDDVVSLISTPSEESKYAKYKEHNWKVVQELKMPGAGNLFVKTHPKSKHF
WADAPMNPEREVAESVYVFDMMNLSKAPIQLNVAKDSGLPESKAIRRAVQ

PEYNKAGDEVWISLWGGKTDQSAIVIYDDKTLKLRVITDPAVVTPTGKF
NVFNTMNDVY
> P55972|IF2_HELPY Translation initiation factor IF -2 - *Helicobacter pylori*
(*Campylobacter pylori*).
MSGMVDLKEFLAELGKTQKELKNVIEQAKDIGLELKTNSKMTPEQAGKLY
KYIVDGIKEQIQANQPAKNPEQDNKDDLNTAVASKSLNKKVSKTPKKEET
KSQPKPKKTKEKKKEAPTPIAKKGGIEIVNTFENQTPPTENTPKVVS
QIEKAKQKLQE IQSREALNKLQSNANNASNANNAKKEISEVKKQE
KRHENIKRRTGFRVVIKRNDEVENESENSVTESSKPTQSAIAIFEDIKKEW
QEKDQEAKKAKPSKPKATPTAKNNKSHKIDFSDARDFKGNDIYDDETD
EILLFDLHQDNFNKEEKEIRQNINDRVVRQKPNPWNESGIKRSKK
KRAFRNDNSQKVIQSTTAIPEEVRYEFAQKANLNLADVIKTLFNLGLMV
TKNDFLDKDSIE ILAEEFHLEISVQNTLEEFVEEVLEGVKKERPPVVTI
MGHVDHGKTSLLDKIRDKRVAHTEAGGITQHIGAYMVEKNDKWSFIDTP
GHEAFSQMRNRGAQVTDIAVIVIAADDGVKQQTIEALEHAKAANVPVIFA
MNMKMDKPNVNPDKLKAECAELGYNPVDWGGHEFIPVSAKTGDGIDNLE
TILIQAGIMELKAIIEGSARAVVLEGSVEKGRGAVATVIVQSGTSLVSGDS
FFAETAFGKVRTMTDDQGKSIQNLKPSMVALITGLSEVPAGSVLIGVEN
DSIARLQAQKRATYLRQKALSSTKVSFDELSEMANKELKNI PVVIKAD
TQGSLEAIKNSLLELNNEEVAIQVIHSGVGGITENDLSLVSSSEHAVILG
FNIRPTGNVKNKAKEYNVS IKTYTVIYALIEEMRSLLLGLMSPIIEEHT
GQAEVRETFNIPKVGTIAGCVVSDGVIARGIKARLIRDGVVIHTGEILSL
KRFKDDVKEVSKGY ECGIMLDNYNEIKVGDVFETYKEIHKKRTL
> P33129|HTRE_ECOLI Outer membrane usher protein htrE - *Escherichia coli*.
MTIEYTKNYHHLTRIAATFCALLYCNTAFSAELVEYDHTFLMGQNASNIDL
SRYSEGNPAIPGVYDVSIVVNDQPIINQSITFVAIEGKKAQACITLKNL
LQFHINSPDINNEKAVLLARDETLGNCLNLTETIIPQASVRYDVNDQRLD I
DVPQAWVMKNYQNYVDPPLWENGINAAMLSYNLNGYHSETPGRKNESIYA
AFNGGMGTGELRARGSNYNWMTDSGSNYDFKNRYVQRDIASLRSQLILG
ESYTTGETFDSVSRGIRLYSDSRMLPPTLASFAPI IHGVANTNAKVITIT
QGGYKIYETTVPFGAFVIDDLSPSGYGS DLIVTIEESDGSKRFTSQPFSS
VVQMLRPGVGRWDISGGQVLKDDIQDEPNLFQASYYYGLNLYLTGYTGIQ
ITDNNYTAGLLGLGLNTSVGAFSFDVTHSNVRI PDDKTYQGQSYRVSWNK
LFEETSTSLNIAARYSTQNYLGLNDALTLIDEVKHPEQDLEPKSMRNYS
RMKNQVTVSINQPLKFEKKDYGSFYLSGSWSDYWASGQNRSNYSIGYSNS
TSWGSYSVSAQRSWNEGDGTDSDSVYLSFTIPIEKLLGTEQRTSGFQSIDT
QISSDFKGNQNLNVSSSGYSDNARVSVNTGYTMNKASKDLSYVGGYAS
YESPWGTLAGSISANSNSRQVSLSTDGGFVLHSGGLTFSNDSFSDSDTL
AVVQAPGAQGARINYGNS TIDRWGYGVTALS PHYHENRIALDINDLENDV
ELKSTSAVAVPRQGSVVFADFETVQGS AIMNITRSDGKNIPFAADIYDE
QGNVIGNVGGQAFVIRGIEQQGNISIKWLEQSKPVSCLAHYQOSPEAEK
IAQSIILNGIRCQIQ
> P69797|PTNAB_ECOLI PTS system mannose-specific EIIAB component -
Escherichia coli.
MTIAIVIGTHGWAAEQLLKTAEMLLGEQENVGWIDFVPGENAETLIEKYN
AQLAKLDTTKGVLFVLDVTWGGSPFNAASRIVVDKEHYEVIAGVNI PMLVE
TLMARDDDPDFDELVALAVETGREGVKALKAKPVEKAAPAPAAAAPKAAP
TPAKMPGPNYMVIGLARIDDRLIHGQVATRWTKETNVSRIIVVSDEVAA
DTVVRKTLTQVAPPVTAHVVDVAKMIRVYNNPKYAGERVMLLFTNPTDV
ERLVEGGVKITSVNVGMAFRQGTQVNNAVSVDEKDIEAFKKNLARGIE
LEVRKVSTDPKLMMDLISKIDK
> P0AFH8|OSMY_ECOLI Osmotically -inducible protein Y - *Escherichia coli*.
MTMTRLKISKTLAVMLTSAVATGSAYAENNAQTTNESAGQKVDSSMNKV
GNFMDDSAITAKVKAALVDHDNIKSTDISVKTDQKVVTLSGFVESQAQAE
EAVKVAKGVEGVTSSDKLHVRDAKEGSVKGYAGDTATTS EIKAKLLADD
IVPSRHVKVETTDG VVQLSGTVDSQAQSDRAESIAKA VDGVKS VKNLKT
K
> Q47474|PMEB_DICD3 Pectinesterase B - *Dickeya dadantii* (strain 3937)
(*Erwinia chrysanthemi* (strain 3937)).
MSLTHYSGLAAVSM SLILTACGGQTPNSARFQPVFPGTVSRPVL SAQEA
GRETPQH YFAHGGYAKPVADGWTPTPIDTSRVTAAYVVGPRAGVAGATH
TSIQQAVNAALRQHPGQTRVYIKLLPGTYTGTVYVPEGAPPLTLFGAGDR
PEQVVVSLALDSMSPADYRARNPHGQYQPADPAWYMYNACATKAGATI

NTTCSAVMWSQSNDFQLKNLTVVNALLDVTDSGTHQAVALLRDTGEGSAGT
KCPFAQPSDTFFVNTSDRQNSYVTDHYSRAYIKDSYIEGDVDYVFRGATA
VFDVRVRFHTVSSRGSKEAYVFAPDSIPSVKYGFLVINSQLTGDNGYRGAQ
KAKLGRAWDQGAQQTGYLPGKTANGQLVIRDSTIDSSYDLANPWGAAATT
DRPFKGNISQDRDLDDIHFNRLWEYNTQVLLHE
> P56060|KDSA_HELPY 2 -dehydro-3-deoxyphosphooctonate aldolase -
Helicobacter pylori (Campylobacter pylori).
MKTSKTKTPKSVLIAGPCVIESLENLRSIATKLQPLANNERLDFYFKASF
DKANRTSLESYRGPGLKLEMLQTIKEEFGYKILTDVHESYQASVAAKV
ADILQIPAFLCRQTDLIVEVSQTNAIVNIKKGQFMNPKDMQYSVLKALKT
RDKSIQSPTYETALKNGVWLCERGSSFGYGNLVDMRSLKIMREFAPVIF
DATHSVQMPGANGKSS GDSSFAPILARAAAAGVIGDGLFAETHVDPKNAL
SDGANMLKPELEQLVTDMLKIQNLF
> Q55653|SYH_SYNY3 Histidyl -tRNA synthetase - Synechocystis sp. (strain PCC
6803).
MGAIQAIRGTRDILPPETNYWQWVEIAKSIILDRALYQEIRTPIFEQTSL
FERGIGEATDVVGKEMYSFTDRGDRPITLRPEGTAGVVVRAIIEQNLQAAG
GVQRLWYTGPMFRYERQAGRQRQFHQLGVEVLGSADPRADVEVIALGTD
ILKALGLSNLSLALNSVGNNGDRQRYREALIAYLTPFKAELDPDSQDRLE
RNPLRILDKAKRTQEIIVQDAPSIDHLGVDSQRHFDQVQQLLTNLGIAY
QLTPTLVRLDYYTHTAFEIQSSDLGAQATVCGGGRYDGLVAELGGPVTP
AVGWAMGLERLIILLQOMATPPAPSPDLYLISKGEKAEPQALILAQKLRN
QGLAVALDLSA SAFGKQFKRADKSGAIACLVLGDGEIATGTVQLKWLADK
AQETLQLQDLMGNITELKQRLAGHREKYPHLTSNFSVTCHDPMDNLV
> P65106|IF1_CHLTR Translation initiation factor IF -1 - Chlamydia
trachomatis.
MAKKEDTIVLEGRVEELLPGMHFRVMLENGVPITAHLCGKMRMSNIRLLV
GDRVTVEMSTYDLTKARVVYRHR
> P48464|TYSY_SHIFL Thymidylate synthase - Shigella flexneri.
MKQYLELMQKVLDEGTQKNDRTGTGLSIFGHQMRFNLDGFPVLTTRKRC
HLRSIIHELLWFQGDNTIAYLHENNVTIWEWADENGDLGPVYKQWRA
WPTPDGRHIDQITTVLNQLKNDPDSRRIIVSAWNVGELDKMALAPCHAFF
QFYVADGKLSQCLYQRSCDVFLGLPFNIASYALLVHMAQQCDLEVGDFV
WTGGDTHLYSNHMDQTHLQLSREPRPLPKLIKRKPESIFDYRFEDFEIE
GYDPHPGVKAPVAI
> HLYX_ACTPL P23619 REGULATORY PROTEIN HLYX. - ACTINOBACILLUS
MKIVSDAKHTGRTRCTIHCQNCISISQLCLPFTLSEHELTQLDNIIERKKP
VQKSQIIFQSGDELRSIYAIRSGTIKSYTISESGEEQITAFHLPGLVGF
DAIMNMKRVGFAQALETSMICEIPFDILDD LAGKMPKIRHQIMRLMSNEI
KSDQEMILLLSKMSAEKLAFLHNLRSQRYAAPGFSAREFRLTMTRGDIG
NYLGLTIETISRLGRFQKSGMITVQGYITINRMDELTV
> P00805|ASPG2_ECOLI L-asparaginase 2 - Escherichia coli.
MEFFKKTALAALVMGFSGAALALPNITILATGGTIAGGGDSATKSNYTVG
KVGVENLVNAVPLKDIANVKGEQVVNIGSQDMN DNVWLTAKKINTDCD
KTDGFVITHGTDTEETAYFLDLTVKCDKPVVMVGAMRSTSMSADGPFN
LYNAVVTAAKASANRGLVVMNDTVLDGRDVTKTNTTDVATFKSVNYGP
LGYIHNGKIDYQRTFARKHTSDTPFDVSKLNELPKVGIVNYANASDLPA
KALVDAGYDGVIVSAGVGNGLYKSVFDTLATAAKTGTAVVRSSRVPTGAT
TQDAEVDDAKYGFVASGTLNPQKARVLLQLALTQT KDPQQIQQIFNQY
> P07464|THGA_ECOLI Galactoside O -acetyltransferase - Escherichia coli.
MNMPTERIRAGKLFDTMCEGLPEKRLRGKTLMYEFNHSHPSEVEKRESL
IKEMFATVGENAWVEPPVYFSYGSNIHIGRNFYANFNLTIVDDYTVTIGD
NVLIAPNVTLSTVGHVHHELKNGEMYSFPITIGNNVWIGSHVVINPGV
TIGDNSVIGAGSIVTKD IPPNVVAAGVPCRVIREINDRDKHYFKDYKVE
SSV
> Q05811|OM3A_RHILV Outer membrane protein IIIA - Rhizobium leguminosarum
bv. viciae.
MNIRMVLLASAAAFVAASTPVLAADAIVAAEPEPVEYVRCDAYGTGYFYI
PGTETCLKIEGYIRFQVNVGDNPPGGDNDSDWDAVAVRFSRKSDEYGP
LTGVIVMQFNADNASDQDAILDSAYLDVAG FRAGLFYSWDDGLSGETDD
IGSVVTLHNSIRYQYESGTFYAGLSVDELEDGVYQGTFTPGVIPGTTDFT
ADDGPNNVGVAFGIGGTAGAFSYQVTGGWDVDNEDGAIRAMGTVEIGPGT
FGLAGVYSSGPNSSYSSAEWAVAAEYAIKATDKLKITPGRWHGHVPEDFD

GLGDAWKVGLTVDYQIVENFYAKASVQYLDPQDGEDSTSGYFACSVRSNH
LVDAPGLRIGSTTISF
> P56146|SYFA_HELPY Phenylalanyl-tRNA synthetase alpha chain - Helicobacter pylori (Campylobacter pylori).
MHTLIERLEKVTNSKELEEARLNALGKKGVFADKFNQLKHLNGEENAF
KEIHYYKQAFEKAFEWKKKAIIELELEERLKKKIDVSLFNAIKTSSSSHP
LNYTKNKIIEFFTPLGYKLEIGSLVEDDFHNFSALELPPYHPARMDQDTF
YFKDHKLLRHTSPVQIHTMQEQTPPIKMICLGETFRRDYDLTHTPMFHQ
IEGLVVDQKGNIRFTHLKGVIEDFLHYFFGGVKLRWRSSFFPFTEPSAEV
DISCVFCKQEGCRVCSHTGWLEVLGCGMVNNAVFEEAIGYENVSGFAFGMG
IERLAMLTCQINDLRSFFETDLRVLESF
> P32670|PTFX2_ECOLI Multiphosphoryl transfer protein 2 - Escherichia coli.
MALIVEFI CELPNGVHARPASHVETLCNTFSSQIEWHNLRTDRKGNKSA
LALIGTDTLAGDNCQLLISGADEQEAHQRLSQWLRDEFPHCDAPLAEVKS
DELEPLPVSLTNLNPQIIRARTVCSGSAGGILTPISSLDLNLGNLPAK
GVDAEQSALENGLTLVLKNIEFRLDSDGATSAILEAHRSLAGDTSLEH
LLAGVSAGLSCAEAIIVASANHFCEEFSSSSSYLQERALDVRDVCFQLLQ
QIYGEQRFAPAGKLTQPAICMADELTPSQFLELDKNHLKGLLLKSGGTT
HTVILARSFNIPTLVGVDDIDALTPWQQTIYIDGNAGAIIVVEPGEAVARY
YQQEARVQDALREQQRVWLTQQARTADGIRIEIAANIAHSVEAQAFAFGNG
AEGVGLFRTEMLYMDRTSAPGESELYNIFCQALESANGRSIIVRTMDIGG
DKPVDYLNIPAEANPFLGYRAVRIYEEYASLFTTQLRSILRASAHGSLKI
MIPMISSMEE ILWVKEKLAEAKQQLRNEHIPFDEKIQLGIMLEVPSVMFI
IDQCCEEIDFFSIGSNDLTQYLLAVDRDNAKVTTRHYNLSNPAFLRALDYA
VQAVHRQGWIGLCEGELGAKGSVPLLVGLGLDELMSAPSIPAAKARMA
QLDSRECRKLLNQAMACRTSLEVEHLLAQFRMTQQDAPLVTAEICITLES
WRSKEEVLKGMTDNLNLAGRCRYPRKLEADLWAREAVFSTGLGFSFAIPH
SKSEHIEQSTI SVARLQAPVRWGDDEAQFIIMLTLNKHAAGDQHMRIFSR
LARRIMHEEFRNALVNAASADAIASLLQHELEL
> P04744|PAPB_ECOLI Major pilu subunit operon regulatory protein papB - Escherichia coli.
MAHHEVISRSGNAFLNIRESVLLPGSMSEMHHFLLIGISSIHDRVILA
MKDYLVGGHSRKEVCEKYQMNGYFSTTLGRLIRLNALAAR LAPYYTDES
SAFD
> P25447|FAEF_ECOLI K88 minor fimbrial subunit faeF - Escherichia coli.
MKKTMMAALVLSALSISQALAAEYSEKTQYLGVVNGQVGVNSVVKVTRT
PTDPVLYRSGSNSPLPAELIIRHAESRPASGGLANITVKEALPDNGEARI
TLKTSMLMVDGKRVALSARQQGEDVVITVPEAQQQIELRTDAPAELEVPVS
YRGNLQIALQVED
> P14756|ELAS_PSEAE Pseudolysin - Pseudomonas aeruginosa.
MKKVSTLDLLFVAIMGVSPAFAADLIDVSKLPSKAAQAGPVTLQAAV
GAGGADELKAIRSTTLPNGKQVTRYEQFHNGVVRVGEAITEVKGPGKSV
AQRSGHFVANIAADLPGSTTAAVSAEQVLAQAKSLKAQGRKTENDKVELV
IRLGENNIAQLVNVSYLIPGEGLSRPHFVIDAKTGEVLDQWEGLAH AEA
GGPGGNQKIGKYTYGSDYGPLIVNDRCEMDDGNVITVDMNSSTDDSKTTP
FRFACPTNTYKQVNGAYSPLNDAHFFGGVVFKLYRDFWGTSP LTHKLYMK
VHYGRSVENAYWDGTAMLFGDGATMFYPLVSLDVAHEVSHGFTEQNSGL
IYRQSGGMNEAFSDMAGEAAEFYMRGKNDFLIGYDIKKGSGALRYMDQP
SRDGRSIDNASQYNGIDVHSSGVYNRAFYLLANSPGWDTRKAFEV VD
ANRYWTATSNYNSGACGVIRSAQNRNYSAADVTRAFSTVGVTCPSAL
> P26877|LIP_PSEU0 Lactonizing lipase - Pseudomonas sp. (strain 109).
MKKKSLLPLGLAIGLASLAASPLIQASTYTQTKYPIVLAHGMLGFDNIG
VDYWFGPSALRRDGAQVYVTEVSQLDTSEVRGEQLLQVVEEIVALSGQP
KVNLIHSHGGPTIRYVAAVRPDLMP SATSVG APHKGSDTADFLRQIPPG
SAGEAVLSGLVNSLALISFLSSGSAGTQNSLGSLESINSEGAARFNAKY
PQGIPTACGEGAYKVNVSYSYWSGSSPLTNFLDPSDAFLGASSLTFKN
GTANDGLVGTCSHLLGMVIRDNYRNMHLDEVNQVFGLTSLFETSPVSVYR
QHANRLKNASL
> P08306|COX2_PARDE Cytochrome c oxidase subunit 2 - Paracoccus denitrificans.
MMAIATKRRGVAAVMSLGVATMTAVPALAQDVLGDLPIVIGKPVNGGMNFQ
PASSPLAHDQQWLDHFVLYIITAVTIFVCLLLLICIVFRNRANPVPARF
THNTPIEVIWTLVPLVILVAIGAFSLPILFRSQEMPNDPDLVIKAIGHQW

YWSYEYPNDGVAFDALMLEKEALADAGYSEDEYLLATDNPVVVVPVGGKVL
VQVTATDVIHAWTIPAFVAVKQDAVPGRIAQLWFSVDQEGVYFQGQ SELCG
INHAYMPIVVKAVSQEKYEAWLAGAKEEFAADASDYLPAFPVKLASAE
> P19845|NOSY_PSEST Membrane protein nosY - *Pseudomonas stutzeri*
(*Pseudomonas perfectomarina*).
MNQVWNIARKELS DGLRNRWLLAISLLFAVLAVGIAWLGAASGQLGFTS
IPATIASLASELATFLMPLIALLLAYDAIVGEDEGGTLMLLTYPLGRGQI
LLGK FVGHGLILALAVLIGFGCAALAIALLVEGVELGMLFWAFGRFMISS
TLLGWVFLAFAYVLSGK VNEKSSAAGLALGVWFLFVLFVDFLVLALLVLS
EGKFNPELLPWL LLLNPTDIYRLINLSGFEGSGSAMGVLSL GADLPVPA
VLWLC LLAWIGVSL LLAYAIFRRRLT
> P09888|OMPC_NEIGO Outer membrane protein P.IIC - *Neisseria gonorrhoeae*.
MQPAKNLLFSSLLFSSLLFSSAARAASEDGGRGYPYVQADLAYAAERITHD
YPKPTGTGKNKISTVSDYFRNIRTHSVHPRVSVGYDFG SWRIAADYARYR
KWN NNKYSVSIKELLRNDNSASGVRGHLNIQTQKTEHQENGT FHAVSSLG
LSTIYDFDTGSRFPYIGMRVAYGHRHQVRSVEQETEIITTYPSNGGGK
VSLSSKMPPKSAHQNSIRRVGLGVIAGVGF DITPNLTLDTGYRYHNWG
RLENTFRFKTHEASLGMRYRF
> P0A9K1|PHOH_ECOLI Protein phoH - *Escherichia coli*.
MVTSC TGHVLDNQRATTRGVFSSGSHLVTLHFQPHPFSCVTD AVNGARS
RFSAFYPKANYGLQGSQPSDVRAHNRAANGACDEYKQLKVL SMGRQKAVI
KARREAKRVLRRDRSRSHKQREESVTSLVQMGGVEAIGMARDSRDTSPIL
ARNEAQLHYLKAIESKQLIFATGEAGCGKTWISA AK AAEALIHKDVDRII
VTRPV LQADEDLGFLPGDIAEKFAPYFRPVYDVLVRR LGASFMOYCLRPE
IGKVEIAPFAYMRGRTFENAVVILDEAQNVTAAQMKMFLTRLGENVTVIV
NGDITQC DLPRGVC SGLSDALERFEEDEMVGIVRF GKEDCVRSALCQRTL
HAYS
> P31550|THIB_ECOLI Thiamine-binding periplasmic protein - *Escherichia coli*.
MLKKCLPLLLCTAPVFAKPVLT VYTYDSFAADWGPVVKKA FEADCNC
ELKLVALEDGVSLLNRLRM EGKNSKADVVLGLDNNLLDAASKTGLFAKSG
VAADAVNVPGGW NNDTFVFPFDYGYFAFVYDKNKLNPPQSLKELVESDQN
WRVIYQDPRSTPGLGLLLWQKVY GDDAPQAWQKLAKKTVTVTKGWSEA
YGLFLKGESDLVLSYTTSPAYHILEEKKNYAAANFSEGHYLQVEVAART
AASKQPELAQKFLQFMVSPAFQNAIPTGNWMPVANVTLPAGFEKLT KPA
TTLEFTPAEVAAQRQAWISEWQRAVSR
> P13907|PSBO_ANASP Photosystem II manganese-stabilizing polypeptide -
Anabaena sp. (strain PCC 7120).
MRYRALIVAFVAVCLGLLTACSDAPASSTRDILTYEQIRGTGLANKCPQL
TETSRGSIPLDSSKSYVLKELCLEPTNFFV KEEPANKRQTAEFVAGKLLT
RYTSTIDQVSGDLKFNDSSSLTFVEKDGLDFQAITVQLP GGERVPFLFTI
KNLVAQTQPLSSLNTSTDFEGTFKVP SYRGA AFLDPKGRGVVSGYDNAV
ALPAQADDEDLTRTNVKRAEILNGKISLQIAKVDSSSGE IAGTFESEQPS
DIDLGADEPKVKIRGIFYARVE
> MALQ_ECOLI P15977 4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.2 5)
MESKRLDNAALAAGISPNYINAHGK PQSISAETKRRLDAMHQRTATKVA
VTPVPMVMVYTS GKKMPMVVEGSGEYSWLLTTEEGTQYKGHVTGGKAFNL
PTKLPEGYHTLTLTQDDQRAHCRVIVAPKRCYEPQALLNKQKLWGACVQL
YTLRSEKNWIGD FGLKAMLVDVAKRGG SFIGLNPIHALYPANPESASP
YSPSSRRWLNVIYIDVNAVEDFHLSEEAQAWWQLPTTQQTLQ QARDAD WV
DYSTVTALKMTALRMAWKGF AQRDDEQMAAFRQFVAEQGDSLFWQA AFDA
LHAQQVKEDEM RWGPAWPEMYQNVDSPEVRQFCEEHRDDVDFYLLWQL
AYSQFAACWEISQGYEMPIGLYRDLAVGVAEGGAETWC DRELYCLKASVG
APPDILGPLGQNWGLPPMDPHIITARAYEPFIELLRANMQNCGALRIDHV
MSMLRLW WIPYGETADQ GAYVHPVDDLLSILALESKRHR CMVIGEDLG T
VPVEIVGKLRSSGVSYKVL YFENDHEKTFRAPHKAYPEQSMAVAATHDLP
TLRGYWECDLTLGKTLGLYPDEVVLRGLYQDRELAKQGLLDALH KYGCL
PKRAGH KASLMSMPTLNRGLQRYIADSNSALLGLQPEDWLDMAEPVNI P
GTSYQYKNWRRKLSATLES MFADDGVNKLKDLDRRRRAAAKKK
> ASRB_SALTY P26475 ANAEROBIC SULFITE REDUCTASE SUBUNIT B (EC
MSHC SCHDKPQHSLAAAYRILSITRHTPLEWNFRVAVD FPAHWGQFVEV
SLPRVGEAPISVSDYGDGWIDLLIRNVGKVT SALFTLKEGDNVWLRGCY
NGYPVDTLRHKPLLVVAGGTGVAPV KGLMRYFVENPQEIGQLDMILGYKN
RDCVLYKEEMATWRGKHNVLTLDEGEADDRYQIGRVTDR LADMTLSDID

TMQAIIVVGGPPIMITFTVKMLLQKGLKPEQIWVDYERRMACSVGKCG HCRM
GEVYVCTDGPFIIFYAVAQRFAD
> P36912|EBA2_FLAME Endo -beta-N-acetylglucosaminidase F2 - Flavobacterium
meningosepticum (Chryseobacterium meningosepticum) (Elizabethkingia
meningoseptica).
MKTANFSFALCLSVVIMLFIKCTRSEQDLSVTKDAIAQKSGVTVSAVNLS
NLIAYKNSDQISAGYYR TWRDSATASGNLPSMRWLPDSLDMVMVFPDYT
PPEAYWNTLTKTNYVPLYLHKGRTKVIITLGDLNSATTTGGQDSIGYSSWA
KGIYDKWVGEYNLDGIDIDIESSPSGATLTKFVAATKALSIFYGPKSGTG
KTFVYDTNQNPTNFFIQTAPRYNYVFLQAYGRSTTNLTTVSGLYAPYISM
KQFLPGFSFYEENGYPGNYWNDVRYPQNGTGRAYDYARWQPATGKKGGVF
SYAIEDAPLTSSNDNLTLR APNFRVTKDLIKIMNP
> P22365|AMCY_PARVE Amicyanin - Paracoccus versutus (Thiobacillus versutus).
MISAKTLRPAIAAIALFAIGATGAWAQDKITVTSEKPVAAADVPADAVVV
GIEKMKYLTPEVTIKAGETVYVWNGEVMPHNVAFKKGIVGEDAFRGMEMT
KDQAYAITFNEAGSYDYFCTPHPFMRGKIVIVE
> P24404|LEU3_AGRT5 3-isopropylmalate dehydrogenase - Agrobacterium
tumefaciens (strain C58 / ATCC 33970).
MTVRSFLFLPGDGGIGPEAMTEVRKLI EYMNSAHNAGFTVSEGLVGG SAYD
AHGVAISDADMEKALAADAILFGAVGGPKWDGVPYEHREAGLLRLRKDL
ELFANLRPAICYPALAAASSLKPELVEGLDILIVRELTGGVYFGEPKQII
DLGNGQKRGIDTQIYDTFEIERI ASVAFELARSRDNRVCSMEKRNVMKSG
VLWNQVVTETHAAKYKDVQLEHMLADAGGMQLVRKPKQFDVIVTDNLF GD
MLSDVAAMLTGSLGMLPSASLGAPDAKTGKRKAMYEPVHGSAPDIAGKSI
ANPIAMIASFAMCLRYSFNMVDEATKLEAAIANVLDKGI RTADIMADGCR
QVGTSDMGDAVLAEFKALSA
> P07862|DDL B_ECOLI D-alanine--D-alanine ligase B - Escherichia coli.
MTDKIAVLLGGTSAEREVSLNSGA AVLAGLREGGIDAYPVDPK EVDVTQL
KSMGFQKVI FIALHGRGGEDGTLQGMLELMGLPYTGSGVMASALSMDK LRS
KLLWQAGL PVA PWWALTRAEFEKGLSDKQLAEISALGLPVIVKPSREGS
SVGMSKVVAENALQDALRLAFQHDEEV LIEKWLSGPEFTVAILGEEILPS
IRIQPSGTFYDYEA KYLSDETQYFCPAGLEASQEAN LQALVLKAWTTLGC
KGWGRIDVMLDSGQFYLL EANTS PGM TSHSLVPMAARQAGMSFSQLVVR
ILELAD
> P24037|C552_PSEST Cytochrome c -552 - Pseudomonas stutzeri (Pseudomonas
perfectomarina).
MKKTLMASAVGAVIAFGTHGAMAAAPADWSSVAATDVTFLYPGVSPVEWI
TKGTEHG GARALKGETCAGCHSEEASDMGEKMASGKKLEPS PIAGKAPF
INAKVQAANDGENLYLRFTWKQPAASGAAPMDADNPVKIAYMLEGGSKVE
LAEAGGCWGSCHGDARTMPGAADTKTKYVKDGLANGVYYDLNQWRSGEN
KAFDGYVATERVMEGGQALVDAQGKLDGDTWTVV FTRKFAGGEDVTLAP
GNLYNFGFAIHDDSATGRYHHVSLGYS LGIDAQGDITAAKQ
> P18103|FANC_ECOLI K99 fimbrial protein - Escherichia coli.
MKKTL LAI ILGGM AFATTNASANTGT INFNGKITSATCTIDPEVNGNR TS
TIDLQAAISGHGT VVDFK LKPAPGSNDCLAKTNARIDWSGSMNSLGFNN
TASGNTAAKGYHMTLRATNVGNGSGGANINTSFTTAEYHTSAIQSFNYS
AQLKKDDRAPSNNGGYKAGVF TTSASFLVTYM
> P74764|SYFB_SYNP7 Phenylalanyl -tRNA synthetase beta chain - Synechococcus
sp. (strain PCC 7942) (Anacystis nidulans R2).
MRISLNLWREL VQVDLEPEVLA EKLTLAGFEVEEIEDRR TWAAGVVVGRV
LEREQHPNADRLSVCQVEIGQAEPVTIVCGASNVRADIWVAVATLGSYLP
CIDLKLKPTKLRGRVSEGMICSLSELGLTKESEGIHIFPEDAGLQAGQPV
GPLLGLDDVVLDTSTANRADALS LIGIAREVRALTAATLTL PEVELQTY
PELPCLAISLQSEACSHYSGT IIEGVTIAPSP EWLQKRLQLAGIRTINNV
VDITNYILLEYGQPLHAFDRQKLQAIAGSSDLAIGVRS AQAGETLKTLD D
QERTLAEALVITAGDCPVALAGVMGGADSEVSQETTQLLLEAAWFEPIA
VRRSARSQGLRTEASARYERGVNVTELP IATQRAIDLLLQIAGGTVISQT
VATTTQTEPEHSITLRLQRINELLGPVQAEDEELKDLGADDIE RLLTAIG
CHLTLVDDAVWQVRVPYRYRDLEREIDLIEEVARLYGYDNFGETLPPLG
SDEGALSIDESLRRQIRAVCRGVGLTELQHYSLVKPGSDRQVHLANPLLA
EYSALRLDLLSGLIDAFQYNWEQNGPLWGFEIGRI FWREEDGFFEADRM
GGILGGDPSRGRWQRGGEQAIDWYAAKGVLEE IFERFGLTIEFQPDRQD
DRFHPGRTASLWLQGDRLGRFGQLHPSLCEGRGLPAEVYAFELD LDVWLD

HLDQPERQVPRFQPYSSFPASDRDLAFFVDQSVTVAELEIRIRROGGALL
SEVELFDQYCGEHPENQRSLAFRLTYRASDRTLTEAEVEFPVHDQVRQSL
VERFRVTLRS
> NDK_SYNY3 P74494 NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)
MERTFIMIKPDGVQRQLIGEIVGRFEKKGFKLVAMKVMTVSQELAEKHYE
ALNDKPFSSGLVNFICSSPVVAM VWEGNSIVSTSRQMIGATDPHAAAPGT
IRGDYGVSVGRNIIHGSDAIETAKREISLWFKDEEVNEWDATLNPWLYE
> P29739|OMPH_PHOPR Porin-like protein H - Photobacterium profundum
(Photobacterium sp. (strain SS9)).
MKKTLVALAILTAAGSANAGINLYDADGVKTDLSGAAEVQYRQTFKEDSD
AELRMDGDGLAVNTTVAISDSLNA VAAVAFEFEDGKVTNDELWVGAGDF
GTLTAGRQYMLADDAGVGGKDYELGGDIDFVQANGDQVVKYVFDNGQFYG
GVGALITETNPDDNADEASVYEGRLGARFGDFDVRAYLYSGEDVNTDNFD
VFGDDKVNVDIDGYQIEAEYIVNAFAFAASFGQVDYELASDSSQKIEADT
AALAGSYTMNKTTFVAVGYTYWSPEAKGTVKKMEEANVFYANVTQQLHSNV
KVYGEIGSSDNDSEFGYVAGMEVT F
> P42512|FPTA_PSEAE Fe(3+) -pyochelin receptor - Pseudomonas aeruginosa.
MKTETKVIKGRQGIARNRHTPLCLGLLLALSPLAAVADARKDGETELPD
MVISGESTSATQPPGVTTLGKVPLKPRELPQSASVIDHERLEQQNLFSLD
EAMQQATGVTVQPFQLLTTAYYVRGFKVDSFELDGVALLGNTASSPQDM
AIYERVEILRGSNLLHGTGNPAATVNLV RKRPRQREFAASTTLSAGRWRD
YRAEVDVGGPLSASGNVRGRAVAAYEDRDYFYDVADQGRLLYGVTEFDL
SPDTLLTVGAQYQHIDSITNMAGVPMKDGSNLGLSRDYLVDVDWRFRKW
DTYRAFGSLEQQGGGWKGVSAEYQEAADSRLRYAGSFGAIDPQTGDGGQ
LMGAAYKFKSIQRSLDANLNGPVRLFGLTHELLGGVTYAQGETRQDTARF
LNLNTPVNVYRWDPHGVPRPQIGQYTSFG TTTTQKGLYALGRIKLAEP
LTLVVGRESWWDQDTPATRFKPKGRQFTPYGGLIWDWFARDWSWYVSYAEV
YQPQADRQTNWSEPLSPVEGKTYETGIKELADGRNLNLSLAAFRIDLNN
PQEDPDHQPNNPFYISGGKVRSQGFELEGTGYLTPYWSLSAGYTYTST
EYLKDSQNDSGTRYSTFTPRHLLRLWSNYDLPWQDRRWSVGGGLQAQSDY
SVDYRGVSMRQGGYALVNMRLGYKIDEHWTA AVNVNLFDRTYYSLSNP
NWNRYGEPFRSFRVSLRGAF
> P43478|CGKA_ALTCA Kappa -carrageenase - Alteromonas carrageenovora
(Pseudoalteromonas carrageenovora).
MKPISIVAFPIPAISMLLLSAVSQAASMOPPIAKPGETWILQAKRSDEFN
VKDATKWNFQ TENYGVWSWKNENATVSNGLKLTTKRESHQRTFWDGCNQ
QQVANYPLYYTSVAKSRATGNYGYYEARIKGASTFPGVSPAFWMYSTID
RSLTKEGDVQYSEIDVVELTQKSAVRESHDHLNIVVKNKPTWMRPGSF
PQTNHNGYHLPFDPRNDFHTYGVNVTKDKITWYVDGEIVGEKNLNYWHRQ
MNLTLSQLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYVRTWVKVGNN
NSAPGEGQSCPNTFVAVNSVQLSAAKQTLRKGQSTTLESTVLPNCATNKK
VIYSSSNKNVATVNSAGVVKAKNKGTTATITVKTKNKGKIDKLTIAVN
> Q2RVM4|CYC2_RHORT Cytochrome c2 - Rhodospirillum rubrum (strain ATCC
11170 / NCIB 8255).
MKKGFLAAGVFAAVAFASGAALAEGDAAAGEKVSKKCLACHTFDQGGANK
VGNLFGVFENTA AHKDDYAYSESYSTEMKAKGLTWTEANLAAYVKDPKAF
VLEKSGDPKAKSKMTFKLTKDDEIE NVIAYLKTLLK
> FRZC_MYXXA P43500 FRZCD PROTEIN (FRIZZY AGGREGATION PROTEIN)
MSLDTPNEKPAGKARARKAPASKAGATNAASTSSSTKAITDILLTVLSGN
LQARVPKELVGESGVELAHLNQLDQFAASEHRKHVAAQEQIDQALDALI
GLVREGDLRWNNTTTEDPQLGPLEGFGKVIETLRTFVREINEAALRLSS
SANQVLAASTQHETSSTEQAAAIHETTATM EELKHASAQIAENAGSVARV
AEETLGAARAGRGAIGEFIQAMQQIRSDGVAVADSIKLSKRVERIGTVV
EVIDEIAADRSDLLNALNAALEGSRAGEAGKGFISIVAAEMRRLAENVLDSTK
EIKNLITEIREATAAAAGAAEASKSATESGEKLGAVAAQAVEGILAGVQE
TSDAARVINLATQQRTATEQVVASMAEIEDVTRQTTQASKQATGAAEEL
TQLAGRLAELIKRFKAD
> P26997|XYLA_THET8 Xylose isomerase - Thermus thermophilus (strain HB8 /
ATCC 27634 / DSM 579).
MYEPKPEHRFTFGLWTVGNVGRDPFGDAVRERLDPVYVVKLAELGAYGV
NLHDEDLIPRGTPPQERDQIVRRFKKALDEGLKVPMTANLFSDFPAFKD
GAFTSPDPWVRAYALRKSLETMDLGAELGAEIYVWVPGREGAEVEATGKA
RKVWDWVREALNFMAAYAE DQGYGYRFALEPKPNEPRGDIYFATVGSMLA

FIHTLDRPERFGLNPEFAHETMAGLNFVHAVAQALDAGKLFHIDLNDQRM
SRFDQDLRFSGENLKAFFLVDLLESGYQGPRHFDHALRTEDEEGVWA
FARGCMRTYLILKERAEAFREDPEVKELLAAYYQEDPAALALLGPYSREK
AEALKRAELPLEAKRRRGGYALERLDQLAVEYLLGVRG
> P0AFL3|PPIA_ECOLI Peptidyl -prolyl cis-trans isomerase A - Escherichia coli.
MFKSTLAAMA AVFALSALSPAAMAAKGDPHVLLTTSAGNIELELDKQKAP
VSVQNFVDYVNSGFYNNTTFHRVIPGFMIQGGGFTEQMQQKKNPPIKNE
ADNGLRNTRGTIAMARTADKDSATSQFFINVADNAFLDHGQRDFGYAVFG
KVVKGMVDVADKISQVPTHVGPYQNVPSKPVVILSAKVLV
> P22320|HOXH_RAL EH NAD-reducing hydrogenase hoxS subunit beta - Ralstonia eutropha (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337)).
MSRKLVIDPVTRIEGHGKVVVHLLDDDKVVDKLVHVEFRGFEEKFVQGHF
FWEAPMFLQRICGIC FVSHHLCGAKALDDMVGVLKSGIHVTPAEKMRR
LGHYAQMQLSHTTAYFYLVPEMLFGMDAPPAQRNVLGLIEANPDLVKRV
VMLRKKWQVEVIKAVFGKMMHGINSVPGGVNNLSIAERDRFLNGEGLLS
VDQVIDYAQDGLRFLFYDFHQKHRAQVDSFADVPALSMCLVGDNDVYYH
GRLRIIDDDKHI VREFDYHDYLDHFSEAVEEWSYMKFPYLKELGREQGSV
RVGFLGRMNVTKSLPT PLAQEALERFHAYTKGRNTNMTLHTNWARAIEIL
HAAEVVKELLHDPDLQKDQLVLT PPNNAWTGEGVGVVEAPRGTL LHHYRA
DERGNITFANLVVATTQNNQVMNRTVRSVAEDYLGGHGEITEGMMNAIEV
GIRAYDPCLSCATHALGQMPLVVSFDAAGRLIDERAR
> P06608|ASPG_ERWCH L-asparaginase - Erwinia chrysanthemi.
MERWFKSLFVLVLFVFTASA ADKLPNIVILATGGTIAGSAATGTQTTGY
KAGALGVDTLINAVPEVKLANVKGEQFSNMAENMTGDVVLKLSQRVNE
LLARDDVDGVVITHGTDVVEESAYFLHLTVKSDKPVVFAAMRPATAISA
DGPNNLLEAVRVAGDKQSRGRGVMVVLNDRIGSARYITKTNASTLDTFKA
NEEGYLGVIIGNRIYYQNRIDKLTTRSVDFVRLTSLPKVDILYGYQDD
PEYLYDAAIQHGKVIYAGMG AGSVSVRGIAGMRKAMEKGVVIRSTRT
NGGIVPPDEELPGLVSDSLNPAHARILLMLALTRTSDPKVIOEYFHTY
> P50500|IRO_THIFE Iron oxidase - Thiobacillus ferrooxidans (Acidithiobacillus ferrooxidans).
MSEKDKMITRRDALRNIAVVVGSVATTTMMGVGVADAGSMPKAAVQYQDT
PKGKDHCVCAQFIAPHSCVVAGNISPNGWCV AFVPKSA
> AAT_ECOLI P00509 ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (T
MFENITAAPADPILGLADLFRADERPGKINLGIGVYKDETGKTPVLTSVK
KAEQYLENETTKNYLGIDGIPFGRCTQELLFGKGSALINDKRARTAQT
PGGTGALRVAADFLAKNTSVKRVVWVSNPSWPNHKS VFNSAGLEVREYAYY
DAENHTLDFDALINSLNEAQAGDVVLFHGCCHN PTGIDPTLEQWQTLAQL
SVEKGLWLP LDFAYQGFARGLEEDA EGLRAFAAMHKELIVASSYSKNFGL
YNERVGACTLVAADSETVDRAFSQMKAAIRANYSNPPAHGASVVATILSN
DALRAIWEQELTDMRQRIQRMRLFVNTLQEKGANRDFSFIKQNGMFSF
SGLTKEQVLRRLREFGVYAVASGRVNVAGMTPDNMAPLCEAIVAVL
> P45678|PEB1_CAMJE Major cell-binding factor - Campylobacter jejuni.
MVFRKSLKLA VFALGACVAFSNANAAEGKLESIKSKGQLIVGVKNDVPH
YALLDQATGEIKGFVEVDVAKLLAKSILGDDKKIKLVAVNAKTRGPLLDNG
SVDAVIATFTITPERKRIYNFSEPYQDAIGLLVLKEKKYKSLADMKGAN
IGVAQAATTKKAIGEAAKKIGIDVKFSEFPDYP SIKAAALDAKRVDAFSVD
KSILLGYVDDKSEILPDSFE PQSYGIVTKKDDPAFAKYVDDFVKEHKNEI
DALAKKWGL
> Q07792|ESTE_VIBMI Arylesterase - Vibrio mimicus.
MIRLLSLVLFCLSAASQASEKLLVLGDSLSAGYQMPIEKSWPSLLPDAL
LEHQDQVTVINGSISGDTTGNGLARLPQLLDQHTPDLVLIELGANDGLRG
FPPKVITSNLSKMSI LKDSGANVMMQIRVPPNYGKRYSDMFYDIYPKL
AEHQVQVLMPPF FLEHVITKPEWMMDDGLHPKPEAQPWIAEFVAQELVKHL

> P0A855|TOLB_ECOLI Protein tolB - Escherichia coli.
MKQALRVAFGLIILWASVLHAEVRIVIDSGVDSGRPIGVVFPQWAGPGAA
PEDIGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAWSALGIDAVV
VGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQWLR YAGHTASD
EVFEKLTGIKGAFRTRIAVYVQTNGGQFPYELRVSDYDGYNQFVVHRSPQ
PLMSPAWSPDGSKLAYVT FESGRSALVIQTLANGAVRQVASFPRHNGAPA

FSPDGSKLAFAFSKGTGSLNLYVMDLASGQIRQVTDGRSNNTTEPTWFPDSQ
NLAFTSDQAGRPOVYKVNINGGAPQRITWEGSQNDADVSSDGKFMVMVS
NNGGQQHIAKQDLATGGVQVLSSTFLDETPSLAPNGTMVIYSSSQGMGSV
LNLVSTDGRF KARLPATDGQVKFPAWSPYL

> P18012|IPAC_SHIFL Invasin ipaC - *Shigella flexneri*.

MEIQNTKPTQTLTYTDISTKQTQSSSETQKSQNYQQIAAHIPLNVGKNPVL
TTTLNDDQLLKLSEQVQHDSEIIARLTDKMKDLSEMSHTLTPENTLDIS
SLSSNAVSLIISVAVLLSALRTAETKLGSQLSLIAFDATKSAENIVRQG
LAALSSSITGAVTVQGITGIGAKKTHSG ISDQKALRKNLATAQSLEKEL
AGSKLGLNKQIDTNI TSPQTNSSTKFLGKNKLAPDNISLSTEHKTSLSPP
DISLQDKIDTQRRTYELNLTLSAQKQNI GRATMETS AVAGNISTSGGRYA
SALEEEEQSLISQASSKQAEASQVSKEASQATNQLIQKLLNIIDSINQSK
NSAASQIAGNIRA

> ALKH_ERWCH P38448 4 -HYDROXY-2-OXOGLUTARATE ALDOLASE (EC 4.1

MKNWKTSAEQILTAGPVVIVINKLEHAVPMAKALVAGGVRVLELTLRT
ECAVEAIRLIAQVEPDAIVGAGTVTNPQQLAEVTAAGAQAISPGLTEPL
LKAATEGTIPLIPGISTVSELMLGMDYGLREFKFFPAEANGGVKALQAI
GPFGRKIRFCPTGGISLKNYRDYLLKSVLCVGGSWLVPADALESGDYDRI
TALAREAVAGATA

> ACKA_HAEIN P44406 ACETATE KINASE (EC 2.7 .2.1) (ACETOKINASE)

MSKLVLIILNCGSSSLKFAILDPATGEEKLSGLAEAFFLPEARIKWKLNGE
KGNADLGAGAAHTEALNFIA SNILNDELKNSIAAIGHRIVHGGEKYTQSV
IVTDEVVKGIEDAAQFAPLHNPALHIGIREAFKAFPHLKDKNVVFDTA
HQTMPPEEAFLYALPYSLYKEHGVRRYGAHGTSHYFVSREVAKYVVGKPADQ
VNAIICHLGNGGSVSVVRNGQCIDTSMGLTPL EGLVMGTRCGDIDPAIVF
YLYKTLGMSMDQIEETLVKKSGLLGLTEVTSDCRYAEDNYDDESKPETRR
ALNVYSYRLAKYIGAYMAVLGDDHLDIAAFTGGIGENSAHVRELALNHLK
LFGIKIDNERNLATRFKGDGVIITDDSAFKAIVLPTNEELVIAQDTAKLC
F

> P0ABK9|NRFA_ECOLI Cytochrome c -552 - *Escherichia coli*.

MTRIKINARRIFSLIPFFFFTSVH AEQTAAPAKPVTVEAKNETFAPQHP
DQYLSWKATSEQSERVDALAE DRLVILWAGYPFSRDYNKPRGHAFVTD
VRETLRTGAPKNAEDGFLPMACWSCKSPDVARLIQKDGEDGYFHGKWARG
GPEIVNNGCADCHNTASPEFAKGPPELTL SRPYAARAMEAIGKPFKAG
RFDQQSMVCGQCHVEYFDFGKNKAVKFPWDDGMKVENMEQYDKIAFSDW
TNSLSKTPMLKAQHPEYETWTAGIHG KNNVTCIDCHMPKVQNAEGKLYTD
HKIGNPFDNFAQTCANCHTQDKAALQKVVAERKQSINDLKI KVEDQLVHA
HFEAKAALDAGATEAEMKPIQDDIRHAQWRWDLAIA SHGIHMHAPEEGLR
MLGTAMDKAADARTKLARLLATKGI THEIQIPDISTKEKAQQAIGLNMEQ
IKAEKQDFIKTVIPQWEEQARKNGLLSQ

> P13811|ELBH_ECOLI Heat-labile enterotoxin B chain - *Escherichia coli*.

MNKVKFYVLF TALSSLCAGAPQSITELCSEYHNTQIYTINDKILSYTE
SMAGKREMVIIITFKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTE
TKIDKLCVWNNKTPNSIAAISMEN

> P80505|G3P2_SYNY3 Glyceraldehyde -3-phosphate dehydrogenase 2 -
Synechocystis sp. (strain PCC 6803).

MTRVAINGFRIGRNFRLRCWLGRTDSQLEVVGINDTSDPRTNAHLLRYDS
MLGKLDADISADENSITVNGKTIKCVSDRNPLNLPWAEWNVDLVIEATGV
FVTHEGATKHVQAGAKKVLITAPGKGNIGTYVVGVAHEYKHEEYEVIS
NASCTTNCLAPFGKVINDFGIIKGTMTTTHSYTGDQRILDASHRDLRRA
RAAAVNIVPTSTGAAKAVALVIPELQKLNGLIALRVPTPNVSVVDLVVQV
EKNTIAEQVNGVLKEAANTSLKGVLEYTDLELVSSDFRGTDCSSTVDGSL
TMVMGGDMVKVIAWYDNEWGYSQRVVDLAEIVAKNWK

> P22318|HOXU_RALEH NAD-reducing hydrogenase hoxS subunit gamma - *Ralstonia*
eutropha (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (*Cupriavidus*
neator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337)).

MSIQITIDGKTLTTEEGRTLVDVAAENGVYIPTLCYLKDKPCLGTCRVCS
VKVNGNVAAC TVRVSKGLNVEVNDPELVDMRKALVEFLFAEGNHNCPS
EKSGRCQLQAVGYEVDMMVSRFPYRFPVRVVDHASEKIWLDRDCIFCQR
CVEFIRDKASGRKIFSI SHRGPESTRIEIDAE LANAMPPEQVKEAVAICPV
GTILEKRVGYDDPIGR RKYEQSVRARALEGEDK

> NODB_BRASP P04675 CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.

MTEFIPLFAVRRNYGDVSGTRSVYLTFFDDGNPFCTPDVLDVLTQHRVPA

TFFVIGTYVANQPELIRRMAEGHEVANHTMTHPDLRCEPAEVHDEVLT
ASRAIRSACQALPRHMRAPYGIWTQDVLATSAGLAHVHWSVDPRDWA
RPGVDRIVSSVLAAIRPGAIVL LHDGYPPGEERSCTDATSRDQTVRALS
LIPALQRRGF EIHPLPQLH

> P08331|CN16_ECOLI 2',3'-cyclic-nucleotide 2'-phosphodiesterase -
Escherichia coli.

MIKFSATLLATLIAASVNAATVDLRIMETTDLHSNMMDFYKDTATEKF
GLVRTASLINDARNEVKNSVLVDNGDLIQGSPLADYMSAKGLKAGDIHPV
YKALNTLDYTVGTLGNHEFN YGLDYLNALAGAKFPYVNANVIDARTKQP
MFTPYLIKDTEVVDDKDGKKQTLKIGYIGVVPQIMGWDKANLSGKVTVND
ITETVRKYVPEMREKAGADVVVVLAHSGLSADPYKVMANSEVYYLSEIPGV
NAIMFGHAHVFPKDFADIEGADIAKGTLNQVPAVMPGMWGDHLLGVVDL
QLSNDGKQVTAQAEARPIYDIANKKSLAAEDSKLVETLKADHDATRO
FVSKPIGKSADNMYSYALVQ DDPTVQVVNNAQKAYVEHYIQGDPDLAKL
PVLSAAPFKVGGKNDPASYVEVEKQLTFRNAADLYLPNTLIVVKAS
GKEVKEWLECSAGQFNQIDPNSTKPKQSLINWDGFRTYNFDVIDGVNYQID
VTQPARYDGECQMINANAERIKNLTFRNGKPIDPNAMFLVATNNYRAYGGK
FAGTGDSHIAFASPDENRSVLAAWIADESKRAGEIHPAADNNWRLAPIAG
DKKLDIRFETSPSKAAAFIKE KGQYPMNKVATDDIGFAIYQVDLSK

> P18187|PHNS_DESFR Periplasmic [NiFe] hydrogenase small subunit -
Desulfovibrio fructosovorans.

MNFSVGLGRMNAEKRLVQNGVSRDFMKFCATVAAAMGMGPAFAPKVAEA
LTAKHRPSVVWLHNAECTGCTEAAIRTIKPYIDALILDITISLDYQETIMA
AAGETSEALHQAELGKDGYYLVVEGGLPTI DGGQWGMVAGHPMIETTKK
AAKAKGIIICIRHLPHGQVQKAKPNPSQAKGVSEALGVKTINIPGCPPNP
INFVGAHVHVLTKGIPDLDENGRPKLFYFELVHDNCPRLPHFEASEFAPS
FDSEEAKKGFCLYELGCKGPVTYNNCPKVLFNQVNVWPVQAGHPCLGCSEP
DFWDTMTPFFYEQG

> P50320|PGKP_RALEH Phosphoglycerate kinase, plasmid - Ralstonia eutropha
(strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Cupriavidus necator
(strain ATCC 17699 / H16 / DSM 428 / Stanier 337)).

MMSLSHASVPHTNPTAPHTLAALLAAGGLAGKRVFIRADLNVPQDAAGDI
TDDTRIRASVPAIAACLOAGAAMVMTSHLGRPQEGAPDRHSLAPVGRRL
SELLGRQVPLLSGWTEGGFQVPPGQV VLENCRMNTGEKKNSELAQKMA
ALCDVYVNDAFGTAHRAEATTHGIARYAPVACAGPLLAEEIDALGKALGQ
PARPLVAIVAGSKVSTKLTILKSLADKVDNLVVGGGIANTFMMAAGLKIG
KSLAEPDLLADARAI IDIMAARGASVPIPVDVVCAKEFSATAAAVKDVR
DVADDDMILDIGPKTAAMLADQLKAAGTIVWNGPVGVFEFDQFGNGTRVL
AQAIAESKAFSIAGGGDTLAAIAKYGI ADRVGYISTGGGAFLEFLEGKKL
PALDVLEQRAAS

> P32676|PTFB3_ECOLI Fructose-like phosphotransferase enzyme IIB component
3 - Escherichia coli.

MAYLVAVTACVSGVAHTYMAAERLEKLCLEKVGVSIIETQALGTENRLA
DEDIRRADVALLITDIELAGAERFEHCRYVQCSIYAFLEPQRVMSAVRK
VLSAPQOQTHLILE

> P06621|CBPG_PSES6 Carboxypeptidase G2 - Pseudomonas sp. (strain RS -16).

MRPSIHRTAIAAVLATAFVAGTALAQRDNVLFQAATDEQPAVIKTLEKL
VNIETGTGDAEGIAAAGNFLEAELKNLGFVTRSKSAGLVVGDNIIVGKIK
GRGGKNLLLSHMDTVYLKILAKAPFRVEGDKAYGPGIADDKGNAVIL
HTLKLKKEYGVRDYGTITVLFNTDEEKGSFGSRDL IQEEAKLADYVLSFE
PTSAGDEKLSLGTSGIAYVQVNIITGKASHAGAAPELGVNALLEASDLVLR
TMNIDDKAKNLRFNWTIAKAGVSNIPASATLNADVRYARNEDFDAAMK
TLEERAQQKLEADVIVTRGRPAFNAGEGGKLVDAVAYYKEAGGT
LGVEERTGGGTDAAYAALSGKPVIESLGLPGFGYHSDKAEYVDISAIPRR
LYMAARLIMDLGAGK

> P37329|MODA_ECOLI Molybdate-binding periplasmic protein - Escherichia
coli.

MARKWLNLFAGAALSFAVAGNALADEGKITVFAAASLTNAMQDIATQFKK
EKGVDVSSVFASSSTLARQIEAGAPADLFISADQKWMYAVDKKAIDTAT
RQTLGNSLVVAPKASVQKDFITIDSKTNWTSLLNGGRLAVGDPEHVPAG
IYAKEALQKLGAWDTLSPKLAEDVRGALALVERNEAPLGIVYG SDAVA
SKGVKVVATFPEDSHKKEVYPVAVVEGHNNATVKAFYDYLKGPQAAEIEFK
RYGFTIK

> P0A1V8|BLO2_SALTY Beta-lactamase OXA-2 - Salmonella typhimurium.
MAIRIFAILFSIFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADER
QADRAMLVFDPVRSKKRYSASTFKI PHTLFDALDAGAVRDEFQIFRWGCV
NRGFAGHNQDQDLRSAMRNSTV WVYELFAKEIGDDKARRYLKIDYGNAD
PSTNSGDYWIEGSLAISAEQIAFLRKLRYNELPFRVEHQRLVKDLMIVE
AGRNWILRAKTGWEGRMGWVWVWVWPTGVSFFALNIDTPNRMDDLFRKRE
AIVRAILRSIEALPPNPAVNSDAAR

> HEMN_PSEAE P77915 OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III
MLDTIRWDADLIRRYDLSGPRYTSYPTAVQFHEGIGP FDQLHALRDSRKA
GHPLSLYVHIPFCANICYCACNKVITKDRGRSAPYLARLVREIEIVSRH
LSRAQVVEQLHFGGGTPTFLSPGQLRELMSQLRTHLNLDDSGDYGIEI
DPREADWSTMGLLRELGFNRSVSLGVQDFDMEVQKAVNRMQTPEETRTIVE
AARTLQYRSINLDDLYGLPKQTPDSFARTVDEVIALQPDRLSVFNIAHLP
ERFMPQRINADDLPSPGQKLEMLQRTEQLAAAGYRY IGMDHFALPDDE
LASAQEDGTLQRNFQGYTTHGHCDLVGLGVSASISQIGDLYSQNSSDINDY
QTSLDNGQLAIRRGLHCNSDDRVRRAVIQQLICHFELAFEDIETEFIDF
RSYFAELWPDLERFAADGLIRPDAKGIDITSSGRLLVRSICMLFDRYLP
LNRQRFSRVI

> ADHI_RHOSH P72324 ALCOHOL DEHYDROGENASE CLASS III (EC 1.1.1
MRTRAADVAVEAGKPLEI MEVNLEGPKAGEVMVEIKATGICHTDEFTLSGA
DPEGMFPAILGHEGAVVVEVGPVTSVKPGDHVI PLYTEPCRQCPSCLS
QKTNLCTAIRGTQGGQLMPDGTSRFSMLDGTPIILHYMGCSTFSNYTVLPE
IAVAKVRPDAPFDKICYIGCGVTTGIGAVINTAKVEIGAKAVVFGGGIG
LNVIQGLKLAGADMIIGVDLNNAKKEWGERFGMTHFVNPSEIDGDVVAHL
VNMTKTPFDQIGGADYTF DCTGNVVMRQALEACHRGWGQSIVIGVAPAG
AEIQTRPFQLVTRVWKGSAFSGGARGRTDVPKIVDWYMEGKIQIDPMITH
ILSLEEINKGFDMHAGESIRSIVVF

> P00446|SODC_PHOLE Superoxide dismutase [Cu -Zn] - Photobacterium
leiognathi.
MNKAKTLLFTALAFGLSHQALAQDLTVKMTDLQTGKPVGTIELSQNKYGV
VFTPELADLTPGMHGF HIHQNGSCASSEKDGKVVVLGGAAGGHYDPEHTNK
HGFPWTDNHNKGLPALFVSANGLATNPVLAPRLTLKELKGHAIMIHAGG
DNHSDMPKALGGGARVACGVIQ

> P07103|GUNZ_DICD3 Endoglucanase Z - Dickeya dadantii (strain 3937)
(Erwinia chrysanthemi (strain 3937)).
MPLSYLDKNPVIDSKKHALRKKLFLSCAYFGLSLACLSS NAWASVEPLSV
NGNKIYAGEKAKSFAGNSLFWSNNGWGGEKFYTADTVASLKKDWKSSIVR
AAMGVQESGGYLQDPAGNKAKVERVDAAIANDMYAIIGWHSASHAENRS
EAIRFFQEMARKYGNKPNVIYIEIYNEPLQVSWSNITIKPYAEAVISAIRAI
DPDNLIIVGTPSWSQNVDEASRDPINAKNIAYTLHFYAGTHGESLRNKAR
QALNNGIALFVTEWGTVNADGNGGVNQTETDAWVTFMRDN NISNANWALN
DKNEGASTYYPDSKNLTESGKKVKSIIQSWPYKAGSAASATDPSTDTTT
DTTVDEPTTTTDPATADCANANVYPNWVSKDWAGGQPTHNEAGQSIVYKG
NLYTANWYTASVPGSDSSWTQVGSCN

> P0A9H7|CFA_ECOLI Cyclopropane-fatty-acyl-phospholipid synthase -
Escherichia coli.
MSSSCIEEVSVDDNWNRYRIANELLSRAGIAI NGSAPADIRVKNPDDFFKRV
LQEGSLGLGESYMDGWWECDRLDMFFSKVLRAGLENQLPHHFKDTLRIAG
ARLFNLQSKKRAWIVGKEHYDLGNDLFSRMLDPFMQYSCAYWKDADNLES
AQQAKLKMICEKQLKPGMRVLDIGCGWGLAHYMASNYDVSVVGVTTISA
EQQKMAQERCEGLDVTILLQDYRDLNDQFDRIVSVGMFEHVGPKNYDTYF
AVVDRNLKPEGIFLLHTIGSKKTDLNVDPWIN KYIFPNGCLPSVRQIAQS
SEPHFVMEDWHNFGADYDTTLMAWYERFLAAWPEIADNYSERFKRMFTYY
LNACAGAFRARDIQLWQVVSFRGVENGLRVAR

> P23031|XYNC_PSEFL Alpha-L-arabinofuranosidase C - Pseudomonas fluorescens.
MINHNKTPNILAKVFKRTCGLVSTGAALAILSQAASAACYTIDSEWSTG
FTANITLKNDTGAAINNNWVNVNQYS SNRMTSGWNAFSGTNPYNATNMSW
NGSIAPGQSSISFGLQGEKNGSTAERPTVTGAACNSATSSVASSSSTPTT
SSSSASSVASALLLQEAQAGFCRVDGTIDNNHTGFTGSGFANTNNAQGAA
VVWAI DATSSGRRTLTIRYANGGTANRNGSLVINGGSGNGNYTVSLPTTGA
WTTWQTATIDVDLVQGNIVQLSATTAEGLPNIDSLSVVGGTVRAGNCGS
VSSSSSVQSSSSSSSTPSQTCELKAP LRWTSTGPLISPKNPGWISIKDPS
IVKYNDTYHYVATYYDTAYRSMYTSFTDWNTAQQAPHISMNGSRVGNNTVA

MQGITSLEEVRVTKD
> P08038|DRNE_VIBCH Extracellular deoxyribonuclease - *Vibrio cholerae*.
MMIFRFVTTLAASLPLLTFAAPISFESHAKNEAVKIYRDHPVSYFCGCEIR
WQGGKGIPLDESCYQVRKNENRASRIEWEHVVPA WQFGHQLQCWQQGGR
KNCTRSTPEFNMQMEADLHNLTPAIGEVNGDRSNFSFSQWNGVDGVTYGGQC
EMQVNFKERTAMPFERARGAIARTYLYMSEQYGLRLSKAQSOLMQAWNNQ
YPVSEWECVRDQRIEKVQGNRNRFVREQCPCN
> P13431|SFAH_ECOL5 S-fimbrial adhesin protein sfaH - *Escherichia coli*
06:K15:H31 (strain 536 / UPEC).
MAYSQPSFALLCRNNQTGQEFNSGDTSEFRVNVSPVVQYDKSISVLDLSQL
VSCQNESTGQNYDYLIKILKSGSFPALDTKTYGRLDFTSRPTGYARQLP
LQFDLQVTEAFYQYGVWVKPFAKLYLYPEPGVFGKVINNGDLLATLYVVK
FSTKQGEAGERNFTRWFYATNDVHIQTGTCTRVSSNNVKVDLPSYPGGPVT
VPLTVRCDQQTQSVSYTLGSPVTGSGNTVFANTAASGAGGVGVQLSDKAGP
VPAGQPRSLGQVSSPVSGLKASYALTGQASLTPGAVQSVINVTFSYN
> P14774|CYCL_METEX Cytochrome c -L - *Methylobacterium extorquens*
(*Protomonas extorquens*).
MMNRVKIGTALLGLTLGIALPALAQPSGPTGVVFRNTVTGEALDVSQ
GKEGGRDTPAVKKFLETGENLYIDDKSCLRNAGESLFATSCSGCHGHLAG
KLGPLNDNWTYPSNTT DVGLFATIFGGANGMMGPHNENLTPDEMLQTI
AWIRHLYTGPKQDAVWLNDEQKKAYTPYKQGEVPIPKDAKQCKPLDE
> P28784|CPG1_PORGI Gingipain R1 - *Porphyromonas gingivalis* (*Bacteroides*
gingivalis).
MKNLNKFVSIALCSSLLGGMAFAQQTELGRNPNVRLLESTQQSVTKVQFR
MDNLKFTEVQTPKMAQVPTYTEGVNLSEKGMPTLPIL SRSLAVSDTREM
KVEVVSSKFIKKNVLIAPSKGMIMRNEDPKKIPYVYKSYSQNKFFPGE
IATLDDPFILRDVGRQVVFAPLQYNPVTKTLRIYTEITVAVSETSEQGK
NILNKKGTFAFEDTYKRMFMNYPEGRYTPVEEKQNGRMIVIVAKKYE
IKDFVDWKNQRGLRTEVVKVAEDIASPVTANAIQQFVKQYEYEKEGNDLTYV
LLVGDHDKDIPAKLTPGIKSDQVYQIVGNDHYNEVFIGR FSCESKEDLKT
QIDRTIHYERNITTEDKWLQALCIASAEGGPSADNGESDIQHENVIANL
LTQYGYTKI IKCYDPGVTPKNIIDAFNGGISLVNYTGHGSETAWGTSHFG
TTHVKQLTNSNQLPFI FVACVNGDFLFSMPCFAEALMRAQKDGKPTGTV
AIIASTINQSWASPMRGQDEMNEILCEKHPNNIKRTFGGVMTMNGMFAMVE
KYKKDGEKMLDWTWVFGDPSLLVRTLVP TKMQVTAPAQIN LTDASVNVSC
DYNGAIATISANGKMFSAVVENGATINLTGLTNESTLTLTVVGYNKET
VIKTINTNGEPNPYQPVSNLTATTQGGKVTLKWDA PSTKT NATNTARSV
DGIRELVLLSVSDAPELLRSGQAEIVLEAHDVWNDGSGYQILLDADHDQY
GQVIPS DTHTLWPNCSVPANL FAPFEYTVPENADPSCSPTNMIMDGTASV
NIPAGTYDFAIAAPQANAKIWIAGQGPTKEDDYVFEAGKKY HFLMKKMGS
GDGTELTISEGGSDYTYTVYRDGTKIKEGLTETTYRDAGMSAQSHEYCV
EVKYAAGVSPKVCVDYIPDG VADVTAQKPYTLTVVGKTIITVTCQGEAMIY
DMNGRRLAAGRNTVVYTAQGGYYAVMVVDGKSYVEKLAVK
> P37387|XYLF_ECOLI D-xylose-binding periplasmic protein - *Escherichia coli*.
MKIKNILLTCLTSLLLTNVAHAKE VKIGMAIDDLRLERWQKDRDIFVVK
AESLGAKVQVQSANGNEETQMSQIENMINRGVDVLVIIPYNGQVLSNVVK
EAKQEGIKVLAYDRMINDADIDFYISFDNEKVGELQAKALVDIVPQGNFY
LMGGSPVDNNAKLFRAGQMKVLKPYVDSGKIKVVDGQWVDGWL PENALKI
MENALTANNKIDAVVASNDATAGGAIQALSAQGLSGKVAISGQDADLAG
IKRIAAGTQMTVYK PITLLANTAAE IAVELGNGQEPKADTTLNGLKDV
PSRLTLPIDVKNKNIKDTVIKDGFKHESEL
> P36431|SYP_CHLTR Prolyl -tRNA synthetase - *Chlamydia trachomatis*.
MRMSLLFYRTSKNANKEASVLSYELLQKAGYLFKTSKGIYSYTPLFQRVI
LKMTEI IREELNAIGGQEVCLPLLQPAELWEKTGRWKAFLSEKLLYVLKD
RENKAMCLAPTHEEVSEFVAQWLTGREQLP IHLYQIGTKFRDEIRPRFG
LMRAKEFLMEDSYTFSDSPEQMEEQYAKLRLAYQRI FDRNLNKYVIVAAD
GGKIGKSEEFHVLCSLGEDTICVSGSYGANVEAAQAI PPSYVYDSNLL
PVEEVATPNIRTIEDLEVFFNTPKHKILKTLVVKTCQKDKSEKFFAICIRG
DRQINLTKVASFLQVDDCELASEEILKHLHVEKGFIPLYCPIPCYADE
TTRPMTNFCANNQKDVHCKHVNWGRDIP LPA FGDFLLAEAGDLCPQNGG
APYEIFQGVVAHIFNLGTRYTESFSVGFQDKNGDKQLCWMGTYGIGVGR
TLAACIEQLADNKGVLWPLAVAPFSITILYNGGDTEGEATALQLYQSLNT
EGFEPLDDRNERLGFKLKDSDLLGIPYKLIIGKSFQSTGLLEIESRSGE

KCNVSPENLLDWCSKNLPCHTRKIPPLREQN

> P49250|AMO_KLEAE Copper amine oxidase - *Klebsiella aerogenes*.

MANGLKFSRPRKALALAVAVVCAWQSPVFAHGSEAHMVPLDKTLQEFQAD
VQWDDYAQMFTLLIKDGAYVKVKPGAKTAIVNGKSLDLPVPPVMKEGKAWV
SDTFINDVVFQSGLDQTFQVEKRPHPLNSLSAAEISKAVTIVKAAPEFQPN
TRFTEISLHEPDKAAVWAFALQGTVPDAPRTADVVMLDGKHVIEAVVDLQ
NKKILSWTPIKGAHGMVLLDDFVSVQNIINTSSEFAEVLK KHGITDPGKV
VTPLTVGFFDGKDLQDARLLKVVSYLDTGDGNYWAHPHENLVAVVDL
EAKKIIKIEEGPVI PVPMEPRPYDGRDRNAPAVKPLEITEPEGKNYTITG
DTIHWQNWDFHLRLNSRVGPILSTVTYNDNGTKRQVMYEGSLGGMIVPYG
DPDVGVYFKAYLDSGDYGMGTLTSPIVRGKDAPSNVLLDETIADYTGKP
TTIPGAVAFIFERYAGPEYKHEMGPVNSTERRELVVRWIS TVGNIDYIF
DWVFDHNGTIGIDAGATGIEAVKGVLAKTMDPSAKEDTRYGTLDHNIV
GTHQHIIYNFRLLDLDVGENNTLVAMDPEVKPNTAGGPRSTMQVNQYTI
DSEQKAAQKFDPGTIRLLSNTSKENRMGNPVSYQIIPYAGGTHPAATGAK
FAPDEWIYHRLSFMQKQLWVTRYHPTERYPEGKYPNRSADHTGLGQYAKD
DESLTNHDDVVWITGTTTHVARAEWPIMPTEWALALLKPWN FDETPTL
GEKKK

> ASG1_ECOLI P18840 L-ASPARAGINASE I (EC 3.5.1.1) (L-ASPARAGI

MQKKSIIYVAYTGGTIGMQRSEQGYIPVSGHLQRQLALMPEFHRPEMPDFT
IHEYTPLMDSSDMPEDWQHIAEDIKAHYDDYDGFVILHGTDTMAYTASA
LSFMLENLKGPIVITGSGQIPLAELRSDGQINLLNALYVAANYPINEVTLF
FNNRLYRGNRTTKAHADGFDFAFASP LPPLEAGIHIRRLNTPPAPHGEG
ELIVHPITPQPIGVVTIYPGISADVVRNFLRQPVKALILRSYGVGNAPQN
KAFLOELQEASDRGIVVVNLTQCMMSGKVMGGYATGNALAHAGVIGGADM
TVEATLTKLHYLLSQELDTETIRKAMSQNLRGELTPDD

> Q59967|SRPH_SYNP7 Serine acetyltransferase, plasmid - *Synechococcus* sp.
(strain PCC 7942) (*Anacystis nidulans* R2).

MSLSPRSDRTEIRRSWGLDSIVSALSQASTDPLPHHLLSDQFYPLPSRES
LGLILHGLRSVLFPRHFGDPELSVETHYFIGNTLDKTLNLLNEQIRREL
WLQHVTVQGTPEATPAVLSQHASELTQAFALPEIKRLLDSVNAAYLGD
PAAQSISEILFCYPGITAITFHRLAHLRYQLGLPLLARITAEVSHSETGI
DIHPGAAIGGSFFIDHGTGVVIGET CVIGDRVRIYQAVTLGAKSFRDET
GALIKQARHPVIEDDVVIYAGATLLGRITVGRGSTIGGNVWLTRSVAPG
SFISQAQIRSDNFESGGGI

> P54354|LEU3_BACFR 3-isopropylmalate dehydrogenase - *Bacteroides fragilis*.

MDFKIAVLAGDGIGPEISVQGVVMSAVCEKFGHKVNYEYAI CGADAIDK
VGDFFPEETIYRVCKNADAVLFSAVGDPKFDND PTAKVRPEQGLLAMRKKL
GLFANIRLVPVQTFKCLVHKSPRAELVEGADFLCIRELTGGMYFGEKYQDN
DKAYDTNMYTRPEIERILKVGFEYAMKRRKHLTVVDKANVLASSRLWRQI
AQEMAPQYPEVTTDYMFVDNAAMKMIQEPKFFDVMVTENTFGDILTDEGS
VISGSMGLLPSASTGESTPVFEPHGSWPQAKGLNIANPLAQILSVAMLF
EYFDCKAEGALIRKAVDASLDANVRTPEIQVEG GEKFGTKEVGAWIVDYI
RKA

> P13041|VRPR_SALTY Virulence genes transcriptional activator - *Salmonella*
typhimurium.

MDFLINKLKIIFITLMEGTSFSIATSVLVITRTPLSRVIDLERELKQRL
FIRKNGTLIPTEFAQTIYRKVKSHYIFLHALEQEIGPTGKTKQLEIIFDE
IYPGLSKNLIISALTISGQKTNIMGRAVNSQIIEELCQTNNCIV ISARNY
FHRESLVCRTSVEGGVMLFIPKKFFLCGKPDINRLAGTPVLFHEGAKNFN
LDTIYHFFEQTLGITNPAFSFDNVDLFS SLYRLQOGLAMLLIPVRVCRAL
GLSTDHALHIKVALCTSLYYPTKKRETPDYRKAIKLIQOELQSTF

> DAPD_ECOLI P03948 2,3,4,5-TETRAHYDROPYRIDINE -2-CARBOXYLATE

MQQLQNIETAFERRAEITPANADTVTREAENVQVIAL LDSGALRVAEKID
GQWVTHQWLKAVLLSFRINDNQVIEGAESRYFDKVPKMFADYDEARFQK
EGFRVVPAAVRQGAFIARNTVLMPSYVNI GAYVDEGTMVDTWATVGS
CAQIGKNVHLSGGVIGGVLEPLQANPTIIEDNCFIGARSEVVEGVIVEEGS
VISMGVYIGQSTRIYDRETGEIHYGRVPAGSVVVSGNLPKDGKYSLYCA
VIVKKVDAKTRGKVGINELLRTID

> P73162|ACKA_SYNY3 Acetate kinase - *Synechocystis* sp. (strain PCC 6803).

MKFLILNAGSSSQKSLYELTGDRLPETIPEPLWEAFIDWTVLANQGRLT
VETAGQKQVILETGDRQQGIARMLDTLVTGDDAVLKS LAEIDLVGHRVV
HGGTDHAATLITPEVQQAIDLIPLAPAHNPAHLEGIEAISALLVLGVE

PQIAVFDTAFHRTIPTPAAEYPIQAWTNLGIIRRYGFHGTSH KYCAQKTA
EILGKPLADLKLITCHIGNGASLTAIKNGVSIIDTTMGFTFLEGLMMGARS
GSIDPAILLFLQETQGLTPAEINTTLNKKSGLLGVSGLSADLRITLQAKA
EGNEQAQLAYVMIHRFRSCLGQMIASLEGLDTLVFTAGVGENAATVRAD
VCQAFEFGLGLDPELNNRSPRDTVISHSDSLVTVLIVHTEEDWAIQDC
WHWWHSQGQRKQS

> P43922|PT1_HAEIN Phosphoenolpyruvate-protein phosphotransferase -
Haemophilus influenzae.

MISGILASPGIAFGKALVLKEEKIVLDTQKITDDQIDAEEVARFYEGRNAA
VEQLNSIRERALISLGEKAAIFEGHLMILEDEEEEEEILDYLRSNKVNA
GVAASKILVAYDMLTSEIDDEYLKERAGDIRDIANRLVKNILGMYIVDLG
DIQEESILVAYDMLTSEIDDEYLKERAGDIRDIANRLVKNILGMYIVDLG
AIVGTNKVTKLVNTGDYLLILDAINNQVYINPTASQIDELKALEAKISEEK
AELAKLKDLPATLDGHKVDVVANIGTIRDCDGAERNGAEGIGLYRTEFL
FMDREQLPTEEEQFIAYKQVVEAMNGRLTVIRTMDIGGDKELSYLDLPKE
MNFPLGWRAIRIALDRREILNAQLRAVLRASAFGKLAVMFPMIISVEEIR
ELKAVIETLKAELREEGRLEFDNNIQVGMVETPSAAVNAKF LAKEVDFFS
IGTNDLTQYTLAVDRGNEFISHLYNPMHPSVLGLIKQVIDASHAEGKWTG
MCGELAGDERATLLLLGMGLDEFMSAISVPRIKKLIRNVNFQDAKVLAD
TALQKPTAAEIDQLIEEFLENSLN

> P18958|INH_ERWCH Proteinase inhibitor - Erwinia chrysanthemi.

MKQLIIATLLSALSGGCMASLRPSAAELSGQWVLSGAEQHCDIRLNTD
VLDGTTWKLADGTAQLKLLPEAPVGVWRPTPDGLTTLTQADGSAVAFFSRN
RDRYEHKLVDSVRTLKKKA

> P12903|FM12_KLEPN Fimbrial subunit type 1 - Klebsiella pneumoniae.

MKIKTLAMIVVSALALSSTAALADTTVNGGTVHFKGEVVNAACAVDAGS
IDQTVQLGQVRSAKLATAGSTSSAVGFNIQLDDCDTTVATKASVAFAGTA
IDSSNTTVLALQNSAA GSATNVGVQILDNTGTPLALNGATFSAATTLNDD
PNIIPFQARYYATGAATAGIANADATFKVQYE

> P19369|FMFL_AERHY Flexible pilin - Aeromonas hydrophila.

MPNFFRNGCIALVGSVAAMGAAHAEGGIAEAAAGKALDSAQSDVTITAPKV
MMVVATVVGILINMMRKA

> P23847|DPPA_ECOLI Periplasmic dipeptide transport protein - Escherichia
coli.

MRISLKKSGMLKGLSLVAMTVAASVQAKTLVYCSEGSPEGFNPQLFTSG
TTYDASSVPLYNRLVEFKIGTTEVIPGLAEKWEVSEDKTYTFHLRKGVK
WHDNKEFKPTRELNADDVVFSFDRQKNAQNPYHKVSGGSYEYFEGMGLPE
LISEVKKVDDNTVQFVLTRPEAPFLADLAMDFASILSKEYADAMMKAGTP
EKLDLNPIGTGPFQLQQYQKDSRIRYKAF DGYWGTKPQIDTLVFSITPDA
SVRYAKLQKNECQVMPYPNPADIARMKQDKSINLMEMPGLNVGYSYNVQ
KKPLDDVKVRQALTYAVNKDAIIKAVYQGAGVSAKNLIPTMWWYNDVQ
DYTYDPEKAKALKEAGLEKGFSIDLWAMPVQRPYNPNARRMAEMIQADW
AKVGVQAKIVTYEWGEYLKRAKDGEHQTVMMGWTGDNGDPDNFFATLFS
AASEQGSNYSKWCYKPFEDLIQPARATDDH NKRVELYKQAQVVMHDQAPA
LIIAHSTVFEPVRKEVKGYVVDPLGKHHFENVSIE

> P44708|GLMS_HAEIN Glucosamine --fructose-6-phosphate aminotransferase
[isomerizing] - Haemophilus influenzae.

MCGIVGAVAQRDVAEILINGLHRLEYRGYDSAGVAVINKQNELQRIRCLG
KVKALDEAVSEKPLIGGTGIAHTRWATHGEPSETNAH PHSSGTFVAVHNG
IENHEELRELLKSRGVFLSQTDEVI AHLVEWEMRTDSDLDAVKKAV
KQLTGAYGMVMDSRHPEHLVAARSGSPLVIGLIGENFLASDQLALLSV
TRRFIFLEEGDIAEITRRTVDIYDTHGNKAKREIHESNLENDAAEKGKFR
HFMQKEIYEQPTALINTMEGRINHENVIIVDSINGAKGILEKVEHIQIVA
CGTSYNAGMVARYWFESLAGVSCDVEIASEFRYRKFVT RPNSLLITLSQS
GETADTLAALRLAKEKGYMAALTICNVAGSSLVRESDLAFMTRAGVEVGV
ASTKAFTTQLAALLMLVTALGKVKGHISVEKEREIKAMQSLPAEIEKAL
AFDTEIEALAEDEFAEKHHALFLGRGAFYPIAVEASLKLKEISYIHAEAYA
AGELKHGPLALIDAMPVIVVAPNNELLEKVKSNIEEVRARGGQLYVFAD
KEAGFTPSEGMIITMPKVN DIVAPIFYTIPMQLLSYV ALIKGTDVDQ
RNLAKSVTVE

> P06970|FAED_ECOLI Outer membrane usher protein faeD - Escherichia coli.

MKKYVTTKSVQPVAFRLTTLVMSAVLGSASVIAGEKLDMSFIQGGGGV
NPEVWAALNGSYAPGRYLVDSLNGKEAGKQILDVTPQDSNELCLTEAWL

TKAGVYVSADYFREGYDATRQCYVLTAKPSVKVDFDVSTQSLALSIPQKG
LVKMPENVDWDYGTSAFRVNYNANANTGRNNTSAFGSADLKANIGHWVVS
SSATASGGDSGDNSTTINMFTATRAIRALSADLAVGKTSTGDSLLGSGTGT
YGVLSLRNNSMKPGLGYTPVFSGIANGPSRVTLTQNGRLLHSEMVPAGP
FSITDVPPLYTSGDVTMKITGEDGRDEVQNFPLSVMAGQLSPGQHEFSVAA
GLPDDSDSLKGGVFAASYGYGLDGLTLRAGGVFNQDWQASAGVVAGLGY
LGAVSADGAYATAKYRDGSHSGNKVQLSWSKQLETTNTGLRVSWSRQSEE
YEGMSSFDPTELWSQSNHGRRTKDEWNAGISQPVGGFLSLSVSGWQRSYY
PASMTGSYRYSDDNGKETGITGSLSTQIKGVSLNLGWSGSRNSRGENNWS
ASASVSVPFLLFDRRYSSASVSTSKGGGTGFSTGVSGSLNDRFSYGLGG
GRDGDGGTSSYLNASYSGDRAYLNGVLNHSQSGGTSGSVSVSGSVLAVPA
AKDIMFSRTTGTDTAVVNVKDTPGVKVTSGDGQTDSDGNLVLVPLNSYDWN
TVTIDTGTLPSTELTNTSQKVVPTDKAVVWMPFDALKVKRYLLQVKQRD
GEFVPGGTWARDSKNTPLGFVANNGVLMINTVDAPGDITLQCRIPAARL
QDTEKLQEITCE

> P07111|PAPH_ECOLI PAP fimbrial minor pilin protein - *Escherichia coli*.
MRLRFVSVPLFFFGCVFVHGVFAGPF PPPGMSLPEYWGEHVWWDGRAAFH

GEVVRPACTLAMEDAWQIIDMGETPVRDLQNGFSGPERKFSRLRLNCFEN
SQGGNLFSDSRIRVTFDGVGRGETPDKFNLSGQAKGINLQIADVRGNIA
RAGKVMPIPLTGNEEALDYTLRIVRNGKLEAGNYFAVLGFRVDYE

> P04377|AZUP_ALCFA Pseudoazurin - *Alcaligenes faecalis*.

MRNIAIKFAAAGILAMLAAPALAEN IEVHMLNKGAEAMVFEPAYIKANP
GDTVTFIPVDKGNHVESIKDMIPEGAEKFKSKINENYVLTVTQPGAYLVK
CTPHYAMGMIALIAGDSPANLDQIVSAKKPKIVQERLEKVIASAK

> P43529|E2BB_ECOLI Heat-labile enterotoxin IIB, B chain - *Escherichia coli*.

MSFKKI IKA FVIMAAALVSVQAHAGASQFFKDNCRNTTASLVEGVELTKYI
SDINNNTDGMVVSSTGGVWRISRADYDPDNVMTAEMRKIAMAAVLSGMR
VNMCA SPASSPNVIWAIELEAE

> P52992|DLDH_RALEH Dihydrolipoyl dehydrogenase - *Ralstonia eutropha*
(strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Cupriavidus necator
(strain ATCC 17699 / H16 / DSM 428 / Stanier 337)).

MSKQFDVLVIGAGPGGYIAAIRAGQLGLNVACCEGNPYDDPKGEARLGGT
CLNVGCIPSKALLASSEEFENVQHHLGDHGITVGDVKVDVAKMLKRKDDI
VGKMTKGI EFLFRKNKVTLLKGYGK FVGKSAEGFQVDVAGEVV TAKQVII
ATGSKARHLPGIKVDNDLVSDNEGALKFPAVPKKGVI GAGVIGLELGSV
WRRLGSDVTVLEALPAFLGAAD EGVAK EAQKQLTKQGLKFS LGVNV NEVT
TGKNGVTVKYTDKDGKAQ TLEVDR LIVSVGRVPNTDNLGLDAVGLAADQR
GFIEVDDHCATKVPGLWAI GDVVRG PMLAHKA EDEGVAVAER IAGQKPHI
DYNCPWVIYTFPEI AWVGKTEAQLKAEGREYKAGQFPFMANGRALGMGH
ADGFVKMLADAKTDEILGVHIVAANASDLIAEAVVAMEFKAASEDIGRVC
HPHPSMSEVMREAA LAVDKRQLNM

> Q01269|PHEC_PSEAE Cy clohexadienyl dehydratase [Includes: Prephenate
dehydratase - *Pseudomonas aeruginosa*.

MPKSFRHLVQALACLALLASASLQAQESRLDRILESGVLRVATTGDYKPF
SYRTEEGGYAGFDVMAQRLAESLGAKLVVPTSWPNLMRDFADDFDIA
MSGISINLERQRQAYFSIPYLRDGKTPITLCSEEARFQ TLEQIDQPGVTA
IVNPGGTNEK FARANLK KARILVHPDNVTIFQQIVD GKADLMMTDAIEAR
LQSRHLPELCAVHPQPFDFAEKAYLLPRDEAFKRYVDQWLHIAEQSGLL
RQRMEHWLEYRWPTAHGK

> Q51434|CHEZ_PSEAE Chemotaxis protein cheZ - *Pseudomonas aeruginosa*.

MQLIQELSQARDRGLYQEVGKLTRELHNAIVDFQIDPHS PHAQEMSQIAD
ATDRLSYVEMTEKAANRTMDLVEQSAPLVN QLGD DSRELHQEWQRFMRR
EIDADGFRELAKRIEQFLVRS GENAGQLSSQLNDILLAQDYQDLTGQVIK
RVTKLVTEVESNLVKLVWV MAGQVD RYAGIEHDHVS MRHQAA LERSAKGEG
PQVAAEKREDEVVSGQDDVDDLSSSLGF

> P36774|LON2_MYXA ATP-dependent protease La 2 - *Myxococcus xanthus*.

MSDEKKKGSAA SAMPTAMAPPGLINKEDIPQVLPIL PLRNSVFFPGGVLP
LAVGRQKTIALIKDAVRDDQVIGVVTQRRAE EEDPGAADLYTMGTVARIV
KLLKMGEDNYSLVVQGLARFRVVELVQEAPYLKARVDAVEDKTSSENVEV
EALGINLKKLAREVIELMPELPAAATELVESITHPGHLADLIAANVDVPI
EEKQAVLETVDL KARMKLVLELLNRKREILKLSNKIDS AVKGEMSKTQRE
YYLRQQLKAIKEELGEMGEEEEELDELQERLKKAGLP PDVEKVANKELNR
LKTIPAASSEYTVARTYLDWIADLPWAKISEDNLDIENARQQLDKDHFGI

KKVKKRILEYLAVRKLKNDMRGPILCLVGPVGGKTSLGQSVAKATGRKF
VRLSLGGVRDEAEIRGHRRTYVVGALPGRFIQSMKKAGTKNPFVMMLEIDK
LGADFRGDPSAALLEVLDPQNNFSDHYLDVFPDLSKVMFVATANQLDP
IPGFLRDRMEI IELTGYTFEEKQSIARIHLVPKQLKEH GLSPDHIDITDE
ALLTLTTAYTREAGVRNLERRIADICRAVAVEVAGGKTEKQTINADRVKE
ILGPEMFYSEVAERTEVPGVATGLAWTAAGDLLFIEATKMAGKGGMTLT
GQLGDVMKESATAALSYLRSKAEQLGISPNFLEKTDLHLHFPAAGSIPKDG
PSAGVTILTALTSLLTGIRVRHDTAMTGEATLRGLVLPVGGIKEKVLAAH
RAGIKRVILPERCRKDLIDVPDQARNELEFIFVTHMDDV LKAALETTPVG
VAGTPGGEPGKEAPLPKPAESAPEVRA

> P17201|DHAQ_ACEPO Membrane -bound aldehyde dehydrogenase
[pyrroloquinoline-quinone] - *Acetobacter polyoxogenes*.

MGRNLNRFLGKDGRRREQASLSRRGFLVTSLGAGVMFGFARPSSANQIFPL
DRSLPGDGAPEPTIWCSIAPDGEITVNIIRAEMGQHIGTALARIIADEME
ADWSKVRINYVDTPKWLMTGGWSVWMTWDVFRQAGAATRTAMVEEG
ARLLGTTDPKCTVASSIVSAGGKQISFGDIVAKGHPSHAFTPEEMAKLPL
KPASERRLIGNAELKALDIPAKTNGTAIYGIDAKVEGMLYGRPKMPPTRY
GSKVRSVDDTEAKKIKGYVRYLLIDDPQVQVQGWVVVLAESYSAAIRATD
ALKVEWTPGETIHTSERDIQDRGRELINNKAGGVYIFNDDGVDQAFGSAH
TVMDQEYTCASVLYHQLEPTNALAFEKDGVEYI HAGNQWQSLILPTLAKS
LQVPESKYILRSYLLGGGFGRRNLNGDYMI PAALASKALGGKPVKLIILTRS
DDMQFDSFRSPSVQVRMAFDASDRITAMDYQAAAGWPTGVMAEAFMEKG
VDGKPYDQFAIAGGDHWYEVGAFRVRALRNDLAEKTFRPGWLRVSVPGWT
SWGVECFLDEVAHRQKDPAQFRLELLTGQGRNKGQAPDSVGGALRQAAV
VRLMEKVNWGTSLPKDTAMGLATTAGQERGMPTWDRCAQVHVDRSTG
VVTCQKLTILVDAGTVVDPDGAKAQTEGAALWGLSMVLFENTEIVNGMPV
DRNLNTYTPLRIADTPEMDIEFLPSTEKPMGLGEPGTTVVGPAIGNAIFN
AVGVRLRHMPVRPADVLRGLQNG

> P54893|P5CR_THET2 Pyrroline -5-carboxylate reductase - *Thermus
thermophilus* (strain HB27 / ATCC BAA-163 / DSM 7039).

MRLAFVGLGKMGRSILKALERGFRLPEEVGVLGRTPEERSRELAEPFGVR
PLTRADLGMAERVLIAVQPRDFPALAPEIAHHRLLGYISIMAGISTSVLAR
RLDNRRVVRAMPNLAVVIGESSTALTALKEAREAEDLAFARALFATVGDV
YEIPEHLFDAFTGMSASAPAYLAVVAEALADAGVKMGMPRALALRLAADA
LAATGELLKGRHPAQV KDEVASPGGTTIHGLHALEARAVRAAFYEAVEAA
TRRGHELGESE

> P43014|SYT_HAEIN Threonyl -tRNA synthetase - *Haemophilus influenzae*.

MPIITLPGDQRQFDRPVSLEVAQDIGAGLAKATIAGRVNGERRDACYV
IEQDATLEIITAKDELDGLEIIRHSCAHLGHAIKQLFPDVKMAIGPTIEN
GFYYDVLDLDRSLTQEDIDAIEKRMLELAKTNYDVVKK RVTWQEARDTFEK
RGEPYKMAILDENIERTATPALYHHLEYIDMCRGPHVPMNRFQHFKLQK
VAGAYWRGDSKNKMLQRIYGTAWADKKQLAEYLTRLEEAARKDRHKIGKA
LDLYHMQEEAPGMVFWHNDGWTIFRELETFVRTKLKQYDYQEVKGFPMMD
RVLWEKTGHWNQYADLMFTTQSENREYAIKPMNCPGHVQIFNQGLKSYRD
LPIRMAEFGSCHRNEPSGLHGLMRVRGFTQDDAHIFC TEDQIESEVTSC
IKMVDIYSTFGFTNIAVKLSTRPENRIGSDEMWDRAEAGLAAALAHNGL
EYEIQEGEGAFYGPKIEFALRDCLGREWQCGTVQLDFALPGRLDATYVAE
DNSRKTVMIHRAILGSIERFIGIITEEYAGFFPAWLAPTQAVVMNITDS
QADYVQKQVAKQLSDVGLRVKTDLRNEKVGFKIREHTLRRVPYMLVCGDKE
IAEGKVAVRTRKADLGTFTVEEFAEILKNQVRSRELKL LNEE

> Q01605|PHOE_CITFR Outer membrane pore protein E - *Citrobacter freundii*.

MKKSTLALVVMGITASASVQAAEVYNKNGKLDLYGKVKAMHYMTDYDSK
DGDQSYIRLGFKGETQINDELTYGRWEAEFAGNKAESDSNQKTRLFAFA
GSKLKNLGSFDYGRNLGALYDVEAWTDMFPEFGDSSAQTDNFMTKRASG
LATYRNATDFGVDGLDLTLQYQG KNQDRDVKKQNGDGFSTVYDFGGS
DFAVSGAYTNSDRNTQQNLQTRGTGDKAEAWATGLKYDANDIYIATFYSE
TRNMTPISSGGFANKTQNFQAVVQYQFDFGLRPSLGYVLSKGDIEGVGNE
DLVNYIDVGATYYFNKNMSAFVDYKINQLSDSNKLGINNDIVAVGMVYQ
F

> P0A2C5|RBSB_SALTY D-ribose-binding periplasmic protein - *Salmonella
typhimurium*.

MNMKLLATLVSAAVSATVSANAMAKDTIALVISTLNNPFVSLKDGAKQ
EADKLGYNLVLDLSDQNNPAKELANVQDLTVRGTKILLINPTSDAVGNAV

KMANQAKIPVITLDRQATKGDVVSHIASDNVLGGKIAGDYIAKKAGEGAK
VIELQGIAGTSAAREREGEGFQQAVAAHKFNVLASQPADFDRTKGLNVMQN
LLTAHPDVQAVFAQNDEMALGALRALQTAGKADVMVVGFDGTP DGEKAVK
DGKLAATIAQLPDQIGAKGVEVADKVLKGEKVQAKYPVDLKLVIKQ
> P14542|IUTA_ECOLI Ferric aerobactin receptor - Escherichia coli.
MMISKKYTLWALNPLLLTMMAPAVAQQTDETFVVSANRSNRTVAEMAQT
TWVIENAELEQQIQGGKELKDALAQLIPGLDVSSRSRTNYGMNVRGRPLV
VLVDGVRLNSSRRTDSRQLDSIDPFNMHHIEVI FGATSLYGGGSGTGLLINI
VTKKGQPETMMEFEAGTKSGFSSSKDHDERRIAGAVSGGNEHISGRLSVAY
QKFGGWFDDGNGDATLLDNTQTGLQYSDRLDIMGTGTLNIDESRQLQLITQ
YYSKQGDDEYGLNLGKGFSAIRGTSTPFVSNGLNSDRIPGTDGHLISLQY
SDSAFLGQDELVGVYRDESLRFYFPFTVNANKQVTAFFSSSQDQDQYGM
KLTLSNPKMDGWQITWGLDADHERFTSNQMFFD LAQASASGGLNKKIYT
TGRYPSYDITNLAAFLQSGYDINNLFNLGGVRYQYTENKIDDFIGYAQQ
RQIGAGKATSADAFWRLSRLRHFLFNAGLLMHITPQQAWLNFSQGLELP
DPGKYYGRGIYGAAVNGHLPLTKSVNVSDDKLEGVKVDSEYELGWRFTGNN
LRTQIAAYYSISDKSVVANKDLTISVVDDKRRIYGVGAVDYLIPTDWS
TGVNFVNLKTESKVNWTQKYDVKTASPSKATAY IGWAPDPWSLRVQSTT
SFDVSDAQGYKVDGYTTVDLLGSYQLPVGTLFSFIENLFRDRYTTVWGQR
APLYYSPGYGPASLYDYKGRGRTFGLNYSVLF
> P24735|AMPC_PSEAE Beta -lactamase - Pseudomonas aeruginosa.
MRDTRFPCLCGIAASTLLFATTPAAGEAPADRLKALVDAAVQPVMKAND
IPGLAVAI SLKGEPHYFSYGLASKEDGRRVTPETLFEIGSVSK TBTATLA
GYALTQDKMRLDDRASQHWPALQGSRFDGISLLDLATYTAGGLPLQFPDS
VQKQDQAQIRDYRQWQPTYAPGSQRLYSNPSIGLFGYLAARSLGQPFERL
MEQQVFPALGLEQTHLDVPEAALAQAQGYGKDDRPLRVGPGPLDAEGYG
VKTSAADLLRFVDANLHPERLDRPWAQALDATHRGYKVGDMTQGLGWEA
YDWFISLKRQLQAGNSTPMALQPHRIARLPAPQALEGQRLNKTG STNGFG
AYVAVFPGRDLGLVILANRNPNAERVKIAYAILSGLEQQGKVP LKR
> SYW_SYNY3 P73655 TRYPTOPHANYL -TRNA SYNTHETASE (EC 6.1.1.2)
MKNCEÑDHRFTTVSSGKAWGQLHRFP SLIKFNFAHRSTTAMDKPRILSGV
QPTGNLHLGNLGAIRSWVEQQQHYDNFFCVVDLHAITVPHNPQTLAQDT
LTIAALYLACGIDLQYSTIFVQSHVAAHSELAWLLNC VTPLNWLERMIQF
KEKAVKQGENVSVGLLDYPVLMADILLYDADKVPVGEDQKQHLELTRDI
VIRINDKFGREDAVPLKLEPLIRKEGARVMSLADGTTKMSKSDSELSR
INLLDPPEMIKKVKCKTDPQRGLWFDDPERPECHNLLTLYTLLSNQTK
EAVAQECAEMGWGQFKPLLTETAIAALEPIQAKYAEILADR GELDRI IQA
GNAKASQTAQQTLARVRDALGFLAPPY
> P43835|SYW_HAEIN Tryptophanyl -tRNA synthetase - Haemophilus influenzae.
MAKPIVFSGVQPSGELTIGNYL GALRNWVKMQEDYECIFCVVDLHAITVR
QDPVALRKATLDVLALYLACGIDPNKSTIFVQSHVPEHTQLSWVLNICYTY
FGEMSRMTQFKDKSARYAENINVG LFDYPVLMADILLYQAKSVVGGDDQ
KQHLEITRDIANRFNALYGNIFTIPEIFIGKAGARIMSL QDPEKKMSKSD
DNRNNVVTLLLEPKSVAKKIKRAVTDSEPPVVRYDVQNKAGVSNLLDIL
SAVTDKPIADLEKEFEFGKMYGHLKTAVADEVSTLLASLQERFHQYRND ET
LLDNILRQGAEKARAKAQETLAKVYEAVGFVAAK
> P39325|YTFQ_ECOLI ABC transporter periplasmic -binding protein ytfQ -
Escherichia coli.
MWKRL LIVSAVSAAMSSM ALAAPLTVGFSQVGSSEGWRAAETNVAKSEAE
KRGITLKIADGQQKQENQIKAVRSFVAQGVDAIFIAPVVATGWEPVLKEA
KDAEIPVFLDRSIDVKDKSLYMTTVTADNILEGKLGIDWL VKEVNGKPC
NVVELQGTVGASVAIDRKKGFAEAIKNAPNIKIIRSQSGDFTRSKGKEVM
ESFIKAENNGKNICMVYAHNDDMVIGAIQAIKEAGLKPGKDILTGSIDGV
PDIYKAMMDGEANASVELT PNMAGPAFDAL EKYKKDGTMPKELTLTKSTL
YLPDTAKEELEKKNMGY
> METK_HAEIN P43762 S -ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1)
MSSYLFTSESVSEGHDPDKIADQISDAVLDEILKQDPKARVACETYVKTGM
ALVGG EITTSAWVDIENLTRKVICDIGYEHSEMFGDGHSCAVLNAIGKQS
ADINQVDRENPLDQAGDQGIMFGYATNETDVLMPAAITY AHRLMEKQS
EVRKSGKLAWLRPDAKSQVTLKYEDNKIVGVDAVVLSTQHSEEVSQKDLH
EGVMEEI IKPVL PSEWLSKETKFFINPTGRFVIGGPMGDCGLTGRKIIVD
TYGGAARHGGGAFSGKEPSKVDRSAAYAARYVAKNIVAAGLADRCEIQLS
YAIGVAEPTSIMVETFGTGKVANELLVSLVREFFDLRPYGLIKMLDLIQP

IYRETAAYGHFGREQFPWEKVDRAEDLRIAAGLK
> P09155|RND_ECOLI Ribonuclease D - Escherichia coli.
MNYQMITTDALASLCEAVRAFPALDTEFVRTRTYYPQLGLIQLFDGE
HLALIDPLGITDWSPLKAILRDPSTKFLHAGSEDEFLNVFVGFELPQPL
IDTQILAAFCGRPMSWGFASMVVEYSGVTLDKSESRTDWLARPLTERQCE
YAAADVWYLLPITAKLMVETEASGWLPAALDECRLMQMRRQEVVAPEDAW
RDITNAWQLRTRQLACLQLLADWRLRKARERDLAVNFVREEHLWSVARY
MPGSLGELDSLGLSGSEIRFHGKTLALVEKAQTLPEDALPQPMNLNMDM
PGYRKAFAKAISLITDVSETHKISAEELLASRRQINQLLNWHWKLKQPNNL
PELISGWRGELMAEALHNLQYEYPO
> P51752|MIP_COXBU Peptidyl-prolyl cis-trans isomerase Mip - Coxiella
burnetii.
MKRLIIPFLSVGLLGTTAHAATPLKTEQDKLSYSMGMVTKGAFRKHDIK
IDPQTFMSGLSDAYLGKETQMTAEMRQTLQQFEKQSLQKMQHKMKQTAQ
QNAEKSRAFLTANKNPGVKTLANGLQYKVLQAGQGQSPTLNDEVTVNYE
GRLINGTVFDSSYKRGQPATFPLKSVIKGWQEALTRMKPGAIWEIYVPPQ
LAYGEQAGPGVIGPNEALIFKVNLI SVKKK
> P22542|HSTI_ECOLI Heat-stable enterotoxin II - Escherichia coli.
MKKNIAFLASMFVFSIATNAYASTQSNKKDLCEHYRQIAKESCKKGFGLG
VRDGTAGACFGAQIMVAAGKC
> P18775|DMSA_ECOLI Anaerobic dimethyl sulfoxide reductase chain A -
Escherichia coli.
MKTkipDAVLAAEVSRRLVKT TAIGGLAMASSALTLPFSRIAHA VDSAI
PTKSDEKVIWSACTVNCGRCLPMHVVDGEIKYVETDNTGDDNYDGLHQ
VRACLGRSMRRRVYNPDRLKYPMKRVGARGEGKFERISWEEAYDIIATN
MQRLIKEYGNESIYLNyGTGLGGTMTRSWPPGNTLVARLMNCCGGYLNH
YGDYSSAQIAEGLNYTYGGWADGNSPSDIENSKLVVLFGNPGETRMSGG
GVTYYLEQARQKSNARMIIDPRYTDTGAGREDEWIPIRPGTDAALVNL
AYVMITENLVDQAFLDKYCVGYDEKTLPASAPKNGHYKAYILGEGPDGVA
KTPPEWASQITGVPA DKI IKLAREIGSTKPAFISQGWGPQRHANGEIATRA
ISMLAILTGNVINGGNSGAREGSYSLPFVRMPTLENPIQTSISMFMWTD
AIERGPEMTALRDGVRGKDKLDVPIKMIWNYAGNCLINQHSEINRTHEIL
QDDKKCELIVVIDCHMTSSAKYADILLPDTASEQMDFALDASCNMSYV
IFNDQVIKPRFECKTIYEMTSELAKRLGVEQQFTEGRTQEEMRHLAQS
REAIPELPTFEFFKQGI FKKRDPQGHVAYKAFREDPQANPLTTPSGKI
EIYSQALADIAATWELPEGDVIDPLPIYTPGFESYQDPLNKQYPLQLTGF
HYKSRVHSTYGNVDVLKAACRQEMWINPLDAQKRGIHNGDKVRIFNDRGE
VHIEAKVTPRMPGVALGEGAWYDPDAKRVDKGCCINVLTTQRPSPLAK
GNPSHTNLVQVEKV
> P0A8F8|UVRB_ECOLI UvrABC system protein B - Escherichia coli.
MSKPFKLNSAFKPSGDQPEAIRLEEGLEDGLAHQTLLGVTGSGKTFTIA
NVIADLQRPTMVLAPNKTLAAQLYEMKEFFPENAVEYFVSYYDYYQPEA
YVPSDFTIEKDASVNEHIEQMRLSATKAMLERRDVVVASVSAIYGLGD
PDLYLKMMLHLTVGMIDQRAILRLAE LQYARNDAQAFQRTFRVRGEVI
DIFPAESDDIALRVELFDEEVERLSLFDPLTGQIVSTIPRFTIYPKTHYV
TPRERIVQAMEEIKEELAARRKVLENNKLLQRLTQRTQFDLEMMNEL
GYCSGIENYSRFLSGRGPGEPPPTLFDYLPADGLLVDESHVTIPQIGGM
YRGDRARKETLVEYGFRLPSALDNRLKFEFEALAPQTIYVSATPGNYE
LEKSGGDVVDQVVRPTGLLDPIIEVRPVA TQVDDLSEIRQRAAINERVL
VTTLTKRMAEDLTHEYLEEHGERVRYLHSDIDTVERMEIIRDRLRGEFDVL
VGINLLREGLDMPEVSLVAILDADKEGFLRSERSLIQTIGRAARNVNGKA
ILYGDKITPSMAKAIGETERRREKQKYNEEHGITPQGLNKKVVDILALG
QNIAKTKAKGRGKSRPIVEPDNVPMDMSPKALQKKIHELEGLMMQHAQNL
EFEEAAQIRDQLHQRLRFIAAS
> P28307|CSGA_ECOLI Major curlin subunit - Escherichia coli.
MKLLKVAIAIAIVFSGSALAGVVPQYGGGNGHGGGNSGPNSELNIYQY
GGNSALALQTDARNSDLTITQHGGNGADVGQGSDDSSIDL TQRGFGNS
ATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTVQVGFNNATAHQ
Y
> P11278|PELP_YERPS Periplasmic pectate lyase - Yersinia pseudotuberculosis.
MKKRALLSMSVLA MLYIPAGQAAEIDRLTVVKYVDNVLNKASD TYHGD
KPSPLLADGVDPRTGQQMEWIFPDGRRAVLSNFS AQQLMRVMSGLSELS
GDPQYQKRAEDIVRYHFQNYQDNSGLLYWGGHRFVLDKTLQPEGPSEKEK

VHELKNAYPPYDLMFVSDSDATTRFIRGFWNAHVYDWRILETSRHGEY GK
PMGALWESTFEQQPPFFATKG LSFLNAGNDLIYSASLLYKYQQDQALVW
AKRLADQYVLRDAKTGLGVYQFTQALKREEPTDDADTHSKFGDRAQRQF
GPEFGPTALEGNMMLKGRSTSTLYSENALMQLQLGKDLGGQD DLLKWTVD
GLKAFACYGYNEQDNTFRPMIANGQDLSNYTLPRDGYGKKGSVLKPYKA
GNEFLISYARAYAVDNDPLLWKVARGIASDQGLGDIGSAPGKEMKVKLDT
TNSDPYALFALLDLYNASQVAE YRSLAEKVADNI IKTRYIDGFFMASPDR
QYADVDAIEPYALLALEASLRNKPQAVAPFLNGAGFTEGAYLMADGSARI
STRDNELFLLNVGETLQPNGRK
> GAL_PSEFL_P11886_D -GALACTOSE 1-DEHYDROGENASE (EC 1.1.1.48).
MQPIRLGLVGYGKIAQDQHVPAINANPAFTLVSVATQKPCPGVENFQSL
GELLENGPPVDAIAEFTPPQGRFALVQQAALAGKHVLEK PPCATLGKAA
LWIKREQASAPCSPCIAYAPAIAAARDWLATRTLQSVQIDWKEDVRKWHF
GQAWIWQPGLVDFDGINALSIVTHLLPLPLFVESAEELRVPSNCQSPIAA
SIKMSDPRLLDVRAEFDFDHGHDELWSIQIRCAEGTLRLDNGGALLSIDG
VRQTVAAEEGEYAAVYRHFQQLIGDKTSDVDVQPLRLVADSFFVGSRVSVE
AFYD
> P38683|TORT_ECOLI Periplasmic prot ein torT - Escherichia coli.
MRVLLFLLLSLFMLPAFSADNLLRWHDAQHFTVQASTPLKAKRAWKLCAL
YPSLKDSYWLSTLNYGMQEAARRYGVDLKLVLEAGGYSQLATQQAQIDQCKQ
WGAEAILLGSSTTFPDLQKQVASLPIELVNAIDAPQVKSRVGVVWPFQ
GYQPGRYLVQWAHGKPLNVLLMPGPDNAGGSKEMVEGFRAAIAGSPVRIV
DIALGDNDIEIQRNLLQEMLERH PEIDVVAGTAIAAEAAMGEGRNKLTPL
TVVSFYLSHQVYRGLKRGVIMAASDQMVWQGELAVEQAIRQLQGQSVSD
NVSPPIVLVTPKNADREHIRRSLSPGGFRPVYFYQHTSAAK
> FTN_HELPY_P52093 NONHEME IRON -CONTAINING FERRITIN. - HELICO
MLSKDI IKLLNEQV NKEMSSNLYMSSSWCYTHSLDGAGLFLFDHAAEE
YEHAKKLIVFLNENNVVQLT SISAPEHKFEGLTQIFQKAYEHEQHISES
INNIVDHAIKGDHATFNFLQWYVSEQHHEEVLFKDIIDKIELIGNENHG
LYLADQYVVKGIKSRKS
> Q06987|TBP12_NEIMB Transferrin -binding protein 1 - Neisseria meningitidis
serogroup B.
MQQQHLFRLNILCLSLMTALPVYAENVQAEQAQEKQLDTIQVKAKKQKTR
RDNEVTGLGKLVKSSDT LSKEQVLNIRDLTRYPGIAVVEQGRGASSGYS
IRGMDKNRVSLTVDGVSQIQSYTAQALGGTRTAGSSGAINIEIYENVKA
VEISKGSNSSEYNGALAGSVAFQTKTAADIIGEGKQWGIQSKTAYSGKD
HALTQSLALAGRSGGAEALLIYTKRRGREIHAKHDAGKGVQSFNRLVLDE
DKKEGGSQYRYFIVEEECHNGYAACKNKLKEDASVKDERKTVSTQDYTGS
NRLLANPLEYGSQSWLFR PGWHLNDRHYVGAVLERTQQTFDTRDMTPPAY
FTSEYVPGSLKGLGKYSGDNKAERLRFVQEGESTLQGIYGTGVFYDERH
TKNRYGVEYVYHNADKDTWADYARLSYDRQIDLDNRLQQTHCSHDGSDK
NCRPDGNKPYSFYKSDRMIYEESRNLQAVFKKAFDTAKIRHNLSINLGY
DRFKSQLSHSDYYLQNAVQAYDLITPKKPPFPNGSKDNPYRVSIGKTTVN
TSPICRFGNNTYTCTPRN IGGNGYAAVQDNVRLGRWADVGAGIRYDYR
STHSEDKSVSTGTHRNLNAGVVLKPFWMDLTYRASTGFRLPSFAEMY
GWRAGESLKTLDLKEKSFNREAGIVFKGDFGNLEASYFNAYRDLIAFG
YETRTQNGQTSASGDPGYRNAQNARIAGINILGKIDWHGVWGGLPDGLYS
TLAYNRIVKVDADIRADRTFVTSYLFDAVQPSRYVLGLGYDHPDGIWGIN
TMFTYSKAKSVDELLGSQAL LNGNANAKKAASRRTRPWYVTDVSGYVNIK
KHLTLRAGVYNLLNRYVTVWENVRQTAGGAVNQHKNVGVYNYRYAAPGRNY
TFSLEMKF
> Q43990|SYK_ACIAD Lysyl -tRNA synthetase - Acinetobacter sp. (strain ADP1).
MAQPNVQSTSEPLLSENDLIAQRHAKLKQIQDKAKETGKSVWPNTFKREH
YAADLQEQFKDIDKAQIEGSDKTYVKVAGRVMLNRRGSF MVIQDMTGRIQL
YVDRKGLPADTLETIKSLDLGDI IAAEGYIGRSGKGDLYVHLEGFELLTK
SLRPLPKDFHGLTDEAKYRKRYLDLIVNEETRKTFEIRAQVVAGIRAF
TNQRFMEVETPMHVI PGGASAQPFVTHHNALDMELYLRIAPELYLKRIV
VGGFERVFEINRFRNEGVSTRHNPEFTMIEFYQAYADYKDLMLTENML
EKLALDILGTTDVPYGVDEVYSFKGPFKKISMFDAILEHN PDFTPENVNDR
EFLAKFTQDVLKEQVKGFGGLGKLQTVFEETVETKLRQPTFITEYPAET
SPLARRNDDNPHITDRFEFFIGGRELANGFSELNDPIDQAERFQAQVAEK
DAGDDEAMHYDADFIEALEYGLPPTAGQGIGIDRLVMI FANAPSIRDVLL
FPHMRRKDV

> P52854|EFTU_TREHY Elongation factor Tu - *Treponema hyodysenteriae* (*Serpulina hyodysenteriae*).

MAKGTYEGNKTHVNVGTIGHVDHGKTTLTSAITAVSSAMFPATVQKVAYD
SVAKASESQRRDPTKILTIATSHVEYESDNRHYAHVDCPGHADIKNMI
TGAAQMDGAILVVAEDGVMPQTKEHVLLSRQVGVNYIVVFLNKCCKLDD
PEMAEIVEAEVIDVLDHYGFDGSKTPIIRGSAIKAIQAIEAGKDPRTDPD
CKCILDLLNALDITYIPDPVREVDKDFLMSIEDVYSIP GRGTVVVTGRIERG
KIEKGNVEIVEIVGIRPTQKTTCTGVEMFKKEVVGIAGYNVGCLLRGIERKA
VERGQVLAKPGTITPHKKFEAEVYILKKEEGGRHSGFVSGYRPMYFRRT
DVTGVINLQGDQMIMPGDNANLTIELITPIAMEEKQRFIREGGKTVGN
GVVTKNIRII

> P12625|PHB_ALCFA Poly(3-hydroxybutyrate) depolymerase - *Alcaligenes faecalis*.

MVRRLWRRIAGWLAACVAILCAFPLHAATAGPGAWSSQQTWAADSVNNGN
LTGYFYWPASQPTTPNGKRALVVLHGCVQTASGDVIDNANGAGFNWKS
ADQYGAVILAPNATGNVYSNHCWDYANASPSRTAGHVGLLDLVNRFVTN
SQYAIDPNQVYVAGLSSGGGMTMVLGCIAPDIFAGIGINAGPPPPTTAAQ
IGYVPSGFTATTAANKCNAWAGSNAGKFSTQIAGAVWGTSDYTVAQAYGP
MDAAAMRLVYGGNFTQGSQVVISGGGTNTPYTDSNGKVRTHEISVSGMAH
AWPAGTGGDNTNYVDATHINYPVFMVMDYVWVKNLNRAGSGTGQAGSAPTGL
AVTATTSTSVLSLWNAVANASSYGVYRNGSKVGSATATAYTDSGLIAGTT
YSYTVTAVDPTAGESQPSAAVSATTKSAFTCTATTASNYAHVQAGRAHDS
GGIAYANGSNQSMGLDNLFYTSTLAQTAAGYYIVGNCP

> P17215|LIVJ_SALTY Leu/Ile/Val/Thr-binding protein - *Salmonella typhimurium*.

MKGKTLLAGCIALSLSHMAFADDIKVAVVVGAMSGPVAQYGDQEFTEGAEQA
IADINAKGGIKGDKLVAVKYDDACDPKQAVAVANKVVNDGIKYVIGHLCS
SSTQPASDIYEDEGILMITPAATAPELTARGYKLVLRRTGLDSDQGPTAA
KYILEKVKPQRIAIHDKQQYGEGLARAVQDGLKGG VNVVFFDGITAGE
KDFSTLVARLKKENIDFVYYGGYHPEMGQILRQSRAAGLKTQFMGPEGVA
NVLSLSNIAGESAEGLLVTKPKNYDQVPANKPIVDAIKAKKQDPSGAFVWT
TYAALQSLQAGLNHSDPAEIAKYLKATVDTVMGPLSWDEKGLKGFEE
GVFDWHANGTATDAK

> P12061|FM_SALEN Fimbrial protein - *Salmonella enteritidis*.

MRKSASAVAVLA LIACGSAHAAGFVGNKAVVQAAVTIAAQNTTSANWSQD
PGFTGPAVAAGQKVGTLTITATGPHNSVSIAGKASVSGGVATVPFVDGQ
GQPFVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVFVTTFGKSTLP
AGTFTATFYVQQYQN

> P05458|PTRA_ECOLI Protease 3 - *Escherichia coli*.

MPRSTWFKALLLVALWAPLSQAETGWQPIQETIRKSDKDNRYQAIR LD
NGMVVLLVSDPQAVKSLSALVVPVGSLEDPEAYQGLAHYLEHMSLMGSKK
YPQADSLAEYLMHGGSHNASTAPYRTAFYLEVENDALPGAVDRLADAIA
EPLLDKKYAERERNAVNAELTMARTRDGMRAQVSAETINPAHPGSKFSG
GNLETLSDKPGNPVQQALKDFHEKYYSANLMKAVIYSNKPLPELAKMAAD
TFGRVPNKESKKEITVPVVTDAQGII IHYVPALPRKVLRFVFRIDNN S
AKFRSKTDELITYLIGNRSPGTLSDWLQKQGLVEGISANSDFIVNGNSGV
LAISASLTDKGLANRDQVVAIFSYLNLREKIDKQYFDELANVLDIDF
RYPSTIRDMDYVEWLADTMIRVPVEHTLDAVNIADRYDAKAVKERLAMMT
PQNARIWIYISPKPEHNKTAYFVDAPYQVDKISAQTFADWQKKAADIALSL
PELNPIYPDDFLIKSEKKYDHPPELIVDESNLRVVYAPSRFYASEPKADV
SLILRNPKAMDSARNQVMFALNDYLAGLALDQLSNQASVGGISFSTNANN
GLMVNANGYTQRLPQLFQALLEGYFSYTATEDQLEQAKSWYNQMMDSA
GKAFEQAIMPAQMLSQVPYFSRDERRKILPSITLKEVLAIRDALKSGARP
EFMVIIGNMTEAQTTLARDVQKQLGADGSEWCRNKDVVVDKQSVIFEKA
GNSTDSALAAVFPVTGYDEYTSAYSSLLGQIVQPFYVNLRTTEEQLGYA
VFAFPMSVGRQWGMGFLQSNQKQPSFLWERYKAFPPTAEAKLRAMKPE
FAQIQQAVITQMLQAPQTLGEEASKLSKDFDRGNMRFDSRDKIVAQIKLL
TPQKLADFFHQAVVEPQGMALISQISGSQNGKAEYVHPEGWKVWENVSAL
QQTMLMSEKNE

> P13626|CYF_NOSSP Apocytochrome f - *Nostoc sp.* (strain PCC 7906).

MRNASVTARLTRSVRAIVKTLII AIATVTFYFSCDLALPQSAAYPFWAQ
QTYPETPREPTGRIVCANCHLAAKPTVEVPPQSVLPDVFVAVVQIPYDT
SAQQVGADGSKVGLNVGAVLMLPEGFKIAPEDRISEELQEEIGDIFYQPY

SEDKENIVIVGPLPGEQYQEIVFPVLSNPATDKNIHFGKYSVHVGGNRG
RGQVYPTGEKSNNLNYNASATGTIAKIAKEEDEDGNVKYQVNIQPESGDV
VVDTPVAGPELIVSEGOAVKAGDA LTNNPNVGGFGQORDAEIVLQDAGRVK
GLIAFVALVMLAQVMLVLKQKQVERVQAAEMNF
> Q00499|CY550_PARVE Cytochrome c -550 - Paracoccus versutus (Thiobacillus
versutus).

MKISIIYATLAALSLALPAVAQEGDAAKGEKEFNKCKACHMVQAPDGTDIV
KGGKTGPNLYGVVGRKIASVEGFKYGDGILEVAEKNPDMVWSEADLIEYV
TDPKPWLVEKTGDSAAKTKMTFKLGKNQADVVAFLAQHSPDAGAEAAPAE
GAAN

> P18895|ALGE_PSEAE Alginate production protein algE - Pseudomonas
aeruginosa.

MNSRSVSNRPSFAPRALSLAIALLLGAPAFANAENGAPKNFGLDVKITG
ESENDRDLGTAPGGTLNDIGIDLRPWAFGQWGDWSAYFMGQVAATDTIE
TDTLQSDTDDGNSNRDNGREPDKSYLA AREFWVDYAGLTAYPGEHLRFGR
QRLREDSGQWQDTNIEALNWSFETLLNAHAGVAQRFSEYRTDLDELAPE
DKDRTHVFGDISTSQWAPHHRIGVRIHHADDSGHLRRPGEEVDNLDKTYTG
QLTWLGIEATGDAYNYRSSMPLNYWASATWLTGDRDNLTTTVDDRRIAT
GKQSGDVNAFGVDLGLRWNIDEQWKAGVGYARGSGGGKDGEEQFQQTGLE
SNRSNFTGTRSRVHRFGEAFRGELSNLQ AATLFGSWQLREDDYDASLVYHK
FWRVDDSDIGTSGINAALQPGEKDIGQELDLVVTKYFKQGLLPASMSQY
VDEPSALIRFRGGFLFKPGDAYGPGTDTSTMHRAFVDFIWRWF

> G6PI_SYNY3 P52983 GLUCOSE -6-PHOSPHATE ISOMERASE (GPI) (EC 5

MNNQQLWQRYQDWLYYHGGLDFYLDVSRMGFSDALVEDLQPKFAKAFQDM
VALEKGAIANPDEQRMVGHYWLRLNPALA PNDGIRAEITEPLRQIKAFVAD
VHQGNIKPPTAPKFTDLLAIGIGGSALGPQFVAQALAPNFPPLAIHFIDN
SDPDGIDRVNLCKAQDKLSTLVVTTSSKSGGTPEPRNGLAETKAVFEAQ
GLHFADYAVAVTMPGSKLSQQAQTEQWLQAFPMQDWVGGRTSELSAVGLL
PAALQGDIDQAMLDGAKTMDIATRVRELRLQNPAAALLALAWYAGDGGGK
DMVILPYKDRLLFSRYLQQLVMESLGKE RDLGDNVHVHGGIAVYGNKGST
DQHAYVQQLRDGVNPFATFIEVLHQRGQPSLELEPGVTSGDYLSGFLQG
TRQALFENQRDSITVTIPEVDATSVGALIALYERAVSFYGSLVNVNAYHQ
PGVEAGKKAASILELQKAILSTLQNESGPIALEALATKVQAPEQVETVY
KIVRHLAANDRGVTLQGDRQFPQRLQIQWRS

> P10908|UGPQ_ECOLI Glycerophosphoryl diester phosphodiesterase -
Escherichia coli.

MSNWPYPRIVAHRRGGKLAPELNTLASIDVGAKYGHKMIEFDAKLSKDGEI
FLLHDDNLERTSNGWGVAGELNWQDLLRVDAGSWYSKMFKEPLPLLSQV
AERCREHGMMAIEIKPTTGTGPLTGKVALAARELWAGMTPPLLSFEI
DALEAAQQAPELPRGLLLDEWRDDWRELTARLGCVS IHLNHKLLNKARV
MQLKDAGLRILVYTVNK PQRAAELLRWGVDCICTDAIDVIGPNFTAQ

> P0AGC3|SLT_ECOLI Soluble lytic murein transglycosylase - Escherichia coli.

MEKAKQVTRWLLAAGVCLLTVSSVARADSLDEQRSRYAQIKQAWDNRQMD
VVEQMMPGLKDYPLYPLEYRQITDDL MNQPAVTVTNFVRANPTLPPART
LQSRFVNELARREDWRGLLAFSPEKPGTTEAQCNYYYAKWNTGQSE EAWQ
GAKELWLTGKSQPNACDKLFSVWRASGKDPLAYLERIRLAKAGNTGLV
TVLAGQMPADYQTIASAI ISLANNPNTVLTFFARTTGATDFTRQMAAVAF
SVARQDAENARLMIPLSLAQAQQLNEDQIQELRDIVAWRLMGNDVTDEQAK
WRDDAIMRSQSTSLIERRVRMALGTGDRRGLNTWLARLPEAKEKDEWRY
WQADLLLERGREAEAKEILHQLMQQRFYPMVAAQRIGEEYELKIDK APQ
NVDSALTQGPENARVRELMYWNLDNTARSEWANLVKSKSKTEQAQLARYA
FNNQWWDLSVQAT IAGKLWDHLEERFPLAYNDLFKRYTSGKEIPQSYAMA
IARQESAWNPKVKSVPV GASGLMQIMPATHTVKMFSIPGYSSPQQLLDP
ETNINIGTSYLQYVYQQFGNNRIFSSAAYNAGPGRVTRWLGNSAGRIDAV
AFVESIPFSETRGYVKNVLAIDAYYRYFMGDKPTLMSATEWGRY

> IADA_ECOLI P39377 ISOASPARTYL DIPEPTIDASE (EC 3.4.19. -). -

MIDYTAAGFTLLQGAHLYAPEDRGICDVLVANGKI IAVASNIPSDIVPNC
TVVDLSGQILCPGFIDQHVHLIGGGGEAGPTTRTPEVALSRLTEAGVTSV
VGLLGTDSISRHPESLLAKTRALNEEGISAWMLTGAYHVPSRTITGSVEK
DVAIIDRVIGVKCAISDHSAAPDVYHLANMAAESRVGGLLGG KPGVTVF
HMGDSKKALQPIYDLLENCVPI SKLLPHTVNRNVPLFEQALEFARKGGT
IDITSSIDEFPVAPAEGIARAVQAGIPLARVTLSSDGNGSQPFDFDEGNLT
HIGVAGFETLLETQVVLVKDYDFSISDALRPLTSSVAGFLNLTGKGEILP

GNDADLLVMTPELRIEQVYARGKLMVKDGKACVKGTFFETA
> P0AET2|HDEB_ECOLI Protein hdeB - Escherichia coli.
MNISLRKAFIFMGAVAALSLVNAQSALAANESAKDMTCQEFIDLNPKAM
TPVAWMLHEETVYKGGDTVTLNETDLTQIPKVIEYCKKNPQKNLYTFKN
QASNDLPN
> P21948|PPB_ESCFE Alkaline phosphatase - Escherichia fergusonii.
MKQSAIALALLSCLITPVSAQTSQNINILENRAAQGDITMPGGARRLSG
DQTEALRASLNPKAKNIILLIGDGMGDS EITAARNYAEGAGGYFKGIDA
LPLTGQYTHYALDKKTGKPDYVTDASAASATAWTTGVKTYNGALGVDIHEN
PHTTILEMAKAAGLATGNVSTAELQDATPAALVSHVTSRKYGPSVTSEK
CPGNALEKGGKGSITEQLLNARADVTLGGGAKTFAETATAGEWQKTLRE
QALARGYQIVSDAASLAAVTQAGQDKPLLGLFAEGNMPVVRWHGPKASYHG
NLDKPAVTCTPNPQRNETVPTLAQMTDKAI ELLSKNERGFFLQVEGASID
KQDHAANPCGQIGETVDLDEAVQRALEFAKKDGNTLVIVTADHAHSSQIV
APDTKAPGLTQALNTKDGAVMAISYGNSEEDSQEHTGSQLRIAAYGPNA
NVVGLTDQTDLFYTMKAALGLQ
> NAHR_PSEPU P10183 TRANSCRIPTIONAL ACTIVATOR PROTEIN NAHR. -
MELRDLDLNLLVFNQLLVDRRVSITAENLGLTQPAVSNALKRLRTSL QD
PLFVTRTHQGMETPYAAHLAEPVTSAMHALRNALQHHEFDPLTERTFT
LAMTDIGEYFMPRLMDVLAHQAPNCVISTVRDSSMSLMQALQNGTVDLA
VGLLEPNLQGTGFFQVRRLLQNHVYVCLCRKDHVPTREPLTLERFCSYGHVRI
AAGTGHGEVDYTMTRVGIIRDIRLEVPHFAAVGHILQRTDLLATVPIRLA
DCCVEPFGLSALPHPVVLPPEIAINMFHAKYHKDLANIWLRQLMFDLFT D

> P37188|PTKB_ECOLI Galactitol -specific phosphotransferase enzyme IIB
component - Escherichia coli.
MKRKIIIVACGGAVATSTMAAEEIKELCQNHNIIPVELIQCRVNEIETYMDG
VHLICTTAKVDRSFGDIPLVHGMPFISGIGIEALQNKILITLQG
> P00956|SYI_ECOLI Isoleucyl -trNA synthetase - Escherichia coli.
MSDYKSTLNLPEFGPMRGDLAKREPGMLARWTDLDDLYGIIRAACKGKKT
FILHDGPPYANGSIHIGHSVNKILKDIIVKSKGLSGYDSPYVPGWDCHGL
PIELKVEQEYKPGKFTAAEFRAKCREYAATQVDGQRKDFIRLGVLGDW
SHPYLTMDFKTEANIIRALGKIIGNHGLHKGAKPVHWCVDCRSALAEAEV
EYDKTSPSIDVAQAVDQDALKAKFAVSNVNGPISLVIWTTTP WTLPAN
RAISIAPDFDYALVQIDGQAVILAKDLVESVMQRIGVTDYTILGTVKGAE
LELLRFTHPFMGFVPAILGDHVTLDAGTGAVHTAPGHGPDYVIGQKYG
LETANPVGPDGTYLPGTYPTLDGVNVFKANDIVVALLQEKGALLHVEKMQ
HSYPCCWRHKTPIIIFRATPQWFVSMQKGLRAQSLKEIKGVQWIPDWGQA
RIESMVANRPDWCISRQRTWGVPMSELVHDKTEELHPRTELELMEE VAKRV
EVDGIQAWWDLDAKEILGDEADQYVKVPDLDVWFDSGSTHSSVVDVRPE
FAGHAADMYLEGSQHRGWFMSSLMISTAMKPKAPYRQVLTHTGFTVDGQG
RKMSKSIGNTVSPQDVMNKLADILRLWVASTDYTGEMAVSDEILKRAAD
SYRRIRNTARFLANLNGFDPKDMVKPEEMVVLDRWAVGCAKAAQEDIL
KAYEAYDFHEVVQRLMRFCSVEMGSFYLDIIKDRQYTAKADSVARR SCQT
ALYHIAEALVRWMAPILSFTADEVWGYLPGEREKYVFTGEWYGLFGLAD
SEAMNDAFWDELKVRGEVNVKIEQARADKKVGGSLAAVTLYAEPELSA
KLTAALGDELRFVLLTSGATVADYNDAPADAQQSEVLKGLKVALSKAEGEK
CPRCWHYTQDVGKVAEHAEICGRCSNVAGDGEKRKFA
> NIRD_ECOLI P23675 NITRITE REDUCTASE (NAD(P)H) SMALL SUBUN IT
MSQWKDICKIDDILPETGVCALLGDEQVAIFRPYHSDQVFAISNIDPFFE
SSVLSRGLIAEHQGELWVASPLKKQRFRLSDGLCMEDEQFSVKHYEARVK
DGVVQLRG
> P73071|PROB_SYNY3 Glutamate 5 -kinase - Synechocystis sp. (strain PCC
6803).
MTMAMQPQTLVIKIGTSSLARPETGQALALSTIAALVETVCKLIGQGHRVV
LVSSGAIQVGCGR LGLTERPKKMAKQAI AAVGQGRMLRMTYDDL FSSLRQ
PIAQILLTRRELIERTAYVNAYNTFQALFELGVIAIVNENDTVAIDELKF
GDNDSLALVASLVEADWLFLLTDVDRLYSSDPRLDPDAYPIPLVKADEL
AQLQVRTDSTGSAGWTGGMATKITAARIATGSGVRTVITHGQKPEQILAI
LQGANLGTQFEAQRSDNARKRWIAYGLVPTGKIFIDAGAVQALKARGKS
LLAIGVVALEGEFS ATDAV IICDPQGQELGRGLVNYNCNELEKIKGLHSE
AIAAVLGYVGPDTVIHRDNLVLQEN
> P04693|TYRB_ECOLI Aromatic -amino-acid aminotransferase - Escherichia coli.

MFQKVDAYAGDPILTLMERFKEDPRSDKVNLSIGLYYNEDEGIIPQLQAVA
EAEARLNAQPHGASLYLPM EGLNCRYHAIAPLLFGADHPVLKQORVATIO
TLGGSGALKVGADFLKRYFPESGVVSDPTWENHVAIFAGAGFEVSTYVW
YDEATNGVRFNDLLATLKTLPARSIVLLHPCCHNPTGADLTNDQWDAVIE
ILKARELIPFLDIAYQGFAGMEEDAYAIRAIASAGLPALVSNFSKIF
LYGERVGGSLVMCEDAEAAAGRVLGQLKATVRRNYSSPPNFGAQQVVAAVLN
DEALKASWLAEEVEEMRTRILAMRQELVKVLSTEMPERNFYLLNQGMFS
YTGLSAAQVDRLEEFVYLIASGRMCVAGLNTANVQRVAKAFAAVM
> P21517|MALZ_ECOLI Maltodextrin glucosidase - *Escherichia coli*.

MMLNAWHLPVPPFVKQSKDQLLITLWLTGEDPPQRIMLRTEHDNEEMSVP
MHKQRSQPQGVTAWRRAAIDLSSGQPRRRYSFKLLWHDRQRWFTPQGF
MPPARLEQFAVDVPDIPQWAADQIFQYQIFPDRFARSLPREAEQDHVYH
HAAGQEIILRDWDEPVTQAQAGGSTFYGGDLDGISEKLPYLKKGVTALYL
NPVFKAPSVHKYDTEYRHHVDPQFGGDGALLRLRHNTQQGLMRLVLDGVF
NHSGDSHAWFDRHRNRTGGACHNPESPWRDWYSFSDGTALDWLGYASLP
KLDYQSESLVNEIYRGEDSIVRHWLKPWNMDGWRLDVVHMLGEAGGARN
NMQHVGITTEAAKETQPEAYIVGEHFQDARQWLQADVDAAMNYRGFTFP
LWGFLANTDISYDPPQIDAQTCMAWMDNYRAGLSHQQQLRMFNQLDSDHT
ARFKTLLGRDIARLPLAVVWLFVWPGVPCIIYGVDEVLGDGKNDPFCRKP
PWQVEKQDALTALFALYQRMIALRKKSQALRHGGCQVLYAEDNVVVFVRVLN
QQRVLVAINRGEACEVVLPASPFLNAVQWQCKEGHGQLTDGILALPAISA
TVWMN

> P20041|PGLR2_RALSO Polygalacturonase - *Ralstonia solanacearum*
(*Pseudomonas solanacearum*).

MNHRYTLLALAAAALSAGAHATGTSVTAPWGEVAEPLPADSAVCKTSLA
SITPIKGSVDSVDGNPANSQPDASRIQSAIDNCPAGQAVKLVKGSAGESG
FLSGSLKLGKSGVTLWIDTGVTLFASRNPAVDNGLGTCGTATTSDKSCN
ALIVARDTAGSGIVGAGAIIDGRGSLVTSGPANRLTWWDIAYLNKTKGL
NQQNPRLIQTYN GSAFTLYGVTVQNSPNFHIVTTGTSGVTAWGIKIVT
LAYAVAGYKCPGSGSTPDKVTPATCFTEPETVKNTDGFDPGQSTNVVLA
INTGDDHVAVKASSGPTRNLLFAHNHFYGHGLSIGSETNTGVSNNMLVTD
LTMDGNDSSAGNGLRIKSDASRGGKVTNIVYDGCIMRNVEKPLVDFPFYS
SVKGSLYPNFTNIVVKNFHDLSAKSIKRTMTFLGYKANKQKNPLTITLD
NVVFDGTLPAFEG SHYGGPASPNGVHFTFGGTGPVSFADAIVTSSTTDVT
VTGTPGTAAAVDCSKAFVPLKSVAPTSP

> P04170|RUBR1_DESDE Rubredoxin 1 - *Desulfovibrio desulfuricans*.
MQKYVCNVCGEYEDPAEHDNVFPDQLPDDWCCPVCVSKDQFSPA

> P45369|THIL_CHRVI Acetyl-CoA acetyltransferase - *Chromatium vinosum*
(*Allochromatium vinosum*).

MSENIIVDAGRSAIGTFGGSLSSLSATEIGTAVLKGLLARTGLAPEQID
EVILGQVLTAGVGQNPARTTLAGLPHSVPAMTINKVCGSGLKAVHLAM
QAIACGDADIVIAGGQESMSQSSHVLPDRSRDQRMGDWSMKDTMIVDGLW
DAFNHYHMGTTAENIAQKYGFTREQQDAFAAASQKTEAAQKAGRFQDEI
IPIEIPQRKGDPKVFDADEFPRHGTTAESLGKL RPAFSKDGSVTASNAG
INDGAAMVVVMKESKAKELGLKPMARLVAFASAGVDPAIMGTGPIPASTK
CLEKAGWTPADLDLIEANFAAQAMSVNQDMGWDLKVNNGGAIAIGH
PIGASGARVLVTLLEYEMQKRDAKGLATLTCIGGGQGVALLAVERM

> P22391|BLO1_KLEOX Beta-lactamase OXY-1 - *Klebsiella oxytoca*.

MLKSSWRKTALMAAAAVPLLLASGSLWA SADAIQQKLADLEKRSRGLGV
ALINTADDSQTLRYGDERFAMCSTGKVMAAAALVKQSESNPEVVNKRLEI
KKSIDLVVWSPITEKHLQSGMTLAELSAAALQYSDNTAMNKMSYLGPEK
VTAFQSIGDVTFRDLRTEPALNSAIPGDKRDTTTPLMAESLRKLTGLN
ALGEQQRAQLVTLWLGNTTGGQSIRAGLPASWAVGDKTGAGDYGTNDIA
VIWPNHAPLVLVTYFTQPQQDAKSRKEV LAAAIVTEGL

> LIPA_ECOLI P25845 LIPOIC ACID SYNTHETASE (LIP-SYN). - ESCHE

MSKPIVMERGVKYRDADKMLIPVKNVATEREALLRKPPEWMKIKLPADST
RIQGIKAAMRKNGLHSVCEEASCPNLAECFNHGTATFMILGAICTRRCF
CDVAHGRPVAPDANEPVKLAQTIADMALRYVVITSVDRDDLDRDGAQHFA
DCITAIRESKSPQIKIETLVPDFRGRMDR ALDILTATPPDVFNHNLENVPR
IYRQVRPGADYNWSLKLLERFKEAHPEIPTKSGLMVGLGETNEEIEVMR
DLRRHGVTMLTLGQYLQPSRHHLVPQRYVSPDEFDEMKAELAMGFTHAA
CGPFVRSSYHADLQAKGMEVK

> P09545|HLYA_VIBCH Hemolysin - *Vibrio cholerae*.

MPKLNRCIAIAIFTILSAISSPTLLANINEPSGEAADIISQVADSHAIKYY
NAADWQOEDNALPSLAELRDLVINQQKRVLVDFSQISDAEQAEQAOQFR
KAYGVGFANQFIVITEHKGELLFTPFDAQEEVDPQLLEAPRTARLLARSG
FASPAPANSETNTPHVAFYISVNRAISDEECTFNNSWLWNEKGSRPF
KDANISLIYRVNLERLSQYGVGSATPDAKIVRISLDDDDSTGAGIHLNDQ
LGYRQFGASYTTLDAYFREWSTDAIAQDYRFVFNASNNKAQILKTFPVDN
INEKFERKEVSGFELGVTGGVEVSGDGPKAKLEARASYTQSRWLTYNQD
YRIERNAKNAQAVSFTWNRQQYATAESLLNRSTDALWVNTYPVDVNRISP
LSYASVFPKMDVIYKASATETGSTDFFIIDSSVNIRPIYNGAYKHYYVVG
HQSYPHGFEDTPRRRITKSASFVTDVWDHPVFTGGRPVNLQLASFNNRCIQV
DAQGRLAANTCDSQSAQSFIDQLGRYVSASNTKCLDGEALDALQPCN
QNLTQRWEWRKGTDELTVNYSGESLGHDKQTGELGLYASSNDAVSLRTIT
AYTDVFNAQESSPIILGYTQGKMNQQRVGDHRLYVRAGAAIDALGSASDL
LVGGNGGSLSSVDLSGVKSITATSGDFQYGGQQLVALFTTYQDGRQQT
SKAYVTNAHEDRFDLPAAAKITQLKIWSDDWLKGVQFDLN

> P17315|CIRA_ECOLI Colicin I receptor - Escherichia coli.

MFRLNPFVRVGLCLSAISCAWPVLAVDGDMVTASSVEQNLKDAPAS
ISVITQEDLQRPVQNLKDVLEKVPVQLTNEGDNRKGVSIIRGLDSSYTL
ILVDGKRVNSRNAVFRHNDFDLNIIPVDSIERIEVVRGPMSSLYGSDALG
GVVNIITKKIGKQWSGTVDVTTIQEHRDRGDTYNGQFFTSGLIDGVLG
MKAYGSLAKREKDDPQNSTTTDTGETPRIEGFSSRDGNVEFAWTPNQNH
FTAGYGFDRQDRDS DSLDKNRLERQNYSVSHNGRWDTYGTSELKYYGEKVE
NKNPFGNSPITSESVTVDGKYTLPLTAINQFLTVMGGEWRHDKLSDAVNLT
GGTSSKTSASQYALFVEDEWRIFEPALTTGVRMDDHETYGEHWSPRAYL
VYNATDVTVTKGWATAFKAPSLQLSPDWTSNSCRGACKIVGSPDLKPE
TSESWELGLYMGEEGWLEGVESVTVFRNDVKDRISISRTSDVNAAPGY
QNFVGFETGANGRRI PVFSYYNVNKARIQGVETELKIPFNDEWKLSINYT
YNDGRDVSNGENKPLSDLPFHTANGTLDWKPLALEDWSFYVSGHYTGQKR
ADSATAKTPGGYTIWNTGAAWQVTKDVKLRAGVNLGDKDLRSDDYSYNE
DGRRYFMAVDYRF

> FABA_HAEIN P45159 3 -HYDROXYDECANOYL - [ACYL-CARRIER-PROTEIN]

MQNACTLNKKSSYSYDDLASGRGELFGKEGQPLPAPTMLMM DRIEMNE
ETGAFGKGYIEAELDIKPELFFGCHFIDGPVMPGCLGLDAMWQLVGFYL
GWIGGKKGKRALGVGEVKTGQILPTAKKVYRIHMKRVINRKLVMGMAD
GEVEVDGRVIYTATDLKVGLFQDTSTF

> OTCA_PSESH Q02047 ORNITHINE CARBAMOYLTRANSFERASE, PHASEOLOT

MNARHFLSMDYTPDELLGLIRRGVELKDLRIRGELFEPLKNRVLGMIFE
KSSTRRLSFEAGMIQLGGQAIFLSHRDTQLGRGEPIDSAKVMRMLDA
VMIRTYAHSNLTFAANSRVPVINGLSDDLHPCQLLADMQTFLEHRGSIK
GKTVAWIGDGNMNCNSYIEAAIQFDFQLRVACPAGYEPNPEFLALAGERV
TIVRDPKAAVAGAHVSTDVWTSMGQEEETARRMALFAPFQVTRASLDA
EKDVLFMHCLPAHRGEEISVDLLDSDRSVAWDQAENRLHAQKALLEFLVA
PSHORA

> DCP_SALTY P27236 PEPTIDYL -DIPEPTIDASE DCP (EC 3.4.15.5) (DI

MSTNPLLDQSMPLYPQAPRFDRIKDCHYRPAFDEGVRQKRVEIEAIVNHPA
APDFTNTLLALEQSGALLSRVTSVFFAMTAAHTNDELQRLDEAFSAELAA
LSNDIYLNALFARVDVAVWQQRHSLGLDDESLRLVDVIHQRFVLAGAQLA
EEDKARLKVLNTEATLMSQFNQRLLAASKAGGLAVDDA HCLAGLSPEEM
TVAAEAAREKGLEERWFIPLLNTTQQPALATLRDRQTRENLFASWTRAE
KGAHDTRAIVQRLVEIRRCQAKLLGFPNYAAWKMAQMAKTPQAALSFM
RGIVPPARQRVLNEQAEIQNVIDGEQGGYTVQAWDMWFYAEQVRREKYAL
DEAQLKPYFALNTVLQEGVFWTANQLFGITFVERFDI PVYHPDVRVWEIF
DSDGVGMALFYGDFFARDSKSGAWMGNFVEQSTLNETRP VIYNVCNYQK
PVDGQPALLLWDDVITLFEHFGHTLHGLFAVQRYATLSGTNTPRDFVEFP
SQINEHWASHPRVFERIYARHVDGSEKMPADLQERMRKASLFNKGYDMTEL
LGAALLDMRWHMLEESVAEQSVAEFEQQALAAEHLDPVPPRYRSSYFA
HIFGGGYAAGYAYLWLTQMLADDGYQWFVEQGLTRENGQFRDAILARG
NSTDLETLYSAWRGHEPHIDPMLQYRGLDR

> P13650|DHGB_ACICA Quinoprotein glucose dehydrogenase -B - Acinetobacter calcoaceticus.

MNKHLLAKIALLSAVQLVTLTSAFADVPLTPSQFAKAKSENFDDKVVILSNL
NKPBALLWGPDNQIWLTERATGKILRVNPESGSVKTVFQVPEIVNDADGQ
NGLLGFAFHPDFKNNPIYISGTFKNPKSTDKELPNQTIIRRYTYNKSTD

TLEKPVDLLAGLPSSKDHQSGRLVI GPDQKIYYTIGDQGRNQLAYLFLPN
QAQHTPTQOELNGKDYHTYMGKVLRLNLDGSI PKDNPSFNGVVSHTYTLG
HRNPOGLAFTPNGKLLQSEQQPNSSDDEINLIVKGGNYGWPVNAVAGYKDDSG
YAYANYSAAANKS IKDLAQNGVKVAAGVPVTKESWTGKNFVPPKTLTYT
VQDTYNYNDPTCGEMTYICWPTVAPSSAYVYKGGKKAITGWENTLLVPSL
KRGVIFRIKLDPTYSTTYDDAVPMFK SNNRYRDVIASPDGNVLYVLTDTA
GNVQKDDGSVTNTLENPGSLIKFTYKAK

> P30125|LEU3_ECOLI 3-isopropylmalate dehydrogenase - *Escherichia coli*.

MSKNYHIAVLPDGI GPEVMTQALKVLDVAVRNRNFAMRITTSHYDVGAAI
DNHGQPLPPATVEGCEQADAVLFGSVGGPKWEHLPPDQQPERGALLPLRK
HFKLFSNLRPAKLYQGLEAFCPLRADA ANGFIDILCVRELTGGIYFGQPK
GREGSQYEKAFDTEVYHRFEIERIARIAFESARKRRHKVTSIDKANVLQ
SSILWREIVNEIATEYDPVELAHMYIDNATMQLIKDPSQFDVLLCSNLF
DILSDECAMITGSMGLPSASLNEQGFGLYEPAGGSAPDIAGKNIANPIA
QILSLALLRLRYSLDADDAACAIERAINRALEEGIRTGDLARGAAVSTDE
MGDIARYVAEGV

> P16869|FHUE_ECOLI FhuE receptor - *Escherichia coli*.

MLSTQFNDRNQYQAITKPSLLAGCIALALLPSAFAAPATEETVIVEGSA
TAPDDGENDYSVTSTASAGTKMQMTQRDIPQSVTIVSQORMEDQQLQTLGE
VMENLGIKSKSDRALYYSRQGFQIDNYMVDGIPTYFESRWNLGDALS
DMALFEGYEVVRGATGLMTGTGNPSAANMVRKHATSREFKGDVSAEYGS
WNKERYVADLQSP LTEDGKIRARIVGGYQNNDSWLDRYNSEKTFSSGIVD
ADLGLDITLSAGYEQRIDVNSPTWGGLPWNTDGSNSYDRARSTAPDW
AYNDKEINKVFMTLKQFADTWQATLNATHSEVEFDSKMMYVDAYVNKAD
GMLVGPYSNYGPGFDYVGGTGWNSGKRKVDALDLFADGSYELFGRQHNL
MFGGSYSKQNNRYFSSWANI FPDEIGSFYFNFGNFPQTDWSPQSLAQDDTT
HMKSLEYAATRVTLA DPLHLILGARYTNWRVDTLTYSMEKNHTTPYAGLVF
DINDNWSTYASYTSIFQPNDRDSSGKYLAPITGNNYELGLKSDWMNSRL
TTTLAIFRTEQDNVAQSTGTPIPGSNGETAYKAVDGTVSKGVEFELNGAI
TDNWQLTFGATRYAEDNEGNAVNPRLPRTTVKMFYSYRLPVMPELTVGG
GVNWQNRVYTDTVTPYGTFRAEQGSYALVDLFTRYQVTKNFSLQGNVNNL
FDKTYDTNVEGSIVY GTPRNFSTITGTYQF

> P26311|PEPT_SALTY Peptidase T - *Salmonella typhimurium*.

MDKLLERFLHYVSLDTQSKSGVRQVPSTEGQWKLLRLKQQLLEEMGLVNI
TLSEKGTLMATLPANVEGDI PAIGFISHVDTSPDFSGKNVNPQIVENYRG
GDIALGIGDEVLSVPMFVPLHQLLQTLITTDGKTLGADDKAGVAEIMT
ALAVLKGNIPIPHGDIKVAFTPDEEVGKGAK HFDVEAFGAQWAYTVDGGGV
GELEFENFNAASVNIKIVGNVHPGTAKGVMVNALS LAARIHAEVPADEA
PETTEGYEGFYHLASMKGTVDRAEMHYI IRDFDRKQFEARKRMMEI AKK
VGKGLHPDCYIELVIEDSYNNMREKVVEHPHILDIAQQAMRDCHITPEMK
PIRGGTDGAQLSFMGLPCPNLFTGGYNYHGKHEFVTLEGMEKAVQVIVRI
AELTAKRGQ

> P45996|OMP53_HAEIN Outer membrane protein P5 - *Haemophilus influenzae*.

MKKTALALVAVGLAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIK
KGLSSSNYGYRRNTFTYGVFGGYQILNQDNFGLAAELGYDDFGRAKLREA
GKPKAKHTNHGAYLSLKGSYEVL DGLDVYKAGVALVRSYKFKYEDANGT
RDHKKGRHTARASGLFAVGAEYAVLPELAVRLEYQWLTRVGKYPQDKPN
TAINYNPWIGACINAGISYRFGQGEAPVVAAPPEMVSKTFLNSDVTFAFGK
ANLKPQAQATLDSVYGEISQVKSRRVAVAGYTNRIGSDAFNVKLSQERAD
SVANYFVAKGVAADAISATGYGEANPVTGATCDQVKGRKALIACLAPDRR
VEIAVNGTK

> P21175|BRAC_PSEAE Leucine-, isoleucine-, valine-, threonine-, and
alanine-binding protein - *Pseudomonas aeruginosa*.

MKKGTRQLSRLFAAMAIAAGFASYSMAADTIKIALAGPVTGPVAQYGDMMQR
AGALMAIEQINKAGGVNQAQLEGVIYDDACDPKQAVAVANKVVNDGVKVF
VGHVCSSTQPATDIYEDGVLMITPSATAPEITSRGYKLIFRTIGLDNM
QGPVAGKFI AERYKDKTIAVLDHDKQQYEGEGIATEVKKTVEDAGIKVAVFE
GLNAGDKDFNALISKLKKAGVQFVYFG GYHPPEMGLLLRQAKQAGLDARFM
GPEGVGNSEITAIAGDASEGMLATLPRAFEQDPKNKALIDAFKAKNQDPS
GIFVLPAYSAVTVIAKGI EKAGEADPEKVAEALRANTFETPTGNLGFDEK
GDLKNDFDFTVYEWKDATRTEVK

> P13482|TREA_ECOLI Periplasmic trehalase - *Escherichia coli*.

MKSPAPSRPQKMALIPACIFLCFAALSVAEETPVTPQPPDILL GPLFND

VQNAKLFPPDQKTFADAVPNSDPLMILADYRMQQNQSGFDLRHFVNVNFTL
PKEGEKYVPEEQSLREHIDGLWPVLTRSTENTEKWDSLLPLPEPYVVP
GRFREVYYWDSYFTMLGLAESGHWDKVDVMANFAHEIDTYGHIPNGNRS
YYLSRSQPPFFALMVELLAQHEGDAALKQYLPQMKEYAYWMDGVENLQA
GQQEKRVVKLQDGTLLNRYWDDRDTPRPESWVEDIATAKSNPNRP ATEIY
RDLRSAAASGWDFSSRWMDNPQQNLNTRTTSIVPVDLNSLMFKMEKILAR
ASKAAGDNAMANQYETLANARQKGIKYLWNDQQGWYADYDLKSHKVRNQ
LTAAALFPLYVNAAKDRANKMATATKTHLLQPGGLNNTSVKSGQQWDAP
NGWAPLQWVATEGLQNYGQKEVAMDISWHFLTQHTYDREKKLVEKYDV
STTGTGGGGGEYPLQDGFQWGTNGVTLKMLDLICPKEQPCDNPVATR PTVK
SATTQPSTKEAQPTP

> P15214|GST_PROMI Glutathione S-transferase GST-6.0 - *Proteus mirabilis*.

MKLYYTPGSCSLSPHIVLRETGLDFSIERIDLRTKKTESGKDFLAINPKG
QVPVLQLDNGDILTEGVAIVQYLADLKPDRNLIAPPKALERYHQIEWLNF
LASEVHKGYSPLFSSDTPESYLPVVKNLKSKFVYINDVLSKQKCVCGDH
FTVADAYLFTLSQWAPHVALDLTDLSHLQDYLRARIAQRPNVHSALVTEGL
IKE

> P40130|CYAA_ERWCH Adenylate cyclase - *Erwinia chrysanthemi*.

MYFYIETLQKRLDAINQLRVDRALEAMKPAFQQVYSLLPVLLHHHPLMP
GYLEGGKPHGICLFSFDEKQHYLDSVELRWGELSAPDRKGELPITGVYS
MGSTSSIGSCSLLDIWVCHQSWLDNEERQLQKCSLLEKWAAG QGVDV
SFFLMDENRFRHNESGSLGGEDCGSTQHILLDEFYRTAVRMAGKRILWN
MVPVEEEAHYDEFVLSLYARGALAPNEWLDLGGLSALSAAEYFGASLWQL
YKSIDSPYKAVLKTLLLEAYSWEYPNTRLLSSEIKARLHKGEIVSFGDP
YCMMLERVTOYLDAINQTRLDLVRRCFYLVKCEKLSRERACTAWRRQIL
TQMVAQWGSDERLVMLDNANWKIGQVREAHNELLDAMMQSYRNL IRFA
RRNNSVVSASPQDIGVTRKLYAAFEALPGKVTLVNQPISPDLSETNLT
IYVPAGRANRSGWYLYNQAPSMDAIISHQPLEYNRYLNKLVAWAYFNGLL
TSSTRLHIKGHELCIDARLQELVSDVSSHFLRVAAPTPKALYSPCEIRH
LAIIVNLEHDPTAAAFRNQVVHFDLQVDFVDFSGQQQCLVGSIDLLYRNS
WNEVRTLHFSGEQAMLEALKTILGKMHQDAALPESLEVFYCYSQHLLRG LIR
TRVQQLVSECIELRLSSTRQEPGRFKAVKVAGETWGLFFERLSVSAQKLE
NAVEFYGAISNNKQLQGLPVQVETNHIHLPPVVDGVASEGIIQFFFDQHD
NQGFNIYILDESNRVEVYHHCEGSKEELVRDVSRYSSSHDRFTYGSSEFI
NENLPPQFYQIVQLDGRGTQVI PFRSSALSHLCVTPSSEDKKNLVLSQLQM
L

> GLYA_CAMJE P24531 SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2

MSLEMFDKEIFDLTNKELERQCEGLEMIASENFTLPEVMEVMGSILTNY
AEGYPGKRYGGCEFFVDEIETLAIERCKKLFNCKFANVQPNQSGSQANQGV
YAALINPGDKILGMDLSHGHLTHGAKVSSSGKMYESCIFYGVELDGRIDY
EKVREIAKKEKPKLIVCGASAYARVIDFAKFREIADEVGAYLFADIAHIA
GLVVAGEHPSPPHAAVVSSTTHKTLRGPRGGIIMT NDEELAKKINSAIF
PGIQGGPLMHVIAAKAVGFKFNLSDEWKVYAKQVRTNAQVLANVLMRKF
KLVSDGTDNHLVMSFLDREFSGKDADLALGNAGITANKNTVPGEIRSPF
ITSGRLGLTPALTARGFKEKEMEIVSNYIADILDDINNEKIQENIKQELK
KLASNFIYERAMF

> P24092|HMWC_DESVH High-molecular-weight cytochrome c - *Desulfovibrio vulgaris* (strain Hildenborough / ATCC 29579 / NCIMB 8303).

MRNGRTRLLRWAGVLAATAIIGVGGFWSQGTTKALPEGPGEKRADLIEIGA
MERFGKLDLPKVAFRHQHTTAVTGMGKDCAACHKSKDGKMSLKFMRLLDD
NSAAELKEIYHANCIGCHTDLAKAGKKTGPQDGECSRCHNPKPSAASSWK
EIGFDKSLHYRHVASKAIKPVGDPQKNCGACHHVYDEASKKLWVGK NKED
SCRACHGEKPVDKRPALDTAAHTACISCHMDVAKTKAETGPVNCAGCHAP
EAQAKFKVVREVPRLDGQPDAAALILPVPGKDAPREMKGTMKPVAFDHKA
HEAKANDCRTCHHVRIDTCTACTVNGTADSKFVQLEKAMHQPDMSRSCV
GCHNTRVQQPTCAGCHGFIKPTKSDAQCGVCHVAAPGFDAKQVEAGALLN
LKAEQRSQVAASMLSARPPKGTFDLNDIPEKVVIGSIAKEYQSEF PHR
KIVKTLIAGIGEDKLAATFHIEKGTLCQGGCHHNSPASLTTPPKCASCHGKP
FDADRGRDPLKAAHYHQCMGCHDRMKIEKPANTACVDCHKERAK

> CILA_HAEIN P44459 CITRATE LYASE ALPHA CHAIN (EC 4.1.3.6) (C

MTTREQRIEKYHADRSVYQAVPKSELSRTAKDRKLCSTLEEAIKRSGLK
DGMTVSFHHAFRGDFVVMVMNKIAEMGFKNLTLASSSLID SHFPIVEH
IKNGVVTKIYSSGLRGLAEQISRGLLNEPVNIHSHGGRVHLVKSSELKI

DVAFLGVPCCDFTFGNANGFTGKSKCGSLGYARVDAEYADKVLLTEEFVE
YPHHPISIAQDQVDLIVQVEAVGDPKKIGGGATRMTPNPRELLIARKCAE
VIFASGYFKDGFSLQTFSGGAALAVTRFLEEKMRRENITADFALGGITAS
MVALHEAGLIKLLDVQSFDSVAAESLARNPNHIEVSANQYAN YSSKGAS
VERLDMVILSALEIDTKFNVNVLGTSDGVIRGASGGHCDTAASAQVAIIIV
APLVRGRIPTVVENVITCVTPGENVDILVTDHGVAVNPKRPDLIEALSKT
DIPLFTIEQLCERAYSITGKPKIEFTNKPVAVVRYRDSVIDTVYQVKD

> P34895|GLYA_HYPME Serine hydroxymethyltransferase - *Hyphomicrobium methylavorum*.

MSSAPAAGTAS TSRFFKSHVSETDPDIFSAIQKEFGRQQHEIELIASENI
VSQAVLDAAGSVLTNKYAEGYPGKRYGGCQYVDIVIDIAIDRAKCLFNC
EFANVQPNSGSQANQGVFNALAQPGDTILGLSLAAGGHLTHGAPVNQSGK
WFKAVHYMVKPDShLIDMDEVKLAQEHPRIIIAGGSAYPRKIDFAAFR
AIADEVGAIFLVDMAHFAGLVAAGLIPSPFPHAHVVTTHKTLRGPRGG
MILTNDADIACK INSAIFPGIQGGPLMHVIAGKAVAFGEALRPFKVIYIK
QVMDNARALGEVLVQNGFALVSGGTDHLVLDLRPKKLTGTKAEKALGR
ANITCNKNGIIPFDEPKPMVTSGIRLGSAPGTTTRGFVGAEFQEIIGRLISEV
LDGVAKNGEDGNGAVEAAVKAKAIALCDRFPPIYA

> P04805|SYE_ECOLI Glutamyl-tRNA synthetase - *Escherichia coli*.

MKIKTRFAPSPTGYLH VGGARTALYSWLFARNHGGEFVLRIEDTDLERST
PEAIEAIMDGMNWSLEWDEGPYYQTKRFDRYNAVIDQMEEGTAYKCYC
SKERLEALREEQMAKGEKPRYDGRCRHSHEHHADDEPCVVRANPQEGSV
VFDDQIRGPIEFNSQELDDLIIRRTDGSPTYNFCVVDWDMETHVIRG
EDHINNTPRQINILKALKAPVPVYAHVSMINGDDGKLSKRHGAVSVMQY
RDDGYLPEALLNYLVRL GWSHGDQEI FTREEMIKYFTLNAVSKSASAFNT
DKLLWLNHHYINALPPEYVATHLQWHIEQENIDTRNGPQLADLVKLLGER
CKTLKEMAQSCRYFEDFAEFDADAACKHLRVPVARQPLEVVRDKLAAITD
WTAENVHHAIQATADELEVGMGKVGMPLRVAVTGAGQSPALDVTVHAIGK
TRSIERINKALDFIAERENQQ

> P48515|IF2_THET8 Translation initiation factor IF-2 - *Thermus thermophilus* (strain HB8 / ATCC 27634 / DSM 579).

MAKVRIYQLAKELGMETQELLELLDQMGVAYKSHASTLEEKDAEAVRELV
KEQRGLQEKLAEEERRKSLPRRPPVVIMGHVDHGKTTLLDYLKRSRIAE
KEAGGITQHVGAFFVKTTPQGTVVVIDTPGHEAFTTIRQGAQVADIAVIV
IAADDGIMPQTEEAIAHAKAAGAKLIFAINKIDLPQ ADPEKVKRQLMERG
FVPEEYGGDAIVIPISAKTGQGVQDLEMLILLAELEDYRADPNAPRGPV
ILESKLKQAGIIANMLVQEGTFRVGDYVVAGEAYGRIRAMMDAGNQRK
EAGPGSAVQVLGFQELPHAGDVVEWVPDLEAAKEIAEERKEERKAREEEE
KARRPRTMAELLRAMQEEGRKELNLI LRADTQGSLEAIQHILARESTEDV
KINILLAQVGPATESDVLQAQTANAAILAFGVNPPGS VKKKAEEKGVLLK
TFRIIYDLVDEVRNMVKGQREPQYKEEVLGQAEVRAIFRLPTGKQVAGCM
VTQGRIPRNAEVRVLRDQVVIWQGRIASLKRKFEDVREVAQGYECGIGLD
GFDDDFREGDVIEAFQMVEVPA

> ACEK_SALTY P51067 ISOCITRATE DEHYDROGENASE KINASE/PHOSPHATA

MPRGLELLIAQTIILQGFDAQYGRFLEVTSQAQRFEQADWHAVQQAMKSR
IHLYDHHVGLVVEQLRCITDGKSTDANFLLRVKEHYTRLLPDYPRFEIAE
SFFNSVYCRFLDHRSLTPERLFI FSSQPERRFRTI PRPLAKDFFPDHGWE
PLLMRILSDLPLRLPWQNKRRDIRYI IAHLTEALGEDALPRCHVQVANEL
FYRNKAAWLVGKLTTPDGTLPFLLPIHRTDEGELFVDTCLTTTAEASIVF
GFARSYFMVYAPLPAALVEWLREILPGKTTAELYMAIGCQKHAKTESYRE
YLCYLAESDEKFIEAPGIRGMVMLVFTLPGFDRVFKI IKDKFAPQKEMSA
AHVRACYQLVKEHDRVGRMADTQEFENFVLDKRQIDPALMALLRQEAPEK
ITDLGEQIVIRHLYIERRMVPLNIWLEQVEGQQLRDAIEEYGNAIRQLAA
ANIFPGDMLFKNFVTRHGRVVFYDYDEICYMTEVNF RDIPPARYPEDEL
ASEPWYSVSPGDVFPPEEFRHWLCADPRIGPLFEEMHADLFRADYWRALQT
RIKEGHVEDVYAYRRRQRF SVRYGAISSTVNSS

> P0C0X7|C554_RHOSH Cytochrome c-554 - *Rhodobacter sphaeroides* (*Rhodopseudomonas sphaeroides*).

QDARQIERMIEGRHGLMTLMAYELGKLGMAKEETPYDAEVAGDAASNLS
ALASVLSPELFPKGSVAGEAEDSEALPAIWEKPD DFAQKISDMEEAAAKM
QAAAGTDLASLQGAMRDLGAGCGSCHETYRQK D

> P44442|RND_HAEIN Ribonuclease D - *Haemophilus influenzae*.

MSKWDNSNIPFLFFSNKKITMIKECQNPFFRVVTDNTALLEVCNLAQQKS
AVALDTEFMRVSTYFPKLGLIQLYDGEHVSLIDPLAITDFSPFVALLANP
KVLKILHSCSEDLVFLQEFDQLPRPMIDTQIMARFLGLGTSAGLAKLAQ
QYLNVEIDKGATRTNWKRPPLSDIQLQYAAGDVWYLLPLYH ILEKELAKT
PWEQAVRDDCELVLAKTHKLQERDSEKAYLDIPNAWKLNPLELSRLRVLA
QWRQNVAIERDLALSIVKSEHLWKVAKNNPRNTSEMLEMGLTENEVRVR
GKEILQLLSQARRISSNDYPKSIERISEDPRYKKTIRLLQEKVNSLTPEG
LTPEIVASKRTLEELIKWVWKYDCSQDKRPELLIGWRKPIGEKLVDAK
> NIRF_PSEST Q52521 NIRF PROTEIN. - PSEUDOMONAS STUTZERI (PSE
MIRPFLLLAAVGLLTACAQQPLRGTGDLGVVVERATGSLQIIESSNQSQI
ARIEGLGDLSDHASVVFSRDQRYAYVFRDGGTLTKVDLLRHRIDRRVIQGG
NSIGGAISQDGTLIAVGNYPGGVKVFDKTELELVADIPATPLADGSRNA
RVVGVVIDVPGRRFYLSLFDTDETWLLDFSQGNEPQITREFEGIGRQPYDAL
LTPEGRYYIAGLFGEDGMAKIDLWHPERGERI LDGYGRGEQKLPVYKMP
HLEGWTVAGNQTFVPAVGQHRVLMDSQNWQQTAAIDVAGQPIFVMARPD
ARQIWNVFAHPDNHRVQVIDSETHEI IADLEPGPAVLHMEFTARGDQLWL
SVRDGEEIQVWDPYTLKLLKRLPAHSPSGIFFSSRAHETGL
> P07110|PAPC_ECOLI Outer membrane usher protein papC - Escherichia coli.
MKDRIPFAVNNITCVILLSL FCNAASAVEFNTDVLDAADKKNIDFTRFSE
AGYVLPQQYLLDIVNGQSISPASLQISFVEPALSGDKAEKKLPQACLTS
DMVRLMGLTAESLDKVVYWHHDGQCADFHGLPGVDIRPDTGAGVLRINMPQ
AWLEYSDATWLPSPRWDDGIPGLMLDYNLNGTVSRNYQGGDSHQFSYNGT
VGGNLGPWRLRADYQGSQEQSRYNGEKTTRNFTWSRFYLFRAIPRWRAN
LTLGENNINSDIFRSWSTGA SLESDDRMLPRLRGYAPQITGIAETNAR
VVVSQQGRVLYDSMVPAGPFSIQDLDSVVRGRLDVEVIEQNGRKKTFQVD
TASVPYLTRPGQVRYKLVSGRSRGYGHETEGPVFATGEASWGLSNQWSLY
GGAVLAGDYNALAGAGWDLGVPGLSADITQSVARIEGERTFQGKSWRL
SYSKRFDNADADITFAGYRFSESNYMTMEQYLNARYRNDYSSREKEMYTV
TLNKNVDWNTSFDNLQYSRQTY WDIRKTDYTVSVNRYFNVFGLQGVAVG
LSASRSKYLGRDNDSDAYLRISVPLGTGTASYSGMSMSNDRYVMAGYTDTF
NDGLDSYSLNAGLNSGGGLTSQRQINAYYSHRSPLANLSANIASLQKGYT
SFGVSASGGATITGKGAALHAGGMSGGTRLLVDTDGVGGVPVDGGQVVTN
RWGTGVVTDISSYRNTTSVDLKRLLPDDVEATRSVVESALTEGAIGYRKF
SVLKGKRLFAILRLADGSQPPFG ASVTSEKGRELGMAVEGLAWLSGVTP
GETLSVNWDGKIQCQVNPETAISDQQLLLPCTPQK
> P45573|DSVC_DESVH Sulfite reductase, dissimilatory -type subunit gamma -
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).
MAEVTYKKGKSFVEDEDGFLLRFDWCPEWVEYVKESEGISDISP DHQKII
DFLQDYKKNGIAPMVRILSKNTGFKLKEYELFPSPGPKGACKMAGLPK
PTGCV
> ASRA_SALTY P26474 ANAEROBIC SULFITE REDUCTASE SUBUNIT A (AN
MAIKITPDEFSLLIQRLNKKWRVFAPSAEFRGGRFSDTDNIYQRISGWR
DLIWEKSHMSPNTIIAPITETLFYFDKDTIQIAETDTSPIIIFARACDI
NAMSRLDYMYSNNGNSDYSYQLLREHI RFVLI ECEESFENCFCVSMGTN
KTDCYSAAMRFSDEGALVSIRDPFIEAAIQGLGQEADYTPSFVSENRETV
VTPDSVCHDPQKIRDILTHHPLWDAYSRCISCGRCTTGCTCCTCYSVFD
VAYDENPQRGERRRQWASCMVPGFSDMAGGHGFREKPERLRYRALHKVN
DYKARNGIEHMCVGCRCDDRCPPQYIKFSLIINKMTAAVRQALAEAA
> P56145|SYFB_HELPHY Phenylalanyl -tRNA synthetase beta chain - Helicobacter
pylori (Campylobacter pylori).
MKLSINDLNVFVNTPKDIAKLCEDLSRLGLEVESCIPIAPKNVVVGKIL
EKAPHKNAEKLSVQVDVGKEVLQIVCGAKNVAPNQFVVPALNGALIGST
TIAKTELRGVESHGMCSSIELGFPKINDGILELDESVELVGLKELNEY
APFNTHVLEISLTPNRGDCLSVLGIAREI SAFYHTPLKPIKALNFTPKSG
LITLSAGENIESHLAYLICNHSLKTPLNKLSLAHNALSSENDLNNFIE
FSTHFSGVIMNAYS LNTPMDLSVKNDENNLESVYINHQRSTIAIKHQV
QKDLSECLLLEASYTDPI SLSLKLHALKDKTLQKDNALYRSARGSNPNL
SDGLNFLSAHLKATILESQTEHSLKDRTLTFQLEDITEILGLAVEKEKI
QGILKNLGFKVSVEKPNKPKQILEVIAPNF RHDIKTIQDIAEEILRFVGI
DNLVSKPLHCVSSKNSPNYDTHRFFENLKHKALACGFKEVIHYVFYSKE
KQQKLGFEVLEDPLELQNPITTELNTLRTSLVCGLLDASLRNKNLGFKSI
ALYEKGSVYNSKREEIQKLGFLISGLQKKEYPDTKGAWDFYSFAECVS
KVIGDFSLEKLTQTPI NHYPYQSAKI IQNHEIIGVIAKIHPKVIQELDLF

ESYYAEIDAFKLRPAMLLKPFISIYSSVRD LTLIIDENTAFSGIKKALK
DAQIPNLSEILPLDIFKESNNSIALSVRCVIHSLEKTLNDEEVNSAVQKA
LEILEKEFNARLKG
> P34945|SYS_THET2 Seryl -tRNA synthetase - *Thermus thermophilus* (strain
HB27 / ATCC BAA-163 / DSM 7039).
MVDLKRRLRQEPFVHRAIREKGVALLDLEALLALDREVQELKKRLQEVQTE
RNQVAKRVPKAPPE EKEALIARGKALGEEAKRLEEALREKEARLEALLLQ
VPLPPWPGAPVGGEEANREIKRVGGPPEFSFPPLDHVALMEKNGWWEPRI
SQVSGSRSYALKGDLALYELALLRFAMDFMARRGFLPMTLPSYAREKAF
GTGHFPAYRDQVWAI AETDLYLTGTAEVVLNALHSGEILPYEALPLRYAG
YAPAFRSEAGSFGKDVRLMRVHQFHKVEQYVLTEASLEASDRAFQELLE
NAEEILRLLLELPYRL VEVATGDMGPGKWRQVDIEVYLPSEGRYRETHSCS
ALLDWQARRANLRYRDPEGRVRYAYTLNNTALATPRI LAMLENHQLQDG
RVRVPQALIPYMGKEVLEPCG
> P04981|TOX5_BORPE Pertussis toxin subunit 5 - *Bordetella pertussis*.
MQRQAGLPLKANPMHTIASILLSVLGIYSPADVAGLPTHLYKNFTVQELA
LKLKGNQEFCLTAFMSGRSLVRACL SDAGHEHDTWFDTMLGFAISAYAL
KSRIALTVEDSPYPGTPGDLELQICPLNGYCE
> P94282|SYFA_BORBU Phenylalanyl -tRNA synthetase alpha chain - *Borrelia
burgdorferi* (Lyme disease spirochete).
MKVIFMKADLNLIKTLHPLEIKVIVNNEEEDDISASIIIEKLGFNQAN
KTIEWLNSKGIIEEIRKLN VFYKATERGLGALRD GFVEEKIINLVSQKA
VLASNLALELDIDVKEVRKAFGNLLKEGILSLDLKQIIINCLDGTETNY
QKVRVLLERAKNSDLLRESLTTEELLLISNFAKKKGADSVFFKIIIEKLDL
KFRLLSSFGLEVKNFLMKSCLTGDDELTKLTPEILKNKTYENKKFRAYNIHI
PSAKTFIGRANSYLDYISKIKDKLVGLGFQEFDGPLVETEFFNNDALFMP
QFHPSRDIKDVYISDPSMQESLPEPYFNSVLAHE TGYATGSRGWRYSF
SEDLKRLVLRTHGTVLSAKQLINAKNPSRYFGVIRCFRYDQVDATHGVD
FYQTEGIVIEDGVSIKTLGLLEIFAKELAGATEIKYVPAYFPFTEPSIE
IHVKHPVLGWFLGGSGIFRPEVTKPLGIDLPIAWGIGIDRMALMHLGL
NDLRDLFTYDIGDVILRRGKIDAKVRNL
> P04738|FMKA_ECOLI K88 fimbrial protein A - *Escherichia coli*.
MKKAFLLACVFFLTGGGVSHAAVQKTIFSADVVASVCHVVVDADSTGNSG
RLTFGTYRKSTGASVPPRDFTVRLYESGATVQGC SAFLAGQVATLDFGNP
GQLDAAGVVTRGAGDGI RVDVRAVDAQADYRGRLTQDNH SVKYPVDFAAK
GQFRFRAQPVFPADVKAGEYSGALTFVVTYQ
> P14898|AMY2_DICTH Alpha -amylase 2 - *Dictyoglomus thermophilum*.
MIYDDKIFGDLCHKEFLVEREVKLEEIYLEEVLPEDPKPEDEIEFTFNC
PLKFHITSGKIVKDNREIYTFNIQERKTQWNDSIFNFSEIIKIKIPPLKE
NGLYQIHLYEMNEKIYEQYLSIDSFEAPLWSEESIYHIFIDRFKDEKE
VEYSENLKEKLGGLKILSRLDYIENLGINTIWIWSPIFKSTSYHGYDIE
DYFEIDPIWGTKEDLKKLVREAFNRGIRIILDFVPNHMSYKNPIFQKALK
DKNSNLRSWFIFKGEDYETFFGVKSMPKINLKNKEAIDYIINA AKYWIRE
FGISGYRMDHATGPDINFWSIFYYNLKFSEFPETFYFGEIVETPKETKKYV
GKFDGTLDFYLFKIRDFFIGKRWSTKEFVKMIDLEEKFYGNKFKRISFL
ENHDSNRFLWVAKDKLLRLASIFQFSINAIPIIYNGQEMGCSQYRDILE
GNRTLHEHARLPIPWSDDKQDKELIDFYRQLVKIRKSHPALYKGTFIPIF
SDMISFIKETQEESILVLINIEDKEEIFNLNGTYRDLFSGNIYTNLSKLG
PMSAHLRLRIDH
> P02943|LAMB_ECOLI Maltoporin - *Escherichia coli*.
MMITLRLKPLAVAVAAGVMSAQAMAVDFHGYARSGIGWTGSGGEQQCFQT
TGAQSKYRLGNECTY AELKLGQEVWKEGDKSFYFDTNVAYSVAQQNDWE
ATDPAFREANVQGNLIEWLPGSTIWAGKRFYQRHDVHMIDFY YWDISGP
GAGLENIDVGFGLSLAATRSSEAGSSSFASNNIYDYTNETANDVFDVR
LAQMEINPGGTLELGVYGRANLRDNYRLVDGASKDGLWFTAHTQSVLK
GFNKFVVQYATDSMTSQGKLSQSGVAFDNEKFAYINNNGHMLRILDH
GALSMDNWDMMYVGMYQDINWDNDNGTKWWTVGIRPMYKWTPI MSTVME
IGYDNVESQRTGDKNNQYKITLAQQWQAGDSIWSRPAIRVFATY AKWDEK
WGYDYTGADNANFNGKAVPADFNNGSFRGDSDEWTFGAQMEIWW
> P05706|PTHA_ECOLI Glucitol/sorbitol -specific phosphotransferase enzyme
IIA component - *Escherichia coli*.
MTVIYQTTITRIGASAI DALSDQMLITFREGAPADLEEYCFIHCHGELKG
ALHPGLQFSLGQHRYPVTA VGSVAEDNLRELGHVTLRF DGLNEA EFPGTV

HVAGPVPDDIAPGSSVLKFESVKE
> P45354|HXUA2_HAEIN Heme/hemopexin -binding protein - Haemophilus influenzae.

MYKLNVISLIIILTCSGAAYASTPDFPQHHTVFGTVTIEKTTADKMTIK
QGSQDKAQIDWKSFDIGQKKEVKFEQNEHAVAYNRVIGGNASQIQGKLT
NGKVYLANPNGVITITQGAENVAGLLATTKDLERISENSNSYQFT RRTKD
RQVLKEGLVLKDGQVVKEGQVINENITAQDFVVLNGDEVINKGNINVEK
NSTINGKVYLLSSGYNFTFTLPDSGISVALEDNTVQGIKNEGSIKAGEIT
LSAKGRKQALDSLVMNNGVLEATKVSNNKNGKVVLSADNVELNNE
SNIKGE IVTFGADVTSNKLKDNKITSKTGSKVTSPKINFTGKSVNIN
GNGFRED STHYKDFEKKLNEVNIDVDPDENIRIADIEDNTGTGTGTSS
FIQT GALSSLLANNGKVNKGNVNVISGRIHIDSFGRSDSLKLTNKGHI
DINN ADIHSKGRFFITSLQNEEDFKSNITITDSKINLNGAMGLGRSV
DEKDY DNRWQKTEGSQRKFDVKMSNVEFNQVDDVILAGGFQVNLKIV
ATGQT NFYIDGGVSRNGRKYEYGVLDLDRKRTQSELNQRRRWGYYD
LELDMNR AYLYRFDLDFATKNTGRSTIKDTEINISNSNINLKNFVH
LLAEKIKL DNS KIDITFDKDNSQDTLAQTNRLGMNGKVS
MINSHIKIVGDEKEGISPTGTY ATMFLIGELIGEKS
SIFVKSHQGYTFKTDGNTKIAGKYSKEDLKITAINT
GGRAAEVLLINGALGSADNDANIANMAFTIGDSANTKTTIENADIT
ALAP NGGTAYLSSKDVEIEVKPNSNFTFELPREKNLNQTKINGAST
KLSERGF ARLYDKINGVRASNLQAEQNLVTDASEKIINTKLVSSLD
VEKLVSVAV CD AGNGCEEQFGDKGNNTKVS
VGELEAEQ

> P0AGJ9|SYY_ECOLI Tyrosyl -tRNA synthetase - Escherichia coli.

MASSNLIKQLQERGLVAQVTDEEALAERLAQGPALYCGFDPTADSLHLG
HLVPLLCLKRQAGHQPVALVGGATGLIGDPSFKAAERKLNTEETVQEW
VDKIRKQVAPFLDFDCGENSAIAANNYDWFNMNVLTFRLDIGKHFVSVNQ
MINKEAVKQRLNREDQGISFTEFSYNLLQGYDFACLNKQYGVVLLQIGGSD
QWGNITSGIDLTRRLHQNVFGLTVPLITKADGTFKFGTEGGAVWLDPKK
TSPYKFFYQFWINTADADVRYRFLKFFTFMSIEEINALEEEDKNSGKAPRAQ
YVLAEQVTRLVHGEEGLQAAKRITTECLFSGSLSALSEADFEQLAQDGVPM
VEMEKGADLMQALVDSSELQPSRGQARKTIASNAITINGEKQSDPEYFFKE
EDRLFGRFTLLRRGKKNYCLICWK

> P0C0T5|MEPA_ECOLI Penicillin -insensitive murein endopeptidase - Escherichia coli.

MNKTAIALALLASSASLAATPWQKITQPVPGSAQSIGSFSNGCIVGADT
LPIQSEHYQVMRTDQRRYFGHPDLVMFIQRLSSQVSNLGMGTVLIGDMGM
PAGGRFNGGHASHQTGLDVIDFLQLPKTRWTSQALLRPQALDLVSRDGKH
VVSTLWKPEIFSLIKLAAQDKDVTRIFVNPAAIKQQLCLDAGTDRDWLRKV
RPWFQHRAHMHVRLRCPADSLECEDQPLPPSGDGCQAEQSWFEPPKPGT
TKPEKKTTPPLPPSCQALLDEHVI

> EFG2_SYNY3 P74228 ELONGATION FACTOR G 2 (EF -G 2). - SYNECHO

MARTVPLERIRNIGIAAHIDAGKTTTTERILFYSGVVHKIGEVHEGTAVT
DWMQERERGITITAAAS TDWLGHHINI IDTPGHVDFTIEVERSMRVLD
GVIAVFCVGGVQVQSETVWRQAERYQVPRIAFVNKMDRTGANFFRVCQQ
IGDRLRANAVPVQIPIGSEAEFEGIVDLVRMAYLYKNDLGTDIQEVPI
IP DSVKDKTEEYRLRLVESVAEADDALMEKYLEGEELTADELVAGLRRGTIA
GTMVPVLCGSFAFNKGVQQLLLDAVVDYLPSPLEVPVPAIEGHLDPGEVATRP
AEDKAPLSALAFKVMADPFG RLTFVRVYSGVLEKGSYVLNSTKEKKERIS
RLIILKADDRIEVDQLNAGDLGAVLGLKDTLTGDTLCDDQEPILLES
LFFV PQPVISVAVEPKTKQDMDKLSKALQSLSEEDPTFRVSVDPETNQT
VIAGM GELHLEILVDRMLREFKVEANVGAPQVAYRETIRKAVQAEKGFIRQ
SGGK GQYGHVVIEVEPTEPPTGFEFVSKIVGGVIPKEYIAPSEQGMKEACASGV
LAGYPVIDLKATLVDSGFHDV DSSEMAFKIAGSMAIREAVGQADPVLL
EP VMKVEIEVPDDFMGNVIGDLNARRGHIEGQETEQGIKVAASVPLAEMFG
YATDIRSKTQGRGIFSMESHYAIEVPRNVAEIVAKSRGYA

> Q04064|OMP_BORPE Outer membrane porin protein BP0840 - Bordetella pertussis.

MKKTLAAALLAGFAGAAQAETSVTLYGIIDTGIGYNDVDFKVKGANADD
SDFKYNHSRFGMINGVQNGSRWGLRGTELDGDLQAVFQLES
GFNSGNGN SAQDGRLFGRQATIGLQSESWGRDLFGRQTNIA
SKYFGSIDPFGAGFGQA NIGMGMSAMNTVR
YDNMVMYQTPSYSGFQFGIGYSFSANDKDADAVNRVG
FATADNVRAITTLGRYVNGPLNVALSYDQLNASNNQAQGEV
DATPRSYGL GGSYDFEVVKKLALAYARTTDGWFGGQGYPVAVT
LPSGDKFGGFGVNTFAD

GFKANSYMVGLSAPIGGASNVFGSWQMVDPKLTGGDEKMNVFSLGYTYDL
SKRTNLYAYGSYAKNFALFLEDAKSTAVGVGIRHRF
> P0ABW7|FMS1_ECOLI CS1 fimbrial subunit A - Escherichia coli.
MKLKKTIGAMALATLAFATMGASAVEKTI SVTASVDPTVDLLQSDGSALPN
SVALTYSPAVNNFEAHTINTVVHTNDSKGVVVKLSADPVLNVNPTLQ
IPVSVNFAGKPLSTTGITIDSNDLNFASSGVNKVSSTQKLSIHADATRV
GGALTAGQYQGLVSIILTKST
> Q05092|XYLS2_PSEPU XylDLEGF operon transcriptional activator 2 -
Pseudomonas putida.
MSMTLVAEHYTKIIATKLETLSSNVSRRKGFVEGNPCFERVVQFIEENVK
RSISLEQLAELALMSPRSLYTMFEKHTGTTMNYIRNRKLECVRACLSNP
TTNIRSITEVALDYGFLHLGRFAEKYRSTFGELPSDTLSLHKMKCIDSRE
SSLSSLF
> Q06529|CYSD_CHRVI Cytochrome subunit of sulfide dehydrogenase -
Chromatium vinosum (Allochromatium vinosum).
MTQSTPRMLAASVLAALGLASNAGAEPTAEMLTNNCAGCHGTHGNSVGP
SPSIAQMDPMVFEVMEGFKSGEIASTIMGRIAKGYS TADFEKMAGYFKQ
QTYQPAKQSFDTALADTGAKLHDKYCEKCHVEGGKPLADEEDYHILAGQW
TPYLQYAMSDFREERRPMEKKMASKLRELLKAEGDAGLDALFAFYASQQ
> P72181|NIRS_PARPN Nitrite reductase - Paracoccus pantotrophus
(Thiosphaera pantotropha).
MRQRTPFARPGLLASAALALVLGLAASAQEQVAPPKDPAAALEDHKTRT
DNRYEPSLDNLAQQDVAAPGAPEGVSALSDAQYNEANKIYFERCAGCHGV
LRKGATGKALTPDLTRDLGFDYLSFTIYTGSPAGMPNWTSGELSAEQVD
LMANYLLDPAAPPEFGMKEMRESWKVHVAPEDRPTQQENDWDLENLFSV
TLRDAGQIALIDGATYEIKSVLDTGYAVHISRLSASGRYLFVIGRDGKVN
MIDLWMKEPTTVAEIKIGSEARSIEETSKMEGWEDKYAIAAGAYWPPQYVIM
DGETLEPKKIQSTRGMTYDEQEYHPEPRVAAILASHYRPEFIVNVKETGK
ILLVDYTDLDNLTTEISAERFLHDGGLDGSRYFITANARNKLVVIDT
KEGKLVAIEDTGGQTPHPGRGANFVHPTFGPVWATSHMGDDSVLIGTDP
EGHPDNAWKILDSFPALGGGSLFIKTHPNSQYLYVDATLNPEAEISGSVA
VFDIKAMTGDGSDPEFKTLPPIAEWAGITEGQPRVVQGEFNKDGTEVWFSV
WNGKDQESALVVDDKTLELKHVIKDERLVTPTGKFNVYNTMTDTY
> P0A9K9|SLYD_ECOLI FKBP -type peptidyl-prolyl cis-trans isomerase slyD -
Escherichia coli.
MKVAKDLVVSLAYQVTRTEGVLVDESPVSAPLDYLGHGSLISGLETALE
GHEVGDKFDVAVGANDAYGQYDENLVQRVPKDVFVGMVDELQVGMFLAET
DQGFVPEITAVEDDHV VVDGNHMLAGQNLKFNVEVVAIREATEEELAHG
HVHGAHDHHDHHDGCGGHHGHEHGEGCGGKNGGCGCH
> LPSA_PASHA Q05770 LPSA PROTEIN. - PASTEURELLA HAEMOLYTICA.
MNNYVISLTSAQERRKHIEAEFGKQNI PFQFFDAITPDLIKEKAKAFNID
ISNTNLTKEGIACALSHIALWHLAKQQLDYICIFEDDIYLGNNAFELK
TNYIPENTHIVK LETLPFDRINRFNKTEKYILNRRLFKLNSRHVGTAGYI
LTNKGAEFLINILKTLNIPIDDLIFDEYLKIKEYKVLQMSPALCVQDFIL
NSKTNFKSSLQDDRAIRCNNEDKIKNQAKLKKPNYFLTKIQKELYRPFKQ
LKQKVFTTYITFK
> P44430|DEOC_HAEIN Deoxyribose -phosphate aldolase - Haemophilus influenzae.
MTSNQLAQYIDHTALTAEKNEQDI STLCNEAIEHGFYSVCINSAYIPLAK
EKLAGSNVKICTVVGFPPLGANLTSVKAFETQESIKAGANEIDMVINVGWI
KSQKWDEVKQDIQAVFNACNGTPLKVILETCLLTKDEIVKACEICKEIGV
AFVKTSTGFNKGATVEDVALMKNTVGNIGVKASGGVRDTETALAMIKAG
ATRIGASAGIAIISGTQDTQSTY
> P12267|FM3_KLEPN Fimbrial subunit type 3 - Klebsiella pneumoniae.
MKKVLLSAAMATAFFGMAAANAADTNVGGGQVNFVGGKVTDSCTVSVNGQ
GSDANVYLSPVTLTEVKAAAADTYLKPFSFTIDVSDCQAADGKQDDVSK
LGVNWTGGNLLAGATAKQQGYLANTEAAGAQNIIQLVLDSTDNATALTNKII
PGDSTQPKAAGDASAVQD GARFYYVGYATSTPTT VTTGVVNSYATYEIT
YQ
> P0C1C0|PEL1_ERWCA Pectate lyase 1 - Erwinia carotovora.
MKYLLPSAAAGLLLLAAQPTMAANTGGYATTDGGDVSGAVKKTARSLQEI
VDIIEAAKDKSSGKAVKGGAYPLVITYNGNEDALIKAAEANICGQWSKDP
RGVEIKEFTKGITILGTNGSSANFGIWMVNSNVVVRNMRFGYMPGGAKD
GDAIRIDNSPNVIDHNEIFAKNFECAGTPDNDTTFESAVIDIKKATNVT

VSYNYIHGVKVKVGLSGSNTDTGRDLT YHHNIYSVNSRLPLQRGGKVHA
YNNLYDGIKSSGFNVQRQKIALIESNWFENALNPVTARNDSDNFGTWELR
NNNITSPSDFAKYKITWQKPSSTPHINADDWKSTGKFPVAVPYSYSPVSAQC
VKDKLASIYAGVGNLAVLTAANCK

> P75948|THIK_ECOLI Thiamine kinase - Escherichia coli.

MPFRSNNPITRDELLSRFFPQYHPVTFNNSGLSGGSFLIEHQGRFVVR Q
PHDPDAPQSAFLRQYRALSQLPACIAPKPHLYLRDWMVVDYLPGAVKTYL
PDTNELAGLLYLLHQQPRFGWRITLLPLELEYWQQSDPARRTVWLRMLK
RLRKAREPRPLRSLPLHMDVHAGNLVHSASGLKLI DWEYAGDGDIALELA
AVWVENTEQHRQLVNDYATRAKIYPAQLWRQVRRWFPWLLMLKAGWFEYR
WRQTGDQQFIRLADDTWRQLLIKQ

> P10641|OPPI2_HAEIN Oute r membrane protein P1 - Haemophilus influenzae.

MKKFNQSLLATAMLLAAGGANAAAFQLAEVSTSGLGRAYAGEAAIADNAS
VVATNPALMSLFKTAQFSTGGVYIDSRINMNGDVTSYAQIITNQIGMKAI
KDGSASQRNVVPGAFVFNLYFVAPVNDKFALGAGMNVNFKLSEYDDSYD
AGVFGGKTDLSAINLNLGAYRVTEGLSLGLGVNAVYAKAQVERNAGLIA
DSVKDNQITSALSTQQEPFRDLKYLPSKDKSVVSLQDRAAWGFGWNAGV
MYQFNEANRIGLAYHSKVIDDFADRTATSLEANVIKEGKKNLFTTLPDY
LELSGFHQLTDLKLAHVHYSKYTHWSRLTKLHASFEDGKKAFFDKELQYSNN
SRVALGASYNLYEKLTLRAGIAYDQAASRHHRSAAIPTDRTWYSLGATY
KFTPNLSVDLGYAYLKGKKVHFKEVKTIGDKRTLTLNNTANYTSQAHANL
YGLNLNYSF

> P55995|LON_HELPY ATP-dependent protease La - Helicobacter pylori
(Campylobacter pylori).

MTEDFPKILPLLVEEDTFLYPFMIAPIFLQNNASIKAVAYAKNNKSLVFI
ACQKDKLNDNEAPYDVGVIQSVMREANMPNGRVKLLFNIGIAKGRILEPA
KENEQGFLEAQISPIEYLEYDKENIQAIVEVLKEKVI TLANVSSLFPPDL
IKALEDNDDPNRIADLIAAALHLKDKQAYS LFANNNTEQRLDLIDIVIE
ETKTQKLEIKPKSVHVKMEQTNKEYFLKEQLKQIQKELGTDKQRDEDLN
QYQKLESIKPFLKEEAFKEIKKQIDRLSRTHADSSDSATLQNYIETMLD
VPPGQYGGKALDIKHVREQLDKDHYS LKRPKERIVEYFATMQLLEMRRKK
KPEKKDKTKGTILCFYGGPGVGTSLANSIAKAIERPLVRIALGGLEDVN
ELRGHRTYIGSMPGRIVQGLIEAKMNPVMVLDEIDKVDRSVRGPASA
LLEILDPEQNTAFRDHYANFSIDLSQVIFIATANNIDRI PAPLRDRMEFI
SVSSYTPNEKEEIAKNYLIPQELEKHALKPSEVEI SHECLKLIIKEYTRE
AGVRDLRRQIATIMRKVALKYLEDNPHQKGRTKKGNKESDQKSEDQKS
ENQKSENKDFCVSITPNNLKEYLERMVFEIDPIDEENKIGIVNGLAWTPV
GGDVLKIEVLKIRGKELKLTGSLGDMKESAI IAFSVVKVLLDNETLKV
PKIPSETDAEGKKKKVLKVYNAYDLHLHVPEGATPKDGP SAGIAMASVM
ASILCDRATRSEVAMTGETLTSGEVLP IGGKELKLI AAFKAGIKTALIPV
KNYERDLDEIPAEVRENINIVAVKNIAEVLEKTL

> P04979|TOX3_BORPE Pertussis toxin subunit 3 - Bordetella pertussis.

MLINNKLLHHILPILVLALLGMRTAQAVAPGIVIPPKALFTQQGGAYGR
CPNGTRALTVAELRGNAELQTYLRQITPGWSIYGLYDGTYLQAYGGI IK
DAPPGAGFIYRETFCITTIYKTGQPAADHYYSKVTATRLLASTNSRLCAV
FVRDQSVIGACASPYEGRYRDMYDALRRLLYMIYMSGLA VRVHVSKEEQ
YYDYEDATFQTYALTGISLCNPAASIC

> P27369|CYSR_SYNP7 Regulatory protein cysR - Synechococcus sp. (strain PCC
7942) (Anacystis nidulans R2).

MVREPASTLLPPTSPATPAPHRLLI GRRGMVPTGANVIWKIQSGLVRSST
WGEEGDMISLGLWPGDLIGRPLSCLDPYELECLTAVEVVAVSDPALESH
ESLVRSLRYTERLLSITRLRRAEAKLASLLGWIGERFGQPGATGWEIDLR
RIPLTHQVIAELSGSTRVTTTRLLGE FRQAGRIHRRDRALIVRYPETLYP
PARLSA

> BTUR_SALTY P31570 COB(I)ALAMIN ADENOSYLTRANSFERASE (EC 2.5.

MSDERYQQRQKVKDRVDARVAQAQEERGIIIVFTGNGKGTAAAFGTAA
RAVGHGKNVGVVQFIKGTWPNGERNLLEPHGVEFQVMATGFTWETQNREA
DTAACMAVWQHGRMLADPLDMVVLDELTYMVAYDYLPLEEVISALNAR
PGHQTVIITGRGCHRDILDLADTVSELRPVKHAFDAGVKAQMGIDY

> P05818|BMAE_ECOLI M-agglutinin - Escherichia coli.

MNLKKAIAIASSVFAITMALTCHAVTVTATHTVESDAEFTIDWVDAGPTT
TDAKDGEVWGHLDMTQTRGTPFTFGKLRNPQGETSPGPKAPFSFTGPDGH
TARAYLDSYGAPIHNYAGDNLANGVKVGSNGTFFVVG TASRLTARIFG

DQTLVPGVYRTT FELTTWTD
> P15279|DHM1_METOR Methanol dehydrogenase subunit 1 - Methylobacterium organophilum XX.
MSRFVTSVSALAMLALAPAALSSVAYANDKLVLSKSDDNWVMPGKNYDS
NNYSELKQVNSNVKQLRPAWTFSTGLLNGHEGAPLVVDGKMYVHTSFPN
NTFALDLDLDPGHILWQDKPKQNPAARAVACCDLVNRGLAYWPGDGKTPAL
ILKTQLDRHVVALNAETGETVWKVENS DIKVGSTLTIAPYVVKDKVI IGS
SGAELGVRGYLTAYDVKTGGQVWRAYATGPDKDLLLADDFNVKNAHYGQK
GLGTATWEGDAWKIGGGTNWGWYAYDPGTNLIYFGTGNPAPWNETMRPGD
NKWTMTIFGRDADTGEAKFGYQKTPHDEWDYAGVNVMPSEQKDKDGKTR
KLLTHPDRNKIVYVTLDRDGDALVSANKLDDTVNVFKTVDLKTGPVRDPE
YGTRMDHLAKDVCLPSAMGYHNQGHDSYDPKRELEFFMGINHCMDWEPFML
PYRAGQFFVGATLNMYPGPKGDRQNYEGLGQIKAYNAITGSYKWEKMERF
AVWGGTLATAGDLVFGYGLDGYLKARDSDTGDLWKFKIPSGAIGYPMTY
THKGTQYVAIYYVGGWPGVGLVFDLADPTAGLGAVGAFKLANYTQQGG
GVIVFSLDGKGPYDDPNVGEWKSASK
> P09373|PFLB_ECOLI Formate ace tyltransferase 1 - Escherichia coli.
MSELNEKLATAWEGFTKGDWQNEVNRDFIQKNYTPYEGDESFLAGATEA
TTTLWDKVMMEGVKLENRTHAPVDFDTAVASTITSHDAGYINKQLEKIVGL
QTEAPLKRALIPFGGIKMIIEGSCAYNRELDPMIKKIFTEYRKTHNQGVF
DVYTPDILRCRKSGLVLTGLPDAYGRGRIIGDYRRVALYGLIDYLMKDKLAQ
FTSLQADLENGVNLEQTIRLREEIAEQHRALGQMKEMAAYGYDISGPAT
NAQEAIQWTFYGYLAAVKSQNGAAMSFGRTSTFLDVYIERDLKAGKITEQ
EAQEMVDHLVLMKLRMVRFLRTPYDELFSGDPIWATESIGGMGLDGRTL
TKNSFRFLNTLYTMGSPSEPNMTILWSEKLPNFKKFAAKVSIDTSSLQY
ENDDLMPDPFNDDYAIACCVSPMTVKGQMQFFGARANLAKTMLYAINGG
VDEKLMQVGPKESEPIKGDVNLNYDEVMERMDHFMWDLAKQYITALNIIHY
MHDKYSYEASLMALHHRDVRTMACGIAGLSVAADSLSAIKYAKVKPIRD
EDGLAIDFEIEGEYQFGNNDPRVDDLAVDLVERFMKKIQKLTHTYRDAIP
TQSVLTIITSNVVYGKKTGNTPDGRRAGAPFGPGANPMHGRDQKGAVASLT
SVAKLPPFAYAKDGISYTFISIVPNALGKDDEVKTNLAGLMDGYFHHEASI
EGGQHLNVNVMNREMLL DAMENPEKYPQLTIRVSGYAVRFNLSLTKEQQQD
VITRTFTQSM
> P13810|E2AA_ECOLI Heat-labile enterotoxin IIA, A chain - Escherichia coli.
MIKHVLLFFVFI SFVSANDFFRADSRTPEIRRAGGLPRGQQEAYERG
TPININLYEHARGTVTGNTRYNDGYVSTTVTLRQAHLIGQNILGSYNEYY
IYVVAPAPNLFVNGVLGRYSPYSENEFAALGGIPLSQIIGWYRVSFGA
IEGGMQRNRDYGDLFRGLTVAPNEDGYQLAGFSPNFPAPWREMPWSTFAP
EQCVPNNKEFKGGVCISATNVLSKYDLMNFKLLKRRLLALTFMSEDDFI
GVHGERDEL
> P0A9L3|FKBB_ECOLI FKBP-type 22 kDa peptidyl-prolyl cis-trans isomerase - Escherichia coli.
MTTPTFDITIEAQASYGIGLQVGQQLSESGLEG LLPEALVAGIADALEGKH
PAVPVDVVRALREIHERADAVRRQRFQAMAAEGVKYLEENAKKEGVNST
ESGLQFRVINQGEAIPARTDRVRVHYTGKLIDGTVFDSSVARGEPAEFP
VNGVIPGWIEALTLMPVGSKWELTIPQELAYGERGAGASIPPFSTLVFEV
ELLEIL
> P19250|HLY2_VIBPA Thermostable direct hemolysin 2 - Vibrio parahaemolyticus .
MKYRYFAKKSFLFISMLAAFKTFAFELPSVFPFPAPGSDEILFVVRDITFN
TNAPVNVEVSDFWTNRNVKRKPYKDVYQSVFTTSGTKWLT SYMTVNIND
KDYTMAAVSGYKHGHSVAVFKSDQVQLQHSYDSVANFVGEDEDSIPSKMY
LDETPEYFVNVEAYESGSGNILVMCISNKESFFECKHQQ
> P0A432|PSBO_SYNEN Photosystem II manganese-stabilizing polypeptide - Synechococcus elongatus naegeli.
MKYRILMATLLAVCLGIFSLSAPAFAAKQTLTYDDIVGTGLANKCPTLDD
TARGAYPIDSSQTYRIARLCLQPTTFLVKEEPKNKRQEAFFVPTKLVTRE
TTSLDQIQGELKVNSDGSLTFVEEDGIDFQPVTVMAGGERIPLLFVKN
LVASTQPNVTSITSTDFKGEFNVPSYRTANFLDPKGRGLASGYDSIAL
PQAKEEELARANVKRFSLTGQISLNVAKVDGRGTGEIAGTFESEQLSDDD
MGAHEPHEVKIQGVFYASIEPA
> P45175|RNG_HAEIN Ribonuclease G - Haemophilus influenzae.
MDAVELLMNVTNPNETRIALVETGMLREVHIERQAKRGIVGNIYKGRVTRV

LPGMQSAFVDIGLEKAAFLHAADIVSHTECDENEQKQFKVKSISELVRE
GQDIVVQVVKEPLGTKGARLTTDITLPSR HLVFMPENSHVGVSQRIESEE
ERARLKALVEPFCDELGGFIIRTATEGASEEELRQDAEFLKRLWRKVLER
KSKYPTKSKIYGEFALPQRILRDFIGTNLEKIRIDSKLFCGEVKEFTDEF
MPELSDKLVLYSGNQPIFDVYGVENAIQTALDKRVNLKSGGYLIIIEQTEA
MTTIDINTGAFVGHNRNLEETIFNTNIEATKATAHELQLRNLGGIIIIIDFI
DMQTDEHRNRVLQSLCDALSKDRMKTNVNG FTQLGLVEMTRKRTRESLEH
VLCDECEPTCHGRGRVKTIVETVCYEIMREIIRVYHLFSSEQFVVYASPAVS
EYLINEESHGLLPEVEMFIGKRVKVKTEQFYNQEQFDVVVM
> P27458|PRLB_ACHLY Beta -lytic metalloendopeptidase - *Achromobacter lyticus*.
MKKISKAGLGLALVCALATIGGNAARRATAQRRGSGVFYDEMFFDIDAH
LAKHAPHLHKHSEE ISHWAGYSGISRSVDRADGAAERAVTPSARRIVRSA
SWRAPTASARRPARSRWRCASRCTSAIPTRQGAGDAGPRQSAAGAVRAFR
RQRAGGRAARRRRVPAGLRPPVQRTAPGQGGFGPLRQGRPGRAAVSPNGL
LQFFPFRGASWHVGAHTNTGSGNYPMSLDMRGGGWSNQNGNWSAS
AAGSFKRHSSCFAEIVHTGGWSTTYHLMNIQYNTGANVSMNTAIANPAN
TQAQALCNGGQSTGP HEHWSLKQNGSFYHLNGTYLSGYRITATGSSYDTN
CSRFFYLTKNGQNYCYGYVNPVPN
> Q47945|CYCA_GLUOX Alcohol dehydrogenase cytochrome c subunit -
Gluconobacter oxydans (Gluconobacter suboxydans).
MLNALTRDRLVSEMKGWKLAAAIGLMAVSFGAAHAQDADEALIKRGEYV
ARLSDCIACHTALHGQPYAGGLEIKSPIG TIYSTNITPDPEHGIGNYTL
DFTKALRKGIRKDGATVYPAMPYPEFARLSDDDIRAMYAFFMHGVPVAL
QNKAPDISWPLSMRWPLGMWRAMFVPSMTPGVDKSIDPEVARGEYLVNG
PGHCGECHTPRFGMQVKAYGTAGGNAYLAGGAPIDNWIAPSLRSNSDTG
LGRWSEDDIVTFLKSGRIDHSAVFGMADVVAYSTQHWSDDDLRAKAYL
KSMFAVPEGKNLGQDDGQTTALLNKGQGN AGAEVYLHNCAICHMNDGTG
VNRMFPLAGNPFVITDDPTSLANVAVFGGILPPTNSAPSAVAMPGFKNH
LSDQEMADVNFMRKGGWGNAPGTVSASDIQKLRTTGAPVSTAGWNVSSK
GWMAYMPQPYGEDWTFSPQTHTGVDDAQ
> P0AEG6|DSBC_ECOLI Thiol:disulfide interchange protein dsbC - *Escherichia coli*.
MKKGFMLFTLLAAFSGFAQADDA AIQQTAKMGIKSSDIQPAPVAGMKT
LTNSGVLYITDDGKHIIQGPYDVSQTAPVNVTKMLLQNLNALEKEMIV
YKAPQEKHVITVTFDITCGYCHKLHEQMADYNALGITVRYLAFPRQGLDS
DAEKEMKAIWCAKDKNAFDDVMAGKSVAPASCDVDIADHYALGVQLGVS
GTPAVVLSNGTLVPGYQPPKEMKEFLDEHQKMTSGK
> P50286|ASPG_WOLSU L-asparaginase - *Wolinella succinogenes*.
MAKPQVTILATGGTIAGSGESSVKSSYSAGAVTVDKLLAAVPAINDLATI
KGEQISSIGSQEMTGKVLKLAKRVNELLAQKETEAVIITHGTDTEETA
FFLNLTVKSQKPVVLVGMAMRSGSSMSADGPMNLYNAVNVAINKASTNKG
VIVMDEIHAAREATKLNTTAVNAFASPNTGKIGTVYYGKVEYFTQSVRP
HTLASEFDISKIEELPRVDILYAHPPDDTD VLVNAALQAGAKGIIHAGMGN
GNPFPPLTQNALEKAAKSGVVVARSSRVGSGSTTQEAQVDDKKLGFVATES
LNPQKARVLLMLALTKTSDREAIQKIFSTY
> P39176|ERFK_ECOLI Protein erfK/srfK - *Escherichia coli*.
MRRVNILCSFALLFASHTSLAVTYPLPEGSRLVVGQSFVTVDPDHTQPL
ETFAAQYQGGLSNMLEANPGADVFLPKSGSQTIPQQLILPDT VRKGIVV
NVAEMRLYYYPDSNTVEVFPFIGIGQAGRETFRNWTTVRERKQEAFTWTP
TPNTRREYAKRGESLPAFVPAGPDNPMGLYAIYIGRLYAIHGNTANFGIG
LRVSQGCIRLRNDDIKYLFDNVVPVGTQVQIIDQPVKYTTEPDGSNWLEVH
EPLSRNRAEYESDRKVPLPVTPLSLRAFINGQEVNVRANAALQRRSGMPV
QISSGSRQMF
> P24251|CRL_ECOLI Sigma factor -binding protein crl - *Escherichia coli*.
MTLPSGHPKSRLIKKFTALGPYIREGKCKDNRRFFDCLAVCVNVKPAPEV
REFWGWMELEAQESRFTYSYQFGLFDKAGDWKQVVKDTEVVERLEHTL
REFHEKLRRELLTTLNLKLEPADDFRDEPVKLT
> P13429|SFAG_ECOL5 S-fimbrial adhesin protein sfaG - *Escherichia coli*
O6:K15:H31 (strain 536 / UPEC).
MVKDIIKTVTFSCMLAGSMFVTCHVCAAGSVVNITGNVQDNTCDVDINSR
NFDVSLGSYDSRQFTAAGDTPASVFHVGLTSCGSAVRAVKLTFTGTPDN
QEAGLIQINSINGARGVGIQLLDKDKHELKINVPTTIALMPGTQTIAFYA
RLKATYLPVKAGNVDAVNVFVLDYQ

> P14283|PERT_BORPE Pertactin - Bordetella pertussis.

MNMSLSRIVKAAFLRRRTTLAMALGALGAAPAAHADWNNQSIVKTGERQHG
IHIQSDPGGVRTASGTTIKVSGRQAQGILLENPAEELQFRNGSVTSSGQ
LSDDGIRRFGLTIVTKAGKLVADHATLANVGDWDDDGIALYVAGEQAQA
SIADSTLQGAGGVQIERGANVTVQRSAIVDGGHLHIGALQSLQPEDLPPSR
VVLDRDNTVAVPASGAPAAVSVLGASELTDGGHITGGRAAGVAAMQGAV
VHLQRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPGGFGPVLDGWYGV
SGSSVELAQSSIVEAPELGAAIRVGRGARVTVSGGSLSAPHGNVIETGGAR
RFAPQAAPLSITLQAGAHAQKALLYRVLPEPVKLTTLTGGAQAQGDIVAT
ELPSIPGTSIGPLDVALASQARWTGATRAVDSLSDNATVWMTDNSNVGA
LRLASDGSVDFVQPAEAGRFKVLTVNTLAGSGLFRMNVFADLGLSDKLVV
MQDASGQHRLLWRNSGSEPASANTLLLVQTPLGSAATFTLANKDGKVDIG
TYRYRLAANGNGQWSLVGAKAPPAPKAPQPGPQPQPQPQPEAPAPQP
PAGRELSAANAANTGGVGLASTLWYAESNALSRLGELRLNPDAGGAW
GRGFAQRQQLDNRAGRFRDQKVAGFELGADHAVAVAGGRWHLGGLAGYTR
GDRGFTGDGGGHTDSVHVGGYATYIADSGFYLDATLRASRENDFKVAGS
DGYAVKGYRTHGVGASLEAGRRFTHADGWFLPEQAE LAVFRAGGGAYRA
ANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPYIKASVLQEFDGAG
TVHTNGIAHRTELGRTRAE LGLGMAAALGRGHSLYASYEYSKGPKLAMPW
TFHAGYRYSW

> CILB_HAEIN P44460 CITRATE LYASE BETA CHAIN (EC 4.1.3.6) (AC

MKLRRSMLFVPGNSAAMLSNSFIYKPD SIMFDLE DAVALKEKDSARLLVA
HALQHPLYKEIETVVRVNPLDSEFGLLDLNSVVRAGVDVVRMPKTESAQD
VLDMDHAITEIEKACGREAGSTKMLAAIESPLGITQANQIAFASKRLIGI
ALGAEDYVRNLKTERSPEGIELLFARCSILQAARAAGIQAFDTVYSNANN
EEGFLKEAALIKQLGFDGKSLINPRQIELLHNLFAPTQKDVEQAKRIIEA
AVEAERQAGVVS LNKMIDAPIIDRAKLVLERAK SGIREE

> Q00971|NPRV_VIBPR Neutral protease - Vibrio proteolyticus (Aeromonas
proteolytica).

MNKTQRHINWLLVAATALPVTAEMINVNDGSLNQAQSQSVAPV
ETGFKQMKRVVLPNGKVKVRYQQTHHGLPVFNTSVVATESKSGSSEVFGV
MAQGIADDVSTLTPS VEMKQAISIAKSRFQQQEKMVAEPATENEKALMV
RLDDNNQAQLVYLVDFFVAEDHPARPFFFIDAQTGEVLQTDWGLNHAQAD
GTGPGGNTKTGRYEYGSDFPPFVIDKVGTKCSMNNSAVRTVDLNGSTSGN
TTYSYTCNDSTNYNDYKAINGAYSPLNDAH YFGKVVFDYKDWMTTPTLT
FQLTMRVHYGNNYENAFWNGSSMTFGDGYSTFYPLVDINVS AHEVSHGFT
EQNSGLVYENMSGGMNEAFSDIAGEAAEFYMKGSVDWVVGADIFKSSGGL
RYFDQPSRDGRSIDHASDYNGLNHVHYSSGVFNRAFYLLANKAGWDVRKG
FEVFTLANQLYWTANSTFDEGGCGVKAASDMGYSVADVEDAFNTVGVNA
SCGATPPPSGDVLEIGKPLANLSGNRNDMTYYTFTPSSSSSVVIKITGGT
GDADLYVKAGSKPTTTSYDCRPYKYGNEEQCSISAQAGTTYHVMLRGYSN
YAGVTLRAD

> P02970|FMKB_ECOLI K88 fimbrial protein AB - Escherichia coli.

MKKTLLIALAIAASAASGMHAWMTGDFNGSVDIGGSITADDYRQKWEWKV
GTGLNGFGNVLNLDL TNGGTKLITVTGNKPILLGRTKAEAFATPVSGGVDG
IPQIAFTDYEGASVKLRNTDGETNKGLAYFVLPKNAEGTKVGSVKVNAS
YAGVFGKGGVTSADGELFSLFADGLRAIFYGGLTTTTVSGAALTS GSAAAA
RTELFGLSRNDILGQIQRVNANITSLVDVAGSYREDMEYT DGTVVSAAY
ALGIANGQTI EATFNQAVTTSTQWSAPLNVAITYY

> P33590|NIKA_ECOLI Nickel-binding periplasmic protein - Escherichia coli.

MLSTLRRTLFALLACASFIVHAAAPDEITTAWPVNVGPLNPHLYTPNQMF
AQSMVYEPLVKYQADGSVIPWLAKSWTHSEDGKTWTFTRDDVKFSNGEP
FDAEAAAENFRAVLNDRQRHAWLELANQIVDK ALSKTELQITLKSAYYP
FLQELALPRPFRFIAPSQFKNHETMNGIKAPIGTGPWILQESKLNQYDVF
VRNENYWGKPAIKKITFNVIPDPTTRAVAFETGDIDLLYGNGLPLDT
FARFSQNPAYHTQLSQPIETVMLALNTAKAPTNELAVREALNYAVNKKSL
IDNALYGTQQVADTLFAPSVPYANLGLKPSQYDPQKAKALLEKAGWTLPA
GKDIREKNGQPLRIELSFITDALS KSMAEIIQA DMRQIGADVSLIGEEE
SSIYARQRDGRFGMIFHRTWGAPYDPHAF LSSMRVPSHADFQAQQLADK
PLIDKEIGEVLATHDETQRQALYRDILTRLHDEAVYLPISYISMMVSKP
ELGNIPYAPIATEIPFEQIKPVKP

> P00154|CYCP_CHRVI Cytochrome c' - Chromatium vinosum (Allochro
matium vinosum).

MKHVLASTAAGLMLGLASSAIAAGLSPEEQ IETRQAGYEFMGWNMGKIK
ANLEGEYNAAQVEAAAANVIAAIANS GMGALYGP GTDKNVGDVKTRVKPEF
FQNMEDVVGKIAREFVGAANTLAEVAATGEAEAVKTAFGDVGAAACKSCHEK
YRAK

> P28581|PHOC_MORMO Major phosphate -irrepressible acid phosphatase -
Morganella morganii (Proteus morganii).

MKKNI IAGCLFSLFSLSALA AIPAGNDATTKPDLYYLKNQ AIDSLKLLP
PPPEVGS IQFLNDQAMY EKGRMLRNTERGKQAQADADLAAGGVATAFSGA
FGYPITEKDSPELYKLLTNMIEDAGDLATRS AKEHYMRIRPF AFYGTETC
NTKDQKKLSTNGSYPSGHTSIGWATALVLA EVNPNANQDAILERGYQLGQS
RVICGYHHWQSDVDAARIVGSAAVATLHSDPAFQAQLAKAKQEFQAQSQK

> Q99289|HLT_VIBPA The rmolabile hemolysin - Vibrio parahaemolyticus.

MMKKTITLLTALLPLASAVAEEPTLSPMVSA SEVISTQENQTYTYVRCW
YRTSYSKDDPATDWEWAKNEDGSYFTIDGYWSSVSFKNMFYTNTSQNVI
RQRCEATLDLANENADITFFAADNRFSYNHTIWSNDAAMQPDQINKVVAL
GDSLSDTGNIFNASQWRFPNPN SWFLGHFSNGFVWTEYIAKAKNLP LYNW
AVGGAAGENQYIALTGVGEQVSSYLTYAKLAKNYKPANTLFTLEFGLNDF
MNYNRGVPEVKADYAEALIRLTDAGAKNFMLMTLPDATKAPQFKYSTQEE
IDKIRAKVLEMN EFIKAQAMYYKAQGYNITLFDTHALFETLTSAP EEHGF
VNASDPCLDINRSSVDYMYTHALRSECAASGA EKFFVFDVTHPTTATHR
YVAEKMLESSNNLAEYRF

> P0A7A5|PIMT_ECOLI Protein -L-isoaspartate O-methyltransferase -
Escherichia coli.

MVSRRVQALLDQLRAQGIQDEQVLNALA AVPREKFVDEAFEQKAWDNIAL
PIGQGQTI SQPYMVARMTELLELTPQSRVLEIGTGSGYQTAILAHLVQHV
CSVERIKGLQWQARRRLKNL DLHNVSTRHGDGWQGWQARAPFD AIIIVTAA
PPEIPTALMTQLDEGGILVLPV GEEHQYLKRVRRRGGEFIIDTVEAVRFV
PLVKGELA

> Q55187|SYFA_SYNY3 Phenylalanyl -tRNA synthetase alpha chain -
Synechocystis sp. (strain PCC 6803).

MTISLEADLKS LQQSAQA AISGCDDLDGLDKLRVQYLGKKGELS LILKGM
GKLSAEERPKFGAI ANEVKEALQHDLESRKANLQNA AIEAQLAAETLDVT
MAGSYRPQGRRHPLNSTVDRVLDIFVGLGYTVATGPQVETDY NFEALNI
PADHPARDMQDTFFLKDGRLLRTH TSPVQIRYMEKHDPPIRIVAPGRVYR
RDTVDATHSAVFHQV ELLAIDKGLAFTHLKG TIQAFIKQMFGEALPIRFR
ASYFPFTEPSAEVDVQWQGWLEVMGCGMVDPNVMEAVGYDPEVYTGFAA
GFGVERFAMVLHQIDDIRRLYN SDLRFLRQF

> P16454|AIL_YEREN Attachment invasion locus protein - Yersinia
enterocolitica.

MKKTLLASSLIACLSIASVNVYAASESSISIGYAQSHVKENGYTL DNDPK
GFNLKYRYELDDNWGVIGSFAYTHQGYDFYGSNKFGHGDVDYYSVTMGP
SFRINEYVSLYGLLGA AHGKVKASVFDESISASKTSMAYGAGVQFNPLPN
FVIDASYEYSKLD SIKVGTWMLGAGYRF

> P44398|XYLA_HAEIN Xylose isomerase - Haemophilus influenzae.

MTTYFDKIEKISFEGEKSTNPF AFKHVDANQVILGKTM AEHLRLAVCYWH
TFCWNGNDMFGLSLERSWQKNSNLLAGAEQKADIAFEFLNKLGV PYYCF
HDVDIAPEGNSVREYVQNFHHIVDIL ERKQVETGVKLLWGTANCFTNPRY
MSGAAATNP NPEVFAWAATQVF NAMNATQRLGGENYVLWGGREGYETLLNT
DLKREREQIGRFMQMVVEHKKHIGFKG TLLIEPKPQEP TKHQYDYDVATV
YGFLKQFGL EKEIKVNI EANHATLAGHTFQHEIATACALDIFGSIDANRG
DPQLGWDTDQFPNSVEENTLVMYEILKHGGFTTGGFNFD AKIRRSIDPY
DLFYAHIGAIDVLLSLKRAAKMLQEETLQKIVNERYAGWNS ELGQHILQ
GKTSLETLAQLVQQKDLAPKPVSGQQEYLENLVNQVIYS

> Q05918|IPHP_NOSCO Tyrosine -protein phosphatase - Nostoc commune.

MKTHHANLALALMLGLSSSATAVAADAPQAVATKAAAPNVK PVAADAHGV
IPDGAPGMCARSPACRATAIPADAFVRTADLGR LTDADR DALAALGVKLD
IDLRTADEEAQSPDLLARDDRFDYQRISLMGTEKMDLQKMMTSFPDSLGE
AYVQWLGH SQPQFKQVFQRIAAQQDGAVLFHCTAGKDR TGI IAGLLDLA
GVPKAEIVHNYAISAHYLEGQPKDS DERADHGAGQAEPGDRPQDGGHGRY
RAGQHGAVALAALHSQYGGAEGLK SIGVSEQEIQLKVR LGQAG

> P42195|PECS_DICD3 HTH -type transcriptional regulator pecS - Dickeya
dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937)).

MARYLEVSDIVQQWRNERPDL DVEPMLVIGTL SRVSL LIDRALDKVFSKY

KLSAREFDILATLRRRGAPYAYSQIVNA LMINNSTLTSRLDRLEQAGW
LRRMPIEGDRRSVNIQLTDEGFALINRVVEEHVENERDILSPFSEEEKTH
LRALLGRVEKHLVNNR

> P24474|NIRS_PSEAE Nitrite reductase - *Pseudomonas aeruginosa*.

MPFGKPLVGTLLASLTLGLATAHAKDDMKAAEQYQGAASAVDPAHVVRT
NGAPDMSESEFNEAKQIYFQRCAGCHGVLRKGGATGKPLTPDITQQRGQQY
LEALITYGTPLGMPNPGSSGELSKEQITLMAKYIQHTPPQPEWGMPEMR
ESWKVLVVKPEDRPPKQLNDLDPNLFVTLRDAGQIALVDGDSKKIVKVI
DTGYAVHISRMSASGRYLLVIGRDARIDMIDLWAKEPTKVAEIKIGIEAR
SVESKFKGYEDRYTIAGAYWPPQFAIMDGETLEPKQIVSTRGMTVDTQT
YHPEPRVAAIASHEHPEFIVNVKETGKVLVNYKIDIDLTVTSIGAAPF
LHDGGWDSHRYFMTAANNNSKVAVIDSKDRRLSALVDVGKTPHPGRGAN
FVHPKYGPVWSTSHLGDGSIISLIGTDPKNHPQYAWKKVAELQGGGSLF
IKTHPKSSHLYVDTTFNPDARISQSVAVFDLKNLDAKYQVLPVIAEWADLG
EGAKRVVQPEYNKRGEVWFVWNGKNDSSALVVVDDKTLKLVKAVKDP
LITPTGKFNVTQHVDY

> P0A433|OPD_FLAS2 Parathion hydrolase - *Flavobacterium* sp. (strain ATCC 27551).

MQTRRVVLKSAAGTLLGGLAGCASVAGSIGTGDRINTVRGPITISEAG
FTLTHEICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRARAAGVRTIVD
VSTFDIGRDVSLLAEVSRADVHIVAAATGLWFDPLSMRLRSVEELTQFF
LREIQYGIEDTGIRAGIIVKATTKATPFQELVLKAAARASLATGVPVTT
HTAASQRDGEQQAIFESEGLSPSRVCIGHSDTDDLSYLTALAARGYLI
GLDHIPHSIAIGLEDNASASALLGIRSWQTRALLIKALIDQGYMKQILVSN
DWLFGFSSYVTNIMVMDRVNPDGMAFIPLRVIFPFLREKGVQETLAGIT
VTNPARFLSPTLRAS

> P0A282|PTH_SALTI Peptidyl -tRNA hydrolase - *Salmonella typhi*.

MAIKLIVGLANPGAEEAATRHNAAGAWYVDL LAERLRAPLREEPKFFGYTS
RITLEGEDVRLVPTFMNLSGKAVGAMASFYRIQPDEILVAHDELDP
GVAKFKLGGGHGHNGLKDIISKLGNNPNFHRLRVGIGHGDKNKVVGFV
LGKPPVSEQKLIDEAIDEAARCTELWFKEGLAKATSR LHTFKAQ

> P14005|PELP_PECCC Periplasmic pectate lyase - *Pectobacterium carotovorum* subsp. *carotovorum* (*Erwinia carotovora* subsp. *carotovora*).

MKRFALSLLAGLVALQASAATPDRLTIVNQYVDNVLTKAGDHYHGQSPTP
LLADGVDPRTGKQMEWIFPDGRHAVLSNFSAQQLNMRVLVGLSNLSGNPS
YKQRAEAIIVKYHFQHYQDESGLLIWGGHRFVLDKTLQPEGPSEKEMVHEL
KNAYPYDLMFVSDKDATARFIRGFVNAHVYDVKIMETSRRHGKYQKIGA
LWQSPFQPPFFATKGLSFLNAGNDLIYSASLLYKYNKEDGALVWAKRL
AQYVLPQDKATGLGVYQFTQALKRDETTDDADTHSKYGDRAQRQFGPEF
GPTALEGNMMLKGRSTIYSENALMQLQLGKDLGAEGKELLTWTTDGLKA
FAKYAYNESDNTFRPMLANGKDLSNYVLPDGGYKKGTVIKPYPADNSF
LLSYARAYTVLPDAELWRVARGIARAQGLGELGSAPGKDVKVDLATKNND
PYALFALLDLYQASKVDYLSLAEKVDNIISTRYQNGFFMAEPNRQYAD
VDTIEPYALLALEAAVRNQPSVAPFLNGAGFTEGGYRMEGSTRVSTRD
NEIFLLNVGETLKPNNK

> P0A3R5|TOX4_BORPE Pertussis toxin subunit 4 - *Bordetella pertussis*.

MLRRFPTRTTAPGQGGARRSRVALAWLLASGAMTHLSPALADVPLYLVK
TNMVTTSVAMKPYEVTPTRML VCGIAAKLGAASSPDHVFPFCGKDLKR
PGSSPMEVMLRAVFMQQRPLRMFLGPKQLTFEGKPALELIRMVECSGKQD
CP

> P25253|OMPX_ENTCL Outer membrane protein X - *Enterobacter cloacae*.

MKKIACLSALAAVLAVSAGTAVAATSTVTGGYAQSDMQVMNKTNGFNLK
YRYEQDNNPLGVIGSFTYTEKDRTEGNSYKNGQYYGITAGPAYRLNDWAS
IYGVVGVGYGKFFQQTENQGLNRTASNSDYGFSYGAGMQFNPIENVALDFS
YEQSRIRNVDTVGTWIAGVGYRF

> P23827|ECOT_ECOLI Ecotin - *Escherichia coli*.

MKTILPAVLFAAFATTSAAWAEVQPLEKIAYPQAEKGMKRQVIQLTPQ
EDESTLKVPELLIGQTLEVDNHLHRLGGKLENKTLEGWGYDYVFDKVSSP
VSTMMPDGPDKKFKFVTAYLGDAGMLRYNSKLP IVVYTPDNVDVKYRVW
KAEEKIDNAVVR

> Q47537|TAUA_ECOLI Taurine-binding periplasmic protein - *Escherichia coli*.

MAISSRNTLLAALFAIAFQAQAVNVTVAQYQTSAEPAKVAQADNTFAKESG
ATVDWRKFDGASIVRALASGDVQIGNLGSPLAVAASQQVPIEVFLLAS

KLGNSEALVVKKTISKPEDLIGKRIAVPFISTTHYSLLAALKHWGIKP GQ
VEIVNLQPPAIIAAWQRGDIDGAYVWAPAVNALEKDGKVLTDSEQVQWQW
APTLDVVVRKDFAEKHPEVVKAFAKSAIDAQQPYIANPDVWLKQPENIS
KLARLSGVPEGDVPLVKGNTYLTPQQQTAELTGPVNKAIIDTAQFLKEQ
GKVPVAVANDYSQYVTSRFVQ

> P13857|RIML_ECOLI Ribosomal -protein-serine acetyltransferase -
Escherichia coli.

MTETIKVSESELELHAVAENHVKPLYQLICKNKTWLQQLNWPQFVQSEED
TRKTVQGNVMLHQRGYAKMFMIFKEDELIGVISFNRIEPLNKTAIEIGYWL
DESHQGGIISQALQALIHHYAQSSELRRFVIKCRVDNPNQSNQVALRNGF
ILEGCLKQAEFLNDAYDDVNLARIIDSQ

> P09394|GLPQ_ECOLI Glycerophosphoryl diester phosphodiesterase -
Escherichia coli.

MKLTLNLSMAIMMSTIVMGSSAMAADSNEKIVIAHRGASGYLPEHTLPA
KAMAYAQQADYLEQDLVMTKDDNLVVLHDHYLDRVTDVADRFPDRARKDG
RYAIDFTLDEIKSLKFTTEGFDIENGKKVQTYPRFPMGKSDFRVHTFEE
EIEFVQGLNHSTGKNIGIYPEIKAPWFHHQEGKDIAAKTLEVLKKGTYTG
KDDKVYLQCFDADELKRIKNELEPKMGEMLNLVQLIA YTDWNETQQKQPD
GSWVNYNDWMFKPGAMKQVAEYADGIGPDYHMLIEETSQPGNIKLTGMV
QDAQQNKLVVHPYTVRSKDLPEYTPDVNQLYDALYNKAGVNGLFTDFPDK
AVKFLNKE

> P16630|GUNS_PECCC Endoglucanase S - Pectobacterium carotovorum subsp.
carotovorum (Erwinia carotovora subsp. carotovora).

MQTVNTQPHRIFRVLPAVFSLLLLSSLTVSAASSSNDADKLYFGNKKYY
LFNNVWGKDEIKGWQQTIFYNSPISMGWNWHWPSSTHSVKAYPSLVSGWH
WTAGYTENSGLPQLSSNKSITSNVTYSIKATGTYNAAIDIWFHTTDKAN
WDSSPTDELMIWLNDTNAAGPAGDYIETVFLGDSSWNVFKGWINADNGGGW
NVFSFVHTSGTNSASLNIRHFTDYLVQTKQWMSDEKYISSVEFGTEIFGG
DGQIDITEWRVDVK

> Q02286|PHEA_ENTAG P-protein [Includes: Chorismate mutase - Enterobacter
agglomerans (Erwinia herbicola) (Pantoea agglomerans)].

MNPDNPLLALRDKISAVDKLLTLLAERLLAVEVAQAKLATHRPIRDVE
RERALLENLIVLGAHNLDHAYITRFLQLVIEDSVLTQQALLQKNLNHPH
AHAARIAFLGPKGSYSHL AARNYASRHFDSMVECGCLKFHDIKQVENGV
ADYAVMPIENTSSGINDVYDLLQQTSLIVGELTLPIDHCVLVNGPTDL
QQIETVYSHPPQFQCSQFINRFPHWKIEYTESTAAAMEKVAALNSPKVA
ALGSEAGGELYQLQVLERNLANQQNHTRFIVLARKAIEVSDQVPAKTTL
IMATGQQAGALVDALLVLRQHNLIMSKLESRPINGNPWEEMFYIDVQGNL
QSERMQQALQELQTMTRSL KVLGCYPSENVVPAEPGR

> CYSE_SYN7 Q56002 SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (S

MFKTLAADFRIIFERDPAARNGLEVLLCYPGFQALVCHRVAHWLYQQRLP
VIPRLLSHLSRLLTGVEIHGARGLQGFIDHGMGVVIGETAIVGDYCLI
YQGVTLGGTGKQSGKRHPTLANNVVVGAGAKVLGNIQIGENVRIGAGSVV
LRDVPDCTVVGIPGRVIYRSG VRVDPLDHSQMPDSEARVIRMLLDRIEA
LEDQLEGLNLPAAEAIQVTLAPVGDRCQLRDRTIEEFLDGAGI

> P56069|METB_HELPY Cystathionine gamma -synthase - Helicobacter pylori
(Campylobacter pylori).

MRMQTKLIHGGISEDATTGAVSVPIYQSTYRQDAIGRHKGYEYSRSGNP
TRFALEELIADLEGGVKGFAFASGLAGIHAVFSLLQ SGDHVLLGDDVYGG
TFRLFNQVLVKNGLSCTIIDTSDISQIKKAIKPNTKALYLETPSNPLLKI
TDLAQCASVAKDHGLLTIVDNTFATPYQNPLLLGADIVAHSGTKYLGGH
SDVVAGLVTTNNEALAQEIAFFQNAIGGVLPQDSWLLQRGIKTLGLRME
AHQKNALCVAEFLEKHPKVERVYYPGLPHTPNYELAKKQMRGFSGMLSFT
LKNDEAVAFVESLKLFILGESLGGVESLVGIPAFMT HACIPKTQREAAAG
IRDGLVRLSVGIEHQDLLEDLEQAFKIG

Positive Training Data

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> gi|51591594|emb|CAF25398.1| yopB; putative Yop targeting protein
[Yersinia pseudotuberculosis IP 32953]
MSALITHDRSTPVTGSLLPYVETPAPAPLQTTQVAGELKDKNGGVSSQGV
QLPAPLAVVASQVTEGQQQEVTKLLESV TRGAAGSGLISNYVSVLTKFTL
ASPDTFEIELGKLVSNLEEVKDKIKIADIQRLHEQNMKKIEENQEKIKET
EENAKQVKKSGIASKIFGWLSAIASVIVGAIMVASGVGAVAGAMMVASGV
IGMANMAVKQAEDGLISQEAMKILGPILTAIEVALTVVSTVMTFGGSAL
KCLANIGAKLGANTASLAAKGAEFSAKVAQISTGISNTVGSVAVTKLGGSF
AGLTMSHAIRTGSQATQVAVGVGSGITQT INNKKQADLQHNNADLALNKA
DMAALQSIIDRLKEELSHLSESHQQVMELIFQMINAKGDMMLHNLAGRPH
V
> Q8XYE3_RALSO
MRIGKSSGWLNESVSLEYEHVSPPTRRPRDTRRRPRAAGDGLAHLHRRLA
VGYAEDTPRTEARSPAPRRPLPVAPASAPPAPSLVPEPMPVSLPAVSSP
RFSAGSSAAITDPFSLPPTPVLYAMARELEALS DATWQPAVPLPAEPPT
DARRGNTVFDEAS ASSPVIASACQAFASPPRAPRSARARRARTGGDWP
APTFLSRPSSSRIGRDFVFGKLVALGYSREQIRKCLKQESLSEIAKYHTTTL
GGGFTHADICRISRRRQSLRVARNYPELAAALPELTRAHIVDIARQRS
DLALQALLPVATALTAAPLRLSASQIATVAQYGERPAIQALYRLRRKLTR
APLHLTPQQVVAIASNTGGKRALEAVCVQLPVLRAAPYRLSTEQVVAIAS
NKGKQALEAVKAH LLDLLGAPYVLDTEQVVAIASHNNGKQALEAVKADL
LDLRGAPYALSTEQVVAIASHNNGKQALEAVKADLLELRGAPYALSTEQV
VAIASHNNGKQALEAVKAHLLDLRGVYALSTEQVVAIASHNNGKQALEA
VKAQLDLRGAPYALSTAQVVAIASNNGGKQALEGIGEQLLKLRTAPYGL
STEQVVAIASHDGGKQALEAVGAQLVALRAAPYALSTEQVVAIASNKGK
QALEAVKAQLLELRG APYALSTAQVVAIASHDGGNQALEAVGTQLVALRA
APYALSTEQVVAIASHDGGKQALEAVGAQLVALRAAPYALNTEQVVAIAS
SHGGKQALEAVRALFPDLRAAPYALSTAQLVAIASNPGGKQALEAVRALF
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> gi|12025046|gb|AAG45729.1|AF229440|2 y4yA [Sinorhizobium fredii]
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GYLAREGLTLAMEPGRALADQAAITVFLISRVKALGPD SHVIFVEGSSFS
ACETWFAS EFLVDPILVPATRPAAQSPPIRAYLAGHSCLDEDVLSNRWLS
FPIAPHAGDLLVYANTGGYQMDLLENEFHRHAMPARLCVVKDAEGHPILV
PDTIGEV
> Q8Y0Z8_RALSO
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> gi|12512890|gb|AAG54470.1|AE005192|12 m ethionine aminopeptidase
[Escherichia coli O157:H7 EDL933]
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IKDGFHGDTSKMFIVGKPTIMGERLCRITQESLYLALRMVKPGINLREIG
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```

> gi|28868585|ref|NP|791204.1| avirulence protein AvrE (Pto) [Pseudomonas syringae pv. tomato str. DC3000]

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> Q7AGE0_ECO57

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RDIDAENHRGTGSD FHCNLNAVEYPCGEGISVVD F HATIVFHELLHVFN
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> CP0144 mxiE MxiE, similarities to transcripational activators of the AraC family, function unknown 123331:123963 forward MW:24552

MEGFFVVRNQNIKFSDNVNHYHFRFNINSCAKFLAFWDYFSGALVEHSHAE
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FLVKKINEKI

> Q3CB18_9CLOT

MIYIISDDLTGANDTGIQYTKQGFRTLVTVKTDVEFLETTSKSYDVISIN
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DASNAKIALVATSFPEVGRKLMNGKLELIDWEGNKSVIDVIELFTDDMKR
KVRGINLSTVKEGISSIVEVVERTSEGVEVFVIDAESDE DLAVIKGAAT
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ITSQQLKVLEEMRIPVLTLMTGEVLNNGGREAIIENTRGEVSSLIDNGCR
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> Q7DB74_ECO57

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> PSCF_PSEAE
MAQIFNPNPGNTLDTVANALKEQANAANKDVNDAIKALQGTDNADNPALL
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> Q8XR37_RALSO
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> gi|28868239|ref|NP|790858.1| avirulence protein AvrPpiB1 (Pto)
[Pseudomonas syringae pv. tomato str. DC3000]
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> HopAB1 Pph race 6-1448A|Genbank: AAZ37972
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TFMDMKKLAQYLADKPEHPLNRQRLDAKNIKYAFKIVP
> gi|12329139|emb|CAC05870.1| IpaH1.4, member of the IpaH family, secreted
by the Mxi-Spa secretion machinery, function unknown [Shigella flexneri]
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> gi|28868581|ref|NP|791200.1| type III helper protein HrpW(Pto)
[Pseudomonas syringae pv. tomato str. DC3000]
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KP
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japonicum USDA 110]
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violaceum ATCC 12472]
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> gi|51591579|emb|CAF25383.1| yop targeting protein yopK, yopQ [Yersinia
pseudotuberculosis IP 32953]
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[Pseudomonas syringae pv. tomato str. DC3 000]
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> Q8XSZ4_RALSO

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LPEVISAASPA

> avrB1 Pgy race 4|Genbank: M21965

MGCVSSKSTTVLSPQTSFNEASRTSFRALPGPSQRQLEVDQCLIGAARW
PDDSSKSNTPENRAYCQ SMYNSIRSAGDEISRGGITSFEELWGRATEWRL
SKLQRGBEPLYSASFASERTSDTDAVTPLVKPYKSVLARVVDHEDAHDEIMQ
DNLFGDLNVKVRQYAYLHGNVPIPLNTRFRVATDTEYLRDRVAHLRTELGA
KALKQHLQRYNPDRIDHTNASYLPKIKDHLNDLYRQAISSDLSQAELISL
IARTHWWAASAMPDQRGSAAKAEFAARAIASAHGIELPPFRNGNVSDIEA
MLSGEEEFVEKYRSLDSDCF

> Q3BTM6|Q3BTM6_XANC5 Xanthomonas outer protein J - Xanthomonas campestris
pv. vesicatoria (strain 85-10).

MGLCVSKPSVAGSPEHYAAHVAEQATPSEEGSGTPAQATSSYSATDPALQ
GLARRGKVDLSRSGLPERVALKTKLLANSLSDAKDAGVRSSIVKYGERT
LKMLAANKQPDEALLKLDIKNLPALASVYNRRYPGLNIQHFDSPIDFLQS
LSEQTTSVVSQRAVLRLERDGEHHVAADVRRRPNGEASVIVLEPARLLTF
VTGHTQLRRQALQGENAKFAFIQVGAQKSAADCLMFDLHFALHAHQHS
SLFDQWHDNMVNHTIDPYGQGAASPDALLEADAGVELMLGEQMLPAIFYK
HTHSSGVVEEVDRSQPGSAYTDVSTSGRQQQHEQSRVQAFRVDRGYSA
SIETSRATKIRSALETAISDRQS

> gi|28869866|ref|NP|792485.1| type III helper protein HopPtoP [Pseudomonas
syringae pv. tomato str. DC3000]

MTMGVSPINRNSNLPIDFSSLSAKSGGHNLGSGDNSTIDPSTLLFGNQ
QTQVNFAPPNSTDSSTSGVNAASGNTASGLVEQIMSLKQLMQMLMNNN
ASGNPQTDSSTPGVGSGNSVSGSGGTGSSLAGSDGGDETSVGVNGGLGDAG
STPTTSAADGVPSD TSLTGSGGLHLPQQLEQYRGDIMDAAKATGVPPSVI
AGQIWAESRGQLNAATTNVNGKADAGLMQVNDTFKSLQQQNPGLLNDV
NDSHTNIMAGALYLRDQNKFEFGDMGAALRAYNSGPKVNKADLSDTGGVG
GSSYPADVLNFAKIIESGQGNLPA

> Q8XUA3_RALSO

MPIETRYSNIIYAQSLVNTREALEDFKQDAHQALDIINSRPAQNQLLSELS
ELCRARRHKITIHIELNSNEEPCSEPV LSRHQIEEYSPENFRENREKACDL
AEKRSGWFGKPKPEGASVIVSWSMSSHSSMTFSANGSPTGTCPNSNDKVSQ
LAHELVAHAKHMVAGTWKGRWGDDRPDPTTSAGKEELRAVGLGKYAETGEP
ENAIRAEHGLPLRRKYY

> gi|24210995|ref|NP|710166.1| AopP protein [Aeromonas salmonicida subsp.
salmonicida]

MNIPPIHIKTDLTNQDEKTTIQEA TKEELQLLIATMERELASGEFFTSHE
NYASIDLGMPLLIEAANNKHVGLNLFVSNPIDLPSEIGRAISNGKEQF
RYVVNMGESGIHFAAIDCKMVDGKLSLLMPEANLNSMGPAAMLAMRVSSC
LKREAEIIPKPHFCIAVMDIQRSNSECGIFSVGLAKKMFSEAPLDALHE
EILSERLPDGMKCDVLEGEALDRLLPPTFYKHAQSQRRLDQYIRAHDPGN
DTSVNKKGELLLDRAKRLMVPVDEK LISSSIHQKRIMEYSAISDDGKSV

> Q4KBD3_PSEF5

MTISNRPRLGCIADDFTGATDLANMLVRGGMRTVQSIGIPSAEVAAGLD
ADAVVIALKSRTTAASEAVAESLALQWLRDQGCQIFFKYCSTFDSTAA
GNIGQVSEALLEALGSDFTLACPAPPENGRTIFRGHLFVQDQLLSESGMQ
HHPLTPMTDANLVRVLQSQTRLPVGLLRYDSIAQGVAVRSRIAELRGQG
VALAIADALSDA DLYTLGAACADLPLLTGGSGLALGLPENFRAGKLRDL
DAASLPKVAGGEVVLGASASLATNAQVDWLEAERPWARIDPLALAAGEA
VVEQALAFAREQQGTVLIYATSTPEEVKAVQRQLGAERAGALVENALGEI

ARGLRDSGVERRFVAVGETSGAVVKALDVRLQLQIGAQIDPGVPATVSSGG
EPLALALKSGNFGGRDFFSKALGQLAGGQA

> Q8X606_ECO57

MITHIPRSSFSANINNTAQTNEHQTLSELFYKELEDKFSGKELATPLLKS
FSENCRHNGRHFISNKDFVIKFSISVLQADKKEITIIINKNENTTLTQTIA
PIFEEYLMEILPQRS DALDKKELNLNSDRKEKEFPVRVKNLNGQCYFPGRPQ
NRIVCRHIAAQYINDIYQNVYKPHQDDYSSAEKFLTHFNKKCKNQTLAL
ISSRPEGRCVAACGDFGLVMKAYFDKMESNDLSVMAAILLVDNHALTVRL
RIKNTTEGCIHYVVSVDYDPNVTNDKIRIMSESKEDIKHYSMLDMFNVDS
LLKWSNDHVINQSVAIIPALPKEQLLMLKGTVEITPPLSPATMNLMAI
GQNHQLKQMIQLQKMPELHRTEMLTAYNSINLPGLYLAINYGNADIVET
IFNSLSEPGYEGLLSKKNLMHILEAKDKNGFSGFLAISRKDKNVVTSIL
NALPKLAATHHLDNEQVYKFLSAKNSTSSHVLYHVMANGDADMLKIVLDA
LSLLIRTCHLTKEQVLDLLKAKDFYGCPLYLAMQNGHSDIVKVI LEALP
SLAQEINISASDIVDLLTAKSLARDTGLFMAMQRGHMNVINTIFNALPTL
FNTFKFDKKNMKPLLLANNSNEY PGLFSAIQHKQQNVVEMVYLALS DHAR
LFGFTAEDIMDFWQHKAQKYSAFELACELGHRVIAELIFNTLNKMAESF
GFTDNPRYIAEKNYMEALLKKASPHTVR

> gi|17547494|ref|NP|520896.1| PROBABLE HAR PIN-RELATED PROTEIN [Ralstonia solanacearum GMI1000]

MSIQIDRPNNHFQTPSTWNHDAGSSIDTSQLQRAVQLLDQVLQQLLEARKL
FGNMLNQPAGADNAGQNHAGGHGGHGGGNGFGENGRFGSPHANSAPAQPD
LELPANKPNNGKHNTSASTPDTQTAPSSTSPPTGTSTPTSTSTATEGKVA
YGVKPPPEPTGVVDVSKPIVVKAGETFDGGGKYRPTKEMGDGSQNEHQKP
LFILEPGATLKNVQYSGGDGIHLLGSAKLDVVNRQVGEDAITIDGAKNR
AHDAKIAGIDPASPGGTPKVEITNSAFYGAQKLAQINGDVLQVKGM
VNGAGKVFRNTNGDQIKATVNVQDSNFQNVSEAVFRDTSKFSSTASFSDD
VKSDAPFDGLAPDKSQVTGTNKVSYKAYS

> gi|51591596|emb|CAF25400.1| lcrV; putative V antigen, antihost protein/regulator [Yersinia pseudotuberculosis IP 32953]

MIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDNIDISIKY
DPRKDSEVFANRVITDDIELLKKILAYFLPEDAILKGGHYDNQLONGIKR
VKEFLESSPNTQWELRAFMAVIHFSLTADRIDDDILKVIIVDSMNHGDAR
SKLREELAELTAEKLIYSVIAEQAEINKHLSSGGTINIHDKINLMDKNLYG
YTDEEIKFASAEYKILEKMPQTTIQEGETEKKIVSIKNFLESEKRTGAL
GNLKDSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRFNS
AIEALNRFIQKYDSVMQRLDDTSGK

> hrpA3 Pma R1|Genbank: BAD20871

MSASSMGTKLVNGIGNGMQGLSDINSADKDRQTSLYKNTGSNDSTDSVYDN
LRKGDKENGKQLDISTEEGAKRREESMMAGFEAADEKLANQIVA KKIENA
VVQF

> A1JQ86_YERE8

MVDIKAGSDRINNILFTTQGANFNQIRDDSTKNLFDVSLGDAVQELASME
QEKHHRVKGAPRLVMPKMTLAQAKSEAAANQPSAEAAAGASISARHGANS
EATSQTSGFNAASLMGSLATVRQIVSDSSLSLGRQLQMINIESSVQRE
RAENLLSAFENSTNELQOSSNEVTKCQLAWQQSVTTVKGTLGQOLELQSS
LNTNQKLTQQLAKTTAELKVI SPPQDLAQLKQHELLTDKVSGLSIR
LSALQVEQQSLSTNLTKLKGTLTKAQLNSTQLENAYKQVLNQATEIAILA
DQDRIAINEFIESSVTPPKIDGERWVNQLAILALLTAELRMVMGKDAIKD
MEKKQEVLETISAASRRDSEKKAKEAEAAQRKADEASKTASCTSKIFSYI
MLAVSVVATIATLGTAAPLTLAIAAVGIALTVTDIVLEETGQGLMQMLA
AEISTGISNMLMTFGMSAEKAKEIGNIVGMVLA AVAFLAISLFSMSFFK
NAGQMINSLAKNGSKLVGNLMKSAVKALPTDLLNSMGKVGTKATNLSKSL
AQIADKTDDVVHADKAASVGKTASVTARKIEMGMNGTNMVLGVTNAAVS
GGLNLQVGTNTRDMKEMMAGLMHNNAMQFIEDLLKSLIASVAKNYDQLN
EMFNSMLTALDQSGTAKANIIKSSFA

> gi|34498071|ref|NP|902286.1| invasion protein [Chromobacterium violaceum ATCC 12472]

MPITGASHAAMRPLSAPPDGTAGPASPLGRQLRDVRSVFPARRHSLAD
LASYQADYARRSVATLFAASPHADKLGELYQASPNRYAKLEIAEFAKVYS
QLKRQPDLPAAAGTLDLDAQQYAARILKDGLGEKSAFGPWTQRTDKHYQ
LRSGLERKLAEIASRHCQGDQKLGNDFMRAEVTTFILSCVETHLGRQLD
EATSRQITGLVDSAAQAFEDLRQRGDLIEQRGFSVGTLRADLDTVAVL

PQLLRSLLEALPPGPGQRAPEEPARDGPARTPSPDPGPAGPGEAQRPE
IHYHIDNSIHWNDNSQDNRRWNRGDTYLGGARQGDRLRS SGGFPASGLA
ASLRTAASQDLKPKQQAVLSGPASPAAGRHPLLNAVDVQVQSLSGLVDA
IGTAGTRPLSPGGAAESSAVRLAGLGS DGLSALPPRDDPGASLHGAARAV
ADSLSAVLTAADGAKIT KIATPARLDAAASGEDAQPAAGEAIPADAGQP
GAGGFDGIRFRDGNLYMLPTQAYLRGLASPRRAENELLRAVRGALEPAAA
QPMAQRREFEALNRILPSDRFDQDKVDRFASGGEDRLADDAARLRQAL
AGHPGLERHRQALRSFARTLI REANLLPSAKPANPLVAGLLDALGIQADE
EARRAPLPSKPCGVVLTDDGLHVDSSRAGRRGAS
> Q8X4W3_ECO57
MPMNTTGMSPFSSFGISCH RENSFRNSFRGKNDVVKCSIGERTISFSVRK
FSGNILETVRRQSTKIDIDEWIKDERIVYPSRVINQEIDNYCFQKNAKIST
EERQRVFFLVSQENQLTLDVKAQSSINHVMGSASFQKMDALCDGMSR
DVKNRTSDTIANLLADKQYQKHIDSDIDIVKLRNDIPDYLMRAIQG
> Q8XB16_ECO57
MDNLIGTPPNHAVPHNYIDMEQMEYLCHLNRF SKLSNDFLINGPREDLFT
YKYVLDGS FSNLQHL LPKGQLQKIQQRLSSLMHKMNFHCFHVFLKLC SI
ESIPLPNADYAFFDDEMPFTLTDEQIENISFLNAYHKEKKGNNDIVTFDF
MSADHYNFSTTIALTND SFHISSINNHNSQVIFDENIHLHPYELPESSQ
WCYQLIKNMISLHCRYNNNFKIN
> avrRps4 Pph race 6 -1448A|Genbank: AAZ38042
MNRISTSSVNSSFSYSAPAEQAQNRVSSAPTNSPPGTTTAV AQASEGQK
KPGAVLSMQAQRRLQ LCESSYQYRQNAL LAKSFD AQRDLINTQAGPSNS
PHLNALNKLQQRDFKPAAGGLEIPFTPKSLGGGKR VYQIGSSSRDVQVC
PRGAGAALRQEIADKQLMVNHLTDELQDAIDEANQAEIANTSQQLRQARS
DLAELQRRFAVLGNEDRRINQ
> gi|15618110|ref|NP|224395.1| similarity to CT119 IncA [Chlamydomonada
pneumoniae CWL029]
MSSPVMNTPSAPNIPAPPTPGIPTTKPRSSFIEKVIIIVAKYILFAIAA
TSGALGTILGLSGALTPGIGIALLVIFVSMVLLGLLILKDSISGGEERRL
REEVSRFTSENQRLTVITTTLETEVKDLKAAKDLTLEIEAFRNENGNLK
TTAEDLEEQVSKLSEQLALERINQLIQANAGDAQEISSELKKLISGWDS
KVVEQINTSIQALKVLLGQEWVQEAQTHVKAMQE QIQALQAEILGMHNQS
TALQKSVENLLVQDQALTRVVGELLESENKLSQAC SALRQEIEKLAQHET
SLQQRIDAMLAQEQLAEQVTALEKMKQEAQKAESEFTACVRDRFTFGRRE
TPPPTTPVVEGDESQEEDGGTTPVSPSSPVD RATGDGQ
> gi|51591597|emb|CAF25401.1| lcrG; putative Yop regulator [Yersinia
pseudotuberculosis IP 32953]
MKSSHDFEYDKTLQAE LAIADSDHRAKLLQEMCADIGLTPEAVMKIFAG
RSAEEIKPAERELLDEIKRQRERQPQHPYDGKRPRKPTMMRGQII
> Q8XVD4_RALSO
MSRTLATPRTPQGNDLSLFASYEAIASLSTEMVEAAEAGDWAGVSALEREC
ALYMERLGRTPSRPVLSEAELRRKRD LMMRILANDARVRALVCPRQDQLL
RPMDAARRSIGARQAYAAVSYY
> Q3BRE0|Q3BRE0_XANC5 Xanthomonas outer protein F2 - Xanthomonas campestris
pv. vesicatoria (strain 85 -10).
MKLQRQNSAPPSIPSGSSANPGAHAHASEPFVPEPQTPRSTVLKGLAEPSP
RLRARAGKTTTTLPSGELSPAKTRQWRPEAGESSRAASERAERQHRAGRHP
GNQQAASSSATQGAYAQRCAACERLKAQLRAGLKARPF AEP SDEQLALQ
AEYVQWADARLQERIEAFGPDAAYEVAGDMKAVGRKASLP IAYESLRSFF
VGALRTPLGISAATAYQSNRPPASEPLSTATLAGVISGMGSHACDTLLIP
SMDRRARVANLPRFQAIDPKILVPDPPVLEITPEGSKRFVRPGENGTP
TRAELTAQAYDRRAGIAQRQSVLDDTALDTMLLRPTISGGFNAARRTS GD
PSTRTAVAEVGLAGLAVGGAGALHKALLDTGKAMGR TGQMTVPDLLGGHQ
RLNLFALALPKT RPPATWSDAVHFPSYLLQTGQEA MALARQAFSTANAA
TTALRDVLRHMVGNVLANMASLGATRLIASPLRGGYGGGSLPGEADNSP
AWVLQQGAQMFFNDVGNALKAKNGTNTTQATRLDHERAIAAAEQDRTIS
RTLQTLAEPLDTALGLLPPPAQGEVPRAMEEGTGVPVPLSADVDRLRNAL
QQLRDQVAAQAVSIATID DALGRLADLPVAGDGEGRAVIAELSAQLHALG
AALRQKQALQQWQQ GRP
> Q8XT97_RALSO
MPI SACKPHRSATTIISGDIQISSSQEAPSKKSAKEPRLETNPLLSKLRP
RSSSVTAGAQSETSSSLRIKAAPFLTVPKSLDAYAIDSSVPYQFQPSKIA

IIGGGLTGVISALKLRSLGHEVSLFESNEDICLEASKIPAHCYGAPGYCH
LPKDEQIEIFRSLGFAKLFPPQAI SLRPTIFALRKNDRVRVTNDQNGRFR
TIDDLKNSVNLAENEYKKAVERSDPKSEVFGPVG KYQSGYTHEQIQALRNQ
PLTGAPGNNDWVANWAHEMSEALSELQYPVFLVKEPEINMLRFRELAR
SALGELGVDTHIGETVNDLTSQAGKPGIMVNQAHFDYAVNCSGAESGTHD
DKREAI SERTVIVKGAGVASLPSVPPFR

> gi|28868073|ref|NP|790692.1| type III helper protein HopPmaG (Pto)
[Pseudomonas syringae pv. tomato str. DC 3000]

MRSRVITTSLVVIMLSCASAAPACFSADMTSPSVSNESSTSEADFQQWLATF
RSNATTKGIDTATLDLAFQNTLDPTVHQLDMAQPEFTTAIWLYLSERLT
PKNIQQGQELLQKREPMVNEVERHYGVDAKIIAAIWCIESGYGKDIGSRDV
IRSLATLAYKGRMDYVATQLMAALHIVQNKDIARAQLIGSWAGAMGQTQ
FIPTTYLDYAVDFNHDNRRDVWSSRADALASTASYLQRSWNSRVV WGQE
VQLPENFDYAQADMSIKKPVAEWQRLGVMGKQAI PGELAQEQASVLLPA
GYRGPAFMVLNFRSILRYNNSTAYALTIGLLADSYAGGTGVSHPWPTDN
PPLGSIAQVTDLQKLLTAKGYSLGAAAGVIGAMTRAAIRAYQKDQHLPPD
GYASTVLLLESLRR

> gi|15618928|ref|NP|225214.1| hypothetical protein CPn1020 [Chlamydomonas
pneumoniae CWL029]

MSSWLSQASEVLLNQDPYIPDAPRSQESSVPKISYSITVAPQEAQKSLPK
FFTQKQFSQCKSEPIITHHKTFI IATPRERILRFGSSFESQLHNTSQAQT
SSPWNLFQKNSTEASKALMQELTMPKSPEKTSEKALDKNLSSKQEGSCK
NFDTLHLQHLKLFGTVDLSLQSLDSEQQELLQSRREERSETYANQQSS
EKKIETKVQIKDLCKDLFSQDQDSNOKKSPFQDTSRKNR IAKAAQAV
PVI PPPSIGVFTLSYLLTKQGILSDFSSYGCHKDSVESTQRELDALHEKR
IETIKVSI EKEKRERLWGSLSDI IGWLAPFVSI GIGIVAILSGGGIFAF
GFFAGLISLVIKCLEKLFKFDWLEKHLPIKNEELRRIITIIQWVVYLT
VILSICTLKVENLGFSP IIEGAIKGIQPAIESTMAALRCAILFSQAEIYK
LKGKLTKIQLDIELKSFDRDDHYERSQELLDNMESSEALSRI LNYMREL
DQVYLHSLRG

> hopAH2 Pph race 6-1448A|Genbank: AAZ34780

MNIRSDRSYDPLMAAREKPV MAGRTTRAVGAGATEANPDTQEKL DAYTAS
DSR SAEAPEAFVYTRTMLS RNARSLESEASPSDMALLASQOTLATQGD
KALRDEVA AVKDNATPSAPETKVTDKDKVASAEPVKIAEKVSRGGANANP
DDIATPAAATKMIQDLKTIGGGTLRFQMTHDQIKDARQMD KLRALLSEG
KQGKVKVQFTFRDNANQGGGNVLTGEEKLQASADISNVVKKFGSRTSFVLD
TFNQGGKSASQDADMOTTLIKAARNSGYKGTIVVEDSNWGGGLTAGPQS
GLVKFADQLKAANGEGNPALIGSFHVYARESEASSRLGKQIKALREAGYK
FQIGEVGNAKFLVGNFTFQKDEATKALQDNMTALKAAAGADILPGKDQFQD
GKLRRRAGFSKSDQFL

> Q7PC42_PSEU2

MTQTPPSLD FNLSTPSPVPMTPSDTWAGASAALKRLELRTLLARELDAL
PQAGEALLSALDGADV SERELQIFGLLQQIDDYWTDPGETGESRRDRLLP
ALQRSLHDEARVRIHERDFDSGYLACL PDSPDQEGPALAYSTVRVQLHDD
EQIEMAGVLVISQDQGRLLMLPGLGISGFATQAMLVATLVQWLNTPTLR
DALLSNAQRQHQLERLTEILQDADLYLEPFTAADVQLQPVVTTAPFIHAFD
RLLNKQRNDI RYACEQGTADRLKRQSLIQQAIDMPGLFGPAAMLELREL
TNRRRQYQRNLP EWMKIASAADLQTYALHLQRYDAAHTAMLSVLGSAASP
ERFAEMQLRTRLANDLGHDLDPRLTIDTRRTL PATSETYRVKLPLTELA
LYGLHPDDETAGSDFLDQTLITLDGQPLDAAYSDLNPAYLARVIDELDLR
AVFGDFQRQAYQQEHNQOMLRALARVRLTTLGWAAKMQGHIRPDDFAIVA
AL TSAATGTHD PALRVQQIRLNDRNVMARLLVCRKQDAQGRTRQLIMFAS
EAPGQQYFKAFD TDTQLLHEMVGWTAS PAMTAWLLDQVEVAARPELAAQL
TALREKPPAKDFLQFIDHPDCETALRRFTDEQTRVLLSEQARHTPDWYL
RASRAQRRELLALERAINGALDNYQAQHTGVQSFKDYVHQRASQQLGKL
LGV PAGTVDPDQIVITSERETQTYTDMLLKGYNDSIDPLSTSAATDATFS
GPPGIDLSALSP AAVAGSVRGQWLAD EYIALIRNTLLNSENDGYAYRRQY
SVMITQLQMKAAALRSLLKGHVEAAQYAWLTQSLDNAHLSDPASRERYPL
YPLQIHVDKPLIASGLTDVDQLVIPSPLLTHIETVQGCLVILPTQIRHAA
LLYTPQAPDGI EFRFVSDFVSSLNSEG MIDYKDRCRIKARRTLSFFLRD
MQKGNANKPPVI PRAFIADVADTCFNRLPERRLRDVEETTGRNDMLTKL
IRVSVEIVATALT LPFPASPFAVGLISLHDSGQALAALSAGDRERATNY
MLSALLNGLGAGSDLLVGLKGLGGALHQLENSQHSTPVLRSFQRQPSLPR

YEDLYPVELQEQVFLGKPNVHGHAIFQASHVASAPPLATGQFAAREIG
GAWQPLPLPPTAQRAPSGLRIDLAVDISLENVPRIAEGHAKGVHAINGK
YYIQLSDQAFEVQYDAYWQYWIIDPANPFAFFGKQPVRLNDQGQWLLVE
RQRLRGGGLDTPGT YRPLPEQASASSSSLNTLSDYEMPSGMRAHLDIVIN
KEVFDPTGAGLDVYFETYFTEVRQTFARREQLYQDAQAFARFTPPPRP
TLPAYGLPGSVDTLIKHFHSHSNGLVFSEAPKSVASKRLLLLNMPLLAEQ
RVEVLYIEHLLTDKHLRKLARYRQLGKKSRSRGSHELKYYLQETNRGALNN
ASSEFDYYHLIKAAHRYGIEVRPLSSISYPFLGHTVLSAADDPAAMKM
SNFFGHRLINHDIEP ASARRWVALLDQKLATTHDQVPGIAEMQGAVSVQV
QDIPAGRPTIRIQGAGEAHENTPSHCDFSIAFADPTLPARPLPPATALDN
TLIRELGDPTAIAEGERWAGEYGFVLDENHTWLRVEADDWSVDRSMTAIQ
QSLTDATYEMPAEDTRTTLHRLANFEKKGLDMEYFFEDIELDTVRNTFDLR
RKNLQKDAASISAAQLPPRPTLPAIEPQTSTAGLLETLYRHTEGLVIGES
HSSVASKKLIIDNLPL LSQQNVKTYMEHLLSDLHQADLDRFLETGQMSK
TLLHDLKTLDRGHHTDPNGVYTFEQLVIRARQGLEIRAIDCASSYHLKG
IAEDEPLIRQQMMNYFASRTIRRHQDVMGSHKWIALVGNSHSNTYQGVVP
GIAEEGGIGLRVVDVAPGHSRGITLDQGELVSGGIADKVIKADYRVE
MEVPRPQPARLPSIEKRLSRPGMFLVQEGEGLNQTIVHRARDTWIHRTPV
LRNAEGKLYIERLRWPR IHLKPFDDIDALVAALEAMNLTRAT
> gi|2695858|emb|CAA74156.1| DspA protein [Erwinia amylovora]
MELKSLGTEHKAADVHTAAHNPVGHGVALQQGSSSSSPQNAASLAAEGKN
RGKMPRIHQPSTAADGISAAHQKKSFSLRGCLGTTKFSRSAPQGQPGTT
HSKGATLRDLLARDDGETQHEAAAPDAARLTRSGGVKRRNMDDMAGRPMV
KGGSGEDKVPTQOKR HQLNCFGQMRQTMLSKMAHPASANAGDRLQHSPPH
IPGSHHEIKEEVPVSTSKATTAHADRVEIAQEDDDSEFQQLHQQLRARER
ENPPQPPKLGVATPI SARFQPKLTAVAESVLEGTDTTQSPKPKQSMLKGS
GAGVTPLAVTLDKGKQLAPDNPPALNTLLKQTLGKDTQHYLAHHASSDG
SQHLLLDNKGHLFDIKSTATSYSVLHNSHPGEIKGKLAQAGTGSVSDGK
SGKISLGSQTQSHNK MLSQPGEAHRSLLTGIWQHAPAGAARPQGESIRLH
DDKIHLHPGLVWQTSADKDTHSQLSRQADGKLYALKDNRTLQNLSDNKS
SEKLVDKIKSYSDVQRQVAILTDTTPGRHKMSIMPSLDASPEHISLSLH
FADAHQGLLHGKSELEAQSVASHGRVVADSEGKLFSAAI PKQGDGNE
KMKAMPQHALDEHFGHDHQISGFFHDDHGQLNALVKNNFRQQHACPLGND
HQFHGWNLTDALVIDN QLGLHHTNPEPHEILDMGHLGSLALQEGKLYHF
DQLTKGWTGAESDCKQLKGLDGAAYLLKDGEVKRLNINQSTSSIKHGTE
NVFSLPHVRNKPEPGDALQGLNKDDKAQAMAVIGVNKYLALTEKGDIRSF
QIKPGTQQLERPAQTL SREGISGELKDIHVDHKQNLALTHEGEVHFQPR
EAWQNGAESSWHKALPQSESKLSLDMSSHEHKPIATFEDGSQHQLKAG
GWHAYAAPERGPLAVGTS GSQTVFNRLMQGVKGVIPGSGLTVKLSAQTG
GMTGAEGRKVSSKFSERIRAYAFNPTMSTPRPIKNAAYATQHWGQGREGL
KPLYEMQGALIKQLDAHNRHNPQPDLSKLETLDLGEHGAELLNDMKR
FRDELEQSATR SVTVLGGHQGVLSNGEINSEFKPSPGKALVQSFNVNRS
GQDLSKSLQAVHATPPSAESKLQSM LGHFVSAGVDMHQKGEIPLGRQR
DPNDKTALTKSRLILDVT I GELHELADKAKLVSDHKPDADQIKQLRQQF
DTLREKRYESNPVKHYTDMGFTHNKALEANYDAVKAFINAFKKEHHGVNL
TTRTVLESQGS AELAKKLKNTLLSLDSGESMSFSRSYGGGVSTVFPVPTLS
KKVPVPIPGAGITLDRAYNLSFSRTSGGLNVSFGRDGGVSGNIMVATGH
DVMPYMTGKKTSGNASDWLSAKHKISPDLRIGAAVSGTLQGTQLQNSLKF
KLTEDELPGFIHGLTHGTLT PAELLQKGIHQMKQGSKLTFSVDTSANLD
LRAGINLNEDGSKPNGVTARVSAGLSASANLAAGSRERSTTSGQFGSTTS
ASNRRPTFLNGVGAGANLTAALGVAHSS THEGKPVGIFPAFTSTNVSAAL
ALDNRTS QSISLELKRAEPVTSNDI SELTSTLGKHKFDSATTKMLAALKE
LDDAKPAEQLHILQQHFSAKDVVGDERYEAVRNLKLVIRQQAADSHSME
LGSASHSTTYNNLSRINNDGI VELLHKHFDAALPASSAKRLGEMMNNDPA
LKDIKQLQSTPFSASVSMELKDLREQTEKAILDGKVGREEVGVLFQD
RNNLRVKS SVSQQSVKSEGFNTPALLLGTSNSAAMSMERNIGTINFKYG
QDQNTPRRFTLEGGIAQANPQVASALTDLKEGLEMKS
> Q121N8_POLSJ
MGKILLGCIADDFTGASDLANNLVRAGMRVVQTIGVPAGPLGAEVDAVVV
ALKSRTIAPAEVAQSLQA LAWLQAQGAQQIYFKYCSTFDSTFSGETRGN
IGPVTEALMDALKTDFIATPAFPDNQRTVFKGYLFAGDVLLNESGMQNH
PLTPMTDANLVRVLAQTRRKVGLIDYRVVARGEAAIRARIDQLKAEGIG
VAVVDALSNDLLRLGPALKGMPLVTAGSGVAIGLPQNFGITPSSKASEL

PPAGGLQAVVSGSCSLATNRQVLAFIKSGRPALAIIEPLRIAAGVDVAAEA
LTWAAPLIQQGPVLVYSTAD SNAVKSVQGR LGVEEAGAMVERTIAAIARG
LVERGVRQLVVAGGETSGACVQALNISQLQIGPQIDPGVFWCHALS DAAA
GQGVHLTLKSGNFGSDDFFTKAFTMLQ

> Q8XZC6_RALSO

MKIGGTQSGPVVSSDSTVEGSPAPLTHGPTSTAPTTPPEPRQVSGEHGGH
LRRRVGAGAAMVSSMTRRAKLPEAVDTRVNASLTRALQTTVKGVVAPAVT
LTGSQLSTVGKAVRQASQAPASSLPLQRA LGGDLTQPDRQMEHRKAVNY
GKHSAQHLDRIVAF LHGVLRLSAGTSTAFGVGRNAGLAAGDALGRAERGV
PQASGVTGSEAPARTMSSQSFAFLAAAGVQQWALGAVTGAAGNLAGQVV
AGPIINMLPRQFQAI DARAVVPQEI VALMNALKPGAGNELRDKAKAMQAD
IANIASDSSVWLGQIAFDSITAARMAAQGGTPLGVAGQISLGLAVSGTAG
AVIGAVIAVRQSTATIDVPKADALRAALEL APADRPVAVLETHAVPLFFAK
HATMPATAAAGDIETGHIATAAQPHQQEQMSRMHAAVQQVKQMVGGGLGGL
VTAPAGAIAKAFTAGPLLEPQPTVEGAAPSGQVSRATATVSNVLASGVRR
TKLMAESTAVTSLMSTGSAMLASATEGPARRAVLALGNAIGIHAAIRPWF
NALANDIPAGDNAMRAERQQHVNAQVPRPEQPEV

> Q8X3G2_ECO57

MTAWTVTSEKRHLHRIVYRVKYFNFTTLHDYN HFCDFIEFKHKNIMNTS
QYTGSSW

> NleF_Crod

MFGMLPSSSSANLYSWMYISGKENPSTPESVSELNHNHFLSPELQEKLD
VMFAIYSCARNNDERENIYPELRDFVSSLMDKRNNVFEVINEDTDEVTGA
LRAGMTIEDRDSYIRDLFFLHSLKVKIEESRQDKEDWKCKVYDLLCPHHS
SELYGDLRAIKCLVEGCSDDFSPFDTIKVPDLTYNKGSLQIG

> Q8XZN8_RALSO

MMFKRIDSSVFSPIYVRPEPSAPPLPEQGAPSGRAANSASHPIRPEPSAP
LLEGGFFPHVPDQAGEQRAYS PPRSAGVSSSPLGGLAAMRLDSSGAGTA
PMLRSRLPPAPSAPQVVRNIEEMPAGVLQHVASF LDRSRRALSQVS
TMTNDAARSSQTHMJAQWNAKMLGQLHRYPNLQSLRRLRGDITLDELKALPK
TLRHIDLGECDPGCGAKSHAAIEYLATLPLESLNVKGAAIGDRGAALLAG
NRSLKTLNVADGGISEVGARKLADHASLES LDMTGNQIDARGAQHLATSE
SIQTLRLCCCGVTDPGIQALAGNRQLKSLDVSGNHINEDALRALAANPSL
TTLDVSCNRQTPVGE PQSVEQGVSMALALAEGLVGRETPLASLKADGNAF
VDFAVEMLAFFPTIRTASLSLKS NF IGPEGAQKLAENPALKSLDLTRNKIG
DAGAEALSHSRSLKTL SVLNC DVKDPGAQALARNPTLTLDLGNLISEKQ
NPAARQQEQDEFDTTANEITENGTRALAQSPSLISLSVQGNLCE DAGVLP
LARSPLTSLNVAYTNMTLESARELASNPVLTSLNVRWNVEHLGTAGVLE
LAKS QSLTFLDARDTCMGEAGALALEANTRIKGTPDDPNFIRDSYRG

> HopAB2 Pto DC3000|Genbank: AY074795

MAGINRAGPSGAYFVGH TDPEPVSGQAHGSGSGASSNSPQVQPRPSNTP
PSNAPAPPPTGRELRSRSTALS RQT REWLEQGMPTAEDASVRRRPQVTAD
AATPRAEARRTPEATADASAPRRGAVAHANSIVQQLVSEGADISHTRNML
RNAMEGDAVAFSRVEQNI FRQHFPNMPMHGISRSELAIELRGALRRAVH
QQAASAPVRSPTPTPASPAASSSGSSQRSLFGRFARLMAPNQGRSSNTAA
SQT FVDRSPPRVNQRPI RVDRAAMRNNGNDEADAALRGLVQQGVNLEHLR
TALERHVMQRLPIPLDIGSALQNVGI NPSIDLGESLVQHPLLNLNLVALNR
MLGLRPSAERAPRPVAVPAPATASRRPDGTRATRLRVMPEREDYENNVA
GVRLNLNLPVGVVRQAVAAVTDRAERP AVVANIRAALDPIASQFSQLRT
ISKADAEESELGFKDAADHHTDDVTHCLFGGELSLSNPDQQVIGLAGNPT
DTSQPYSQEGNKDLAFMDMKKLAQFLAGKPEHPMTRETINAENI AKYAFR
IVP

> Q8XQI9_RALSO

MPPPIRNARTTPPSFDPSAAGDDL RATPPRVAAATP THRTAPSQLAGLPS
RPRLOPPQDPDPTPLAPRGNTHTGSATGRLIALALANPAANRTPGRLAG
GLHLPSIDNGNPNVSLASLNVASGELAEIGAAALLATRLRLPSIALDGP
GPAATLLAGLEHRTRALS LAQEPGG LGPGHPPLAVLPDIVAAALANSNSL
RDLLDRHPASVLANRLRGVGPAPQPAADPSLGHAAQRAAQIILEGWAQQCQLP
PKTVDAWRPVLNQEESRPFVSL LARLNGCASFRPAHRAESL KELGGILQL
AAHNDAYRTRCFDICGGADANCHDNVDVIFGNLRLAARDPSYHGNAQLHE
VLSYHNRCMPWTLIDDFVSHRFGRGDQLERALALRVLSDILPITTPAML
HHDIARIDNAHEREARAYISAHLGTQEHLLRNLSRSPAWRQFLEQQRPVE
FAANTLLWESALQDVMAPAGDGA VADAPRAASTTAPGSRTEALAQAHAM

PGIGTGQAFQHRQENATAMLAETMTRKLVMEASPPPDETGAHAALLTDPD
WLAYLQKEHPEDRAFSPADMHAAERHDLMLRLTRQEIAEARGMVQPHAGA
PTDHG

> gi|34496429|ref|NP|900644.1| probable tyrosine phosphatase
[Chromobacterium violaceum ATCC 12472]

MSTIQGTGIQLGGRQLDLSRLDLSLGSVNADKARIGIRKDGTLVVYTGRSYL
LHPDQTRRADQFLKHDLLIPGQKPREFRLAQLFDRPMDALTQRNTQANE
TIAKPTQQDQDVTVTRGGKPKLRWADQAAARPSGEPSPRGERASLKQRRGAE
HLKLAQPRAEARPEKHDAIKTELASRLGSSDQPSGLLLQLKAQVGSSEAG
ARFLNDVGVQARFRDIPTAAATQVRAPDGAPLPANRVQVGGVNVAIASQYP
KAAQLESYFGMLAANRTPVLVVLASDADMAKQGRDGKADLPDYFSQSGRY
GRVEVESKSKGSTTLEGGLEVRAYHLNVRGADHKSVSIPVLHVPNWADFG
AQGATALKALAQHVDAVADKKTAFYRDNNSALNDPDKLLPVIHCRAVG
RTGQLIAARELLKPGASSLESIVADMRGSRNMLMVQTSQGQLSTLVDLAQQ
QGRAILQPETAAEPIYANQAQAEPIYANDAPPPPPRRPR

> Q8Y125_RALSO

MKVSSANAGVPASSADNTSARPSQTNADTTPLGRRRRAPDDAPGSPARR
QRQDSDPESDAQTMFRRAGMTSLPPSPATSEHVPLLDNRPTLERMGVDHPL
PGRTWYETGHTTASLADRTSTASAAQVASSRSAGPATAARPQPTRTSAG
QQATVGRRLRTQVTGFLSGALGKLQALSQNMDPELAQFRVLDVDRAIMPL
LIVAENARNPGLNLVPLHMDMAEDEEVRTQPPMAGSRHIAEFVASARPGR
YRAVIDDGSHTRAADIRKSDASGTSVIVVDPLRKEKDESAYVDYADNVNME
FGEHAKCAFI PVDIQKSFDCRILSLSLALKMHDKDDAFAAFHETLRNGG
DPSHHVSRAQQTEELGATLVLDGAPLVDARMMKHGQAASSVSRYLGNHPE
QSTVPVKNRNETLGERTRHLVKKVRNRADSEGRVTSGETKEITFSNSV
EQKRIALLNRAASYVNSAPPVVMMAKLLQDSSLDTN

> gi|12329054|emb|CAC05785.1| OspC2, probably secreted by the Mxi -Spa
secretion machinery, function unknown [Shigella flexneri]

MKIPEAVNHINQNNIDLVDGKINPNKDTKALQKNISCVTNSSSSGISEK
HLDHCADTVKSFRLKSIQAQSYKMFSGQTSFKSLNLSIEAPSGARSSFR
SLEHLDKVSRLYLSIEIIQKTHPLSSDERHLLSIIINSDFNFRHQSNANLS
NNTLNKISFDKIKSENIQTYKNTFSEIDIEEIANHDFVFFGVEISN HQETL
PLNKTHHTVDFGANAYIIDHDSPTYGYMTLTDHFDNAIPVVFYHEHQSFLL
DNFKEVVDEVSRYVHGNQGKTDVPIFNTKDMRLGIGLHLIDFIRKSKDQR
FREFCYNKNI DPVSLDRIINFVFQPEYHIPRMLSTDNFKKIRLRDISLED
AIKASNYEEINNKTVDKMAHQALAYSLGNAKSDMALYLLSKFNFTKQDV
AEMEKMNNMYCELYDVEYLLSEDSANYKVLEYFINNGLVDVKNRF QKAN
SGDTMLDNAMKSKDSKTI DFLKNGAVSGKRFR

> gi|21231556|ref|NP|637473.1| avirulence protein [Xanthomonas campestris
pv. campestris str. ATCC 33913]

MWSQPVWNPYASFDTGTASSHSQAVQGTATNYLRGPANYSKLSSEEQSLV
GAARWPDDAPGLNINSNKSNQDNKKYCKSLYKASRIAGGSIASGQINSFN
DLWQKATQWRLSRISGDASKGDFAAERMPNTRFVTSLRRPYHSVIERAR
NHPDAETELYEGEYFKEIEVKVYRQCAGAISGETIPMTTVAAVDDNAISA
RLRNLPKDKRQQARQSMASHPNMITHSAEYIKTIRDHLESYLAIDP
SLEKHEAFELIARLHWWAASAAPDKRGSAAKAFAARSIASAHGIEMPPF
RHGIVPDIEAMLRSESQFVADYPNFFERFPI

> Q8Y3D9_RALSO

MPLTKINPSASAD T'LLPASVPVEVEASQDHPAARAKTAELSALAKARLR
NAAGGTAFSLRAKLRVAHQVGKDAVHYRNVQHRLNAQMKQLRPETGFQD
QLHFSASLAEVESILRHIAVSPALLSASRSKSAVTALFTKTFMLPLLDG
GQLRLHEFRSGRAQDEEDPHRHRWNLKTEHLKGAYVQQVHEETHADAP
GARLYQKHQLEATPKDKTERRFTHLGEVHVRQSATKLYSEEQRPHDFPLA
ETHSVADLSRHAGM TLTARTGKAIYADS IAYNAGTEILTAPLGRAPDE
QAFIERLHRSIAIILQLVQLQRELEAYLRGKAPASLTAGEQRHLEDAKAPN
YFETSLPALATLDLATAAGQASDEFSPETVAYLDSALDRIRSTSLRQII
ADNDAHLQAGHFCAELSNFEQLKSLIRTTE

> A0B2L3_BURCH

MTASASRPLLGCIADDFGTGATDLANMLVKSGMRTVQTI GVPADGAAADTI
VDADAIIVALKSRTI PAADA VAQSLAAYAWLRAQGCRRQFFFKYCSTFDST
DAGNIGPVADALLDAAGGDFTIACPAFPENGRITIRGHLFVGDVLLNESG
MENHPLTPMKDANLMRVLQRQTKSPVGLIRYDTIALGAAAVRARIDQLRA
EGARFAIADALSDRDLYVLGEACAGLPLVTGGSGIALGLPANFRRAEQLP

ERDNAASLPRIDGLSAVLGASASKATNAQVAWRATRPSFRIDPLAASRG
EPVVDQALAFARSHLPQPVLI YATATPDEVKAVQQALGVDAAGHLVESTL
AAIARGLRELGVRFVAVAGGETSGAVVQALDVKSLQIGAQIDPGVPATAT
IDAQPLGLALKSGNFGTTDFDKALRALDGAAR

> SIPC_SALTI

MLISNVGINPAAAYLNHNSVENSSQTASQSVSAKDILNSIGISSSKVSDLG
LSPTLSAPAPGVLTPGTITISFLKASIQNTDMNQDLNALANNVTTKANE
VVQTQLREQQAEVGFDDISGMSSSA VALLAAANTLMLTLNQADSKLSGK
LSLVSFDAAKTTASSMMREGMNALSGSISQSALQLGITGVGAKLEYKGLQ
NERGALKHNAKIDKLTTEHSIKNVNLGQNSVVKLGAEGVDSLKSLNMKK
TGTDATKNLNDATLKSNAAGTSATESLGIKNSNKQISPEHQAILSKRLESV
ESDIRLEQNTMMDTRIDARKMQMTGDLIMKNSVTVGGIAGASRQYAATQE
RSEQQISQVNNRVASTASDEARESSRK STSLIQEMLKTMESINQSKASAL
AAIAGNIRA

> hopA2' Pmp 5795|Genbank: AAP23125.

MNPIQTRFSNVEALRHSEVDVQELKAHQIEVGGKCYDIRAAANNDLTVQ
RSDKQMTMSKFFKAGLSGSSGSQSDQIAQVLNEKRGPAQPRLLIRQGQTH
LGRMPLNIEEGQSSATTSVQKSGLPNGRLVNSSILQWAEKAKANGNTSS
GALYQIYAKELPRVXXXXLLPRAEHRACLAH MYKQNAKDGISIWQFLD
GVRGVQLKHDTKEFMMNNPKAADEFYKIERSGAQFPDEAVKARLTINVKP
QFQKAMVDAAVRLTAERHDIITAKVAGPAKIGTLTDAAVFYVGGDFSSAQ
TLAKELQALLPEDAFINHTPAGMQSMGKGLCYAERTPQDRTSHGMSRASI
IESALADTSMLSLEKCLRNAFKSAGYNPDNPAFRLE

> gi|20139269|sp|Q9RBS2|POPC|RALSO PopC protein

MPRDTPQTVPGHSPFWPLFFFTHNNKREARHDLARLSLTMPILPRLFHR
TSRTSSADTQRDARTPPNASPLHGEPGRTPRSRGELGRNLRLSNAQTSG
TPGTPARPQIRASASRTAPSTPQHPQGTGTRTPVNSPLHNDARVFRERA
DHTGLSAWRTEMLTRFIEHSRKHGLANDFEQVRVYDRLSRAVDHLKSVLR
MSGDSVQLKSLVPPELDPVTFEIAHLKNELETVDLHALPATLENLFLLE
TSLSLKGAKNFKALPDVWRLPALQELKLESETGLKSLPPVGGGSALQRLTI
EDSPLQLPAGFADLDQLASLSLNTKLEKLSGGIGQLPALKSLSLQDNP
KLERLPKSLGQVEELTLIGGRIHALPSASGMSSLQKLTVDNSSLAKLPAD
FGALGNLAHVLSLNTKLRDLPASIGNLFTLKTLSLQDNPKLGSLPASFGQ
LSGLQELTLNGNRIHELPSMGGASSLQTLTVDDTALAGLPADFGALRNLA
HLSLSNTQLRELPAANTGNLHALKTSLQGNQQLATLPSLGLYLSGLEELT
LKNSSVSELPPMPGPGSALKTLTVENSPLTIPADIGIQCCERLTQLSLSNT
QLRALPSSIGKLSNLKGLTLKNNARLELLSESGVRKLESVRKIDLSGCVR
LTGLPSSIGKLPKLRTLDLGCTGLSMASLPRSLVLPDGLNVIFFPEHLK
TDVGNARIQQNPRARLLEGLHLERQNEAMNHAMFGDDES SVGSMTSVPDNEA
GVVSMFAHAKHAYKRLERLRQEAGSSMAAPMRNDAESMRRALAYAFRSM
SDLPTFFKLDNAARSLSYEVQEQADLVAAPVGQKLVKAI AEGAYGAGR
ARAIEQMLPELATRIANHPEIQQLREQAKRYPSSLPPEKLAAKLTPLIQP
LWDGTRAVAPMPGQLRQALQDLLVTAEGRQLASEIDRAAHSHRAGDEGKA
LRGLLPVLAAKIGSDPRVVRVREFVSRHTFGSPQORAESLAQTLTPVVQE
LWAQTQAEVAKQGQTPAASPSRQR

> A3JVV6_9RHOB

MAHKMATVLGCIADDFGTATDLAGLLARSGVAVSLRIGVDPDPTDAAF
EVIALKSRTAPVAEAVAETKAALAWLRAAGAQRFFWKYCSTFDSTSEgni
GPVAEGLMDELGAQTVYCPAFPENGRSVFMCNLFVGGQPLAESPMKDHP
LTPMNSNLMLRLDPQTSQDVGLVNRLVVEQGVAAVKSELAALANKNCAH
VVVDAVANSDLNTIA TACQDMPMLTGGSALAMPLPQLYAEQGLFDLKAAL
SKHVAPGSPTLILSGSCSEMTNKQVDAYLKTGAPSFQLDPLALATDGVEP
VLEWLSKQDLECAPLIYATATPESVKATQDRLGVKEAGEIVENALAACAI
AARNAGARRFIVAGGESSGAVTKGLNVDALDIGPEIAPGVPTFCISSGT
RIALTLSKSGNFGAETFFTDATAVLDAI

> gi|2496787|sp|P55730|Y4ZC|RHISN Putat ive cysteine protease yopT-like y4zC

MHSPISGSFTSSTQVHDPIHPANSDFRETLANVELRTPSPAECPKMG
CCASKPQASDPNNPSTSSPARPSTSLFRYRTAELAQANADGICVGLTAEW
LRNLNSHPSIRMEALVPGSQRHASATVRQKEYENLKVHLRRQGAGPSEAD
FAAQNTMLQKAGLAPSGKEKVKVGEPNFPRMLTKITADGSNHLISLYFA
EGGAHTVATSAMDGN TTLFDPNFGEFTVQSDQIDDLFRSLANRYSNPNRQ
HLTTVTTQKMT

> Q3JLF5_BURP1

MSTDQALRPLLGCIAADFTGATDLANMLVKSGMRTVQTIQVPAAGA AVPA
DAIVVALKSRTI PAADAVAQSLAALDWLRAOQCRQFFFKYCSTFDST DAG
NIGFVADALLDALGGERAFTIACPAFPENGRTVYRGHLFVGDALLGESGM
ENHPLTPMKDANLVRVLQRQTPSKVGLIRHDAIALGTC AV RETIDTLRRE
GVRITAIADALTRDRDLYVLGEACADLPLITGGSGVALGLPSNFR LGLLPE
RGDAAALPAIGGASAVLAGSASKATHAQVAAWRAERPALRIDPFAAARGE
PVVDQALAFARAHLPQPVLIYASAAPDEVKQVQALGIEAAGHLVEATLA
AIARGLREMGVRKFVVAGGETSGAVVQALGVKALRIGA QIDPGVPATATT
EGSPCGTTEGSPCGATEGSPRGTPDAQPLGLALKSGNFGSV DFFEKALRA
LEGA A

> gi|21233646|ref|NP|639563.1| avirulence protein [Xanthomonas campestris
pv. campestris str. ATCC 33913]

MPNASPALPRRLPARLLAAAL IATGLLGAASTASAACTAGPWTARANE A
GMPPVRYETTHFAFRWNGDGVSSADVRAAGEHLEMVWDTFINRLQFPEPA
CNSTTKTKASIHLDPGFGLSGGVTGSGNMGMW MAPGGLRDHWGLAHELTH
ALQGQTQSLRSDYTGWIWESHANWMTHQLPEFHASDVHCS SMLVNYPHL
YLGSTRDRYCNWQFLEYLKNRYGYAIVNDLWAKAPKPGDPAQRSADPFSV
LRTNMGWTQAQLNDVFGDWALRNVNWDYTNPDGSDQGALYRARYGSNLAF
DPQRTQDWDNRDRALRMTVLDPVAGQANRYRVPF EWAPQRWGYNLVQLIP
AAGATYSIGVSFEGQVQTAPAVTALPGLVTD PAS IPTPDSDRWGWVSIDS
SGRARYSALQRGAKASVTVALRSGDRAVYLMVMGAPT NMHKIKWDQSYA
IYRYPWSVTLSNAAAAGSQPGAPTPTPVGRRHANGGGWVANTANVASTAY
VGFARVLAGNVLGNARIDGHATVMGGTVQGNV LGGTLVWHPGAVIGNT
AQAQTVFMGPGAFGAVAVAGTTQVRGDLELREGTTPSQGVFYGYADTETM
RNPEFGADLRQAVPEITARPAGW

> Q4ZPS9_PSEU2

MGLCISKHS GSSYSYSDSDRWEVPVNP SNVRSASSHQTVSASDRASDKVD
ERPATFSHFQLARCGEDYTL SMVSLAAYQAERRHRGNLIKDRS QSALPWV
QVYHSETGLDYSFQIDRTTTVKVAGFNYNVPNDGETRHLYSAGTSQV NMP
VITDNMSACIAVACAENVDAGTGERRPGAKVRV FHLLPFRREDLMPEQV
LASVRDYLRDIKEQGLTMRVALHGGNREGDFSVSTAEALKSLFADEG IPI
EFDETCANRTSETLLGAVILNDNSTQFIKHLVAL

> gi|21233603|ref|NP|639520.1| leucin rich protein [Xanthomonas campestris
pv. campestris str. ATCC 33913]

MSAGGRVLQRSTQLRSYESV LLEWRDQCAANADQWREAWISANESVTGAE
LNLEVALRISAAHLARAASHNVASLDLSYLPLPRFPEQTFRFHGLQDMSI
AGAGLLELPESISDLANLRTLTLSONPIGALPASISRLGELQELTIFSCP
NLTELPEHLAIRNTAGQREGLVKLRTLTL SRTGIRSLPSSLEYLKD LTHL
KINSSPLTELNTSIHRLPLLEEVDLRGCTRLRHYP S ISGQQWSLRKL SLQ
DCSSLQTLPSNIDALRN LQELDLRGCNNLRALPPSISGLPDHCTIRAPAH
LQASLDQLRPRRPLARPWDVAGPSTPQVAGASS SAARPSDDDPAITQAR
QKIEDTVYALFAAIDEDRNPFVQNPYF IPEKREEGTP IVLGEVDGIQQM
LKES SREVFKNKLI GLANSLQORRI PHPWKASDR LDTAEHKAFVN SHLGT
FNEHSPINGVSLYKAAQMWK TRELLVHNDPTNRDFL PPIPTYSLPEQATD
ASES

> gi|17549106|ref|NP|522446.1| hypothetical protein RS01656 [Ralstonia
solanacearum GMI1000]

MRTAKCKASIRPNG SAFAAAGSRTAGMRACWKRSPTRRDMRCIAMPKHGL
RFPSILFRHAAQPARDATAQDNAPPSTAPSRQRQGLFRGLLP I GKR RGAD
NPPGAGTQTGSPPRVTAASPRLSRQASRAGETGSGRIDADALAGNPDQSD
AGWGIRLLRNARLNTTREAGGDATTAIQPHAGPTPEIEAVPVPI PPTPAP
APVDAGTKPARGIAVLP LN RQTSPSPSVSPTRAKASINRLPSGPKMDGIS
EPSTSLHRLNETILS TITEALGLGPLKATALAREAQIKQAGRRL LGSVIE
KPELPSAGTVKNLPPFYEGLVPGLRGQLGLATSRADCVISEHTQLSKLGAP
RHLLRVQFRASIDRGEYRLASQRGSPNYEAVA EAVAQRLAE AIDPQYRTDQ
RQYGIEFVGARGRKSSAEV FIEHFARHARVKPRQIRSTPSTINDANIRN
ADVFRALSPEQMNLARA AHVSHLSFKEETSTTRDGTVRHDLYLFFGGSE
NLRRDYGQAAA SAVGR VGHVFGAAKKAAWIVAQAVEQRQRDGHVHFESI
GGVSMGGASAVFAAALQGSVKLVAPAAPLVLLDPQLLNDAQARHATKGG
AHDYDFGGSRGVAITLDYPAAPRKS LMGRMKGLGYQSPGLVRIK LALQDD
DSVKQLDNGEWNRPKPYGPPLTGYHGD LALYTKALLRFTASPLPKPAD
AVP

> A2U5B4_BACCO

MQVKLAVIADDLTGANDTGVQFAKQGFRVTVLFAQTQLQPLHLNEDVVV M
NSDSRGLQEYEEYEAUVFKIAMHSRKLGVSKIIFKKIDSTMRGNIGLEIDAV
MDAFQFETAFIVPAFPKSDRITIGGYHFVNGVLIENTELAQDPVCPVNES
YLPTLLQSQSKRKVELLSISDVRKGGKHLSELMNKLASEKIPKLIIVVDAT
TDSELKMIVEATRNLNDFLWAGSAGIAYHLFDTGQAEELGKAEIKDRP
PVLAVAGSVNSIIDHQIRNLKEKHHVVEIVLSPEEFFYEDRKKREIENVV
TIGQDLLKKGDLVVTNREAEICRVKELQRRFGLSNFVQGTIAKSIGM
IAARLIGSVPCGVILTGGDIAGATCKVLKGDGIRVIGVEAGIPYGKLF
GGPYDGMPIVTKAGAFGTAQALSLSLQTTITQVYALDDKNKLTQ
> gi|21231996|ref|NP|637913.1| leucin rich protein [Xanthomonas campestris
pv. campestris str. ATCC 33913]
MDKNLNLWDMSTFIQQYGALTADHPHTHPEDSPQTVPSRSPSSSAHSPEIQ
ELRSLQETRPARGARSQSSSSKHGLQCCSSSPDESFRHLHAELAAWCER
VETKPSLLAKLGCAPVVDHREQRREMERIMRCLDAGQAGTQLTLR
DLNLSQLPPGLHRLAHLRDLVDADNVNLTLPEDLSLCKHLERINADGCS
IAALPSKIGALKNLSEISLAFNELRTPDSIGQCSSLTIVVPGCKINKL
PASLANLTQLKLDVAANIELSELSPHMNLDDVAVHSTQTRLGLMHRI FK
APTFFDPETRQRLSYQASALRDRWAALSHHLSPOARARVDQMREGASTTLS
SQDHKASTAWKTATEKVSSWAEEGAPITLDRIFKLNQLLLPEGDDNDPI
GGQLRKVGIQAAPSNTWTECRYPPPETLKDEMAKFSGWLEHSEQQAHARD
ALGHIEFAAQHLQRLVSLHPFDDANGRTARLAMDWALQRHGLPPAPPVGE
ASRLPASFLGGKRVSEPKVVLETLEGIATVMNQVHQ
> Q8Y2S8_RALSO
MDFPRRHSLSPLRFLTPSRSPQTERTPGASPAPGNTPRRASGPLSGLTKG
FNALFKADPEKAALRQAFSMAEAGKAEPLAGLLQSHPHLVMVAVNANGTTL
LASAAKRGHLEVVRILILARPESAILINQINKRGETPLQRAVEAGRTAVVG
ALLQHAIEDPNRVDKHGQTPLHIAAGNRHADITRALVEHPRTEVNRPRDR
GNTALHLAVRKRGLDAAGELLRHPHIDPNQPNAKHHTPLTMAIAKLHVDC
VHALASHPGVQVNLNPGTGDGHPVWQAVAQFVEHLESGSFARHRVRTGKEL
DCLFELASPHIDLNVLGPGGHTPLTRLACAKPHRYVQAGRDTTFTEIQH
KQRVVDVAVRAFLQGSSEGRNGFNPARNIDGQVAVQIALRNGHDALASRL
LQDPRTDPGAAVTRLIDKPGRLSRLNPPGPEPKTHGAGQAFVLEQLERS
IRFRNPDGTANPWSLALCEYAAARFEITAEAQRASAESRSCRPAASYA
AQALEFSMAFQQAPIIKVAAQALIHHAAPRHQAHFNLGGIDVSRSEIQAWA
AGDVPEAVLNAHIEQYVRDGRINVHADALLTRGQQLLNAMKRLTPEDQRR
SVEQSAADLRAVIGQRSDQLKQALKAEASEAALEALAAFEAFETVEAMEA
MAAEQAEDAEEAREEEVEEDAQEEAAQARAHEAEHQKARLKGRIDDL
NAGKGIKHLKMGPTKEDPDYAFHANVALADTWSYVQSRKDPKLDNLTA
ALLLRLADVQKDVPCNTGCIQRVAFASEGIDTSLHQGEPRGAMYEEIVS
IAKAVNERYKARYGEVEAFDPAAPGTSSAPSVTARDRQAAILRYTKGAEID
DDVVTDVCRDMVRADVLADLVGRRGWTRATVEELLAPILDNVEYLDEFVS
KASGSPDVHAGP
> gi|33596828|ref|NP|884471.1| putative secreted protein [Bordetella
parapertussis 12822]
MVPNGRNDIGQFAAWNLPRAQGYSAACVFQLEGALMTIDLGVSLTSQAGGL
QGIDLKSMIDIQTLMVYVQGRRAELLTAQMOTQAEVVQKANERMAQLNEVL
SALSRAKAEFPNPKPGDTIPGWDNQKVSRIEVLNDALRAAGLTGMFEA
RDGQVTPAGGRGTQVVNGTGMAGSMTYKELESAYTTVKGLMDTASNTQQ
MDMIRLQAASNKRNEAFVMTNTEKRRSDLNSSITNMC
> Q8XQL0_RALSO
MSRIFRSSSTQPTQAPSTSGGTSSTQATPPQVRQRSASFQKALARKTGR
ALGLVSAPRAEPQIKPGDKGPLGLVLMHRERPSKLTRAFVGPVQPGDSQPS
SRASSRASSHHTPERTSSSSSSSHSASVSGESLPHLPVHEKGLVQFAAVA
KWTVQGEVSDASQHNGVDERISMKINIDNETHKPKGLAHMDETRAGA
QGDLSVAVSQMVNLLKERMRLNGNPDEVAEAEIREALAQHQFPESLVYE
AKHFGLRTEENRAAVVARFYEWAADDAELAEDAAQHEEHPATHEAR
> Q8XPQ6_RALSO
MPPSIRGLGTSALLQHSPGDAAAGETSPPSNTVVRARTASAAFDRLQRRPS
LERTASQTPDTADIAHAAAAAIPYVRSLLPLKSDNKDYGEDDARIPPSKL
ARYHEDARDNRTIILNKIQCEIYALEATWRQSRQAPDFGALARII TSKGA
SAAGNCYEQAVLAYDFLRMRLTDANLPIDIVSLERPGDHNFAIGQSTDG
NGQYPKQFSDWHPDAFIVDPWTRIIACRAADYPRQWSEKMEKWAARGLRVD
DASPLDSSLLDALRDNNKISRKAFPV

> hopAU1 Pph race 6-1448A|Genbank: AY803995
MKPVQSVSATQHYNPLTNLQGEASCSHEISGITQTEGMQATAATTQTAEQ
LTTARVRDITAAAKVIPDGTTVMSR KPEDLSQLQTAYLAAKNAPTHPDLY
LKLCEFTFRVHDERHASEGHENICAKTMTARIDDDAIRVMAYASRGMHGGD
VNNFLKFSFNSGLPNPISALPSMLTFGASSFIGAVHGPWSGFGSALAF
AAKPFMAGGIQPAIVSLCDNIRGRNAPTVLAKGEVNDEIWLDAQAQTLEG
LNEDTRRALTSFDDAVQAAITSVGIRDPKFLETDEGLELFFDHLSDTHFN
CLREALQEVNNAALQNTAPQTRESLRA LEEASRPNMLEQRETTLKAEFSNL
RQKEGNDWQRI PRSLRASGGTTLTSGLSGLKRDEI PTRMNPALDRKSHFEG
LNALASPAVGTSYAAAAISLLQSPMAGLDERNKQKFNVKAIVFYDAFTPE
GKQRYLAGEEMDPDRDQAKLRGVFTSVSEYMVKSTQENLKQRQKVLGV
EISEAGHALNALPENTSSITPPEIRAKVERYKALSADMSAVTQAIAREGNP
NFLTDLDPDGEVKKAFDDCVNSGGMHVL ENMTKVYAKQGELKAQWTQKVS
TDVSMFGLAGQFTPSIVNKLAAAICGGAGHIPNAVVGFLGAYSLAASFIG
AQTQFAAINAKNNFREGNPKPTSLETFRGNLAPVMQASANRHSQHALQG
AEQAISTARQALNSSLGQNLRRRPSARTQQE#
> Q8XRI5_RALSO
MPNLPRVWRVAPAPQSTPPSPPEMGGGGTAALVGRAPRQRGPLSGLKARV
LPKSSSETEFSTMFGGKRYAGKPVNALKAYPP PALSEASALQPATAREQAR
AARSQAATAALVQRTQQGLQMRGTDNSHAAAASAE PGARQPVTVPE SARQ
YRQLLAQQFAATRDTGAVARLSARLEALAPPADAVGEHLRYARPTLVAEA
LAHTCGHDAAAALRVLASLENEARLDTAAFGTPDAPARASVSSATFHDAI
SEQEGPDEPDGPPQSPSARSSASSEAFFDAMSVLEEPGEPEDAGAART
AQLLSRYHAGFEALCDLMRLPQTPAHRHAAHA FLQAADALQGAAGQAAS
PQALLQRCPPGSGTPDDSLAIKTLHAAAQLRGEALSPEQTGALFAWRQG
FRAEGPGSDLAKVKARTAKFVSRTIRRVENHGWRSTLWQVVGKKKSPLSA
ARLGMQAHRVSLDKEYTAYAASLRALGMLGARYREALALSPAHADLPW
KQAEQMQGAILQHWASLPADAPLSAYVLTHDTLRTIGEQLRHTVLRVRE
ELTISLAHSAEAGDTPDPGMLDKLRTLVELSRQ ANLNLGASNLVPTPPPQ
FIDAYPSGAVLRKWEQVDAGAASGPLRKALDATERIEQQDDLKQEA
DAARGVIESLITTEGGGKLRSLASGTS LGVNTGTISTGLQNAQALAVPV
AIQADFHASHKRQAVVEIARGSHGRDLFVGTDKTVLAAAGFGASVGYDFK
VLQNRIRAMVGASVVPIDVEKGERVGMVYRAVRQVTQAAGPHADWDVAVKY
DDAATREMIALS NWLFQQATEHRERPPGADAVW NALAQHCSGAGADAIS
VGWVDQRKHLRHLKRVGGGVNVRVTAPAAPVRVGVVRLTGEITSRDTT
AMRETTGIMRAEQYSQGHGGHMTVRAGVNYAVGKRFYTS PAQDAAAAGPT
ASVPSGGRRSITQGFNGGTPLTYTKQFAEHSHTAKLKTVHLDGRLADRVC
YFDKEYKSAKEYLALIRSAQDTWIDMLSRKPGGTVEKARKEFEDYCATVE
QHTGPHIRYLLRERLRPAAAREVEGHLDLANLHRA TATGTPSGQADAPAM
PEAGAMATPPARKTSHMPRLRNLADKVTGRSQQA EARRMIDAIRARLA
SGQPEPGRMIRALQREAEHRQATARPPAEADAQACEAKADAVLFAEASWL
PEKLAIVENVSKRESRGVSLTVQMSTTEASGQRELNSLKFG
> gi|12620504|gb|AAG60780.1|AF322012|85 ID185 [Bradyrhizobium japonicum]
MSELFKGNNDWRHQFPGRDEIT STIAFRVTHPLVENAGDILLEHQIQIDG
NKPLVLSSHSSNPEAKARAAALGFLEVS DMMVLDPTKHDDKWKNEGGNWQ
RAGKPPLYLAATEDNSGNKYTESVAKPANDPYDEEYDFM
> gi|47013795|gb|AAT08443.1| outer protein J [Vibrio parahaemolyticus]
MKVNLEQNHYEQRGGSDLREQLSSYIDLMDDAIRQGGKQLPKDTAAANDI
ALMDDFIAIANQK KEGLNAHFFRSPLDMVNYVKSLIPSEDTTARFVVMNG
SGGIHCIAVDCAIKNGKCSLIGIEPVTMNSLGASMLAIRLQSVCKRELPE
TSLVIMETDMQRSQGECLMFSFLVKKMHKECDEFQYLHDKNINRELPLT
QGLIVSVKDADSLPPLSMKHTQSPNRLQKYLEMRPEAMNCVNNKGETL
KTRQQRHITTELGKTVSYSNSIEQKRRIKEAKGLLNNL
> Q8XAJ5_ECO57
MNIQPTIQSGITSONNHQTEQIPSTQIPQSELPLGCQAGFVNNIPDDI
QQHAPECGETTALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLD MFGLF
NVTQMALEIPSSVSGISGKYGVQLNIVKPDIHPTSGNYFLQIFPLHDEIG
FNFKDLPGPLKNALSNSNISTTAVSTIASTGTSATTSTVTTEPKDPIPF
GLTAQVVRNHGVELPIVKTENGWKL VGETPLTPDGPKANYTEEWVIRPGE
ADFKYGASPLQATLGLFEGAHFKWDLDNPNTKYAVLTNAAANALGALGGF
AVSRFASTDPMLSPHIGAMVQAAGHAIQYNT PGLKPDITLWWAGATLGA
ADLNKAEFEVARFTDYPRIWWHAREGAI FPNKADIEHATGADIRAMEEGI
PVGQRHPNPEDVVIDIESNGLPHHNPSNHVDIFDIIQETRV

> Q8XT99_RALSO

MLGGNITERSIRAPADPFVSPAGPDTERAGSPQHRPPATRPAALEGLAR
PPVCASAGTSMAAVALRQAEPLRALPAAMLQTPEGVVLTKALKYGALLQ
TLVSDASVSTDKREHAKRGVEQAKAGIEALS DLSRKGGLPSVAAVLGDL
LHHLAQAAAMVGIKAYHRMLNEEWDARTERFGIRSEHATAMSAYEGLRSAL
TEKPFQAMDELASYRAALDHFVEACKPSRPNDSPARLERNLPAVLSGR
VRCSARQSLDALHLALCGFSLRRIAVVMGLPDL SQRVSALAGAMKYRRD
EVETAIRRLDAVAMWYPGAEGAPPERLTVRQLAECKALVRAYRDGIDRVG
TQLCMDAAARIEAADTSPLWKTLLEVVVEVIARYKGWLDELCD SVRGGDPE
PAAAPGTSGQAPVSAPEIASSMPDPADALAVSDTVDPADATDATDATEAT
EATEATEATEATVTRTEDRGSPAPVRPLAAAPRPPDTRTAVQKQADGLLKR
CPVDSETAARFQGDAVAIADVFGKDRDIERLMDGRKTSAAVVATSMRQE
VDGWFFERRERLEQARSGLCAEDPRTGHLTDRLRALDIIDRYVTTWEADAA
KCALFPKAKHLERLLEMEGIEHVDAVPVLRSGKDKRNRDRVFEIRIQPRR
LSSPDGIEDGDRLPLFVHLHLSRPVDAGKLHTLSYGDFNAVHLKLAQK
GQGRNWEKMMHAMGYRDAKVERAMVGDALLRRLFALAGRDDASASAVAGA
PGAH

> gi|12025045|gb|AAG45728.1|AF229440|1_y4yB [Sinorhizobium fredii]

MEYCLLSPAQLIPTEEVNLDSVDALQAQILQAGSWTAPITAEKDALFVMD
GHHRLTVAHRLRLTTPVVLDDYDSVRVESWRPGENITPAEIFAMARSGR
KFPYKTRRHIFAHGLPICDVPLELSSPAPMDMAPAFSAGAL

> YPCD1.26c yopM secreted effector protein 16336:17565 reverse MW:46203

MFINPRNVSNTFLQEP LHRSSNLTEMP VEAENVKSKTEYYNAWSEWERN
PPGNGEQREMAVSRRLRDLDRQAHELELNNLGLSSLPPELPPHLESLVASC
NSLTELPELPQSLKSLLDVNNNLKALS DLPPLLEYLGVSNQLEKLPPELQ
NSSFLKIIDVDNNSLKKLPDLPPSLEFIAAGNNQLEELPELQNLPLFTAI
YADNNSLKKLPDLPLSLESIVAGNNILEELPELQNLPLFTIYADNLLK
TLPDLPPSLEALNVRDNYLTDLPPELPQS LTFLDVSENI FSGLSELPPNLY
YLNASSNEIRSLCDLPPSLEELNVSNNKLIELPALPPRLERLIASFNHLA
EVPPELQNLKQLHVEYNPLREFPDI PESVEDLRMNSERVVDPYEF AHETT
DKLEDDVFE

> hopJ1 Pph race 6-1448A|Genbank: AAZ37567

MMLARWFTACTASGKLNTRKKQTPNNRRRSPRNPNTDLNLSLRTSLRSG
EHVFADTLAFIAEGYDYPQPFRNGAV DNAAGQNEGSCKTGLLALLEGLS
DEEALLAFGEHYRSVQATPEGSDHGNI RALIEYGLAGVKFEGEPLKRKA

> Q8XQA2_RALSO

MKVNPPASPGASVSSPSAVQEAAQTQ PATEPSASRAHAAGSPLASLAELS
QTRRAGVKRPAGDDGAGSSSEPPRKM PRRSVK FAMSFRDGAPRRPALARH
SATDAEQADINRQIETNQRAFLVQKLGAKQPVVRLQSELGAEIARHLPA
QDQHRLDATLARSPEARYEHARLLPPQMGGAYLNRDEEALALALAETDSH
GAPLSADARLD RAGWLLLAGTRAAALPDVQLIGRMRRAVRQARVTLFQTF
DRAGPAAQAEALSRLIGACAYAGSQADALRW TREALGEQRFYSLPPGERA
DALAEALAEHLDNAEAMEWDRLLDDFTDLAMRAEHERTLARLHTNGLASTLP
MMLDAARRIGMPSPDAEELMQSVVN MARRSMPAPATQQVMLDLFSILLP
HLQGNARADGGARLM AMLPELPAIGDQLRLFNGLRRPPGTPPSENRLSH
LDVAGQYALTQAVFSQLANMGEHVMREEMKLLDNQLAPGRLGRFPGAAL
ESLLTDAARLPVPASSRPQLLSIVERALEALPGGRIARPLRKLLEIRAIQP
PAWHLDAREAAA WHDISPRLMQAWHLLPRLPAVQCADALAFVTRVPGL
LPLALGQLAAVTVDEHRAMLRGIEDPLRTAFADTIAHTLVGSPGLLYDAI
RHALSIA PVERRTTVV ASLAATLAWTATAVSSPLRDNVALLMEAI GRQCL
GAVPREQLESTLAAFFRRGELPSLPSLAAQHLSLNLADEARVLAGLTNA
VASLDPPTRALVFSFVMERLAAQAAGQAGAFARIAAGLPPDVARTWAGQL
QTELD AELGLRLASGPRATVDPHLERLAAEAGRALEFRLSSQPGPSEAR
GDawnRYGTAVAMIEALHAHHPGPGPYA

> Q8XRH2_RALSO

MSSPAPLSADALIDRIRTDIRSTG DAPDVAARHEHFYLMQALRS DILAL
SNREPDDERVVRCIRVFHEEVA AFKEAHA IARLPYSPAVDRRYPPFRDAAG
EPVYVATLAPTGPQAQGSRRYGAEAVWPYLDAAEAPEGLGALYLGRHLHCR
TMMAADLRDPRESALVGERGVFAARRIERGECLGIYGGRLMTPATYYTCL
DDAFVLSSTTAEGIESAVDGENILAMANTVFAYEGEHAVSQAADGYNMEEA
VFQATTRCGRRFAIRAFFATEAVPA GDELRWNYRYAPALIRQRFGLPA

> Q5GYE5_XANOR

MQIKTASHSPNAHPHPVAGDGSSPADRSIEIEAGHGSGTVRPADGTQAR

ACPSPASETTVCLADLLS ISSQRPSRPEVIPAIVQAGGDEGVDPVLPQPA
RSGASQPRLANPGEARDVESRLLMRDCSSRIA AFLGNLSVVQELRQFDSS
AFVGGKLRNELVTEPGCAEPKTL LAAIGEKVAELWSHLDDKASTPEEAEFL
AEARRYLEPVL T SLETDIHTLQHDASA AKRIYQGAL TLLLYPLPLATLFT
QKTGTYYAAFNIASYTYTAIQLVSLMRPPTDAKLFMKHAINRHSLVFFIS
LIYAVPTFYAKASPLQRNAGFTAGAAVAQGTMMFGLRLGQNLMSMRLRF
NGAFNRRRDLDPGFRDAIEGVVGLR TGLSNVNR SVGEFQQDRRITPHMD
RQLTFFKQDL SRVVTGLERLLATGTRKETPVAARDDAPGSLEAVRRTLEA
SFANNPDLK GKLA LATVAFAVLGSNIALMRNNGLALPDFIADAVVSSTFL
LSEALSPHVTHAGMND SVSDTVGGMTIGLPFSVA VMSSYMDPRANPSG
FIAGTVGYTAAYLLFGRVAGDVLSKGLMATSGALGWQQQAIRLGRSAMA
LGFELVAGHSSPAAADVHDVAGVEMAGVPHEPLFFSPSQRASAERTLVGT
LEQIGDEWH DARDEWEGESEATAGRDAPWVDAPAELMQPAPQSE
> hopF1 Pph 1449A race5 & 7|Genbank: AF231452
MGNICNSGGVSR TYSPTSPVYGSVSSPSRFVGYTLT SIHQLSSEERE
NFLDAHDP MRVYDLNSETS SVYRTTQREYVRNGYATGNPNSGAI IALHEEL
QESPYAQHIGARPQADAYRPRTAHVSSLNTPSLNVMAGQGALSALRGYA
GSDHVTTEMRLGDFLDQGGKVYS DTSAMSAGGDSVEALIVTLPKGRKVPV
NILD
> gi|55977841|sp|Q05 608|YPKA|YERPS Protein kinase ypkA precursor (Protein
kinase A) (Targeted effector protein kinase)
MKS VKIMGTMP PPSISLAKAHERISQHWQNPV GELNIGGKRYRIIDNQVLR
LNPHSGFSLFREGV GKI FSGKMFNFSIARNLTD TLHAAQKTT SQELRSDI
PNALS NLF GAKPQTE LPLGWKGEPLSGAPDLEGMRVAETDKFAEGESHIS
I IETKDKQRLVAKIERSIAEGHLFAELEAYKHIYKTAGKHPNLANVHGMA
VVPYGNRKEEALMDEV DGWRCSDTLRTLADSWKQ GKINSEAYWGTIKFI
AHRLLDVTNHLAKAGVVHNDIKPGNVVFD RASGEPVVIDLGLHSRSGEQP
KGFTE SFKAPELGVGNLGASEKSDVFLVVSTLLHCIEGFEKNPEIKPNQG
LRFITSEPAHVM DENGYP IHRPGIAGVETAYTRFITDILGV SADRSDN
EARLHEFLSDGTIDEESA KQILKDTLTGEMSP LSTDVRRITPKKLR ELS
LLRTHLSSAATKQLDMGGVLSDDL TMLVALDKAEREGGV DDKQLKSFNSL
ILKTYRVIEDYVKGREGDTKNSSTEVS PYHRSNFMLSIVEPSLQRIQKHL
DQTHSFSDIGSLVRAHKHLETLLV LVTLSQQGQPVSSE TYGFLNRLAEA
KITLSQQ LNTLQQQESAKAQLSILINRSGSWADVARQSLQRF DSTRPVV
KFGTEQYTAIHRQMMAAHAAITLQEVSEFTDDMRNFTVDSIPLLIQLGRS
SLMDEHLVEQREKLRELTTIAERLNR LEREM
> Q7DB68_ECO57
MEANLSPSGAVMLATSLSGNNSVDEK TGVIKPENG TNRTVRVIAGLAL
TTALAALGTGIAACSETSSSTEYLALGITSGVLGTLTAVGGALAMKYA
> ECs4550 ECs4550 EspF 4589257:4590003 reverse MW:25252
MLNGISNAASTLGRQLVGIASRVSSAGGTGFSVAPQAVRLTPVKVHSPFS
PGSSNVNARTIFNVSSQVTSFTPSRPAPPPPTSGQASGASRPLPIA QAL
KEHLAAYEKSKGPEALGFKPARQAPPPPTSGQASGASRPLPIA QALKEH
LAAYEKSKGPEALGFKPARQAPPPPTSGQASGASRPLPIA QALKEHLAA
YEKSKGPEALGFKPARQAPPPPTG PSLPLA QALKDHLAAYEQSKK
> Q8X394_ECO57
MDFSWEGRELEFLIYFNCINILNGLHRVNSSTPYS LAYNTCCNLHLSAM
KKHHL SLYEILD LPSANLSFQSTFKYCIYLP TRSYFRKLN MNDNIPTARN
HKQSTCITEKTCLYF
> gi|16764579|ref|NP|460194.1| secreted effector protein [Salmonella
typhimurium LT2]
MPITIGNGFLKSEILTNSPRNTKEAWWKVLWEKIKDFFFSTGKAKA DRCL
HEMLFAERAPTRERLTEIFFELKELACASQRDRFQVHNPHENDATIILRI
MDQNEENELLRI TQNTDTFSC EVMGNLYFLMKDRPDI LKSH PQMTAMIKR
RYSEIVDYPLPSTLCLNPAGAPILSVPLDNIEGYLYTELKRGHLDGWKAQ
EKATYLA AKIQSGIEKTT RILHHANISESTQONAFLETMAMCGLKQLEIP
PPHTHIPIEKMVKEVLLADKTFQAF LVTD PSTSQSMLAEIVEAISDQ VFH
AIFRIDPQAIQMAEEQLTTLHVRSEQQSGCLCCFL
> hopAW1 Pph race 6-1448A|Genbank: AY803997
MRVRSNTLQPAVEHTTQATIGGCSSSTASRIKEIPFKQADELARVGDQR
AACVVLTAAWLDRVHHHSQPAEARIDHMRHRATLEQVAERQQTYRNHEIN
NPRTPYEILFSPTRFDYSLRLSNARILDIMSDEEQAMGSMANTLRDPNSS
HVLVIVRMNGDNHAIATH CTGNKLHVFDPNHGEYSFKADTGTVEESMRDI

IQAYSSRFVPEIHILPVR#

> gi|28871468|ref|NP|794087.1| type III effector HopPtoE [*Pseudomonas syringae* pv. tomato str. DC3000]

MNRVSGSSSATWQAVNDLVEQVSERTLSTTGQTAMGRNLNKPESDADA
LMTMRAQQYTDSAKRTYISETLMNLADLQQRKIYRTNSGNLRGAIE MTP
TQLTDCVQKCREEGFSNCIDIQALEIGLHLRHKLGISDFTIYSNRKLSHNY
VVIHPSNAFPKGAIVDSWTGQGVVELDFKTRCLKFKHREENYAVNANMHEW
IERYGQAHVID

> Q8X782_ECO57

MLPTSQRLRPTGTFTCSYSAETSADIKSEITPIQIEEARASGRLYIKDCDIE
YLPQLPNEITSVFIENCNNLTLTGLPVNTQNLVINCEKLOITDMPSTV
KNLHIELTDSFPIHFISEGIE CLTVCHCYISGVPESVRYLEIKGSATDSI
KNVPNGLSSLSINSYNPENQARIDNLSPSLKTLSLTGCSNIILPEKLPE
SVTSVTIHAEQKTTWNIGVEGMPDGLDLQNVLLSPDVVKAKNITFQGN
ALDVALHFREGDIVYGLSSPREKLVNSIKLVNDFSKKDIITQNTLTNAVW
DPRTPRKYKQDPLIKRALNEHERGIKFKQHLKNHNNYNVTMADLSVYNRD
KLWAKTSKAGLEFQTLTRNKTV IFCADELVNSLKLIAANKSEGYQQSITAS
ELRWIYRNKDNQIMKNIKFYLHGKEIPAERILDTPWKDYRPKYSGSTY
KYS

> A0TW66_9BURK

MDRRRRHSPGSAQVRRVSTSRRALGCRIEGQAPARQQPEGAHARRHEVH
LPAPAAVNALAPHAARLLIVADDLSGAADCAVAGLRHGLTATVVLDAAHA
AAPPHGVDILSIDVSRRLPKDVAARRTVDAVASLSSAGTRLYKKVDSTL
RGNFAAEVAALTSRAGMAIVCPAYPASGRTTIDGRQWVRGVPVEASEYWR
NEHIPGTADLVALLSAEDLRVAYMAIGTVRGNANALTAHLRGLQSDRMQA
VVCDAESDDDLQRIARASAALDGVFWVGSAGLAPGVIEALGPPHGASGPT
AGGPHSKGPVLTVVGSMSSISHAQLDCLKANAGTHLVALEVSVCALDDPR
SDVTTVVSDALRGRHVVVLSQARRGDVDDGLLFSTRLAALLAPAVRHA
GAI IATGGETARALLTAAGASALRVVDEIEDGMPLLECRHLGHALPVVTK
AGGFGQPESIYHAWRRLANTGEPADTAQPNQ

> SOPE_SALEE

MTKITLSLQNFRIQKQETTPLKEKSTEKTSLAKAILAVKNHFNKLSNLS
ERFISHKNTLESSATHSHRGSASADRAVLTNKVVKEFMLQTLNDMDIRGNA
SKDPAYASQTREALSAVYSKNKDQCCKLLISKGINIAPFLKEIGEAAQN
AGLPGATKNDVFTPSGAGANPFITPLVSSANCKYPHMFINQHQQASFKIY
AEKIIMTEVAPLFNECVMPPTQQFHLILENIANKYIQNTP

> gi|17549774|ref|NP|523114.1| SECRETED PROTEIN POPf1 [*Ralstonia solanacearum* GMI1000]

MSTNISSAASPTLPLAGPGVNGPAEGKSDMPGSLFFQFDHSTGSTRPDL
TDLFFSFGDSISRVAQDASNQSPEQAPAADPAPASPDG QSCQPSQPATPP
VGS DVTWNGGTLNDTQLQIIGILNLHKDKGDISWDKLDKINDPDTPPDL
KVALQALSQDFNLQAIQSQDGRFGGKIKGKDLAEFAKSHSQVLTWNSG
TLNDSQLEIMSILARHKDKMPVDWSSIQDKINDPSTPSDLKAALQALAND
PALFFAIGSQDGNCKGKIKAGDVSKFADNHPQVEEYNRKKAEGYVKNYI
PSDAKPGDKPSAMTQNDALRELYRYSYDLPKPKLDMEAFQ RIVDGDSDVKK
APPQVIAAAEYFLQNRNEWASLNKMDPDKRVGKSDFLQRAASAVHLSKE
DLQTVSTINSNLDVFFKDGQKITRDLAAMSQDESLSPAVRNAKQLLQD
PLLYGLINNANSYKTKNGFFSFGGPTVDSGVIGKDFEKFMSMTDANK
TVQARKTHPANSEASKSAVADMGMGMEDQPDIAVKKSGGALKKAMDKIL
TIYSKVMDIASQVVGALGVIPLGGEIADALSMGMAAGASA AKVLSTLLNG
GSLKKALAEAGINLASAALGAVAGPEARVALKNGLTKMLVEKVANTGIDL
AVDKAKSFVDGYLQDLKGRQLQATAANAANTVNTSVNWWSDKTKDFLENPV
QNLTPRVNIPGITPYQPGYPMVAAAA

> Q8X395_ECO57

MLQLSSNIGWKKGAENALKNKIHSFSFVNPDEFSCDTQFLKCPITLCVP
EKGVFVKNALNSNICTLYDKSAFMNLTREHLPHPLSREKIVKEMIIERNM
CYFDTISQHFIMDADQQKQCHCK

> hopAA1' Pph race 6 -1448A|Genbank: CP000058

LFDRHFAALLSRNYSFRTSPPQRFVQTPHINRSAPQPPGIEMESFRTAS
DASLASSSVRSVSSGAQNNLHAITDYLDKDHVFAAHKLPPLTDSLEDHAAIH
AHNEQIDALIDARARLSEQGEPRASIGETFKAKEKFDRLATTASSALRA
TPFAAASVLQYMQPAINKGDWLPAPLKLPLTFFI SGALSGAMDQVGTMMMD
RATGDLRYLSTSPDRHPXXXXDAMATSVKRHSPGLGRQVDMGIAVQTY

SARNAVRTVLAPALASRPVQSAVDISVSTAGGLAANAGFGNRMLSVQSR
DHLRGGAFVLGLKDKPEKADLNEETDWLDAYNAIKSASYSGAALNAGKRM
AGLPLDIATDGLKAVRSLVSATSLSVQNGVALAGGFAGVGLQEMATKNIT
HPATSAAVSQTNLNLAGSAGVFAGWTTAALATDPA VKKAESFIQDTPVKSTA
SSTTGIVADQTVKLAKTVKDKGGEALVNTGASLRNTVNNLRHRPAREADI
EEGGIAASPSETPFQPGRS

> Q4ZX80_PSEU2

MQAPTVMNRNTGNVIAPEATARADNPSNIRQQTEQPTQRSSSHSLGSMGKRL
LKSVMGKVFQKSRAPRQSAARPPSTQPPSSPPRSSREAGRNTSRDTRLDP
NPPPRNDPPPKSILRTRANTSGETTKHEIEQGSTRADTAPRNNRRVTFNLP
QDQLTRASSSEQLAAPMTDEEAVASAMRERRNPGGRLQGPDPGTRQSMQPV
DPNTASSSGTQADDDPGPLARRNTGLESSTGGSELRSQELIRDTRPQAT
IRLSADGKPDFSSFKTPGMAALLNDILAKPGQTYLAQQSEQGVQDHQLLQ
ANGHLLHLAQGDSSLAVIRSSEPTLPVAGGKPPVNMQREENHIHLDTLD
GRRSQELPGKAHIAHLTDVHQTTNGDRLRVHEDRLYQFEPLAARWKPVDE
IEDIAFNRLITGGNGSVYAKSDDVVVDLSSPFMPHADFNLDKSFVAPDD
TAALLSGSDVQTVLLTDMSPVIGGLTPKKTKTLELDGGQAQAAEVALSND
RLFIAQTQGRLYSTDRSAFESNEPTLRLMPERAGYRLDDQPMGGHNSVSG
FISGDDGRVHALIRNRQGEVHSHALDEQGAKLESGWNLTNALVLDNTRGL
TVMFAPVADRLHLDRAGLVGLNAGRIQRWDATPQCWKDAGIKDVDRLQR
GADSNAYLDLGGKLLRLDVPKHPNVAFDHNTALAQIARSTKVAMGKEIA
GLENRVVTAFAVMVSDKRFVALDDQNRLTAHAKDHPIDLDTSIDGDIKD
LALDEKHNLYTSLSTGKLYCMPREAWQATRFGGQLAAKWTPLAAPDGGQPV
KALYSNDDNRLSVQVEDAAGQLMQLKEGQWQAFEQRPVEKNGLNDVYNR
ITRAHKTWRIPGTGLTANLDINAFGRSGMEKSNRPTASEAIRANVYKHTL
EPPRWMKNVGNNIQHRYHGREGLEKELYKKELIAFKQLELVHEAAGAPPTP
GNDLKARIARLQLGPEGAELAKELEVFRDELEKHARTALENIGKDYGKLL
NLKQNDGVLNQHSALAKPSKRTQLGKKLAEELGSIILNFKSSGHDFVKELDD
ALTRIAPSANPTARTLKLKLDNGVKLSHTKTDIGLQRRDANEDHGLSK
ARLALDLVTLNLDGALIGKVELLARSDDLRLQAEELTSLRDVTYGENPVK
QVTDMGFTDNAALEGAYDAVKAFSNALKKSDHAVSVNMRAATGSQNQSEL
ADTLKAMLKNLEHGDDIEGVQRSYGLNLTSPWVVLADKSTGPWPNAGATG
NRNYLFSACERCEGGVTLYLTREAGNVNGGVGGKDYWPGFFDENHPARS
VDIGNNRKMTPNFRLGADVTATAAASQRAGVIFNVADDEIDGFVDDLFEG
KLNPLQLLNKVKDHETYEARRFNFDITTFGSADMRVGFGLSEADSAPLSA
VARLGAANVTVNLSSYTDYSLTQKNDKTELDRDGGKNRPRFFNSLIFGGQ
ARGQISGTHSNSTATPTSAAGPTPATQSAANNLGAANVTIDDKTVKRVK
FRFNVATPMTTESLDKLSKSLGAAFKDKATTARLAELQNPLNALYVDMNP
EQAIQARVLDGLKALFAERPSQNDTQYKALRDLKRAQVQHEASINNHSVLD
NARFETSKTSLSGLSKESILTRIMGSLRDASAPGNAARVAEYMRQDPTLS
AMVKQLENSQGTLARIRLEPKDSLIDEIDEGSRRGTLTQTELSGLENRN
NMRIRKLVVFTPRQTFENFTSPTPLISYNSGASLSVNKPLGRINFIYGED
QDKPIGYTFDGEISRPSASLKEAAGELKLSGFVKS

> Q8XT19_RALSO

MKFNTRHRLNPPAHVGHTRGHAPAPAGPQRSRAPRARPDLPGSSRGAA
RTARIPSSAPGEALSRLNYCEYNLAGERRTRLENERSQQQNELGHKSGI
DFPARCIDMARNNVLAESNNGHWALVFLFPGGSDTNTLLGDYLAKLGD
CEHGRVEPALSGRIRACAEELCAHYLLHTSWFEGAPAASYAYPASKFSKFP
DSRPCMEALDWIARQALQARNLQPMGDRKASQFVSGLAKNTRSDACRDAV
QRIVHWLLENSAVRARLDAIQVPTLLNALS KWATHDGATSLALQVADLLA
SKPRLREALDRQIGNCLNALS KWSTEPWAENVVMQLAGRLTAEPDLRLS
LRGQELVNSLNALS KWAHCEPAKQAILQLADRLATEPQLRRQLNASLLSS
GLNALS KLSGERQAKEAALQLAHSIAIEPRLQKIDAQAVANALNALS KW
PADERAIRAARLLADCLVSNPGLRRALKPQEFTSTLNALS KWQHEDTIKQ
AALLLAERITTEPALRAAMRERDIANAMNALCKWPGADVSKQAVLLLAKR
LEAEPQLRNAMNDQHVSNLTGALS KWPDDEEQASRTALLLVKRLVDEPRLR
QSLEAQGVANILNALS KWPHDLAKQGALLLADRVA SEPSLLTAMDTQET
INTLSALS KWPGEPATLAAQRLTAASTGRWATLDARNLSNALIALSRWP
DESWARQAAMPLAERIATEPLAWNSADPQSVSNALSALS KWPDENQTRLA
TRELAGRILADEKLRMAFDAQALAHSLNALAKWPNEPEAMRALWQLSTLP
GRASHPWRTFNLDMAQISNAFARLLQDDGEDLERARGILQHLAVHLELH
PECFERSSVGHIGVLFKSFANLRILPSLRPLSRPVLNRVMTLCRETQLRD
EPLETIGNLCLGLLPLARSPELVHRASALRAF DALQPIVARKIDSYLRQ

GERATTGAALLVTDGQEQACGTRGPALTFYQILKAYTLVARQWKRRYIQDA
RQTVHDRQAALQQVWVNDTLARTRSVIEADLQEKSWNLIAQIEAGDDVLNA
LDLRIIGKDLEHITQRHPPTRFDLAGAHRMGTAPGRVVRVPTAGVGDTRHV
TVDLQGRELKVDDGIHPPYSLYARLTGQPLVEVRLPGKLSFMLARTFYQY
QGEPWRFDLFGGSRLTRGRSNRVVSI LAGDRPLPSVLP A IRYADSAPGSA
FMALTHKLAPQREDWSRMQRALLEMPHDHVVEGTMRIGWFKDVSGPQHP
FKLTGPGGQRIALCPNDGCGFLKWEVAMQIPAVREQIEAWHAVRRGRATD
AQQQRIADQAPGFNTMPPQALMHFPRDEAVLVEAHEALQHRLDKLRAEVQ
GRGAPASKLEAEAGALSPDAVDLLTLYQMATSGGYQRRIRAVPSADDKL
YLPTIPMNGFARPA GDLLVGKPPYDKNLLPIGPERVGTAVHG DATGRFL
DQCFAIQYSYTFDDGSGLAADMLHSGMLIIPPLGYWSAAHGMDLACS
TEDLKVLSRWKQGRDRDSVPARMLSTGSLRVKDILLPGRLGALPIPELRK
RNMDTDGDDAFVYAGYPKLAAHIRRVMDDRSDRRGTEHSFKPPKTANPAF
DSQGQYQAGRAREILAEQRGGQLVGVASNAATRFLSQPDELREAMATSMM
FGTYDGIERRLRNGLRALLEGREPAPALQELQALAHQAIARAHLPEAHAV
AVLLHTLTTLTQLGAAEAQVPVQLAADVTQRFSP LAEAWSAADTPARIHAI
LDHY PVCRLSHEQFPKGQPGYVKGQPELTMRNLFTLAVKVGTDALKSDTG
TELF TT LIQKCEAVERSFPGRVRYVPHTKQTAREFRNERFDPERAVATLE
RIPTLAAGVMQDAVSSIQQAGLLVARPAPAERLRTVSPEAMDRAAIVLNE
RAHTASAQITPLQLTNLRAWIGADLGADAARLAGLEHAVKSAGSLKDKLG
YMTAAKQLPDLQDALS RVNDALRYSIVLPPDTFVAASRILAGLEKHGHA
MTARTNHFSQPGTAFGALSVTLQAPSGDFLWEIQFHTEQTFELKARHHNL
YKQAQQERHQGASSDAIRALLRP AWQDFRAVPVPAGCEEIDDWQQESVDT
APPSHPVREVQSAQPIAAYLRPLVRELGTQHRMEARVSPKLOPLVQKHG
GKLREDKPGNWRQFI FKKERSIARKIALRQRANEHLTPEHAAARVRD TLR
YEVILPAEGFGKAVDTILKTLGRHGLKAMRLKNAFMRPDTTYAGLNVNLR
LADASAPGD FEIQFH TAHSLSLTKLKMHRDYEKVRELPPADARIDGDEAGL
DFNAERERRLKMRDAAALVERPQGIETLIPFDLYQDA

> gi|29840502|ref|NP|829608.1| hypothetical protein CCA00745 [Chlamydomonas
caviae GPIC]

MKVQKITALICSLVLGFQISGSAKTLVQKNACSDLDLFEHLLDVKYAPKE
WKHKLFHWDLKDATDQARLKLCEENPSTSYCQGVLAEYISDLKDFHAGI
TFFRTENSHLPYTVKLSNSRRCFIVDVHTYNSEISVGDEILEMDGMPIME
VIESIRTGRGALS DYAAAARTLFSRS AALGHQIPMGVATLK IRRPSGLTR
TVKAKWRHTPEYIQDLSLISPLVKDPIIQMRSSRACPLSSASENCLFTN
EMVPYFWKELRQQYKRGSLSSDYNIGSKRGFLPDFGHV TWKAKSGPYHAYV
FTCTDNHGQSHSIGFLRISTYSWTDMEDRTAMNMESPWDDFSEIISVLQE
KTEALIIDQTNPNPGGSVFYLYALISRLTDRPLETPKHRMILTQSEVQSAV
QWLNLLLEGVETDEQARNALGEDMEGYPIDMNAAGYLQTF SNT VLK CWANG
DINLSTPMP LLGF AKVHPHPEHRYTRPICVLINQEDFSCGDLFP A IMKDS
GRALIVGTATAGAGGFVFNVEFPNRTGIKCSLTGSLAVRPGSYIENLG
VSPHIFLDFTD TDVQTGKYSDYISTVKS LVLDLIEREADNKAS

> gi|58579718|ref|YP|198734.1| HpaI [Xanthomonas oryzae pv. oryzae
KACC10331]

MNSLNTQFGGSTSNLQVGPSQDT TFGSNQGGNQGISEKQLDQLLCLISA
LLQSSKNAEEGKGGQGGDNGGGQGGNSQQAGQONGPSPFTQMLMHIVGEIL
QAQNGGGAGGGGFGGGFSGDLGLGTNLSSDSASMQ

> Q28MT1_JANSC

MTVPRLAWYGD DFTGSAAVMDELAQAGLTAVLFTRMPDDATATRFAGYDA
VGLAGTARTRGP AWMRRELPGVFDWMERTGADHLHYKICSTFDSSAELGS
IGLAAEIGLAQLGGWAPCLT AAPSMGRWQCYGTLFARGPDGAAHRLDRHP
VMRQHPSTPMAEADLARHLAEQTDLP IGLLTLDQLAGVPERDRDGI VLL
DAQREADMVLGAILADNAGLLLSQGVEMALIAHWRAAGRLGSEQPRT
PLRPARLAVVSGSVSEGTAAQITAAKAAGFATFALD TASLLDGAVPDLTK
ATAALRQGASILCHTALGPQDPRLSATRDRQ RSLGLSPEDTAERIGTALG
QVLARLAPTAERL VVAGGDSS GFVTTALGVDALTALAPVDPGAPLMRVHG
GAADGAELVLKGGQMGARDL FVRLRNGDR

> gi|15618718|ref|NP|225004.1| hypothetical protein CPn0809 [Chlamydomonas
pneumoniae CWL029]

MSISSSSGPDNQKNIMSQVLTSTPQGVPPQDKLSGNETKQIQQTRQGKNT
EMESDATIAGASGDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVS
GAAATTASNTATKIAMQTSIEEASKSMESTLESLSLSAAQMKEVEAVVV
AALSGKSSGSAKLETPELKP GVT PRSEVIEIGLALAKAIQTLGEATKSA

LSNYASTQAQADQTNKLGLEKQAIKIDKEREYQEMKAAEQKSKDLEGMT
DTVNTVMIAVSVAITVISIVAAIFTCGAGLAGLAAGAAVGAAGAAGA
AAATTVATQITVQAVVQAVKQAVITAVRQAITAAIKAAVKSQIKAFIKTL
VKAIATAIKSKI SKVFAKGTQMIAKNFPKLSKVISSLTSKWVTVGVGVVV
AAPALGKGMQMLSEMQQNVAQFQKEVQKLAQAADMI SMFTQFWQQASK
IASKQTGESNEMTQKATKLGAQILKAYAAISGAIAGAHKTNNF

> Q8XYB9_RALSO

MPSRMGYSRISSGLNASRGASAPQPDPPTPPDNRRTMRDMPLEGL
HHARRSAVPGAGSSGGMPQTARSLPRRMESRVSEPEREVPERAT SEPRP
EDASTSDPMRSAGRERSCISPPGSRAGADAGPTPAQLAEYERWLDAAAL
RQLDAQVREEEQWQLQALVQDAWNKVDLQCAQLTSDNILARRNGCGQAL
VFLDGAQSAENARRVGDYLVLSQSSAQAGRHRGQRQLERCVDLAASYLF
KTDWFDGVPQAQLSNLGNLLSKYPTRPAAMEAVAWIAGQVLAPVRLPRLN
GKQLALLANAFSNTDSLRCERAVARIASQGLDHCTEALATQSISL LFNA
MSKWPDNVAVCQTAERLAAWLAEAGTLRAMTAQEVASTLNALSKWPDS
ACRQAVERLADRLAKESRLRQALSAQQVANALNAMSKWPKAQACRTAALQ
LVGRVADDERILLTLNAQGVALLNALCKWPDADACGQAVERLAERLARE
RGLLQAMSAQNVANALNALSKWPNNKACRLAAVLLAERVAKESRLRQAMS
AQQVANAVGAVGKWPDEAFCKAAAECLAVRLADEADLRWALSAQQFV STL
SGLSKWPKSNDCGRAAQCLAVRLAQDAVLRQALDALGIASTLSALGKWE
ASDCRIAAGYLAARLAQDGGRLQALDVQGIANALNGLSKWPNADDCRTVA
KHLAARLAEDAALRRALDAQGVANALNALSKWSDVEGCRVAAEHLAERLA
TDADLRQALDAQGVASTLNALSKWPDVAVCKAAAEHLAARLADEAGIRRA
LSPQGMANALNALSKWPTAANCCLAELLAGQLLRDPALWQAMNAQEF AS
TLSALSKWPDTDCCRLLAERLAAYLDKQADLRQALDAQGIANALNALSKW
PDTAVCKAAADHLAARLAEEADLRQAMDVLGIVGALGALSRWPEADTCRM
AAERLAARLRGGRPELLRAMSAQQFASALNALSKWQPSEACQQAALGLADA
LGGSGRPFQAFDMGSLAKLANGIARFAAGLAGAAVPPDEDEDGQANAA
LSMMHACLRLAAHLSVRPAGLDAEETRDVAMVFKALATAGLKDGLKLL A
RQGLQRLQVLHEQTLRLRPSLETGLS LAAGLLPLVRS PDLKPFRIDALRL
LERMQPDVARKVQHYTDAHAASAALAKARSPEGEAFGVRPGLTFFLLK
TYAVVAGQWKQRNAADDRARVAQRREALQAWIGNTLEQVRGAI EGDLD
SWNLIAQIEAGDHVLDALDLKLRDMDRITTAHPPTRLDVAVRRELRGL
SAVRDLMGSEAGAAALQVDMRGNP IRSGPDALANYSFFTRLTGGKPLI
EVELPGKLSAFMLARTLQHNGDLLRMDLFGGSHLT PPNTRVFEMLSQAQ
AAKRYGRIPAIRLADTVPHAPLMKDVIRKLNPPQREDWYRMQRALLEVPR
DHVVEGVPRLALQADRPQGT E PAFALRLPTGEP IHLVSHDGCFTRESLA
RRI PAMAAAMDEWARSRRQAEPPAPRMTSLPPQATHHYPRNAAAI EEA
RTHLRRTLQEDATLWQAEVDPDGT HRLGTTRLYELLVGAGITGVQGIAPS
ADSKVYLPGEKSGPFD RAGGPVLLGKPPYDKPNLMP I PAERVGT PGQDA
TARFLDTAFQYSYTAWDESRTRTPSDDAPMLHGKGVTVVVPDALWPKG
NDAQVWVSTEDMKIHSWTRRRERDRLPARMDTVGSLRVKDI FAPGALIA
VPIDELGKRDCDGDVVFYAGAPKMAQAIDGFFSARERRIGRMP SFKP
VKTARA AVDEAGQYHAGRAVEVLSAVRGQELVRRMSTFQFHFQGPQALR
ERIAEQAILGTFEETRRELRRGLRRLLYSPGAATPASLQALCERARLGAA
HAQHPVARTQAALRDQLEAFVQAPDAPPAPAGQPQALPSALAQRF TSLA
EAYAQAAGTARERLEALASHYPTALLPHPGTALPEDCADDPLPLPEMQLGY
VPAAPMETLRNLLTLGVKVGTDAPKAATQTDVYLKIAERLDRALRSE PDR
IRLMPYTKNGLVKKLREGIDVPAERLLL RDNPTLAAGL MEMALEELQPLG
LIDTAPAPGAVSAETASRVWQLAHALHAAAEQAEARVTGMVERAIDGIGE
SRGEAHLKSSASSLFDKLLRLMHKGR LSPQAAAATVEDALRYSIVLDAQT
FVQRYADILGRDLTGLTRTQVRNSFVLNHTAFKGVNVGFTAGDGDGKAV
RLEIQFHTQET FALKARFHDDYKQAQSLYLAGADTEQRHAALDQAREFA
PVATPPGGEHILDWDSAPPRTERPRAAAAAA PAAGTHPARDGLAGHVERV
TAQARAIQREVTPLEAIGLAI AKQHSTPKPASSVRKKIERYQALKGLSL
EQAAAASVRDAMRWVLLPADQFGAGFRQARQALEAKGLRIMRIRNGFAVL
GTTYAGLNVI VRS PAGRDFEMQFHTEDSL RARNTSHPLYRAWQDQELRIG
LEQDPAKRLRLQANALRQQLRRERAAQVALPTGAKSIVDFDALRDAAPP
RATSPHRPQRPERPQQGKRAGHRP

> gi|51591628|emb|CAF25432.1| yscM, lcrQ; putative type III secretion
regulatory [Yersinia pseudotuberculosis IP 32953]
MKINTLQSLINQITQVGHGGQAGRLTETNPLTENSQISTAEKAFANEV
LEHVKNALS SRHDIACLLPRVSNLELKQKGAGEVIVTGLRTEQLSLSDAK

LLLEAMRQDTAADG

> hop01-3' Pto DC3000|Genbank: AA058038

MNINPSLGAHGSAYSSPQSDTSKATGKAPAPSPFFKQLGGCFSPCLGSHAS
SSQQLSASHAQTLSQNYSSNIQGTSTRQPRAPSPRLSDTPMKQALSSMI
ERERLRLQGLSGGMFSGIDSADAMIGRALTKKDSNPKAARFSDEFLLAVH
LYTTCLYRPIHHHLRYQHXXXXXMSDEEVMKRFNSGRPYRDEAFMSTSTD
SVIANSLTSSVTLHLQSTSAVNVSPFAMNAYEKEAII PPQTPFEVVGGLKK
MHSTWHVDLKEVQDNADGS

> Q4ZX47_PSEU2

MNISGPNRRQGTQAENTESASSSSVTNPPLQRGEGRRLLRQDALPTDIRY
NANQTATSPQNARAAGRYESGASSSGANDTPQAEGSMPSSALLQFRLAG
GRNHSELENFHTMMLNSPKASRGDAIPEKPEAIPKRLLKMEPINLAQLA
LRDKDLHEYAVMVCNQVKKGEGPNSNITQGDIKLLPLFAKAENTRNPLN
LHTFKSHKDCYQAIKEQNRDIQKNKQ SLSMRVVYPPFFKMPDHHIALDIQ
LRYGHRPSIVGFESAPGNIIDAAEREILSALGNVVIKVMGNFLOYSKTDC
TMFALNNALKAFKHHEEYARLHNGEKQVPIPATFLKHAQSKSLVENHPE
KDTTVTKDQGGHMETLLHRNRAYRAQRSAGQHVTSIEGFRMQEIKRAGD
FLAANRVRAPK

> gi|28868774|ref|NP|791393.1| type III effector HopPtoJ [Pseudomonas syringae pv. tomato str. DC3000]

MGLCISKHSGSSYSYSDSDRWQVPACPPNARSVSSHQTASASDIASGDVD
ERPATFSHFQLARCGGEYTLMSVSAAYQAERRHRGNLIKDRSQSILPWV
QVYHSHKGLDYSFQIDRTTTVKVAGFNCSIPNNRGRTRHLYSAGTSQTNMP
VIADNMSACIAVACAAENVDAAGTGERRPGAKVRFVHLLPFRREDLVPEEV
LASVRDYLRITKEQG LTRVMAMHGGNTEGDFSVSTAQALKGLFANEGIPL
EFDETCANRTSETLLGAVILDDNSTHFIKHLVAQ

> Q139Z8_RHOPS

MTLALGCIADDYTAGSDLANTLTRQGLRTVQTIQVGPADDLALPEVDAVVV
SLKRSIAADQAVAKARAAEQWLRGRGAAHVLFKICSTFDSTDQGNIGPV
MDALRADAGDAMVLVTPAFPETGRTVYQGHLEFVGASPLNESPLKDHPLNP
MLDPNLVRLVARQSHTK ISLADLSVIAQGPAAALRKHLDDLATRGVAVVA
DAVFERDLETIGAVALAHRVSVGASGLGLGLARALVGAGRVELNHAEASD
RESIGGFAACLVGSCSRATLAQVADAERSMPVLRLLDPSAIVAGDGEAORA
AEWAIARIADGPVLIASSGTPDQVAAVQAKFGRVAAGHAIEQVMADIIVR
LVESGVRRLVIAGGETSGAVVDRLAIPGFLVGPVIAAGVPLRAVAGCRS
GMLLALKSGNFGGPRFFT DALGLMS

> gi|28868614|ref|NP|791233.1| type III effector HopPtoB1 [Pseudomonas syringae pv. tomato str. DC3000]

MRPVGGPAPGYPPPTYEAERPTAQAAAGNDRARSSQASSSPAASVAPETPM
LGDLRFPAGRYPDMKVENIRLKIIEGQEPGGKDGKHTRRRKPDAAGSSH
VHGGQSVASTSASAQSKALQDTNFKASDLAELARWCESPHYPY ALAPSKAA
GKSSQLSANVVSILLQEGKHALEQRLEAQGLKLADVVSSEGRDHLHINLN
YLEMDSCLGTSKGLWAPDSNDKLIKAARYFDDFNAQKLPALPLTKMK
SKDSLGMVRELLRDAPGLVIGEGHNSTSSKRELINNMKSLKASGVTTLFM
EHLCAESHDKALNNYLSAPKGSMPARLKNYLDLQSQGHQAPEELHTKYN
FTTLVEAAKHAGLRVVDLDTTSTYMAPEKAEIKRAQAMNYAA EKIRLSK
PEGKWVAVFGATHATSCDGVPGLAELHGVRSLVIDDLGLKSRATVDINVK
NYGGKLNPDVRLSYKV

> gi|21230674|ref|NP|636591.1| HrpF protein [Xanthomonas campestris pv. campestris str. ATCC 33913]

MSLNTLSTGSTAGLFLPLTDDASSPGLLGSDSAMNDSDLLLAMDNLFLQQ
IYRLIAATYGNSTLNGPGSGIPGLDTPSA DDLQASQPIEKRTSWPTLSAP
FNVKDIKGSRLPPAVDGSSTWEGGTLTPSELQIVSTLNQHKDKTPELFA
KLDDKINDPSTPPDLKALQGLQKDPRLFFAIGSQDQKCGGKIKAGDLW
DFADHHQQVVALGGKNAEFNPKNIKATPPPAEAGSSVTWDGGTTLTQSQL
EIVSTLNQHRDMMPIEFAKLDEKINDPATPPDLKALQGLQDQDPLFFAM
ASQGHGKHHDDQKCNKGLIADNLYDFAD RHPQVTAQGGKNATYNPEKM
KGRDLPPPVDGSSVTWDGGTTLTQNELEIVATLNRHKDKCPVKWTDLDAKS
KDPAIPPDLQKAFADLQDQDPAALFHAIGAQSGKSGCDGKFTKDLTRFSVP
EKHAQIAQYAEQQAKGYTQNYVASDSPDKTEPTVMTESDAMRELYRSDY
LPKDLNQDAFKQLVEGDSTTKKSPQVIAAAQYFREHPDQWKALAGDKES
MSTADFLQKSTSEMHLTAPELKTLDTINSHQ EAFFGDGKEVTRDKLDTIV
KDDKADPAVRDAKQLLGDPLLFGLLNNAITGYKKPHSFFGGGHVVDSGK

ISNKDFQQFYEHMTAVNKTLDTPPHTAATSPEQKKAVADMLMGKADQPEI
KRKKHDVGTFSKGLHEFLKWDSKILDGIVSVALSAMNGIPLIGEVADAAAL
AFESEAAQAVIDTALQGGNLSLAWKLAGINMAGAVVAVGGPTARLAAK
GAAKGVAEGAAGATQGTTKGAAKGGKGVAE REKPLDIAKGYIIGTSIN
RPTMLKTPVLAGLHYEVRDKEKKKGEIRKNLEAAGGVPLGKQFIPKA
IADNFEADTKENLRHVRGRK

> Q8XZP6_RALSO

MPTRVPSPTLGRSHPVGTGAASTATSTAATATRS GPATAPASGRSREGLLA
ELPTGRTARTPSVSAAGAHAGRPANVQGAIEAMAALSPEREKRLFKKSA
SPQYRYAKGLTAEQRGQLESALQFRNPAAPAEARDSALAMWLSVQ QAR
LRHTHTAGHRNHNDLEQFQLAALSVP I PLLALGYRRQRRRYSSPLRPEYR
TAFNNFMRVIGDPSLSEAVRQTVAQRLEYHRRSEETIARHERQLLGEHGV
MGLAESGYQIGTNYDHNLTALEREAVVESRSGSVPALHIQALQTERS
VESGALRHQWLTRRLRDAQARAGQGEAVAASAGPSSVRQVDAESSAAAA
RLRRDTANDIRRLRPLAAEIKQWLKLAHAEPLDPKAFDNELYANAF AR
LLERRRPLSLISYFARWDPVVVDGAKVIQAIKANDLRKEVFAAAETALG
TCGDNVADGFANIVTMVDTHQLVDDVRSKGLDQPALEAWGRQYRLDSLI
TEVNQWMMASRRRQAGQHSIMTERRVAREPLETMLHAKVALKTVLDLPKNL
PSSMRHRLASALKPDDLKRLAETVQAKEADPVELARYLLSNDAWRGAMKA
LHPAAFAALRRKRFAPKDALAKEIPPQPTDPEGLEFLDERMAYAERTDA F
TQKCRAAEDTLLLSLAGRYALVPAVVGAGPSQGSR

> Q8XU25_RALSO

MPPVLP SILRCFRPAVSRPEAETAAPSSSQEHNRPSPERSPRRAPAALQ
GLTPRAGSSRRQAPEAPAGPARFLTDGERQFGGYLMARDVDQRPVHGEP
LDTLRSANETLLQTRRILTHGRGNVEDDIDATHGLSTHIAQGGRSIQESM
WRAHPKPVVWAAIAMVAGAGNCGEHADLATFLHAAKLEGEAVDNVHIDD
FDHFVAIVHRAEPDLERDVYIDAWGKGP AIFAVDGM MYRPGERRTKFGY
DKASGEEAHADMEMLATV LATRMRGGISNTMRLGPDYRYPPEVWAVTP
IVAQRFTDRVKAEMSKPADLGKLMVPPDCATPSSVEPPVTNERLMQPLRH
EIHARTLGAHSVDTMAHAARRIVAVASDLQGYPIEAHPLQAKKDAE
DIAAAERRRRARRAALGKGEPPATES

> gi|57434450|emb|CAI4386.7.1| translocated intimin receptor [Escherichia coli]

MPIGNLGHNPVRLI PPAPPLPSQTDGAGGARNQLINSNGPMSRLLFT
PIRNSVADAADSRASDI PGLPTNPLRFAASEVSLHGALEVLHDKGGLDTL
NSAIGSSLFRVETRDDGSHVAIGQKNGLETTVVLSDDQEFSSQLSDPEGK
NKFVFTGGRGAGHAMVTVASDIAEARQRIIDKLEPKDTKETKEPGDPN S
GEGKIEIHTSTSTSSLRADPKLWLSLGTIAAGLIGMAATGIAQAVALT
EPDDPTTDDPDTAASTAEAAATKDRLTQEAQDPDKQKVNIDENGNAI
PSG ELIDDVVAQIAEQAKAAGEQARQEAIESNSQAQKKYDEQHAKREQEMSL
SGVGYGISGALILGGGIGAGVTAALHRKNQPAEQITITTRTVVDNQPTNNA
SAQNTDTSGPESPASRRNSNASLASNGSDTSSTGTVENPYADVGM
PRN DSLARIPPEPIYDEVAADPNYSVIQHFSGNSPVTGRLVGT
PGQGIQSTYALLASSGGLRLGMGLTGGGESAVSTANASPTGPARFV

> Q4ZX84_PSEU2

MSIGINSSTSYQPASTQLDFSALSGKSPQNTNFSDESTAQGVDP
SALLFD TARQKDVDFGQPDNTVFNPTDSSAATDPQSNVVKLLSALVTSLLQMLMNL
NKKQDTGQDSNEWQDPFQNEGGLGTPSAEGSDGGTQEASGGDEGGTT AA
TGGDGGGGTSPTEGDDGGTSPTEAGDGGGSYVSTGADGSGAPSTEDGTG
GGGSDGVTPQVTPQLANPGRNSGNGTVSDTTGSLEQSGEVNVV
KDTIKV GAGQVFDGHGATFTADKSMGTGDQDEHQKPLFELAE
GAVLKNVNLGENEA DGIHVNAKNSEQVTIDNVHAQNVG
EDMITVKGEGGAKVTNLNITNSSANG ADDKVIQLNADTHLKV
DGFKATDFGTLVVRTNGGKQFDDMSVELNGVDAT H GK
FALVKSDDDLKLATGDIAMTDVKHAYDKTKASTQHTL

> A1FFLO_PSEPU

MACPTPNGKPKSTRKKPAPTSKRRLKKNLVTDLNTLRASLASGKHA
FADT LAFIAANYSYQPQAFNTNGGVENAAGQNEGSCKTLGLALLEGLSDQ
EALLA FGEHYRDVAATPEGTDHGNIRALIAHGLAGVKFTAQPLSRNA

> gi|3414586|gb|AAC62314.1| HrpW [Erwinia amylovora]

MSILTLNNTSSSPGLFQSGGDNGLGHNANSALGQQPIDRQTIEQMAQL
LAELLKSLSPQSNAATGAGGNDQTTGVGNAGGLNGRKTAGTTPQSDS
QNMLSEMGNGLDQAITPDGQGGGQIGDNPLLKAMKLIARMMDGQSDQF
GQPGTGNNASASSGTSSSGGSPFNDSLGGKAPSGNSPSGNYSPVSTFSPS

TPTSPTSPLDFPSSPTKAAGGSTPVTDHPDPVGSAGIGAGNSVAFTSAGA
NQTVLHDTITVKAGQVFDGKGQFTTAGSELGDGGQSENQKPLFILEDGAS
LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGEDAITVKPNSAGKKSHVEI
TNSSFEHASDKILQLNADTNLSVDNVKAKDFGTFRVTRNGGQQGNWDLNLS
HISAEDGKFSFVKSDSEGLNVNTSDISLGDVENHYKVPMSANLKVAE

> Q8XSA6_RALSO

MLIQTYQPGFYIATASDNQREADRYAGKVNEALGKIASGR SGDELLRGIS
SLSATRQRKLTISEIDSDDDPGTEAVLTRPQIAAYEPSDFRANKRIAKQF
ARGEVSSEPAGCSAIVNWNPKTSIKLSRNGSPKRLHKDPKESFAVLAHEL
IHARHVMAGTSKAWSGDRYNETSEAGQEELRAVGLGAYAHAYTGEPTENS
IRAEQQLQARSKYKPRNA

> gi|34498034|ref|NP|902249.1| probable secreted protein EspA
[Chromobacterium violaceum ATCC 12472]

MNTAVNQPPSGVNVPTGTADSSDNDYLRAARNYSLLGQAITTMEEVML
LFTELSNAKFAQMSKKMEVSRDAQEKANVMEAVLASLTDPNKGLPPDV
IEYIRENGILVGNQTIIDDFIRENGQFVGCVSEGRFEKMDEYIKRLANLIE
SCDRTGSDLHPFERMKAFSDFMDALGVKVDGKSVSDLINETLYIDENGYE
RVPVAVLEKMQNALEEAKMPVFNI SSLTAVKSSLESFSGRASDFVQQSQL
KMQQLIQNFNTAVTMANSLQSMNAESTKSIQAIR

> gi|12329095|emb|CAC05826.1| Spa32, secreted by and component of the Mxi -
Spa machinery [Shigella flexneri]

MALDNINLNFSSDKQIEKCEKLSIDNIDSLVLKKRKRVEIPEYSLIASN
YFTIDKHFEHKHKGEIYSGIKNAFELRNERATY SDIPESMAIKENILIP
DQDIKAREKINIGDMRGIFSYNKSIGNADKNFERSHTSSVNPDLLESDNR
NGQIGLKNHSLSIDKNIADIISLLNGSVAKSFELPVMNKNTADITPSMSL
QEKSIVENDKNVQKNSMPTYHFKQWAGHSVSI SVESGSFVLKPSDQFV
GNKLDLILKQDAEGNYRFDSSQHNKGNKNNSTGYNEQSEEEC

> gi|28867732|ref|NP|790351.1| type III effector HopPtoF [Pseudomonas
syringae pv. tomato str. DC3000]

MGNICGTSGRHVYSPSHTQRITSAPSTSTHVGGDTLTSIHQLSHSQREQ
FLNMHDPMRVMGLDHDTELFRTTDSRYIKNDKLAGNPQSMASILMHEELR
PNRFASHTGAQPHEARAYVPKRIKATDLGVPSLNVMTGSLARDGIRAYDH
MSDNQVSVKMRGLDFLERGGKVYADASSVADDGETSQALIVTL PKGQKVP
VERV

> SPTP_SALPA

MLRYEERKLNNTLSSFSKSGVSSDTRLYIAKENTDKAYVAPEKFSKVL
TWLGKMPLFKNTEVVQKHTENIRVQNQKILQTFLOALTEKYGEKAVNNAL
YMSSINMNKPLTQRLLVQITECVKGADGGFINIIKKNKDNVGMNAALVIK
GGDTKVTEQNNDVGAESKQPLLDIALKGLKRTIPQLEQMDGNSLRENFQE
MASGNGLRSLMTNLQSLNKIPEAKQ LNDYVTTLNKIQIGADRFSQWGTC
GGEVERWIDKASTHELTQAVKKIHVIAKELKNVTAEFEKIKAGASMPQTM
NGPTLGLARFAVSSIPINQQTQVKLSDGMPVPVNTLTFDGKPVALAGSYP
KNTPDALAEAHMKMLLEKECSCSLAVLTSEDQMOKQLPAYFRGSYTFGEVH
TNSQKVSSASQGGAIQDQYMQLSGCEKRYTIPVLHVKNWPDHQPPLSTDQ
LEYLADRVKNSNQNGAPGRSSSDKHLPMIHCCLGGVGRGTGMAAALVLKDN
PHSNLEQVRADFRNSRNNRMLLEDASQFVQLKAMQAQLLMTTAS

> Q8X5T9_ECO57

MRYNGLNMMFFPLCLINDNHSVTSLSHTKTKSDNYSKHHKNTLIDNKAL
SLFKMDDHEKVIDLIQKMKRIYDSLPSGKITKETDRKIHKYFIDIASYAN
NKCDRITRRVYLNKDKEVSIKVYFINNVTVHNNTIEIPQTVNGGYDFS
HLSLKGIVIKDEDLNSNFA GCRLQNAIFQDCNMYKTNFNFAIMEKILFD
NCILDDSYFAQIKMTDGTLSNCSAMHVQFYNATMNRANIKNTFLDYSNFY
MAYMAEVNLYKVIAPYINLFRADLSFSKLDLINFKHADLSRVNLNKAILQ
NINLIDSKLFFTRLTNTFLEMVICTDSNMANVFNANLNCHFNCSVLT
KAWMFNTRLYRVNFDEASVQGMGISILRGEENIPINSDTLVTLQKFFED
CTSHTGMSQTENNTHEVAMKI TADIMQHAD

> Q4ZPQ3_PSEU2

MNTINRNYYPVSGIPAQDAPAQTDQLPQQGQIKPGHNSNLIDFGLTQQA
NGPHSSLNTLGSRVQPTDNTSSNMPGGNGEQVLNKLVAIRNINLNNLLS
LLEGNLHNGSGPAQQRDQPTLAQSPSSASPPSSPPSTPQNAEKPFV
QNDHPSEKPVSLQKNTPTSAAQSPQAPRTTERSSATPDKTPARPDVNP
AVVHDLALPKTSTDPTAKPDNTVNAAK TATPAAHGQGADMSGIMGFAKEA
NTTGGNGGEVTVNTVADLKKYMEDDKARTVKLGLANLSADSKVTINFGAN

KTLLGTDKGNLSLHNIYLASGKTASNDIFQNLNFDHDSRYRENGDMQMFIS
SGQKYWIDHNTYSGTQKDNQAKGLDKLLYVGGTADNVSLTNSKFQNNYEGV
ILGQPDDSAQAKAEYKGYPRMTIANNVFNLDVRAPGLMRHGQFDVLNNS
IDNFHLGFTATGDATILSQANYFAKGVV VSDKASNSGVLDYDGAHFKDI
GSNVSFTQKSAVTAWTPSYQRDIKTAEEARAYDQANAGAKTVS
> gi|34497729|ref|NP|901944.1| hypothetical protein CV2274 [Chromobacterium
violaceum ATCC 12472]

MLGFNGERLDPASGAFHLGNGYRAYSPALMRFHCPDLSLSPFGASGVNPYA
YCAGDPANRADPSGHLSWQAWTGIGLAVASLALAAFTAGT SIIASGGIVA
ALESASAITLAEGGLAVVSDMTAIACGAMEASDPQAAAALSWSLACGAM
GMVHAGYGAVRGIDRKLGAFLQENSRLGKITRGERDSLGIPLGGGLTKC
FRPASEMEGASAGIALGRHLRHSSTPDMEAFALPAKRRKRIGSGVSGVV
YEAGRQWVVKIAIDPLPIETMEREAEIFRAVHGPSALVAENMLWMKRIP
GVPVNTLNLLEDEKAEMWQKTLAEVKRLQEMGIHHDGDPDPSWN NLLFDQQQTG
TVSFIDFGKSRYLDFAPAT

> SOPE_SALET

MTKITLSPQNFRIQKQETTLLEKSTEKNSLAKSILAVKNHFIELRSKLS
ERFISHKNTESATHFHRGSASEGRAVLTKNVKDFMLQTLNDIDIRGSA
SKDPAYASQTREAILSAVYSKNKDQCCNLLISKGINIAPFLQEIIEAANK
AGLPGTTKNDVFTPSGAGANPFITPLISSANSKYPRMFINQHQQASFKEY
AEKIMTEVAPLNFECAMPTPQQFQLILENIANKYIQYTP

> Q8XYN5_RALSO

MKSSDRIKSSARSREWPATFEDADDLQPSITNAARQSQRETPRHPLASP
TFLEKFTQOTSALLLYAAIRCLIGVALTFYSFHRNRCQTLHRSIDSAPK
KKKAAQKSNRRRIKTNLRRNKIHIQPIRFDLCEKRIRKFKQIRRAVR

> gi|27376900|ref|NP|768429.1| hypothetical protein blr178_9 [Bradyrhizobium
japonicum USDA 110]

MATMESVVRMVPQDYAEMQERLVGMGVQFETRLDERLAEHGLTGDADA
EPVLGARYETRLPARSKARSCIRSSGSAFSYERTSEGGSDVPPRRSQKS
KFNRRRLPGRACMTDCLHEPLPNELC

> hopAN1 Pph race 6-1448A|Genbank: AAZ35071

MSLNNARPLLGCIADDFTGATDLANMLVRGGMRTVQSIGIPSAEM AAGLD
ADAIVIALKSRTPSADAVAESLALEWLREERGCEQIFFKYCSTFDSTAA
GNIGQVSEALLEQLDSDFTLACPAPPENGRTIFRGHLFVQDQLLSESGMQ
NHPLTPMTDANLVRVLQAQTRHKVGLLRYSIAQGVGVRNRIAELEAEG
VSMIAADALSDADLYTLGEACADLPLLTGGSGLALGLPGNFRKAGKLRDI
DAAKQVAISGGEVVLGASASVATNGQVAAWLEDNRPALRINPLDLA AGKP
VVEQALTFARDAGQTVLIYATSTPDEVKAVQKELGVERSAMVEAALGEI
AKGLLNAGVRRFVVAGGETSGAVVQALGVQLLQIGAQIDPGVPATVSSGA
QPLALALKSGNFGARDFFAKALKQLAGAA

> CP0133 ipgD IpgD, secreted by the Mxi -Spa machinery, modulates entry of
bacteria into epithelial cells 116362:117978 forward MW:59895

MHITNLGLHQVSFQSGDSYKGAETGKHKGVSVISYQVRKNGERNKGI EA
LNRLYLQNTSLTGKSLLFARDRAEVFCEAIKLAGGDTSKIKAMMERLDT
YKLGEVNRHINELNKVISEEIRAQLGIKNKKEQLTKIKQIFTDYLNKN
WGPVDKNI SHHGKNYGFQLTPASHMKIGNKNI FVKEYNGKICCASTRES
DHIANMWSKVVDDEGKEIFSGIRHGVISAYGLKK NSSERAVAARNKAEE
LVSAALYSRPELLSQALSQKTVDLKIVSTSLLTPTSLTGGEESMLKDQVN
ALKGLNSKRGEPTKLLIRNSDGLLKEVSVNLKVVTFNFGVNELALKMGLG
WRNVDKLNDESICSLLDGNFLKNGVIGWAAEAIEKNPPCKNDVIYLANQ
IKEIVTKKLQKNDNGEPYKLSQRMTLLAYTIGAVPCWNCKSGKDRTGMQD
AEIKREIIRKHETGQFSQLNSKLSSEEKRLFSTILM NSGNMEIQEMNTGV
PGNKVMKKLPLSSLELSYSERIGDPKIWNMVKGYSSFV

> CP0128 ipaB IpaB, secreted by the Mxi -Spa secretion machinery, required
for entry into epithelial cells 111248:112990 reverse MW:62172

MHNVTSTTTTGFP LAKILASTE LGDNTIQAANDAANKLFSLTIADLTANQN
INTTNAHSTSNILI PELKAPKSLNASSQLTLLIGNLIQIILGEKSLTALTN
KITAWKSQQQARQQKNLEFSDKINTLLSETEGLTRDYEKQINKLKNADSK
IKDLENKINQIQTRLSELDPE SPEKKLSREEIQLTIKKDAAVKDRTLIE
QKTL SIHSKLTDKSMQLEKEIDSFAFSNTASAEQLSTQQKSLTGLASVT
QLMATFIQLVGKNNESLKNLDLALFQSLQESRKTEMERKSDEYAAEVRKA
EELNRVMGCVGKILG ALLTIVSVVAAAFSGGASLALAAVGLALMVTDAIV
QAATGNSFM EQALNPIMKAVIEPLIKLLSDAFTKMLEGLGVDSKKAKMIG

SILGAIAGALVLVAAVVLVATVVGKQAAAKLAENIGKIIIGKTLTDLIPKFL
KNFSSQLDDLITNAVARNKFLGAAGDEVISKQIIISTHLNQAVLLGESVN
SATQAGGSVASAVFQNSASTNLADLTLSKYQVEQLSKYISEAIEKFGQLQ
EVIADLLASMSNSQANRTDVAKAILQQTTA
> hopM1' Pph race 6 -1448A|Genbank: CP000058
MNTPRIGGSGAIELSRINQQPDAIPAQTAHPNAVTPGMNPPLTPNQAGPH
AAESSATGAARLNVAARHTQLLQAFKAEQATAPVSGAPMISRAALLIGS
LLQAEKLPFEVMAERLSPERYQLKQFHGSDLQQLLDKFTQPGQVPDKAEV
GQLIKGFAQSVADQLEHFQLMHDATPTKTGPHANEDRATLAVSQ TALGEY
AGRASKAIGEGLSKGIVSLDDHIAALDVSLQSAEEGAKDALHSNRQALVD
AKTTLVGLHADVFKSPEAKRLASVAAHTQLDVTVSDLVARTNSVGGWKGGA
GPIVAAAVPFLSSMTHLGYVRLSTSDKLRREEVETSSDASMLKAAITGM
VTGIAHETVNSVVKPVFQATFQKTGLNERLNMVPLKAIIDTNSVIPDPFEL
KSEHGELIRKTPPEIAQDKAFVKGERAVLNQKKVQGSSTHPLGEM IGYS
FGGSHAVRQMLNDLHQINGQTL SARALASGGGAVSVSSQTLQLKSTYV
DPAGRKIPVFTPDRAETELKKDLAKGMDLREASVRTTFYSKAISGYSELG
ADLGTAAACDSPAGRARYAQCGEYPAQ(siteofframeshift -downs
treamsequenceisnotsimilartootherHopMfamilymembers)
YGSGRNGLDFLSVHALRQPVCHRRSQVEGCGDGGRNADAGSYRNS LEQH
PPSEQGIAATYLP AEHVERYSKGYKRLSHGTRRVAANPDGRGHGSSVG
RRC AERRVNSTRCAYASKTA (whatfollowsistheHopM -homologu
ssequenceinthealternateframe, post -frameshift) MALVA
TGSISYLSSTLYANQSVTAEAKALKDAGMGGATPMLDRTETALNNIRHPNR
ASLPHTFQ PSTLSGI PRAMESAYHMGRGALQLPTQMAVDTVRVLADG ALN
GVSSARAALTPAKPPEARVSVDELRN TAPT PPSPTVQR PAPS VPLDDEQ
LRALEESLLAPR
> Q8XXH5_RALSO
MSIGRSKSVAGASASHAPASGENGSTQPQTVTPLAGATRRRRNSGLLCEL
QSMCKRTLRAASQTIIFFPYSKTGTTPTRAQPKPDVVPALKPAPRRMRPP
AAPGRKHQRNVDAVVP PAMATSPRAEIRFPLTTADAQRYLRAQWRQAETG
GRFDQAAVDRLTTTLTARLL ATSAATGNGVHEDSGEKACARAIMVCDALA
QATGGDPARAH DALLALLD TTSHADARVRADVLALQ TALGMTAIGLDTLL
AIAPHVLPQRGSAAPEIQREALRHALRAADHLLRRKPADAPGPTSLEALA
ALADPVLPAVERGRPGSSAGASVAPPKAPAWLADPGNALAIKALHAANA
LRADPAAQC PPHLAQAYLAWRNGFDREGPGTDLAKAQQLFKLFAYAERA
ARTGMAARAAAGFFGTQKSPL SALQNFGTAGVMLGHPDDEFARFTAALAP
VKTQLADRLKAASTSRALKTRCAVRLAAIEQWERRMASKGLRSTFRFSSR
DLETVAARARPLLSNRVALHADGSPADLALDPHRNRDAIRAEVKPLRGMT
PAQLRTWADEAWRLSGQAVPEPIRANIDLVESRLAGDIRPKPGDTNAQLD
AIGALVKQMPDIYDIRVSSGGTVGLGGVPSQSLAALSSHLGVPVHSVLPD
GGYLQGRHAVIDIGSNQHFGHL FIGTESRKS LYGGLGGYAGWSFGQDGM
NVGVSGGLRRSRDWGGPRGVTIRTRRSDEQGRPDARTMLEVELHATR
SAGPNSDAPRNAREMWGSLARRFWNDPACSINWTD SRST SATSGSASAT
ARVGTADTKWGPALGATLRHVARAAHRQWDKTGNHAI DVSTHNSGRATAV
AATLVEALPGIPVNGSGHLAALSFP TQP YVIGITTLFTTQTNAALRIGR
DSGRIIPKHTFRDTEFGTFKAFK QFVDTHRSEWLTALGGTDDARRRLEDEM
VATVKARATAGNLIMGERMHMTDEAARRLDLFLHRKQRFDRIPAPT PVQA
RERASIDADIRQMLASENSWRRQALYVLEALGVQRTVGLSFLLNQSTQA
VSGVRELGLSPE
> Q1UBI8_9GAMM
MSIRHSDVSALLNGLNKKAI GFNDVLFIDDFYRYTPVKFSNGDLVNAV
QNEGS AKVFGFAKHHGLNQLD TLK LFAEHYDAVVAAPKGTDPHPNIR NFIH
WGWQGFLMEHNPLTARPSVDVKNI
> PIPB2_SALCH
MQRSLDSLGMATSAFGAGTSAAMRQATS PKTILEYIINFFTCGGIRRRN
ETQYQELIETMAETLKSTMPDRGAPLPENIILDDMDGCRVEFNLPGENNE
AGQVIVRVSKGDHSETREIPLVSFEKICRALLFRCEFSLPQDSVILTAQG
GMNLKGAVLTGANLTAENLCDADLSGANLEGAVLFMADCEGANFKGANLS
GTS LGDSN FKNACLED SIMCGATLDHANLTGANLQHASLLGCSMIECNCS
GANMDHTNLSGATLIRADMSGATLQGATIMAAIMEDAVLTRANLRKASFI
STNLDGADLAEANLNNTCFKDCTLTHLRTEDATMSTSTQTLFNEFYSENI

> gi|15618212|ref|NP|224497.1| Inclusion Membrane Protein C [Chlamydomonas
pneumoniae CWL029]
MTSPPIPFQSSGDASFLAEQPPQLPSTSESQLVLTQLLTMMKHTQALSETVL
QQQRDLRLPTASIIILQVGGAPTGGAGAPFQPGPADDHHPHIPPVVPVPAQIE
TEITTIIRSELQLMRSTLQQSTKGARTGVLVVTAILMTISLLAIIIIIILAV
LGFTGVLVQVALLMQGETNLIWAMVSGSIICFIALIGTLGLLILTNKNTPL
PAS
> gi|53722632|ref|YP|111617.1| hypothetical protein BPSS1609 [Burkholderia
pseudomallei K96243]
MPRIQSSSPITPSITANQPTNGANARAATVTRQKRPAGHATLSKCLASSGK
KVLHARMRPKGLAQPGANSSGAATSKPAVPKADAPPAAHQVQANAHEGD
LIDLSDPPPTTKPAGMQPSLLDAQPNDLHALHTPVLQPTVLHSAAPAAH
GAQPLGQTLAAAGMPSLQDIHHTTDQAIAMQHAIGQANQRLAIAEMLNSF
MQKVIDMIKKAASQP
> gi|53722413|ref|YP|111398.1| putative ATP/GTP binding protein
[Burkholderia pseudomallei K96243]
MTSMLFLKEIMPVIIRSSGASIHQSDLSSRRSEADASDPAAAGPAREPDR
VAGAERSRFVQPAPLNKTADKVKGGTPAIPLSLQVLGLYQRDKVCAQPVR
PDHASLPESTRAEGLPRLDGKLPKRIETAPFARALVQGNAGSGHNSRDVF
LNVTTGGVS GKAAPSNADHLTDVLLSDCRPGESLAGTPDDNAFVIGGHSEI
IDVATRPDGLSRADKARQMAIVMFGVTDPAHQIAFAERKLTALENAEAR
HLAMSLFTGEEGREALSQWIAFDGGAARLQRMHQLMYAAAVLQKNGR
AAARLLRNYCGMSTERPDLQKQSYSMQRVLVSARGTSLDILGIPPSIT
GREHHAEQKSVYRNALAIQYLHEKLDAAKPDSDLEMLAAAQIVSAEAL
GGSGDRTEREYHFSRVVDNLGSIYQEERLSIDALACAANLISIDRDNGAK
ALGAVAMLSSEQADVMDALEQAGELVRLPLGIRRDIA TVADLDKVLNA
NAEGPGARASVSSVDPMGQASAQKAIKGLRAALAVAPDIGNIPIGAAARA
AIPMQQKIAYFKWRNGLADERKARLVFERLYKLNKYADRAIPRGKNTGR
LRRIGDDIAGAFKRNKPVGMLEEGLLGGFLREDVFNEKIAPAFHSLIE
KYRESGAGAGAGAGAGVAKARSEVVS RVFEKLIKIDGFSKIEIKSDDL
KKWVALAVAGGRNDVAVKRSLEFESIRRD LKNGFSVDVLERWAAEAGLDDG
NFRRLNDLRSVSNNGYGEIPELGDRTSVFSAFSEIVARYRAGKSLKFSS
GGVGLALGDSQSIGPLVSVSPTLGAGGGRVATVEIGGASGRGLIIVTR
ANSQKLVKVGASVFAGPQFIHVVRAGGSANLELVSAEQTREKGAIVRFVPR
AGSLGGGEAWR GWAQDCLSIIGNSADSADLLERLAEYVYVNAEIGIGMTE
KEENVISSAAVAGAVKASSGGDFRGGAGVSASIGVKREWRHKAVREL
DNKMGNHKFDQSSSTSVTWNAGLNASESYQLNPTPDFSTSASASAQAFSI
GGTLFSVKEGTSVAIRLRDGMVDAELAILDRTRNGGRRRAVDLIARDYPIW
VKAMGKTDAEGEALNRFFASELGRGVNRPLRPEVPETVYVASYRMTKEAA
SALNHYRAQIDLEQMLGTNKSRSVSELRRRYAEVIENSASWRPSSIQHYPE
TSSAKSVGLHNVFVEAKKSSSTSTVQVLAHQAASEYVDPVALARHPVSV
GSVQAGGDAPSDVGGRSTHGSVAVKTGE
> Q415V5_KINRA
MSDYGTAPVIGAIADDFTGATDVAVAFRRAGLRVAVHFGVPTAASAAVEA
GLDAVVVALKSRTEIETPEAVEQSLQAARWLQDQGVRLYFKYCSTFDSTA
RGNIGPVADALLELTGAATTV VVPASPAHGRTOYLGNLVFGDVP LAESPM
RHHPLTPMTDSNVQRLLQGQTTHTPTALLTRSVVARGAAVRSQSLQAAAAA
GTDYVVVDALDEQDLLTIGQACVDLPLLTGAAGLAGGLGAALAQRRERAVS
QRAAGTASPPVEGTLSDAPGADATGGDVPGGDVPGGGPAAVLAGSCSAR
TLEQLTALRTAAPGSSAHPAHFLDAVQTPDAAALAEQALNWEQQDPAGP
APLIYSSQPQQLRAAQQALGV ERASLILEEATGLIARGLAERGVRRLVV
AGGETSGAVVTALGVSDGLIGSEAAPGVPIWIRTARPETGRGATQGADDGD
GRHLWLLKSGNFGDPQLLVRAADTASPASSGDTGSPASSGDTASPASSG
DTASPASSGDTATETAVPA
> A0WHJ3_9GAMM
MLLGVIAADDFTGATDIAGFLVENGMRITQVNGIIPANMEINADAVVVSLK
SRSCPTQAEIQSVAALKWLQAQGCKQFYFKYCSTFDST TKNIGPVVTD
LLDVLGEDFTIVCPALPVNGRTVFNGHLFVLGQLLSESGMRNHPVTPMTN
SNLMDLMDAQSKGKTGLINYQSIEQGADAIIGEFALKAQKRYAVVDAF
TAEHLNEIGKAVSSKLVTTGGSLAAGIAKNWGEHLQDQTAQKQAGHPAK
APTIVIFSGSCSVMTNKQVELYKAKASFFALDIEQCMSNENYVNEVFDWVI
SHANESLAPIVYATADA EKLKTIIQQYGAEESSQAVETLF SMLAIKLDQS
GIRNFIVAGGETSGVVTQSLKVDSFHIGPQIAPGVVWKAINQDLSLAK

SGNFGDENFFTTAQGYF

> Q8XRH4_RALSO

MAGSHCSPPRRPMPANNRIGSQRLVAPQYRRRTADQENIAPRKQORSQDKQPR
TRQEPFKGLAPMARAPLQARNLNIGASQPQPRPQKAAAPAKPHLIRTPGH
GVAASTAIQNRQREIVRRQIEALGRREGASATGRPQQVMKLLNARTPDLDP
AKSIELLRQLQVILRLPNPASRNSHLMFVANNRLVAGAAVAKPATAAAP
APAPARQASRPAPMRQAARPAPPPARAPQAARPAQAARPAPAPQQAQPA
QRIFKSFQDLATQGPFPARPARPAPQPSRPSRPAQRFDDFKPRNGAAPARS
RPAATAAPLRTASAPPQYGRTASISAEPTQQPILITIGDFIRFAQDDAEQE
SLRRYSMPETIYAKAQKNFDAYLTRLEGRTEPQPRPARTQSAPPRMQTVPA
ARMDTSSWHGKVDQETDDRNRYHNERGGHQSAREDYAARQQPAAYSTAPRP
RRTQSLPELTAQIDSIHRFEDQRADQENEYPNHDEAVRRYKQQNGYR

> Q2RPK8_RHORT

MPLLGCIADDFTGATDLAAMLVGNMRTVLMMLGRPKAATESPKADAVVVA
LKSRTTPAAQAVSDSLDALTLWLRAGARQIVFKYCSTFDSTAQGNIGPVA
DALAEALETDFALVCPAFPANGRTVYQGHFVGDHLLNESGMRDHPLT PM
RDASVVRLAAQTPHRVGLIALPVVEAGVPAIDEALRALRATGVRYGVID
ALTDHLRTIGAAAAGHRLITGGSGVAMGLPENFRQQGLLPFRDSDASLP
KVDGGA AVLVGSCSQAATRQQAQARPHLPTLILDPLATPEAGALMAIARA
WIDAQPAGAPLMIVGSAAPEAVAALQKRLGAGPAGALIE TVLAGLAEDLV
ERGIRSLVVAGGETSGAVVSR LGITSLRVGAEIAPGVPTWLADHPAGPL R
LALKSGNFGSATFFLEALGLPL

> Q8XTK9_RALSO

MKFFSFRSSVHTASTAAPAARDAASSASAAPQQPASASAGSGRISHALHG
LKRCLRPSAINVTAVPGFTKTTIDPLPIPKRPPPNL PKAPKQAGHKLD
RIDRQVHNLTQKLYPPLPSGLHADPEAKRAIASSRAFVSAVEALFVPSGA
GVYAVPGLQTLIDGLAGMAEAQPDVDTTRYAGMLQCARALATATGGRAD
EACRALEHLRDR FSLTDGSNGAPPTPAQMHAWSTAKLLAHTASGFDALLA
LRPTLAEVDATLPDDNMNMRMKREGLRFLQAADLMAARLPAGVVPQT
PHAQLQDARARLDAADRASLAGDGLALNALVCAAQVHAEPEAAHAVDD
RAQVAAYVAVRSYREGGKGSALERSLGRMHKFTTWARRAEHRATHPLAA
FDPRRLGLMRKSP LTAAYGTGGANLGLLNQEAQALHDTVKHGIEAMQAH
STALRALNGRHAL STEQRGLLVREAVLQHWASIGTTWRSSKLLSDHD
KRAIADRVRKAAPGARVD AEAVLAYREFRKLDKLDTLVRWLDEARAFD
PRASEPTLRAAADNIVKAGDIERGRPIKPRGTTLADFREALTGAIGQMP
LGNVRYFDGATYGVNTNMTVNQH EFSSHNSLVPSMGLPGGARELTGRHAF
VEIGSSSYGGEVFIGTDKRSSTGVGAGLYAGFKVGIKNWLSAGFSAGVA
HAHDRSAPVGVIVR TGLTYGADGKATS AWRDNVADVTRFLQTAEGQAA
RPVPPDRMWEQFSARFFRTPDISVNWRDQRRSHTVTKHGSGAVRVAAGA
VRVGPAPSVGHQVVLASKNDRVDTNGWLRGVERARARASNVHVSGLAAV
AQGVGHFSNRSGFPESVTLPSVPIVGASANILPSGTSVTLRRVDEHGRLN
PRFIRRLVEFIDPSAFLSHMQARLPQIAHSDASRAKVGAFMSAMRDMGTQ
GNLAYGESWKIRPEV TEVLNAYTDEIQMLKCAKAAPGAGGQAIQPAQAA
QTYHDLIERIFETVERETAMPPEQAQAFRQALAGLRDQEVQDQILRLANE
TIRVLKDVQSWKLSGYAYDITTHGYTAGPAMLLQATASTSVAGERVLAE
LAVRDLELMDDPAHAAQDKDPAAGEVL

> Q8XB17_ECO57

MVAKLKPDVFNTPFLEAMYKERLSHKGYSDKIALSINDKKYVNSKDI
ENILDGKGLDFKKRTLWEFVRDLF PGSHIKEVKGLIYEFVTKVDNKAEVF
DKIKSLAKKEQQWRFSKTDFTTNENNEVIVSRSFNLYTGATSNENEKKQ
VSSERLTLDNYLDDLHFDNSPLVRLTFDNYSVKLATLIKNIPIINTTIN
LSSLKSDVLNSLYCSFKNVI FSGVINSNLEGPVFENCYFDDCKFNNIQ
LYETNDDTVESGNKPIKGMFKGCFISKCKIENYRCETSKIYTVTQPDSI
QEKLGSYLFMQSFVQDCI IQGGCCP GSSILLSHFYNCNIIGLDAHGMDFL
ANSFNKSNYDEIRGPDGTGFYNCNLKHIKINDGLREDGSDRTMFPNKEY
FSDYIERRSRNLKLDNFSKCVESIKKGTDSFSKKNTENNNVFFKNSNL
IGANLGYYSRGDRCKDAIDPNTNYSKDGLTAQKMYMDLDGAI SKEQIP
DFLKKVSAINIDVINFYNSESKTKEYKNAFLELESFSLSTLYVENKSYEE
KYHFDNSRVEFFIFKDMQENAQNIIN NMIESDRIKFVESIINKMIPPPDG
TILTENPKEYVQKQIKESHKESATNVTFDYKELAPIFEGVEEKQIKALSN
QLEHIKSFKTDYDRLNKYARDFYFSSAFAINWEDLLKNYQEIRASIKD
YDDLLEIKELIISRNKSLDKRTLFDNKRDNWNSIEVQDEVNALNAKIV
DCDDKIRSKLTIVRNRLNENQYKDDKNI SDAMRNILDFWERYPDIVQNTIT

QA

> gi|16766251|ref|NP|461 866.1| secreted effector protein [Salmonella typhimurium LT2]

MPVTLSTFGNHQNYTLNESRLAHLSSADKEKAIHMGGWQVQDFRAEKKD
HALEVLHSIIHGQGRGEPGEMEVNVEDINKIYAFKRLQHLACPAHQDLFT
IKMDASQTQFLLMVGDTVISQSNIKDILNISDDAVIESMSREERQLFLQI
CEVIGSKMTWHPELLOESISTLRKEVTGNAQIKTAVYEMMR PAEAPDHPL
VEWQDSLTADEKSMACINAGNFEPPTQFCKIGYQEVQGEVAFSMMHPCI
SYLLHSYSPFSEFKPTNSGFLKLNQDYNDYHAKKMFIDVILEKLYLTHE
RSLHIGKDGCSRNILLT

> gi|29171488|ref|NP|808672.1| type III effector HopX1 [Pseudomonas syringae pv. tomato str. DC3000]

MKIHNAGLTPPLPGISNGNVGKAAQ SSITQPQSQGSYGLPPESETRPD
RARANYPYSSVQTRLPVVASAGKPLPDTFSSLPGYLLLRRLDHRPVDQEG
TKSLIPADKAVAEARRALPFGRGNIDVDAQLSNLESGARTLAARCLRKDA
EAAGHEPMPANEMNWHVVLVAMSGQVFGAGNCGEHARIASFAYGALAQEN
GRSEYENIYLAASTEEDHVWAETDESQSGTSTIVMDPWSNGSAIFAEDSR
FAKNRNAVETDFTNLSTAAEAGKIT RETAEKALTQVTTTRLQKRLADQQE
QVSPKISGRYRPEKSVLDDAFVRRVSDKLTSPDLRRALQVDIEAVGVAMS
LGTKGVKDATRQARPLVELAVKVASPQGLARRDV

> Q7ADG2_ECO57

MSQNDIIIRTHYKSPHRMHIDSDIPTSPSEPINQFAPQLITLLDTSDLSS
MLSYCVTQEFTANCRKISQNCYALFTINFATSPIHAENIFITLHYKKE
IISLLETTPIKANHLRSILDYIEQEQL TAENRNHCKMKSCKIHKRETIQ
PTVNLNGSAFFSQSPDAIFCRHLSLQYALDSLNGKGVNLIKHYSSVE
SIQQHVPLVRDAEFRALLRHPPAGSRVIAASKDFGFALDIFFCRMMANNVS
HMSAILYIDNHTLSVRLRIKQSAYGQLNYVVSVDPNNTNAVVRGTHRTA
RGFLSLDKFISSGPDQWADRYVRNCAIAILPLLPEGVPGAIIFTGIATR
MPFAPIHPSAMLLIMATGQTQQLITLFRQ LPILPEKEIEIEIITAQNSIGT
PALFLAMMNGHTDNVTKIFMQEIQSLVDNHI IHEDNLVKLLQTKSANETPG
LYISMLYGFDEIIDIIFLNALTPPIAQELLNKKLVMSILAMKIHDGEPGLY
AAMENNHPLCVTRFLSKINGIAFKYKLSKANIMDLLKGATAQGTALYIA
MSKGNEDVVSYSISTLGAFKKSFSQHQLFTLLAAKNHDNMSAVHIAIH
HNHYKTVETYYAAINVISQSMSFSADELKT YL

> Q8XXI4_RALSO

MKATTRASLFGWSLARVGTGKRRRSRNALMESTEIKGVRKMRPRSAEP
DVSTPFRHDTQAGRVAPACSAHGAQRALVPTGEQLVECERALLHCAEFQQ
LRAQHVSRLTKLAEDSRLRKQVSVHECVDLACANVLAKRNGYGLALVFLA
AGATPEENVRQLTNYFFALQAASLRASQPERRQLGQCADLAAHYLFKTPW
FARAPLRPFVMLGNLLSKYPDHPACLQALSWIAD QVLAPAQMPALGEKDL
ALLANALSKNSGCRSEQAVARIGRHVVVRAGAGDFRAQSVSLMLNACSKW
SGNADCRDAVEVLAARVSEDAALQRDMAAQAVANALNALSQWPERIGCRN
AVLALAVRVATDVALRCRMKPQEVANALNALSQWPDRIECRNVLSLATH
VEGHGTLRQAMNAQHVANALNALSQWPEQGECCDAALPLIRRVADDAALR
SSMDALVTSNVLNALSQWPDRECRDTAVTLALRV ADDAGLRHDMGVQAV
ANALNALSQWSEQACRDAALSARMVGDASLRHMSAQNVANTLSALS
KWPEQAGCRDAVLSAARVADDAALRLDMNAQNVANVLNALSQWPERGEC
RDAMLSLAPRVADDAALRYDMSAQAAANALNALSQWPAQTGCRDAALRLA
ARVAEDAALRHSMDAQVANTLNALSQWPEASSCRHVTTTTLMSLGESEGC
PWRQFNMINLAQIANASARLFLSASDEVEIQALART KLRALAAHLGLHRE
RFETASASSIGTIFKAMEALQLPAEMRSLVCAAMNRIERLCSQASLRSES
RESLGMRLRAGLLPYIDTNRGLSDSPGMLEAAAPRLTAWAARHRLEIDL

> gi|28868095|ref|NP|790714.1| candidate type III effector Hop protein [Pseudomonas syringae pv. tomato str. DC3000]

MDKNKPNLILVSELVDVSEVVS IRSLYPIDAWTFIYLLLEDLLGQAGEA
LNRDGHFVIRDFAVHTEVEKVFQGIARKYSVTAVIPNDEFVYIAAWAND
CWQLPGLTFDVATRFDRKRRMKKIAQKFNIPAKELSLDDINRGATFPV
ILKPRSLAGSVGVRIITEVQQLSEAYATEIDDYQDMNEHQYLIETYSQP
LYQIDAVVLKQQLAFLSAGKYLKGPIDYLAECPLGYFSLAEDDLHTLWRP
FIERVLSAFEGPDGVYHIEAFGDAG DGFELLEIAYRPGGASTVDMIKIAY
GIDDLRFIHLAVQLGLVDALHVDKGEAFGYMTFPPKHLAKEMLYVTRVSL
SSMETLQTLKMKKIAQVGDIASGEFFCHKDCLGAFVFCGDRGSVAHDLKH
VEEHYQVHAEAARG

> Q4ZT52_PSEU2

MTTLTTRQIQLAHVTSVHTGAGLALDWDVAEKVEEVAIKADALSRDL
HRARNLSRSLGRVSTTPMGIGFFGLSQAGKSYLISALAADEKQQLLT RLG
TRQLDFIKHVNVPVGGGKEATGLVTRFTRTAAPSLDPQFPVELRRLFREVEI
AII LANAWFEDFDHQRLNSQVTDQAIDALLQRFQDGQSAAAPTQVSSDDV
VLLWDYLEHHYANAMRPLNARYWPCVIKLAPRLSVRERAQLFEPLWGGIG
KMTETYEQLASALHRLGLAETVFAPISALVTERDQGLVQNSIINVDILS
RLGGSADSPIEVRPAHEGTLRSVSVNRAELAALTNELIFRLDNEPAN AI
VNSVDLLDFPGYRSRQKLMSEINEASEVDSNGTANNPVARLLLLRGKVAYLF
ERYTNEQEMNALVMCTSTFKQSEVSVGVPVLSKSWIDKTQGTSPQQRDGRA
SGLIWLTMDCDGFIGGALNGETVQFPEGCDNMLKLTMIERFGNEDWMKQW
GSTPFKNTYLVRKPRFKTSFIELAADGEERAYSSDSSHTALQALQQAFSNS
ELVKRHVAEPQEAQWQAMLTLDNGGMRFSASFPIANIDFKLQRIAEQL D
ELMVQLLPRLEEYEAAGGEDERAKKVIANMIARPFATTPHGKHLVGLL
GYMALPEQQLRDLVNGDFGSPASEATAAVQAVGKPEVEYDIFGEAIAAT
ATVETPAAAAPVQYQSHHRFARAAFDLWATHLRNLSRRQHLLDLELP
AEAIALLVKELVCAERLDLPLQLSNALLKRAQSGVRENLVQRQVLTQAQ
LLLNDFAAWFGHTAQFAGQRPTGLLQAKQPLFAFYQKEMPGRFPHLAAQA
DDQSVIFADDWISGIAIHTQKNVGHKKEITPEQNEAMGRVIAQAFKAR

> gi|12620564|gb|AAG60840.1|AF322012|145 ID322 [Bradyrhizobium japonicum]

MATGFTSQRWRELFPGRTDVTSIVDFQVAHPLVGNAGDILLEHQLGRDGE
RPLVNWPRPANDEARARAEQLGFVHVDPDDMVLDPDPTQSKQWRYRDGEWQRA
TNSSMYLSKASSDDEPSEPSDSDGDFM

> hopAT1 Pph race 6-1448A|Genbank: AY803994

MVGINNWSSNLDAYRILQEAQSLTEEPHFDTAFPIEPESIAPEHHNHR
YVIGQEEHRVRLAANRNKGRPSARAFGNARNNSTRN

> HopAB3-2 Pma ES4326|Genbank: AF458391

MVGSINRAGPSGAPYGHATAPEPAPERAHESGSGASFNSPQLPAHSSDAP
TSQARDREMLLRARPLSRQTRREWVAQGMPTA DAGVPIRLHERAATAVP
DARAEERHTPEEPADAAAPQHLGARAHANGIVQQLVDAHADLAGMLSMIQ
DGRRG

> gi|15599036|ref|NP|252530.1| exoenzyme S [Pseudomonas aeruginosa PAO1]

MHIQSLQQSPSFAVELHQAAASGRGLQIEARQVATPSEAQQLAQQRDAPKG
EGLLARLGAALVRPFVAIMDWLGKLLGSHARTGPPSQDAQPAVMSSAVV
FKQMVLLQALPMTLKGDKASELATLTPGLAREHSRLASGDGALRSLST
ALAGIRAGSQVEESRIQAGRLLERSIGGIALQQWGTGGAASQLVLDASP
ELRREITDQLHQVMSEVALLRQAVESEVSRVSADKALADGLVKRFGADAE
KYLGRQPGGIHSDAEVMALGLYTGIIHYADLNRLRQGGQELDAGQKLIDQG
MSAAFEKSGQAEIQVVKTFRGTGGDAFNAVEEGKVGHDGGLSTSLNPGV
ARISFGQGTISTVFGSGIDVSGISNYKNEKEILYNKETDMRVLLSASDEQ
GVTRRVLEEAALGEQSGHSQGLLDALDLASKPERSGEVQEQDVRLLMRGL
DLA

> SopD2_Stym

MPVTLSFGNRHNYEINHSRLARLMSPDKEEALYMGVWDRFKDCFRTHKKQ
EVLEVLYTLIHGCERENQAEINVDITGMEKIHAFTQLKEYANPSQQDRFV
MRFDNMQTQVLFEDGKVIDKCNLHRLNVSENCIFKVMEEDEEELFLKI
CIKYGEKISRYPELLEGFANKLKDVAVEDDDVKDEVYKLMRSGEDRKMEC
VEWNGTLTEEEKNLRLCLQMGSFNITQFFKIGYWELEGEVLFDMVHPTL
SYLLQAYKPSLSSDLIETNTMLFSDVLNKDYDDYQNNKREIDAILRRIYR
SHNNTLFISEKSSCRNMLI

> Q8XQB2_RALSO

MTRITHASSHDYPRSHDNQAPASSTHPRKRNRDPAHDASSSFDGLPRRTD
SRRHPEHV PAKQRVRSVADRQETASHASAPHPQHRARTTAEAPRRQRS
REPPARQAKRARHDRSDAIRTETGRARTAPAPAQARDRHDPDARRRPA
AVPQRPTPEARASFRKQFARTRKLDDESDLLWTIASDALSHRDCGKALR
LLERPAVDFMDSLACFANFVRAVSALLESAGRLGLSERATDQLKRKWEES
SHAFYAVHDMADIDNERFVSKLASLGNRSQAQPAQAGCVAVARILES
GMRYGPGLLRNRLADTNPLGRDMSLLINAFSKWPEDEACRVGAQLLAGV
VADEQDALLSPVQYQPQALARLVGGVSKWPDDKTCRQAAAAMAGALWQRR
QELDNPEAFKQELAMCLNGLSKFTDAACEQAAMAVAGAVLSRKAQLLDP
GTCPSQHLSMI LNGLSKWPLREPARLAAVEVAAALWHRRRDMTDTGQFNA
QDVSNCLNGLSKWHDATCRQAAVALAEALPRHRDAHNDLPDFLPMHLAS
CLNGLSKWPEEASCRQAAAARALLWRKADLDDAERFSAQHLSNCLHGL

SKWPDEDESCRQAALAVADALVRRRLGTPGGADAFTPQQVSNCINGLSKWPE
EPACKLAAVAMATALWRRRDALDDAAQFTGOGLANCLHGLSKWPTEDPCR
KAALAVVGALMPRWSSVAVAGDPFLPQLLSNCLNGLSKWPEEDSCRKAAL
TVAETLMRHRRALADPRQFTPQELSNCLNGLSKWPEAPGCREAALAVAEA
LLLRDELGDT EAFGAIGLAACLNGLSKWPEATCRRALAVAEALLLW
DTLAADGQLTPQRLANSLNGVSRWLQDAASQEV SIRI I GMLGSGGQPFGA
FTMAQLAQLANGTARF I LELGHAGEADDGDAIQSDASMALAQARLRELA
HLDSRPDRLAQAETRNVALILKALASTGLKDGRLRLAHQGLTRLAALYAE
TGFKPDNLEALASVAAGLLPVARAPELKAYRADALRLLDQMOPAVDRKIR
LY IDAHLAAADP RRPAAAEAPPSLQIRRDGEAFGTRRPGLTFFLLLKAYS
VVADCWKRNSVPDI PLPAHARRDALRTWVAEMLDRTRGAIETDLDDEMSWN
LIAQIEAADQVLDVAVDLKLHKDLDT I LAHPPTPLNVGDVRRELRLAPEV
RDMHSDAGAAAEV I DLAGRNLT PHRPDETRDTAASQYAFFTRLTSGRL
PLLEVQLPGKVSFMLTRVIRRGDLLRMDLFGGSHLKP TKVHMRSLLGA
SGTKGGIKRYGRI PAMRLADTAPDAALMKDVIRKLNPREDFWFRMQRALL
EVPFRDHVVEGPIRLALLPDRLPSPAFALRTPEGAAIQLVPNDGCGFI
RESLACRIPVIRQAMHSAQALEGESQRMSLLPPQATHHFPRDQATIEEAR
AHLRASLRDDPELVWANPDDGTRDIKTHKLYEALAGALIMGTQGIAPVPSG
DDRLHLPRDKSKVFDATGGTVLLGKPPYDKANLMPVTADRI GTCDNGDAT
ARFLDTAFAFQYSY TAWDETGNNPAAADDVPMHLHGKGVTI VVPDKMWPQD
NDAQWVSTEDMKVHSSWTDGRRRDLAPRMDTVGSLRVKEIFPPGALMA
LPINELKKRDADCDGDKVFLYAGLPRMTQAVTRFFEEERERRIGKLGSKFP
PKTAHGVLDAGRYQAGRAAEVLSALHGQELVGRSLTLQFLFFGQPPALQ
QTLAERTLFGVYETERELRRGVRLLRGERATTPQVMEDLLL RAGLVQ
HACHPVALEVARALE AQLLEVMREAQPPVRAVSPDTASRAPQALSGGSTL
LFAPLTQAYESATTPRERLAALVTHYPRARLPHPATI LPTT PPKQPDPLA
QPAPLDDAPIGQSGYVPGAPLETLHNLTLGVKIGTDPKAVTQTDLFLD
IADHLEGTLRSSPERIRFMPYTRSGVMQELSQGRFNAQATLQRLRDNPTL
AAGLMEMAIEELLAHGAI EGT PPLRTT PAETEQLRHCARTLHAAARLVE
PEITPVIKAAIEGIGA LRGQAHRVKTERALHDKLRVLLHRGHSPADAAA
MVNDALRYSVVLKPDFAAGYAEVLGNLDRAGLIKTRVHNAFKPAWDPFK
GINVKFMGRDAAGQSVRLEVQFHTDETFALKMRYHDNYKQDFELQMQGAS
VEQRVACLEEARQACRQVATPAGCEHIGDWNNEPPQVNRRAQAKAAQLP
GAGAGKRPDAMATQVERLLQAAVRIEREVGPLLQTMQLHVIREHSVVKKA
KSIEKKIQRCLVNGIT PEQAADRVRDAMRWI IQLPHETFGAHAQKALET
LTANGLRITRVNNSFMARNRTYAGLNVKLTQREALNFEIQFHTGDSLYTR
NKTHKIYRQWQD TDVEQRQATDPAQRQALQKANADRLAALKTYAATVPTP
IGAERIPSFDRYRRDGASASDRARAERTAAPES

> gi|15835481|ref|NP|297240.1| hypothetical protein TC0867 [Chlamydia muridarum Nigg]

MSLSSSSSSDSNLRSVLSQVITSTPQGVPNADKCLTDNQVKVQVQTRQNR
DDLNMESDSAIAGAAGKDRASSVSQMEGQEVIEQQGLAAGKETASASTAS
LTQNASTGAASQKRVEDTNSKLELSSLSLSSVDASQLQEIQNIVASATR
STNETSLKNLDTPLGPKPTTTPRQDVMEISLALAKAITALGESTQAALN
FQSTQTQASNMNKSLESQGLKIDKEREEFQKLQEIQKKAGNNSTMDTVN
KVMIGVTVAITVSVVAALFTCGLGLIGTAAAGATAAAAGATAGATAAAT
TATSVATTVATQVTMQAVMQAVKQAI IQGVKQAI VQAIKQGLKKGIMQAI
KQAIKAAVKTLTKNIGKI FNTGKNVSKSFPNLSKVMNTLGSKWVTLGVG
ALTAVPQLVSGIGNLQSDMQKDLAKIQKEVGALTAQSEMMAFTLFWQQ
ASKIAAKQTESPSETQQAQAKTGAQIAKALS AISGALAAAA

> gi|34498030|ref|NP|902245.1| secretion system effector [Chromobacterium violaceum ATCC 12472]

MDINKVGSNTVPTVPPQLSGQSVDKGSTGVYATIDNLIAMLQKMNIDIR
DMERDFHAAGQQRAAAQVLSIDTKLESIELKYKAAWKNASAKVLSGFLS
AGGAAIGGVAGSGGDL MSTGLSGVGKAAEGGINWGTASLTRDAEQKNILG
EFQADHAAERYKALSAAA EKAAEASSRMHDLTRQLMSMQERMMSVVKI

> gi|29839805|ref|NP|828911.1| hypothetical protein CCA00037 [Chlamydomonas reinhardtii GPIC]

MELNKTSESLYNCKTDRHSVQVEVGPDPKDNRDVKVFSLEGRQOSKQDRQ
DKVSSKDSRQESRGADDKHVEEKTS AVSSKEEDKEESDGF MAYDNPTAGM
AFVDVAASVSSEAVVESTTVAIGSADLQWVQDVI ASTVESMMVADVNGQQ
LIELVLDAEGNVPDI FAGANLTLVQTGTDLSVKFSNFVDNAQMAEAMSLI
VNNPSQLAGLVEALKNRHLNLTELVGSSIVQLPTIEEVQTPHMI AATI

HQRDEERDQEGDQDQQQQDQEQNQYKVEEARL
> gi|140232|sp|P19520|YAV5_XANCV Hypothetical 50 kDa avirulence protein in
avrBs1 region
MSDMKVNFSKIIDS TPSEEEVATQQDSYTKSGLVAPSLDSQALKKAPRK
RVIKENIAALHTSSLERVHQKKVLVQNLAQLQRGLAKINGRVELEELIDG
FSVKELLIKRNPKIAEYEGGNPLMIRSLRFSNPQEVTSKLGAEKTPAK
REVDTICNKSTLHDIVMTPASLVKKEVRMNLISEVPRAKDKQKYRGLPSV
VYGQSSRRSESDYLTSRNGFGDVHSLKSNNAFNSDYEKICGSLSHAELG
LIERNLTPFIRHDPDR ISTDVHVSIEELAELHQMQLQSRKPASALRHNEYC
TKLELWDAKAI AVGESRALAVATLIEFNLEMLSIAQEIDDDGHKSKMVAD
FIERQLSWLGPQTALDSKSTLERVSAVTIQEREFIANEISRSLRQGVSLC
TYDKDEAGSHIREMSLLDFRVEEIEGISEFISSKLLHVTNAGEA
> A1JUC5_YERE8
MIGPISQINSPGGLSEKETSSSLISNEELKNIITQLETDIADGSWFHKNYS
RTDVKVMPALVTQANNKYPENLNFVTSPLDLSIEIKNVIENGVGSSRFI
INMGEDGIHFSVIDYKHINGKTSLILFEPANFNSMGPAMLAIRAKTAIER
YQLPDCHFMSVEMDIQRSSSECGIFSLALAKKLYTERDNLKIHEDNIKG
ILSDGENPLPHDKLDPYLPVTFYKHTQGGKRLNEYLNTPQGVGTVVNKK
NETIFNRFDNKSIIDGKELSVSVHKKRIAEYKTLKLV
> A0VTH1_9RHOB
MATVLCIADDDFTGATDLAGLLARSGAAVRLRMGVPDGPQDTAGIEVIA
LKIRTPVAEAVAQARAALAWLRAAGAERVFWKYCSTFDSTPQGNIGPVA
EALMADLGVQQTIIYCPAPPENGRAVFMGNLFVGRDPLDESPMKDHPLTPM
RDANLMRL LAPQVTRPVGLVDRLCVARGAGALRAELGR LDAAGVAHVVD
AVADADLGVIAEACHDMPLMTGGSVAAPLPGLLSGGAAEAAAAPDLAP
GAVVLS GSCSAMTRAQVSAYLRRAPGYKLDPLVLRTEGAGALAWLEAQA
LQDAPLVYATAEPEGEVRAAQALGVAEAGALVEDALARIAVAARDRGARR
FVVAGGETSGAVTQALGVVQLDVRREIAPGVPWCFAESGGVDIALTLKSG
NFGAESFFADALALVDTL
> Q8X837_ECO57
MLSPIRTTFHNSVNIQSSPCQTVSFAGKEYELKVIDEKTPIILFQWFEPN
PERYKKEDEVPIVNTKQHPYLDNVT NAARIESDRMIGIFVDGDFSVNQKTA
FSKLERDFENVMIIYREDVDFSMYDRKLSDIYHDIICEQRLRTEDKRDEY
LLNLEKELREISKAQDSLISMYAKKRNHAWDFFRNLALLKAGEIFRCT
YNTKNHGISFGEGCIYLDMDMILTGLGTIYAPDGI SMHVDRRNDVNI
NSAIIVNRSNHPALLEGLSFMHRSKVD AHPYDGLGKGVKKYFNFTPLHNY
NHFCDFIEFNHPNIIMNTSQYTCSS W
> gi|16764446|ref|NP|460061.1| secreted effector protein [Salmonella
typhimurium LT2]
MPITNASPENILRYLHAAGTGTKEAMKSATSPRGILEWFVNFFTCGVRR
SNERWFREVIGKLTTSLLYVNKN AFFDGNKIFLEDVNGCTICLSCGAASE
NTDPMVIEVNKNGKTVTDKVDSERFWNVCRMLKLSKHNIQQPDSLITE
DGFLNLRGVNLAHKD FQGEDLSKIDASNADFRETTL SNVNLVGANLCCAN
LHAVNLMGSNMTKANLTHADLTCANMSGVNLTAALFSGDLTDTKLNKAG
LDKIALTLAKALTGADLTGSQHTPTPLPDYNDRTLFPHPIF
> OspE1_Sflex
MLTQTIFFPCLPQKQENIILEVSNPVLSSSTVTTDGYTVFNKKAAYELQI
PAASRTKTLKFTATEMQWLTKINEAGIDEKQSQRYSDF
> Q8XRC8_RALSO
MGLARLPSGSHRWAVSPESGNDPSQHSNSNQQTPSLTRRARASGHLEPL
ARSPGHRAHASARALAVEAAGTDRSSTQSGSGMACAGPREDGADPLERV
SHSRQASRIPLKRRKREAGDDTDVRPTSLPRRGEIAAFHTAACDADAPTTP
PTTPRAESRREPTAEQLTDYGRWLGHTEFGRLAALREQQCARLWKLVASA
RRGKVDPDFCLHVARNDNTLAQRNGYGLALMFLDGSVPEENARRLDGYLF
ALGAASAPTHAEPHRQVRGLEQCVEMAACYLFKTRWFMDAPLEKLAELGN
LLSKYPRQPASMAAIAWIAGQALKPGPLPRLGAKELTLLANAFSKNGDSG
RCEQATARIGRHLLHDGGEQTFEARQIGLLLNAFSKWP GDTDCRAAAEYL
AARLERSPGLRQAMDAQAVATAINGLSKWPETAVCRNVAEHLAARLVHEA
ALLERMTATAVAASNLGLSKWPKAEICGAAVECVAEQLVKAPGLRQAMSA
QEI ANAFNAL SKWPDS AACRAAAECLAVRLADDPRLQASMNAQEVASTLN
ALCKWPRTTACREALGLAARIRSEADLRDALDAQQLANTLNALGKWPDA
DVCRAAAERLAIRLGRDAALRDGLNGQHIGNVFNALGKWPESAACLA AAA
CLTARLTDEVALLSMDAQGVAAALNGLSKWPESAACRTAAERLIARLSS

DADLRQGMDAQAVANVLNALS KWSREDHCRALAEQLAMRLVDDAELRQAM
NAQEVANAINGLSRWLEQPHCRRSLLLLTARMGEADLPWRNAEMSALAQ
ANAFARLFLSAPDDAELQAPARIKLQALAAHLDLRERFETCSAREIAIV
LKAMASVQLQHDMPFLARPALERLAALCPTTGLRNENLETMTGLCLGLLP
LARSRLVIAYRRRALCVLGLTQPIVARKIERFVQPRLGTAEKALAADTAM
REESHATRRALTFYQVLKTYSVVSDMWKTRYIEGSRRSVRDQRDLAAW
VKQTLERSREAI EADLGEDSWNIIARIEADADVLNALLDLRIHQHTALITQ
NHPPSRFDLGAHRMRTLKPGAPVPPARGAGDTHYVVVDMAGKELKHNR
DEPSKPYSLYARLTGLPLVEVKLPGELSAFMLARTFRYQGEFWRFDLFGG
SRLSRGGGLRPHDILSNHAAPAAMLPAVRYADTAPGSSLMQLAAKLAPLR
EDWARMQCALLEMVPSDHWVEGTLRLGFFDDVDGPEHPFKLQSPDGQRIQ
LCPNDGCGGLKFEVAMCIPVFRDHVMAMWAMRAGRATPAQQKLETSNDR
KRIAPQALQHFPRDEAALEEARRAIERKLAQLAPKASGQAPSVDPLTL
YHLTVSGGYEGEQIRAVPSADDNVHLPQRSFADLHGGALLIGKAPYDK
ENLLPFPDEQVGTVERGDATASFLSRCFAIQYSFTGFND DAGEGAEMLS
KGM LIVPPPQYWS PDHAGMDMACSREDLKTLSRWITGRNRATLPPEMRST
GSLRVKEVVVPGRLGALPI TELRKRDMTDGDDAFVYAGYPKLAAHISRV
MDDRKKRRGQQRSEFKPRKTAAPAQDPKDGQYQPGRAAEILAEQRGRRLRG
TASVFAKRFLAQSSDMREAMARDMMFVYDGIERPLRNGLLEQFEAEQAD
PQALDALRNHAFEDIANTHLPEAEAAAQLLHDEVFRLQSVPAKAAGMPA
GLADRFPLLAQAYEQAGDTRARVQAILENYPVCRLSCEQFPEGQPLVRG
SPELTLRNLCTIAIKVGTDALKSDTGTELF SKVIETCLRSERTFRERIGS
VPYKETAAYAMHDGRFDPEQAKAELRHNPTMAAGVMIHSVEALQQWGLLA
PAPTPOARFANTPALDVSQAIRLLADRASRMDAAITPTLRNIAQAAGQL
AGLRHRLKSSGSLKEKLMVAHKHMTLEDAVPQVNDALRYSVVLP SQDF
AAGCRRIQAALDEQGHARVKLVNHFVKRYE PFSAINVTLRDP EGHLEIQ
FHTPQTFDLKEHYHDL YKRSHHLRLQGVPAARLQELTRPARDAFRAVPMP
PGCEDIIDWEAEQTSVALPAVRAQLVPEPVYAE LNVRLHQAAKAMEPEIT
PVL RALLQHVQHHLGDGPELHRHVFKK PASTHRKIELLRHQHALPPEQA
AARVDALRYEVVVLQHEGFEVASVQWVSRQLQSEGLEVMRNNTFATADTT
YAGLNMNLRSGAHHEIQFHTPDSLRIKQKTHRLYEKLRRIRARPEAMP
NGQNPPASERESLEHGLRSAAATVRRPEGIEAIGSIDRYEG
> gi|10567542|gb|AAG18480.1| avirulence protein [Xanthomonas campestris pv.
vesicatoria]
MTSSINRYSYNPTNFPQFEQLSASQNAERSHPSAPLKDRSHEEAFFVRL
ASTRIKRSSGAGREFALS RNKPIKGVGYSTQPAVTA STGT SKPGVLCMTD
GMDLCVGVAVGGEKPSQNA GKARV FHVMPENRRAQWEIKS YIESLRSQGY
AAKAAIHGGDSSSRSSVSKIQAIEATLGAMDVPIEFSS TGAGANNNGNPL
GAVVEENGT VRFVNLVK
> A0GFG8_9BURK
MGWHRASDLRRRALHRS AVHVGRRHSRASGWARRRRDERAPGMGGGAGGH
AVAGVRRAYAGVATRLGVFRQPRVNASGDTEQEMSDEANSRGPAYAFYGD
DFTGATDTLAHLARAGLRTMLFFAPPDATRLSMLGPLDAIGVAGAARTMP
PAAQRQE LERVGAFAALGVRVMHYKVCSTFDSAPETGSGVAIRTLREY
CANELVAVVGGQP NLRRYCVFGE LFAAAGADDDAQSIYRIDRHPTMSRHP
VTPMNEADLRVHLQRQGVKNVQSIDWRCYAHGDAELQEEVQRRLDAEPDA
VLFVDVLDSSHQAIGRVIARHAAASAPLLAVGASSVAQAYALAHDNRVKD
AAAENRTTPLLPRAHGPVFLAGLSPLTEVQIGAAQSYLRVELDPLKMT
GDAASSYL AERVAIAGPLRDGRNVLAFTARRASSEGGALPQLAHACASL
LQQVLAAVRLRRIGIAGGDTSSFAVRALGAWGLSYLAPLSAGVTVCRLHA
DRAELDGMEIMLKGGQMGDANLFEQLLDGNG
> Q7DB76_ECO57
MFSPTMAGRSLVQATAQTLKPAVTRAAMQAGTGATGMRFMPVQSNFVIN
HGKLTNQLLQAVAKQTRNGDTQQWFQQEQTTYISRTVNR TLDDYCRSNNS
VISKETKGHIFRAVENALQQPLDMNGAQSSIGHFLQSNKYFNQKVDEQCG
KRVDPI TRFNTQTKMIEQVSQEIFERNFSGFKVSEIKAITQNAILEHVQD
TRL
> gi|27377169|ref|NP|768698.1| hypothetical protein blr2058 [Bradyrhizobium
japonicum USDA 110]
MYNRVDGEYAHTEQAESSWPADGSECAQTLTEIARLES LAPGELFDRMG
LCFSKPHTSDAIDSSNTSGLSTSSLSSELSVATSPVRPLFDYRTAEL
PQANVSGICVGLAAEWLLDLPSASSRMGVLLPGTENHRSAARRQEQSEK
LKTQLKEDKAEGSHNFQAKSTILRDAGLEPSAEETRYRFGTSSCIDKIVN

ELAQDPSVHLVSLKVFQPGAGTHTIATATSNGTTILSDPNYGEFTVPSDR
VGGLFKSLAERYSTLNKRDISAVVTQRIRYGHPNATDLALFPRAEHR

> A0UL57_9BURK

MSMLIIADDLSGAADCAIGFASAGYRTVVTLDVPTQGLDATVADVIAADT
DTRRLTPAEAAQRTSAAWRALREPGRRLYKKIDSTLRGNWAAEVAALQPL
AGLAIVAPAFPATGRTVLGGRVFRGEFLETTDTWKLENAGRTADLHAML
AQNGVSTAQLDVALRESSQTLIARIAAVAASGTEALVDAETNDDLIAL
ARATAQMDDALFWVGSGLAREIASVESLFDARAARTGAAASQRQPRHAP
VLALVGSLSAVSERQCAMLRRERAGMMELTVPPAVLRGGERHADVPQWQAR
IGDALRTGADLLLRIGSDDAFDPAEGALLSATLAALVKPHFAVLGGLIAT
GGETARAMLSAVGVGSVELIEEIEAGVAVGKPIGASVCQPHLRIVTKAGA
FGTDHALFAAWRYLRETPAASVRAGARSHGSA

> Q8XZC7_RALSO

MDTHDLAPPNACAADGAQLAGGNLDTLMQRAHELTHAAARALGLDEPAA
AQADDGGVVLNGTLVTVTPMPLEGLAGEAGDGALVVSATLGCRVGALDA
RALCALFAHAPGLAVYNAAGCQPNGELVLRHMVPVHDVVDTLAQDLV
VTQQLAVLLGDAATQVTRPQ

> gi|21241166|ref|NP|640748.1| HpaF protein [Xanthomonas axonopodis pv.
citri str. 306]

MFNINRLLRSRPTDADQAPAEDRPSHQPSAAEGLLSPLLARPRRRESA
AAPRNAGQSRPFRSPLRASGQPAALAGASSAPPRSIEHDDWLAQSLPM
AERVRTGYNLHDGQRDTSREVLQSVADAIRRAATRHSSTELVLDYGLPATT
LPDAIGRLDALQKLTLLHTGLQSLPDSLGLHLRHLQIAGALGLKTLPP
SLTRLSNLRTLQLTMIPLDELPGVIGRMQGLRSLTLGGGHYARLPASIVE
LSGLTELRRPHSSHRELPEINIGLMQGLRSLEVASNSELEQLPGSLTQLH
RLEKLTLSNRRLAHLPEDIGQLRGLTELSLKNCAALRQLPDSVGDALQ
QLLDLRGTGLQTLPPQSLARLPAQCEDIKVPDHLAQGLLQIRDPERAAREPQ
RAAQRLAERRRRAPVPAQQAGASWNRMPFARVLRVTVADLGERFDKWT
QGLAQRTARISGASITPADMPLLDQVVTEAIRSPEFRSSFGQFLSDHTLKT
LNMDGMTQVGGFPAVRGDVKTAFAEMLKHKLMHTQDHQTALGLLQDALQ
NPDGLSREMLLRSRNELTGRVEMWPPKAYISMHDVEGQAAQDAAITWT
MAQFEEAQGGIGDAEAKQESERAQANANRFIEQRRARVLLREWDIR

> Q221V6_RHOFD

MKKILLGCIADDFTGATDLANNLVRAGLRVQAMGVPAQPLDADADAVVV
ALKSRTLVPDEAIAQSLAALRWLQAQGAQQIYFKYCSTFDSTAQGNIGPV
AEALMDALGTDFTIATPAFPDNQRTVFKGHLFVGDVLLNESGMQNH PLTP
MTDANLVRVVLQGCRRPVGLIDYKVVAQGEAAIRTRIDQLRAQGVGLAVV
DAISNDLLRLGAALSMDPLVTGGSGVAIGLPANFGIAPSSTASALPRAT
GLQAVVSGSCLATNRQVLAFIQAGRPALGIDALQIAAGVDVTTQALAWA
APLLSQGPVLIYSTADANAVKAVQAQLGVEEAGAMVERTLAAIALGLVAL
GVRQLVVAGGETSGACVQALNITQMKIGPQIDPGVPWCHAQADAAPG AGL
HLTLKSGNFGADDFSKAFALLA

> Q4ZX48_PSEU2

MRIHSSGHGISGPVSSAETVEKAVQSSAQQAQNEASHSGPSEHPESRSCQA
RPNYPYSSVKTRLPVASAGQSLSETPSSLPGYLLLRRLDRRPLDQDAIK
GLIPADEAVGEARRALPFGRGNIDVDAQRSNLESGARTLAARRLRKDAET
AGHEPMPENEDMNWHVLMAMSGQVFGAGNCGEHARIASFAYGASAEKGR
AGDENIHLLAAQSGEDHVWAETDDSSAGSSPIVMDPWSNGPAVFAEDSRFA
KDRRAVERTDSFTLSTAAKAGKITRETAEKALTQATSRLQORLADQQAQV
SPVEGGRYRQENSVLDDAFARRVSDMLNADPRRALQVEIEASGVAMSLG
AQGVKTVVRQAPKVVRRQARGVASAKGMSPRAT

> gi|15723919|gb|AAL06366.1|AF311901|18 SepZ [Citrobacter rodentium]

MEPTNLSPSGVVLPLATAINGNGPVDENTGVMQAEGGASRNVRVVFAGVAL
AVSALAATGAGIAAMCIDNSSQTEKLGGLGIAAGVLGGLTSVGGALAMKYA

> Q8XBX8_ECO57

MLSSLNVLQSSFRGKTALSNTLLQKVSFAGKEYPLEPIDKTPILFQWF
EARPERYKGEVPIILNTEKHPYLSNIINAANKIENERIIGVLVDGNFTYEQ
KKEFLSLENEYQNIKIYRADVDFSMYDKKLSDIYLENIHKQESYP ASER
DNYLLGLLREELKNIPEGKDSLIESYAEKREHTWFDFFRNLAAMLKAGSLF
TETGKTGCHNISPCSGCIYLDADMIITDKLGVLYAPDGI AVHVDCNDEIK
SLENGAIVVNRSNHPALLAGLDIMKSKVDAHPPYDGLGKGIKRHFNYSSL
HDYNAFCDFIEFKHENIIPNTSMYTCSSW

> gi|28871725|ref|NP|794344.1| candidate type III effector HolPtoU2
[Pseudomonas syringae pv. tomato str. DC3000]
MIKTVDNSIPGTYGIAFTRVDTAAQISRVPVSDIQRNSSIEKAVIEHIA
DHPAAKVVMMSALVEALTGVFVKAQGEIKGWAEIVQAASRPHDSNRKGTGV
LSPRFDVMGCVGWNAATIRATCRVGTLEKGTFTNLMLSDNFKRILERS
MTDPALQRKLEGLVDLDYLKTTDGNLYAMSGWAARASESREQIGKAAFES
ASNLSAQISARELAFHRHNPVNHPSNQARVGFGISSPANNDLQVLRGHG
SSVWVKVPGSDFARLASASGKPVIAAGPSGTASRFMAVARFISPGCLRDLG
LDSEQAFKELVRYACYGYFGQDDHHSMLVNLGIAPHGLDEQWDDKLYTE
PFSHVIMGRGFSVDNAAQQHIVARATDEPVEHSAADRVG
> STM1183 flgK flagellar hook -associated protein 1265468:1267129 forw ard
MW:59109

MSSLINHAMSGLNAAQAALNTVSNINNYNVAGYTRQTTILAQANSTLGA
GGWIGNGVYVSGVQREYDAFITNQLRGAQNQSSGLTTRYEQMSKIDNLLA
DKSSLSGSLQSFFTSLQTLVSNAEDPAARQALIGKA EGLVNQFKTTDQY
LRDQDKQVNIAIGSSVAQINNYAKQIANLNDQISRMTGVGAGASPNDLLD
QRDQLVSELNKIVGVEVSVQDGGTYNLTMANGYTLVQGS TARQLAAVPSS
ADPTRTTVAVYVDEAAGNIEIPEKLLNTGSLGGLLTFRSQDLDQTRNTLQ
LALAFADAFNAQHTKGYDADGNKGDFFSIGSPVVYSNSNADKTVSLTA
KVV DSTKVKQATDYKIVFDGTDWQVTRTADNTTFTATKDADGKLEIDGLKV
TVGTGAQKNDSTFLKPVSNAIVDMNVKVTNEAEIAMASESKLDPDVTGD
SDNRNGQALLDLQNSNVVGGNKTFNDAYATLVSDVGNKTS TLKTSSTTQA
NVVKQLYKQQQSVSGVNLDEEYGNLQRYQQYYLANAQVLQTANALFDALL
NIR

> gi|28871720|ref|NP|794339.1| candidate type III effector Hop protein
[Pseudomonas syringae pv. tomato str. DC3000]

MKKSAGTQAYALFASATGSSSKGVLSTIARHLTGCFAPNKTALHSATAV
SYELLPGNYSVAASVHGLSVDH ROPALTRLSNVLFNQALALDLERFDEGA
PADEMFRPSLKREGAHPRLADSLGGEQLAVQTMKGLKRLAEDPAQSFAR
CHSFFYPISDTSPOASLHSVASSG

> Q8XRE0_RALSO

MGNQFSINRNRPANAGEAHASSTEAKPAPDAASPSRQVRVATAPSILEGL
RKLRLPFNFGARVPPLPEETWAEIARRVDTKTLHRMRAVSKTLKAAADTE
IRQLTVNTVEALQAAKRYACLETLMKMDGYFG DADLEGLPASLRELDLFST
RYVSAKGLAHLKPLVRLKVRANGIHAEARALAASTTLTALDIRNGI
GDAGAQAALANTSITSLDASFNDIGVAGARALAANTTLTSLDLGFNAIGD
EGLQALATNTSLTSLTVGSCIEGDAGAAALANNTALTSVDLTCNHIGEEG
AEGLAANTVLTSLDLTRNSISDRGAAALAGNTTLTSLCVNFNDIYGRGAR
WLAENTTLTLLDISYNPIDWGALGLADNMTL RLSVAVAGRIGVEGARAL
AGNTTLTLLDISVNAIGNEGAQALANATLTTLSLRSCELRAAAAEAFKA
NTTLASLDIGENRIEAGAQAALADNTALTTLRVGTGNQIGMAGAQAALANR
SLTKLNISQNDIRSAGAQAALANTSITSLDVSSASIGAAGAQAALANTS
I TWLNINDNHIGDAGAQAALAAHPALTSLYACDNFIGTAGVQAALANTRLTS
LSIWGNRIGDAGVKALAANTTLTKLTIGKRVDK QLGEQIGDLAWQELMAS
VDRSGMTFHSL

> gi|15618613|ref|NP|224899.1| S/T Protein Kinase [Chlamydomonas reinhardtii
CWL029]

MDCRGGIPLPEPQVIGGYHVKKILSKLRSRVVHGLHPETRHSTVIKVF
PSPSFTSRVYVNFLEAQLHQITHPNIVKFHRYGKWQDCLYIAMEYIEG
ISLREYILAQFISLPQAIDIIIFDIAQALEHLHSRNILHKD IKPENILITP
QGKIKLIDFGLADWDEIQRHPSVIGTPYYMSPEQRQGESHPASDIYA
LGLLAYELILGHLGLGRVFLSLVPERISKILAKALQPSNNRYSSTREFT
QDIHHRMSGDMQEDLRIKDHTVALYEQLQTRFWLAPETLRFPDFISGV
LYHQGYPLYPHAYDTLLEGDVFNWLWGYSPISNATIALSVVKSVCQDL
QRPLLDVCEINECLIRMKIPIDEMGISILCLEISKENKEL SWIACGKTV
FWIKRQGRVVQDFESFSPGLGKITSQIRETKVAWEIGDEAVVCTLELEE
SVASLKTLSLAELQDRRQKAI FCP IESIHGGIQSRQHGNSPSTLISLKR
IR

> gi|15596903|ref|NP|250397.1| type III secretion protein PcrV [Pseudomonas
aeruginosa PAO1]

MEVRNLNAARELFDELLAASAPASAEQEELLALLRSERIVLAHAGQ PL
SEAQVLKALAWLLAANPSAPPQGQLEVLREVLQARRQPGAQWDLREFLVS
AYFSLHGRLEDDEVIGVYKDVLTQDQGRKALLDELKALTAELKVYSVIQS

QINAALSAKQGIRIDAGGIDLVDPTLYGYAVGDPRWKDSPEYALLSNLDT
FSGKLSIKDFLSGSPKQSGELKGLSDEYFFEKDNPNVGNFATTVSDRSRP
LNDKVNKETTLLNDTSSRYNSAVEALNRFIQKYDSVLRDILSAI
> gi|34498031|ref|NP|902246.1| hypothetical protein CV2576 [Chromobacterium
violaceum ATCC 12472]

MTDFSVARFSQSTGANGVPGEYSVNSKKTGELPKLPELQIGADPLHNVLN
DLKSLDFESCGLAEPIDGLNYTVQLLAGNEGFGALDLHGTFSIGDLMAK
LQSLYGQQREGFWAMQAEELLPLVAAVALLAVQQRSEAAELNARALQENAA
SEVVGAGQVFSAVGGETARAVASKGAAQISEAISLHAVGHEVQGAQEET
SGELAQKLANSIGQHLANDARQETANRQEYIPLMEGMIAVLAKDQGSWVR
R

> gi|28868578|ref|NP|791197.1| type III effector HopPtoN [Pseudomonas
syringae pv. tomato str. DC3000]

MYIQQSGAQSGVAAKTQHDKPSSLSGLAPGSSDAFARFHPEKAGAFVPLE
GHEEVFFDARSSFSVDAADLPSPEQVQQLHSLRLLPDLMVSIASLRD
GATQYIKTRIKAMADNSIGATANIEAKRKIAQEHCQLVHPFHQSKFLFE
KTIDDRFAADYGRAGGDGHACLGLSVNWCQSRAGQSDAEAFFHKLEDYQ
GDALLPRVMGFQHIEQQAYSNKLQNAAPMLLDLTPKLGMTLGKGLGRAQH
AHYVALENLDRDLKAVLQPGKDQMLLFLSDSHAMALHQDSQGCLHFFDP
LFGVVQADSFNSMHSFLADVFKRDVGTWHRGTEQRLQLESEMVPRAADFHLR

> gi|28871243|ref|NP|793862.1| type III helper protein HopPmaH (Pto)
[Pseudomonas syringae pv. tomato str. DC3000]

MNTINRNIYPVSGISAQDAPVQTDQLQPQGGIRPGHNSNLIDFGLIQQA
NGPHSSLNTSSSRIQPTDTSTSSNRLGGNGDQLLNKLVFAIRNINLNN LLS
LLEGNQHQQSSPAQTQREQTPTSTQSHASPSSSSSSPSTSSQSSPSVPS
TPQGNAEKPFVQSDHPAEKPVSLQRTSEPTSVTPPQTPPQAVERNISITP
DKAPAKPEAVKPAVVNDPVLPKTSPAAAKPDSTVTAAKHATPAARGQGA
DMSGMIGFAEKANTTGGNNGEVVTVNTVADLKMYMEDDKARTVKLGANLS
ADSKVSIINFGANKTLLGTDKGNTLHNIYLASGKTASNDIFQNLNFNHD AR
YRENGDMQMFISSGQKYWIDHITATGTDQNPKGLDKLLYVGGKADNVSL
TNSKFQNNYGVILQGPDDSAAKAEYKGYPRMTIANNVFSNLDVGRPGL
FRQGFQFVNNNSIDKFHLGFTATGNATILSQANYFSNGVDVSNKASNSGV
LDDYGDAAHFKDIGSNVSFTQKSPVTAWTPSYNRDVKTAEARAYDLANAG
AQVVK

> Q7AAV1_EC057

MPIINKSASNYVEYISKNNPPYLSKKRD ASINLNGKVSDCNGEI IWCRI
ASYWSEFFCSNSGKIDYETFSSPQLLSKAIIVIENKGTNNIKGDVYFVEN
ESWGSVIYNLFLQLEKENKSHTSLEVHSPGHAMALGIKIKNDKENKFVIN
FYDPNQATATHKRVFCTNNICDIINLTAYDFLSEQCLKCYGLKEDTSLF
VDKTKSNDNNNVFIKKLPDNLQGVVINFAMGAGLREI IKKVYNDTRFTD
LTKSQMKILCESKNVNNVPGLLLLALQNGH DNVIDEYGTLIKKSINLKEEL
IHILSARTLDGTIPGLYQALQNGHAQAISYGNLVLDTINKNIDLEYLLS
AFKYEAHSSNKYTPGLFSAFQNGHADAIKAYCGVLGNSNLKRGEIIRMLE
ARNYDGAAGLLAYQNGDINTIQSFFDSLIMLDISKDFIEELLTAKHYDF
TGLSLAISHRHDHVVKLYGKLFKKLDTSFYKMSIILALADCERNNANI I
IDSEYKSNKAVKEYVEILKEFNICEKVAE YLSEFSGKHFLDVYNYYSN

> gi|19749310|gb|AAG45731.2|AF229441|2 Y4yA [Sinorhizobium fredii]

MTKIGHGLPPIILRSATADLLTKYGPLLFDWAARHGSPLNLVWPDALREN
AALKGVLTERVQHAIIYGAAGKNSPGLMQAALSASAGLDVSSLYELRDA
RRLGADGARLVATGPAKTNAFHQALINCNALISVDSPEELEDLIHGLPAD
AGQQPILLRLRPRDQS KSRFGMPPDAIVHCLVRLAGEGRLEFRDGLHFHLS
GYRRETRVAALSEAADLIAEARRMGFFPGMIDIGGGLPIQYVDRARYDAH
LAAQAPEDYRTGKIPDSFYPGSTLSAADWLHRLLEAEMNQGRSVAGYLA
REGLTLAMEPGRALADQAAITVFRI SRVKAVGPD SHVIFVSFSACETWFA
SEFLIDPILVPATKATVQSPVVRAYLAGHSCLDEDVISNRWLTFTPAPRA
GDLLDTPTPAATRWTSS KTSSIAIPCPLASASSKTPKGGPISFPDTIGEV

> A0TES8_9BURK

MDSRRRHSSGPAQVRRVRSSTSRVGGRGIEGQAPARQQSEGADARRHEIH
LQPPAAMNANAVAQHAARLLIVADDLSGAADCAVAGLHHGLTAMVLLDTE
HAPAPTNGVDILSVDVDSRRASKDEAARRNVAEIESLSHSDTRIYKKVDS
TLRGNVATEVAALASHLGMIVCPAYPASGRTRDGRQVWRGVPEASEY

WRNENIRGKADLVALLCAEHLRVAYAAIGTVRAEPGALAAACLRMQSEGA
QAVVCDAESDDDLQRIARASATLDNVFVWGSAGLAPAVIEALEPRRGIAE
PAAAGDDPQGPVLTIVGSMSSISHAQVEYLKANAGASLVALEVAVSALDD
PRSDVTTAVCNALRHGRHVVSMSQTQRGDVNDGLLFCNRLASLLAPAVR
HAGAI IATGGETARALLIAAGASALRVVDEIEDGMPLLECRLOGKTFPVV
TKAGGFGQPGSIHHAWRRLANEGKTANTAQTNL

> Q7AE34_ECO57

MITDLILHNHPRMKTITLNDNHIAHLNKTITTKLEYLNLNSNNLLPTNDI
DQLISSKHLWHVLVNGINNDSLAQMQYWTAVRNII DDTNEVTIDL SYNLA
ITNIDTSDEHLVEVSDNSEGNYIKDNDSMSIRYRSKYYSRDSALIEEETI
FSDAELKAILPMRMYGVSDYKSNSSSLSSHSGLKDPGTGTPVCYIHNES
KPSLGYGPTSNNWLSQSFTTEL

> Q8XQK6_RALSO

MLKVTPNFLRPGTGTSAPAEYPHNEKAVSYQSEEDGTSMADFEASPKGRR
VAGQYRAGIDKLDKDFLRVNGTPERDTA IHALDAFGKRIGAGHEGMYSTQI
SRMYGEGKVAFDGFCSGVGNPAIPMGVVRVSAVEELAKGLLECSEGTASNL
DIAAQALHLSQHGLL

> Q1I4Y7_PSEE4

MTDLNLTLSLSSASGEHV FADTLAFVAAHYSYQPQAFDNGD VHNAAGQNEG
SCKTLGLALLEGLSDQEALLAFGEHYRSVVATPEGSDHGNI RALIKHGLA
GVKFAEQPLARLA

> Q8XQ26_RALSO

MKLARTPPPSTSAAGASAEFSAPSPSVGSKRPRSPGALAYLSQAAMPNK
RLRLSASDGSL SAGPEVKAPALPTLIGTERAADLDVRFGLQPVRTKDG
GIHDWEKDAEGRPLAHPRFIALQGGDAPPDWDTPAVRKAFDIDALKAGDK
QYIWAASALGRV FIGEEEPVGHDPDSGKQRRRGHPLLVS GGPARI CGEFR
FDAETGKLVVINKLGRYSRYEDRREAQLQEVATI IRAAVAPLGLLEVET
RSGKTPDALVLP SLDPKYREPPAD

> Q7PC45_PSEU2

MF IASPKNVQECMLINPVKHNFSHLGFSNAQST SALGPASNKVPNFVSR
GRGKGVPEQFN TAECECRLAGRQDSVLD SIDGKEFMRL LQKYTASETTEE
EFADLRASIPRYSIELAKSDQPKV LYRGISLDDEAASLLN TSRGYRSRE
IAHGLIHGLRVVKGVYATATGVASASTVSNVSQGFALVNAKRKKETPVLV
LKAMPVPALNHS GAKGVTLSESRPLSAASKSEHEVILDI TNRYEITQA
RRSGEFIVVDMT VLGSRKRGGEFALVETDKWKQLSGAKG SNPGLFQAPN
GVKWKVKTNP SANRLLNEVLASRLYRAAGIDVPDIELASRKGKPALISKL
IVGNPKDLDTLAKNSQLKCGFAVDA WLANWDVIGL TGDNVI FNHRNKPVR
IDLGGALVFR AQGEHKGNQFGTTPMELVTMLSREDNSSRAFRKIERNDI
REGIAAIEKI PDARIAALCAEHGPGNH SERIELGKR LISRKKWLVD MKQT
LPYIHRKNERGDVVTVKKPTSPSAADTWRDRYATAVFVPHSAVRGSMNN
LPFRSFTPPD TMDGWRRTTRAVNFTEPEFKRSQHLAPASGAI IFEPDGR
VWITEPTNHPFGATHAFPKGQEAGL NLR TNALKEVYEETGLLVEFHGFI
GDYDR TTSRTRYLAKRIDGIPSDMGFESQSVKLANITEAKRLLPNAVDI
AILRDAERAYLKGPFK

> Q5EN61|Q5EN61_XANCV Early chlorosis factor protein - *Xanthomonas*
campestris pv. *vesicatoria*.

MQIKTAGLGPNAHPHGPVSGDGSSPADRSIEIEAGHS DTL SRACPQPAS
ETTMGLADLLS ISSQR SRPEVMPAITPAGDDEGVPDLRSQPARGASQP
CPANPGEARDVESGLLMRDCSSRIAAFLGNLSVVQELRQFDDSEFV DKL
NELVTEPGCREPKTL LAAMGERVNE LRSHLNKQASTREEAEFLAEARRYL
EPVMTSFETDIHTLQHDASA AKRIYQGAMTLLLYPLPLATLFTQKTGTYA
AFNIASYTYTAIQLVSLMRRPTTDAKLFMKHAINRHS LVFFISLIYAVPT
FYAKAAPLQRNAGFVAGA AMAQGMMFGLRLGQDLMDSMRLRFNGAFNRR
RDLPDGFRDAIEGVVGD LDRAGLSNVNRSVGEFQQDRRI TPHMDRQLTFFK
QDLSRIVTGLERL VATGTRQESPLAASDDPPGPLEAVRRTLEASFANNPD
LKGKLALATVAFVAVLGNIALMRNGLALPDFIADAVVSSTFLLREALSP
HVTHAGMNSVSDTVGGMTIGLPFSVATVMMSGYMDPRANPSGFIAGTVG
YTAAYLLFGRVAGDVLSKG LMATSGALGWGQQQAIRLGRSAMA LGFELVA
GHRSPAAADVHDLAGIEMADVPLEPLCFSPSQRASAERTLVGTLEQIGDE
WYDARDEWEGESEGTAGR DAPWVDAPAELPVQPVPQSE

> A0IP74_9ENTR

MLLGVIAADFTGATDIASFLVENGLPTVQLNGVPRDDL PVEAQAVVISLK
SRSCPVAQAI EQSLQALAWLQRQGC RQFYFKYCSTFDSTA QGNIGPVTDA

LLDALGESQTVISPALP VNGRTVYQGYLFVSDQLLAESGMRHHPVTPMTD
SNLLRLMEAQAQGRCLVNAEMDRGAGAVAEKLRQLALQGMRYAVLDTL
NEQHLLTQGAALKDMKLVTTGGSLAIGLARQWAQPGQSPQAAGAPQGAK
AVVLSGSCSTMTNQVARYRQQAAMAVDVARCLNDAERTAYITELADWV
QQQASAPLAPLLYATAEPEKLQVQVQGYGMAAASQAVESLAFAGVVKQLQQ
RGFSRFIVAGGETSGVVT QALGIRGFHIGPCISPGVPWVRAIDQSI SLAL
KSGNFGDENFFARAQTEFPL

> SOPB_SALDZ

PAKEAYRLAAATFRDAQVKHLNSQPWQTIKNTLTHNGHQYTNMQLPAADM
KIGTQDIFPSAYQKGVCSDWTKNIHHANNLWMSTVSAHEDGKDKTLFCG
IRHGVLSPYDVKDPLLRQTGAENEAKEVLTAAALFSKPELLTRALEGEAVN
LKLVSVGLLTASNVEFGKEGTMVEDQMRAWQSLTQPG KMIHLKIRNKDGEL
QTVKIKPEIAAFNVGVNELALKLGFGLKTSDSYNVEALHQLLGNDLRPEA
KPGGWVGDWLAQYPDNYEVVNILARQIKDIWKNLHKKDGGEPYKLAQRL
AMLANEIDAVPAWNCKSGKDRGTGMMSEIKREIICLHQHTLNAFGSLPD
RSGQEIQKVLNLSGNLEIQKQNTGGAGNKVMKNLSPEVLNLSYQKRVGD
ENIWQSVKGISSLITS

> Q8XRI4_RALSO

MTNPFVSPCAPPAQSPSPSAAAAPGDPPPAPAGKAPRKRGTLSL PARLL
PKASETEVSTLIGASKHSGRPVNTVADYSPPARTVSAPPDLPTTADRDR
SRSLARTAGLVQRAQRGLQKLQGTTRHARAPKPDASSTRLPVTVPDSAPRY
RQLLAQGF AATQDAGAVGRLADRLRALAPPLAEAGERTRYARPMLLAKV
LEHTCGQDAAAALRVLDRLTGGMRLGAPTFAAPDGSPDAHESALIRQASA
ASDAFFDALSDFHDAAPAAETGAAWRTAQLLARYHAGFDALCSLMQIPDV
PEQRQAHAHAFLOAADALQHGSVKPAGSPQALLDKHPIGSGTPEESLAIKT
LHGAAAVLRGEAPTPEQAGALFAWRQGFREEGPGTALDKTKARIGRFVRR
VIPRVEKHGWRTMLWQMIGKKASPLSSARLGLQAAHRKNLAGEYKDYVDA
LRSAVTTLAARYAQAEAAPLDPPGALPWRSPQEMWSSAVLKHWSALAQA
SPQDCVL TDDILAAIGLQLRDTVTRAFDALAAGIAQATEHDDGLREHLRA
SLATLTRLSDQAGLFPARDSPHPPGLIGLAPSGALLRSWSPAAPAGPL
EKALKSAERIEQDDQLREKTIEAARELIESLLTTIDAGGKRLRLASGSA
LGVNTGTLSTGLQNAGHALAIPLSVQADFHASRKRQAVVEFGRGHGRDL
FIGTDKTVHAAAGCGGAI GYDIQVLTNRIRASLGMSVVPIDVERGKRVGV
MFRAVRQLDRAQQTVGGYHDWEAVKYDDTATRQALISLSNWLFEQATEHR
QRPLEREAIWNALALHCGTGNTISVGWVDQRKRRLRHKLRLSGGVQARIS
SKGAPIRVGPSARLTAEATSRRDATATRETAGIMRVEQSVQGHGGHLTLRA
GLTYSAGKMFYTS AAPDAATGSDATGGRHRITQGFNGGTPLSWSKQFAEL
GHTVEVRTIHLNGLRADRVSYS DKRYKSGTEFLALIRTRQRVWIDMLS RK
PGMTREAAEQEFKVFCDMVERHSGPNVSYLYRERLKP AIAREIEGQLDLA
DMHRALDIDALAGLPADSERASTEEGTSPQPASPAPKPSLP GKHAAPAPA
PDIMRGEAEASGPPSVAGSPPPAAE SVPLLTRPAMRKT SRLPKARNLL
DKYTAKVQTAQAAGLNDALHTLLTGNAMTKGRSIRAVQREVAKRI SEGT
WSPNSRARTAVPAGYATLPGSPLEAAA AVAAAHA PGSPPSASHLARAQS
TGLTRRESEAALAEETHAQACEMAADAVLFDEASWLPERLAIVENISR
RENKGLSTTLQLYGTSEASGQRDLHNLKFG

> HopAB3-1 Pma ES4326|Genbank: AF458050

MVGISGRAGPSGSYNSGHTDNPEPVSGRARDSNSEANSNSPQVPPPLN
APASEMPAGRPRFLRSMALSSQTREWLEKGMPTAEAEAGVPIRLQERAANT
APQARAEERHTQPADAAA PHARAERGRTLQAPASTSPLYTGA VPRANRIV
QQLVAGADLANIRTFRNMLRGEEMILSRAEQNVFLQHFPDMLPCGIDRN
SELAIALREALRRADSQQAARAPARTPPRSSVRTPERSPAPRTATESSSG
SNQRSLLGRFAGLMTSNQRRPSSASNASTSQRPVDRNPPRINLMPTGANR
VAMRNRGNNEADAALQALQNGINMEDLRAALEAYIVWLRPIPLDIANAL
EGVGITPRFDNPEEAKVDNPLMNLSSALKRRLDA

> Q3BZN0|Q3BZN0_XANC5 Avirulence protein AvrBs2 - *Xanthomonas campestris* pv. vesicatoria (strain 85-10).

MRIGPLQPSIAHTAAPALPHTSAISPTQVPHMPGNTPPLRERPRRRAGN
MPPLVPLNDSAMTGKPALVALDSEFSEQR LAEVQARQITVQTLQGKLATH
LAQAGTALKPDSIAARFAAGTLEPVYLDTAAFNAMSRGLPARARAAAGPV
LIDAQQGRIIFNLQRAFAPGDTFSDAALAALGKQLNLSGHGLATPNWLQP
AAGTPGRKLLQQAARYHGHEVPARDGGAGFFKANDHRLLEGGQVLLRNHQ
KSLVHNHYFEAPSTRAF GKDV MVHRGLFDNHAGI PENSLASIDHAYEQGY
RNLELDVEVSSDGVVPLMHDFSIGRMAGDPQNR LVSQVPPFAELREMP LVI

RNPSDGNVYKTDQTIAGVEQMLEHVLKKEPMSVALDCKENTGEAVAMLL
MRRPDLRKA AAAIKVYAKYYTGGFDQFLSNLYKHYQINPLHSQDAPRRAAL
DRLLAKINVVPLVSLQGMLNDRERLGRFFRSNEQGAAGLADTAMQWLDLSDTK
MRPVIVEAVATDDSDAGKAMEMARTRMRQPDSAYAKAAYSVSYRYEDFSV
PRANHDKDYYVYRNFGEQKLTNEAFGVKRTTAGAFRDDGESLLTDQPEA
ELLAILNLRALARGHTGNELDVPPEPPIIDINRDAEIVKQRTQQFQASSIP
ADPNHISAVREGKQHDHTADMVNDPAATRALDKRAKALGLLTDKYRGAPV
THYLNEQARQTETD
> Q8XUB9_RALSO
MKRIDVHAIPPEPAREPSEAPASAPVIAQPTDATALLEAAVRKLLQELNG
NPAPARHAKRWRIGQTEVAVLVFVTERKNANGHSEWIVERVRLGERALG
MDVLSNGGELASPGSADIGPVQGDGTTGTVAVVVEQYASRTTAADAGTT
TRPA

> gi|15605594|ref|NP|2203.80.1| predicted Protease containing IRBP and DHR domains [Chlamydia trachomatis D/UW-3/CX]

MKMNRIWLLLLLTFSSAIHSPVQGESLVCKNALQDLSFLEHLLQVKYAPKT
WKEQYLGWDLVQSSVSAQQKLRQTENPSTSFCCQVVLADFIGGLNDFHAGV
TFFAIESAYLPYTVQKSSDGRFYFVDIMTFSSEIRVGDDELLEVDGAPVQD
VLATLYGSNHKG TAAEESAALRTLFSRMA SLGHKVPVSGRTTLKIRRPFGT
TREVVRVKWRYVPEGVGD LATIAPSIRAPQLQKSMRSFFPKKDDAFHRSS
LFYSPMGPWFHWAELRNHYATSLKSGYNI GSTDGFLPVIGPVIWSEGLF
RAYISSVTDGDGKSHKVGFLRIPTYSWQDMEDFDPSGPPPWEEFAKIIQV
FSSNTEALIIDQTNPNPGSVLYLYALLSMLTDRPLELPKHRMILTQDEVV
DALDWLTLENVD TNVESRLALGDNMEGYTVDLQVAEYLSFGRQVLNCW
SKGDIELSTPIPLFGFEKIHPHPRVQYSKPICVLINEQDFSCADFFPVVL
KDNDRALIVGTRTAGAGGFVFNVQFPNRTGIKTC SLTGS LAVREHGAFIE
NIGVEPHIDL PFTANDIRYKGYSEYLDKVKKLVLCQLINNDGTIILAEDGS
F

> gi|58580860|ref|YP|199876.1| avirulence protein [Xanthomonas oryzae pv. oryzae KACC10331]

MGSLAVSTEISHNPLPILHAGPGSPSCLRLTLVVEGCQDHPKLC TAMRPG
KLCRDHRPLVWRRPCKEVCLMDPIRSRTPSPARELLPGPQDRVQPTADR
GGAPPAGGPLDGLPARRTMSRTRLPSPAPSPAFSAGSFSDLLRQFDPSL
LDTSLLD SMPAVGTPHTAAAPA EWDEAQSGLRAADPPPTVPVAVTAARP
PRAKPAPRRRAQPSDASPAQV DLRTLGY SQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVA VTYQDIIRALPEATHEDIVGVGK
QWSGARALEALLTKAGELRGPPLQLD TGQLVKIAKRGGVTAVEAVHASRN
ALTGAPLNLPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVA
IANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQR
LLPVLCQDHGLTPDQVVAIASHGG GKQALETVQRLLPVLCQDHGLTPDQV
VAIASHGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETV
QRLLPVLCQDHGLTPDQVVAIASNGGKQALETVQRLLPVLCQDHGLTPD
QVVAIASHDGGKQALETVQRLLPMLCQDHGLTPDQVVAIASHGGGKQALE
TVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLT
LDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQ
ALETVQRLLPVLCQDHGLTPDQVVAIASNGGKQALESIVAQLSRPDPALA
ALTNDHLVALACLGRPALDAVKKGLPHAPELIRRVNRRIGERTSHRVAD
YAQVVRVLEFFQCHSHPAQAFDDAMTQFGMSRHGLVQLFRRVGVTEFEAR
CGTLPPASQRWDRILQASGMKRAKPSPTSAQTPDQASLHAFADSLERDLD
APSPMHEGDQTRASSRKRSDRAVT GPSTQQSFEVVRVPEQRDALHPLS
WRVKRPRTRIGGLPDPGTPIAADLAASSTVMWEQDAAPFAGAADDFPAF
NEEELAWLMELLPQSGSVGGTI

> gi|28871829|ref|NP|794448.1| candidate type III effector HolPtoAA [Pseudomonas syringae pv. tomato str. DC3000]

MNRISTSSVNSSFNYTAPTKEAQNR FASAPDNSPLVATTSIT QTLVQPG
RLDKNHRMLDSKIINFSVAFNLGRTRSIAGGSA

> Q3BSU7|Q3BSU7_XANC5 Xanthomonas outer protein C - Xanthomonas campestris pv. vesicatoria (strain 85-10).

MKTSSASKSHYTGQFPQGD LQPKTPIPVGRNSEIPKDAALSAQLKGLRPL
DRKPSKMPTSSSDLQAVNKMIAENRSNDVGGQFLLSTQSLGSAERVDSQ
NYHSRNEGSKAPLFFSEFATEKPSLQSVKLSQGGQDYAVRVHVGKRGRD
LFTDEPIEGENSKLGR LKTSPLLSTQSQGTRAIRAFAATATIDKSRGEYV
ARLHRHVVEALGDEGGVHLLRPTRDHYAEDSTLNFFTFCEQTELASSLN

SLEAISAKKEDRKPVFTDHSKSLVGLSRTSRTEASPIGRVQPPYFVTS
LKRGDVVITDDHIQAGGSMLEAAAKEAGVDLALATLSAHPFSPQLT
MSSEVSAFLDETLAAWDPQGVKTERLAAIGMPREKLTNSEAMILIAY
PASDSAILRFESIQQNLFKRAHLHNVGIDPDAPDTLEQMQKLSMQEM
TDSARHFVDDAKVLEGEHDSLIPILKMKPASPDEIVKELDQVSLASR
QASEVQVQVVLDWDDCLRDEKGLNYKLMHNALAITAREHASTLPEL
AVLHSHKLNAGAEVDEEAPLLMKNQKDFSSYLMGRQSIYKRHIIE
DFVVRKMLPGISEHKAASINNAVYSNFVREYKMLVKPEVSKKNYSR
DVPFDPDIELSLPGAKEILEKSRNANSRVILISNRGHGDLENEINH
LGMHYFDVVSGAEEVTLEKSHLPPSQMPEDLQKRLINSLNGSDEEAL
RATLSEAAIYAHDPDSTIERIDKKPDPSTRLAESLERLSVQPNVPI
TSYGDQPSDIKQLKSVAEPKSRVLKGVIVNAQRDDVGREIDV
DVGVPTRVVSKITEL

> gi|15835056|ref|NP|296815.1| adherence factor [Chlamydia muridarum Nigg]

MPVSGSIVASKENTSASLQPATTLNNGSSVEFFQQITVYDDARNFTNHTT
EDVIKIGEQLRKFYNMTEGTQVPFTTSPAYHTGNWKTAFIYNLAQVIAN
LFPSTIQPIRVNSTRSSPFSTNSSVEKRNRFSTKDTKVQPPHTTRS
VSPRKRKSVIVTRSVNIHNHTPDKKSSGESLRNISLEKPVLSRKR
RDVEKNKEIKNEPSVNKYDLTYKNIAEKLGLSSEQQTSVKELLNKLR
KAITNYNALIEKNSSEGQSLLRQAKLVEEIQEKISPAVSDKKGN
EKKTEEKSKVSIKDVADIIKAEFSGHLVPVDKIIHGIWIAGAP
PEGIEQYMRVFLDTPDYSFYFWVDSNAYGAAGFSGILKRM
AFDVAIQELRDSTEESTKVFVKEYDDLKKEYQRIAQTHSTK
KNEYLQDLQSLLEKYKTVSDEVGRFRDVLFLKNVITQDNFF
NYCLLKGVGNISDETRMEYLEKELKFSKEEIEEYRKLKESN
KEKIASVVKLNEQLGSARVHIKDIKELNSMKHSQNIYNYE
MEMFLRWNYAAATDQVRMYMLEEYGGLYTDLDMMPAFS
QEVLEVIVKHSVGDVDMFEDMTSRRRAISDAVLKLA
VGETTTSVIEDIGKIDISRLTEEDKTKLGELEFFV
KKTQNSSKLGKAKSFFQPMNDIVRDTMPI LRRYHY
YPELGFVFRGLNGLMVSHKGSAAVSHVIGQDAYQ
ELAAMRQEVLSGEFFRSLEDLTHRQHKDLIGHLV
SDYLAKSLFFDYRQDSIMPEAVSTLGTGPD
LVAQKLVLEFKDWGLGRDFLTPRGKLGDM
AFLGSYKKIPLDPSDPRKYTFDWMNPLTVGSND
VTPADESTWCGSKKRCVAELLFSDSSTKLST
NKLQGVTRTKIDTSTFTSLWKEESK
KLPGLLESFNRFITEKTVDILKLELDQKI
YVTQSAIQDDNIAKASLFSLQLLAHLLRF
APYPTNHVHFFPQIQKELDSYVKA
IKLFLKTSSTTTVVWLWSSQQNLSLFF
KELLAISERRVAIYNLLNPEEA
AKARKALEKKERDKKGGQEKDSSE
GEDQQGDQKKNFSEYAE
LLKQYEQHKAKDSLGLLSEAEQ
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IEAEISSGYVFRALESQVSKW
FSLPEQORRQIILNLLKELEKDA
IKNSKQDKKHKNWLETLYDQAEQ
KWLQEPKKKLQDLIKNSGDN
SRVILKDSDQLLSRNE
LQSMIKKGYPFADFANILRFM
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PENLQKELKNIAPEHLLTPP
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SVMASIGSGFFNPSSYS
MARYMEAIFELQQKIVNGEL
QTVETVKNILQKGAESLY
HADRAALLVQFSELRYHLSL
TEVQKGLADLDNLGQAPS
YLLTGPLPGLGHIMLRDR
DFGLPLATSMTDPIGLSTY
DFSGIGGRKDVFTSPSEVPS
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ERYSGIWDLA
FRLGAESLRTHPQTFIYDTE
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LHFFDGAFRVTDPNFG
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FSGIRTTWATL
FAMGLTLNGNRIDERT
KESDLDTQINGDLLTS
FLSKNVLDERGVALGR
TLVETLFPVAGTR
LVSSGAIVETPNDV
ASLLQASRERLSHF
KDVIQVLLRELAT
KIHGKGLKDS
DKVSVKSVTV
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SVKIKSLRDA
FQNFGKSLNEL
ANTGVMDELGLS
VLSLIQYARLV
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FNILDVKELTE
MTVGTVIQALQKQ
FITPAGIDGFR
TETLLARQIQK
VGT
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VARVLELPVLET
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VEDLLHADS
YS
DRVA
AKVQISFDVIT
LALTLSS
SALPLAMLAVG
PIAIGMGAAS
IARNVARKE
ERHYAWVEY
KQFLDSAAK
LVKAYPESHLL
DLSGNRVLGN
LYLDLSQNP
LLKGDVSR
NYDSLIGHV
GDWSDRQVRNRL
G
YR
SSPERALAK
GHANTRW
PREIPHI
AKGVYETV
YLG
YGIQYKVYTE
IVYLSNQV
AWRDAVMD
P
TSRYIPPL
VEEGKSAT
I
IAGNTPL
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VQIGGGG
TYTTLTGDV
SAKNTIS
FRAIPPLG
VCFNLSNH
AMQNVPM
MRPNGTK
IEALKIQ
QTGFSVIAGS
AEGYDIL
TGEKDT
HFYISSGG
KIFSG
LGNWYH
IPK
LKGRLD
IILAKNSAE
HLLMDDYS
YNWQSLG
TNLTLIPR
GEGNNNS
GIFVSN
FDASPS

FEQWVNKFTVKMADGITLFLNKSSEDQNFSLATTNTIVTLGVHVSVDQTI
WSNRLPEEPSYIENIFNWLKFKCWWLAPKVTVLQREGTADFYRDQKLIY
HPKPPFAELDLHPQPGYHTYVNGSIGDITYIFSESPWVNLSTVKLSLADDLG
HSQTVDLSSLVPTFVVRGRMTSQTVNGPSIDLEISSPRYTLPLQISWGSV
LPRNTRFDVMPNHSPTLGEWYDKLNTNTSEWHTLFHNSMLIPKSLVSVLS
LNNTVTVMVRHLERKNEHILGVENRDSINRKVHGQLYAGFITHTIENRHW
YTLQPNLVEFDITVPAKSIKYFVFRGRLLFRSYLEPKTLEVRSGTPIDFH
VWSQYDKIHVHATTLKLEKFQVYNVTATDALNRYLMYAQNLAYIYGRDF
VLKFFFIRSGTGIGAIQLVFKDLFKDSFGTEKTLGKEAKSTTPLYSIINP
SYKDHLKFFLGEGEYDLTQYIQEISDTSHIIEMLRDPPTHELQEPShLPK
NPiVLTYITIDPQKASAGGKQLQFLDKTIKAYQLPPTMAEHYYMDPVS
DLYITCIALTNPVERAFSLRRLPKFKLNWLEFQNIIFIgTHSRTSQALGSS
GTGVMFVGP EILYMEIDL SRVIADRSFPDRVSSRSSVVFPTNDQVVLN
SLAKKFYSYSESMIWNLRDRAGESDRAKAYDIYLLDACTSKDKNLNWA
PPKLLDFALAYR A WSHVWKQSLKKG YLIQLPAGSIQVSLIT TQSEYFA
RQRKQGFQVYFSIYGLQGVIPKQFPGDMLCDIKEDVVLTVKAVDES
DYD NRKIYVVLDLATEEERKL RADKNVIVIPGGEQSKY
> hrpA1 Por 1-2 (1-1?) | Genbank: BAD20931
MPAFPSITSSLTQAGTGVANGIGGALQGANTIASAANMQGNVLAGTGMGN
SLSLAAQNKASAEMDANGAQLIAMQAEETKKKQTM DVLN AIEAGKEDSTN
KKISATAQNARGIRY
> Q8XRI9_RALSO
MQSLTGIATSPSDPTAQEPAQAEPAAAPSSLVARLSRALRRALQVRPPTA
AGHANPAPVAARAHTT IMPRHERRPAAEPSRAQHOMRADAARAAQRLQOP
AGGLHAHHARGTVPFADGNRWMVAVCDVAGWQQEMVRRVSRYSGLLPDA
NRPT EQGLALAA T RMLLAMQ QKSRHLV LDSI PVMRLPSALCNAEQVEVLT
VHDCDVFEW PASGGLPPNLCSLHFSRNRRLTAIPGRMGQLQQLRELVIDL
SPLRALPTAVS QLPQLERLVLQGS DLRIVPVELGALQRLQTLTLASSRLL
TQLPTSLGQLRHLQNLNRGNPVL PALPETV GQLSVLES L DLRENTGMTT
LPRSLGSLRRLRHLDCSGMTALTALPADLGACTSLRTLRLRDCVALRTP
ATLGG LKRLTHL DLRGCVGLTDLPEALRSLPATCRIDVPPHLAERLVQRR
RTVAQAPSVP LPNPGEGADWGRLLQNRTRGLGYDTEYGSDAFRIVVERS
ANAAMPDEVRSRRDARRLGFLVDGLCNSATLRCLVFQRAHERYALGHLDD
EGLAIP ELMALLTEECVRNGPSFADRAATLMRHEAWSSLEGATGNDFIG
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> Q7PC44_PSEU2
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> A4XN96_PSEME
MIRPIPNASSILHIPSVARAASPATPLAQVRSGAATTTGTSAQQASKFAA
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RKTLKNGQLLRMERGKLLKQIVDSMAGDAAKAHALLQAAARQAKGEKSLN
EQQALNQQLQLLRQHG RNP RPLFNTGNNTRI LARGGEDPQRDKLRS LY
SVAVTEQLNVVGLIEALLNSTQDDGQKDGREGFEAVLREIRQVVARMAE
LDGSASPQLR TMMYAMSTAQYVATLFGGCEHLLGRMRNKNPAMQVETSA
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GP IVAAVPQFMVSMHLHGYIRTATSDAMKDAVPEKSADASMKRALAVGL
TAGVAHEGVTNLLKPMVQAGFQKAGLNERLNMVPLKGI DTDSVIPDPFEL

KNDNGALVRKTPPEAAEDKAFVASERAVLNQKKVQVSSSTHPLGEMIPYGA
FGGGQAVRQMLN DFNLLNGQTL SARAVTSGIAGAISATTQTIAQLNSTYV
DPRGRKIPVFTPDRANADLGKDLAKGLDLREPAVRTAFYSKAVSGVQSAA
LNGALPSVAVQPQGASGTL SAGNIMRNMALAATGSVSYLSTLYANQSVTA
EAKALKEAGMGGATPMVARTETALS NIRHPDRASLPHTFQPDTLGGVPRA
VENAYHMARGALQLPTQVVVDTVRVVEDGVASGVSSLRDAHKPAETSSPT
ADDAAAVELTAME EGRRR
> gi|17233490|ref|NP|490528.1| hydrophilic protein [Salmonella typhimurium
LT2]
MPINRPNLNLNIPPLNIVAAYDGAEIPSTNKHLKNNFNLSLHNQMRKMPVS
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LGAQFTLYIKPDQENSQ YSASF LHKTRQFIECLESRLSENGVISGQCPE
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> Q8X9Y4_ECO57
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NYDRLVKLSLNSNTLESINI HQGRNVSITHISMNNCLRNIDIDRLSSIT
YFSAAHNKLEFVQLESCEWLQYLNLSHNQLTDIVTGNKEELLLLDLSHNK
LASLHNALFPNLNTLLINNNLLSEIKMFYSNFCKVQTLNAANN QLEKINL
HFLLTYLSSIKSLRLDNNKITRIDTENTSDIRSLFPI IKKSESLNFLNISG
ENNCPTIQLMLFNLFS PALKLNTGLAILSPGAFEDHSDGLDVDNELFHYT
INKAYTPYNIHTYKTEEVVNQRNIKIKNMTLDEINNTYCNNDYYNEAIRE
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> hopAV1 Pph race 6 -1448A|Genbank: AY803996
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VDELIAEVQAAPRFKSRQTLDVAQRHLLAALNIDIDQYKKG VHKAGLYE
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GMAVNGVAAIGTVVSTTVPVVGVQVAGPAILASTIPLQWGAGYLDERRNKH
RYNLRANTKWGDFLKDNAANIHFKDLTVEHISESKLRQSFLTQPEVQIAA
IREVYEDTIGELMRRRLEMQKDIDVQREAGRPM RALALKQLRELD A EIDV
TKMHADQFESFNMDRWSAIPEDSVIGRCLDDLDNLQKANRRARLRKPGEG
AQIVQRYVQAFQGGVSTGTTL PVVDASIDSFHVHDSQGHDHGLQPAPL
AVAAGTGAAGGAVFTGATGEVRMSKADNKIMTQLRVDEPVYTADA EHW
FRAGNRDVLRTSAGYKQHAHTRWDELALVAQALKHGLTSGPVGLKNLAV
AKVELRQARASLQ S ALDALAASGLPHRTPDSARA PTISSMKDQLYDYSEV
RRHLGV@
> hopZ2 Ppi 895A (race 4A)|Genbank: AJ277495
MGICVSKPSVRHDY NEDYGRNYGADTAQASSNTSSSDSEWEQSPPHSPRQ
PVAADIPDRAKDKISALRESYRSQMNSNPDLLHYAKNILDNIEYRQSN
DTLQLDAQNLSLAAA YNTSFSQLNLHCFDSRIAFLDHLQSHNEPGAWRG
VFRNLNPPSLHHVAVDVRNHSNGQKTLIVLEPIT AYKDDVYPPAYLPYPQ
LREEVNTLRGNKMSVIETDAQRSWHDCVIFSLNFALCSYQKDSAFDSL
HEKLAESGYCFPNEDSRSLARGIELIDGKQVLPVAVFYKHAHSRGTVTA
VENAQPHIANDNVSTNRSSSRETLNERAEAFRVHREGGDPENYSMSI
ESS RARKIRKALESQ
> gi|46395936|sp|Q93Q17|AEXT|AERSA ADP -ribosyltransferase toxin aexT
(Exoenzyme T) (aexT protein)
MQIQANTVGTQAVAHSDATTGVGRMGQMEARQVATGQDA ILLGSRSEPO
KGQGLLSRLGAQLARPFVAIKEWISNLLGTDKRAAAPKAQTAVSPEDLQR
LMKQAAFSSGLGFAKADVLNNITGELQKGDHASLATNGPLRSLCTALQ
AVVIGSQPQLRELATGLLARPIAGIPLQQWGSVGGKVTELLTSAPPELL
KEAMSQLHTAMGEVADLQRAVKA EVA GEPARSATTA AAVAPLQSGESEVN

VEPADKALAEGLQEQFGLEAEQYLGEQPHGTYSDAEVMALGLYTNGEYQH
LNRSLRQEKQLDAGQALIDQGMSTAFEKSTPTEQLIKTFRGTHGGDAFNE
VAEGQVGHADVAYLSTSRDPKVATNFGGSGSISTIFGRSGIDVSDISVEGD
EQEILYNKETDMRVLLSAKDERGVTRRVLEEASLGEQSGHSGKLLDGLDL
ARGAGGADKPKQEQDIRLKMRLDLA

> STM2066 sopA secreted effector protein 2141570:2143918 forward MW:86783

MKISSGAINFSTIPNQVKKLITSIREHTKNGLTSKITSVKNTHSTLNEKF
KTGKDSPIEFALPQKIKDFQPKDKNTLNKTLITVKNIKDTNNAGKKNIS
AEDVSKMNAAFMRKHIANQTCDYNYRMTGAAPLPGGVSVSANNRPTVSEG
RTPPVSPSLSLQATSSPSPADWAKKLTDA VLRQKAGETLTAADRDFSNA
DFRNITFSKILPPSFMERDGDIIKGFNFSNSKFTYSDISHLHFDECRFTY
STLSDVVCSENTKFSNSMDNEVFLQYSITTTQQQPSFIDTTLKNTLIRHKAN
LSGVILNEPDNSPPSVSGGGNFIRLGDIVLQMPLLWTENAVDGFNLHEH
NNGKSILMTIDSLDPKYSQEKVQAMEDLVKSLRGGRLTEACIRPVESLVLV
SVLAHPPYTQSALISEWLGPVQERFFAHQCQ TYNDVPLPAPDTYYQQRIL
PVLLDSFDRNSAAMTHSGLFNQVILHCMTGVDCTDGTRQKAAALYEQYL
AHPAVSPHIHNGLFNGYDGS PDWTTRAADNLLLSSQSDTAMMLSTDTL
LTMLNPTPDTAWDNFYLLRAGENVSTAQISPVELFRHDFPVFLAAFNQQA
TQRRFGLIDIIILSTEEHGELNQQFLAATNQKHSTVKLIDDASVSRLATI
FDPLLEPKGLSPAHYQHILSAYHLTDATPQKQ AETLFLCLSTAFARYSSA
IFGTEHSDPPALRGYAEALMQKAWELSPAIFPSSEQFTEWSDRFHGLHGA
FTCTSVVADSMQRHARKYFPSVLSSILPLAWA

> gi|28867301|ref|NP|789920.1| candidate type III helper HolPtoY
[Pseudomonas syringae pv. tomato str. DC3000]

MNITPLTSAAGKSSAQGTDKISIPNSTRMINAASIKWLNKV RSAISDHI
RTSIEKGLFELASLGSNMFGVPALSARPSTLQPVLAFAEADPNHDLNLVR
VYMQDSAGKLTWPDPNNAVTTTTSNPSEPDAQSDTASSSLPRRPPAGSVL
SLLGIALDHAQRHSPRADRSAGRPGREERNGARFNAKQTKPTEAEAYGD
HQTFNPDLRHQKETAQRVAESINSMREQQNGMQRAEGLLRAKEALQAREA
ARKQLLDVLEAIQAGREDSTDKKISATEKNATGINYQ

> Q8X4X1_EC057

MPLTSDIRSHSFNLGVEVVRARIVANGRGDITVGGETVSIYVDSTNGRFS
SSGGNGLLSELGFGNSGPRALGERMLSMLSDSGEAQSQESIQNKISQ
CKFSVCPERLQCPLEAIQCPITLQPEKGFVKNSDGSDVCTLFDAAFS
RLVGEGLPHPLTREPITASIIIVKHEECIYDDTRGNFVIKGN

> gi|41834168|gb|AAS13306.1| VopD [Vibrio harveyi]
MLDKISNTGRADLYGLGELGKTTQAEKTSETRTEAAAIRSSNDSAVTGAK
NYQLDGPKPATGQARVVEKLSALAPTIVNLLMQTTTEKALNGEQVVKSP
SDTISQSLSLITLTYQVSKLSREQQVLQREIAVEANVASIKSQAEELNNS
AKAMIAMAVVSGVLAGVTAII GAVGSFKAGKEIKAEVAGNNVLKMQKAGF
DQVEELMGNTNLSKTQQDQVRRAHAFKDSITDNTLSSGGHKFDKIMG
ANQSKNAVQLGLGQMANAANAQTKAQARSKEDEVLATRAQADKQRADE
NIGFQEGLLKELRELFRSIADSNQAWRASIPTV

> A3NLD2_BURP6

MNMHVDMGRALTVRDWPALAKTMPADAGARAMTDDDLRAAGVDRRVP
EQKLGAAIDEFASLRPLDRIDGRFVDGRRANLTVFDDARVAVRGHARAQR
NLLERLETELGLGTLDTAGDEGGIQDPILQGLVDVIGQGKSDIDAYATI
VEGLTKYFQSVADVMSKLDQYISAKDDKNMKIDGGKIKALIQQVIDHLPT
MQLPKGADIARWRKELGDAVSI SDSGVVTINPKLIKMRDSLPPDGTVWD
TARYQAWNTAFSGQKDNIQNDVQTLVEKYSHQNSNFDNLVKVLSGAISTL
TDTAKSYLQI

> Q2LDQ5_PANAY

MWHNINPYGAPPFSNRAPDGEPPAADPPPQGTAGGTPYPEDEVLTWEFSD
CATIGGTDHGVIIIDYGRALRRFSGFLSQN GLPALSAPGRLDDPDLRRLRDA
HVYIDRFPPQPTNKKYLIPLSNRLIDLVTSGADRITIRGPKRPRRTVPDAD
EAQIKAAFPDRDGYSVNLTTSARAYSAWLHANGRPGLSDTDWLLSEQADA
DAVAYSWAHPGYAGRVNIVLAHLRARAGGEVPLIAKNQTRTIPLADQRL
ARAYRDVAEDRAGACGIVYKKGKDGDAIDRSITVLRFSAWRTARGLPA
LTDHLHDPTLLTDAQMFEKESQAGRALNT TRRTLYMLNAALELLRASFP
PGTFVTLPEEPADSFALPGSDWSGWDMSLSLPGAEGGPAPADSDSVSGRP
ADSFALPGSDWSGWDMSLSLGGHPADSDSVFGGLAPLDSRERFSSDGLS
GALASGWPEPGEVNPQPGSGTFFVNMRYATPPFRPDGVGFASGEGLSCLL
DSILQRYHNIRRGPGTTPRGLTDWLDGVEVRRVREALSAQGVDLLPARGEID

IYGGAGSYLAGAMNVRQLQVIQAEFQEEPDGT YVRYTSHPEMGRSDAPLVR
LLHTPGHFQPLWG
> Q8XQK7_RALSO
MNHARQTWEALLDQAVREFAQQQHRGMADYALYEIHLANGYRNHLAEEYG
VAGRVDSFVPPEVGRHLAACKAFVRQRVTAGAMVRRMAEACLGEVHERLK
LYCQRALTADEAWQFYRDYDKSLEAALEMRYGNIPSDVLINPHQGRGTKD
APYSVIETPTLLARAIARNLRQCELEPFKFLRMAPTPDGHSIKDVGDD
FYVKMRSQDGEKGYRPLMIADLHKSAWHHGPIAVRKAALMNTTDPGQLKT
LEPEAVWTLIRQHKDPMGWLEDLSHPAVRRYREAEPADDAFLVAYALATI
RKQSPGAQQRALLQVLRQGERALAEQLCAVVDRADRADAAGNTALHYAAE
HGFDQLLAELLPKSESPDARNVRRPMLRAARHGKASAVGTLVLAGACV
EAKNARGETALFLAARVGDAAASVGVLSRHVTSLDDQAASGKTALMAASEN
GHEGVVTMLLSLRANANRGNNTTPLIAACRGGHFACAEALVKAGANVN
AHTKDGTTALMAAIDAGHMALVRLLI PKAKLNRFRDHGKTALMCAVARGN
AEGVSALLQANARVDLPKAMLLALKHGHVEVVGVLNDAWAKQAGNPSRR
> gi|21264239|ref|NP|644739.1| avirulence protein [Xanthomonas axonopodis
pv. citri str. 306]
MRRSEAERSPPNLL QSLQEIKMGLCSSKPSVAGSPVAGSPEHYLTHHTTE
QTPSTPSSPEAPMSPSLHGLVALGSSGTRRDRFRQPTLQPEVQQAAYQ
LGMRLSGRPIEDASDRQLADATETVHETRLALHRGRGNVDSLRLSNGR
SATYSSLSYCLGENDERLLAGSALAAGAGNCDHNAAINARRHAVRMEG
QMMNVRDYEQTHLYALYQPPSSAEAEESPVVLD SWGDGPAVLLRDSHWAE
TYGTSTNVIERFDKR DAIDALARTNAFRAEIEDPQTDLHANARDLETAFL
ANPAPGDI FSAMPVIAPELAQSTRQLQEYSPRTRQALAADAARQAYGLD
NAQPISPRTTAAIQDAERLDALGRPPLSW
> Q8X393_ECO57
MAASGGGEITVGGQTVRITYSETDGRFLASGGNNSLLSGLLLTGLNGGPE
ALRDIMLRMVSGSNTQSHGDI EGKISQCKFSVNTESLQCPSEAVRCPII
LDKPEEGVFVKNSEGLVCTL FDSVSFVSHLVRDGGKHPLTREPITSSMIV
SQEQCIYDQTKGNFVIKDK
> Q8X5C9_ECO57
MDAFIVDPVQGEGLYSGLSHTELADI IRLADSVENQLNGGNSFLDVFSTYM
GQVISEFMHSNDNRIELLQRRHLHSCSFLVNI EEMS YIDEALQCPITLAI P
QRGVFLRNAEGSRVCSLYDEMALSRI INDGMHHP LSREPITLSMLVAREQ
CEFDCSIGHFTVRSDCYSV
> gi|9885643|gb|AA G01466.1|AF282857|15 HrpN [Pantoea stewartii subsp.
stewartii]
MSMNTSPLGTSAIQVTLGGNGLMGTDLRTDGLGLLSQPGLGEGKGHNES
IDLLAAAL TGMMMSMMGGGLSLLGSGTG MGNSPFGGSGSAPGNTLS
GTSGGSPGGTTGAGSSLGLDPTQTGDDSLSGAGQTS GMSPMEQLMKIFAD
ITQSLFGDQDGASGGNAGRQPSQDEQNAYKKGVTDALTA F MGGGLSQVAG
NGSEGGLDGGMGLGGNGLGGKGLQDLSGPAD FQQLGNAIGTVGMKAGI
EALNNIGTHSDSSTRSFINKEDRALAREVGFMDQY PETF GK PQYQKNAD
SAVKTDTKSWAEALSQPDDDGMT PASMEQFNKAKGI IKSAMAGDNGNINL
QARGAGGSSMGIDATLTGDAINMALTRLSAA
> gi|21229530|ref|NP|635447.1| avirulence protein [Xanthomonas campestris
pv. campestris str. ATCC 33913]
MRIALLQPAATPTTALATPAHTSAITPMEVPQPPGPNPLRARPRRQAAV
LPPLVPLDDSAMTGKQALVALDGEFSEQR LAEVQAHQITLQAAQSALAKQ
LPQATPAPRPDSIAARFAAGTLQPVYLDTAAFD EMTASLPEHSRAAAGPV
LVDAQQGRIVFDLGHAFAPGDTFSDAARTALRKALDLRAHGLETPGWLKP
AAPTPAQPRRKLQQAARYHGHEVPARDGGAFFKPN DHHLVAGKDALLRK
HRKELVHDAYFQAPSTRALGKDV MVHRGLFDNHAGI PENSLAAIDRAYEH
GYRNLELDVEVSADGVPVLMHDFSIGRMTDDPQNRLVSQVFPQAQLREMP
VIRNPVDGNFIKTDQSIAAVEQALEHALQKPEAMSV ALDCKEDTGEAVAM
LLMRRPDLRQGAAIKLYAKYYTGGFDQFLSNLYKHYQINPLHSQDAPRRA
ALDRLLAKINVVPVFSQGM LADAQLRDFFP GKDDGPEGLADTAVQWLESW
NRMRPVIVEAVATDQQAAGKAMELTRTRLRQPDSSYAQA AFSGGYRYED
FSLPRANHKDYVWRNFGEMQKLSGEAFGIQRTTAGAFRDAGESLLTDQ
PEEELLALLENRTLARGHTGMELDLPETPID SARDAAIVEQRTSEFRAA
SRPADPAHVAAVREGRLDRSADHSHDAAARQAVDARADALGLLTDQYRG
APVTHYLNEQARQIEPGE
> OspD3_sflx

MPSVNLIPSRKICLQNMINKDNVSVETIQSLLHSKQLPYFSDKRSFLLNL
NCQVTDHSGRLIVCRHLASYWIAQFNKSSGHVDYHHFAFPDEIKNYVSVS
EEEKAINVPAIIYFVENGWGDIIFYIFNEMIFHSEKRALEISTSNHNM
ALGLKIKETKNGGDFVIQLYDPNHTATHLRAEFNKFNLAIKKLTVDNFL
DEKHQKCYGLISDGMISFVDRHTPTSM SSIIRWPDNLLHPKVIYHAMRMG
LTELIQKVTRVQVLSDSLSDNTLELLLAAKNDDGLSGLLLALQNGHSDTIL
AYGELLETSGLNLDKTVELLTAEGMGGRI SGLSQALQNGHAETIKTYGRL
LKKRAINIEYNKLNLLTAYYYDEVHRQIPGLMFALQNGHADAIRAYGEL
ILSPPLLNSEDI VLLASRRYDNVPGLLLALNNGQADAILAYGDILNEAK
LNLDDKKAELLEAKDSNGLSGLFVALHNG CVETIIAYGKILHTADLTPHQA
SKLLAAEGPNGVSGLI IAFQNRNF EAIKTYMGI IKNENITPEEIAEHLDK
KNGSDFLEIMKNIKS

> gi|16765466|ref|NP|461081.1| putative cytoplasmic protein [Salmonella typhimurium LT2]

MARFNAAFTRIKIMFSRIRGLISCQSNTQTIAPTLSPSSGHVSFAGIDY
PLLPLNHQTPLVFQWFERNPDRFGQN EIPIINTQKNPYLNNIINAAIEK
ERIIIGIFVDGDFSKQRKALGKLEQNYRNKVIYNSDLNYSMYDKKLTITI
YLENITKLEAQSASERDEVLLNGVKSLEDVVKNNPEETLISSHNKDKGH
LWFDYRNLFLKGSDAFLEAGKPGCHHLQPGGGCIYLDADMLLTDKLTGT
LYLPDGAIAIHVSRKDNHVSLENGI IAVNRSEHPALIKGLEIMHSPYGPDP
YNDWLSKGLRHYFDGSHIQDYDAFCDF IEFKHENIIMNTSSLTASSWR

> hopQ1-2 Pto DC3000|Genbank: AA058166

MSSPALERSKSAPTLLTSAQREMLAHPVDQYLRDVQKSALKGLWEGIQAG
LLPGLDDSWFFRTFMPNAQIEAAQMDKNKERSFDDIWPKVTELNLYDLLT
LMASVPGAALKLFPKATHSEGFGVLEQVGPDDVTHPEKAKLLMSALS
ALVQSTAVPD

> gi|12329042|emb|CAC05773.1| o spF, secreted by the Mxi -Spa secretion machinery, function unknown [Shigella flexneri]

MPIKKPCCLKLNLDLNVVVKSEIPQMLSANERLKNFNILYNQIRQYPAYY
FKVASNVPTYSIDICQFFSVMYQGFQIVNHSGDVFIHACRENPOQSKGDFVG
DKFHISIAREQVPLAFQILSGLLFSEDSPIKWKITDMNRVSQQSRVIGIG
AQFTLYVKSQDECSQY SALLLHKIRQFIMCLESNLLRSKIAPGEYPASDV
RPEDWKYVSYRNELRSDRDGSRQEQLREEPFYRLMIE

> Q8XYF7_RALSO

MKPVAVPGQSSAADGVRAPSADAQPGPPAPGPAPARPARSAAGSSLLQGLA
QLLSLCQPRPARPLPQLPPDIFREIARRSDPLTVQRLRVASKPVKAAIEA
DMRELVIKDRAGLAGVLRAGNYPALEKLTLAGTFTDDDLRGLPASLKALD
LSRCRGSITAAGI AHLRLPLVRLNVRNKRI GAEGARLLANHPRTLTLNLV
SNGRIGPEGAQALANTRLTTLNVSGNRIGVAGAKALANQTLRSLDVSD
NRIGDEGARELAECTQLTTLNANRNGIGVDGATALAASRTLTLTSLAIGGNE
IGDAGVLALANARLTLNVESTGVGADGVKALAASKTLTWLRLDGNDIG
NAGATALAASTSLTTLHLEHSRIGAEQAQALANTKLTTLDLGYNDIGDA
GVRALSANATLVWL SVRRNNLEDASAVSLAAGKLTTLTLDISNGIQDQGA
KALANPTTLTLDVSSNDIKNAGARALANARLVSLDLRNNRMEESGTRA
LLANRTLSSLGVS LNCCGQHIAELMAWANHNGVTMRH

> gi|62868683|gb|AAY17522.1| elicitor of the hypersensitivity reaction [Erwinia amylovora]

MSLNTSGLGASTMQISIGGAGNGLLGTSRQNALGG NSALGLGGGNQON
DTVNQLAGLLTGMMMMMSMMGGGGLMGGGLGGGLGNGLGGSGGLGEGLSN
ALNDMLGGSLNLTGSKGGNNTTSTNSPLDQALGINSTSQNDSTSGADS
TSDSSDPMQQLKMFSEIMQSLFGDQDGTQSSSSGGKQPTGEQONAYKK
GVTDALSGLMGNLSQLLNGGGLGGGQGNAGTGLDGSSSLGGKGLQNLG
PVDYQQLGNAVGTGIGMKAGIQALNDIGTHSDSSTRSFV NKGDRAMAKEI
GQFMDQYPEVFGPKPYQKPGQEVKTDKSWAKALSKPDDDGMPASMEQ
FNKAKGMIKSAMAGDTGNLQARGAGSSSLGIDAMMAGDAINNMALGKL
GAA

> STM1959 fliC flagellar biosynthesis protein 2047658:2049145 reverse MW:51612

MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSKDDAAGQAI
ANRFTANI KGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSA
NSTNSQSDLDSIQAEITQRLNEIDRVSGQTQFNGVKVLAQDNTLTIQVGA
NDGETIDIDLKQINSQTLGLDTLNVQQKYKVSDDAATVTGYADTTIALDN
STFKASATGLGGTDQKIDGLKFDTTGKYYAKVTVTGGTGKDGYYEVS

DKTNGEVTLAGGATSPLTGGLPATATEDVKNVQVANADLTEAKAALTAAG
VTGTASVVKMSYTDNNGKTIIDGGLAVKVGDDYYSATQNKDGSISINTTKY
TADDGTSKTALNKLGGADGKTEVVSIGGKTYAASKAEGHNFKAQPDLAEA
AATTTENPLQKI DAALAQVDTLRSDLGAVQNRFNSAITNLGNTVNNL TSA
RSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLR

> gi|33600601|ref|NP|888161.1| putative outer protein N [Bordetella
bronchiseptica RB50]

MTRIDAAPNPFHAAMQGRHDASANTSSGWLQGGRIAPAPTGISLADAAEE
LSLHMAQAAEEKHHSERKVTAEPRMLWLDAAQLAELFSHTHPDAQAKLE
ALTAELLRGRGAPMQLAAQAFVTGVTQQYLALQHALQRGEHEDAAPHALEA
LRDALADLELAHGPEIRAGINTLPTAGAFARSADELAFQHAYRDIALGQ
LSLARTLDLVLERVGNDDIHGALGALIQALGHDLAAATPSTDGVRLQVLA
SDLYQVEVAATVLEECNALKQRLGNAGSQECADAQGLMRDLVGI SEDKWI
APARFEKLAERHGANALSERIAFLGGVRQILKDLPTQIYADMVVRATVLA
AAQDALDNAIAMENA

> gi|50121144|ref|YP|050311.1| putative virulence effector protein [Erwinia
carotovora subsp. atroseptica SCRI1043]

MLATITDYKQRITLIQDSGIQFLDFALKPQFSAEQPNRYVRKSANGPLLH
LLYDEHTDKYLLPSATGMPPEVVKPELSASLDQSLKLENIWLPLPFFRF
NPPRTFMGGPDNWARMRILALDTPDQGNTHRICLAFDTKYPEGHEYES
LAPNANDIKTGGNFALAYHSDELGEFLDETWVDGWLREIFTQQVKAQEKR
DSDHVKVALRGFEYQAHYLNVLDMNGNQLIPEIRINTSTLQEPAVNVDL
ILDVGNSTCGILVEDHADESNGLKQTYELQLRDLSEPHYLYNELFESRV
EFSQAKFGKENFSVESGRDDAFIWPSTRVGREASHMALLRQTEGSSGI
SSPRRYLWDEESYAPGWRFSQTDHQSQTEPLATAMPLTIMLNDEGQPLYN
QPLDERLPVFSPHYSRSSIMTFMSELQAALMQMNSAAQRSKMIHSRAP
RQLRNIILTLPSAMPKPEREIFRRRMHEAIALVWKAMDWHPMEDDFTTLA
DKQQRSPVPVEKTLIEWDEATCGQMVYLYNEAQVNFVGGRAEDFFASMARPD
KELDEGEPAGKTLRIASIDIGGGTDLAITQYLLDDGVGNVVKIIPRLLF
REGFKVAGDDIILLVPIQLYILPALQAALKTAGMASPDALMAKLFNGNEGRM
DAQLTLRQQVTLQVFIPIGRAILEAYERFDPLDTSAEIESTFGELLEQAP
TEKVLEYINTEVQRELPSVSDTVFDIILQVPLILKLNKLHGFEFLSNKMNIQ
NLRMLSEVVSLSYCDVLLLTGRPSRFPGIQALFRHLQPLPINRMLSLDGY
HTNDWYFPNKRGRIDNPKSTAAVGAMLCLLALDLRLPGFYFKVGFQFPYS
TVRYLGMMDSNALTLDNVYYSIDIDLAPDFVLDPKHSFQVRGSLCLGFR
QLDNERWPASSLYMLSIVDQDLARKVVGDSKLRVRLAVTKGDDQDSPERF
EIADAVLEDGTRVPPHHLRLKLNLTLSANGSGATHYWIDSGSVFKK

> gi|21233160|ref|NP|639077.1| avirulence protein [Xanthomonas campestris
pv. campestris str. ATCC 33913]

MVAAQNHIHPNLVDKVFSDASASEPHALRQAI VNTGRGQRWRVAVNVERIH
GKGAPSHGIAVDVSGGRGKVSVLAVDSVWGCADTL SVMTAALKGVK NATL
TILNTGTQKDVINCKTFALANAKAMADNDLMDLHKKNFRGKIVGTGDT
VNDVDVTIARGSDVLYVSFFQHTTSKDVFDLPEHIREPLEESFDQNFRE
IEAGGKRRAYNTSIQQERLKYLRDALLFADAEYWS

> A4SZD3_9BURK

MAVLLGCIADDFTGTDLAGMLVKSGMKTIQ LIGVPTEPAPHD VDAVIA
LKSRTNPAPAEI EESLRALEWLK SQGCQ QFFFKYCSTFDSTPKGNIGPVA
EALMKALDTKFTIACPAFPANKRSIYKGLFVGGDDLLSESGMRNHPLTPM
TDSNLVRVLQQQVQSKVGLTDYSVVKGGAGVIQKRFADLRKDG NQFSIVD
ALS DIDLYSIGAACADLPLVTGGSGIALGLPENFRKKGLLKIIGDASKLG
TVRGLKAVIAGSCSVATQEQVRAMKEKSPAYFVDPLALVDGRDVVTEALE
WVAQKIVKGPVLIYATSSPETVKS IQDKVGIEKAGEMVEHALAQIAKGLI
KLGVGQLIVAGGETSGAVVKALGISGLRIGPEIAPGVPWKAI FTEVNHD
PLVLALKS GNFGSPQFFNEAWDYIQ

> gi|33600605|ref|NP|888165.1| putative outer protein D [Bordetella
bronchiseptica RB50]

MSVSPTSPGSFGAGPVFDSELQAPAPSAQRRGGAAPVPPPVDRRGVEPGD
PTLGMPLPAPDLLAGGAVSRTRAALDDLDAAARLGEDIYTLMAVLQQASQQM
REAARIARDAEATRQTALGDAASQMRQAANERMAGAI VAGAMQIAG GFV
QLGAGLAAGLQAMGAAAQAKGA AFSEQASTSRKVAAGLHDAPELQATVQ
ARATQLEAQAASFGADAARSSAKSQRVSSVAQAGAATAGGI GGLTSAAQE
RRAAEHEARRAELDVEAKVHETASRRADEAMQQLDIIRGIREKLAGMEQ
SRSETARSVARNI

> Q8XTZ4_RALSO

MRAASPGAPCPSRPWPTHKAPQLPVWPAGTASHSHASPSGKRPLSHESA
GRHPVSTNAKRAGTMKFDPNYRHRPPLHLVNAGRGHAPAPSKPQGHRAPR
ARALDLPRPARAPAGVAQQDRASPSAVEGALS KALNYPERDL DREAMQL
DIQREEQQYELWCKSGLGFPERCLDMARDNVLAERNHGGRALVFLMPDSD
AEANIDLLGHYLAKLGDGGPGRVDPALRDGIRACAELCAGYLVHTSWFEG
APVATY AHLANKLSKFPDRAACMEGLAWIARQVLLARHLYRLGDRQATTL
VGG LAKNTRSEACRDAI LRL TGGLLGDNAMRGR LNAIQVPM L LNALSKWP
THDEAKSFVLQ LADLMAPPSELLHALDGGVANS LNALS KWPGEARAEKL
ALRLAKRLVADPDL LLSMREQEVTNS LNALS KWAHREEAQAMLRLAARL
ADEPQLRRAVQNLQSVANALNALS K LSEEPQAKQTVLLADR IATEPRLLO
ALEAQGVANALNALS KWPGETRAFRAHLLTERLAADPPLRRALKVQEFK
CTLNALS KWPREDAMK HVALQ LASRI PAEPGLL PALGAQDIANV LNALCK
WPGAEGAKRTVLL LARRLEMEPQLRSALS ALELANS LGALAKWPGEAQM
RTAMQLAERLMAEPKLRQALEAQGVANV LNALS WWSHQDTAKLVAMQLAD
RVAAPELLKAMDHQQLANTLSALS RWPDEQRAGHAARALVAHLTAEPAG
RWRDL DARHTSNALFALS KWS DENWATQVVLQ LAER IATEPALLDDADAQ
GVSDALCALS KWPGEDSARLAT RELAGRLLADTALQA AHDAQRLANTLNA
LAKWQREPEAMRAFQ LSTLPGRASHPWRAFNI VDMAQIGNAFARLVQDE
GEDFERARTVLRQ LAIHLELHPEC FECSGSGHIGVL FKS FASLRMQREL
PLGT PALNRVMTLCRETQLRDEPLETVGNLCLGLL PLARS PELARHRVPA
LKVFE SLQPVVARKIDS YLRHGVRASAGSALRVMDGQEACGTRGPALTFY
QILKAYALVVRQWKPRYIQGDRO AVQARQATLKQWVDATLARTRGVIESD
LQEMSWNLIAQIEAGDNV LNALDLRIGRELTAITQRHPPTFRDLGARTR
MRTEPGKVRPVKAGVGATRHVTVDLQGRELKV DGGAEQPY SFYARLTGQP
LVEVQLPGALSTFMLARTFQYQGE PWRFDLFGGSRLTRGRMRQVKAILAN
NPPLASVLPAMRYADSAPGS AFMTLTHKLAPQREDWSRMQRALLEMVPD
HVVEGLRVGWFE DVKVPGT PPHF RLKGPDGTRIALCPDDGCGFMKWEVA
MRI PVVREHVEAWQAVRAKRATPAQQERVAGQEPGANAMPQALMHPYPRD
EAVLAEAHDMQRLLDRLRAQVQGP GTNVQNAQAPALSPDAVDL LALYQM
TIGGGYEGRRIRAVPSADDKLYLPTIPMDGFARPA GDLLV GKPPYDKENL
LP IAAERVGTAAKGDATAHFLDQCFAIQSYTGFD DSGPAADMLH SKGM
LIIPPPGYWSSAHGMDLACSREDL KVL SRWKQGRDRAGLPDTMLSTGSL
RVKDI LMPGRLGALPIPELKRKNMDTDGDDAFVYAGY PKLAAHIRQVMEE
RGGRRKTEYAFKPKTASPAFDEQQYQAGRAREILAVQRGGQLVGAASN
AATRFLSQPDALREAMARDMMFGTYDGVDRRLRNLRLRARI GGSADAPALG
ELLALAHQIGRAHLPLAREVALLLHTLT TQLGAAGARPAPPI SAELTQR
FGALAEAWTAAPDTHARIHA ILDHYP VCRLSHEQFPNGQPGYLEGEPELT
IRNLFTLAVKVTGTLREKSDTGTNLFSTLIEQCAVIERTYHDRVRQVPHTK
QTAREFRDGRFDPAAAAALERMPTLAAGVMQDAVGALQQAGLLASPPAP
AERVRTVSPSDIKRTAATLNDQAHASARITSL LQANLHG WAGPGAGAVR
LAGLKHAVKSAGSLEDKLYLIAGKQLDLPEAVSQVNDALRYSIVLPSPT
FVPASRRILAGLEE HGHAMTERTNHFA RRGSAFRALS VTLRDPDGLLWE
VQFHTEQTFELKERYHDLYKQAQRARHQGASFDALRTL LQPAWKDFNAV
MPAGCDEIDDWQQEPAQA AVPGPQPGPDGQGAQRTIAPYLLPLARRLGAQ
ARRIETLVSPKVTVLR TCGGKLRDQPGDWRNFLFKKERSIARKIALRQ
RAGQLTPETAAGVGRD SLRYEVVLP AEGFGKTVTAILKMLGKQGLRTMRM
KNAFVQPDTTYAGRLNVNLR LRAVGNLPGD FEIQFH TAQSLSIKLRGHKDYE
KLRELPSANTHDEHDEAGADFAAERERLLKMRDAAARVERPQGIETLIP
FDHYRDAQPSGTSRRTG

> Q8XS09_RALSO

MAAPVSTRNAPLPSNPATADTGT PRGNPNSGELAYTPTRSSAGVASSPLG
GLASRLGLPAATSPSSGPRILPPAAHGDPRTAALPRATHLQIHDRRALS
LRDHPHLESVHLKGDFTLADL KALPTTLRHLDLSECTGSAKSFRAIA YLA
GLPLESLNVAGAEIGDGGARLLAANPSLKS LNAA SGGISASGARM LAESP
TLESIDL TQNAIGDAGA QALAGSRS LRHLAVRNGLVTDL GTRALALNPAL
VSLDLGNLVTETGNQVEQDGYDKTANNI TAQGAWALAQNRSLKLSVQGN
DLCGGDGV RALARNRTL TSLNVAFTNMTSASAKALADNPVLTSLSVRWNY
GLDDAGAMELAMSRSLTSLDARDTGM SARGALALAAANARISVWHDHAN PV
RAPLGEPPSLGLAGDPGQASRTAPGGAIWSSAAQARHVS AEAPANSAMTA
STREGFALIDPFFNRVARESGLNVQAPQEMPWTRLRPSASEANHGNAGAH
GASAEGLASSRMAASIREGLGLIDQYVDRMGREYGLPV RAPAAQPD SAAP
EATQPTLPADVWQTIAAQADPRVRRTLSTVSKPLRAAALAAATKHLTVWDK

AAFSRLRNPYPALESLSFHGPLSLADLRALPPSVRHLDLGCTGSVSEA G
LAYLARLPLASLDLSDTGIGNRGAQALAASASLTSLNLSGNGIGTAGAEA
LGRNTVLTALDISANPIRNAGAALAGSRSLTSLELRDTGIEDGGIEALA
ANTVLRSLDISGNLSDQSAAALANRRTLTLKANGCGLTNDMAQQLARI
RSLRTELVGSNSIGDAGVLTIANASLRSLNLSRNPITPQGLYPLALSRT
LKSLDVSRIKCGDRGALLSGNRALTSKLGFNRSSEGARRLAANRTL
SLDLRGNTIDVAAARALANAEPASLNVSDCRLDDAVACALAESRTLTL
DVSWNRLSHRAARALANNPVLASLYISHNDIGPEGAQALADSASLTFLDA
RANRIGEAGARLLEANTRMRGTPQNPFLAQDVPE

> gi|15835482|ref|NP|297241.1| hypothetical protein TC0868 [Chlamydia
muridarum Nigg]

MTTGVRGDNTPDPSLLAQLTQANASASADK NGAAKTQQQEEASFEDLI
QDSQGTGKSKKASTSQTSGKSEKAQKSSGTTTTTVAQASQTATAQAV
RGARSSGFNNDGSASLSPSPNPVNGVVLKKNMGTLLMGLIMTLAQAS
AKSWSSSFQQNQAIQNVAMAPEIGNAIRTOANHQAATELQAKQSLIS
GITNIVGFVAVSGGILSASKSLGGLKSAFTNETATAASSATSAAAKTA
VNALDDVANVAATAGTKAASGAASAASAATK LTQNMDDTASQTAS
KATGGLFGNALNTPNWSEKISRGLNVVKTQGGRAAQFAGRALSSAMSISQ
MVHGLTAGVDGITGGIIGAQVANEQRAAGMAEAREAEELKSLNSVQSQYAS
QAQQLQEQSQSQSFNSALQTLQSIADSSLQTTGAMFN

> gi|28871846|ref|NP|794465.1| type III effector HopPtoD2 [Pseudomonas
syringae pv. tomato str. DC 3000]

MNPLQPIQHSITNSQMSGQQLEAEGSQAHNSYSHPDRLSLSQLSQAHL
ALDHLSTQPNTHQVRVASLVRNAVQDGKFLQSSNDTQVYKTSVCPAN
ADTMGAAHLINNELTVQARLNDQLEYDIVSAHLYGPSEASISIDASSPPSA
NDLASSGLSERTHLGMNRVLLRYAVPRETEDQCVMVIDKMPPPKHGKMS
FFRTTNDLSKPLGMEGTGGLSDDLKLAGCERISSVEQVKSIRAALGG GPLT
VLDLREESHAIVNGLPITLRGPMDWANAGLSQVDGAARESAMITELKRTK
SLTLVDANYVKGKSNPQTTELKLNLRVSEREVTEAGATYRRVAITDHN
RPSPEATDELVDIMRHCLQANESLVVHCNGGRGRTTAMIMVMDMLKNARN
HSAETLITRMAKLSYDYNMDDLGSISALKRPFLEDRLLKFLQAFHDYARNN
PSGLSLNWTQWRAKIALE

> gi|12329122|emb|CAC05853.1| IpaH9.8, secreted by the Mxi -Spa secretion
machinery, function unknown [Shigella flexneri]

MLPINNNFSLPQNSFYNTISGTYADYFSAWDKWEKQALPGEERDEAVSRL
KECLINNSDELRLDRNLSSLPDNLPAQITLLNVSYNQLTNLPELPVTLK
KLYSASNKSELVLPALLESQVQHNELENLPALPDSLLTMNISYNEIV
SLPSPALKNLNRATRNFLTELPAFSEGNNPVVREYFFDRNQISHIPESI
LNLRNECSIHISDNPLSSHALQALQRLTSSPDYHGPRIFYSMSDQQNTL
HRPLADAVTAWFPENKQSDVSIWHAFFEHEEHANTFSAFLDRLSDTVSAR
NTSGFREQVAAWLEKLSASAE LRQQSFAVAADATESCEDRVALTWNNLRK
TLLVHQASEGLFDNDTGALLSLGREMFRLEILEDIARDKVRTLHFVDEIE
VYLAFQTM LAE KLQLSTAVKEMRFYGVSGVTANDLR TAEAMVRSRENEF
TDWFSLWGPWHAVLKRTEADRWAQAEQKYEMLENEY PQRVADRLKASGL
SGDADAEREAGAVMRETEQQIYRQLTDEVLALRLFENGSQLHHS

> Q7AGC6_ECO57

MDCSKCNGYATMLLNMVQSDPVLNLELHGFLHFAYVVSFGKFNAGHR
YNAFKKFVSEISEISANDINMTIKTGQSRHENVISINMNDAI PRDEKGIT
VRIDNINGKKNNSSDVFIPIVNTFPDLKKNILRMKIELTEGSGFSKSL
SDSQIEMHILRTVNSLNVGEKLNDDNLADHSIFTNEFSVIIPPSYDATS
AVNANNIVREKLFESDSKVVDIVDDMSNH DVESEKDI FVIGGMIEKLNSL
ADESFNDSTDNIQVTKDLLTQLTDGMELFALRDIVAFPSTIIAKLIKSP
NSDHELVMRALD TYLCYFRNKNLNNAE IINFFHALFLKRPPELMVAENYR
FIQFIDLLFENG NVEEKLAFDLYHNYLSLSEIKQFVTEEIKLNFNEQQG
LLDKDNKCYILLSSDN SGRVMRLSHQALISMLEPEVKKKT IWNYSIYPS
LQDTHEVVRDDPETICMRAFPLFAKWEYAQKNKKHQLILNALGFKGYIR
DIFMSAIMRKTDFVLECNQPTLELNSFS SLMNDS DQWQQHTLKD KHYAN
LLTMLDLNDASESDKSKIFFCLSAVFANISHSNVFNGIPDASKTLKRYAF
ALLAKAHS LDESMISNQTFNTYKTVLLDFNNLSNEEANQLRIS SLYRDMV
RYAQYRFSKVLSEWTPDAWL

> Q4ZLM6_PSEU2

MGNICVGGSRMAHQVNSPDRVSNNSGDEDNVTSNQLLSVRRQLAESAGLP
RDQHEFISSQAPESLRSSYNLYSHTQRTLDFADMQRHFM TGASGINPGM

LPRENVDMMRS AISDWSDMREALQHAMGIHADIPSPERFVTTINPSGSI
RMATLAPSPHRNW
> gi|53722552|ref|YP|111537.1| putative cell invasion protein [Burkholderia
pseudomallei K96243]
MSIGVQSSGINISHAELSRLVDAGKSEQGDKAVRDDGRALARADAALAAV
VGERVAARRDAVAGSGAQRVELARPKPDAQTRATDRRTVSGLEREHKRLA
ASQTPRVTMHMDALVQRHVSLDGAKAAHGEGVKRAAGDAPRAAADAPQRF
AFADDKAFDAMLALGAAMQKNVQSDLAMQGKLTMLAHDAMMSAAAQDRSI
GAAQMTAAIAGGALQATTSLGGAMQQMKSLSSTKSMSIEKELKPQAEKQF
HAEQALELRGINKPVLNSNDEVS HVKIKRDTGETVRHEIDHGGERSDEHA
SVLAQEA PARQHRIDMHGMRHEENLVKAGRQQMKGDLQSGGQIGKNQID
GASAQQQADRAEQKEDENAAQTAMAASTRDEAAHRSREAAQKAIDAAK
SQVANDNAVAAQVAGNLRT
> SOPE_SALDU
MTKITLFPNFRIOKQEATPLKEKSTEKNSLAKSILAVKNHFIKLNSKLS
ERFISHKNTESSATHFHRGSASEGRAVLTNKVVKNFMLQTLHDIDIRGSA
SKDPAYASQTREAILSAVYSKYKDQYCNLLISKGIDIAPFLKEIGEAAQN
AGLPGATKNDVFSFGAGANPFITPLITSAYSKYPHMFTSQHQKASFNII
AEKIIMTEVVPLFNECAMPTPQQFQIILENIA NKYIQNTP
> gi|15723942|gb|AAL06389.1| EspG [Citrobacter rodentium]
MILVIKIFVIDETERAFMLNGLNNSASLVLDATIKINSYKPKWNEMTC
AEKLLKILTLGLWNPKYSQDERQQFQGLLTVLEPVS PAHNELGRVYAKFS
DGSSLRISVTNSELIEAEIHTPNNEKFLVLEANEQNRLQLSLPINRHMP
YIQVHHTLPQEELTDLLSMHKLLSFTSKLSATLIPH NNQTDPLSGLTPFS
TVFMDTSRGLGNSKLSLNGVDIPADAQKLLRNTLGLKDTNSSPDLVIRN
GIPRHYAEQIVKESSTNEQKAAVDFLCQPEAPTAICSAFYQSFNVPAL
MLTHVRISQASAYNAQRSLDMPNACINISITQSSEGSIHVTSHTGVLIMA
PEDRPNQLGMLTNRTSYEVPPGVKCEPNEMARMLKAKYASSETYLNNA
> A1B7G2_PARDP
MLLGAIADDLTGATDLSLILSRAG MSVIQVVGVPDEGDDFGNADAVVVAL
KSRTIPAAEAVEQSLASARVLRARGARQLYFKYCSTFDSTAEGNIGPVTD
ALLDLIGETRIVACPAFPQNGRTVYQGHFVGSQLLSDSPMKDHPLTPMR
DADLRRVLAQAQTARPVDLVAHATVAQGAEEAVAAALAGAQGIATDAICNA
DLMTLGKALAGYGLVTGGSALALGLPQNFRAAGLLAEDAGNADFTAPKGP
GIMLAGSCSAATRQVARAEANGIA TLALDPLAIASGETRIEDALAFIAA
HAGDPRPPLLYSSADPEAVAQAQEKLGRAQAGVVVEAFLSGVARKLAEAG
TRRFIVAGGETSGAVVEALEAMAVRIGPEIDPGVPVWVSTDFVAPMALAL
KSGNFGCEDFFAKAWDMLA
> gi|15605406|ref|NP|220192.1| S/T Protein Kinase [Chlamydia trachomatis
D/UW-3/CX]
MLRSGVSFSSSKTNYLLTRELSRK VGLTVYQGVDEHSSRPVVIKTLVSPG
IHDRRFLRAFEEEARIMQLVTHPAFVRLEDRGECEQGRYLVSEYILGSSL
RDSILSSQISLDKAISIVLQVAQAITTLHRHGVLHLDIKPENIVLSQSGE
IKLIDYGLSAWQFNHWGSPAYMSPEQSRQEPSPASDVYSLALLAYELIM
GQLALGKVVYVLLPSKISKILIQALQPSPAARFSSMQEFAEALQDYLLHD
VHEDYRKKDHVVAQIEQWHNQRAWL SPEKLSAPEEICVHIYSQKEPCYLH
NIYYDMLTSGNVAEFWFCYAPGNCSFALSMMKQFLNQREEKAKDIQTVIK
SMDTLCKTMHIPCIEEGISCCCFIFFLEELMCFSCGKTDFSLKKQTGGGQ
RFQAESQGIGEETPLEIHEQSFLWEPGDELIVHTPKARDLVYLYCPSFLK
LQDRGQIDIFCQTDNLQKGIQKYDRSLYPSTLISLKRVR
> Q4ZX85_PSEU2
MHINRTGSSQPSIELERFYSA SQSLASSSVRELSPAEHANLQAITDYLKD
HVFAAHKLPLESAVDQDAVHAHNEQLDKIIDARARLLDEGETPATIAD
TFAKAEKFDRMATTASITLRATPFAAASVLQYMQPAINKGDWLPMLKPL
TPFVSGALSGIMDQVGTVMNRRATGNLHLYLSTPPEKLHDAMAASVKRHS
GVMRQAVDLGIAIQAYSARNVARTVLAPALASRPVQGAVDISVSAAGGL
AANAGFGNRMHSVQARDHLRGG AFVLGIKDQEPKADLSEETDWLVAIKAI
KSASYSGAALNAGKRVAAGLPLDVATDGLKAVRSLVSATGLAQNGLALAGG
FAGVGKLEMATKNI TDPATKA AVS QLTNMAASTGVFAAWTTAAVATDPA
VKKAESFLQD TVKSAASSSTSYVADQTVKLA KAGIDASGEAIAATGASLL
DTLRRRNAREPDIEEGGIAAGSPSAVPFQPGRS
> Q4ZXP9_PSEU2
MTDLNSLRTSLSSGEHAFADTLAFI ADGYDYQPQAFRNGDNDNAAGQNEG

SCKTLGLALLEGLTDEEALLAFGEHYRSVQATPEGSDHGNI RALMANGLA
GVKFAGEPLKRKA

> hopD1 Psp race 6 -1448A|Genbank: AAZ37970

MNPLRSIQHNITTPPISSGQPLDAVGPQAQQSHPKRISPSQLSQAHQAL
ERLSANAHEQRLASLVRNALQDGTFFQFQSSNHTQVITYKASICLPADTDTV
RTDHLINNELTVQARLNDQS EYDIVSAHLHGSSKAISFDVSPPPAHGSA
SSVLSERTHLGSSVLSQDAVDSSSLETPLVSSPDHSRPPSQPKPVHIGS
VRRDSGSLVSDNPVQALLSFVQADQAFPPQAASIAGVQLEMRSRRDIEQ
ALEELKGAFTVEKAQLMSGGSSSERVEDVDNADIHIPLLLKAIERGAGAF
GPGALIEIADGGQISAKAFLASCAPTITSNDDVLSEFINQKLGDDDLQV
RLGAQELLHVATKKEFQLGGL AGSIGVSSILGSAWELGASELLKNAIFGK
NFSPSQYALQLAGIDSVPPPIIEAMDSFCVLVIKGMKGELWSMKDLLPK
ALKAGAISSAMSPNNVLQYAGFKSRVADLAANSITTEAAIFGAASGIPP
EVKESEELMRAGLFQSMKDGVMMAHPGEGMDTKETIERMTRHALDIAPGES
TAVKSMGLAAIVGMIPLIASSKATGLVSEQILRIFRNAVFNP IEAIALNA
LALGGRVNVPGFLFSDNAKHAR VAQTILARASQHMEAGDREISAEELHQM
LAPRSEFLRHVGSIAVNGMNASFEAIPALVRKLGYGAEPLAERI PYQDLA
VPDTSRQPAP

> gi|12329059|emb|CAC05790.1| OspC1, secreted by the Mxi -Spa secretion
machinery, function unknown [Shigella flexneri]

MNISETLNSANTQCNIDSMNRLHTLFPKVTSVRNAAQQTMPDEKN LKDS
ANIKDFFRKTIQAQSYSRMFSQGSNFKSLNIAIDAPSDAKASFKAIEHL
DRLSKHYSIEIREKHLPLSAEELNLLSLIINSDLIFRHQSNLSDSKILN
IKSFNKIQSEGICTKRNTYADDIKKIANHDFVFFGVEISNHQKKHPLNTK
HHTVDFGANAYIIDHDSPIGYMTLTDHFDNAIPPVFYHEHQSFLLDKFSEV
NKEVSRVYVHSGKIIDVPIFNTKDMKLGGLYLIDFIRKSEDQSFKE FCY
GKNLAPVDLDRIINFVQPEYHIPRMVSTENFKKVKIREISLEEAVTASN
YEEINKQVTNKKIALQALFLSITNQKEDVALYILSNFEITRQDVISIKHE
LYDIEYLLSAHNSCKVLEYFINKGLVDVNTKFKKTNSGDCMLDNAIKYE
NAEMIKLLLLKYGATS DNKYI

> gi|27377015|ref|NP|768544.1| hypothetical protein blr1904 [Bradyrhizobium
japonicum USDA 110]

MEILMNTGQAQWSAGSSAAASEEGEQESYLSGFSRAVADLLEAMTGYRTP
ASARAQLLDNWAEEGQGEAENRRQGRARIRGADNTGSHSLDLSSLSLTA
LPAALPPRLLELRARHNELSSLPASFPPLQHLLISHNRLISLPDALPAT
LSRLEVADNLSLTPANLPAGLEILNASDNRLTSLPDALPSRLTSLAVSG
NQLTDLDPDYLPSGLIELDVSSNQLADLPAPLPST LQSLNLSGNRLTSLPE
DLLEGRVPNLSLSYPHLENLEFGDNPLPDDVLANLATAEAPPQLAQQSLY
EAAAQWLADDPATLAKWQHFADEPGAQDYAQFLERLRETVNYGNDEFRQA
VADDLQQAANPTLREQFFAQASEANASCEDRVTLHWNGMQTARLNADVE
DGVYDDRDLGDLIQRGRVAFRLEALDEIARDRINSLASGNPNVDDIEVYLA
YQHRLREPLELSHVAPDMRFLAVSHVSEDDATEAL DLVREEREASQFTDFM
ASRWQPWETVLRRIAPDEHAAMQDRIVEAMGEEFQSRLDQRLAEHGLVGD
VDAERVLGAQVRNQIAGEIKGEVMHRLLAERGLEQ

> Q8X4Q6_ECO57

MPVNATGVSFSSFGISYHKDNSFRGTIRGKNDEVVKCSMGERSIRFNVNK
FSGCILETVSRQSTKDIHGWVSDERTVYPSRVINQEIDNCCLOKNAKISS
EERKMVFLSVSKEFELTLDVKAQSSINHIIIGNAS FGKMDALCDGMSR
AVKNSTTDYIANVLADKIFYQKHIAPGVDIVKLRNEIPGYMSRVIQG

> gi|57434478|emb|CAI43895.1| EspG protein [Escherichia coli]

MISVVESFIINEIGESLMINGLNNNSASLVLDAAIRINSDFKKQWNDMSC
AEKLLKVLVFLGNPTYTRSERQTFQELLTVLEPVSPAPNELGRIYANFA
DGSSLRISVTNSELVEAEIRTPDNEKILML LESNEQNRLQLSLPINLHMP
YIQVHRALSKMDLTDHKSMHLLSFTSKLSATLIPHNTQTDPFSGPTPFS
SMFMDTFRGLGNKLSLNGVDIPVDAQKLLRDALGLKDTHTSSLARNVINN
GISRHHAEQIARESSGSDKQAEVVEFLCHPEAATAICSAFYQSFNVPAL
MLTHTRISQAREYNVERSLDVPNACINISISQSPDGSIHVASHGTGILIMA
PEDRPNELGMLTNRTSYEVPPQGVKCEIDEMV RTLQPRYGASETYLKN I

> Q8Y2V5_RALSO

MSSRISGSWGRYWPDLSSQS DERDEKMPAVSKAQAREVYEHSVLFHGTTL
RSRRSIQRNGFRLENKSAGSITAYAGIQSNFDAAVASSSHHYFAEKRRLR
SASPEWSAVIAAIAPHWFVP

> Q12HJ4_POLSJ

MQASHKDSTLKIAYYGDDFTGATDTLATAARAGLRTLLFLGLPTATQLER
AGPLDCLGIAGAARAMTPAEMQLELEPVGRLFAA LGAPVMHYKTCSTFDS
APHIGSIGAALRILRPHAGNALVPIVGGQPNLHRYCVFGNLFAGTGNGGA
IHRDRHPTMRQHPVTMHEADLRLHLAQQGLLENLSAIAYPDYAQLDEAL
DRQLDALLAQGPDAVLFDAHPDNLAAVGRLIWQHARRQRLLAAGPSSVV
QALAAHWQSGAGPARTAIPAQGPVVLVLAGSLSPLTARQVKAATSYEHIA
LDAPRLAGDENYRMMARQIATRLDQGAHVLACTS GADGATVSTSSSTSS
SPTDGRALAQACGDL LAHVLA TRPIRRLGIAGGDTSSHAVQALQAWGLSY
RAPLAPGVALCRLHSEQASLDGLEIMLKGGQMGGETLFEELLAGTPLPV
> gi|16766189|ref|NP|461804.1| translocation machinery component
[Salmonella typhimurium LT2]

MLNIQNYASASPHPGIVAERPQTPSASEHVETAVVPSTTEHRGTDI ISLSQ
AATKIHQAQQTLQSTPPISEENNDERTLARQQLTSSLNALAKSGVLSAE
QENENLRSAFSAPTSALFSASPMAQPRTTISDAEIWDMVSNISAIGDSYL
GVYENVVAVYTDYFQAFSDILSKMGGWLLPGKDGNTVKLDVTSKNDLNS
LVNKYNQINSNTVLFPAQSGSGVKVATEAEARQWLSELNLPNSCLKSYGS
GYVVTVDLTPLQKMQDIDGLGAPGKDSKLEMDNAKYQAWQSGFKA QEEN
MKTTLQTLTQKYSNANSLYDNLVVKVLSSTISSSLETAKSFLQG
> Q3BRD8|Q3BRD8_XANC5 Xanthomonas outer protein N - Xanthomonas campestris
pv. vesicatoria (strain 85-10).

MKSSASVDSASRSAGSHLPEIQETELATASTSAAVTHQSAPDPALSPLGR
APVRRSGANTLGALLARPEQDAQALVPQPVTSNATKATLARLRQQLAS D
NARAIAPDLAADLISRLRPMKSPGTTGAQARAATHADLVSRISEHDVIDW
YKAQGLNENDVATLRRTALLSGMPNPSGSFLTVMQYIVSPWINYATRQP
WAGAGFGLATMLVAAPVNAGQQSAVVSLCESIREHGAHVIVPDKKQINDK
HWLPELAHALKEKIEETFAKACDVFREIQSDPNSSSKERAAAADVLLAAEK
ELHQAQHDFVMTQGAHDRQCQGNRRQAVPRIMRSPVASTLGLLSKTGAMR
ALSPTAQTVGAMLMTAAQHVAAGFDEQAKQEANNKLNLLYADVLT DAGKQ
KLASGAAVSADDIKTDKLRSLIQSPTQALVKRVTAGVAELEKLLADAVTA
EGTQPGAITAEEDRDI EAGDASKAMQELRLVRNDLEALREGRLEIDPNGT
ASKLLIGA EKSVLSQQLFN DIAKKYNYLEFTAQTAQRIGQMFHLIFLGS
ASSVISKLV SASQGGTRNVPLPQSLAVSAISGMAAVGALNQHTAITIKN
NRREGSTDIGLKGQLGRGVLGAMYETFQRRTKASKAINALLEGNDVEA
LLATARALSVQEASTSSSQPDLPSTSRAPPRRHVSAPSSPNRSRLEP
TNNEITRSKSARNLGTTELHEFARMAGKHSKHLV

> gi|12329105|emb|CAC05836.1| VirA, secreted by the Mxi -Spa secretion
machinery, function unknown [Shigella flexneri]
MQTSNITNHERNDSSWMSTVKSTTEVSWNKLSFCDILKIITFGIYSPHE
TLAEKHSEKLMDSFSPSLSQDKMDGEFAHANIDGISIRLCLNKGICSVF
YLDGDKIQSTQLSSKEYNNLSSLPPKQFNLGKVHTITAPVSGNFKTHKP
APEVIETAINCCTSIIPNDYFHVKDTDFNSVWHDIYRDIRASDSNSTKI
YFNNEIPLKLIADLINELGINEFIDSKKELQMLSYNQVNIINSNFPQQ
DLCFQTEKLLFTSLFQDPAFISALTSAFWQSLHITSSSVEHIYAQIMSEN
IENRLNFMPEQRVINNCGHI IKINAVVPKNDTAISASGGRAYEVSSSILP
SHITCNGVGINKIETS YLVHAGTLP SSEGLRNAIPPESRQVSFAIISP DV

> gi|2897963|gb|AAC38401.1| SepZ [Escherichia coli]
MEAANLSPSGAVLPLAATINGNPNVDEKTVGMQSEGGTSRSVRILGGVLI
GAGVLA AIGTGIAAMCVD DPSQRLGLGIAAGVLGGVTTVAGGLAMKYA

> gi|57434460|emb|CAI43877.1| SepZ protein [Escherichia coli]
MSKLDNGEKLMDAANLSPSGRVLPLAATINGNPNVDETTGVMQPENGTNR
TIRILGGVLISAGALAAIGAGIASLVEDPSQKLGLGIAAGVLGGVTTLG
SGLAMKYA

> gi|12329039|emb|CAC05770.1| OspB, protein secreted by the Mxi -Spa
secretion machinery, function unknown [Shigella flexneri]
MNLDGVRPYCRIVNNKNESISDIAFAHIKRVKNSSCTHPKAALVFLGEK
GFCDSDNVL SIMGQIPRVFKNKMLYDYVFKNEKSKNDFLKMAESWLPQS
EPIVINDDDDALNAAAYFSVKKAKIKTVNDTDFKEYNKVYILGHGSPGSH
QLGLGSELIDVQT IISRMKDCGILNVKDIRFTSCGSADKVAPKNFNNA
ESLSCILNSLPFFKEKESLLEQIKKHLENDESLS DGLKISGYHGYGVHYG
QELFPYSHYRSTSI PADPEHTVKRSSQKKTFIINKELD
> hopAA1 Psy B728A|Genbank: AAY36237
MATPTNSWNPRHCCDHTALS VLFADGPPDVCNCHSR TDASLPCLFASKS

SGQTRLGALLRNLSNREGVSMHINRTGSSQPSIELERFYS ASQSLASSSV
RELSPAEHANLQAITDYLDKDHVFAAHKLP LSESAVDQDAVHAHNEQLDKI
IDARARRLLDEGETPATIADTFKAKEKFD RMATTASITLRATPFAAASVL
QYMQPAINKGDWLPMLKPLTPFVSGALSGIMDQVGTVMNRATGNLHYL
STPPEKLHDAMAASVKRHS PGVMRQAVDLGIAIQAYSARNAVRTLAPAL
ASRPAVQGAVDISVSAAGGLAANAGFGNRMHSVQARDHLRG GAFVLGIKD
QEPKADLSEETDWLVAYKAIKSASYS GAALNAGKR VAGLPLDVATDGLKA
VRSLVSATGLAQNLALAGGFAGVGLQEMATKNITDPATKA AVS QLTNM
AASTGVFAAWTTAAVATDPAVKKAESFLQD TVKSAASSSTSYVADQTVKL
AKAGIDASGEAIAATGASLLD TLRRRNAREPDIEEGGIAAGSPSAVFPQP
GRS

> gi|15618717|ref|NP|225003.1| hypothetical protein CPn0808 [Chlamydomphila pneumoniae CWL029]

MTSGVSGSSSQDPTLAAQLAQSSQKAGNAQSGHDTKNVTKQGAQAEVAAG
GFEDLIQDASAQSTGKKEATSSTTKSSKGEKSEKSGKSKSSTSVASASET
ATAQAVQGPGLRQNNYDSPSLPTPEAQTINGIVLKKGMGTLALLGLVMT
LMAAAGESWKASFQSQNQAIRSQVESAPAI GEAIKRQANHQASATE AQA
KQSLISGIVNIVGFTVSVGAGIFSAAKGATSALKSASF AKETGASAAGGA
ASKALTSASSSVQQTMASTAKAATTAASSAGSAATKAAANLTD DMAAAS
KMASDGASKAGGLFGEVLNKPWSEKVS RGMNVVKTQGARVASFAGNAL
SSSMQMSQLMHGLTAAVEGLSAGQTGIEVAHHQRLAGQAEAEV LKQMS
SVYGQQAGQAGQLQEAMQSFNTALQTLQNIADSQTQTTS AIFN

> A0VG66_COMAC

MTLLLGCIADDFTGATDLANNLVRAGMRVVQSIGVPAGPVDEGVDVAVVA
LKSRTIAPADAIQSLQALQWLQAQGANRAPQIYFKYCS TFDSTPQGN
GPVADALMDALGCEFTIATPAFPDNQRTVFKGHLFVGDVLLSDSGMRNHP
LTPMTDANLVRVLQAQTGRKVGLIDHVAVAQGEAAIRARIAALQAEGVGM
AVVDAVSNDLLRLG PALAGMPLVTAGSGVAIGLPANFGI OPTAQAAALP
TATGLQAVVSGSCSAATNAQVAHF IASGRPALALEPLRIAAGEDEAGKAL
AWARQHIASGPVLLYSTAESAVKAVQGH LGVEQAGALVEQTIAAIARGL
VEMGVRQLVVAGGETSGACVQALGIEQMRIGPQIDPGVPWCHAASPLAPQ
GLHLTLKSGNFGTTDFFTKAFGALASA

> gi|15618924|ref|NP|225210.1| hypothetical protein CPn1016 [Chlamydomphila pneumoniae CWL029]

MKKKGLGAI VFGLLFTSSVAGFSKDLTKDNAYQDLNVIEHLISLKYAPLP
WKELFLFGWDL SQQTQARLQLVLEEKPTNYCQKVLSNYVRS LNDYHAGI
TFYRTESAYIPYVLKLS EDGHV FVVDVQTSQGD IYLGDEILEVDGMGIRE
AIESLRFGRGSATDYSAAVRSLTSRSAAFGDAVPSGIAM LKLRPSGLIR
STPVRWRYTPEHIGDFSLVAPL IPEHKPQLPTQSCV LFRSGVNSQSSSSS
LFSSYMPYFWEELRVQNKQRFDSNHHIGSRNGFLPTFGPILWEQDKGPY
RSYIFKAKDSQGNPHRIGFLRISSYVWTDLEGLEEDHKDSPWELFGEIID
HLEKETDALIIDQTHNPGGSVFYLYSLLSMLTDHPLDTPKHRMIFTQDEV
SSALHWQD LLEDVFTDEQAVAVLGETMEGYCMDMHAVASLQNF SQSVLSS
WVSGDINLSKMPMLLGF AQVRPH PKHQYTKPLFMLIDEDDFSCGDLAPAI
LKDNGRATLIGKPTAGAGGFVQVTFPNRSGIKGLSLTGS LAVRKDGEFI
ENLGVAPHIDLGF TSRDLQTSRFTDYVEAVKTIVLTS LSENAKKSEEQTS
PQETPEVIRVSYPTTSAS

> STM1960 fliD flagellar hook -associated protein 2049402:2050805 forward
MW:49835

MASISSLGVGSNPLDQLLDTLTK NEKGR LTPITKQOSANS AKLTAYGTL
KSALEKFQTANTALNKADLFKSTVASSTEDLKVSTTAGAAAGTYKINVT
QLAAAQSLATKTTFATTKELGDTSVTSRTIKIEQPGRKEPLEIKL DKGD
TSMEAIRDAINDADSGIAASIVKVENEFQLVLTANS GTDNTMKITVEGD
TKLNDLLAYDSTNTGNMQELVKAENAKLNVNGIDIERQSNTVTDAPQGI
TLTLTKKVTDATVTVTKDDTKAKEA IKS WVDAYNSLVDTFSS LTKYTAVE
PGEEASDKNGALLGDSVVRTIQTGIRAQFANS GSNSAFKTMAEIGITQDG
TSGKLKIDDDKLT KVLDKNTAAARELLVGDGKETGITTKIATEV KSYLAD
DGIIDNAQDNVNATL KSLTKQYLSVNSIDETVARYKAQFTQLD TMMSKL
NNTSSYL TQQTAMNKS

> gi|28871726|ref|NP|794345.1| type III effector HopPtoS3 [Pseudomonas syringae pv. tomato str. DC3000]

MNISPVSGAHGSSYP SAQSTASTASKGPSG SFLKQLGGCFSPCLGSSSTG
AILSPAHEQVLSHTYSSNIKGLRTPPKGPSR LSDTPMKQALSSMIVQ

ERKRLKSQPKSLASDIERPDSMIKKALDEKDGHPFGERFSDEFLAIHLY
TSCLYRPIINHHLRYAPNNDVAPVVEALKSGLAKLAQDPDYQVSSQLHRGI
KQKMSDGEVMSRFKPKTYRDEAFMSTSTHMVSEEFSTSDVTLHLRSSSA
VNIGPFSKNPYEDELISPLTPFKVTGLRKQDDKWHVDLNEIADNSDE
> gi|21264224|ref|NP|644725.1| avirulence protein [Xanthomonas axonopodis
pv. citri str. 306]

MDPIRSRTPSPARELLPGPQPDGVQPTADRGVSPAGPLDGLPARRTMS
RTRLPSPPAPSPAFSAGS FSDLLRQFDPSLFNTSLFDSLPPFGAHHTEAA
TGEWDEVQSGLRAADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPA
AQVDLRTLGYSSQQQEKIKPKVRSVAQHHEALVGHGFTHAHIVALSQHP
AALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRG
PPLQLDGTGQLLKIARKGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASN
IGGKQALETVQALLPVLCQ AHGLTPEQVVAIASHDGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIA
SHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRL
PVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVA
IASHDGGKQALETVQRLLPVLCQAHGLTPQVVAIASNIGGKQALETVQR
LLPVLCQAHGLTPEQVVAIA SHDGGKQALETVQRLLPVLCQAHGLTPEQV
VAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETV
QRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTLD
QVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALE
TVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALE
LDVAVKGLPHAPALIKRTNRRIPERTSHRVADHAQVVRVLFQCHSHPA
QAFDDAMTQFGMSRHLLQLFRRVGVTELEARSGLTPPASQRWDRILQAS
GMKRAKPSPTSTQTPDQASLHAFADSLERDLAPSPMHEGDQTRASSRKR
SRSDRAVGTGSAQQSFEVVRVPEQRDALHPLSWRVKRPRTSIGGGLPDPG
TPTAADLAASSTVMREQDEDF AGAADDFFAFNEELAWLMELLPQ

> Q3BM44|Q3BM44_XANC5 Xanthomonas outer protein Q - Xanthomonas campestris
pv. vesicatoria (strain 85-10).

MQPTAIRSTVGLPGADMTADLRDPAPVAVPAHSAADAAAPPPGALQTVG
RPPRPDGPVRRRAQSLPARLTPAQRGMLAELGVADTSVLTPTETAVLREL
RLHRPPLPLDTLFTDPNKDPD DVVYTYIAKQLQAEGLRLTDVVVTLGD
ADMRSQRAQLAKGVFDRLLALPEVVRVARGQDYPMTSTQAREHSKFLAEGAA
LRAAPDAVHTDGVVRAMRERLATS PHKLG MVVIAGMTDASALLAEAGDLVR
EKLASITIMGGIDPARDADGLVQPDTRAYNNATDIHAARALYRRAQQQLGI
PLRILSKEAAYRAAVPPAFYEGEIA RNHGPVGEYLRDVQKNALKGLWEGIQ
ANLIPGLDTAWFFRTFVAAQPD PAAADQQGAMSFDAIWPQVTKLNLYDP
LTLAALPGAARLLFQPTPMHREGASPVHVGHAEVVRPEKARLLLSALA
KAALAQQDEGQRGR

> SIPD_SALPA

MLNIQNYASPHGIVAEERPQTPSASEHAEIAVVPSTTEHRGTDIISLSQ
AATKIQQAQQLTQSTPPISEENNDERTLARQQLTSSLNALAKSGVLSLAE
QENENLRSTFSAPTALFSASPMAQPRTTISDAEIWDMVSNISAIGD SYL
GVYENVVAVYTDYFQAFSDILSKMGGWLSPGKDGNTIKLNVDLSEISS
LINKYTQINKNTILFSPQTSGMTTATKAEAEQWIKELNLPDSCCLKASGS
GYVVLVDTGPLSKMVSVDLNGIGSGSALELDNARYQAWQSGFKAQEENLKT
TLQTLTQKYSNANSYLDNLVSVLSTISSSLETAKSFLQG

> gi|16764750|ref|NP|460365.1| translocation machinery com ponent
[Salmonella typhimurium LT2]

MNRIHSNSDSAAGVTALHHHLSNVSCVSSGSLGKRQHRVNSTFGDGNA
CLLSGKISLQEASNALKQLLDVAVPGNHKRPSLPDFLQTNPAVLSMMMTSL
ILNVFGNNAQSLCQQLERATEVQNALRNKQVKEYQEIQKAIQEDKARK
AGIFGAI FWDWITGIFETVIGALKVVEGFLSGNPAEMASGVAYMAAGCAGM
VKAGAETAMMCGADHD TCQAIIDVTSKIQFGCEAVALLDVFQIGRAFMA
TRGLSGAAAKVLDGSGFGEVVERVMVGAGEAIEELAEKFGEEVSEFSKQ
FEPLEREMAMANEMAEAAEF SRNVENNMTRSAGKSFTEKGVKAMAKEAA
KEALEKCVQEGGKFLKFRNKVLFNMFKKILYALLRDCSFKGLQAIRCA
TEGASQMNTGMVNTEKAKIEKKIEQLITQQRFLDFIMQQTENQKIEQKR
LEELYKGS GAALRDVLD TIDHYSSVQARIAGYRA

> gi|15605404|ref|NP|220190.1| hypothetical protein CT671 [Chlamydia
trachomatis D/UW-3/CX]

MELNKTSESLFSAKIDHNHPRTAHEPRDQREVRVFSLEGRSSTRQEKAD

RMPGRTSSRQESSKSGSEEGAVHESHTAGVSSKEEEESKGDGFFFTGGNPTSG
MALVETPMAVVSEAMVETSTMTVSVQVDLQWVEQLVSTVESLLV ADIDGK
QLVEIVLDNSNTVPAAFCGANLTLVQTGEEISVSFSNFVDQAQLTEATQL
VQQNPKQLVSLVESLQKARQLNLTELVGNVAVSLPTIEKIETPLHMIAAT
IRHHDQEGDQEGEGRQDQHQQHQEKVVEEAI
> HOAE1_PSEU2
MMPSQITRSSHSSLPEVAPASGDAAGVSEQTPQQARTVAFFASGELAVAF
GRTSTAPAQDSVRLLSALQRELDKQPSWPTVAQLCHSLAEVAKTEQG WH
QLASEDQAPAPALKDLLERCIGRLADMPASHASHDSLACEGLRTARLH
QSVARLTARPPALARAI PDLLALTHLDPETLGAEPVVSSTLFSHFVHT
AKQRTAELNDSLQRFQPEAVVSLLRSHADTLNDLETLPALQALTENCQDA
PACNELRELAIEVVGALLQLLREHGILPRLEAISIEPGEAPAPGHEAAEPR
LTRSQALLKAGGNLVRKFDAYGALAPMDDKGLLALMRTPAPHLSPDQMH A
FLNKHVHLHTQEQRDIVSNTPLPFAPEGDIEARCGMGFDEKLRLALANGS
LVLSEEQLARLGHLPAAATTTSDVVKTLLEKFPSSALSEAERDMLGAIVQA
NGQGQLDAWRAHNEQLPAVLSRSGLPDVKDELSSLNQMNAELGTLKNG
ASFKSRILASPAMLLALAPLPLAVAFVSKDNSYSSSLVAHFTKNAVFMAG
LMMNELTNRARTNVDHGLNRYFVTVLANAIVAQPTFARNEHLLQVGFQIA
TAVASGAATLGVFNRESIVAFAKLSKLSRQDTGNASIPEDHLAVVRH
FDVSEHFQAQMKVATELYKQDKSITDIMNSSLYLGTGKSEFQARFESVD
ALRAGLQLAEGERKADPDFYTKLGLVALTASIGAALVMLMKSMVKGADYA
ADGVWCVSEMLKLANPEVDMQKAVQVFEIVGLNLVMTGFLGVNKVWNF
LDKGIKGYASGAAVLTAAANLTLPGMVGEVAGAAAGKLSYLTDKGAAHQ
AGRAAASWAGNYVGT SRLGSVGT LQTAIPGRIAGGQVVAGLYDRFRYLT
GSHPTPAQQAAGEP
> gi|29840709|ref|NP|829815.1| hypothetical protein CCA00954 [Chlamydomonas
caviae GPIC]
MSLSTSGPDNANQKNIMAQVLASTPQAVPTPKLAGNETKQIQQTRQGKN
AEMQSDAGIAGTQKKEKTSAVSEAQGADNIMAGQGIAGQETEAEEAAAG
ANQTAGAAAFRANLQASLEETNKLTLETLSLSSLDSTQLHEVQELVASA
VSRSSNSAIRGLETPDLPKPSISKPRQEVMEISMSIAKAI AALGEATASA
LSDYQSTQAQASTMNRSLSESQGLKIDSEREEFQKMKELQAKADGNKTLE
TVNTVMIAVSVTITVVSVAALFTCGLGLIGTAAAGATAAAAAATAGATA
GVTAATSVAATTVATQVTVQAVMQAVKTAIVQAVKTAVMEAVKSAIKQGVK
QAIIKAAVKAATKLMKNMSKIFKTGQKALSKSFPKLSKVINTLGNKWVTA
GMGVVVAVPSLVKIGDLKLSMQTELADIQKKTGMLTAQAEMMMNMFMTF
WQQASKIAAKQTD SANEMQQQATKLGAIKAFQSISSGLAAAV
> YPCD1.67c yopH putative secreted protein -tyrosine phosphatase 47122:48528
reverse MW:50870
MNLSDSLHRQVSRVLVQQESGDCTGKLRGNVAANKETTFQGLTIASGARE
SEKVFAQTVLSHVANVLTQEDTAKLLQSTVKHNLNNDLRVSGNGNSVL
VSLRSDQMTLQDAKVLLEAALRQESGARGHVSSHSHSALHAPGTPVREGL
RSHLDPRTPPLPRERPHSTSGHHGAGEARATAPSTVSPYGPEARAELSSR
LTTLRNTLAPATNDPRYLQACGGEKLNRFRIQCCRQTAVRADLNANYIQ
VGNTRTIACQYPLQSQL ESHFRMLAENRTPVLAVLASSSEIANQRFGMPD
YFRQSGTYGSITVESKMTQQVGLGDGIMADMYTLTIREAQKTI SVPVVH
VGNWPDQTAVSSEVTKALASLVDQTAETKRNMYESKSSAVGDDSKLRPV
IHCRAVGRTAQLIGAMCMNDSRNSQLSVEDMVSQMRVQRNGIMVQKDEQ
LDVLIKLAEGQGRPLLS
> gi|2865295|gb|AAC38388.1| rOrf10 [Escherichia coli]
MNEQFCKDLAHTFGITLEEQT DALAFHDNDGHEWILECAPQSEILFFYCY
LSTNEPDQINKILEINNREMLGMFFLSLKDDKTFLNIAFPKNKIDITEF
TNLMENGYLLKKEI IKLLSL
> Q7DBA6_ECO57
MINPVTNTQGVSPINTKYAEHVVKNIYPEIKHDYFNESPNIDKKYISGI
TRGVAELKQEEFVNKARRFSYKMTMYSVCPEAFEPISRNEASTPEGSWL
TVISGKRPMGQF SVDSLYNPDHALCELDPDICKIFPKENNDFLYIVVVY
RNDSPLGEQRANRFIELYNIKRDIMQELNYELPELKAVKSEMI IAREMGE
IFSYPGEIDSYMKYINNKLSKIE
> gi|34498073|ref|NP|902288.1| cell invasion protein [Chromobacterium
violaceum ATCC 12472]
MAQPKSLLKPEDAGVLSWLA AKREDAGFTAGVEHTANKLEQIIDKELE Q
RGAEQDPGFDISGLSTRMAALLSQAI VLMSALRTADNALSTKLSLVSFDA

TKATAASMVREGIANLSSSIVQSVGQVAITGVGAKKSLNGLNAERGALKN
NAPKLGKLGDEGRNVQATLSRQNTVKLAADADGLKQVGLKFPQNGAARPEV
AELSAQPNAASVADGMAGDKISLQSSNSKLARQHEAALGSSTEDLTAKS
QAEQLAMDDTKLKAQAKQTTGKAIMDSSAAAGNIAGGSGRYAATLEQSEQ
QISQASSRVASTASEETRESSRKADSI IQELLRTLEGISQSKSSAMAAIA
GNIRV

> A0G5K3_9BURK

MKILIIADDLSGAADCAIGFASAGHRTVVVLEATCMPAHDGADTIAVDTD
TRRLTPQDAATRATAAAYAEMSARGQRLYKKIDSTLRGNWAAEVAGLQALA
GMAIVAPAFPATGRTVRDGRVVFVHGEPLEQTATWKLEHAGQPAGIAAOLE
AVGLTTERLDAQWALGDEPETLAVCIGAMAA NGVQALIVDTHSERALRALA
RATLRSADAPFFWVGSGLAREIAALDSRVDPAGRGPGNTTFPGGPILILV
GSLSAVSERQCAMLRRERGGVKELIVPPAVLRAGATHRDWHVLQEQIGVSL
KADVLLLRIGRDDAFDPAEGAQLSAAALALVEPHFTRTGGVIATGGETA
RAMLAAARIGNLQLLAEVEAGVAVARPLDATRTHCPGVVTKAGAFGTDHA
LYAAWLTLRNQTERDVVPH

> Q8XA51_EC057

MTDGISTSPHCLYKSNIVDDVIINKTRQNELVKVFCEYKTEFFLILFDDFF
RSQDLPKPSPVLLHFFQYTHLRDAHFYRCKLIEHTVQFSFFKHKGITLLR
LDVFDRTSECLSEEIKIYQECHEKFIKFLKANFNQEIYPELYTPEIFYE
ACRNLQSFYDHQETSQNAKYSIVKKSIFYNKEIRNLIKKNIYPELYNEQ
CNKIPASSTDDNQKITWQNFKTSNAAYSQICEKLSLLKSSPSRLIEKS AY
CSNENMITDKFDVVFVSYCGDNVKEFILLLPYNKSLEMHELNEQNIQYLTA
LNINIHKLLSNITIEKSNLSYGYFVCVLSNISCESDLSNTIFSNGEI
NNLFIKKSNIFGTSFTNTMIKNLRCEIMPGRWTTQLVNKHLGYRYTGVE
KTLASIDDKPSRFELIPLVQTLVRDNVKNNDVYKELKKFMHDYDKTSP
EMRKYLQSINESMFLMKKISHQD

> gi|28868097|ref|NP|790716.1| candidate type III effector HolPtoQ
[Pseudomonas syringae pv. tomato str. DC3000]

MHRPITAGHTTSRLILDQSKQISRTPESSAQALSQQASMSSPVLERSK
SAPALLTAAQRTMLAQVGCNAHLTSDENMAINELRSHKPLLPKDTWFFT
DPNKDPDDVVITYTLGKQLQAEQFVHITDVVATLGDAEVRSQRAEMAKGVF
NKLELHDVHVSRRGRD YAMNSLOSKEHAKFLEGHALRAGPGEIHRDSLQD
MSRRLARAPHGVGIVVIAGMSDINALITTCPDMVRERVDITIMGGVEPL
KDADGFVQPDARAYNNATDMAARSLYRKAQELGIPLRIVTKEAAYKTAV
SPSFYEGIAGSGHPVGHYLRDVQKSALKGLWEGIQAGLLPGLDDSWFFRT
FMPNAQIEAAQLDNKNESSFEDIWPKVTKLNLYDPLTLASVPGAAKLLF
KPKAIHTEGFGVVEQV GPDDVTHPEKAKLLMSALAKSALVQSTVAPD

> gi|5070694|gb|AAD39255.1|AF156163_1 avirulence protein AvrBsT
[Xanthomonas campestris pv. vesicatoria]

MKNFMRSLGFGSSRSSSSSNWNEQQADNDEQTPASSPSTSPSQTSSAF
SGLPERPRKKAIALESLSNNSNI PYEMRMYAEAALSAANDGSSEAITKA
DVENKYYLAHAYNERFP ELHLSCHDSAQSFFSEFMTSEKQAWRSIVRLSP
SSMHAAIDVRFKDGKRTMLVIEPALAYGMKDGEIKVMAGYETLGKNVQN
CLGENGDMAVIQLGAQKSLFDCVIFSLNMALCAYQKDSVFDNLHDCLRRN
VRCFSSGERKSIHLKNIIEFIEGDKFLPPIFYKSHSRGVVGEFISNQPEY
AHKNVSTGRNTNPSEDLSERVENFRVRRGDLSSYSMSIEASRLRKIRKTIES

> gi|16520028|ref|NP|444148.1| Y4xL [Rhizobium sp. NGR234]

MDINSTSPLNASPQDPPANASAFQALSGFQYSPPHAADSLLPQVEA
DSPYLDTRHPYSQYLDAYPYPSPCEWQHDLTYTRTRERSHPSEQRPHAR
VLQGAPEHDQDQHLAAGPREGSWQVGPSSRGPSQAGLSPSATPLNPSPP
PHATDLETKHPYSQYLDWANPSLLDWQDLHTRATASPAPLTAERGRSPQ
PSEQQPHARALQVPEYDQDLIWQRVDAAGPQAGPWQVGPSSHSGPSQARPS
HAWPSSSAGAEPALSDFVMDSGVRAWDHWFAPHMASEDQMSMLRATGL
MPTAEVPTTTFLMMGMRHVAEFRGEGVIRIRPSVDFDI

> Q3CIL9_THEET

MYRVIVIADDFTGSNDTGVQLVKHGYVITLIGTAGVKKYEDVADALVID
TETRIPALVAYEKLEISNIVGEYKEAVVYKKIDSTLRGNIGVEIKALR
EGLKPELTIFAPAFPKNGRTEKGVHYLKGVPVDKTELARDPKNPVTTAD
VKKILEEGLKVPVHKVLEEI SRDLRKDIEKEMREYDVFSFDAKTDDDLI
KIATSVLDDLKKTLLWVGSAGLAEALIASLEKKEKKNPVLVIAGSVSQVTR
RQVFALEDSRIVLVKLDVKRALSHPEEIDRIRKIVLDFMNAAKDVIIA

SAAEEDAVSEALIAARGKGLSPQDTSEVLAQFLGEVACSIWEAKRPGGLV
LTGGDTAIHVVKSLSTAGCRINSELEPGIPELVLIKGSVDGLRVVTKAGA
FGNDESILNAVKFLRGDGR

> hopT1-1 Pto DC3000|Genbank: AF458399

MMKTVSNHSIPSTNLVVDAGTETSQAQKSQPCSEIQRNSKIEKAVIEHIA
DHFAAKMTISALVDTLTDVVFVRAHGEVKGWAEIVQAVSRPHDSNRHGSGV
LSPRFDVMGMSGVWNAAIIRATSRVGTLREKGTFTNLMLSNFKHLLKRV
VNDPALQQKLDGGLDLNLYLKACEGDLYVMMSGWAARASESREQIGKARYET
ASNLSQTLISARELAFHRHNPVNHPSAQTKVGFDDKGLPEESDLQVLRGHG
SSVWSVKPGSDFAKRAEVSGKPIIAGPSGTASRMVAVARFLAPACLKSLG
IESEQNLKELVRYACYAYFGQDSSHSMLEVNLGVASHGMPEQWDDTLYNE
PFSNSIKGRGFGIDNLAHRQVVRQAAQKS

> NleD_Crod

MRPTSLNLTLP SLPLPSSNSISATDIQSLVKMSGVRWVKNQQLCFHGT
DLKIYQHLEAALDKIESTDTGRTLNCIELTSRLKSEKLAIHLSAELGV
IAHCNADAENSRTGSDFFHCNLNAVEYPCGQGISLVDFHACIVFHELLHV
FHNLNGERLKVESQPELQTHSPLLEEARVGLGAFSEEVLSENKFREE
IGMPRRTFYPHDSSLIHDDNTVTQRFQRKHLHPLL

> gi|58579791|ref|YP|198807.1| avirulence protein [Xanthomonas oryzae pv. oryzae KACC10331]

MRSFMRIGPPQTSIAHTDALAIPTHTSASSPTQVPHVQNGTNPPLRERAPR
RAVSIPPLVPLNDSAMTGKPALVALDSEFSEQRLAEVQARQITVQTLQGGK
LAAHLAQAGTALTPDSIAARFAAGALEPVYLDTAAFNAMSRLPARARAA
SGPVLIDAQQCRIVFNLRQAFASGDTFSDAALTALGKA LDLPGHGLATPD
WLQPAARTPTRRKLQHAPRYHGHEVPARDGGAAFFKANDHRLLEGKQALL
RNHRKALVHDHYFEAPSTRALGKDMVHRGLFDNHAGIPENSLSSIDNAY
AKGYRNLELDVEVSADGVPVLMHDFSVGRMAGDPQNRVLSQVPPFAELREM
PLVIRNPSDGNVYKTDQTI PGVEQMLEHV IKKPEPMSVALDCKENTGEAV
AMLLMRRPDLRNAAAIKVYAKYYTGGFDQFLSNLYKHYQ INPLHSQDAPR
RAALDRLLAKINVPVLSQAMLNDEHLRGGFFRSNDDGAEGGLADTAMQWLE
SWTRMRPVIVEAVATDDSDAGKAMAMARERMRQPD SAYAKAAYSVSYRFE
DFSVPRANHDRDYVYRNFGEQKLTNEEFVGRKTTAGAFRDDGESLLTD
QAEAEALLAIENRTLARGHTGNELDVPPETPIDINRDAEIVKQRTREFQA
GSIPADPNHIAAVREGKQRDHRADMVHDPAAATRAVDKRAQ ASGLLTKKYR
GAPVTHYLNERANQTEPE

> Q7ABH4_ECO57

MERRAVALERQLNGGVDFLRVSVNNYFQSVMAEHRENKTSNKILMEKINSC
VFGTDSNHFSCPESFLTCPITLDT PANGVFMNRNSQGAEICSLYDKDTLVQ
LVETGGAHPLSREPIITESMIMRKDECHFDSKKESFVASDA

> Q8XWW1_RALSO

MRPTAPRIGPPSATVSGEPAADAVPQHAEPGRTGRPPRARGLPLEQRRTG
PAARNPRGAVTQGDAGASDALHGQALSAPRRSNVAGPPADRAESVPSR
VRGGTQPQASKELRARRQLPAEVVRQLSETVHMVQVLLANGFAWSSSLADD
LDDVRLDSARQLSAIAHRDVMPPESANLVFAKLVKGRALILNSAQDQGGC
RSPALAGLLFLGEHHRWKAHNGMPSHTLPALIYGGQSDGFAAAISGS
GGFGTSHLHVGRKAVNNASVIAHESVHEAQYNKRLGLFNALMLRAPTHV
DTAAHARAGFLEAARTLPVLPPTDVS AETAKICYVSDPTEAQAYLEEAQL
RSLLPSDQGMGAYVPRQDARLHELADLLAEVADALNVAGPQEQQAARGILA
EFDPAYPEAGEALERILLSAASLHEMAESTAWDAGAADAWKGTLEILRQ
RCDAIRTEPPLGSGLLGLADALERFLVD TAKQSAQALALIADTLEVFLE
RVAQTHGHAVHALKARPVTPEAFDAKQDP IGVLGQLLERCGFAHAQGLP
AAISAARSASGFSSAVADLKTRLGKEEPVAADDLREVVVLLASRLGLGLAP
SQLPAALVPAVNLYASPVVVL PNVAGLNGVSHQKRKAADFVATWQLHI PR
NVFDAPERLESRLAGLAADVAYA AVSLREDKQFETNHPLFALWYGPLSKR
FTNALAAEEVAASSRDFLARHPDSAAAALHAIVQAVRVDGIEARAWHLG
PRAEVKRASHAGTELPDRAWPGEDEARPDADAARHAYQSRTFERWQVYSV
AFRRIAHL

> Q8XA11_ECO57

MKVSVPGM PATLLNMSNNDIYKMSVSGDKMDMKMNI FQRLWETLRHLFWSD
KQTEAYKLLNFVNK KAGNINASKYFTGAVNENEKEKFIHSLLELFNELKT
CAKNPDEMVAKGMSWVAQTFGDIELSVTFFIENKEICTQTLQLHKGPGN
LGVDLREAYLP GVMRDCYLGLKTMKGHNKVLYLEPGWVANLDGATLDGA
TLDGATVDGATHLYDEVIIINKITPKKIDTEE VATKQSTAEQITDNAIEE

> gi|2865297|gb|AAC38390.1| Tir [Escherichia coli]
MPIGNLGNVNGNHLIPPAPPLPSQTDGAARGGTGHLISSTGALGSRSLF
SPLRNSMADSVDSRDI PGLPTNPSRLAAATSETCLLGGFEVLHDKGPLDI
LNTQIGPSAFRVEVQADGTHAAIGEKNGLSVTLSPQEWSSLSIDTEG
KNRFVFTGGRGSGHPMVTVASDIAEARTKIL AKLDPDNHGGRPKDVDT
RSVGVGSASGIDDGVVSEHTTSTTNSVRSDPKFWVSVGAIAAGLAGLAA
TGIAQALALTPEDDPTTDPDQAANAESATKDQLTQEAFKNPENQKVN
IDANGNAIPSGELKDDIVEQIAQQAKEEAGEVARQQAVESNAQAQQRYEDQ
HARRQEELQLSSGIGYGLSSALIVAGGIGAGVTTALHRRNQPAEQTTTTT
THTVVQQQTGGNTPAQGGTDATRAEDASLNRRD SQGSVASTHWSDSSEV
VNPYAEVGGARNSLSAHQPEEHIYDEVAADPGYSVIQNFSGSGPVTGRLI
GTPGQGIQSTYALLANSGLRLGMGLTSGGESAVSSVNAAPTGPVRFV

> gi|53722438|ref|YP|111423.1| hypothetical protein BPSS1411 [Burkholderia
pseudomallei K96243]
MRANRNNGLTAGALPPNSAAPDDAAKAAPPVAQSDRGAG PLAGLTALKAD
RAQCMSARPSIRSTTKAPAVMSHARADTSRELTPEARIAQT FVRPEHLR
AIAAAAARAGSAFVSRFRASGQLSLKRLANGAPAKGHDI LEKTIKPGSVQEV
YGADSEERRLAIDGYVGHWRDKLLGLYMGPAANERDTPMLFAAL
RSTPSGHRYY PVDHDDLEGLLALLKRTQGPSGTAGSFWMSLPYTGDDYDTH
DMINMAGHRTVPVSGSRDEHRIMRSLNVAIEAIDPIRKAS GSHRLIQHG
PQHNYVAHMRTNEQGAVIDEAVARASFFLAMCDRGTWSVIETPEALAAFY
RQHGVVLKEKWREKRANTFTA

> gi|21241060|ref|NP|640642.1| avirulence protein [Xanthomonas axonopodis
pv. citri str. 306]
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TRCVPRARRGRSGKPTLQPHEVQQAAY QLGMRLSGRP IEDVDRDRQLADA
TATVHETRLALHHGRGNIESDFRLSDGRSSTCSYLSYSFSLYWPBKHDID
LMAGCALAVSAGNCDQNAAVNTRRHAVRMEGGQITNVCEACAHMYALY
QPPGSAEADDSAVVLDSDGPAVLLRDRSRWAGTYRRTSTYPIERFDKPG
AIDALARTRALQAEIEDPQTEFHHLRGVESVVRTPPVPGKIYASTPVIA
PDLVQRTRQRLQELSPRTRKALAADAAR QAYGLDDAQPISPRTTTAILKD
AARLDALGRPPLSWAPTSHTRLKRFVTSARTNARQAFWYRSGWRPPVTVA
R

> gi|34495751|ref|NP|899966.1| hypothetical protein CV0296 [Chromobacterium
violaceum ATCC 12472]
MKIGVLNAGLRQFAAEFGERAARAGRGLAGMFRAANVAEAPRRSAAAI
EQGWQRFSARFLGARGADKPAPTTLTRGGAA RSPLSPGDVKAMIRSRLDS
LRDGMADPVYRRQALESTYATIYSEAKQAFYRANGGKMEGYLRELGEAA
RAAGLPGENKHGVFIPSGDGASPFVNYLLIPVQKEFGHRLRNESQQLFR
DFARQLSMELVAPHAERGWEPPAFAARLEAVGRPWLAQA

> gi|16765569|ref|NP|461184.1| leucine -rich repeat protein [Salmonella
typhimurium LT2]
MPFHIGSGCLPATISNRRIYRIAWSDTPEMSSWEKMKEFFCSTHQTEAL
ECIWTICHPPAGTTREDVINRFELLRTLAYAGWEESI HSGQHGENYFCIL
DEDSQEILSVTLDDAGNYTVNCQGYSETHRLTLDTAQGEEGTGHAEGASG
TFRTSFLPATTAPQTPAEYDAVWSAWRRAAPAEESRGRAAVVQKMRACLN
NGNAVLNVGESGLTLPDCLPAHITTLVIPDNNLTSLPALPPELRTLEVS
GNQLTSLPVLPPGLELSIFSNPLTHLPALPSGLCKLWIFGNQLTSLPVL
PPGLQELSVSDNQLASLPALPSELCKLWAYNNQLTSLPMLPSGLQELSVS
DNQLASLPTLPSELYKLWAYNNRLTSLPALPSGLKELIVSGNRLTSLPVL
PSELKELMVSGNRLTSLPMLPSGLLSLSVYRNQLTRLPESLIHLSETTV
NLEGNPLSERTLQALREITSAPGYSGPI IRFDMAGASAPRETALHLAAA
DWLVPAAREGEPAPADRWHMFGQEDNADAFSLFLDRLSETENFIKDAGFKA
QISSWLAQLAEDAELRANTFAMATEATSSCEDRVTFFLHQMNQVLVHNA
EKGQYDNDLAAALVATGREMFRLGKLEQIAREKVRTLALVDEIEVWLAYQN
KLKKSGLT SVTSEMRFFDVSGVTVTDLQDAELQVKAEEKSEFREWILQW
GPLHRVLERKAPERVNALREKQISDYEETYRMLSDTEL RPSGLVGNTDAE
RTIGARAMESAKKTFLDGLRPLVEEMLGSYLNQWRRN
> SIPB_SALDU
MVNDASSISRSGYTQNPRLAEEAFEGVRKNTDFLKAADKAFKDVVATKAG
DLKAGTKSGESAINTVGLKPPTDAAREKLSSEGQLTLLLGKLMTLLGDVS

LSQLESRLAVWQAMIESQKEMGIQVSKEFQ TALGEAQEATDLYEASIKKT
DTAKSVYDAATKKLTQAQNKQLSDPADPGYAQAEEAAVEQAGKEATEAKE
ALDKATDATVKAGTDAKAKAEKADNILT KFKQTANAASQNQVSOGEQDNL
SNVARLTMLMAMFIEIVGKNTEESLQNDLALFNALQEGRQAEMEKKSAEF
QEETRKAETNRIMGCIGKVLGALLTIVSVVAAVFTGGASLALAAVGLAV
MVADIEVKAATGVSF IQQALNPIMEHVLKPLMELIGKAITKALEGLGVDK
KTAEMAGSIVGAI VAAIAMVAVIVVAVVVGKGA AAKLGNALSKMMGETIK
KLVPNVLKQLAQNGSKLFTQGMQRITSLGLGNVSGKMGLQTNALSKELVGN
TLNKVALGMEVTNTAAQSAGGVAEGVFIKNASEALADFM LARFAMDQIQQ
WLKQSVEIFGENQKVTAELQKAMSSAVQQNADASRFILRQSRA

> gi|53722415|ref|YP|111400.1| putative membrane protein [Burkholderia
pseudomallei K96243]

MAISPTIATNRQVVGSGSENVPGPA AEALQSVESQLHQLMARQLQGGVA
MAQRQGGGIRAAQYAPLDDYTRMYDQADRDRWADLAALQGGVSLERPLAA
MQILSGERQPSAAQTAALQFVNDNPSLKTAMQNTGGLKPDGSDVDPGKVA
DLLKEVEANLAKADEVDKAYLNDHPDADR DALDTVRAAALLEAYEPIVQ
SAGHQSSGKNHYSYTGKNNGGGLTTKQQVADLQNNGGFSAALKSAKAW
STSGAFDNLDRAGDDKATEKVDQIFSA NNLHHFITKDAPTS DAAEHAFLE
KASLENITAGTDISKLNQDIFANPQDYSPOQKAAMVVKLMETLVDVQAGG
ADKLRDVTATVSALKQDIMMLANDPETNAYLHQMVPPEMRDLNATFEQAG
GLEGDTGAAGDMSVADNANRVSARNIVDQTKDALDEAEKVAKRLGKLGNE
GAGEATDATQS IADGAETAADGAVQGGVEEVGGAAASAVDGAEGAITGVA
DGVEAADGAVTGAEGVEGALAGTEGAV VGAEAGAGVAEGVMGAVAGGMA
AAAPVLAVGAAIAGIAGIVLAIIVEAVKKAQNRKAF AENVNPTLNQFGIPL
PT

> gi|51591604|emb|CAF25408.1| yopN, lcrE; putative membrane -bound Yop
targeting protein [Yersinia pseudotuberculosis IP 32953]

MTTLHNLSYGNTPHLNERPEIASSQIVNQTLGQFRGESVQIVSGTLQSI A
DMAEEVTFVFSRKEKLSLDRKRLSDS QARVSDVVEEQVNQYLSKVPELEQK
QNVSELLSLLSNPNISLSQLKAYLE GKSEEPSEQFKMLCGLRDALKGRP
ELAHLSHLVEQALVSM AEEQGETIVLGARITPEAYRESQSGVNPLQPLRD
TYRDAVMGYQGIYAIWSDLQKRFPNGDIDSVILFLQKALSADLQSQSGS
GREKLGIVINDLQKLKEFGSVSDQVKGFWQFFSEGKTNGVRPF

> hopR1 Pph race 6-1448A|Genbank: AAZ37024

MVKVTSSGFTANPLPHHADSVPANSPPQLPEPLPLVDES PSSHKGMRN
RAHASLNSQVLGLQAVPLQRGRHVRIRSHTDGVSVIN DWLAKRPSVQSET
SLDNNGKLVRYTAMHHEPLAPRNEAFFTSVPGMLMAVLT VHPDIEYGISG
EITADAVARLARLEPPIGLLTGVWQSSHD RAYIERGGVVHTANMEERWTSL
TLPGADPREPLRMIGL QADGDVYLHNGRQLWRATD TSAESVPTERLPEGA
AVRIGAGREVQWLHEGAVHSNGISR PVELLRPEASGLGVEQSPARPVDLL
PLPRGNAALILDDKGR IYQADLKGIGPVEAHR LKLPGDFAQGGKAWVTM
GLSRDNTVHMLQDQNGRRMSLQRAQNEV LFRPAYLLDRPLLLLYTEGLH
VPSETAVQSHVQLDGHAQVGHIDGVLHYQPAPDQPWERLRQPGGEPLTGV
TALYSSALGFI DRKPVF ALLGDARQVVELKLEGR TSWLPTDAELPRHPAG
GPLAVIPDVELRARLIAQFDEPVQALAVHNNRQSV ALMESGLLIAADAD
GKVRRLPLLQRPIALAI GLNDQLLVLHHPRNQR PQLKRLSAKDDWEPVPI
ILPGIDHPSNLRATR TQGIQLQLGDNWHTLLPAMT SHDNRPLPARVKPEP
EADELPSNF LAGTNRNVNQQASRISTPHHDASAV TTMGTAAANNPLTM
TSSVQAVVDTTA QVQAL ARDVLGGVTKNTMRAMA HKLGVVLPPTTQERR
LASFHYEAKQAYTSGKTLFEQLPTLAQVRV ASAVGPSDGEKFGLSHQQTQ
RLNLNREEKLEALLRDLRKIGFHEGVIMGDMGDGESAGDLTSTTSTPTFR
LAELWRRQHSQVNKALSSVGLSRSEDILPNLNQSI KALAGGAALHADRMG
EREAE LLSVLCEVSEKIMRAGVRLPADDGSADS ASSHAPHGLRTSGLMAG
LVDYDALLTSTDTQALEMA ERLQDARLPLGLCKLGLSSWVQLAAFDVVVT
TFREQISLPGSARRTQLLKNLGLPPDAAPDEMAARMSDLFLDLFNRSTFF
STQSRGLEIRGSLGADWKHLN AFSVGITGEALQVLGVERIGDGKGDGAG
LVAFFVRHAKASVSATSGVIGDFKPLGLTGGRVLD SRPGRSMNSTWGGSA
NLGISGTYQHGGAAV IAPSTISDFVRL LFDVNHPDSTQILRTGVNNGGS
IGLDL FETNLNGSVGANVSV SPFSLSQYGPQKPSADAAASGADNRRSTA
SGALSVGATAQAGAHWGQ MELHLHDHAWAEIIGLEFQGR TDFNLEFN SNLN
LGGALSSALGDRPQK LINASTGNGNLQLAGIRVASSDVQLPTDSVVDK R
RGPFLSTASYKRTFDTQVAKPITADEWSQMRQLASAFP DNIGELGALAY
STSPSERIATINQ MIDRIQSSKARNVEAGGALDGNALRRQRLDAAREMSN

AGNSVWQASSEIDRASVVEML HQLRQQEQSAVQHARAIPGARVEFNLFGR
RESLETVVFAIGHI GLGSKLNDMAELRRKTPGLDQVMRCFQSLPNINQV
RYVFEMRPQARFAINDALLAREQQASARALGLPGSSASELNWRGVLDKIK
NTPDLYRLAAIAVHNTDENPVTSRIGLPLLNVSATGATSHQLFEAEIQFR
YGLYDGLQGIEVLEAGSRALQSPLRVLQQSGIQALGQRTQAGDVPYGPSS
PRKEATMRTAGEAAALTTNDVW RQLDGKIQRMNSAHEREANAIGSFQHAY
GTASAHVDRLLLRIPELPAPEIDDRNADGESVRGAFASLKRNHQALDEDV
KAMRQASEMVYSIPGERTRQTETSALAHVLSVEKSRRLGHAMEILAGKG
VEAGTATGLELNRVSSQVNALVVRDELLTQLERGAQEGGSNSEEMAMEL
QQTTSLLQRLRADLLGERQAMDATAKRRLDQANRVALEGERSFSDAVRDMT
WGELDKMPQ

> ECs4561 ECs4561 Tir 4599930:4601606 reverse MW:58023

MPIGNLGHNPVNSI PPA PPLPSQTDGAGGRGQLINSTGPLGSRALFTP
VRNSMADSGDNRASDVPLPVNPMRLAASEITLNDGFEVLHDHGPLDTLN
RQIGSSVFRVETQEDGKHIAVGQRNGVETSVVLSQDEYARLQSIDPEGKD
KFVFTGGRGGAGHAMVTVASDITEARQRIELLEPEKGTGESKGGESKGV
GELRESNSGAENTTETQTSTSTSSLSRSDPKLWLALGTVATGLIGLAATGI
VQALALTPPEPDSPTTTDPDAAASATETATRDQLTKEAFQNPDPNQKVNIDE
LGNAPISGVLKDDVVANIEEQAKAAGEEAKQQA IENNAQAQKKYDEQQAK
RQEELKVSSGAGYGLSGALILGGGIGVAVTAALHRKNQPVETTTTTTTTT
TTTSARTVENK PANNTPAQGNVDTPGSEDTMESRRSSMASTSTFFDTS
IGTVQNPYADV KTSLHDSQVPTSNSNTSVQNMGNTDSVVYSTIQHPPRDT
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APGSHRFV

> Q8X5G5_ECO57

MKITNYILPSTRTHGSFSTIKSWDTMNYIKHLIRHTNDPIFEEQFYKITQ
SHIDFDKRAKDEKNDTINIYDNFFYSSNDDLDSKIRSM LNLYEKSLTFR
RIINYYVKEINLSDYGLFKCKILPAYAYNYEMENDAPPK ILIPIDHNLNF
IDAKYNGEITYRGNEEFAINLFLQHILHNDIQEQTSIDLYTSI INKELDSN
RKSYNNEIFNNFSPDKSVKLSYNYIADDIEQVIDKGSKVQLEVYNLLSE
EKIFEHKIMNNWTRSIKNILTYYLFMSSGAVTARNVQTFSP TINNESRIR
LPRALPVGHYPYEEHKASGFSPFMMGGLSGDILPEILTGNGPSIFFNGKH
NNQHDGAFGKI IDFTQNGNKISAKDKEIKRYIFDKINVL IKEYFIRTGK
NSHTPFVEVFIKERLFNQYDIFKTLARDILAHPLVIYDAGYKNYHESLNAA
IAINSRPLQEIHYGDVLYHYHKNDISLGVDTLYGRESFDIVLDAMNVYRK
SKKMRVISNNEMKKS IKISELVIHNI IKKGLTNCLLKKDVLNARYDLIRD
ILRYSLNIRQGIKHDDVNRIAENI IKKYGITEGMNPKPRNARISKELLLL
AVDRQIEWAKKHFTKDVLENVVSKCDLSSIFNVNKVLQNT ILEFVHEIN
NISSARWMSKSKENNKQKEAIEKFKKEVSHMGGQQF IWGFDKVIQEGLS
GLIELSIDINDSTNHRDKSSLSPDGRAVLHFLGTIWNMAMGAVPGYNALS
GVSSILHSAIVKESSNICDYIQGAVRIGMDFVPGTRSDLHSRSLQIKYEA
LKHIEKNINDNI IYHPSNNANFYSVIESIDGNDFIYNEKQSKILEMKQDR
GGNRYSAVDLNSSKYGYEYKVGGFYRYIESFNPI SSETPNK IVYKGESV
DLTKEPNSELYSGRYSINNKQVNVYFRDADGTFYKSEGLHGGGVIRYID
KPYSQLREGDIGYDEDLLDIYDDSPVLEDTLPALSS EIVPTPEHSIKQIY
SKIKEGHIELSDSDIILCRGTTGIQAENIVEYKTAGGLPDSNPNVKAPDE
YMAQQQVRIGRILPEYTS DLSVADRF SREHYLIVVKVAKAYITRGSVTES
GWVIDKTAPVEPLAIDRTFGMKENISMVNASK

> A1JU68_YERE8

MFITPRNVSNFTLQEP L RHSSDLTEMPVEAENVKSKTEYNAWAVWERN
PPGNGEQREMAVSRRLRDLRQAHELELNNLGLSSLPELPPHLES LVASC
NSLTELPELPQSLKSLQVDN NNKALSDLPSPLEFLAAGNNQLEELPELQ
NSSFLKIIDVDNNSLKKLPDLPPSLEFLAAGNNQLEELSELQNL PFLTEI
HADNNSLKTLPDLPPSLKTLNVRENYLTDLPPELQSLTFLDVSDNI FSG
SELPPNLYYLDASSNGIRSLCDLPPSIVELDVRDNQLIELPALPPHLERL
IASLNHLAEVPELPQNLQLHVEHNALREFPDIPESVEDLRMDSERVTD
YEF AHETT DKLEDDVFE

> gi|21243817|ref|NP|643399.1| leucin rich protein [Xanthomonas axonopodis
pv. citri str. 306]

MPPTVGASPLRRSPAIRPYRDVLSQWQRHYSADRNR WHSAWRQANSNNPE
VERRTSRALKATTDLLEDATAPERVALELRSVPLPQFPDQAFRLSHLQHM
TIDAAGLMELPDTMQQFAGLETTLTARNPLRALPASIASLSRLRELSIRA
CPELTELPEHLASTDASGEHQGLVNLQSLRLERTGITSLEPASI ANLQNLK

SLKIRNSPLSALGPAIHQLPKLEELDLRGCTALRSYPPIFGGSAPLKRLI
LKDCSNLLTLPDIHRLTQLEKLDLRGCVNLSRLPSL IARLPANCIILVP
PHLQAQLDQHRQVALRELNKVALERIEDTAQAMLSTVIDEERNPFLEGAPS
YLPEKRPPGTPPTTFGEIPVLQKMLEESRDPHFLQRVSDMAGPSPRIEDES
EEGLRLHYTNVSNWKAQQSAHLGIVDHLGQFVYHEASQLDAASLAKAVQM
WKTRELIVNAHPQDRTSFPDFTLHIPEQVSDADDEQQTSPAPSRDQ
> Q8XXL2_RALSO
MRRATSRPAAQGGDPAPSPPRFVVS TPMQIRNVPRSDLTPIRSGDNVST
PAPNSVPPRRARSASDLQAMGLCARGTPSSAPLALPAIGIATHHEAVQET
HLSAAAALETELLELPHATDAGLAPRIAFRLMNVATRIAEHCAVKPSPGEP
QAPIPEAWRCLEALASRLRLHPAQGLARQMLLGAVEASTHAPLDKALL
QDILKAVTQADGPGLEDEYVARRAYDGLCLGQLKADDEAEPPTRTFNSI
LPSLAASTYDYNPLGRTLLWEGACRLF DGPSAQRRRAALQTAVFSLPNVP
APGKQPLDNLIEFVLAIDDMKLYETTPASEPRAA
> gi|28871821|ref|NP|794440.1| type III effector HopPtoI [Pseudomonas
syringae pv. tomato str. DC3000]
MLIGHSLHHRPTAVDSSLPTSATSQTISNTKSRLDPHRVRELTFIGVGS
SVAYLLNELNGRFADSGVTTTFLGKVSIVGKDDSWAENVRGKG YINHQTE
IISQWDQVQPKYDPNYAARAEFSASNRRLTRTVELGAEHLKAQVTGISR
LDDGCFRINLDNGQILQSRQIVLGTGAGPHTSIWNSVTSHTQAEKRLDNI
KLHEQKALRGKVLDDDEFMRASDASPQTFAGKTVVIHGPNAGIDAERAG
ELGANAVWFTRSTNPVLLDGNQLKFAPELAKSAIHKVDKLDIRPTKLENG
FALRLHYSSSLGQDSREPKKVLDADYVYAMGQDIHKPGSAAAIL GSLLDH
LEPIYDYDQVYSQPFKTVIGLQSRGSNSDNGLIIVGAAVAQLATNVQHS
YKDHALDRILEEMTRLPEKQTEKLSQMLLEGAPSVQIQTYLKTWQLDSGQ
PPDKQVLQNVENYLAARDYFQRQTNEQKGNLDGVAAEVKNQTLTEVASV
IVSPQLGTIKASAAALSGLMPAYVANGENNFTTDRNTMLRAGIAARYPNI
GNAEASAFIDEVTLRHLNSQRFIEKVAGEMMDKGAQPLVSLRPP VLGVP
ASVRTAYEAYLHALNSGAHDGTPLSQRWLPKK
> GogB_Stym
MKIGFQPAILQYAYTSNEATSNLELLNKWRIESPDIEKEERNSIYDKIEE
ANHTGSLSTITAHHVTSIPVFPDNLSELNLSSCYTTLESIPNLPDGLKSLTI
SGNQTIKISYFPDSLESLSIDMQAYEENYTFPALPYGLKSFTACYGKFLP
PLPPLLSSLSLQNFSEILCAELPYKLDKLDLQNCPPFLPLMKMLPEELKEL
SIELIRTVPGTVIDDILPDKLKKLSINFCDNIKLPVKLPVNLKSINLSSR
TPIAWEIPTCNLPAHIDISTDGYVKLNPEFLTRSDITFSNKPAGDVLSFQ
PGDVVYGLCKARDRVNTLVNSLYYFSKDI IQNTLTDVWDRKNRAVFN
KDEKIAERLNDVQRGIFFRFLSQHKYINITEKYSDLNSNEECWIKTSKA
GLEFQTRLRERSVIFVIDNLVDAISDIANKTGKHGNSITAHLELRVYRNR
HDDLKQNVKFFLNGEAISHEDVFSLVGWDKYKPKNRNR
> hopZ1 Psy A2|Genbank: AAR02168
MGNVCVGGSRMSHQVYSPDRADTPPRSERNTPDRRQRAAGDAERTQSMRL
QQKINDLKPYVRHARGPIKAYGQAALDRASGKTSVSFAELDATHLDAMV
YIENQRNPNGLNLKHFDRHKELIQALQSDGPSAFRAIFPQTCPETGQTLKH
HVMADVRLHQQGAPTIIITEPAVIVGARYQQL QRHNLTELDLSESGVPLS
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MKRPDGRMAGRNVNSEGHSEANLVQRNQAFRVKRRRELLDDETPSNTQFSA
SIDGFRLQEIKRVLAEEQR
> Q8X2S5_ECO57
MRLSALYLMKPMGVFYPAAVVGDCLLSYSFMGLITALKLFAGCSVCFR T
QVKHNRKRVRFRTKYLNVSFLLVQEISSARQSLFSVQLH
> P0A0W1|YAV4_XANCV Hypothetical protein avrBs1.1 - Xanthomonas campestris
pv. vesicatoria.
MEREMAHDERLHVHCGMGLGRTTIFIVMHDILRNAAMLSFDDIERQRKF
NPGRSLDNNKDVSDKGRSEFRNERSEFLPLFYEYAKQNPKGQPLLWSEWL
DHNA
> gi|53722548|ref|YP|111533.1| acyl carrier protein [Burkholderia
pseudomallei K96243]
MTAGPHLSDAALAAAKTLLAGMLGVPEAQIAPPQRLDLDLAMSLELIE
LAMELDERWNIRLDRARLAEVATVADVAALLGAAARADDSGGA
> hopAI1 Pto DC3000|Genbank: AA054440
MLALKLNTSIAQAPLKKNAEAEELRHMNAEVRHAHTPTRFTLNHRAPTYEV

AQSALGENHGGWTA VNKFKVTESEVFIHMERSDSRSKGFAGDKIHLSVA
PQHVASAFNAIGKILQADDS PVDKWKVTD MSCASSDLQPEKKRVTQGAQF
TLYAKPDRADNTYSPEYMGKMRGMISSIERELHTAGVQQSNNRPASDVAP
GHWAYASYRNEHRSERAGSSSQANELEKEPFFQLVSPDVAASPVKSGAS
SRSLMPPPWTR

> gi|16764755|ref|NP|460370.1| secreted effector protein [Salmonella typhimurium LT2]

MKPVSPNAQVGGQRPVNAPEESPPCPSLPHPETNMESGRIGPQQGKERV
AGLAKRVIECFPEIFSWQTVILGGQILCCSAGIALTVLSGGGAPLVALA
GIGLAIADVACLIYHHKHLPMADHSIGNAVFYIANCFANQRKSMIAIA
KAVSLGGRLALTATVMTHSYWSSGLGLQPHLLERLNDITYGLMSFTRFGM
DGMAMTGMQVSSPLYRLLAQVTPEQRAPE

> Q8XB62_ECO57

MSIKNCLSLINNALNIQKTSYSLTKMEQAGKLLNRKITPENTPPMLLSY
RNADLTQEKNI TERVLSIFKIKRDFVAVRIQNNQFTDLKNKKIQGHQNTV
ASVMDWYNPQKNALGITMGTTPRKSADIAKEEHRNALNFMIMEKNTFHEKI
LNSNDNLQKSYSKTEDSSWVAASVGSLLDKGAKVYPDTSCSLRLGEPFIF
TLPESVRVDVDIYPLKK

> Q8XRI6_RALSO

MRPLSFPRFFSSTTSTSRRTTAPHTTEATPEPAAQPPALPRARKTSNLP
LRGLLDSRTAKYEKRTMAKLSDDTELHQALLGQRPGMNGRMTRAVHQEAKR
RMDSGQWNPQPAATQAAHAPTSPPLPEAPKTSHPGPLRNLLDHHTAKYE
KASTRFADDARLQQVLLGQAPGINHRMTRAAYQEAKKRADHGAWNPPPA
APHPDGTETTAHADHAQTSAPAPTQMLALDNKPAQDANRPPSRSSMRS
STVHPEPHTTEAPHAAPAGPVIDPDTGALNKANLRKLVNDLTHALPAVPQK
GSQTRKLSQALKDQLDAIATIAADGSRKPPHETGLAVRDAFAKAAQAASQ
LSRNVGGDLADVYQGIAALLNEFKRTHLSASAHDMVM SHYANKEANLER
KAPGIGQGGKGSNI VSTTTGGLTYSLLPKVG YTGPDISVGAGGGKGRIF
ADDDGDIHWPSGQAYLRASLGGELGKWAARLTGRD LLLAGDTWFEHNDL
GEMVKLVANRDANRSWMRSAGPNARKVRQALETLVNTLSTAVGRNYTESA
GKPLYLNDAKIAKGFNTFKMTLLAAAIDEKLEKMG SASRFGNLVSKAYPS
TVEVLTQRLHSGGEQPLPLPPRHDPDSVGYADGALYRQATASVDASIG
NQTHGGTNLEAGGIFGLNLRGNVAQYFMEFGDAPHAQLDPGHQKDYRSVF
KQHQLDDACNGTTPAQLYLYDKMRRTLQIDMGTPAFPFKTEQHLYG
DNACVPAQFRNAIAHASREQLLHVNEQLEQLKQTYLEFVASASAVLSKTD
KFMPAGAGRTLSDSREAAFNLINRGIWQGRYPRKDALAHPEAFIAKSHAA
LSLALGCAGTHMSVIKQMAQRHAQDPHPQDPNAGNEG AHPVDDNQAAI
READSTYKTVREMKD KTYLPLKNYDVRTKSPLKEAGLWQRWDTALRAQAS
GGAQAGLFNTIMSLRTRKSTQVPLGDLTGTISVSDSAGQVLSAEARLLY
ADHQLNPSRTGKFWQLTFTAQGGAPITGALINLAVKAAIEKFMNMRLED
EKFDPEHII RQAQGLLFDITDGTSIVVKLRQAPDVEHAAMQLQYVRVLRN
KSSGPNVSLSIPTPVGAFTPSISHNDSGQSLAGEIVGTDKSYLIMQHPAF
SKVVDPFFARIAADPSNANA IAGELRQALDADPALRNRYLASPTMMADV
KEHFDAMAELAAAAENRPPRILNEFLRYATEPFAR AANVSAQVASHAP
GSTANGGDPFKIARSPLDERVSADTVNDLQ GKREHLQGLKTEARADYLC
GAEGRP LLEAFTKIVGNMRAINSAAFFHSNPQNI GFRSMLRDPRALAREN
KRIDAALNGKPESTGV LNRVRAHLQPDRINLKEASVTELRALAEPNPQPG
QATGRRQRQIAEAAQRELARREQLGAALPPSGGGAPEA

> Q3BY60|Q3BY60_XANC5 Xanthomonas outer protein X - Xanthomonas campestris pv. vesicatoria (strain 85-10).

MEIKKQQTAGPSSLAPLHDIHTDNAPVADATSPTQTPLHPSLAALTPRSR
SRASSADSEHGASVPSHDTEPQADSPERASGPSTAATLAARANAALASG
VQQAYAAVSKGASNLWSLADLRTMLQIHADDP AFLQMV RHTDPEQSAPHT
LAACRQOITQLRDAIEAATGLEARFRQQLLGD IKAVEDALQPLE HGT PAT
GRALKSLANLVNLWPLMVPSPLLGNQAKTFAYSIAAATKGVMTLSASALR
PTADGLPFP LMGGLGRDANEMHFYSVLLNGLFLTTEL PKKFGT PSMRHQ
AEAVENNLGF AAAASTACAAMVLT PFLWNSLNV LGNRLQHKLSHLGAGIA
ENAGFQSQAQRLRRLRTPGQVSAQLRTQLNEICAALEHGREA FQQARRDF
TDPSQGRELTRTLNAQCTH LLETLDRC SKRLS AALQVDQDQ PATL PRQVT
NHDIAPKLALALLGAGVTGLTVYLIQPDRI GTVDLLADSVVV TAVMMQSA
VNAHATRQDAMERFKAMCSGSLVMALALGVEKLSKTFADKSLIEASSSSP
YYAGAIMSLMSMTMPGPMARGAE LAMNWGGGQIMRVFRGPDGTALATRMP
SSPEELIQHVQDTARYVQSLSPEQAQEQYAQT VADSALQGIEDAGAAQTR

PASSVTITEITEANEEEEALAAASASPEQRSPARTHPSPDQAAASTV PSS
> Q8X2S4_ECO57
MPFSIKSIFSGHTWHQPEISRPIADKSSTKNCILDSTTCNVDGFTVFNRR
SCSFDMRPPGSADRTPLRLSISEVAWMSKI IETETNNTNKS
> A3T0G1_9RHOB
MTTALGCIADDFTGATDLAGLLARSGVRVSLRIGVGPSEPPADPAAFEVIA
LKSRTAPVGEAVAETRAALKWLQAAGARRFFWKYCSTFDSTAEGNIGPVA
EALMADLGTDTIYCPAFPENGRSIF MGNLFGVGRQPLAESPMKDHLTPM
RDSNLVRLLEPQVTRPVLADRLTVARGPQALRAELEALKAQGVAVHVVD
AVANEDLAVIAEACRDMPLMTGGSAVAMPALYLADGTLADAPRAEAP
RLDTGTIVLSSGCSAMTNKQVADYTSRGVPAFQLDPLALAEHGPQEALDW
LAQQDLDKAPLIYATANPDSVRAAQEKLGVAGAGEIVEATLSACAVAARD
RGARRVIVAGGETSGAVTRALGVTQLD IGAEIAPGVWPWYCCSGGHQVAL
TLKSGNFGAETFFSDAQERLGS
> gi|21231082|ref|NP|636999.1| avirulence protein [Xanthomonas campestris
pv. campestris str. ATCC 33913]
MGLCVSKPSVAGSPDHYATHALEQTPPSTPSSSEAPMSPSLHGLPSLGAR
RARRAGAGPTLQPHEVQQAAYQLGMRLNDRPIEDARDRQRLADATATVHE
TRLALHLGRGNVSDLRSLNRSATYSALSYTLSRNDQNSWAGSALALGA
GNCDENAAINARQHAVRMEDGGQMMTVRDYGVPHIYALYQPPGAIEAEES
AVVLDSWCDGPAVRLGDSRWAETYRTTTTVVERFDKPDIAEALDRNTNGFR
AEIEDPQTTRHAYARDLGAVFLANHAKHAPGYIFSSMPVIAPDLAEGTRQ
RLQEYSQGTLEDLAADAARQAYGLDEAQFISPRTTTAAILEDALERLDALGR
PPLSW
> gi|51591586|emb|CAF25390.1| yopM; putative targeted effector protein
[Yersinia pseudotuberculosis IP 32953]
MYGFVCSKELDNKNI FRKAFNMFINPRNVSNFTLQEP LHRSSNLTEMPVE
AENVKSKTEYYNAWSEWERNAPPGNGEQREMAVSRRLRCLDRQAHELELN
NLGLSSLPELPHLESIVASCNSLTELPELPQSLKSLQVE NNNLKPDL
PPSLKKLHVRENDLTDLPPELPQSLESRLVDNNNLKALS DLPPSLEYLTAS
SNKLEELPELQNL PFLAAIYADNNLLETLPDLPPSLKKLHVRENDLTDLP
ELPQSLESRLVDNNNLKALS DLPPSLEYLTASSNKLEELPELQNL PFLAA
IYADNNLLETLPDLPPHLEILVASYNLTELPELPQSLKSLRVDNNNLKA
LSDLPPSLEYLTASSNKLEELPELQNL PFLAAIYADNNLLE TLPDLPPSL
KKLHVRENDLTDLPPELPQSLTFLDVS DNNISGLSELPPNLYYLDASSNEI
RSLCDLPPSLVDLNVKSNQLSEL PALPPHLERLIASFNYLAEVPELPQNL
KQLHVEQNALREFPDI PESLEELEMDSERVVDPYEFAHETTDKLEDDVFE

> gi|16520035|ref|NP|444155.1| NolX [Rhizobium sp. NGR234]
MSASNLLPMISSNPAQFAQASLAKAFAPRVAQG QQSVLSFEAMLSTNMLD
RIGPLASREDLPPDAESTLEDLQKDLALLPPHMRAAIESMDQTPQSAV
VIDDHVAPAPIQSSRITWNGGSLTKPELQIVAVLNRHKDLCPLSWESLE
AKANDPSTPPDLKAAIEALLQDPELFYAIGSQDGRCGKISAKDLSEFS
KHHPQVA AFQESQAQSYAQNYIPSDSAENAQPSVMTENDALRELYRYSEY
LPKNLSLADFKQIVDGEAKTGKCPPQVIAAAQYF VSHPEEWKQLYGGNID
KVHKEDFLQVASSMSLTQAELDTLKTINSHQELFFGSGDLTRDKLASMA
DDKSLDPKVREAAASQLLSDPLLFGLLNNAITGYKTHHGFFDFGGGHTVDS
GNVSKEDFGRFYTNMTTANRTVQQPKFHVPEEAAQNAVADMKMGADQP
DIKSPKNGGALMHVVDVLRVGSKVLDDWAATAVGVLSFIPGIGQVADLV
SMTLACEAQAANLLRTAITGGNMKQALIEAGIGVA AQAVGLVSGPGVKLA
IRNGLARKAIEEAATAGINLPLSMAQHAYEGYLNLDL KARLAADHPA
> Q8XA03_ECO57
MKVRNPEQISIPASNTTKDPGLTNSQIIRMANLVKKTENMNI FEELWETL
RNLFQSDKHSQTAAARQILKDAFYFQNSDDYSKYFTGAVD GKARDKLTHWL
IKFNELEKEYAKDPENMAAKASLSPEGLCVSFFIGDEAIFLTELQLKKST
RTGGIDL SNAYFNGVVICGIDCLEV DLSNAETNNSRWYD
> O34208_PSEAE
MHIQSLGATASSLNQEPVETPSQAAHKSASLRQEPSPGQGLGVALKSTPGI
LSGKLPESVSDVRFSSPQGQGESRTLTDSAGPRQITLRQFENGVTTELQLS
RPPLTSLVLSGGGAKGAAYPGAMLAL EEKGMLD GIRSMSGSSAGGITAAL
LASGMSPAAFKTLSDKMDLISLLDSNKKLKL FQHISSEIGASLKKGLGN
KIGGFSEL LLNVLPRIDSRAEP LERLLRDETRKAVLGQIATHPEVARQPT
VAAIASRLQSGSGVTFGLDRLSAYIPQIKTLNITGTAMFEGRPQLVVFN

ASHTPDLEVAQAHHISGSFPGVFQKVSLSDDQPYQAGVEWTEFQDGGVMIN
VPVPEMIDKNFDSGPLRRNDNLILEFEAGEVAPDRGTRGGALKGWVVG
VPALQAREMLQLEGLEELREQTVVPLKSERGDFSGMLGTLNFTMPDEI
KAHLQERLQERVGEHLEKRLQAS ERHTFASLDEALLALDDSMILTSVAQQN
PEITDGAFAFRQKARDAFTELTVAIVSANGLAGRLKLEAMRSALQRLDA
LADTPERLAWLAEELNHADNVHDHQQLLDAMRGQTVQSPVLAALAEAAQRR
KVAVIAENIRKEVIFPSLYRPGQPDSNVALLRRAEEQLRHATSPAEINQA
LNDIVDNYSARGFLRFKPLSSTTVEMAKAWRNKEFT

> Q8X2I7_EC057

MGSLFNIYKDFIPTLGMYSGLK ACHEKNNLPFDINTEIETIQKQINYDIN
HLNDGLIKRNLNLFILHLSNPDNLELTLNRYSSSTEQIIGRTRKRNGLHEF
DDGDLKIIIFNRQDDNESVLTVDKDKDKDKDKDKDKDISSHHCNVKTEQLQ
QFIKIMEQKAQLPIYIDKNNLKESIFSVLHNDPQQVDKQHLPCFKFLKH
ACKSSNSFEVKLDATHQYQHLNFMISFDPVENQLTIRDNNNKTETFSFT
NLQWENLLQYYKENHQPNIAQS RNLTDNIDKIKNTISTSEIIECASPEI
RSSVLNDLYSIANFLPDNNLTPNESWKRFCETCERFYVAQKSITGDKSER
LTRKLSISDAGITMTFKIGDVVINTISTAIPEDATGQRCIEGLNLAEMDL
TDIDLSKMALRNVFNFSILRNAKFSGTICEGVDFTDCLRNAEFENASL
ENNDFRKRVRHLTYVNFKANLRNSNFNGKVLTVGVTFTGSDLSNAYLEHID
FTTVILYETSNIPIPGTPQIPGT PKVILTGAILNYSDLGKDLSEYNLT
GILCMYTNSANLTPNCKISNANFSNAKFYNTNCTGANCSNIFLDYAWFD
NTIFIKTLFKNTCFYNVRAKNVYLEGAYLNNDNIVNQANNSTEKQSIDST
DKQANDSTVQQSIDSTVQQANDSTDKQANDNIDKQVNDSTDKQAKNSTEQ
QDSNSFNQARLKKEVNRFRSIPGLTSYQPTYIVEE

> gi|17548381|ref|NP|521721.1| hypothetical protein RS05518 [Ralstonia solanacearum GMI1000]

MRAGIEADIVLKGRIERNIRAPAPSAAPPTPIDPDRAVSPPVGGHQAVR
PAALADLAKAPAAVSVDTAGSFSRRAALPAAPADPGDVLNALKKRIDVW
KQLVVAEQDPRGRADSPEEEVQYASPVMAVWTGLDALALRMQGRATDS
DANQKAEVMLLTVLTKASDVVLDVDRDRMLRAEWAQLRAVQADTAEAESGPA
EEEDPGPDFEQLPRLWDDLRQVRDALDEVMKRFKSSSEPAAVRAGLQPIIM
PAVTVQQSFCRTAMQTAHGIIISDRVGLLMLAEWKGLPGVVARVAGELRQ
ALRHRREEVAAASSALEAEADDSWKRPRPGVQSADRPTLQALLKHHEVLQ
DYGRQLDQVGHDMCLDAATMIEMNDADGLWQCMMDIAHSIAGYQEGLEAL
CRAAGNVRPARVEPPPLRVAEPPPAPPAQPSGSSQRKHGKPGKQPGAIA
GAVPAPRPVSVDKRDTQKTADGLLRRYPVDRKTLAQFDGDLVRIAQSLG
RDTRTLQRELADPRRDAAITADYLRVAVQDWLGDVQKRGLLREAVAALSS
QDVRVQGLTGRIKALERIERRLDTEADLLKRDACPRAPHLKRLNNAKEN
PIRSVQPARLPAERPNDRLGTLFEMRIALKPLSNGQQVAPWVVIHTRE
PVTADMLGTMPSGDFAAVHLKTDWEKNLGRWEAVMRALGYPEAKVHRGP
IGMELLGQLFARVKLPASG

> Q8XT13_RALSO

MGNLQIKASSAPYALLSDVSPDPSGSPPTPKLTRVASPPQALADLPTKG
TGKRPQVSAQPSKATTGPSRTVSAELPLSSPAPLQLTSLLPSESGET
PEKLGAVPISGNLQIKNGQLTSNNETIRSLIHYLGAADKAFANQANLNGM
QVTIRPNPYATAGHEALKEYCSVETALVHADKPPRRKPSKDPLRQPLRQT
PPPSQLKSEDIENGLVMP LLTSVIESGPAAFGTNDRIMLSGQEVVPHALL
AALAPRVEVNDPDLQAFNSKLSANTQANAKLGAATLLQMETHKTFALKE
LGMSLAVSSGLGTAWELVAAEGIKGGLKHMGLTAKEYILAAAGIDSSSAI
GIETSDSAIVLSAVQSMNRATASFLRRVWDALPAAVAVGLKSAVGSYPNN
LLQYMSTGSYAADLALNSVTTEVAIILAAASGVPGEVKKNEANLQAAIVEK
LRDGLLAVPPREPHMSPEQ YTEIVEKHVQALTRRALDMSPGDGIQAQKSLA
FATMVGLIPLILGNKVTNLVAESALRIVRSTIFNPIESIGMNALVLTSKI
DIPGLMSSDATKHAQTVGRILQEAALGKPLQDGEVHKIFHQWDGLTLGGR
AILNGMSATMDAPPEKVMSSMLKDDSPPLSQRIAYESIDYDRV

> avrD1 Pph race 6-1448A|Genbank: AAZ37987

MQDLSFSTIENHLGPAKDRFFGDGFKHVEYSARHV NLTESEANASISLSY
PANWSKKNDSGELIPLHSSIDALTIINLSQDILLNRFKSIDHCWVRRIS
IRAGKKPEEDLRNINAKITKESQGLDSQGDNTLIFGGNVGTMVQLEFII
PAAHEVDTIKDSKTEKNCYSLHFKNRTQFIDDIIFYSPINAISKLFVANDN
EPHFPLPGGIEANYPNIINPVDSLVSQAQIAQALLYKLDGLTRGESNTLWM
RNLNIIAENPAKRRAATRLLVTELKRANIVSLKGEN WRVAEVAGHMNGIT
FSSVAHLLPL

> SOPB_SALDU

MQIQSFYHSASLKTQEAFKSLQKTLYNGMQILSGQGKAPAKAPDARPEII
VLREPGATWGNYLQHQKTSNHSLSLHNLNRRDLLTVGATVLGKQDPVLTS
MANQMEELAKVKADRPATKQEEAAAKALKKNLIELIAARTQQDGLPAKEA
HRFAAVAFRDAQDKQLNNQPWQTIKNTLTHNGHHYTNTQLPAAEMKIGAK
DIFPSAYEGKGVCSWDTKNIHHANNLWMSTVSVHEDGKDKTLFCGIRHGV
LSPYHEKDPDLLRQVGAENKAKEVLTAAALFSKPELLNKALAGEAVSLKLV
VGLLTASNIFGKEGTMVEDQMRAWQSLTQPGKMIHLKIRNKDGLQTVKI
KPDVAAFNVGVNELALKLGLKASDSYNAEALYQLLGNLDRPEARPGGW
VGEWLAQYPDNYEVVNTLARQIKDIWKNQHHKDGGEPEYKLAQRLAMLAH
EIDAVPAWNCCKGKDRGTGMMSEIKREIISLHQTHMLSAPGSLPDSGGQK
IFQKVLNLSGNPDSEPNTEGGAGNKVMKNLSPEVLNLSYQKRVGDENIWO
SVKGISSLITS

> gi|16764946|ref|NP|460561.1| secreted effector [Salmonella typhimurium LT2]

MPITIGRGLKSEMFSQSAISQRSFFTLLEKIKDFFCDTQRSTADQYIK
ELCDVASPPDAQRFLDFLCKLYELSSPSCRGNFHFQHYKDAECQYTNLCI
KDGEDIPLCIMIRQDHYEYIIMNRTVLCVDTQSAHLKRYSDINIKASTYV
CEPLCCLFPERLQLSLSGGITFSVDLKNIEETLIAMAEKGNLCDWKEQER
KAAISSRINLGLIAQAGVTAIDDAIKNKIAAKVIENTNLKNAAFEPNYAQS
SVTQIVYSCLFKNEILMNMLEESSHGLLCLNELTEYVALQVHNSLFS
LSSLVETTKNEAHHQS

> gi|28901182|ref|NP|800837.1| putative exoenzyme T [Vibrio parahaemolyticus RIMD 2210633]

MKVCRihtENIGSDLKINSRHSFRIHSINSSISEKQLLEKLKSCFPSAR
AINNITTHSQRVSSLSAAEKMAVNLYSGDSYESLNRLKRSQSMTPAEQL
LDIGLSKAVAKEPLDVLTKTYRGSRLRDAFGSVAEGEFGVDPAYLSTSRD
PEIACEFAEEHKRSFAFSVIFGVSGFDMALVNGDTVEAEVLYPKATPMRVL
LRDVNKGKESRVLEELSSETQGHVPALLDALDLAK

> Q12HD1_POLSJ

MADNRWPDGLLLAYYGDFTGSTDVMEAFSAAGVPTVLFRLRPPTADWLKR
FPEVRCVGLAGQSRGRSPDWMRELPQAFASLAKLGAPILQYKVCSTFDS
SPAVGSIGRAIDIGVPLMPGNWSPMVVGAPRLKRYQAFGNLFAAVDGVGY
RLDRHPTMSRHPVTMAEADLR LHLAAQTPRRSELIDMVQLRTGDAAARV
QALAGADVPPVLLDVLDEETLAAAGRLVWTQRGRGLFTASSSGLQYALAA
HWRSQGLLPEQPSLPVAAPVPVIAVVS GSCSPVTAQIAWAQGGFQAER
LNLPRLLDARESEVEIERVVAAVGAIALGVSPVLSAAGPDDAAVRQFD
ATATQAGLARGEAAQRVGEGLAEVMRRLERAPLQRIVVAGDSSGEVAS
ALDITALS SVAGLAPGAPLCKAW SERRERDGLEIVLKGGMGTASFFGAV
RAGRLLD

> Q1YN89_9RHIZ

MSFWCRNAMERPPFGSCICMQEPVRHQAGSYSMILGCIGDDFTGSSDLAN
TLAKGGMRTVQYSGVPTGDAAPDVEAGVVALKSRTIPVAEAVRQSLEALA
WLRSQGCRRQFFKYCSTFDSTDEGNIGPVGEAIARELGAGAVIVCPAFPA
TGRTVYQGHVFNDRLLSESGMENHPLTPMRDADLRRVLRQTDAVPVSHV
PYGVVAKGEDAIADALRQAGADGLCFVITDAVLADLHATGHAARDPLI
TGGSGIALGLPENFRAQGLIGSSTALWTVGVVGRAAALAGSVSTATRRQVG
VHRDAGHPTFELGADAVMAGEVTAASL TEWVLAQSGVPLIYSSADPETVA
AAQQRHGKEAVATAIERLFAATAAALVEAGITRLVSAGGETSGAVVTGLD
VQSLEIGPEIDPGVPAVRVEGRELALALKSGNFGADFFAKAAARLGGEA

> gi|28868583|ref|NP|791202.1| type III effector HopPtoM [Pseudomonas syringae pv. tomato str. DC3000]

MISSRIGGAGGVELSRVNQQHDTVPAQTAHPNAV TAGMNPPLTPDQSGSH
ATESSSAGARLNVAARHTQLLQAFKAHEGTA PVSGAPMISSRAALLIGS
LLQAEPLPFEVMAEKLSPERYQLKQFQGSDDLQORLEKFAQPGQIPDKAEV
GQLIKGFAQSVDQLEHFQLMHDAS PATVGVQHAQADKATLAVSQTALGEY
AGRASKAIGEGLSNSIASLDEHISALDLTLQDAEQGNKESLHADRQALVD
AKTTLVGLHAD FVKSPEAKRLASVAAHTQLDNVVS DLVTARNTVGGWKA
GPIVAAAVPQFLSMTHLGYVRLSTSDKLRDTIPETSS DANMLKASIIIGM
VAGIAHETVNSVVKPMFQAALQKTGLNERLNMVPMKAVDTNTVIPDPFEL
KSEHGELVKKTPEEVAQDKAFVKSERALLNQKKVQGSSTHPV GELMAYSA
FGGSQAVRQMLNDVHQINGQTL SARALASGFGGAVSASSQTLQLKSNYV

DPQGRKIPVFTPDRAESDLKKDLLKGMDLREPSVRTTFYKALSIGIQSSA
LTSALPPVTAQAEGASGTLTSGAILRNMALAATGSVSYLSTLYTNQSVTA
EAKALKAAGMGGATPMLDRTEALNNIRHPNRESLPHTFQKSTLSGIPRV
AENAYHMGRGALQLPTQMAVDTVRVVEGVLNAVASAREALKQPTKDDDA
LRALEEGLLDPR

> gi|1351732|sp|P14727|YAV1_XANCV Hypothetical 122 kDa avirulence protein
in avrBs3 region

MDPIRSRTPSPARELLPGPQPDGVQPTADRGVSPAGGPLDGLPARRTMS
RTRLPSPPAPSPAFSAGSFDLLRQFDPSLNFNTSLFDSLPPFGAHTTEAA
TGEWDEVQSGLRAADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPA
AQVDLRTLKYSQQQEKIKPKVRSVAQHHEALVGHGFTHAHIVALSQHP
AALGTVAVKYQDMMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRG
PPLQLDTGQLLKIARKGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASH
DGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPV
LCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIA
SNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALL
PVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVA
IASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASHDGGKQALETVQR
LLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQV
VAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNNGGKQALETV
QALLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPE
QVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALE
TVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLT
PQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQ
ALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQALLSRPDPALA
ALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAD
HAQVVRVLGFFQCHSHPAQAFDDAMTQFGMSRHGLLQLFRRVGVTELEAR
SGTLPPASQRWDRILQASGMKRAKPSPTSTQTPDQASLHAFADSLERDLD
APSPMHGEDQTRASSRKRSDRAVTGPSAQQSFEVVRVPEQRDALHPLS
WRVKRPRTSIGGGLPDPGTPTAADLAASSTVMREQDEDPFAGAADDFPAF
NEEELAWLMELLPQ

> gi|53722414|ref|YP|111399.1| hypothetical protein BPSS1387 [Burkholderia
pseudomallei K96243]

MRRVLLDRSDEVMRFVADRTGESRYDDYATIGLERDGRIVAGVVYQGHGG
PNVLMHFALDGSRHATPAFVCAVFTYPFKVLRCNRVTGLVRTDNHEAQ R
LDEHLGFVREGVMRAGASDGTDFILYGMLKAECRFLSGKYVEALRVELAG
SIDGVLASVHS

> hopD::IS52 (h) Pto DC3000 |Genbank: AE016873

MNPLQSTQHSITPLISGGRPDLAVGPQAQQSHPKRISPSQLSPGAHQAL
KRPSANAHEHQRIASLVRNALQDGTLLQFQSSNDKQVTKAPVCLPADTSTD
TDTDTVRTERLINNELTVQARLNDQSEYDIVSAHLHGSSRSI SFDVPSPP
PAHGSASSALSERTHLGRRCKNSQLSPPLAHXXXXXMSRVLSQDAVDGSG
LESPLLSSRAHSRPPSQPEPVHIGSVRRDSGSLVSDNPVVHALLAFAQAD
QAFPPQAASIDGVQLEMRPTRDIEQALKKFKDAFTVEKAQLMSVTNSSER
ADEDINADIHIPLLLKAI EQGAAAFGNASIGQNSAKAFLASCAPTITSN
DDVLSAFINQKLGDDDLKVRLGAQELLHVATKKEFQLGGLAG SIGVSSI
LGSAWELGASELLKNAIFGKNFSPSQYALQLAGIDSVPPLMIESMDTMCV
LAI IKMGKGEWMSDLLPKALKAGAISSVVSFPNNVLQYAGFKSRVGD
AANSVTTEAAIFGAASGIPPEVKESEELMRAGLFQSMKDGVM AHPGEGVD
TKETIERMTRHALDIAPGESTAVKSMGLASIVGMIPLIASNKATGLLSEQ
VLRIFRSVFNPIEAIALNALALGGRVNVPGLFSDNAKHARVV QTILAR
ASQQMEAGDRNISAEELHQMLAPRSEFLRHVGSIVNGMNASFEAIPALA
RKLGYGEAPLAERIPYQDLAVRDSRQPAP

> gi|28871237|ref|NP|793856.1| ATP -dependent helicase HrpA [Pseudomonas
syringae pv. tomato str. DC3000]

MTDESPSIDQLLKNLDHAMISERHRLRRLQHELRKKPDEAKLAQWVARVQ
ASCAQVTARRE SVPAMRYDDNLPIAAKRDEIKEALLKHQVLI IAGETGSG
KTTQLPKICLEIGRGQHGLIGHTQPRRIAARSVASRVAEEIGTPLGALVG
YQVRFEDQSDSNTLIKLMTDGILLAETQNDRFLERYDTIIVDEAHERSLN
IDFLLGYLKTLLPRRDLKVIITSATIDLQRFSEHFNDAPVIEVSGRTFP
VDLWYRPLTSEQDEEGNSVEEDLTVQAILATLDELA AFERSERKSPGDV
LVFLPGEREIRDAAEVLKRAQLRHTEILPLYARLSPA EQQRIFQSHPGRR
VVLATNVAETS LTVPGIRYVIDTGTARISRYSYRAKVQRLPIEAVSQASA

NQRKGRGCRVPEGLCVRLYSEEDFNDRPEFTDPEILRTNLAAVILQMLHL
RLGEITDFPFIEPPDGKAI SDGFNLLQELSAVNRENQLTFLGRQLARLPV
DPRMGRMLLEAAKQGSLEVLIVASAMSVQDVRERPPERQQAADQAHQW
KDADSDFAGLVNL WRGFEEQRQTLTASPLRNWCRRNFLNYLRLREWRDSH
RQLSLICRDLQLTVNKEPADYPKFHKAILSGLLSQIGQKADEGDYLGARQ
RRFWIHPSSGLGKKRPQWLMAAELVETTKLYARMVAKIDSDWIEPLAGHL
IKKNHFEPHWEKKRGQVVAFEQITLFGILVVGRRPVHYGPVDPQVSRELF
IREGLVRGEILSRAKCLSANTRLLEQLDELEAKARRRDILADEDTLYSFY
EARIPAQIHQTATF DSWYKTESQNNPQLLIMREEDVLAREASEVTAAQYP
DTLNLGDL SLSLSYHFEPNHPRDGVTLRVPAPL LLSLPAERLEWLVPGLL
ETKCIALVRNLPKAVRKNFVPVPDFIKAALQRLTFEGESLPQALGRELLR
MTGVRVSDAEWAEEAAQQLEGLHRMNLEIVDGSQKFLGEGRDLAELTARFA
EASQAALAVPQTAKSQPVQAKAFAVAQKTQQNIAGLSMTVYPALVEEG
GAVKEGRFSTQAEAE YQHRRALQRL LLLQQLAEPAKFLRNKLPGQTE LALL
HRELGRIDALVEDILLASL DSCVLEGEAELPRDGAGLLS LAERKRADWTE
HAERFAKLAL EILKLWHGLQKRFGKIDLSQAVALNDIKAQLSKLVYPGF
VRETPAAWLKELPRYLKAIEMRLEKLPQVQKDRVWSIELAGLWAQYQAR
ADKHAQEGKRDP ELLALYRWWMEEYRVSLFAQQQLGTMKPVSDKRLSKQWSQ
VDS

> CP0132 icsB IcsB, invasion protein 114564:116048 reverse MW:56420

MILKISNFIDASNKGP I RVEDTEHGPIILIAQKFNLDLDFRTLSTINAK
INSQILNEQLKNYRLENQKSL LLLFNLT LASEKSAESAF AA YEAAKNSIQH
SFTGRDIKMLN TAERFHGIGTAKNLERHLVFR CWGNRGITHLGHTSISI
KNNLLQEPHTHTYLSWY PGGNVTKDTEINYLFEKRS GYSVDTYKQDKL NMI
SDQTAERLDAGQEV RNLNLSKQDQNNK KIFFPRANQKKDPYGYWGSAD
KVYIPLSGDNKTKDGKISHNLFGLDETNMSKFI CKKKADAFRQLANYKLI
SKSENCAGMALNVLKAGNSEIYFPLPDVKLVATPNDVYAYANKVRQRIES
LNQSYNEIMKYIESDFDLSRLTQLRRSYLKSFNKINLIHTPKTFKPLSIS
LYKHPTENVSS EDDAVINACHSYLVKSAPS NMTRVLNELKTEATDKK EE
IEKSIKIIDYNSLKS PDLGTKLYIHDLLQINKLLLNNSHSNI

> Q3BY51|Q3BY51_XANC5 Xanthomonas outer protein B - Xanthomonas campestris
pv. vesicatoria (strain 85 -10).

MKAELTRSHSLSSLERIRHPESDMGND CDLEVGAQPKHSGFCQSEDSRLP
TTRPPRRRSTSSGATSPKSTVQSGHTDN SGLTPLLISLTGLQKPRHMG
LVRRESSRLVSADPVVHALLSFAQVDQFPFPQVASTDGVRL ELVSRRDPE
KALEEFKDAFTVETAQLMPAANSSERTAEQIDADIHIP LLLKAIERGSAA
FGPSALIE MADGSQISAKAFLASCAPDVMSNDDVLSAFINQKLGDEDLQ
VRLGAQELLYVATKKEFQ LGGLAGSIGVSSVIGSVWELGASELLKKAIFG
KNFSPSQYALQLAGIDSVPLI IETMDTMCVLAIIKGMKGEDWSLRD LLLP
KAMKAGAISSIVSFPNNVLQYTGFKSGLGDLAANMTTTEAAIFGAASGIP
PEVKESEETMRAGLFQSIKDGVMACPSEKMGPEEAIEQMARHALDVAPGE
STAVKSMGLAAIVGMIPLIAGSKATGLLSEKVLRIFRSTVFNPIEAIALN
ALALGGRIHVPGLFESDN AKHARVVQTILARASEQMESEAREITAEELHH
ILAPRSEFLRHVGTAVKGMNASFEVLPALARKLGYGETPLNKRI PYQDL
AVSNTSHQPAPEP

> Q8X3G1_ECO57

MPFSIKNR FSSSQVHYPEISGPIKDKPASKNCILTSTTCNVDSYTVYQKK
ACSFDMRPPGAGERTPKLKL SVTEMTWLSKTIETEIHN TKE

> NleC_Crod

MKIPSLQPSFNFFAPAGYSA AVAPNRS DNAYADYVLDIGKRIPLSAEDLG
NLYENVIRAVRDSRSKLIDQHTVDMIGNTILDALSRSQTFRDAVSYGIHN
KEVHIGCIKYRNEYELNGESP VKVDDIQSLTCTELYEYDVGQEPILPICE
AGENDNEEPYVSFSVAPD TDSYEMPSWQEGLIHEI IHHVTGASDPSGDSN
IELGPTEILARRVAQELGWTVPDFIGY AEPDREAHLRGRNLNLRQAAMR
HEDNERTFFERLGMISDRYEASPDFTEYS AVSNIEYGF IQQHDFPGLAID
DNLQDANQIQLYHGAPYIFTFGDV DKHNR

> avrB4-1 Pph race 6-1448A|Genbank: AAX121 08

MGCITSKPLVSSPQWHNSATNSENLETGQRSHKASLYGAMSGSPERSELT
WHQQSLVGVARWPDKEYNRDHVPLQMEYGRSFWNESRKIGSALANGEIQN
FEDLWEKARDWRCSMANHDENIFKKPRNSYNEFPFTTPLINQYNIKERY
SARTDGS LQKLDDEGLLPKAKEFLITDKIFGEPISLTKIVCSSDSSAHRD
QRRYSDLWSRGLDYGEPHYIQHTSSEEVPKILHHVNDL FNEVLQSNLST K
KALKFLGEIHWL AHAMPDERGSAKSEL CVRAIAQAKGLDLPPMKSGIV

PDLEAMTMSREQFIKQYPSMFDD
> gi|18677797|gb|AAL78294.1| XopA [Xanthomonas campestris pv. vesicatoria]
MINSLNTSHLGVDSFSFMQVNPDPQFQKFDNSNQSGISEKQLDQLLTQFIF
SMLLQDDNADDSFNSDKPTDFSPRTQMLMNVIGDILQAKNGGRLGGLSD
GGLNTSLSLSGDTASMQ
> gi|15605307|ref|NP|220093.1| hypothetical protein CT578 [Chlamydia
trachomatis D/UW-3/CX]
MSLSSSSSSDSSNLKNVLSQVIASSTPQGVNADKLTNDQVQVQVQTRQNR
DDLSESDVAVAGTAGKDRAASASQIEGQELIEQQGLAAGKETASADATS
LTQSASKGASSQQCIEDTSKSLSSLSLSSVDATHLQEIQSIVS SAMG
ATNELSLTNLETPLPKPSTTPRQEVMEISLALAKAITALGESTQAALEN
FQSTQSQSANMNKMSLESQGLKIDKEREFEFKMQEIQQKSGTNSTMDTVN
KVMIGVTVAITVISVVSALFTCGLGLIGTAAAGATAAAAGATAAATTATS
VATTVATQVTMQAVVQVVKQAIQAVKQAIQAIKQGIKQAIKQAV
KAAVKTAKNVGKIFSAKNAVSKSFPKLSKVINTLGSKWVTLGVGA LTA
VPQLVSGITSLQLSDMQKELAQIQKEVGALTAQSEMMKAFTLFWQQASKI
AAKQTESPSETQQAAKTGAQIAKALSAISGALAAAA
> SOPB_SALBN
PAQEAHQVAVAAAFREAQVQYLLNNQPWQTIKNTLTHNGYRYTNTQCPAADM
KIGAQDIFPNAYQKQKVCSSDNTNTQHATNLWMSTLSVNEKGDKTLFCG
IRHGVLSPHYVKDPIILRQVGAENRAREVLTAAALFSQPALLTKALQDEV VS
LRLVSVGLLTTSTIVGNEDAMVQDQMRWQSLTQPGNVIHLNIRNKEGEL
RTVKIKPEIAAFNTGVNELTLKLGLGHQASDNYNIGALHQLLGHDLRPEA
PPGGWVGWLAQHPDNHAVVNTLVRQIKDIWNSKLHHTDGNPEYKFAQRL
AILAHEIGAVPAWNCKSGKDRTGMQDAEIKREVISLHQKATLTPLASLPD
SDGQEIFQKVLNLSGNLEIQKQNTGGAGNKVLKKNLPPPEVLNLSYQRRIG D
ANIWQLVKGLSSSLVTS
> gi|21243950|ref|NP|643532.1| avirulence protein [Xanthomonas axonopodis
pv. citri str. 306]
MGCTISTTNNAPHSPRQEDAPPLPPQTRQSFVGVNGLLSDLPKRRRRGG
SLSDPDISLAGYLLSKAVIGDPVEPQDIPRLHKANNMQETRARFPYGRG
NVATDIAVSDHASSQHAQAAHDVFDLVRAAPPASMLTNPT LGHAVVSEF
VQGGHCAGYAAVATMRHVQKLQPEESVHYVQHNNQGHDWAESRVPDGHK
TIVLDPWAQGPVAFASDSRFAANAQHTQERLALNAKGDGDDIAAKTAAGAQ
YLLENCLPLTETHLKRKAQEFHCAPEEVWQPQPVVSDAFRRRRVRQSLAT
LTNSSELGLSRAEQSSKALKMSIKSACALGFGKKAASAAAEGIAAAAYQ
LCEQSQ
> gi|28868061|ref|NP|790680.1| ribD C-terminal domain protein [Pseudomonas
syringae pv. tomato str. DC3000]
MKVTVFSQISIDGKLTMGKGASSKPLFQNFDDDDMRFIHKFRGEVDAIMV
GRNTIVTDDPQLTNRYESGRNPIRIIPTTSLDLPTSASIFKSPEKTIIAT
SEQARDHEMVKHIRACGKEVLFAGAKHVDFTRLFPMLEARGINHIMVEGG
GHLNWQVFNLDLVDIILMQVPIIIGGAAT ATLADGVGYRDINMANSFTL
HALEARPHYNLMHFKRESNNRSPY
> A2I8A2_PANAY
MWHNINPYGAPPFSNRAPDGEPPAADPPPQGTAGGTPPLRDDPRAAPYPE
DEVLTWFSDCATIGGTDHGVIIDYGRALRRFSGFLSQNGLPALSAPGRL
DDPDRLRRAHVYIDRFPPQPTNKKYLIPSLNRLIDLVTSGADRITIRGPK
RPRRTVPDADEAQIKAAFPGRDGYSVNLTT SARAYS AWLHAN GRPGLSDT
DWLLSEQADADAAAYSWAHPGYAGRVNIVLAHLRARAGGEVPLIAKNQNT
RTIPLADQRLARAYRDVAEDRAGACGIVYKKGKDRDAIDRSITLLRSFS
AWRTARGLPALTDHLHDPTLLTDAQMFVEEKSQAGRALNTRRTLYMLNA
ALELLRASFPFGTPVTLPEEPADS FALPGSDWSGWMSLSLGGHGPADSD
SVFGLLAPLDSRERFSSDGLSGTPASGLPETGEVNRPGPDGAP FVSMRDA
VPPFRPDGVGFASGEGLSCLLDSILQCYHNIRRGHGAPRGLTDWLDGEVR
RVREALSAQGVLDLPARGEIDIYGGPGSYLAGAMGLRLQVIQAEFQEEP
GTYVRYTSHPEMGRSDAPLVRLLHTPGHFQPLWG
> VP1667 VP1667 putative outer membrane protein PopN 1783656:1784549
reverse MW:33232
MSIINSQIATNTKFDASVRNGLESS RADSAVKGSYRGETVVRVHNATQSLF
DAMEELTSLGSEKAEKDLTKRKIKDGGVVRVNEAHELVS DYLRKVPDLEKN
QKIKDLAAKMAGGNISTIAQLQAYLNGFSEEKSHQYLALKAVKKYLSANP
ESKHLALIDQAILKIEQNPDSWSQIDTEIRVSHFADEF SKEQEFSSSLHQ

LRGFYRDTVHSYQGLGSAYQDVVERFGEQEVSTAVDFMLQGMSADLSVQG
SNIDSVKLQLLMSMQKLTNTLQD QVGRLEFQMFKPERMSHGLSGF
> hopV1 Pph race 6 -1448A|Genbank: AAEZ0100000
MLNKPTLNIGIAPTAAQAAASHAVEGPTSPTPMRLDAAQQRPLPPMDAPSS
LRLRASGTSSGGEQAAQENSGSAAADNNGAARAQREPGIDPVRFSVKLM
VGTALSTGCRLTRHPDDFAKDPGGS IWAAMSLKHRSSQNDLDQGNRTVL
ERYGAYIPKDSNCFKAKADVTHDIPPGVAGQWNV KTRQVKLNPNIALESH
PAEVAGHEFIHCYTHPEFRGRHIDHRHWKALNEGLTTHLTKLPTPKRLL
PIPLAKDPYHGFKLATGDSWPAAAKRIEGAVGEDTLLKAFFGGDDDAISE
VAKAAAQIYPRLASSRTEQELYRAGMMRGSQQLAECYAGALLASGQPLPE
SWSRNMLPVFVSFSDMQPEQAKKARLQAEQSQERMGIIFDAFFSPDLKTQ
RQALGMLREDLLMHWENVVDPKGCPIEALALKATG KERCSSPPGRYRFHF
DQRTGQRQRHYLQSGARRFQGLLGGAEKLRVTGLQACKVKLAAGFLGPHQ
KHPQLHDIAQIKVLLPEHIAQFVEHRNSLDLSPVCGRRTRRGVWVSEVR
QGAADHEHQAGRGRHGHLRWDKIADAGTLNAVAHGVTPOWMLMLQ
> Q8X834_ECO57
MKIPSLQSNFNFSAPAGYSAPIAPNRAENAYADYVLDIGKRIPLSAADLS
NVYESVIRAVHDSRSLIDQHTVDMI GNTVLDALSRSQTFRDAVSYGIHN
EKVHIGCIKYRNEYELNEESSVKIDDIQSLTCNELYEYDVQGEPIFPICE
AGENDNEEPYVSFVAPDTSYEMPSWQEGLIHEI IHHVTGSSDPSGDSN
IELGPTEILARRVAQELGWSVPDFKGYAEPEREAHLRLNLRQAAMR
HEENERAFFERLGTISDRYEASPDFTEYSAVSNIGYGFIIQQHDFPGLAIN
DNLQDANQIQLYHGAPYIFTFGDVVDKH NQQ
> Q3BW96|Q3BW96_XANC5 Xanthomonas outer protein P - Xanthomonas campestris
pv. vesicatoria (strain 85 -10).
MPKIESTKQAPPDPAQLIQTAPTSPSGSGSAASSAASAAPSQGLGSLIR
PRRLGRASRANLPAASSTNAQDVMAALFAAAPVPPQGPDPFEVLSKASSRL
KRFNDLAQKRDPADIRALEARLESKSAIESARQALQALAE NIQKRMP
VDNVEEHNFLVPHFAVAASLHYGACEKMIQKMATFEGHVNTQRVEMVV
LSADAMRLQPPGFWLALRGHLLNALAAMEEVCQRIRSPMTGQGPDRDSLND
HLPVVRAMMGSCHEMOTVRGMLVEIHSRRLADEASECGLPQVLDGLREL
EEIDSLHHAEVGEALKHVIQVHVERFSSTEHSLTPEGLARCKKVLVGYAE
IRGRAGMQLCVDAALIEAGEHARDHLWPTMLDLAALADQQA IVDMCE
FAVQDRQLIGAAAAQAPASLTSSVPTTTTTTGKSSRRRARVRTPDA
SSSAAAPARRVMDERSAAQKQADEILKGRLESPLVAELGGDFIALAKRL
GKDTTDERLIGDSRYDAATAFDSARITMQGWFSSSERVLQLKGLRAGD
ARIDHLDTRLRLQRIEHDFKRREADALKTDPPRAPHLERLLAMNGLAR
VTSRRLREDDIGDRGRLEFVRIDHTPQSNIGNIPRPWFVHVHAK RPVTP
RRAARARL
> gi|53722553|ref|YP|111538.1| putative cell invasion protein [Burkholderia
pseudomallei K96243]
MSSGVQGGPAANANAYQTHPLRDAASALGTLSPQAYVDVVSAAQRNFLER
MSQLASEQCDAAQPAHDARLDDR PALRAPQERDAPPLGASDTGSRASGAA
KLTELLGLVMSVIGASSLDELKQRS DIWNQMSKAAQDNLSRL SDAFQRAT
DEAKAAADAAEQAAAAAKQAGADAKAADA AVDAAQKRYDDAVKQGLPDDR
LQSLKAALEQARQQAGDAHGRADALQADATKKLDAASALATQARACEQQV
DDAVNQATQQYGASASLRTPPQSPRLSGAAELTAVLGKLELISGNVKEL
ESKQKLFTEMQAKREAELQKKSDEYQAQVKKAEEMQKTMGCIGKIVGWVI
TAVSFAAAAF TGGASLALAAVGLALAVGDEISRATTGVSEFMDK LMQPVMD
AILKPLMEMISSLITKALVACGVDQKAE LAGAILGAVVTGVALVAAAFV
GASAVKAVASKVIDAMAGQLTKLMSAIGKMLVQLIEKFSEKSGLQALGS
RTATAMTRMRAIGVEAKEDGMLLANRFEKAGTVMNVGNQVSQAAGGIVV
GVERAKAMGLLADVKEAMYDIKLLGDLLKQAVDAFAEHNRLAQLMQQMS
DAGEMQTSTGKLILRNARAV
> gi|29840710|ref|NP|82 9816.1| hypothetical protein CCA00955 [Chlamydomonas
caviae GPIC]
MTSGVSGSNNTDPSLAAQLAQNASQAASKSQGQKSGNAQETQEAAAAGFE
DLIQETQTQGTSSKEATSQTTKSSKTDKSAKSSSSTSVASASSTVTAQAV
KGPKGLQQNNYELPQLPMPENTEVNGVVIKKGMTLALLGLIMTLAQSS
AKSWSSQFQQNQAIQNVAMAPEIGNAIRTQANHQA SATEAQAKQSMIS
GIVNIVGFVAVSGGLLSAAKSLGGIKSAAFAKETAGAAGSAASSAASQA
SKMATDAATTAAKTASTAASGVAGSAAQGAAKAAAGLTDDIAAATAKATA
GTAKGGGLFGKVLNTPGWKDKLTRGMNVVKTQGGRAAFAFRALSTSMQM

SQMVHALTAGIDGIVGGVMGAEIAHHQRQAGMAEAHAHEELKQLSSIQQQY
AGQAQQLQEQQSQQSFNSALQTLQNIADSQTTTSAIFS

> A1JQA7_YERE8

MAIGPVGNSRFLVGGQRDKSSAAQASDDADEAARGQGVINDNSSEYASMS
MLAASHVRRRGPTTDSKEEWTRFSEIILDAQADEKILRVEGALNNKLMTO
QQLHAFLLOQYFTDPSDLLMVLAALIHRSRLKRKQLEQLEALREOLEAEDF
DRSAQAGINIALVAKAFAQKMQQSAGNLRMLYREFLCYDGPAYLYEQWA
EEMVAQERENIIRYLARALACDLQALPLGNINVSEF GALFNRSRLREMK
SLDDTFRQRFSTDFAFINQSGENMLSKLFI SGIRGQENFNDSLLTFYSR
QLGALSTDMRARFLQILIIAFSILPTGIFSSLEEREHFIDGLKENMSHFM
EQELAMARRVLHDEEENIP

> Q3KHX5_PSEPF

MSDLNLTLRASLKSGEHVFADTLSFIAAGYDYQPQAFNNGGVENAAGQNEG
SCKTLGLALLEGLSDEEALLAFGEHYRSVVATPEGS DHGNIRALIQHGLA
GVKFEAQPLTRR

> hopPmaA_Psyr

MSPAQIIRTPHSFPPSFTGTSSSAENSHAQSPQQVLTRAFVASGELNAAF
GRTSTASEQDFTSLGLTQRELERKTLSPDIAELANQLAEAAKGDQGGH
WLGREDOQLTKGMIDRCKSQLAHTHASDASYDPLAQVCENLKTARLHQSI
SQMTGEAHAKVRGVPDLLALIQLDPDVLAEKPVGMTSYVNFSGFICMAKA
RTAELSEDLRSDPNEVALLLHPHADT ILELERLPDALAALTENCPTPTR
DDLRLSLAKETGELLQQLRANDLLPRSEEVSSYQGETSVRSREVVEPKLTL
CQAGGNGQQGLEASSARPESLRYAPTRAASSGSEARVPGQAVGGKIADDA
QKVAGLYAEKKRTNWTQANGVAGKISHKIQSLLGMRDAGSRVQAFVAFMA
DGKGRPGATMLDLGDGWMRATRVIKGEAALIDFQCSDGKVV DARHPGRF
PVL PQGNEREAFKTVLQELKFRGAETL SKVPVYVNRNTRGYV IPTHGYV
VAGHPNRGRKSGAVLYGVGGDPKRGVVALDEKLLGHLVGRSDSKTSSKLS
APVKA AISALAGASFATREDFYDAYCAVRGDAVDPLERHNEISSIYRLLP
LSTMEMWPKKADSYRVARPAAPERDLRAFENLPKDIGRKAQLKKVSNVDS
IDLLEAKRQFTLHQLYQDEMLGRNGTGVPSADFKPKVDAQRRDQVLVASTP
KFQRLPPHTTDKVGNCNTGASSLLQRAV DTYTEKNLPPPEKVTAASIFGI
GSSHLAIWDPLDGSSSNKSSKDR

> gi|34498029|ref|NP|902244.1| secretion system effector SseE
[Chromobacterium violaceum ATCC 12472]

MQEMNIKPDVVTQFLLSQGLVPEAEYFGNSHVLVGQRVKLLDCELVYRLE
DEELIICDFVAKQPVQGSASAVAAFIHLIHKIEKSVPTVKRVRGLFLESM
TRPELNQIRMRLSKVLEAQGATWRDIDGELWLVEIGLAQAV

> gi|27376898|ref|NP|768427.1| hypothetical protein blr1787 [Bradyrhizobium
japonicum USDA 110]

MSAATPLQAWLNRRARRRRDRWTAISIDPRAKRRLDSLHCLQWVLVAEAY
PGHSCL SARLWDRSTLLVGRWRVSHSGGLAVLRCAAPAHSLHFATEETIS
MNTEQLVTRIPSATSDLESS EPGSPAAPLWGETLAGVHTSAGAVASPEE
VLANWAAEDGGQHGDRQQAVSRTSAWRGTGDLNQLPLDSSRSLTALPAP
ILAEVRRNLNVDHNQLDSL PETLSTGLQRL

> A3HQ93_PSEPG

MMPAKRCTACPTPSGKPNTRKKPAPNNKRRSKKENLVTDLNLTIRASLASE
QHVFADTLAFIADNYSYQPQAFNNGGVENAAGQNEGSKTLGLALLEGLS
DQEALLAFGEHYRDVVATPEGS DHGNI RALIKQGLAGVKFAGQPLSRKA

> A0FZ98_9BURK

MAQALLGCIADDFTGATDLANMLVRRGMRTVQTIGVPDANIRIDADALVV
ALKSRTAPAREAVRQSLHALEWLRAQGCRRQFFFKYCSTFDSTNKGNI GPV
ADALLDALKDDFTIACPAFPENGRIFRGNLFVGDVLLSESGMEAHPLTP
MSDPNLVRVLQRQTKSKVGLIRYDTIAKGAEAIRARIEELKEDGVRI AIA
DALSDSDLYMLGKA CRNLPLVTGGSGIALGLPQNFHSADLLVYAGDAADL
QEIDGRSIVLAGSTSKATNAQVADWRASKPSFRIDPLALSRGEPVVERAI
DFTLNKNDETVLIYATSAPDEVKAVQKELGAAKAGRLVEDALASIARGLRD
KGGVRKFI VAGGETSGAVVQALNVRSLRIGPQIDPGVPATQSIGRECELP
LGLALKSGNFGTVDFFTKALKALDGGTQMSEF

> STM1401 sseD translocation machinery component 1486467:1487054 forward
MW:20592

MEASNVALVLPAPSLTSPSTSPSPSGEGMGTESMLLLFDDIWMKLMELAK
KLRDIMRSYNVEKQRLAWELQVNVLTQTMKTIDEAFRASMITAGGAMLSG
VLTIGLGA VGGETGLIAGQAVGHTAGGVMGLGAGVAQRQSDQDKAIADLQ

QNGAQSYNKSLTEIMEKATEIMQOIIGVGSLLVTVLAEILRALTR

> Q8XYF8_RALSO

MGYHFWAGWRPTSVADSAQASTSAPQAGAPASQPARPARAPAGSSILRGL
ARLRARWVAPPVPPFPPEIWIETIARGTKPADMQSLRAVSRVAVKMGAEASI
PQLTITHRDSGKRPPSVAGCLELNRLTLVGHFTDAYLQRLPASLTALDLS
RCEGPITSAGIARLLALPLERLDVSGCGLDAESARLLASHPTLTVLNISR
NAIGDDGAAALANPKLTSLVNVRNGISDAGARALVACAGLTKLD ISDNR
IGDAGARALAGSAKLNKLDAGDCGIGPEGARALAASQTLRLDLRYNEIG
VGGAEALANPRLTSLNVCGNALGSAGAALLAASAALTELDIGNNGIGNA
GARALGANATLVKLSVANNGIEEAGARALAASTTLTALDIGSNRIGDAGA
QALAANDTLVTLDASANWIGDPGALALADNTRLATLVNANRIGEAGMRA
LEASTTLAVLKT

> Q8Y164_RALSO

MKRLFRALGVSQPTRTYT PTTDTTSPAAATPESSRNSSPSSRSPPVRS
RSRNHPDLSDLPSRPRRKAEMLAESIQSARDRGVDPEFISYAETTLHNL
SHTQPSVMETNLDIRHLDITVQSYRYNNLNLAQAFNSREAFVASLVEGQGS
GRAERGVVRDYNLHHFAADVRRHEDGRRTTVIILEPASAGNQENLPGYTE
LASALRYNLGSQCRMVVEAEAQKSLSDCVAFALDFALAAAYQERRTTFDQ
WHENLAAYGTIADNGVQDK KYGPFDRGLYHNYGIHLIKGWGLPPVIFYKH
AHSRETLKGVKRPQGSLETDVSTGRNKDGAESLEERMEAFSDRHGFRPR
NISIEASRARKIRHALES

> Q8XE85_EC057

MMKTITKQPILFTDVPVADLRNSMKQDLNQNLIERLWKNKIRDFFLDSKQ
KAFKSIHKYINTLSVLNYSALTPDPNFNIDATSDLDSYLKLDLDFRLSPK
QKQTTLCFFWNKIASLPEPYNSTIKHNIIFYKDGEM LMIRGTISIVNEV
VKTYSLPIEKDDNGYDFSGLYLAHSNISGKDPNKDPDIDFGIDMGNCNC
SNVNFHEITYFYGVKFTNANCTNANFNCRFKKCDLTMNCTGAILDNAMI
YGKEKEPEMQYPEADQIIQRITYQKSDGNETKGMILTNCSCVKTTFNWAD
LSESDCQNVDFSEANLNTILPDIVRMKGTKLYRTDLFNPILKTEAESTE
EKDISPLAKIILDYIESDKNPESLNFEKSTVIKIKQD IDNFIFYNQHLK
KIFNRAMNLQEKISRKKYNEFFKYIQAEAKQYFKDQYKLTKNDYLLKVP
TAQLIAKYKMDQDLQQLLVTREIQDEIKSKIQDKIDELSKNLFNTMTETI
ENNFDDIFRQQSENMSNYEFVD

> Q08678|AVRV_XANCV Avirulence protein avrRxx - *Xanthomonas campestris* pv. vesicatoria.

MCDSIRVQFRSIQKMVVMKMKFFRSLGVG GSSSSRFQHHIPEADSAPSSK
ASTPPASPPDPSPNSAFSALPTRPRKKAELS DAVESRGLHAPPPLSVS
YANATLDQLRRNEPISESLRLMDIENLPHLVRSYDNRLNLLNLRSFDTPG
QFLHDLRWHKTGLPLRAVRLDEDPRRWHRVAFDVRNHESGHTTIIALE
PASAYNPDMHPGVFKMRENLT SQFGRKISFAVIEAEALKSIGGCVIFSLD
YALAAAYQERSTFDQWHKDLRKKGNIKGMTP ESQHLNELGVYLLKGRLLP
ANFYKHAHSRRTIDELEADQPGASGTDVRSGRAAVYKESLSRRLEEFQVQ
RDKTYSMSIEASRARKIRHALES

> gi|17546893|ref|NP|520295.1| PROBABLE TRANSMEMBRANE ABC TRANSPORTER PROTEIN [*Ralstonia solanacearum* GMI1000]

MADVMHGSRLALPVSLERLALPSRAMAYASPLIALALTLVFGLLLFALL G
KDPVAGVRVFLIEPLATKRAIGEVLKTVPLVLCALGLSVCYRANVWNIG
AEGQLIVGGIFAAATI IHFDTPPAIPGGAALLAVVAGLAGGMLWAGLT
ALLRDRFHANEILVSLMLTYIAQLLLLLYMNGLKDPNGMNFQSMVFD
AFVLPVTLVAGTRLHVGFMLAMAAAMTLFVFRSFAGYRLQVGGAPQAA
RYAGFSSRAALWTALLVSGGLAGIAGAFEVAGPIGQLLPSISPGYGFAAI
VVAFVGRHLPLGLTGLGAIVMSLFYIGGELAQSRGLPAAITGVFQGMLLF
FLLACDTLIEYRLRWAHR

> gi|16764754|ref|NP|460369.1| secreted effector protein [*Salmonella typhimurium* LT2]

MKIHIPSAASNIVDGNSSPPSDIQAKEVSFPPPEIPAPGTPAAPVLLTPEQ
IRQORDYAIHFMQYTI RALGATVVFGLSVAAAVISGGAGLPAAIILAG AAL
VIAIGDACCAYHNYQSICQQKEPLQTASDSVALVVSALALKCGASLNCAN
TLANCLSLIRSGIAISMLVLPQFPLPAAENIAASLDMGSVITSVSLTA
IGAVLDYCLARPSGDDQENSVDLHADPSVLLAEQMAALCQSATTPALMD
SSDHTSRGEP

> gi|28871892|ref|NP|794511.1| type III effector HopPmaI (Pto) [*Pseudomonas syringae* pv. tomato str. DC3000]

MINLTHIASLARAALSDSTKPKMERAINVASHIAGKVALQVTSLSLEQK
GLLNERQQKGLSMILKALSGKEPVNNVETHEGGGRFNLARAADFVASVW
ERDKSMHNVMSFLGVSDSKGKMLFSLGKKLADAMAKPEPGKDNSEATNAR
HAYFSSNLKLNKLMNDLTDQVFNKIRQSNQDRVRRPMPPEFWRPYGAQQQ
ARPQTTPGTRPQANSAPPPPKAEPASGRP DGAQQQARPETPPRTRPQ
ANSTPPPPPKAEPASGRP DGAQQQARPETPPRTRPQANSAPPPPKAEP
PRPASGRPDGAQQQARPETPPRTRPQANSAPPPPKAEPASGRP DGTQ
QQARPETPPRTRPQANSAPPPPKAEPASGGERPSTARPNNTSAADASAR
VGDSAPAKPPVKPLYEHLGLTDMVSDLSAVKKAYRDAAMKNHPDKNRGNE
AEAAERFKVISNAYKILSDPELRKAYDNGRINE AGNRA
> gi|34497721|ref|NP|901936.1| probable SPI2 translocated effector
[Chromobacterium violaceum ATCC 12472]
MAENGRSGLFALALKNREVQPSPAGEGKTLDHKRLVIGDSLSDTEGRM
RSKTLGIMPSSRQYYEGRFTNGFAWPDFAASRAFLDKPLVNYAEGGAVAG
KYSKLNPTFMFISNMGRQIKKHDFKPGDMAVLELGANDYMTF GKTNVDKV
IHVYEKQIGKLVAKGVKNILVAGVPDLSKTVSARSQKQKPGHADKLAALS
RQHNEQLRQSVEKLRERHRGEGVEIRFFDIGGKLDYLSLAGEVDYDTRF
NKHEGYIDLPRVFGAGDTRPLDTSRHRVHFHDEVHPSQEVHQILASHITD
FIREEYGRPEEAAAATDSRLERAGVYAGASSAEQPV
> gi|28871729|ref|NP|794348.1| candidate type III effect or HolPtoZ
[Pseudomonas syringae pv. tomato str. DC3000]
MKISGSTSPAHTSTNSAQKSSSKGLLSGLAKHFKGMLVSGNTSGHSALGH
YASSSSGSKGKAPVRDDYSNGPQTRLNNTPLKRALARELDRFGYGSSATE
SFDRSLQRKDKNPELGKV
> gi|4760784|dbj|BAA77400.1| translocated intimin receptor [Escherichia
coli]
MPIGNLGNNNISNNLIPPAPPLPSQTDGATRNGSSSLISSTGSLGSRLLF
SPLRSSIVDTVDSRDVPLPEHPLRFATSETCLHGGFEVLHDKGPLDTLN
QKIGSSVFRVEQQPDGTHAAIGVKDGEVSVTLNSSELQSLQSLDTEGNG
RFVFTGGRGSGHAMVTVASDISQAREKIIAKLDPDNHGGRQPKDIDTRS
VGVGSASGMGDGVVSEHTSTTTSSVRSDPKFWVSVGAIAAGLAGLAATG
IVQAVALTTPAPDDPTTDPDEAANAEEAATKDQLTKEAFQNPDNQKVNID
ELGNAIPSGELKDDVVAQIADQAKVAGEQARQQAVESNAQAQQRHDDQQA
KRQQELDLSSGIGYGLSSALIVGGGIGAGVTAMLHRRNPTEQTIATTHS
VIQQQTGGNTRAQQGADTTGVENASLRRDSQASVASTQWSDTSGDVVNP
YAEGWMSRNNPSLLAPEEPIYDEVAPDPNYSVIQHFSGNPNVTGRLVGS
GQGIQSTYALLASSGGLRLGMGGLTGGGESAGSAANAATTPGVERFV
> gi|15596906|ref|NP|250400.1| translocator protein PopD [Pseudomonas
aeruginosa PA01]
MIDTQYSLAATAAIPSEPIAPGAAGRSVGTTPQAAADLPQVPAARADRV
LNAPRQVLDPVRMEAAAGSELDSSVELLLILFRIAQKARELGVLQRDNENQ
SIIHAQAQVDEMRGATLMI AMAVIAGVGALASAVVGSGLGALKNGKAIS
QEKTLQKNIDGRNELIDAKMQALGKTSDEDRKIVGVWAADQVQDSVALR
AAGRAFESRNGALQVANTVIQSFVQMANASVQVRQGESQASAREGEVNT
IGQSQKQKVEDQMSFDAGFMKDVLQLIQQYTSQSHNQAWRAAGVV
> gi|50282917|ref|YP|052973.1| pilus subunit precursor [Rhizobium sp.
NGR234]
MSKIGTLTSAVGAGAAAGQNVAAKAGAGAAAFQAQIAELAAVSAEATARS
LLRTVTTELQTTKKAADERVQ
> gi|50121145|ref|YP|050312.1| putative virulence effector protein [Erwinia
carotovora subsp. atroseptica SCRI1043]
MAKFLFRSGSLDDFLALGENGQPVYASALQLRETLRLRQQQIADCLAIP
QPNEHGDRIDWYSPVD GNVTSWIAASEEEREKALSLETYKAAVADISQR
AQNAEKAGQKLVGVLAKAIQFPGANHVYLVDMGMPVLTWFVGNLDDKSR
LDALDCLRPPIKEAEPLFVAPAPAASAPTLPLVDPVPEPEPQPIVQDPDV
EPTPAPATLPTRPAFFRLWLLPAAALLAILSLQIRGCVSEQEKPTSEQA
ATVKPEKRALSSSTPAEPTPPPAPVVEKEIVKAAEPPISAPPVVSAPPI
VEAAKPEAPAAVEPKPEP VEPVVEQVPALPAGKDDLMPADAVKIGSIKFL
NGNWRVIVDSKAPITGRPPSLRYQIQNGKGTARITHGDGVTCRANVEAGL
MGSGNLIVNSRSGARCSDNSRFQMPPELVCKQGASGTAAECIGRYDADTVF
PMTIKRESK
> Q8XPN7_RALSO
MKIGRITGFALHGGDTASVSPPKSETASKGKSRAFAFAGLKPAAGTLEPT

QP SLRRTASVRMAVSDDAEPRRLERTLSCAGSLQRAPFGFDPQK YRARHG
KTLTEKYGSRQPARAKSGKKAIQPDEREKLPDGWWRTRVNPTRILVTSTG
IQTQADIEHCGLTKDAQAEPRSLDQLIDVARLRNEPRKFQYKWDMSANGT
FIIGNIHVQKPDGKGVHHLGHPTLVGGRRIPPEARISGMLYADETGRLIIN
NDSGRFSEYPDRDPSQLEAVAAFLRQHGLIVEVEWIDMQNGKAKKRPPIP
LVNDPQLDW

> Q8X5W5_ECO57

MLGHI SKFDGNNSLIKHG VV QGNNIVDFD LLRNFNNGG PGLNRENFIYISN
IFLNIKQRNEKNHSINMFREVSISGDIVSVKFYRNEKIECACDFMMAKDA
QGYIDLSELDLTSCHFVKGDVISKVSFISSNLQHVTFECKEIGDCNFTTAI
VDNVIFKCRRLHNVI FIKASGDYVDFSKNILDTVDFSQSQLTHSNFCECQ
IRNSNFDFHCYLYASHFTRAEFLTDKEISFIKSNLTAVMFDHVRISTGNFK
DSVTQLMVLSIDYSDIFGNEY LDGYINNI IKMIDSLPDDPAILKSVLAVK
LVMQLKILNIVNKNFIENMKKIFSHGPIKDP IIRSYIHPDEDNKFDNFM
RQNRFSKVNFD TQQMIDFINRFNMNKW LIDRNNNFFIQLIDQALRSTNDT
IKENAWHLYKEWIRSDDVSP LFIEIEDNLRFTNTNELTRNDNIFILFSSV
DDGPMVMVSSQRLHDM LNPTKDTNWNSTYIYKSRHEMLPVNLTPETLFGS
KSYDKHALFPIFTASWRANRIK NNGI

> Q4ZN85_PSEU2

MPSRFTHRPLRQLIAASSLVALVACA EKPTAADATPLQSSKVQTNAPAV
APTALVDDNLTIQPAVSFSEWQAGFRAQALKAGIRADVDFLAFAGVTP
DMSVVKADRSQPEFSRPVWEYLDGAI SAARVRKQALLSQYADDLQKIEQ
QYGVDRQTLVAVWGMESNFGSLQGTQSVIRSLATLAYEGRRPGFAQSOLL
AALEIIQHGDITPKMLG SWAGAMGQTQFIPT TYNTHAVDFDGDGRRIW
NTPADALASTAHY LQSSGWQRGQPWGFVVLGSGFDYSLADSTTRKSLVE
WQQLGLKQPDGSAIPVAASQQQAALLLPAGYRGP AFLVLDNFRAILKYNN
STSYALAI SLLSDRFKAGYVVG SWPRGDLPLSRSERIE LQTLLSARQYD
AGAPDGIIGANTRKAIRSAQQSLGW PADGYPTHELLENLRKPVGQ

> A1HLP5_9FIRM

MQKLAVIADDLTGANDTGVQFAK QGLTVEVLLG SQDAAATQADIIVIDTN
SRAISSAEAYRRVAQAAAIVKASGIAAVYKKIDSTLRGNLGA EIDAIMDT
CGQAAAIVAPAYPQNGRCVIGGYHLLNNI PLEATEIARDPRCPVKESHIP
TLIAEQTRRPVGHLSFKTLLKGEDATQAAL EELIGCGKEVIVCDAWEDKQ
LALIAAAAANLGPVLWVGSAGLAQWLPTVLGLTARKQSSPVLVIAGSVS
GVTRGQVAKLKQNAVVKGIEVDAR ALLAEPTRSGEV KRCCAEAAAALREG
YDVVIASGYAEVEVHTKAQGAALGYTAQQVGDIVAGALGEIGKGLASEL
TLAGMVLTTGGDIAVSVCRALGAASLSVASEVAPGIPVGF LTGGLCDGLKV
VTKAGAFGGEDALVKAVHCLKS

> Q7ACZ9_ECO57

MFPLNDLSLKTQSVQLNKITSNTESTIKQHELVSDDAIINELSSSELV SCL
GNDKFTPVSEDSNLLNMLSEFKLLREQC FRWGN YTL LF ENYGAYDKT GSI
TIEKSQEGEGLPIRHKLEFISTNIAELLDKLT KITDARLCKGFS DWASSV
KEGASNDLKENVDRALVRMFKCVKLHSNELNLSLGLSVPPLPEWIEML
SLVYNELDSIQVPE SCKELELDFNNLTFEPQVPDGITLISVNNNLISYID
SFPPKAKKIFICHNKLSEIPALPDTAKVDFDCSENNIKEIRWFPKNLKEAY
IEYNKIEVIPAIPGNLKL LCMKCNPIKEAFLMPWTLTGI RYEISQRKYIV
MNPADYDKYS DMVKKHVIDGEEFIIKYYM

> gi|29171493|ref|NP|808677.1| type III effector Hop01 -1 [Pseudomonas syringae pv. tomato str. DC3000]

MGNICGTSNHNVSPPISPQHASGSSTPVPSASGTMLSLSHEQILSQNY
ASNIKGYRTNPRKGPSRLSDTLMKQALSSVITQEKRLKSQPKSIAQD
IQPPNSMIKNALDEKDSHPFGDCFS DDEF LAIHLYTSCLYR PINHHLRYA
PKNDVAPVVEAMNSGLAKLAQYPDYQVSGQLHRGIKQKMDDGEVMSRFPK
GNTYRDDAFMSTSTRMDVTEEFTSDVTLHLQSSSAVNIGPFSKNPYEDEA
LIPPLTPFKVTGLHKQDDRWHVHLNEIAESSDE

> gi|28868090|ref|NP|790709.1| candidate type III effector Hop protein [Pseudomonas syringae pv. tomato str. DC3000]

MKINLPALRTTSSRVQICLTAVLLCTPLLFSAHAQAAGTASEQANVEVMI
RQLNALEAVAQRSVDLPQDPAQRYHLDY PRLVSDIARIRQGLQDYLSPSR
AQPRDPVELSGHYNVSGDHTP

> gi|12329070|emb|CAC05801.1| IpaD, secreted by the Mxi -Spa machinery, required for entry of bacteria into epithelial cells [Shigella flexneri]

MNITTLTNSISTSSFSNN TNGSSTETVNSDIKTTTSSHPVSSLTMLNDT

LHNI RTTNQALKKELSQKTLTKTSLEEIALHSSQISMDVNKSAQLLDILS
RNEYFPINKDARELLHSAPKEAELDQMI SHRELWAKIANS INDINEQYL
KVYEHAVSSYQMYQDFSAVLSLWISPGGNDGNSVKLQVNSLKKALE
ELKEKYKDKPLYPANNTVVSQE QANKWLTTELGGTIGKVSQKNGGYVVSINM
TPIDNMLKSLDNLGGNGEVVLDNAKYQAWNAGFSAEDET MKNLQTLVQK
YSNANSIFDNLVKVLSSTISSCTD TDKLFLHF

> gi|28868580|ref|NP|791199.1| type III effector HopPtoA1 [Pseudomonas syringae pv. tomato str. DC3000]

MHINRRVQQPPVTATDSF RTASDASLASSSVRSVSSDQOREINAIADYLT
DHVFAAHKLPPADSADGQAAVDVHNAQIT ALIETRASRLHFEGETPATIA
DTFAKAELDRLATTTSGALRATPFAMASLLQYMQPAINKGDWLPAPLKP
LTP LISGALSGAMTQVGT KMMDRATGDLHYLSASPDRLHDAMAASV KRHS
PSLARQVLDTGVAVQTY SARNV RTVLAPALASRP AVQGAVDLGVSMAGG
LAANAGFGNRLLSVQSRDH QRGGALVLGLKDKPKAQLSEENDWLEAYKA
IKSASYSGAALNAGKRMAGLPLDMATDAMGAVRSLVSASLTQNGLALAG
GFAGVGLQEMATKNITDPATKA AVS QLTNLAGSAAVFAGWTTAALT TDP
AVKKAESFIQD TVKSTASSTTGYVADQTVKLAKTVKDMGGEAITHTGASL
RNTVNNLRQRPAREADIEEGGTAASPEIPFRPMRS

> A0WN29_9GAMM

MNSTVELAFYGD DFTVGSTD VLESLSLRGKKTILLLRVPEKKDSIIYSDYD
CVGVAGISRSKDPVGMKAELPKVYQFLNSFDPKYIHYKVCSTFDSNLHKG
NLAVATQVGDVLSPSWTSIVVGT PKIKRYVCFGELFADSKGETYRIDRH
PVMSCHPATPMTEANLVKHMHLGEVDCASVNL SMYSDSAATKLQQFIA
ENKVVIFDSVDHSSQAKVGALINEHCQ EGLHFSVSSSGFEDAVYSQNKLV
ENINITSKRILALSGSCSS ITSSQIDYALSHGFIPVELDIARLLMLESR
PQYLDEIVQTCIDLLSSNKSP LVYSALGPQKSGSTTASQDGLHFDEMLG
SFLGAIALAVTKTGLIERLAVAGGDTSGYCIQSLNLDALTFIAPLCPGVP
LCRAHAQDSDIDGLELALKGGQMGSEDFVRLCSGGE

> NOPP_RHISN

MYGRIDSSSDFHYTQSASKQMDAETQEFADTFARMHLDRSNGGSSSAARY
TLDHEPPVVPIDLETFRREIR KFHGKEITDIANNPQEYSDFVSAKARRTA
DVAQQYGI RRDS ENARYFSYQLGNQCVGLMRTEGGF SMEEEFESKSWRDQ
FPGHQEITSTVDLQVAHPLVENAGDIL LEHQLRDGERPLLNWRAENPEA
KARAAMMGFVEVDDCDMVLDPKQHPDKWTQTSAAEWRRKDKPPLYLRKFE
DAETAQCSTSCSYETYEDDFM

> gi|34498035|ref|NP|902250.1| probable secreted protein EspA [Chromobacterium violaceum ATCC 12472]

MSTAISISSFNGQVDSV GKAGDGNIDYLRAARNYSLLGQAIATMEEV
MLLFTELSNAKFQMSKKMEVSRDAQEMANKVEAVLAGITDPKDTKKLPQ
DVL DYLKANGISVDSVENLEGDLSQADLTAVKSALESFSGRASDFVQQSQ
LKMQQLIQNFNTAVTMANSLQSMNAESTKSIAQAIR

> gi|28868613|ref|NP|791232.1| type III helper protein HrpK (Pto) [Pseudomonas syringae pv. tomato str. DC3000]

MRIS SSPFVIVNQPTPGELALAVESPLAKALPTVGGGGQAGVQFGQPAG
NTQGAPTGAEQTASSILALLLQSGGAAANANVNNQVQPFCADSPAEEA
PTEATAPAAPVEQVAAPTNTDATDASNAPKAADAAFLDNSEYSSPEALKR
WEPMV AHL PPEEREQA AKELNRPIAAAWMARDGPDAGKAMDFINANPAL
KTAVDVAQGGGNADGKI TNKDLKTF AKNMEKAADSADKDLANYTKDNPDA
DPQSLEMVRSAAVMRANMPLAIAADPHHAVDAADKTKVDGNVDAEDLKGL
AQSNPGLSGALKQSCSTWSQPGFLGQVDEAGMSGRKKAHSPDKMFDANK
LSEWIKKSAPTNGGQFASMLSDSATLNAVAGIDISKLDKDVDFDKPKSYSG
AQKAAVMVKLQQTQQSVIAGRSLRNTDKTEQGLNDRI SQLQADPDVQAYL
NKSIP EQERNLVRSDASLQKAVVEQTKNVNSGQALQTDMDKADKAVNKHN
PNADYSGAISGLSAQLQLQKDLFPDSKVPTTNQVLENKPDLDQKIATSIV
TNFSEGGALQQLGQKSDASQSLQTADNQKAIYDSVLPDPFTENQHENY
MNSTLGTLDQSKGRKLLLEGKSDEGGPSMLTQLAEAGVGGKALNSIVGFA
SVSSLI AHGDKLGATQAIYDSTRMGAEAIKGGIDAGAKMMGREASAGLGR
LGGQMIGRAVGMVAGEATGLAAGAALGAAIPVVGWAIDGALAVGFGISMI
IDAVKKHKAQKAFDHNVD PVL DQFGIAKAH

> gi|28871842|ref|NP|794461.1| type III effector HopPtoA2 [Pseudomonas syringae pv. tomato str. DC3000]

MHINQSAQQPPGVAMESFRTASDASLASS SVRSVSTTSCRDLQAITDYLK
HHVFAAHRFSVIGSPDERDAALAHNEQIDALVETRANRLYSEGETPATIA

ETFAKAEKFDRLLATTASSAFENTPFAAASVLYMQPAINKGDWLATPLKP
LTFLISGALSGAMDQVGTKMMDRARGDLHYLSTSPDKLHDAMAVSVKRHS
PALGRQVVDMGIAVQTFSSALNVVRTVLAPALASRPSVQGAVDVFGVSTAGG
LVANAGFGDRMLSVQSRDQLRGGAFVLMGK DKEPKAALSEETDWLDAYKA
IKSASYSGAALNAGKRMAGLPLDVATDGLKAVRSLVSATSLTKNGLALAG
GYAGVSKLQKMATKNITDSATKAQVLSNLVGSVGVFAGWTTAGLATDP
AVKKAESFIQDKVKSTASSTTSYVADQTVKLAQTKVSDMSGEAISSTGASL
RSTVNNLRHRSAPADIEEGGISAFSRSETPFQLRRL
> gi|58583878|ref|YP|202894.1| avirulence/vi rulence protein [Xanthomonas
oryzae pv. oryzae KACC10331]
MGDVAGGVEGCQPPKLCCTAMRPRKLCRDHRPLVWRRTCKEVCLMDPIRS
RTPSPARELLPGPQPDVQPTADRGGGAPPAGGPLDGLPARRTMSRTRLP
SPPAPSPAFSAGSFSDLLRQFDPSLLDTSLLDSPAVGTPHTAAAPAEC
EVQSGLRADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSDASPA AQVDL
RTLGYSSQQQEKIKPKVRSSTVAQHHEALVGHGFTAHIVALSQHPAALGT
VAVTYQDIIRALPEATHEDIVGVGKQWSGARALEALLTKAGELRGPPLQL
DTGQLLKIARKGGVTAVEAVHAWRNALTGAPLNLTDPQVVAIASNIGGKQ
ALETVQRLLPVLCQAHGLTPDQVVAIASHGGGKQALETVQRLLPVLCQDH
GLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPAQVMAIAN NNGG
KQALETVQRLLPVLCQDHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQ
DHGLTPTQVMAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASH
GGKQALETVQRLLPVLCQAHGLTPDQVVAIASHGGKQALETVQRLLPV
CQDHGLTPAQVVAIASHGGKQALETVQRLLPVLCQAHGLTPDQVVAI
ASHGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNSGGKQALETV QRL
LPVLCQDHGLTPDQVVAIASNSGGKQALETVQRLLPVLCQAHGLTPDQ
VVAIASHGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALET
VQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTP
DQVVAIASHGGKQALETVQRLLPVLCQDHGPDGPGRGRHQWRQAGA
GDGATAVAGAVPGPWPDPGPGRGRHQPRWRQAGAGDGA AVAGAVPGP WP
DPGSPGGHRQPRWRQAGAGDGA AVAGVVPDPGPGGGHRQPRWRQA
GAGDGA AVAGAVPGPWPDPGPGGGHRQWRQAGAEDGA AVAGAVPGP
WPDGPGGGHRQWRQAGAGEHCCPVILP
> STM1172 flgM anti -FliA factor 1257046:1257339 reverse MW:10568
MSIDRTSPLKPVSTVQTRTSPTVQKTRQEKTSAAATSASVTLSDAQAKL
MQPGVSDINMERVEALKTAIRNGELKMDTGKIADSLIREAQSYLQSK
> gi|33600606|ref|NP|888166.1| putative outer protein B [Bordetella
bronchiseptica RB50]
MTVMSTTISTAPSGAALAPSRIDMRAPEPGSAGEGAGILAPVTTLALAAG
RPAFPASPRLTAPVLDPPVRDLSPADLADLLRVLRSRAVDGQLATAREN
LQDAQVKAKQNTQAQLDKLDA WFRKAEAEESKGLSKVFGWIGKVLAVVA
SALAVGFAAVASVATGAAATPMLLLSGMALVSAVTSADQISQEAGGPPI
SLGGFLSGLAGRLTLALGVDQSQADQIAKIVAGLAVPVVLLIEPQMLGEM
AQGVARLAGASDATAGYIAMAMSIVAAIAVAANAAGTAGAGSASAIKGA
WDRAAAVATQVLCGGTAVAGGGVGVSMVDRKQADLLVADKADLAASLTK
LRAAMEREADDIKKILAQFDEA YHMIAKMISDMASTHSQVSANLGRQAV

> A4VIM7_PSEST
MTDLKDFRASLRNNAHAFSDTLAFIASNYDYQPSRFVNGTLENAAGENE
SCKTLGLALLEGFSTEEALLAFGEHYQAVLANPNGSDHRNIRALMETGLP
GVRFDSQPLHRK
> A0FNY1_9BURK
MAAKTIRPSSRFSPASTCRRSAEREDRDMTTSASKPLLGCIAADFTGAT
DLANMLVRGGMRTVQITIGVPAADTRVEADA LVVALKSRTIDAADAVAQSL
AALEWLRAQGCRRQFFFKYCSTFDSTDKGNIGPVADALLDALSPIGGGTPF
TIACPAFPENGRTRIYRGLFVGDVLLNESGMEHHPLTPMTDANLVRVLQR
QTRSTVGLVRYDAVARGAEAVRASIDALRHGVRMAIADAVSDADLYTLG
EACADLPLITGGSVALGLPANFRRAGLLGDAAADAGELPRIEGASAVLA
GSASKATNAQVAAWRETRPAFRIDPLAAARG EPVVEQALSFAREHMNARE
KQPVLIYATASPDEVKATQRELGVAGAGELVERTLAAIARGLHQMGVRKF
VVAGGETSGAVVQALDVRMLRIGKQIDPGVPATATIGAEPLALALKSGNF
GAVDFLEKALRHLDGGTQ
> gi|57434439|emb|CAI43856.1| EspF protein [Escherichia coli]
MLNGISQAVSTLGRHITSASRVSSAGLSGFSVSPQAVRLNPIRAQSPFS

PGTSNINARTTFNVSSPATSFTPSRPAPPPPTSGQASGASRPLPPIAQUAL
KDHAAAYEKSLSLEASGLKPSRPAPPPPTSGQASGASRPLPPIAQUALKDH
LAAAYEKSLSLEASGLKPARPAPPPPTSGQVSGSSRSLPPIAQUALKDHAA
YEKSLSLDTSSSLKPSRPAPPPPTSGLVSGSSRSLPPIAQUALKDHAAAYE
SKSLDTSGLKPSRPAPPPPTSGQASEASRPLPPIAQUALKDKNRY
> gi|15835055|ref|NP|296814.1| adherence factor [Chlamydia muridarum Nigg]
MPPSAISKISINSTTPQVQSSSAPNLTMLEGKGISVEKSFVYSEEENQNH
TTEDVVRIGAMLQQQFYNMTTGRNESFTVSPAHHSGNWKTSLLYNFAQLV
AHIFSLNTVPAKIIHHENGTKQNWESKQPTVSSEKSSNKRDVSESIQAVVQ
RVNPEVITKSSLKATKSIRRRKPRSVEEKREQLVKDP ADKIVYDLRADTI
ASRLKLTTEEQIKCRISLNNLKKAIQRYLNIDESERNRKRQDQLLVKQSI
FLNNILENAKMEESEEFKNVMSVIKTEFNHRVKIDSHFHGIWIAGAPPE
GTDVYIKTFLQTYEEFDFLFWVDRQAFGAAKFSSILKKIAFDSSLKELRS
ITSQETQDFVKEYDELQAKYQTSGRREERRELEKDLRKLFDYKHLSSQEI
RTNFDALFLKNMVLSDGFFNYCLLKGIGTIDDQTRIA YLQDELHLPPEE
IQQYKDLIKANEQKIKDIVGKVNTDLGKERVFIKNIRDLSMQDRTNTYN
YEMEMLLRWNYPAASDQIRMYMLKELGGIYTDLDMMPQYSPDVLQMINET
GGDRFFEELPIRRVSDGVLRLANGESGITIDNIAQDIDISKLTRSDRTQ
LEKLLTDIENKQKSSGTSKFSFLQRMADPSVRDFMPIQLQRHHKWSTGWNV
RGLNGLMMAHKGSAMVDAVIKQQRQAYRELKSLRETIVLS GEFFKTLDDLK
HLNHKALIGGHLVEDFLGKSLFSEFRQDTI IAGALSTLGITGPDIVDEM
KTYFRSLGPIGKDYLEGKKLGNKAFGLSYNKIVKEGKQTFDWLHPVTVGA
NDVTPADESTWCGIKQRCLAELLSDESFRPETPKGISRTKIDKKTFTK
LWSEQSKRALSPELLDRFNELIEAKNFDLIKFTDVRALYVLRNQVCDDA
SASAAVFLQLQLAELLRGTSFPPIANQLNVFPDLNRNIAS SLEKTIKLYL
QSHSQTTETVIWHSASIDRVMFLRDMMLATAERMRLVKESIFSKEETPLTTE
EIKLLNSWAELQSKDNLGILSLEEVDKLLDVTSSIMENSKLKKRVSAIED
SIVAGYFYLRLEETLSEWVRI PPKDLKKRVIRFMEGMDANQQHPDERGGR
WYSQLYDESFKKRVTAPVKKIQELAKKYLNEQRVHVLEIDDYLTKNPLFN
RLHEEGYAFSDLTETRYMLAEYGISGIFSEGNILPSPSAR LVNI IKTYV
GGDYHDMQDVLPKIYDWLASGGAADLTNERFAAI PESLRKNLEGLHGTDL
LTPPVDAVSGWGMFSGVENGVESDHTMISIAPGFFNGASYSMQHYLSAL
YEIHRHIHLGSLTSDLIKKELESKGAGCFVHEERFDSLLKASSEKQYLSL
TEIHKSLSNQVHLAEAVSHLMNTALPGVGKIIEREGDFGRLGITTTTETS
AMRSYDYRGIGVSKDLFSLPQEVPTIQNVVEQAKYTLLSWPE FYNRYANA
WSDLATHYGAEILEAHPQSFLYEVEGRCMGLSLLYMSIEDEGGYRTLQGN
LDTVSALYQKERDHLPLSSKDQSLSRDLSLINWLQYQGNKVLLENRGF
NHAKVDVLQLTSTFEKSLTKSLITTPHSLTLNFMGSGFRVTDPNFGHV
DFPSLAAALYFIEDMVQVSPHIKQRYGFSETLSVREQLQVYFLDAPEGIQ
SLLSFTDAGLLSSHQATTLEKMRERGPVIERIQTTWGKLYEI GGSIHHR
RIDEFTSETDLDEMKNLGDVLTDFLTKHVLDSSETVSLILVLETRGLEEG
TKHVSRSLIVETPDEAASLFQFLKNKTAKTREMLVSLSEVTDKLSAQL
DGEDVEVSRVFSDNSDEITVEVKKGSLKLSIRGGGIFDSFKQFSKA
NELGATGVMDELGMSIVSIVQYMRLEEGGKGDPLAVANLVMDVKETAE
MTVGAVIQGLSKKFI TQEGVDGFRLETAIASQLKASSRVGGSV GKVFSK
TAAVLELPVLETALGAWNLYDSVSLKEAQTHSDRMAARVDIAFNISITLG
ITIASVALPSMLAVGPLAAIGMASAIARNVALKEERYDQWLVIKFLT
EGGSHILFADPDRHLLDFSGNYVLGNFLDLRQNPPI LKGDRSYNSNWRI
GNKAGWTDWQIRDRIGYGRISPTSALARGHANSFWPPELPTIPKGDYRT
VILGYGTTYEAVTEVVYLSNKVVWREAVMESSRYRPPPTAKSK LSTII
GGDSPLTVIPVRLIEKDEKENIDHAASYKDYKINIKGGKGLTVQIGGAG
FYNLTGTLPATNTISFRAIPAPFGVKFNLSLVEQDVPLIRPNGTEEKFLK
IRQTGFNTILGSSGNDTLTGGNDTKFYSSPGGGTIYSGKGKVEYHIPQL
THPLHIILSKGSSAHQLVTEINADQVKPVLGSLSLTSSMELISKQEIHVS
SEDTKEDLGWVKERYEVRLDGITATPIDQMNAGTRLVMTGMVKTCD VAKW
QKQHPTEITSYPEDILDWLTQKSWFLAPEVLFVLENGTAKFITNRKHIVYS
PKPYSELAVTQSRDIKAFVQGNQTCYSYVFSTIYRSSQKQTELTLDVDD
VYAQTIDVSSILPTLILAKKSGDNQIDFEFSSSHHLMAIRVSWKGVIPER
TRVKINNETILRLGWLNAKLMASRNPSYWNLLYNNRNVIPERVEDVKS LN
NTVILMPPNTRNGEHVFAIENQEGVDVKVLGFLQSGHVLGEYEEDL MYK
DVFARKITHFAVTVAHKTKYLFFTDDEESLANPEDNVLFYSKLGSNLQA
SQKPLTQFARQLWASYDEISVSDTSLKLENFVRYLMEAEETIELYRQLLYA
QNLLRIHNRDLVLKLFYVRQSEGMGAVLITFKNFFIESMEGISAPTLERE

AKPILASDPMGLINPAYREHLDFLGEDKLNLAIVQEFSMLQYIVSMQE
GKALGSLTTPRYKDMNLAVLTYTVASSWEGRREASWLKAPIEYKLP ET
TLTASYLXPVSGDLYVTCLMNRQPQAFVIRFKGYKFKGAFRSIALI
SSHVSGESRIAKTVLQFRGQELFHLEKSAPNKSAVLQLDSKLLSLRMLF
YGGDQVIRYTPLSVQQFLSLDDDLWLADLKERVMNANEEGFKLISQMHDSY
LMESCMNLRDAVPQWKINPNVINNAITYYRVVVPFWIRNRLTKGSLIRIP
AHSIPIALTTTQNDVFKTIYAPGFSIYFSFLGLDAFLKPRTHNRVGDML L
ELEKEVVVTVKVDETDYNNKRVYIVTELTKEEERVLKANKNVITIPMKS
SYTKK

> A0RRK8_CAMFF

MKISSNIFILSFALFITLLNYKFFFEFAINKAGFYENKIVILTLPLVFFAL
LIIAFSLFLPYLTKPLSIFIGISGIAGAYFMNTYGTIIDSDMIRNAVQT
DVKEVKDLLNWDIILWILGAVFVVIIVVTKIIYSKVLYEIKRSIFIVA
ALAIFGASFGIFSKNFIPFFRNYPEIRFF TTPFYPIYSIIKFTKSLTPKA
EFQKIGLDATLKDCKRFLVFLVGETARAANYSLNNYMKNDTNPYSKENG
VLSFTNFYSCGTSTAI SVPCMFSNLTKKTFSPSKANNTGNLLDVFTVANI
DVSWFGNNSGWCKGVCDRLQNAKNYGGEGFDEVMLKDINSKIQNASKNSF
IVVHLQSGSHGPTYFKRYPKEFDKFNPTCDTAVLKDCTHDEIVNTYDNTIL
YTDYVMNKIINMLKDSKFETGLLYVSDHGE SLGENGLYLHGMPYAFAPDF
QIHVPAILWLDNKKLDELSRLKDENLSQDYVFHSMGLGFFSIDSNVYDNN
LDLFAKDIK

> gi|34498072|ref|NP|902287.1| pathogenicity island 1 effector protein
[Chromobacterium violaceum ATCC 12472]

MYGIQTSASLPLTRPQALQAAAPQSDAPDASAGQTRAAPQGSAAAPALA
AARAKADELGQAA REVRASVERQTAYETRLAAQRSAAAFSGGEPQARRE
APGAELDEARNAQTVSARLFEGNLKGVQSGHAMSAEQKQALQSGLDDVF
ADAPPQARSAGAPMLYSANAAAGQGMADSDLWDMISDQIGKIKDNYLGVY
ENVVGGYTDYKAFSDILSQMANWIKPGGDGNKVKLNDALKAALKLKK
DFSLGKNDNKKAVLFPAQSKDGGIQQGSESDARKWAKEMGLPDAPPPGF
SCVQKAADGNWVVLVDMTPIDTMIRDVGALGSGTELELDNAKFAWQSGF
KAQEENLKNLTQLTQKYSNANSLFDNLVKVLSSTISSCLETAKSFLQI

> gi|53722546|ref|YP|111531.1| putative G -nucleotide exchange factor
[Burkholderia pseudomallei K96243]

MTYNPRIGGFTHVKQASFDVHVKRGEAQPRTSFAQQIKRIFSKIGETLQ
LFRHRAPDSAPGRV RLQGVRYVGSYRPTGDAKQAIRHFVDEAVKQVAHAR
TPEIRQDAEFGQVYEATLCAIFSEAKDRFCMDPATRAGNVRPAFIEALG
DAARATGLPGADKQGVFTPSGAGTNPLYTEIRLRADTLMGAEALARPEYR
ELQPYARQQAIDLVANALPAERSNTLVEFRQTVQTLQLEATYRRAAQDASRD
EKGATNAADGA

> A1JU90_YERE8

MSRIIALIISFLLVGCATPPMPAQRIVGEVMSRPLSRT AHIDVSIFGLY
EGKVREVQRTRFETGNLPLFFSIKLNPAQRGEGELYLRSTLSFPERGVQA
VAQQKLIGKNKVVLMIPKTCYPNCQSPNTR

> gi|53722545|ref|YP|111530.1| putative intercellular spread protein
[Burkholderia pseudomallei K96243]

MINVDAFVASARSGARVVVGGDARGPVVSAARLGMKERLFAFLAHVPLLK
HCDAVRRYAEQVRMENRRSLEVFVLALSRYGPEGAKAAFDYGARRDGP
LDQRRVRNMVSI AEHFHGTGDAKPLARQMVFRSWECEGLDHPGHASLTIK
NQADADAGRHVYEHVSWWPNQRLGSKHEFDRIEPTLDGYRIDKRSEISS
ATEQRLREGDAARRKILADGFKYANQDERHDARFFPRAGQKLDKDAEWGL
SARKVYFPAIGFNHRRDTRPRAFVFLGNEAAMLRDARTVKEGAKSGE
LMYQMISKKENCASMLRVL RAGGAEHFVPTAAWI SEDPNHAHAYALAV
QARIDALNQRADVERRCERLRDSASVRQAWRAFSEAGGASASPLAEDAG
RGRASAHMRQARLDEHAREVERIGAYFAELSAGRSKGHRDRADAALADAM
KRCAPSARDVAALTRKASVLVETLGRHLDAPPPSDSSALRRLAAHAMIG
RIEAFMAAIIAA

> Q3BYL8|Q3BYL8_XANC5 Xanthomonas outer protei n F1 - Xanthomonas campestris
pv. vesicatoria (strain 85 -10).

MKLSSDIGTAASRGAASHPPVQPTQAEDVAAPREERAPTGPLAGLASSA
ALRGRRASLAGRASPHADEEGAMLGGSHRSQSSQSSQASDATFYTAQVVS
PAREIDTPDVPAAAATYAERSTAAAEEVKAQLRARLDALPFAAPSEEQTA
LQASYLEWADARVQERINAFGPDAGYQAVGDMKTAGTKAAL PIAYECLRS
FIIGAMRIPVGLATGAAYASRRPADAEELSTAMVAGVAAGSASYTSDTLL

IPAMDRRAPVSNLPRFQAIIDPKILVDP PPPVILEITAEGRFTRPGENNA
PTLADLKAQTYDRRLGITQRQSTLDDKSLDTLLLLKPVINAGFNAARRTGG
EPGLLTPVGGWGLSALAIIGGAGVVQKALLETGKAVARTGQMRVPDLVGG
QRLNLFALALPDKARRPAQWSDAVHFPPPTYLLDTGKEALALA RQGFNSAN
AVATTARDLLTRHMLSNVMASFGPMGAGRIITAPLRGSHIRVAGEAVNS
TAVVVQAVQTLFNDTFWNALKAKNGANTSQAARLDNERAALAAEHQRTI
ERTLEALAEVPDQAIARLSGPTPAEAEERAMEEGMRAAPGPGPLGQTLRTA
LQTLRTEIGTQSVSIATIDAVRTALREGWSQTFSGVPRDAATQALDGQLQ
TLKRALHDSEALRQWQSGRA

> gi|12054313|emb|CAC2_0124.1| harpin protein [Erwinia chrysanthemi]

MQITIKAHIGGDLGVSGLGLGAQGLKGLNSATSSLGSSLDKLSGTIDKLT
SALTSMMFGGALSQMGSGSLARGAGNQLGASLNTFGSGAQGAGNVLSKPQ
SGSDALSKMFDKALDDLLGHDTVTKLTNQS NQLANSLLNASQMTQANMNA
FGSGLNDALSSILGNGLGQAMGGFSPLSL GAGGLQGLNGAGAFS QLGNAI
GMGVGQNAALNALS NVSTHVDGNNRNFVDKEDRGLAKEIGQFMDQYPEIF
GKPYQKDGWSSAKTDDKSWAKALSKPDDG MTGASMDKFRQALGMIKSA
VAGDTGNTNLNLRGAGGASLGIDAAVVGDKIANMSLGKLAANAV

> VP1698 VP1698 hypothetical protein 1808583:1809581 reverse MW:38503

MRRRTQMKKQHWRRRSLFPDSIVTQRKVTVLQRGARYESASQPLQ DLNVV
HVNHRQLLSEGLVNDQDQLSLLQRLDRSVVDSL CASQLVKTYLRLGTSID
RFAMRFLFLEIGAQLSDSQRVATFEQRLEYINSRLGFRFNLATPKTLILCC
YLALTEWIHRQTDQSALHASVKVEQLMNQLDIQKEYWSKLSGEDTSAIFV
EQQLALIESQQTQLKAQLNLTLEQQSQVIESHKALVDKWQPSLSNLKELA
DYTSTTDMFISDWKTCSEARLQAPDLNEVWDACDVVYNDLNAVAK VWQW
FKDMQIVGDVDHYFYFDIQSGQCGQACNHLSQI

> gi|29840317|ref|NP_829423.1| putative cytotoxin [Chlamydomonas reinhardtii]

MTLPEKTTSVASSAQTHSNYTAASNSSSLRQNNNTTRAASLDERLALYDEA
VNQNNSTETVVEIGKKLQEEFYNLTSQPTRTTASPSNHTGNWKT SFLYN
LAQLIAHIVPPQLLPAKIAKPTIIPPAANATGNSTTEI SQRASNASISQN
TTSLSQPVIIGGGRPRTAKKKVLGTLVKKSASRYRYKKT LKTAKRAPRHS
KSSSVIASSAALEPSFIEKTENQLIEKTVSADSVQNVEDSPSFSRRKRAL
EEEAQEAAGAEKYDLTPENIVDKLGLTEAQKTCRAS INNIKKAIGYNNL
AEKNSRKGQDLLVKQSVFLETIQKKAGLPETHASAKVMTTIKTEFLSHRV
AVNKHHLGIWIAGSPDDVSPYIKVFLQTYEDDFDFFW DESAYGAAKFS
STLKRIAFDASITEIKEKTPEAAKDFIQNYEELKKKYDSAEDAEQKEQYQ
KDLHDFSEKYDKLNKEVKENFNALFLKNMITSQDGFNF CMLKGTSTVTD
ALRIEYLEQNLKLPQEEIEQYKKTIEDNKKKIQDIVAKANKGLGSERVKI
KDIKELTSMKDKTNLYNMEMFLRWNYAAASDQIRMYMLKEYGGIYTDL
DIMPSYSQEATDAIFSKGGRFFENLQIRRVISTAALKIA TEETPV TLEE
ISKEIKTSQLTREDKKKLKELIPELEKLHKDEGGGGK GKSKKGLFQTMAP
DTVRDTPVLRRYHKWSTGWNVRIINGLMMAHKDSAAVDAVIKQQRAYA
ELKDLRENVLSGTFNTLDDLTHLDQKDRVGHYLVKDYLGKSLFYNFRQD
SII PGAVSTLGITGPDLIKELVKYFKDFGPMGKEFLNENGRNLGDSAYL
GSYKQIKDEHGETTYDWNPLSVGANDVTPGDESSWCNVRQ KCAGELLEFS
DSSKLRVETPKGIERTKVNEADFTKLWKEESRKKLPNRL LARFNELIDNP
NIDVAKLSDLDYDILKAKLAI TNPAATTSLSLQLQLANLIRGVQLPVG
NQMNFFPDLYKNVEDDLEKAIKLYLKSHTTTITLWYSSSGNLSLFLRDM
LSVAERQLAVGNLIDSVGQAPLSEKQINLLTTYVELKSKEILSSFSSDED
LTNFLETLSITEDAQLRPQIEKIEEKISSGHFYQDLEELIN KCLGLPEH
KRRKLILD TMKDITRFSGLDKQEQQSAQKWEKIYDTTLEKRVLN PQKKL
EALLKKFESSERVLENLDLFLRDRSLFSRMHRDGYAFADSNDLYRFMVA
EAGISGIFSVDSVLP PPSKHLVNMKTTLNADYEDMHDTLGAVYNYLALD
PETEEAKAALDKIPEGLREKLQNSHIPDLLIPPIDSHVSALGMQYGVVEEG
GESERIMASIMPGEFNPTS YIMSSYLD TLYQLHQRIHDGSLTL ESAKKLL
NENHIYCFVEDTRLQELVNLAQEKKYLSL TEINKLLSKKNFAQAASALL
DGVLPGANQILQRDADFGRPLATTMLEPTAMNPPYD YRGAGLSKDLFSTPP
DVPTLPNVVERAKYSLMAWPDFSREHIHPWSVLARTFGSNI VHVHPQTFL
YDLEGRMGLAMLYMSAKTPVEYAFLTQNLMTVSSLFQTKERDHLPLSEA
DNKFLLSQSYIDWLQYRGNKEIKTQGILTPHTWDIAALSEKFS KSTGSK
SLLVTTPTHSLVVQHLDWGYRFTDPNFGHCD FATLQQALS FLESSVQLSE
EVKLRYGISEHKDIKEQLKVYTLDSQAENS WFPSTNLKFLSYDQHMITL
DKMILRGDVYVGRKKISWRHLYAAGATIDHKRIDEKTRETDLKLQINGE

IILSDFLSRNTLDAPLASTIQYLLD TYGTEPGTKEVSRSLIVETPRDFASI
IGGFKTKAHQMSAMLRNVMDSIRSSIKDIPPGNQDRVSVTDIEVD GEDRI
SFKFKCGSSPEKKIQIPSHGLVKVFRQLGGMLNDLAGTGVMDMELGMSAV
SIIQYARLVEAGKGGALAI FNLSLDVKEMAEMTLGAI VQGVGKFFITEK
GIDGLRLESVLSKQLIKVSNKVGTVGKALFRVGMLELPILETVAGVWG
LYNSVEELMQASSHSDMMGARVQVAFDVISLALTL SAVVAPAAMLAAGPI
AAIGMGASSIARNVAKTEGRHKEWGKYYKFFLEDGSEHVVTAFPERG LIDL
SGNQILGNIYLDLTHNPPIFK GERSYNANRWIGHKPHLSDHQIREKLGYA
FRITPTYALALGHANSYWPPEVPHIPAGTYNTVILGYGITYKGTTEVVYL
SNKIVWREAIMDPESRYFVSPLTAQNHRSTVITGKTHTTIVPVRLLDDDS
KERLDQALEYKNYEIRIQGGSGGVSVQIGGAGYNYLTGAPGAENVISFRA
IPPLAVQFNLSQGLQDVPLIRPNGTKINMLKIKQKGFSTIIGSSGG QDT
LTGHRDTKFYVSPGGKVVYSGAGTNWYYPKLNENLTVLATNSTDHSLH
LNMHSYELHSVENNLNLLGLNGDKHKGIYIENADKSSLFDRWIGHFIVKF
SDGITVEAVERPIPGNHTNATTLGFTKCDQSTWALKHPEEPGFVDNIVKW
MKKYLWWFAPEVSI TQQHGHVSYFDQEKLFVYKPKDKHSELEIRAQEEFLT
TVQGSVGSYI LSSAPNKQAKRIDIVLAKDEDAPQYLDLSSLI PSLVK GR
ITNGSNSSIDLEISSPRYTIPLSLQWDP EALPEKT VIEVHPQNRPTLGEW
YKILKKDPTQWHTLYRYSVLI PERLEGILSMNNTATLMLSESRKNEEHIL
GVENKGDVNLKIWGT LWAGHIK GAMRHLHWKTFNNYRALEKFGITIDAHG
FQYLA FEGTEKSGDNILFHSVLESY PFKAKQTPQTELSHHKWKFYDEIQV
FATTLHLQDFNRYHIA SENKALSRQLLYAKNLVSI SNRDFIVKLFYVRE G
FGIGAMRLVFNFFNEHMEDITEKTLEREAKPWMA SNPHAFIDPSYQNH
ELILGKERLNLATLVREFCASSHILP LSEDEDHRLILPERYQANLAVLT
YTIDSNKIHN GPANTLRFFDNTMKEYRLPLTTILKSSYLDPVTGDLYIT
RLVAEQTDIQHQA FVIKLGFKRHWESYKHIFISGAHVGLTRSKGTALTF
IGPELRHLEIDFPRNTTHHVFPERLVSRSGLVFP TNDQV VNYDPRIDKQF
HTILDYMLWNLDRAWGSKRAKAYDSYLLESAMHIYDKNPQWKIPESMLH
YAI GYYKVVQPRWRSHMRPYTLVKMLKGSITLSLITQNEIFAHKRGSG
FN IYFALLGLNKHVEPHSNKPGDMTLRLKQDVILKVRKVDSEYQKKRVY
VVAE IATEEDRS LRPN SQVLIFPGGEKIRYRRSLKNPKESNSTITD

> gi|12329086|emb|CAC05817.1| MxiL, secreted by and put ative component of
the Mxi-Spa secretion machinery [Shigella flexneri]
MINQINASNALQQRLNSEE FVNLNERLSSSQSFDEDI IYEIMQYFSQSEL
NSIDNDELHNKIEQLFNSRFPYLTAAQKSSLLNKLIDANQYVDLHEGFYA
SLSIYNNIDFYIKTTTFDSLISVFEAGREADDSTW

> gi|15618211|ref|NP|224496.1| Inclusion Membrane Protein B [Chlamydomphila
pneumoniae CWL029]
MSAPIPTPQELSDQITCLNVQYQQVSELARENKGDIEGLKTLTAALTADA
GIQPSADEIYSLQTA AALILSASEKPGSGPSGSTE GSVTVQSPCKFKKVL
AVVLTIIALIAIAVLIACIIAACGGFP LLLSALNLYTIGACVSLPII AST
SVALICLCTFVANS LIKPVITVRTR

> gi|15835057|ref|NP|296816.1| adherence factor [Chlamydia muridarum Nigg]
MEQALCTMTLSNTASSTVSPKSTQLNHTLSNQTHPVAQSNRNIDFQIYDE
QIHNNHSTEDVVAIGRRIQQEYANLTTSKQVNF SASPSNHTGNWKISLLY
NLSMLVANLFP TTIQPVQPQKVI FKNQDSSKETQLTKSSKVVSSRSSLKE
IFSKKSPPLRKSFSSSKISR AIPRRKRSND DDPVQATNTYDLTAENILEK
LSLTQEQQIKHDNLSNLKEAINRYS DLNRKNSRKGQSLLV RQAKILDEI
LSQTKSTEERASNSVMTTIKKEFTSHRVPVEKNIHG IWIAGSPPEGTDEY
IKLFLHTYPEFSFLFWVDK TAYGAAKFSSTLKRIAFDAVNSLREATPEP
VKQFVQRYDKLKKSYDTSRDFDEKQRLSEQLVELYDNYNKF SKEIQSNFD
VLLLHEMITIQDSFNYCQLKGVGAI TDETRIEYLEKVLKVK EEDLSHYK
ETIKRNKESIEKLVKEINDSTGRERVVIKDIRD LKSLQDLTNSYNYETEM
LLRWNYAAATDQLRMYMLKEYGGIYTDLDIMPQYSQDVLQKIMDVGGSRF
FEHDKLRRTLSFAALKLGSGKQTTVSFEEAKKAMTLPFTLQDKSQISEI
FKYLETETQAKKSLFQPM DVTVVRDFMPILQRYHKWQTGWNV RGLNGLMM
AHKDSAVVD AVIARQRAAYDEM RALRQNVVSGEFFRSLGDLEHV NREKNI
GGYLAKNYLGGSLFFDFRQDSVIPGAISTLGISG PDIIMDTMSDYFTNLG
PVGEDFLYEGKLGKAAFLGAYQAQKTPKGELTYDWLHPLSIGANDVTPAD
ASTWCETRQHCAAE LLLSDSISSEHPKGI RRERNVNDPNSKLSKEAQQ
ILSSDFADLLPRFNLLI ESSALDIHTLSALDRDIQH LFTKVQKDPVASVA
VFSLQLQLAEMIRAI PPIRNQVHILPEAQAHFEADWKKAI QLYLHSHPO
TEVVIWYSS THTQIVFGKDLLAVAERVA AAKSLMSDHDPSLITSYLKYKT

QSHLGLVTEFDQEDDFELMVDIAEPELHKQLLKIEEQVNSGLYSHVEHS
LGEWLKLSKEERKSKFLKILKETFQEEEREDSQQHKWTFEELYEKRHQE
RVKDPAKKIQELITVVFQESQRVQAQDIDTYFAHKPFYQDLMKDGAFEDI
SVITKYLLASDGVSGIITTDPIFPFPPSKQLIDAMKQSLGEDFGELHYTLQ
MVYDWLSKETNSVTSEQAKQKLPQKLHEKLEGYTTHDLLIPPIDGSVSAL
GLRFSTEEGKVS DRVLT SIAPGVPNSASYAMTSYLYGLFLITKDIQSGRL
THEILKERLQTYGGAYFINESKIDVLLALSRRKKAQISLIDAHKALTGFSS
FSEASLALLTGRMPGTSRVLSREVEFGRPSAIVMEGATAIRAQSYDAVGL
RKDFLLPHTVPSIQSIVEQAKYTVLSWPEFYENHADKWNDLANRFGAED
LSVHPQTFLYDTEGRCMGLALLYMLADDSVSYRLLQONLMTLASLFDEQN
RRNIPLTPADQKFLNKGLSLIEWLQFKGNQQLQTEGFFHTLDWDIPQLMK
HFASSTVKSRLITTPAHSLVLSLMGNFRVTDPNYGHDTDFPSLEAAITFL
ERMVQVSPAVLERYGFDKEKSVTSQKLVHSLETSELQNAVFASSDLGFTS
RYFTTTLEEMTVRGPITMNRHTDWATLYKIGGTVQGKRIDSRTRESDLN
FLKINGDILEEF LTRTVLDSDLVELIQSLLKTHGLEPGTTLISPSIVET
AIDHVSLLQAVKTKSRMHTILQSLGERIFKLFKNSGVQSDSKISIDRVQ
LVDES DSATIDFTVIKDKQRSQKKSITVGIESLAGSFRKFSASMHEVIGT
GVLDDLGMVTVSVLVQYVRLVEAGQGDALAVANLVMNLKIALEVSIGNV
IQALGKLLTQEGLNTRLETELARQLHKVGARVGGTVGKTLTRVAHVLE
LPFILESAIGTWNLYNSVNELLHADSWSQVAARVQVAFDSISLGITIASV
VSPALMAAGPIAAGMGAASIARNVARKEERHSQWLKYKSFLDNGSKHT
VAAFPHKGLIDLSENVLGNIVLNLRVYPLLTGDRSYNANRWFNGKPGW
SDWQVRERLGYAYRSSPSYALARGHANSFWPLSMPSIDKGVYRTVILGYG
IQYKAVTEVVYLSNEMVWREAVMQFDSRYVEPLTAEKECATVLAGDTPL
SVIPVRLLEESLE REKNAASYKNYQIIIEGGKGLTVQIGGAGYYKLT
QPGKGNILSFRAIPGYLSVTFDLRLEQEVPLTKQNGTALKILKVRQTGF
DTIVGSSGSDNLTGNHNTKFYLS TGGGHVTS GSGKNWYNIPSLTRSLGF
DFTSNAIEHKASVEMLLADFS PANNL SLIVERFANVSIHVFNYSNKTAPY
TVNLKDGVSLEQKGFSGSLEVASFDQTLWQKSY PEDRGFVEDILSWL
LKLQWSLASRVRI L QGGTAQYETTQKSLIYRDPHSSISIQATDSYNTQ
VYGNVCSYILFSSPGVTAKTLDILLFEDSGLPQIIDLSTLVPTS IQGFL
YPGGFINFQVSSARYAFPFSVSWRRHHYTFPAQTIIQVLPRLRFELGDWF
TILQKSVGKWTLYQHDMIIPERIEGVLNNTATLMSHHNQTHMLGVE
NRGDL SLKVLGILQSGQIKGSKSENSASGHFSKLLSVPAAHTIKNLSFKEE
EGTKSKNILFYSVLEE TFLKATDKPLTIKRDKWSLYDEIQVFATTLNLQ
NFLRYHI SEETPMLSRLMYAQKRVS IQNRDLALKFFYVRERSGIGAIRL
VFNFFEESLQGI LHGT LEREVKPMLAENPNTLIHSSYRNHLELILGEET
LDLAIIVQEFSSKNIVELQKDLATHRLIYPQGKEALS LAIYHTTFSKES
LVTSKQRSEGLKFDPSMQEYRLPETTILENSYLDPS TGDLYLTKIIAQ
PSQSRAFLIKFKKYKRH WLD FQKLVLSGSHLELIAS TGTALTFVGP ELRH
LEIDFP GALNGTIAKEHISSRASIVIPTNNQVTHYDPRIAKQHYSSINYM
LWDLRDRATLSKRAKTLDSYLLEVCMLNLDSSNPTWNI PNDV LNYAVGYR
TILPSVWKNKIRVGS LIKVEADTAKTLSFSLITTQNDLFPVVDKGFYIY
YSVSKLANHVKLRNVTGDMMLLDIDKETTFIVRGVDES DYDKKQIYVVL DL
TTEERKLR TDKNIIIP GGERLNR

> Q8X5G6_ECO57

MLPTTNI SVNSGVISFESPVDS P SNEDVEVALEKWCAEGEFSEN RHEVAS
KILDVISTNGETLSI SEPITTL PDLLPGSLKELVLNGCTELKSINCLPPN
LSSLSMVGCSSEVINCSIPENVINLSLCHCSSLKHIEGSFPEALRNSVY
LNGCNLSNESQCQFLAYDVSQGRACLSKAELTADLIWLSANRTGEESAE
LNYSGCDLSGLSLVGLNLSVNFSGAVLD DTDLRMSDLSQAVLENC SFKN
SILNECNFCYANLSNCIIRALFENS NFSNSNLKNASFKGSSYIQYPPILN
EADLTGAIIPGMVLSGAILGDVKELFSEKSNTINLGGCYIDLSDIQENI
LSVLDNYTKSNKSI LLTMNTSDDKYNHDKVRAAEELIKKISLDELA AFRP
YVKMSLADSF SIHPYLNANIQQWLEPICDDFFDTIMSWFNNSIMMYEN
GSLAQAGMYFERHPGAMVSYNSSFIQIVMN GSRRDGMQERFRELYEVYLK
NEKVYPVTQQSDFGLCDGSGKPDWDDSDLAYNWL LSSQDDGMAMMCSL
SHMVDMLSPNTSTNWSFFLYKDGEVQNTFGYLSLNLFSSESFPIFSIPYH
KAFSQNFVSGILDILISDNELKERFIEALNSNKSDYKMIADDQQRKLACV
WNPFLDGWELNAQHVDMIMGSHVLKDMPLRKQAEILFCLGGVFCYSSSD
MFGTEYDSPEILRYANGLIEQAYKTD PQVF GSVYYYNDILDR LQGRNNV
FTCTAVLTDMLTEHAKESFPEIFSLYYPVAWR

> hopAL1 Pma ES4326|Genbank: AF458049

MDVRSAPSNHATAVPTAQPSAPSISKSTLSKLFRAQCSDPVFLSSSSSTER
IAPPRVTANYSAVVDISKASHSKTNADTAEKNSFSLKLNKSTVSENQQ
KKQAIQNFIAQVSDQYINVEEDVAKLAVAASGAYRQLRFEETQQQRVHACL
QDTEALTAMIDL ATRKPLTYKVMGLDSSDCSFDPIARISDHILTEAEQ
CQVVRSAFASADKVCVVTSYGIKPLGAPKSDALSPTIASVLQGFASKQHD
KDFTGVFFYQKSDAIQNYTTEDEKRTNISIKENDWAKAVTLFNAAVERGEI
EGPKEGLK

> PA1698 popN outer membrane protein PopN 1847227:1848093 forward MW:31319

MDILQSSSAAPLAPREANAPAQQAGGSFQG ERVHYVSVSLSLADAAEEL
TFAFSERAEKSLAKRRLSDAHARLSEVQAMLQEWKRI PDLESQQKLEAL
IAHLGSGQLSSLAQLSAYLEGFSSSEISQRFLALSRARDVLAGRPEARAML
ALVDQALLRMADEQGLEIELGLRIEPLAAEASAAGVGDIAQRDRTYRDAV
LDYRGLSAAWQDIQARFAATPLERVVAFLOKALSADLDSQSSRLDPVKLE
RVMSDMHKLRLVGLGLAEQVGLWQVLVTGERG HGIRAF

> Q8XQF0_RALSO

MLRTSLDRASGVASVPTHPQEATGSTPAPAHTPSGRAPSAELSALRTLSS
QSSRTESGRLSIGSQRPASAQESAEMASHHSPTSPASPRALLSGQSER
SNSDVSQWFSAASIRAQSIGSIESNSPPGGSPHTADPGQTGRGIDIPH
WMPIADQLRDIRFRPHFDGTNDAQFEILIQRAERLQAMGETPATVAAVLA
KGANRDRLAQTTVGFVRSVPPFGIASRFLDV KQALTAFAKTARVGVATVGA
GSGTADAFGGTLLGKATSNTQWLAASPDHLEPVMAQAHKAVQPSLGRLLA
EVSLAFQTYSLRNVIRTGVAPLATHALGAARAANVDSWIAAVGGPVAGAA
AYMAMQHMNETHHRTGAEYLLGRTDWEDQFKQLKQSTWTDPLVGAGKRTA
KLLVADLATETLAATRSFLTATNLIKNMGALAGGFAGVLTQAQTAAGKAAT
EAGYTEAAVAARRAVSTVLSAPVYAAWTTA DVMAGPAIDAAAGHIQQAF
TPLMPHAAPPAHTAIDMV

> hopG1 Pph race 6 -1448A|Genbank: AAZ34904

MQIRNSHLYSASRLVQNTFNASSTKEAANTIKNESAALSATQTARTHE
GDSKKGSSNGSRSHLRSMRYAAYLAGSAYLYDKTVNDFLSTTSLNDGKQ
GFTSDARLQKAEKAEANYHAYHNANRANFGGVAPTRSSLLPKLCGENLFVT
MLDFRAATKVHMKNLIDTKEA HDSIANNISCI MGERVKPELLKKHGIVQT
PPDFDITKGASYDCKNKYSLSGVPNQETGSYGYASRSVSNPPIEKGENHH
ARAINSERALTPRNCVDALQPLLQKSERLSPEAQFRAGQALLILRPLYCS
SENWGDHAKVLMPLFLEKKGLVSSQENQKLGATRPFQTDMEKGIARRNTS
LAGPTLNKLNIFLQKSIYNKDEKAI SDLTAKKLGEMKYPIAHFKMNEDV
SSFEDSSGLADSFRTGYNVSAYI NHARLLSGEDRLSKKDVIIVGCLNAYI
DNASSERHTLREIAHGCFVVGAGYTVEDAEDFYNDACKAAAATEFYGGRAIN
VQSQLYSSSVDKPDS

> NleH_Crod

MLSPAPVNLGCSWNSLTRNLTSPDNAVLSVRDAAACSDNGTQVKVGNRI
YRVVVTDNKFVCVARENHSGCFTNMLHRLGWPKGEITRKEAMLNTSPVNL
AMERGSVHLKRPDLPPVDYMQPELPRVDYNKSPVPGNVIGKGGNAV VYED
MDDTTKVLKMFSTTSQNPEEVTNEVSCFNQYYGSGSAEKIYDANGDIIGIR
MNKINGESLFNIQSLPTQAEQAIYDMFDRLEQKRILFVDTTETNVLYDRV
RNEFNPIDISSYNISDVSWREGQIMQSYHGGKQDLIRVVLSRI

> Q7DB50_ECO57

MILVAKLFITNQIGESLMINGLNNDASLVLDAAMKVNSGFKKSWDEMSC
AEKLFKVL SFGLWNPTYRSERQSFQELLTVLEPVYPLP NELGRVSARFS
DGSSLRISVTNSELVEAEIRTANNEKITVLESNEQNRLQLSLPIDRHMP
YIQVHRALSEMDLTDTTSMRNLLGFSTKLSTTLIPHNAQTDPLSGPTPFS
SIFMDTCRGLGNAKLSLNGVDIPANAQKLLRDALGLKDTHTSSPTRNVIDH
GISRHDAEQIARESSGSDKQAEVVEFLCHPEAATAICSAFYQSFNVPAL
TLTHERISKASEYNAERSLDTPNACINISISQSSDGNIIYV TSHTGVLIMA
PEDRPNEMGMLTNRNRTSYEVPQGVKCI IDEMVSALQPRYAASETYLQNT

> NleE_Crod

MINPITNTQNLISINTKHAEYVVKNIYPEIEHNYFNEPPNVYDKKYISGV
TRGVAELKQEGFINEKARRLAYMQAMY SVCPEEFKPI SRNEASTPEGSWL
TVISGKRPMGQFSVDSLYHPDLHALCELDPDICCKIFPKENNDFLYIVIVY
RNDSPLEQRANRFIELYNIKRDIMQELNY ESPELKAVKSEMI IAREMGE
IFGYVLEEIDSYMKNMNNKLAQIEARRSAT

> hopAH2-2 Pto DC3000|Genbank: AA056771

MNIHTARSYDPLMATSEKPATADRTTRAVDAGATEPTPEKQAKLDITYTAS
DSRSAETAEGSPVYTRMMLSRNTRSLESESDSSSDTALLASQKALVSQNDT

KAVGSEVAAVKDSTALSDAEKKAKEAEKAASTEAAKTAQTVARGGANVNP
DDIATPAAATKMIQDLKAI GGGTLRIQMTHDQIRDVKQMDKLRALLNEGK
KQDVKVQFTFRDNANQSGSNVLTGDKLKQAAADISSVVKKFGSRPGFVLD
TFHQGGNSASQEWSDMQTTLIK SARNAGFKGSIVVEDSNWGGGLTAGPQS
GLVKFADQLKAANGEGNPALIGGFHVYARESEASSRLGKQIKALQEAGYK
LQIGEVGNASLLIGSTFRQKDDATKAMTDNMAALKAAGADILPGKDQFQD
GKLRRRRVGFSKS DQYS
> gi|15596905|ref|NP|250399.1| translocator protein PopB [Pseudomonas
aeruginosa PA01]
MNPITLERAGLPYGVADAGDIPALGRPVARDVESL RVERLAAPAAASASG
TGVALTPPSAASQQRLEIVANRAEIASLVQAVGEDVGLARQVVLAGASTLL
SAGLMSPPQAFEI ELAKITGEVENQQKCLKL TEIEQARKQNLQKMEDNQK
IRESEEAKEA QKSGLA AKIFGWI SAIASII VGAIMVATGVGAAAGALMI
AGGVMGVVSQSVQQAADGLISKEVMEKLG PALMGIEMAVALLAAVVSFG
GSAVGGLARL GAKIGGKAAEMTASLASKVADLGGKFGSLAGQSLSHSLKL
GVQVSDLTLDVANGAAQATHSGFQAKAANRQADVQESRADLTTLQGVIER
LKEELSRMLEAFQEI MERIFAMLQAKGETLHNLSSRPAI
> Q4ZX76_PSEU2
MTIMSSLAGAGRGVVNTIGGAAQGIN SVKSSADRNAALVSNTGSTDSIDA
TRSSISKGDAKSAELDGTANEENGLLRESSMLAGFEDKKEALS NQIVASK
IRNSVVQF
> hopAR1 Pph race 3|Genbank: M86401
MKIGTQATSLAVLHNQESHAPQAPIAVRPEPAHA IPEIPLDLAIRPRTRG
IHPFLAMTLGDKGCASSSGVSL EDDSHQVLSDFSVASRDVNHNNICAG
LSTEWLVMS SDGDA ESRMDHLDYNGEGQSRG SERHQVYNDALRAALSND
EAPFFTASTAVIEDAGFSLRREP KTVHASGGSAQLGQTV AHDVAQSGRKH
LLSLRFANVQGHAIAC SCEGSQFKL FDPNLGFEFQSSRS AAPQLIKGLIDH
YNSLNYDVACVNEFRVS
> A1JRY5_YERE8
MKITPTIIQT PFPFNNSHTDIVTQPILGKLIGEGSTAEV FEDVNDSSA
LYKKYDLVGNQYNEI LEMAKQESDLFN AFYGDE ASVVIRHGGDVYLRMLR
VPGTPLSDIDTADIPDNLES LYLQLICKL NELGIIHYDLNTGNMLYDKES
ESLFPIDFRDIYTEYYSATKNDKEIIDRRLQ MRTNDFYSLLN RKYL
> Q8XQ11_RALSO
MVFLVRSINVAQSSHDPSTSDDQPFAMSPSPGERPARRSPA AVLGLVG
FSRRRGAGETAHGHEGGRSLRRFRAPRYMNLRAQGPSSPREPLAVWAQA
CELQPETVEALRALRDQEGSGPF MSLLAKLDACESFEKEPHRADS VQELG
AVLKLAAHNDAYRAFCDVAGGADADCYDNAEVI FGNLRLAARDPTYHGN
ASLEQVNLNYHKRCVPWSLVDDFVSERFPLFAESLENV LALRIRLSDILPI
RTPAMTFDNMTSVNQGV EAQARAYIARHCDREAKLQRNL CRSPAWRQFME
RQHPVEFTANTLLWASALQAVMEQRPEGAAMAVPPEVNTV SFGSRTEALA
RARAMPGIGTGHA FRHLQONATVL LSEDLTRRLVVEKRPPRTEAKAY AHL
LRDPDWLTYLEQEHDPDPAFSSDGIGTPDRHERLMRLTQQEIVAARGG
> gi|20139268|sp|Q9RBS1|POPB|RALSO PopB protein
MSHSKIKAGGHGSSGIGNDFTPAKTPAPATPAPQSQVNDLLGRGVGNAL
NKS NLGSDSQWTWP GSTMVSLKSRSSSSHKPD TGGDTKPDSTSGGKRKR
DETDPNAETEGGKKKKR DENDSSQAGGA GSSAGSSGSPEDALMNIALQ
RAIQRQTQTRQKMQEAMKIKDDDD
> Q4ZV89_PSEU2
MITPSRYPGIYIAPLSSEPTAAHTFKEQAEKALDHISAGPSGRELLQEIS
KLASKKDRKVTLKEIEINNQC YTDVLSRRQLEKYEPEDFNENRRIASRL
SRKGTFTKGECSNAIIGWSPDKASIRLNQNGSPLRLGMDNDDKITT LAHE
LVHVRHVLGSSSLADDGDRYNPRTGSGKEELRAVGLDKYSYS LTKEPSEN
SIRAEHGLPLRMKYRPHQ
> Q2RKJ5_MOOTA
MEQISIIADDLTGANDGTGVQFCQHGFRTMVIIDAANVERVGDQKDVWAIN
TDTRHLAAPEAYQRVYEITLKLKKAASRVYKKIDSTLRGHPGAELEAVM
DAWQADLALVVPAYPANRRLVVDGHL LI SEG METAAASVSLTPGDARAAL
CHIPTVLQGEMGRRVGQINLATVRQGVKELVAALEAARTNSQVLV LDAAD
EEDLRNIARAI SRFQRDVIVAGAAGMAAHLPLAWNLPV PNNPLNKKGAI
LLVAGSRNPVTAQVQRLAEVSACQAVKVE TEA ILTGEPAVEIERVLQEV
TTQDAGAGLIIIAVDSL FQTI DRDRVSN SSKAIALALGTITSRLLMRR
ISALVVTGGDTAVHVCRALEARGINLAADLLPGIPLGYLEGGRGDGLPIV

TKAGGFGSPDSLKVNFLQQRMKSEMELV

> Q8X4X3_ECO57

MPVDLTPYILPGVFS LSDIPQETLSEIRNQTIRGEAQIRLGEMLVSIKPM
QVNGYFMGSLNQDGLSNDNIQIGLQYIEHIERTLNHGSLTSREVTVLREI
EMLENMDLLSNYQLEELLDKIEVCAFNVEHAQLQVPESLRTCPVTLCEPE
DGVFMRNSMNSNVCMPLYDKMALIHLVKTRAAHPLSRESIAVSMIVGRDNC
AFDPDRGNFVLKN

> STM2879 sicP secretion chaparone 3023689:3024081 re verse MW:14449

LQAHQDIIANIGEKLGLPLTFDDNNQCLLLDSDIFTSIEAKDDIWLNG
MIIPSPVCGDSIWRQIMVINGELAAANNEGTLAYIDAAETLLLIHAITDL
TNTYHIISQLESFVNQQEALKNILQEYAKV

> Q8XQT8_RALSO

MDAGRLPPSFVPPATLSPDATAGDHTIQTQNEPPRSPRKRASDVTSNLPR
PARQPSAEPLPASPQAPSGFRTPVPLPASTSSTVTQTEAIQ PAPANIDP
PLLQQSMAAWLPADVDNARFTARSIREYAQEQGLPNDADVVAHLFNAL
PEDQRTEPNRELLDKAMQHSVNASGAAMLVNTDAGLQLVANSQRHKIV
IQTNGACEKGESIRQTVRREFKEELGNPAPNGILLGTLSEANLRAVNGLN
YIGHTAAEIAAHIVKVEADPSELFNVTSLFVNRAVPTMQALEAEVAHLN
ERLARAKPFYQEAHVHYIYGDAKTTFQQDAQVRGEAANVVKRFR QACPDNI
TENFAQCLDAIKADGTDDMDALKQALAAIIDLAENDAIKLIDEPTFAQAM
RLATRMDSDAAKTALENDYFDMSFIGGALHLGDAAPEAFMAQLKAGETA
PAIGRPVLNKDDAAQPEAAIRQAA

> gi|34498093|ref|NP|902308.1| hypothetical protein CV2638 [Chromobacterium violaceum ATCC 12472]

MTPDVTVAIHLNLSRQLAEGSGES LDIRECARLSLQMEKLAGKLPADSPLA
ELSERLALQGQAAWAQLARAEAEQTLLPQFQRYDRPGAGSEKHAGASVGA
GLGLGEGGAGAKATFSVGLGWGRSMDNDEGFFVFNKSHSASASAGVKG
VGIASLSGGVEGRVQKTRYREYNSAKAFVHLNAERLRHGSRRDTLGVGAR
AAVGALIRLFRPGHGNELQHYHRLQQQAADQQRLGVLQGWLGQRDASSA
LPGGRAPVVPVSGDVVSVKGSANAR AAAAGVSAGAAVSVERIDIQADSLTP
YWQALSAPEGAARSAVVAAQRQAGIEAKAQALFDGPKDKAGTRPLSRLTG
GGAASSAALRECSPAALRQAAERLGAELDHFCAVAQQLDAGVGKRQGGAQ
IEKSIVSSWQKRRDALANMALAHAALLIAARSRGDAGEAERALKDMAA
RLYAPPVRHNAEALSKRVAFRDTLELQIRNRSYALDLGGVGVPLGVKLEA
SLTEQHRVHLNPNVFRAGDYKDLRVTL SGSLGDAGALNKLKDALAAQLAPHG
LADALPAALAGMETALTGQLGAGATLLLRFYRPQYQQGADFPQEAAGFRL
QLARVVASGDASVALSGGVPLQPGVSLLELGLSAGGSASVVAYERWGDNTL
TAPMMHYLHLQGVGEFERWQGMADMQKPALSGLFRQLADPGSAVRKEAEY
FLKRQPQDGFGERFFAAMSGFSSGEVDFDARTALDEMQRQLPLWQADK
LAFPLVEQPLAA

> gi|34498037|ref|NP|902252.1| probable secreted protein EspA [Chromobacterium violaceum ATCC 12472]

MNTTVNQTTPGVNALTTGAADSSDNDYLRAARNYSLGQAITTMEEVML
LFTELSNAKFAQMSKKMEVSRDAAEMANKVEALLASITDPNGKASLPEDV
IEYMRKNGVAINGKSIDFLRDDADLDSRWALNNIHSYTIHTYFCLDSA
QAIAKNLDDAGVKI DGQKASDWLKNQENVVGSYSKEAMAKLFSNGRQLLG
RADLTAVKSALETFSGRASDFVQSSQLKMQQLIQNFNTAVTMANSLQSMN
AESTKSIAQAIR

> gi|53722547|ref|YP|111532.1| putative invasion protein [Burkholderia pseudomallei K96243]

MSARRAEARPRGYAARIARVAAAFAGIVSAGGVAHADCIDDAARRYGV
NADLLRSIAYYE SGLNPRALHRNGDGSTDIGLMQINSVHLPALRDQGIDR
LRLYDASINARVGAALLRRQIDQYGDTRAVGAYHSRTPGLSERYARAVH
DVYVARPWAAKAAARRDAAHTMPARAPGLVIEEASVQ

> Q8XAL7_ECO57

MLPTSGSSANLYSWMYVSGRGNPSTPESVSELNHNHFLSPELQDKLDVMV
SIYSCARNNELEEIFQELSAFVSGLMDKRNSVFEVRNENTDEVVGLARA
GMTIEDRDSYI RDLFFLHSLKVKIEESRQKEDSKCKVYNLLCPHHSSEL
YGDLRAMKCLVEGCSDDFNPFDIIRVPDLTYNKGSLQCG

> hopX2 Pma ES4326|Genbank: AF458041

MGLCVSKGSTASSPQHYAVRYTEQVTPSPSPSVASTSPSLHDSTAIGSPL
ARRSVLLPHEVQQAAAYQLAMRLNGRAIEDASDRKRLVDATATVHETRLAL
HRGRGKVDSDLRLSNGRSATYSSLSYCLGEDDENLLA GSALAAGAGNCDH

NAAINTRRHAVRMEDGGQMMTVRDYEQTHLYALYQPPNSAEAEDESTVVL
SWGDPVALLRDRSHWAESYGTSTHVIERFDKPDATDALARTNAFRAEIE
PQTALHANARELETAFLANPAPGDI FSAMPVIAPHLAESTRRRLQECS
TRNVLAADAARDA YGLDDAQANS PR TKAILKEAKRLDALGRPPLSW
> Q8Y1T1_RALSO
MRRIGNFFRTRSHASGSSRGR THERE EGSSGRAARSPSPALSDLPSSPRS
RHSVTVASPTRFDDGRVTPGHIQYQTSERERYPDLAEAVGHSRYTG
PGSPRPERFPISGYFPDQYF SVTGLRGP AIRSGDDAVIDRQHASHVIDH
GEMSDAQAGRFMDWQNR SIYPTYETSGWEYSNCVHGHAEVGRSVFGWDVY
PDQHARPDLDLADQMGNLVRNYSNDSDSG
> gi|28867816|ref|NP|790435.1| type III effector HopPtoH [Pseudomonas
syringae pv. tomato str. DC3000]
MITPSRYPGIYIAPLSNEPTAAHTFKEQAEALDHISAAPSGDKLLRKIS
TLASQKDRKVTLKEIEINNQCYTEAVLSRRQLEKYEPENFNENRHASQL
SRKGTFTKGECSNAIIGWSPDKASIRLNQNGSPLHLGMDNDKITT LAHE
LVHARHVLGGSSLDAGGDYRNPRTGSGKEELRAVGLDKYRYSLTKKP SEN
SIRAEHGLPLRMKYRAHQ
> gi|28872465|ref|NP|795084.1| type III effector HopPsyA(Pto) [Pseudomonas
syringae pv. tomato str. DC3000]
MNPIQSRFSSVQELRRSNVDIPALKANGQLEVDGKRYEIRAADDGTISVL
REQQSKAKSFFKGSQQLIGSSQRAQIAQALNEKVASARTVLHQSAMTG
GRLDTLERGESSTATAIKPTAK QAAQSTFNSFHEWAKQAEAMRNP SRMD
IYKIYQDAPHSHMSDEQQEFLHTLKALNGKNGIEVRTQDHDSDVRNKK
DRNLDKYIAESPAKRFYRIIPKHERREDKNQGRLTIGVQPOYATQLTR
AMATLIGKESAITHGKVI GPACHGQMTDSAVLYINGDVAKAEKLGKELKQ
MSGIPLDAFVEHTPLSMQSLSKGLSYAESILGDTRGHGMSRAEVI SDALR
MDGMPFLARLKL SLSANGYDPDNP ALRNTK
> Q8X9A5_ECO57
MPKISSVVSSCYHLFSEHQLSNETTMTNPVSRRIVHKEYGISLKSVPVW
LATAKTPLALLNGRHRTRSHSFI IAGTPGMGSRSGAQYYAINSDDKRSRID
IDSLFLKLNVRNQNKFPI DVKETVIKLGQKFTCIEDFYKRYNETRLK
ANTNIQQEQIADDEVKSLTYLIPSEKKEMWIYKNNGKDNAKPNLGERDVRM
FENISSDDTDKITGRKFSELGEYLYSGNVI KLSQLSIRYLPNISSISLIE
TKQSLLLHRLYSDEVLQRNGTLIPTPLHEEKSIPADNIKTMLNNIPTYKM
LPPFTETQGNCSGAATFLRKSGAEKDI LACSPRNYGLHHNIKTWDPLV
RN
> gi|12329056|emb|CAC05787.1| IpaH7.8, member of the IpaH family, secreted
by the Mxi-Spa secretion machinery, function unknown [S. higella flexneri]
MFSVNNTHSSVCSFSPSINSNSTSNEHYLRILTEWKNSSPGEERGIAFNR
LSQCFQHQEAVLNLSDLNLTSLPELPHKHSALIVENNKLTSLPKLP AFLK
ELNADNNRSLVIPELPESLTTLSVRSNQLNLPVLPNHLSL FVENNRLY
NLPALPEKLFKFLHVVYNR LTTLPDLPDKLEILCAQRNNLVTFPQFSDRNN
IRQKEYYFHFNQITTLPE SFSQLDSSYRINISGN PLSTRVLQSLQRLTSS
PDYHG PQIYFMSDGOQNTLHRPLADAVTAWFPENKQSDVSQIWHAFEHE
EHANTFSAFLDRLSDTVSARNTSGFREQVAAWLEKLSASAE LRQQSFAVA
ADATESCEDRVALTWNLRKTL LVHQASEGLFDNDTGALLSLGREMFRLE
ILEDIARDKVRTLHFVDEIEVYLA FQTM LAEKLQLSTAVKEMRFYGVSGV
TANDLRTAEMVRSRENEFTDWFS LWGPWHAVLK RTEADRWAQAEQKY
EMLENEYSQRVADRLKASGLSGDADAEREAGA QVMRETEQQIYRQLTDEV
LALRLSENGSRLHHS
> Q471Y7_RALEJ
MTAIQQQDRPLLGC IADDFTGATDLANTLVRNGMRTVQTIGVPAHAVRD
VGQADAI VVALKSR TI PAADAVSQSLAALEWLRAQGC RFVFKYCSTFDS
TDAGNIGPVAEALLAALDSDF TIACPAFPENGR TI FRGHFLVGDGLL NES
GMENHPLTPMRDANLVRVLQRQSKAKVGLLRYDAVARGPAATTARIEALR
ADGNHLAIADAVSDADLFTLGEACANLPLITGGSGIALGLPENFRAGLL
PQRGDAASVPRVDGHGVVLAGSASRATNGQVARWLEQGRPALRIDPLALA
RGEAIVDTALAF AANHDEPVL IYATSSPDEVKAVQAE LGVERAGHLVEQA
LAGIAAGLLARGTRRFV VAGGETSGAVVQALGVRALRIGA QIAPGVPATV
TLDAQPLALALKSGNFGGEDFFAEALAQ LGGQ
> Q8XUH6_RALSO
MRVLSRFSFTAQPRADS AEPKAPVAGSRGAAARPAALEKLTAFSRSNAA
KQANSFVRSPLPLRGDRYSSEPGVLP SAGQFDAHIWDELPTQMAQCAVAR

TRQGLAFRRRFGAESAQHYSGSCVGLSAVWIRLHEAAPATHAVNRVNTAG
SFDGMAHAKVYQRAYEANQSDMLQGRASKRFGKSDMARLDAIAQEQPSQI
LGLTIGTEAY SHKSVGSTARVLTEFDGYGLLALRMAGSRGAINGHAAALH
RQPSSSHITFFEPNLGEFHI PLHDTKDFLQAYAGMQKSLGQPVSQFDLLP
VGVHGSIHDTPLQTLAHSLSV

> A3M1Q5_ACIBT

MAQELLAQLQAGTAKFSDVLAYIEARYQHTPTAFQNGAQHNAATENQGS
KVFSAKLQGLDQVQTLTSLFAEHYASVLATPEGTDHQNIRQFMQNGWDG
VFEGQALTEK

> Q8XTS6_RALSO

MNGGFSVNRHGPVVPQDVGPRASADVDTPAASPAHPARTASGPLLGLRS
AQAQHAVAASGQAADGEIGPAIGAPDRLPEPRTEMAPPMSRAEQHLP
AVAGDEASRTDAEPLSGARKLPPEMWTVIAHRDPVAQQRLRVVSRTRAAAE
VGIRQLIVKTPPEGLAAVKRPGSYPNLRELTLVGNFWGNDLIGLPATLREL
DLSGCSGLRVTGLDPLLALPLDQLNVSGCRLGAEGARQLANHPTLTSLDM
RGNQIGDEGATYLDNPRLTVLVDVGNRIGDPGVIALARNTVLASLHLDG
NTFGLDGIKALAKSATLTTLNVGKNRIGPEGAEALAEHAALTLLIEENA
IGDRGAORLAANKILTTLNVRNNGIGPDGGLALAASTSIVSLAIGHNRIG
SGAVLALANRKLTSLDVEYTEISAVADAADAQAAAAVAEVAASALAAS
TLVHLNVGNTCLGDEGARLAASKTIKTLNISKIRLDGARALANRMI
ASLDLAGNVIGTPGVKALAAANTALATLNLRSQIEPEGVVALAANKTLAS
LDVGANKLDPDSLRLMLLTQMNLAVLDAFSGCEPGAGAEALTALAARIGVT
LRI

> gi|34498074|ref|NP|902289.1| cell invasion protein [Chromobacterium
violaceum ATCC 12472]

MSDASAIRSAYLHNPKLAETAFESVRKDGTFLLDAADKALKAVLATKAGE
ADGKAPIRERDLATPALTOPTAKAKEELDAGKLTLLLGQLMSLLGNVSL
SQLESRIATWRAMMEAQVAMGEKLSQEFQDAFKAASEATEALKDAVGN
YDSAKQAADAQKADAAQAKVDGMSDPDFGYAEAQAASQQAADALQAKQK
ADKAYDAAEKARVVAVEKGVADDLGKVVQGANVNADVARKTGEDNLSNV
AKLTLLMAMFVELVGNSEESLKNLALFQALQEGRQKEMDKKSAEYQEE
VRKAEELNRTMGCIGKILGALLTVSVVAAAFTGGASLALAAVGV
ALMVADEVVKAATGVSFMQEAALKPLMDKVLKPLMDLIGKAITKALEGM
GVDDKKTAELAGSIAGAVLAAVAMVVVMVVAVVVGKGAAGKLGALSKLLGDAIKKIV
PNVLKELAKGSKMLTQGFQRLANSLGLQTDAAAKQMMANTLGRVVVGG
EVAQATSQAGGNVAQGVFMKNASDALADFTLARAAMEQIEQWLKQAVEVFA
STQKVTQELTAMSAAVQQNAEAGRFLVLRQSHA

> Q8XB12_ECO57

MSVGNEEKYSITHKIDITNLIAGDRQSFLKLTWELFDLDFPMYHIKEAKE
TIVEFVTKTEDKVKRFERIKSLAIPPEKWRFTTTEFTVDENKDIIVSRV
FKININSKDNHNNAEENTMRSVLSEERNYSYKHDHIFDEKAFQSGILKM
QFPNDNEKLSVYLKNIIPFENMIDLSALKKDVLSLKQCCFKKMTFTGN
ISYENLNGPVFENCFEECNFESVSLVGFDKVTCESYDVLGNVKNPNNKIP
IYGMFKGCFLYQCMEKNFKIETSKIYSINQDPQRGDKKVGAYLFMQSFVY
ASNLDQGVCKEASVIASSLLSCNIAKLNQVGMDFIETSFYKTRGGFRDS
NNFYDCDFRYVNMTCRKGIREDLRDYDPRKYFGESENKNKLNLDKALLN
FIHDDIFQNIKHTHYNIKDDIDKHLNLNHCCLYAACLGELTGGNPLYDCAI
DTHTTILSGNLAAN TQVKIPVYMYHRGATAEKDILPFMEKVTNIYSRIED
IYKYSNNMKNNYKALADLQSLLVNLHNIMPGYDVKDFQLNDETIKYIID
NVLYNRKKDIASEIDTDKVNFMHKIYNNLYWYRHYDENGNEKTYRTANPN
GNRFYFDFAGLQVLYDYENKKNPTKEKFLEKQNLFLTVMKFKAEKINQ
EKYIEKPANVAHEIASFFDIEQYLLGGIDRNNNYINENFTYKFDLANLS
GTRDAQLERKVYFNEKMLNLDNDEKVKIENDIKKIDKIEIDNAIRDL
SSETERFKIKYQQENTLNDVVQNI RTWLKENQNMVKAIKKIDTE

> CNF1_Ypse

MKNQWQHQYFLSYSELVANFSPPEKVVSDYIKHKFSTTLPWFGWADPDNL
YFIRFTQSRSNKSYTGWDHLGKYAIELTLTLTQAAIVNIGSRFDIFDEAN
STAGIYKTNNSDFDETNEAKMLPSEYLYFLRDCDFSNLKALSDYWAE
NYEKFSTLLQNYIISAYLYKDSAIKDEYEFSDAIFNKKSKILRYFF
DVYGYSSDMFVAMNDNKTMLFIPGATNPFIFADNITDLRDKIKALISDK
NTRELFASKHFLYDRQDGNLYLGVNSMLEQIVSGVVDNTYIMYSNKNIRE
RNVFGSMAFSTRERSFNDGDVIKSNAEVQRDYALNVLQTIILSLSPIFDI
VLPEVSIPIISLGITASSVGISFDELINGDTYEERRSAIPGLATNTVLLGI

SFAIPFLISKA EENKLI INNLVGS DENILNKNLGD FLEKYNISESDIPE
NGSLVINLKNNTNVPVRLV LKLNDEEGEIVA IAKGSTLSGIYYEVD TETGYEI
LSRRVFRTEYNEKIYWTRGGGLKGGQPFNFEGLDI PVYFIDKPYSELASS
VELS FVNDDSP LFPFEMDSRLPKPT PELDIKYYSSNLS SFKEDTVILMRG
TTEEEAWN IANYKTAGGSNKDLEENFIEAGPQFNLSFSEYTS SINSADTA
SRKHFLVI IKVQ VKYI SNDNVLYANHWAI PDEAPVEVLAVVDRRFIFPEP
PVKPKLSFIQKIANRFLTENVAEISSINFRR LNSGNINVLKGRGVFSSRR
LREIYLRFDAANADELRPGDVYVKKTKFDSMGYDSHFYNEGIGINGAPTL
NTYTGEYVADSSSQGATYWLKYNLTNETSIIKVSNSARGANGIKIALEEI
EENKPVVITSGTLTGCTVVFARKGEYFYAVHTGNSESLIGFTSTSGVAKA
IEVLSLSELEVPALPDVINNTLVEYLSDNFDSALISYSSSSLKPNSMI
NISRENVSTFSYTDIQLPSFGT SVTILVRTNDNTVVRSLSESYTMNSN
SSKMVVFNVLQKDF

> CP0125 ipaA IpaA, secreted by the Mxi -Spa machinery, modulates entry of
bacteria into epithelial cells 107178:109079 reverse MW:70065

MHNVNNTQAPTFLYKA TSPSSTEYSELKSKISDIHSSQTS LKTPASVSEK
ENFATSFNQKCLDFL FSSSGKEDVLSIYSNSM NAYAKSEIILEFSNVLYS
LVHQNGLNFENEKGLQKIVAQYSELI IKDKLSQDSAFGPWSAKNKKLHQL
RQNI EHLRALLAQHTS GEALS LGQKLLNTEVSSFIKN NILAELKLSNET
VSSKLDDLDVAQAKLAFDSL RNQRKNTIDSKGFGIGKLSRDLNTVAVFP
ELLRKVLNDILEDIKDS HPIQDGLPT PPEMDPDGGPTPGANEKTSQPVIH
YHINNDNR TYDNRVFDNRVYDNSYHENPENDAQ SPTSQTNDLLSRNGNSL
LNPQRALVQKVT SVLPHSISDTVQTFANNSALEKAFNHTPDNSDGIGSDL
LTTSSQERSANNSLSRGRPLNIQNSSTTPPLHPEGVTSSNDNSSDTTKS
SASLSHRVASQINKFNSNTDSKVLQTD FLSRNGD TYLTRETI FEASKKVT
NSLSNLISLIGTKSGTQE RELQEKSKDITKSTTEHRINNKLVTDANIRN
YVTETNADTIDKNHAIYEKAKEVSSALS KVL SKIDD TSAELLTDDISDLK
NNNDITAENNNIYKAAKDVTTSLSKVLKNINKD

> gi|46400191|emb|CAF23640.1| putative CPAF (chlamydia protease -like
activity factor) [Parachlamydia sp. UWE25]

MNFFLNTFRSCAIFVLFYASLSFAS TEDIKKESMIEDLKM IKHAFDVGY
APLEWKKNYTG LNLDEELNKSIDLILSNPTLTHKDFQRIVKNFLASTKDY
HVDVIFFFSTETATLPFDVKG VNNRYFITWIDELKLPSTYTIKVGDEIIE
FDGRPLGDVIEELKQHGSKN SNPLTDQALAEIKLTNRLGWLGDII PQGPV
TIKVHSRSKEVPLSYQLIWDYRPELIFSPSFFLQTVESFFPNKKISVRS
CMTMMNLTHRKMSETKR DGTLCARKS FIPTLGP RVMMFDKIDKEKEISW
YAYIYKISEEEKIGYIRIPHYIGYKEESKEFGELLNYLEQKT DALVIDQV
HNGGGYASFQYELASMLALNPLKTPKHQMKITQKDVLTAYQILDVIEKIQ
QGIDDEIEEGPIDYQHLLFLKAFYEF TIQEWDGQRTLTDPHLEGCDWIN
PHSDYRYTKPILMLINELDFSGGDFMPA IMQDNQRAVLFGRTRTS GAGGFV
LQASFNNNGIAAFSYTGSIAERPETLL KIENLGVT PDIVYSLTVDDLQN
GYQGYKAAVNEAIQALIKK

> Q8XAL6_ECO57

MLSPSSINLGCWNSLTRNLTSPDN RVLSSVRDAAVHSDSGTQVTVGNRT
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TIERGVSVHSNR PDLPPVDYAQPELPPADYTQSELPRVSNNKSPVPGNVIG
KGGNAVVEDMEDTKVLKMF TISQSHEEVTSEVRCFNQYYGSG SAEKIY
NDNGNVIGIR MNKINGESLLDIPSLPAQAEQAIYDMFDRLEKKGILFVDT
TETNVLYDRMRNEFNPIDISSY NVSDISWSEHQVMQSYHGGKLDLISVVL
SKI

> gi|16764975|ref|NP|460590.1| secreted effector protein [Salmonella
typhimurium LT2]

MPLSVGQGYFTSSISSEKFNAIKESARLP ELSLWEKIKAYFFTTTHAEAL
ECIFNLYHHQELNLT PVQVRGAYIKLRALASQGCKEQFIIESQEHADKLI
IKDDNGENILSIEVECHPEAFGLAKE INKSHPKPKNISLGDITRLVFFGD
SLSDSLGRMF EKHLLPSYGYFGGRFTNGFTWTEFLSSPHFLGKEMLN
FAEGGSTSASYSFCNIGDFVSNTDRQVASYTPSHQDLAIFLLGANDYMT
LHKDNVIMVVEQQIDDI EKIIISGGVNNVLMGIPDLSLTPY GKHSDEKRR
LKDESIAHNALLKTNVEELKEKYPQHKICYETADAFKVIMEAASNIGYD
TENPYTHHG YVHPGAKDPQLD IC PQYVFNDLVHPTQEVVHHCFAIMLESF
IAHHYSTE

> Q1LMB1_RALME

MNRPLLGC IADDFTGATDLANTLVRNGMRTVQTIGVPASAVEADAIVVAL

KSRTIPASNAVAQSLAALRWLREQGCRQFVFKYCSTFDSTDAGNIGPVAE
ALLDALGSDFTIACPAFPENGRTIFRGHLFVADAL LNESGMEHHPLTPMT
DANLVRVLQGGQSAKVGLLRYDTVAQGANAVRARIDALRGEVVKLAIADA
ISDSDLFALGEGCAALPLITGGSGIALGLPENFRAGLLPARTDAAEVPP
VHGHGVVLGASASRATNGQVAHWIAQKRPALRIDPLRLARGDTVVENALA
FAGNHDEPVLIYATAQPDDEVKAVQAE LGVARAGELVEHALASIAASLKAR
GTRRFVAVAGGETSGSVVQALGVQSLRIGPQIAPGVP ATVTLDDAPLGLAL
KSGNFGGENFFDEALQALGAPQ
> gi|21231833|ref|NP|637750.1| avirulence protein [Xanthomonas campestris
pv. campestris str. ATCC 33913]
MLESADGCRRRYQKLNSTFGEPPDRRYVANVAKAHPKRDTRRYVTEAEPETV
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THVIPLTPLSSATSIVKSLTGKTRADQASWRFTVVVSLDAQAHPRYAPLVA
VDGTASATASFPLQGGKGI THYLVTATPYRYSEVPTGEEQLAGQAAARF
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> A2A0X5_ECOLI
MINSINSFFSGLPRS ISSAIRSSTFTVSQHKSTPNTVKTSSPFSNSNSPA
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> hopT2 Pto DC3000|Genbank: AA058036
VFCRRSCMNGCRITPARVGS PKTEASGLQLNSRIEKVVVEHISGHPAAKI
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> Q8X831_ECO57
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> Q8XQ98_RALSO
MRPDHHAIDIDPPAPQAEPPRAGAI AAPPVVPWRRPATLRALSHVQATV
SAVASAGFLAHRHLPGYGLDKAALGLALANVPLTWAIVHGQLQAIRAEAE
GLRHPPELRGQALDQVVKGFCA PDSAAARFDWNASGLFVNTMGMDMADEVS
HILARAFAAARTPAGSAIAPELRYADNLASS ATLRAALAQTA YEANVAC
DDRVGVRLEGELMLAGIMHMARDTTTEPRTVVGTLLVLAATRAEQRISAL
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ARLAHLAKPLQATAQRELATLDATLETLSDQQYRDDADKVKQDYDTAVAQ
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> gi|2865308|gb|AAC38400.1| EspF [Escherichia coli]
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QSGTGGLAGTGGGLGTPSSFSSNSSGVKGDPLIDANTGPGDSGTTSGEAG
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LKGLEATLKDAGQTATDVQSSAAQIATLLVSTLLQGTRNQAAA
> gi|55977843|sp|Q06131|YOPD|YERPS Protein yopD
MTINIKTDSPIITTGSQLDAITTEVTKQSSEIKKTEDTRHEAQAIKSSEA
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PEQVADQNKLALLDKEFRMTDSKANAFNAATQPLGQMANSIAIQVHQGYSQ
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> ECs4555 ECs4555 EspD 4592002:4593126 reverse MW:39083
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SKFGNVANKIGSSVVKVVEKAAEALVKNVFAKISTVAEGVTNGIRSAGTT
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MGVSFNGSPLKKK
> gi|15834669|ref|NP|296428.1| serine/threonine -protein kinase [Chlamydia
muridarum Nigg]
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> gi|15834868|ref|NP|296627.1| hypothetical protein TC0248 [Chlamydia
muridarum Nigg]
MKMNRILLLLLLTFSSAIHSPHGESLVCQNALDKLSFLEHL LQVKYAPKT
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SFFAVESAYLPYSVQKSSDGRFYFVDVMTFSSDIRVGDLELVDGQPVAE
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VKDVRAKWRYTPESVGDLATIAPSIKAPQLQKSMRGAFPKKESVVFHQSST
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HAYIFPLVDENGRSHNVGFIRIPTYGWQEMEDLDSIGTPPWEEFGKIITL
FSEKTEALIIDQTNPPGGSVMYLYGLLSMLTDKPLDLPKHRMILTQDEVV
DALDWNLLNLENDTNAEARIALGDNMEGYPIDLQAAEYLSFAHQVLACW
KNGDIELSTPIPLFGFEKIHPHPRVQYTKPICVLINEQDFSCADFFPAIL
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F
> Q8XTA1_RALSO
MGCFNVTGTSGTASNYVAREHSVEASPTHPTQQTGRRRAPGTPPSRASNT
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STAQNRLAQLEGRVNSFYTTNPVGHQDLQSDRFSDTASHASDIYHPSDS
FRFMSYRPGR
> gi|15834667|ref|NP|296426.1| hypothetical protein TC0042 [Chlamydia
muridarum Nigg]
MEVNKTTESLFSAKVEHNHAQAESHEPRDQRDVKVFSLGGKSSSKQEKLD
HSGRTSSRHETSRSKESIEDKSAEVSSREEEENRDGFLSGGNLTAG
VAFTDTPMAVASEVMIEETNAVMTMSQIDLQWVEQLVLSSTVESLLVADVDGK
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VQONPEQLTSLVESLSKSRQLNLTTELVGVNAVSLPVLEKVVETPLHMIAAT

IRHHDQEGDQEGEGRQEQHQGRQEQEKKLEEAQI
> YPCD1.06 yopE putative outer membrane virulence protein 3600:4259 forward
MW:22987
MKISSFISTSLPLPTSVSGSSSVGEMSGRSVSQQTSDQYANNLAGRTESE
QGSSSLASRIIERLSSVA HSVIGFIQRMFSEGSHPVVTAPTPAQMPSP
SFSDSIKQLAAETLPKYMQLNSLDAEMLQKNHDQFATGSGPLRGSITQC
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AANEIKGLAQMQKLLSLM
> gi|50121031|ref|YP|050198.1| harpin [Erwinia carotovora subsp.
atroseptica SCRI1043]
MLNSLGGGTSLQI TIKAGNGSLFQSQSSQNGASPSQSGFGGQRSNIAEQ
LSDIMTTMMFMGSMGGGMLGGGGLGGALGGGLGSSLGGGLGGGLL
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> gi|17428371|emb|CAD15058.1| GALA PROTEIN 4 [Ralstonia solanacearum]
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GELTLEALKALPPELEHLEIGRCTGSAISAEGLAHLASMPKSLNLNGIE
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RDGAQALAGAPLVSLNLHNNEIGNEGARVLATSRTLTLSDVSNNGVGNAG
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ALADSESFVSLKLGNEIGADGAELARNVVLQSLNLSYNPIGFWGVN
GRAKLRKLDLCACAIDSDGASALARNTSLASLYLGSNRIGDDGARALAKN
STLTLNLSGNNIHAVAQAALASNDLITLTLNRSNIGDDGTAALACHPR
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TLNVSYNAIGEAGARALAESVSLTSLD ARRNGIGEDGAKVLEANTRITGT
PQNPFLAEDVPRPDVWRD
> Q8XC43_ECO57
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EGSSPPQSFL
> A1WKP8_VEREI
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ALKSRTIAASVAVARSLAALQWLRAQGAQQIYFKYCTFDSTAQGNIGPV
TEALMQGLSDFCIATP AFPDNQRVFNGLYLVGERLLNESGMQNHPLTP
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DAVCNADLLRLGAALKGMPLVTAGSGLAIGLPGNFG LAPGNEADRLPAAQ
GLQAI VSGSCSVATNQVMDFIAAGKPALAIDPLRIASGMDMVAEALAWA
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GVRQLIVAGGETSGACVQ ALGIAQLRIGAQIDPGVPWCHARSPLAPEGLH
IALKSGNFGRSDFRAAFARLPA
> gi|28867285|ref|NP|789904.1| type III effector HopPtoK [Pseudomonas
syringae pv. tomato str. DC3000]
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PVNDQDRAPFRALERLHAELFRGGPIEFVPRGSNVLASNVRDVMDEFDV
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> NleB_Crod
MLSPNLVQLQFNFRGETALSAPLQTVSFAGKDYSMEPIDKTPILFQWF
EARPERYKGEVPI LNTKEHPYLSNI INAAKIENERVIGVLVDGDFTYEQ
RKEFLSLEDEHQNIKI IYRENVDFSMYDKKLSDIYLENIHQESYPASER
DNYLLGLLREELKNI PYGKDSLIESYAEKRGTWFDFFRNLA VLKGGGLF
TETGKTGCHNISPCGGCIYLDADMIITDKLGVLYAPDGI AVYVDCND RKS
LENGAIVVNRSNHPALLAGLDIMKSKVDAHPPYDGVGKGLKRHFNYSSLQ
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> gi|15723940|gb|AAL06387.1|AF311901|39 EspF [Citrobacter rodentium]

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KDHLAAFEASKSLEASSLKPARPAPQSPPTNGQSTGRSQSLPPIAQALKDHLAA
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G

> gi|12329057|emb|CAC05788.1| IpaH4.5, member of the IpaH family, probably
secreted by the Mxi-Spa secretion machinery, function unknown [Shigella
flexneri]

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QAVRLLKICLDTREPVNLNLSLLKLRSLPPLPHIRELNISNNELISLPEN
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> gi|17427254|emb|CAD13773.1| HYPOTHETICAL/UNKNOWN PROTEIN [Ralstonia
solanacearum]

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> Q8XQE6_RALSO

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QQAQWKPHALPGKMRAPITLLGRQLDGEAWARAGSMLLKLGAAGGIRAYEV
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GEIKARRVGVVPRMPGSADGWGVETLATSPGSPDKGAALH AVFRSSEGGQR
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GGSQLLALELGGNMRALPARPGVAVAAVPAQRVVSQVSVLAASAAPIRDF
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FALAHSPSQDGGAAPQLSLLRYDHASASWADCQAGLSVLDPE TVRLGISR
LGTLQLTTGGADGEQRTHRVVPPLGAQKRYRLLATGTTEPTVSQALTGNR
PKRVRIPTGTVVATLHRTAGGVTERVQSNFRTAVGHVERVFLAMPKGA VNR
AMEHLRGRRDMAEYDDMKATHLELEPLLHHRHWPLPPTVAAGPAVAVPV
PEATAQACAALRGDAIDKMLGALAQIGVAARVLGPDLLDAAAGRRKQRR
PAKAKPDPDDL PKMHSWLDEFVRRAEAQAKPSPEAGAKAPA PVFDPARL
GDLHRIVELMHTLSEHGKLPAPDLTGQRDTRDRFALITGAVGRHLLTLD
LATRLVTLPTQTVAVIGSDSAVEVLRQSVETDKVLRRLARFGFSNWHDAEF
WETAQTFKKEVMKPGSPFNKFAESHAVRDASSPAEMALKFAEAMKGLSN
RSTLFGIESKASAGVTSAGVVLPKRVGAFGFVAVLGVDRITMVGVERTA
DKLAEGPLVAFFVRQSNKGLTMGGMGMDFKPLRKVLGFRLLQGAQASAS
VMHGKGAAMLVAPDNIDEFARRLFDPAHDPGRLLLELGLNQGAIGLDMIE
QQNLNSANAGGLGGYADKIPGFGPAHRHGDGSSSAFQQTGLQRGFVGN
VNWGVRDFFLKQLHAWEPISGYEYQGGRGWSANAFASLVQQGGLPHVSD

AFTLVLRSLNITLLGASVELSGVESFKRTLWDKTAARVTPQEWSQLAALA
REVFPSSQAIGHFDGPHLKAI IATTLQAAKSTWAARTEHERASFV DRAEQL
LLQDQLASGGRAMLLPGAKIEFNI PNFRSLVDTRKNSKAHRSLGALMEAA
ERAREAVPGLADAMRAMSERDGVNDVRFVFMQDPSY INAVNRLMLEGKLS
WAEFNTMARTVPAPYRLTEICAKSDSNRSAFTLNPLPLLAFNDAEVS
SLFAAEVHLRYGLNGRLLGADLLPGAQRAVAGQKVLQPFVDAGVQVPVAA
GGAAPAQAPDLPRQRSQSLPSERPAGPALKARSLERSKSLE

> Q8XC86_ECO57

MNTIDNTQVTMNSASESTTGASSAVAASALSIDSSLLTDGKVDICKLML
EIQKLLGKMVTLQDYQQKQLAQSYQIQQAVFESQNKAIIEEKKAATAAL
VGGI ISSALGILGSEFAAMNNAKAGAGEIAEKASSASSKAAGAASEVANKA
LVKATESVADVAEEASSAMQKAMATTTKAASRASGVADDVAKASDFAE
DLADAAEKTSRINKLLNSVDKLTNTTAFVAVTSLAEGTKL PTTISESVKST
HEVNEQRAKSLNENFQQGNLELYKQDVRRRTQDDITTRLRDI TSAVRDLLE
VQNRMGQSGRLAG

> SIPA_SALEN

MVTSVRTQPPVIMPGMQTEIKTQATNLAANLSAVRESATTTLSGEIKGPQ
LEDFPALIKQASLDALFKCGKDAEALKEVFTNSNNVAGKKAIMEFAGLFR
SALNATSDSPEAKTLLMKVGAEYTAQIIKDGLKEKSAFGPWLPEKKA
EAKLENLEKQLLDI IK NNTGGELSKLSTNLVMEVMPYIASCIEHNFGCTLD
PLTRSNLTHLVDKAAKAVEALDMCHQKLTQEQQGTSVGREARHLEMQTLI
PLLLRNVAQIPADKLPDPKIPAPAAGVDPGGKKAEPGTGINININIDSS
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ESHSTNSSNVSHSRVDSTTHQTEETAHSASTGAIDHGIAGKIDVTAHA
TAEAVTNASSESKDGKVVTSEKGTGETTSFDEVDGVTSKSIIKGPVQAT
VHGVDNKKQSQTAIEIVNVKPLASQLAGVENVKTDTLQSDTTVITGNKAG
TTDNDNSQTDKTPFSGLKFQNSFLSTVPSVTNMHSMHFDARETFGLVI
RKALEPDTSTPFPVRAFDGLRAEILPNDTIKSAALKAQCSIDDKHPELK
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IGDGSWRAGPAYEYSLNKPQVDRVITTVDGLHMQR

> gi|34498032|ref|NP|902247.1| secretion system effector [Chromobacterium violaceum ATCC 12472]

MPGAGLPADWAEKEEGKSGAARKVGDVAVKMSRPLAEVQSQQLGQLASPR
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QQDKAKKAGILSVVFDWVVAAVEVVTGVAKMIGGVMGTGNVQAAGGAMDL
VAGMAGLVKAMANTMALIDPENAEKYQKVADIAGKIQLSFEIAGAVVDVT
SAARNLLVTKMI PKVAGKVLKEGAEQMVSTAIKKGTTAGAAKNAANAVGKQ
VADQVATQVAQALGKAAVDAKATTKKTVEKFAQKFTNQMLERFTHAIE
KMVSKSVEKVIKKAKEGVELTAQEVTKRNVNQVFADV KATIKATLKAP
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FEFYEQEKKEVIKKTRELLDSKSQVIDDGLQAMSQAASTQAQIASSMV

> gi|58579689|ref|YP|198705.1| HrpF protein [Xanthomonas oryzae pv. oryzae KACC10331]

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AYMSLNLSTGSNPSQLLGTSSNESSSELFGSDSSNDGSDLPSTMDTIF
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SWPSLGYDFDPKNIKGKDAPPALLEGSTVTWNDGTLTKSELQIVSTLNAHK
DQMPIEYKNLDDKINDPSTPPDLKALQGLKQDPRLLFAIGSQGDGKCGG
KVSAQDLWDFSDSHPQVKDLGGKNDEFNPKDIKGSNPPQAAEGSTVTWND
GQLNQSELEIVSVLDRHKDQVDSLQDLDAKINDPSTQPDLLKALKGLQ
KDPRLLFAIGSQDGKCGGKIKAQDLTDFSYHPQIAEYNDKKAQSYTQN
YIASDSPDKTKASVMTKSDALREMYRYSYDLPGNLSEDEFKIVDGDST
GKCPPQLIAAAQYFRDHPDEWKEFGDAGTMSTPDFLQKSTSEMHLTAE
QKTLDTINSHQDAFYGDGKELTRDKLDAISKDNKADPAVKEAATQLASDP
LLFGLLNNSITG YKPPHFFGGGHVVDGSKI SQNDFRQFYDHMSAANKTV
NTPATHEASSPDQQKAVADMLMGKDDPPAIKPKKDVGTFFQQGLHEFLKW
DSKILDWMSVGLSALNGIPVIGEIAAAAAIALESEAQAQVVDTAIQGGD
MSLALKLAGINMAGAVVGAVGGPTARIGAKGAAKGVAEVAKEAAEGA
GAKGTAKGAAKAGAKTAAERPSAAAFKGYVAGSTISKSTEILKPKVMAGLHY
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IRRR

> Q8XR46_RALSO

MERISTNAISKTVARSDLNSGSSAPPRKKNKNGSPRRRAHAPLLPLADRSLT
AISKPNETLGSRLAPVQRAVHASAVPSAAGNWNPLSRLKPEELAGIPET
VVEKLGKDLHDLYEDVQSKGLNYVPVFGYLSLRYKNFHELKGRSQDEVRE
GKDWPASLDNHALDFVMSTQYRGHHQHHPGVVAGLSQSEGSAMDG VILKL
PVGNAEELLARVIRRELLDENDLIHPVPATPPAGTTGLAGSATAGPATPL
SPKKPRSNLMYSSAVRPVTLPNGAKVRALVFVTNPDSAKSLASVFKDREG
VSPQRLAYLMTSTSKGDLGGPAIDYWKRFVETCETAKTAVPPIVSAIRL
ASDWPDAFTGEPAPDDMPRQHQAAWFRAMAGAAAPRRVWHERKPEPSP
DGASAGGTLGTQPKPD
> gi|53722549|ref|YP|111534.1 | hypothetical protein BPSS1528 [Burkholderia
pseudomallei K96243]
MPPSIHRTSSINSTPAVTAAGARRASGPGVLSADVARVASARRHTMPEI
GARRGVDGDRAAPAPRESFRRRLETVSSRAPTPPEADSRANARTTGAA
DGAGATGAAAGPSHGATSLDAARAYLAELAGDRGGALTTLVAQLNGHRR
ALDHLALTVHALHLSVDDASHAKTFAGIGDALASFL AAAARANAKPGSTP
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LGGRMDGHVRTNGMVNRHGGDAQRRMADAAQRFALGARHATNLVDMVGT
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TGSWSRDPASGRWLRAGGGVPLRSTEGFGRIDPFAGVQ RNASATGASAVS
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VTSNVTSNVASGVTSGVTSVAPDGTAWTRPSALAPRNIDPRRMNRAQLE
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> Q8X2D5_ECO57
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PAPTTPVQNEQSRPLPDVAQRLMQHLAEHGINTSKRS
> hopAC::ISPsy5 Pto DC3000|Genbank:
MRPIVAGLQVVAQTSAPQARNGKPVMTQKLPPLAITPTPLTPADTWPAAS
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FATQALMLATVARWLNTPTLQDALNLTLEQDHQDPLFTISQEADLYLEPF
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IRSTLLNPESEGYAYRRQINTLITQLQMKAAALRSVLKGHIEAAQYAWLK
QSLDNAHLNDPASREQYPLYPLQVHVDKPLIASGLNGVDQLVIPSPLLTH
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GRESXXXXXwcvllkengstasgvsqwlemwgswigyresapvlrsfqrq
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vvngrhyvelsgrtfqvyhdthlrgwqivdpenpfaffgqqpvrldeggg
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rdtwihrtplvnaegklylervrwprihl1kpfddmdalvaaleemnltr
vg

> gi|15723927|gb|AAL06374.1|AF311901|26 unknown [Citrobacter rodentium]

MNEQFLTDLAHTFGITLLEPTDALAFHDNDGHEWILECAPQSEILFFYCY
LSNTEPEQMNKILEINSNREMLGMFLLSLKENKVLLNIAFPANKIDITEF
TNLMENGYIIKKEIINSFLL

> Q7ADX5_ECO57

MPVTTLSIPSISQLSPARVQSLQDAARLESGIRISIGSGQYSVHYVQLLD
GFSVEPVRGGLLDRLGREGHRMDRRAVALERQLNGGVDFLSSVNNYFQSV
MAEHRENKTGNKILMEKINSCV FGTDSNHFSCEPESFLTCPITLDPETGV
FMRNSRGAEICSLYDKDALVQLVETGGTHPLSREPITESMIMRKDECHFD
AKREAFCKK

> STM1398 sseB translocation machinery component 1483934:1484524 forward
MW:21495

MSSGNILWGSQNPVIFKNSFGVSNADTGSQDDLSQQNPFAEGYGVLLILL
MVIQAIANNKFIEVQKNAERARNTQEKSNEDE VIAKAAKGDAKTKEEVP
EDVIKYMARDNGILIDGMTIDDYMAKYGDHGKLDKGGLOAIKAALDNDANR
NTDLSQGGITIQKMSQELNAVLTQLTGLISKWGEISSMIAQKTYS

> gi|28867731|ref|NP|790350.1| type III effector HoptoS2 [Pseudomonas
syringae pv. tomato str. DC3000]

MNINRQLPVGSRERLLTPDVGVSQACSERHYSTGQD RHDFYRFAARLHV
DAQCFGLSIDDLMKFSKDKHFRAEHPEYRDVYPEECSAIYMHTAQDYSSH
LVRGEIGTPLYREVNNYLRLQHENS GREAEIDNHDEKLSPHIKMLSSALN
RLMDVAAFRGTVYRGIRGDLDTIARLYHLFDTGGRYVEPAFMSTTRIKDS
AQVFEPGTPNNIAFQISLKRADISGSSQAPSEEEIMLPMSEFVIEHAS
ALSEGKHLFVLSQI

> avrB2 Pph race 6 -1448A|Genbank: AAZ37967

MGNVCFRPSRSHVSQEFQSEFSAASPVRTSERPSDASLDAGLESSSACH
RSLGRGPAKHSMLSLEEIGLVGAARWPDDAPGLNINSNKNTQENKRYCES
LYQAARIAGGSIASGRVTSFDGLWRNATKWRLSRILSGDASKIDFATVRM
PNTRFVTSLRRPYHSVIERVRNHS DANSEIYEGEYLGGIETKVYRQHGTI
SSTTIPMTIVSAVADDDDIHERLKS LPKNERR HLKDLMAASHPNMITHTD
AVYLPMIKDHLESYLYQAIDPSLEQHEALELIARIHWWAASAAPDRRGS
AKAEFAARSAIAFAHGIELPPFEHGAVPDIEAMLRSEEQFVEDYPNLFERP
PQ

> NleA_Crod

MNIQPNIHSGITTQNNQQHHAEQVPVSSSIPRSDLPPNCEAGFVVIPE
DIQQHVPECGETTALLSLIKDEGLLSGLDKYLAPHLEEGSLGKKALDTFG
LFNVTOQMALEIPSSVPGI SGKYGVQMNIKVDIHTTGNFYFLQLFPLHDE
IGFNFKDLPGKLNALTNSSI SATASTVAPTNDPMPWFGLTAQVVRNHG
VELP1VKTENGWKLVGETPLTPDGPKANYTEEWVIRPGEADFKYGTSPLO
ATLGLFEGAHFKWDLDNPNTKYAILTNAANAIGAAGGFVSKVPGIDPM
LSPHVGAMLGQAAGHAVQCNTPGLKPDITLWWAGATFGAADLNKAEFDKV
RFTDYPRIWFHAREGALFP NKQDIARVTGADIKAMEEGVPVGHQHPKPED
VVIDIEGGNSPHHNPSNYVDTFEIIQETRV

> hopAH2-1 Pto DC3000|Genbank: AA056770

MNINSIRSYDLSMAAPEKSAVTNKATLPVNAGNNDAPTTRQSKLDITYTAS

HKYDSSGRPAEAPETAPVYTKALLNRNAQLQKSAAPSDTAPAGQQQVATA
VTKNALQSNNAVTVEEKVSGPTPNASNADTGSHTGGANVDPGDIATPAAATK
MIQDLKGIIGGTLRIQMTHDQIQDTKEMDKLTALVNEGDKQGVKQVFTFR
DNANGGGSVLTGDKLNQASTDISNVVKKFGGHSSFVLDTFNEGGSATQ
GWADMESTLIKSARNAGYKGSIVVEDSNWGGGLTAGPESGLVKYADQLKA
ANGKGNPGLIGSIHEYASGADASARLNEIKALQONAGYKQI GEVGNANW
LGGDKFEERDGTAKAVRDNLAALKAAGADILPWKQFQDQGLRHHVGF
SKSDQY

> AvrA_Psyr

MWNVSKSSNNLGGAYKLPLEAQTPEKISPFDAMSAAQPEGKAPHDQLQND
QYPIQQAEDRGRHLKVEQAEIQAHVQHCHSKAPEIGDATKTSVSEKLGTA
KNSSCDASQILIGLISKNDDFHKNKAGSNGDINKSSDPSALRCSLSPAPRRV
PKSKKSYGAATIGGKVYHPHEKTDSTIADFLSRSLSNAYRSEHRLKRA
LAYLNHISAEKEITSNACFAMKDVNSFAHKQSEWLC HLESLWRDEPALQ
FHDRQQLGNEVLGLKPPDDQSPYFKPRAWKISDEAASAFAMMLKGESGPF
TQDQVKVGFIEICQEGELLAGRLKIQPRMAFRLKNRHDANRSGTHSVKSLS
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LTIDQAKHALIDLSDMDFRRNGPAVVMALRMNSLRKNQGLPYKEVDRCEV
FTHSYAEIHGAISLTDIGVDPADKVEVKNRLYGYTLD AKATLMKIADRSI
RRGVRSKVDIRSTSTSLQTPQLRRVLEKKKIVQKVAELYSEMKGAGNSAT
LKEAITKSSVKELLVNDKPVVSRDYALGEPLMVRSLRFSHDHEATSSFGS
AGKTPAKREVDTLCDNSTAFDIVMTPFSVINAKAKGDTISEMKVPHRPKW
KGLPSVLKYVTASVDLPEYAVARPGFGDIHSFNSNKAFFSSEFSSVRNSLS
HAEKMGFIENSLKPYIKHDPDRESFDFKHSIDELADAQ CMLQSRKPNSTL
RHNEYCAKLELWDAKAIIEVGMSRPVAVATLIEFNLEMLSAARYIEDEGYD
GKLIITNFLERQLSWFGQNAALNKEVTLKKLWGLPFDERKAVAEEKVCEALR
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PTVKSRL

> A1HAK7_BURPI

MSAAPTSTRPVLCIADDFGTATDLANMLVRAGMRTVQTIQVPGAGGEAIA
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DAGNIGPVAEALMAELGTDFTLACPAFPENGRTIFRGHLFVGDVLLNASG
MEHHPLTPMRDNLVPLVARQSASKVGLLRYDTIMRGAQAARDRAQQLRA
DGVKLAIAADAIISNDLIVLGEAFADLPLLTGGGSLALGLPAQYRRAGLIT
AHGNTAQLPIVADSAIVLSGSCSRATNAQVAHWRASRPAFQVDPALAEQ
KPVVVEALDFVHRHAGQ TVLVYATSAPEQVARVQQTGLGVERAGKLVEDAL
GRIARTLHADGVRFRFVAGGETSGAVVQALDVRALRIGPQIDPGVPWTAT
IDSDPLALALKSGNFGTVDFFEKALAQLAHATTEPIA

> CP0127 ipaC IpaC, secreted by the Mxi -Spa secretion machinery, required for entry into epithelial cells 110137:111228 reverse MW:38 861

MEIQNTKPTQILYTDISTKQTQSSSETQKSQNYQQIAAHIPLNVGKNPVL
TTTLNDDQLLKLSEQVQHDSEIIARLTDKMKDRSEMSHTLTPENTLDIS
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LAALSSSITGAVTQVGITGIGAKKTHSGISDQKALRKNLATAQSLEKEL
AGSKLGLNKQIDTNI TSPQTNSTKFLGKNKLAPDNISLSTEHTSLS SP
DISLQDKIDTQRRTYELNLSAQKQKQNI GRATMETS AVAGNISTSGGRYA
SALEEEELISQASQAEASQVSKEASQATNQLIQKLLNIIDSINQSK
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> avrB3 Psy W4N 15|Genbank: AAN85189

MGCVSSKASVISSDSFRASYTNSPGAFAESSSVHNRARTPRYGELQGPQ
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GEIGSFQELWDEARDWRASRAGADADVFLSPRDPNSYREYATPLAEQYSY
IKDRFANRKDGEVGS PADFLPKSKTFRISGKIDGQIPLTRITVSKDRHA
DRMADPYPRLRNQGHGDLGEPNLSHTSAEYVPMIMSHVESLHQSATDPS
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> gi|1330244|gb|AAB00 675.1| putative

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AQVDLRTLGYSSQQQEKIKPKVRSVAQHHEALVGHGFTHAHIVALSQHP
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VLCQAHGLTPEQVVAIASNIGGKQALETVQRLLPVL CQAHGLPPEQVVA
IASHDGGKQALETVQRLLPVLCQAHGLTLDQVVAIASNIGGKQALETVQR
LLPVLCQAHGLTPQVVAIASNSGGKQALETVQRLLPVLCQAHGLTPEQV
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QRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPA
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QLFRRVGVTELEARSGLTLPASQRWDRILQASGMKRAKPSPTSTQTPDQA
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> Q84H14_PHOLU

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ESVFNQLYVGGQKGFHIDSLVSIKQLQMDGLDPYAEQSQITESWLR ENG
IQPRSPLEVSGETGSKGTKDLLNAILDTGDKGSGYKKISFEGQMAGHTVA
AYVDDQKGVTFDFPNFGEFSFPDKTSFSNWFSDQDFWSKSMYNKEIGLGQN
FYVSNFEPKTR

> gi|53722631|ref|YP|111616.1| hypothetical protein BPSS1608 [Burkholderia
pseudomallei K96243]

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IGTLEMHGRLPRVEIGLLTSFAPGRVTRAWSEMLHRFLGWLIAQPGVYR
IEAFCSVTGKAAPLMPHFVCEATVRNYEARPNRGMASAGDLYLFAITKA
PQALRGAVEDEARAPSRQAA

> hopAX1 Psy 61|Genbank: AY349161

MNPIRNSPSFIPPAHSPATQAPSPGTALHSVVSRDSKA VAQLRNEGARA
NKLDAQGHSPDLVDLDMRDIDERSRSLRMALLQSLNPTAQLGYTKPEAL
HGTPWGLEILQSGALRGGVNDKGGTQSLEGKVFFSDRTRESASAETTRA
DFRSKPRVYARGEGMHPNSAYSRAQQHRMAQVILHALDNGRSLSTNELAP
SIEVSSPETLYIEGAAWLQRLHGGYINKLGGPLPFINAPLGEHLDSLRLP
GSIELRVDGQVKKLQGEELNRFYHQAASELQRSLENGKAP YLGLLNKGAI
VPLVGFGEKINNLSTHEIKLRSKTTQHSYQDTEHPLAGSPENGGKLEVE
VRS LGDFATLCLGAGQAGALNCLPT

> gi|19749309|gb|AAG45730.2|AF229441|1 Y4yB [Sinorhizobium fredii]

MEHCPLSAAQLIPTEEVNPDRVDALQAQILQTGSWTVPIAEKDALFVID
DYHRLTAAHRLRLTRMPVLLLDNDSVRVESWRPGGNITPAEIFAMARSGR
KFPYKTRHVFAGHGLPTCDVPLELLSSPTPMDIAPVFSAGAL

> gi|22658444|gb|AAN01357.1| avirulence protein [Xanthomonas oryzae pv.
oryzae]

MRPGKLCRDHRPLVWRRPCKEVCLMDPIRSRTSPARELLPGPQPDVQP
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DPSLLDTSLLDSMPAVGTPHTAAAPAEWDE AQSGLRAADDPPPTVVRVAVT
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TV ARHHEALVGHGFTHAHIVALSQHPAALGTAVTYQDIIRALPEATHEDIV
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QVVAIASHDGGKQALETVQRLLPVLCQDHGL TPDQVVAIASHDGGKQALE
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TPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQ
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GLVQLFRRVGVTEFEARCGTLPPASQRWDRILQASGMKRAKPSPTSAQTP
DQASLHAFADSLERDLDPSPMHEGDQTRASSRKRSDRAVTGPSTQQS
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> gi|16764411|ref|NP|460026.1| secreted effector protein [Phage Gifsy -2]
MPFHIGSGCLPAIISNRRIYRIAWSDTPEMSSWEKMEFFCSTHQAEAL
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DEDSQEILSVTLDDVGNVTVNCQGYSETHHLMATEPGVERTDITYNLTS
DIDAAAYLEELKQNPINNKIMN PVGQCESLMTFVSNFMNEKGFNDIRYR
GIFIWDPTEEIPTNHFVAVGNKEGKDYVFDVSAHQFENRGMNSLNGPLI
LSADEWVCKYRMATRRLIYYTDFSNSSIAANAYDALPRELESESMAGKV
FVTSPRWFTFKKQKYSLIGKM
> Q4ZYH0_PSEU2
MGCVSSTSRSTGYSGYESHEEPRAASRPTNSDDRGYETDSEPSSGNLIP
NARSVYSESVLWHGTSMSQSKIDLRKGFDAGRKTGGA TAGGNANMFMNLS
REAQSETRRRHHYLSSSQKEAKDFAMFADTSNPTLVRTIGVRNNLSLITDP
RTGGTALMTDQSI PRKFVLGSKSSAPGENAKVFRDEMRAAGHNVSTKQAG
ELLREVQSDSDDDNFDPDDFIMSRTG
> gi|11611727|gb|AAG39033.1|AF221058_1 avirulence protein AvrXv4
[Xanthomonas campestris pv. vesicatoria]
MKNIFRSLGLKSSRSSAPEPSYQAPSSSDNSPQSSPDRSSPARPTTFSGL
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KIRHALSRS
> avrRpt2 Pto JL1065|Genbank: L11355
MKIAPVAINHSPLSREVP SHAAPTQAKQTNLQSEAGDLLDARKSSASSPET
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> A2UK49_ECOLI
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> STM1184 flgL flagellar hook -associated protein 1267144:1268097 forward
MW:34175
MRISTQMMYEQNMSGITNSQAEWMLGEMSTGKRVTNPSDDPIAASQAV
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YKTF TDMQMSLFLQNLN
> Q1LK60_RALME
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DASNQLDTPAYVWVSGGLARSLSTVAQVTRAETTSPTVYHQGPVLTMVGS
MSGISGKQAAYL CERARMEALVVAPQTLRDGPGHPAWTTTRQSI TNCLSA
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> gi|4494850|gb|AAD21323.1|HpaA [Xanthomonas campestris pv. vesicatoria]
MIRRI SPGTLRPSVSI EHGSHHHGDH HADASGTSAGSPTDIAARAPRLR
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> hopAP1 Psy B728A|Genbank: AAY36934
MDPEKRVVISKTDQGESEANMPGHWTGCARPTRDPFVFPVAGRGESVA VRY
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VDEDSGAAEEELRTVGIQYEDEYPSENAIRREHGLAPRTSYSNGTGTNL
REPPERN SQYTEARLRSLNARRWSDM
> hopF3 Pph race 6 -1448A|Genbank: AAZ37227
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RLGDFIDRGGKVYLDNSAAGGDRQKTIPLVITLPEGQSVPAEKIVSAS
> Q8Y2V4_RALSO
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GSPAEGNARIFK GEMEADGHSISLEEAGDLLRAVQSDSDSDG
> Q8XAN6_ECO57
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> Q8Y166_RALSO
MGCVNVTGASGKASDYVAERHANQPSTEQAT QRPAARSAGQGV LQGLQRQ
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> hopAS1' Pto DC3000|Genbank: AAO54018 (N-term), AAO54017 (C-term)
MTLRINTRSATPVVPLETGSTSQPTPPPVTARATEPPP VANPAAPKSAPG
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> gi|12620462|gb|AAG60738.1|AF322012|43 ID84 [Bradyrhizobium japonicum]
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> Q8Y2L4_RALSO
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> gi|51591623|emb|CAF25427.1| yscH, yopR, lcrP; putative type III secretion
protein [Yersinia pseudotuberculosis IP 32953]
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> NleG_Crod
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> gi|28868062|ref|NP|790681.1| candidate type III effector Hop protein
[Pseudomonas syringae pv. tomato str. DC3000]
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> gi|17431349|emb|CAD18028.1| POPA PROTEIN [Ralstonia solanacearum]
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> gi|28871145|ref|NP|793764.1| avirulence protein AvrPto (DC3000)

[Pseudomonas syringae pv. tomato str. DC3000]
MGNICVGGSRMAHQVNSPDRVSNNSGDEDNVTSSQLLSVRHQLAESAGVP
RDQHEFVSNQAPQSLRNRYNNLYSHTQRTLDMDMQHRYMTGASGINPGM
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> Q6RK52_ERWCT

MADMTITLSIQPGAGLSSTGLNSPLSGSNGGASPRSGQQDSQLMEALSTL
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RSLLDQDSAGSALNNAINPTADGGGQLSGNDLLKALLELIGNLMDSQKGEF
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FDGGGKTFTASSKLGDDGQAE GQKPLFELAQQATLKNVVFQDAAADGVHV
RGDAKIDNVHWTNVGEDALTVKSNSGK PANVEITNSSAQGASDKIFQLNA
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> Q8XQI6_RALSO

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> gi|15595242|ref|NP|248734.1| exoenzyme T [Pseudomonas aeruginosa PA01]

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MRGLDLA

> Q1QSJ7_CHRS

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> Q8X9A7_ECO57

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TCFCFYALPIYPLQNSI
> gi|15618615|ref|NP|224901.1| hypothetical protein CPn0705 [Chlamydomonas
pneumoniae CWL029]
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SKGNTRTESRKFADDEEKRVDDIEAEVGSKEEEQE SQEFCLAENAFAGMSL
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ELVLDASSSVPEAFVGANLTLVQSGQDLVSVKFSFVDTQMAEAAADLVN
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> gi|1772618|gb|AAC31975.1| HrcC [Erwinia chrysanthemii]
MRNALYALLFNLYRFLCWSLVLMGMLPGAHAATPPDWSKGAYAYSAEQTP
LSAVLQDFANGHGVLDVNLGNIEDVNI EAKIRADNAVAFDLRLALEHRFQW
FVYNNVLYVSPQDEQTSVRIEVSQDAAPDMKQALTGIGLLDSRFGWGELP
EEGVVLTGPTHEYINLIRNFSQQRETKEDRRKVMIFPLRYASVSDRTIQY
RDQRLVPIPGVATILNELMDGNRNTPAGAAGAGSGIGSDGGMATADGAGGG
LDASKSIEMNARSMARLASRNSGAAASASRKKDQLNGRVSADVRNNALL
VRDDEKRRDEYQQLIDKIDVQNLVNDIAIILDVDRALTALSRLEANWQGKL
GAVTGGANMMSGSTLFLVSDFKRFSADIQALEGEGTASIVANPSVLTLEN
QPAVIDFSRTAFITATGERVANVQPVTAQTSQVTPRVVGHGTSISSIQLV
IDIEDGQVETNTEGTASGVKRGTVSTQALIGENRALVGGFHVVEESGDRD
KRVPLLDGDIPIWIGKLFTRQHEVSRERLFI LTPHLIGDQNDPFRVVSAD
NRRQLNDAMGRVAQRNSKTDLFGTVENALRDLAGSQTPAGFTIDGSGPKL
SEICRTSPSMSYQSNRYQWYNSLSLTVGVVKNKTGTQPLRFDEASCANS
RTLAVAAPKPTTLAPGESTEVYLALLPAKNAQPSRASLIK
> Q0FF52_9PROT
MVTFLGCIADDFGTGATDLASMLARSGVNVSLRIGVPRTEPKNTADIE VIA
LKTRSI PASDANVESLSALKWKLQAGAKKFFLKYCSTFDSTSKGNIGPVS
EALMGQLGINQTIYCPAFPENGRSIFMGNLFVQKLLSESSMKDHPPLTPM
KDSNLRVLLLSAQVTNSVGLADHMI VNNGADILKEKLI ALKKGVAHVVD
AVA EKDLEIIANACEDMDFITGGSALAMPLAELYKLSGKISENNNIYRNH
ELTFGSSVLSGSCSEMTILQVKDFIERGAVAFQLDPIDMAENGIKKVL DW
LTEQDFTKNI I IYATADPNIVRTVQDR LGVENAGRIVEQGLSECAVKAKE
IGAKNFIIAGGETSGAITKALNISQLDIGIEIAPGVPTFFGTKNNQMAL
SLKSGNFGKVDFTEALSKLENL
> Q8XZK9_RALSO
MAGGRVGARAVRESAQTPVSADASTSTSAASPPAAAAARQAARPAELRGL
ASAPSSRASSSTGGLSRQASLPARAVARETPEAPVDVFNRTMRHVNAWR
AVAERERKLEALGPEHKGLSPEREMRYACDAIASIQTCQLAALAMKRQQE
IPPGWDVDGQEAELLQLLIVAADIGVCTRHE TLNKLADQDAVFRQRSGT
AEAETVSGPDGPRPDTIEEPEPAGATAPSPSEQAAISPLSALERE PGKIQ
AWLAEFTSCRSALDQIIRRAEVC GASRTVQTALDTMLPNAIYDKLRCCSG
MQALHGILAAASANRFVELSRQMALPDLAVRADELLAAWHKENAAMEAAV
DALVMHGAPDKPTQRLTPKALDGHQAVIEAYAEGLDVGLNLCLDAAADI
EMDDADGVWRSMMEVVHAI SAYSASLLELSETAGRAKTQPEAPQPEPESS
EAAPEPALSEPPAARPAGASGGMRRKHKRPGMRAAGPSVPEPVSARALV
PADTRTVAQKQADTLRRRCRIDRATVAQLGGDIVELAQRLGEDTRLVLSA
LNDRTDAVIAAKFIWGSVGRWFGEPRVRSKASLHAGDHDRIGRLTNW
LGALELIERHMA PLEADMLKRDYRYPKAKHLEKLLQAKGIEFVGVPGRLPP
TEDVNAVGTFLGMRIQFKPLSNRDQVAPWFVHLHTNRPVTAQALSTLAFE
DFTAVHLKTRDRDNKGAQWEAAMRALGYTEAKVHRAAIGEALLHKLFLVQA
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> YPCD1.20 yopT Yop targeted effector 12610:13578 forward MW:36308
MNSIHGHYHIQLSNYSAGENLQSATLTEGVIG AHRVKVETALSHSNLQKK
LSATIKHNQSGRMLDRKLTSDGKANQRSSFTFSMIMYRMIHFVLSTRVP
AVRESVANYGGNINFKFAQTGKGAFLHKI IKHSDTASGVCEALCAHWIRSH
AQQQSLFDQLYVGGGRKGFQIDTLYSIKQLQIDGCKADVDQDEVTLDFWK
KNGISERMIERHCLLRPVDVTGTTESEGLDQLLNAILDTHGIGYGYKKIH
LSGQMSAHAAIAYVNEKSGVTFDFPNFGFHFHS DKEKFRKWFTNSFWGNS
MYHYPLGVGQRFVLTFFDSKEV
> gi|28898430|ref|NP|798035.1| putative translocator protein PopD [Vibrio
parahaemolyticus RIMD 2210633]
MLDKIGGTGRGELYGLGDTIKTTKAEKTPETKLEAGAVKSNGESNVSGAG

RYQLDGPKAPAIISNQAVVANLMGELAPTIDLLMSTTAKVLNGEEVIKSP
SDAVSQSLSLTLTLLYQVSKLSREQQVLOREIAVEANVASLOSQAELNNS
ASAMIAMAVVSGVLAGATAIIGALGSFKAGKEIKTEMASNNVLKTQKAGF
DQVEELMNNGLSKTQQDQVKRAHSLAKDSIADTTAQLTSGGRKFDKLS
SNQAKNAILQALGQMANSASNVEQTKAQARSKDDEVQATRAQAAKQKADE
NIGFQEGLLKELRELFRSISDSQNQAWRASIPTV
> gi|58579719|ref|YP|1987.35.1| Hpa2 [Xanthomonas oryzae pv. oryzae
KACC10331]
MINSTIACQYVGKACNWQLEASPGPSPKRRVHAQLSRCGRWAGTGPQRIL
FAAALACAAPFARADCFEAAAGYQHVPNPWVLRRAIAWQESRGRADAIHRNN
NGTVDYGKMQINSIHLRRLFGYGISKEALMQPCVSVYVAAWRLREMTNKY
GNTWAAVGAYHSETPGERDKYAHAIHSILLRRGVIGE
> CP0130 ipgB1 IpgB1, secreted by the Mxi -Spa machinery, function unknown
113520:114146 reverse MW:23684
MQILNKILPQVEFAIPRPSFDSLSRNKLVKKILSVFNLQRFPPQKNFGCP
VNINKIRDSVIDKIKDSNSGNQLFCWMSQERTTYVSSMINRSIDEMAIHN
GVVLTSDNKRNI FAAIEKKFPDIKLEKSAQTSISHTALNEIASSGLRAK
ILKRYSSDMDLFNTQMKDLTNLVSSSVYDKIFNESTKVLQIEISAEVLKA
VYRQSNTN
> gi|27376899|ref|NP|768428.1| hypothetical protein blr1788 [Bradyrhizobium
japonicum USDA 110]
MQTARLNADVEDGLYDGRLEGELLQNDRVLFRLEALDGIARERVNSLRRAD
PDADVDEIEVYLAYQAQLRDALELRHNAPDMRFMNVSQVTEADVARAEAS
ARDGKRRNFGTI
> gi|15605308|ref|NP|220094.1| hypothetical protein CT579 [Chlamydia
trachomatis D/UW-3/CX]
MTTGVRGDNAPDPSLLAQLTQNANSASAASTGKNGQVAGAKQENVNDASFE
DLLQDAQGTGGSKKATANQTSKSGKSEKAQASSGTSTTTSVAQASQTATA
QAVHGARDSGFNSDGSATLPSPTGTEVNGVVLRKGMGTLALMGLIMTLLA
QASAKS WSSSFQQNQAIQNQVAMAPEIGNAIRTQANHQAQATELQAQQS
LISGITNIVGFAVSVGGGILSASKSLGGLKSAFTNETASATTSATSSLA
KTATSALDDVAGTATAVGAKATSGAASAASSAATKLTQNMESASKTLSQ
TASKSAGGLFGQALNTPSWSEKVS RGMNVVKTQGTAAKFAGRALSSAMN
ISQMVHGLTAGIDGIVGGVIGAQVAQEQRMAGMAEARAEELKSLNSVQAQ
YASQAQQLQEQSQSFNSALQTLQSI SDSALQTTASMFN
> A3LKPO_PSEAE
MICKRFAVNTPHPSLRRSCLAALACSALVAQGAFAASASEQANLEVMIRQ
LNALEDTARRSAQGADEPGQRFYFDYSRLAADLQRIRQGLQDYMTPSRAQ
PRDPSDLSGNYTLRGGPMP
> A0GC88_9BURK
MTATTKRALLGCIADDFGTGATDLANMLVRGGMRTVQTIGVPASNETVEAD
ALVVALKSRTI PAADAVAQS LAALDWLRAQGCRQFFFFKYCSTFDSTDAGN
IGPVTDALLDALS AEGKAGAF TIACPAFPENGRTIFRGLHFGVDTLLNAS
GMENHPLTPMRDANLVSVLQRQTESKVLVRYDAVAQGVSAVRDAFDTLR
NEGVRMAIADAVSDADLYVLGEACADLTITGGSGIALGLPANFRAGLL
KEQADAAQLPQVKLSAVLAGSASKATNEQVAQWRSARPAFRVDPLAAAR
GENVVEQALAFAPQPYLDKAEP MLIYATATPDEVKAVQRQLGVNEAGHLVE
NTLASIARGLHERGVRKFFVAGGETSGAVVQALDVHTLRIGAQIDPGVPA
TATTGAEPLALALKSGNFGTADFFEKALRHLNAAQ
> Q4ZX50_PSEU2
MATMRISSSPSPALGSIVNQPTSGELAAETPLAKASLTQGSAGGGQAFVQ
FGQANDSPSSFSGTQNGSSLMSLLTRS SSSDSTSSVDQDSEVSPMTSVS
STASASPTTASN PANAPSATD AAFLDNSEYSSPEALKRWEPMVANLPPEE
REQAAKELNRPIAAAWMAREDGPNAEKAMAFINANPALKTAVDVGKDGGN
ADGKITNKDLKAFAKNMEKAADNADKDVAKYMEDNPGADPQSLMVRSA
VMRANPLATAADPHHVAAGADKTDVDGNVSAEGLKALIKSNPGLSGTLK
QSSNMWSQAGFLSQVDEAGLTGRKKAHSPDQVFDASNSEWIRKSAPKN
GGQFASMLS DAATLNSVAGIDI SKLNAQVFEKPKAYTGAQKAAVMIKLQQ
TQQSVIAGRDLRNTTEKTEAGLNERIAQLQADPDVQEYLNKSIPEQERSLV
RSDSALQKAVTEQAQNVNSGKALQTDMATADKAVDKHNPDPYSGAITGL
SVQLQLQKDLFPDAQVPTAQQVFNNQPELQTKIADSYVRNFSEGGALKQ
LLGQKKS DAGESLQTADNQKAAYESVLPADFVNGERESYTASTLSELQNS
KKGRKLEGGTDEEGGPSLAAQL AEQGIGGKAFNSVMGFASVSDRLASGD

KLGAASQSIIDSSRLGAESIKGGIDTGAKMMGREASAGLGRGGQMIGRAV
GLVAGEATGLAAGAALGAAIPVIGWAIDGAMALGFGISAIIDAVKKHKAQ
KAFDHNVDPVLDQFGIDKAH
> gi|50121143|ref|YP|050310.1| putative virulence factor [Erwinia
carotovora subsp. atroseptica SCRI1043]
MKRLTPKQLSTRLHGQLQAVAQGVQAIQDWVETTRQNAPRLDIEADRLIV
KLRRNHNKAQHLSQVAQKEIAIGFFGLSQAGKSYLISSLAGGKLETS
FEGQQLDFVDHINPSDRATALVTRFSRQSGVKNKSPVQLQLSELDIGK
IMANAFLNDLNQETTFEELDERHIAEHIKTLLMHRQPEPVEGISRDEVVE
LWDYLVVRHDVQRKQLEAHFWPVAVELAPYLTVDRAQLFSVLWGELNSL
TSAYRHFNHTLQHLGASKLLAPLRTLVDDELNPADGLVDGSALERLHST
DDPSVLVRPVQNGRAGKTAELSLAELTMLTVELLIPLQSPKALFEQVD
VLDFPGFGEVRETRAAPPKAGQNTLYPLAHTLLRAKRAYLLERYTDNQEM
NVLVCSAAGDRADVGVGKALDHWVKQTQGENAQVRSRKPGLIWAIVTR
HDRRITHGQNYDAAVQRYVGNPGDAWGTMLAMDKRGVTRMATWLGTEVHR
EVKLGRISEQLNEIQRELSNLLGNWYLPVDVDDPAEKQRI AETLLKSLQ
TRTGTVHGELLERLLPSRDELRRLYLQQKGASYGGFHTDAEDLSAPLANS
PFGVIEIDLFADEPIAIDQPVMPVLTIDHGYEADYAHGVYRWINYLRG
LPENAPLLDLLNPKSTIEMLVEELITGSI RLRIEEALVDMLVDGEQLGI
NRENKADQVSRVLTILGDFVAWLGFQQQLDESLRPASRINRGHKIFAKPE
KQSVSFGASQRLTKLSLTPNTAFYIYDWLVGLNEMI IQNAGYSAAREV
SAEQREQLGTILALIKPAEK
> Q8XT98_RALSO
MPTSYVNLQDLTTEQDTSPI DAMPQMYIMGAPMVHVS PFESGSAVINVT
PECTYVENGEARSKESTRSQVELSEHMRSVMTSAGKGPLYRTNNMISELG
KLMPRMFGGAPEAF LGGHVCTVGSSDQRGTSITSVTDNALTIIAPKATSA
VTLDLAGKISTASRFNVH LPLKQEGDLQIRMDRDVLADKAAAKARKMGLP
VGMSRVLDRQPGQVQKSGRFASEFILPRGAEKMATGDVFDAAFRDRSGRM
HVVIDGIAYGQDRRLGSGFGGEAFIYRDPATSHEIVVKEYFRLRSQASPG
DMDVNPPKDAGKRAELEKI QMQDFMIEKSAFDALATHPAAKNIAHALRAG
TVDGRFTIVMPYFRGGSVRDLCKNLDKAVEDGII SVGQRRDSALYIMQGI
LNGMKYLSSTLIHRDLKPD NVLLHIEKERDGRVLI PKIADFGTSVLGTS
SDLPVVTTTPQYKSP EYLRAEQQGRGQHTAAQDVWSAGISLHELLTGHRPF
DGDLPKDEHKIYDAIKNYAAGNTEILPADQSKAADLIRIMMNPSSDRATP
AELLDHEAFHGINEKECQKTL SLIHQS
> Q8XUL4_RALSO
MKVGNQSNNVGHDFSVKGVAGSSRRD GAGLDIGGDTGGGLVDAVQRPRQP
TMLDVLPRLLK FATR I KQQRKMPSSHRL GRPSDLTEGGSSSGTEAGNGRF
KSRLANELASSGKPLKFNKWE PADRFQLSSESDSIVKRGARVQAADRNI P
SSNRFMSDLTSAQSTARALAKRPLQRLTLESRLDIHAHGND SYVEDLTAA
ELA AKLHDAGLEEVGLKIQACDVGKGHYLQALLEHLASRGVKVGYLCP
KGALTDTRTVENLGGGEQYVKKDVSFLPGKYVGWLPETFGLNVIKGNVDV
AFGGTRYNLSR
> Q6FEZ2_ACIAD
MVQELLKQLQNGEAKFADVLAYIESRFEHQPTAFKNGQQQNAATENQGS
KVFSLAQIEGLNQ TETLSLFAEHYAAVLNTPEGTDHQNIRQFMQHGWDGV
TFEGEALQAK
> gi|29839807|ref|NP|828913.1| serine/threonine -protein kinase
[Chlamydomonas reinhardtii GPIC]
MDCQSEMLSHNQVIGAYHIKLLSKKEGSTVYQGVHPDTLQPAAIKVLAT
PLVTDTPRVHNFLEKARIIEQISHPNIVKLYQYQCREGLYIAMEYIQGV
SLRHYILSQLIPLSRAIDIILHIAQAI EYLHSGILHRDIKPENILITSQ
GNIKLIDFLAISSIDKDARPLYLGTSPSYMSPEQRQGDKISELSEIYSLG
LIAYELILGNLALGKVVLSLIPDRVSKILAKALQPSPTDRYASMKEFIID
LHRYRHGEDLQKDLRNKDHTAMVNDQLYHQRFWLSPLEIVVPEYLA VSIH
EHGYPTHPHVYIEAYMSGDTFRLWFCYLSGNPTLVLTVMKSFVVSQWGHE
ENIRSTIRKMHSELMRINVPINGKISLFCVTIPKEKELSWIACGKTSF
RLKKQGVKPEIFTTSSAGLGKISSLQIQETKVAWEIGDGAVLHTLQADDS
MSSLHSPLFTELKDRGQT AIFCPIESVRYGIEENHDGNLCPSTLISLKRI
R
> Q4ZNB6_PSEU2
MINLTLNASSLARVALSDSTKPTIDRAMNVVSHIAGKVA LQVNSSLLEQK
GRLNERQQKGLEVILDALLGKEPVTHVETHEGGGRFNLARAADFVASVVW

ERDQSMRNVMSFLGINDSKGNLLFSLGKTLADAMARPEPENGGKHNSEANY
AFFSSNLKLNKLMNDIADQVINEIRQQNTDRVRRPTPGPSWRPESTQQQA
RPQTPPSARPOANSAPPPPKAQPDAGAQRPSTERPPKTTPTGASAKVDDS
APAKPPVKQLYEHLGLSDMTADLSAVKKAYKKAALKYHPD KNAGNVAEAN
ERFKKISNAFRILSDPELRTKYDNGVIDENGNEFKT

> gi|28867817|ref|NP|790436.1| type III effector HopPtoC [Pseudomonas
syringae pv. tomato str. DC3000]

MTIVSGHIGKHPSLTTVQAGSSASVENQMPDPAQFSDGRWKKLPTQLSSI
TLARFDQDICTNNHGISQRAMCFGLSLSWINMIHAGKDHVTPYASAERM
FLGSFEGVVHARTVHNFYRTEHKFLMEQASANPGVSSGAMAGTESLLQAA
ELKGLKLPVLEDKSNSGLPFLIACKQSGRQVSTDEAALSSLCDAIVENK
RGVMVIYSQEIHAHALGFSVSSDGKRATLFDPNLGEFHTHSKALADTIENI
SSADGLPLIGVQVFASKIH

> gi|12620505|gb|AAG60781.1|AF322012|86 ID186 [Bradyrhizobium japonicum]

MFQNTKALSNSERASELDEMGTSDDGSHDSDPRFLDVFALS LAPSSCS
VDASLAAVPPYALVDERPVVEISKSSFENKLADFYGGDIEDIAANPQRY
RWVSEKAHAQRTLHFASARSLFRNRRAFS AISLGRTRASGF

> Q3BYJ5|Q3BYJ5_XANC5 Xanthomonas outer protein D - Xanthomonas campestris
pv. vesicatoria (strain 85 -10).

MEYIPRYEALAEKVPVVRVRF HAYLRGDGSGFGPLPGILRYMTPDQKKRLLYL
ASERRKQALAAAPKSKPTPKSKPLKGVFRTLHQKPNLLLEISSKFSNRAYS
INDSSSGYLSQADLEEMVDEETGELTRLGEAVISGASQGIQTAIRANFRM
RYQQPDLPPYSPQAFHRPEETWNPHTPAGSSYSSLPPTPSGGWPQNAS
GEWHPDTPAGYSHRAWPAQPEASSSTFDDLES LDYRQNYGYREFDLNTPQ
EIEQPGWQQATPAQSTDST FDGLSSMSHYGSEFDLNI PQQEEYPNNHGT
QTPMGYSAMTPERIDVDNLPSQDVADPELPPVRATSWLLDGH LRAYTDD
LARRLRGEPNAHLLHFADSQVVTMLSSADPDQARAQRLLAGDDI PPIVF
LPINQPNAHWSLLVDRNRKDAVAAYHYDSMAQKDPQORYLADMAAYHLG
LDYQQTHEMPIAIQSDGYSCGDHVLGTGIEVLAHRVLDGTFDYAGGRDLTD
IEPDRGLIRDRLAQAEQAPAE SSIRQVPARSNEQKKKKKSKWKKKF

> Q8XR44_RALSO

MRGGTALISITRRRPAQPVAPAHHFS PGSA TSAPAPENTPRQQRRAGSAL
QRLAEIQTAQSASRPVVTG PSASGTGDATRVHRSMRDFLAEAPELHAGDT
AGGASPAEPAAPQKSSKSLAKFTGKVKKLVGKAKTAADRNFVSSQTSVF
GLHTETTGVKPVMTSATRPRPEVLQSRPVPAGTRPEDLPSVPATGPAQPA
ARQRKIDATVKA AFNPSSSIAESMRSHLGLGQDKVARQSVSIAEAMSSEA
GMRVHLARLLSQPLHAPAVRALHGALLDSL PQATESASGRGFAQHVVLLAE
ALVNACGGDTRATAALRALKAGEFLPTAHGTGDAASPRPSDAGAEDAAT
AQAEPAQHLARRIGNASANA IHPTRQTPVEHAML DAMHAAQGLAGIGDVG
MQALLAVMPPLQPAKREPLEFVLQAVEQVSVETKGAQVLLPDIIGHAEKM
AGTRDDTLACKVL RAEVKALRAADTYDALSRADKSAVFAWRQGF LTDDKH
SLLSQTQQRLAKFRKYVSRAETRNLNEARQD PARSTAATARLVANNVQR
AFSRKKSPLLAMGKYGSLAAGTRHVPTDQVELDKHMRTAIDALKDRLQTR
SSEARFSLGRYGEVPTVALRGAIL EHWASAASESKRPQGYTL DGNAMVDIA
ERLHRAIGESVVRADGRLPQQLERLIGTRLSHATLATWARDAMPQRTET
GEETA FSSAMRRAR NILEPGKDKPVDMTADSMRAFLKNFTGEHNVGNAMT
FTDGGALGVNTGALTLNLASLVKRFKGGFALTPVFDAQGSVARSAAFNIG
TTAHGGEI FIGRQRQVVGQLGGGLTAGYTTPTDADENSFSAGVIGSNVT
LFGLEHTNPTGVRLRF TTQRKDDGSAMNSDAMRKQMSDMVDMFEACGPD
KRHLSPSALWEDFAVHHFDQKNLSVAWEDYASVNSKMGASVTLTARAGVT
TQDQGTVRAGGSVGY GFTWNPFTIGQRQEKSGIAPILREDRGSAHLHAVT
VAASVQLPAGPLPDPDGAANSLGVPSPVPIASATYMLGNGGFNATIR TLM
ERGR LSEAFTYRDLSE RNINDFIKFANDPARRKEWEALCSAEQ GAYAAHG
EADAGPGKKRLDDFLDKIQEMARPNQAHYMRWRLGEQERLAMDDYMAAAR
MADRGGRGKDAKACLQAVEQIAAREASWRPAALFTMHGNSKQTD TGLNFG
LQATARTA AVSDRELI FIGLPLPISDAWTQAARDQADPTA

> gi|16519844|ref|NP|443964.1| Y410 [Rhizobium sp. NGR234]

MQLSRRAEIGNPSSRNLSPRINEKVELLQQALEHARRAGMSSSLMEYGRQ
VARHLSANVQPDEKILSLDIRNLPLLAASYNRRYPDLDLRHMDSPARFFD
ALNDRSSDGAWRAVRLADGEQHHVAADVTRAGAAPTII VMEGANFYTF
VASYFKLRGDSFRQLGTQA KWAFIEVGAQKSAADCVMFGVQFALAA YREL
PTFD AWHDLNHHHGTIAHEGDYSSDYMPRRHAGICANKPFSWGEVPPSDL
LQALSLOQC

> hopAG::ISPssy Pto DC3000|Genbank: AAO54435 (N -term) AAO54438 (C -term)

MNPITHSFSHLGFNSAQSTALAPGGNKVPNFVSRGRGKGVPLEHFNTAD
EYRLARQQGGVLSIDGREFMLLQKYTAAETSDEEFA DLRAAIPRYSID
LAEPGQTKVLYRGLSLPEKTAARLLNISWGYESREIAHGLIHGLRVVKEG
LKXXXXXVTLSESRPLPSVASKSEHEVILDITNRYEITHARREGAYIVVD
MNVLGRSKRGGEELEVIETDKWSQLSGAKGSNPGGLFQAPDGVKWKVKTNP
STNRLRNEVLASKLYRAAGIDVDPDIKMASRQGPALISKLIGGNHKDIKT
IEGSGQLRSGFAVDWANWDVIGQTDNIIFNDRNKPV RIDLGGSLLEFR
AQQGGHKGNGFGNTPMELVTMLSRKENTSSHAFRKIERNDIRMGIAAIERI
PDDRICALCAEHGPGNYSERIELGKRLISRKHWLVNMKQALPHIHRQNE
GGDVVIVKNRTPSPDVRALSDSSATAVFPVPHRVRGSLNNIPFKSFAPPD
TVDGVRRHRHTHAVDFKEPEFKFSNHLAPASGAIIFEPDGRWLWITEPTNHP
FGATHAFPKGKLEPGLNLRNALKEVYEETGLKVELHGFI GDYDRTTSTRT
RYYLAKRVDGTPSDMGFESQSVKLARITEAGKLLTRGASGISEIDHTILV
KAAEVFRLNPF

> gi|27735216|sp|Q04640|MXIC|SHIFL MxiC protein
MLDVKNTGVFSSAFIDRLNAMTNSDDGDETADAELDSGLANSKYIDSSDE
MASALSSFINRRDLEKLGKGTNSDSQERILDGEEDEINHKIFDLKRTLKDN
LPLDRDFIDRLKRYFKDPSDQVLALRELLNEK DLTAEQVELLTKIINEII
SGSEKSVNAGINSAIQAKLFGNKMKLEPQLLRACYRGFIMGNIISTTDQYI
EWLGNFGFNHRHTIVNFVEQSLIVDMSEKPCSNAYEFGEFVLSKLIKIM
IRTSDVIFMKKLESSSLLKDGSLSAEQLLLTLLYIFQYPSSEQILTSTVI
EVSRAHEDSVVYQTYLSSVNESPHDIFKSESEREIAINILRELVTSTAYK
KELSR

> Q3BWS7|Q3BWS7_XANC5 Xanthomonas outer protein O - Xanthomonas campestris
pv. vesicatoria (strain 85 -10).

MINTSVKAINSHHTSSSSEEPKRQSRQADAGADPTRIHPALEGLPSIRQ
GMQATRRDATKTSLSLEHSRTEAFKAQRQAISMQPGPSNPHLTALDKLQ
ERDFEPALGGVKIPLTLNLSLPGGKRVQVAGTSSRDVHVVPAGIRSELQE
AITDKQLLIQTLRQDLQEARNQG NPALIAQNERLLEQANADLRSLLGQVA
VYGEESRRINR

> A0UH23_9BURK
MTASASRPLLGCIADDFTGATDLANMLVKSGMRTVQTIGVPAESASIDAD
AIVVALKSRTI PAADAVAQSLAAYEWLRAQGCRQFFFKYCSTFDSTDAGN
IGPVADALLDAAGGFTIACPAFPENGRTIYRGHLFVGDVLLNESGMENH
PLTPMKDANLVRVLQRQTSSKVGLIRYDTIARGAADVRACIAQLRADG VR
IAIADALSDRDLYVLGEACAALPLVTGGSGIALGLPENFRRAAELAARDN
AASLPRIDGTATVLAGSASKATNAQVAWRATRPSFRIDPLAAARGEPPV
DQALAFARSHLPEPVLIIYATATPDEVKAVQALGVEAAGELVERTLAAIA
HGLRALGVRKFVAGGETSGAVVQALGVKSLQIGAQIDPGVPATATIDTE
PLGLALKSGNFGAVDFDKALRALDGAA

> gi|16767411|ref|NP_463026.1| putative cytoplasmic protein [Salmonella
typhimurium LT2]

MIPPLNRYVPALSKNELVKTVTNDRDIQFTSFNGKDYPLCFLDEKTPLLFO
WFERNPARFGKNDIPIINTEKNPYLNNIIKAATIEKERLIGIFVDGDFFP
GQKDAFSKLEYDYENIKVIYRNDIDFSMYDKKLEIYMENISKQESMPEE
KRDCHLLQLLKKELSDIQEGNDSLKSYLLDKGH GWFDFYRNMAMKAGQ
LFLEADKVGCYDLSTNSGCIYLDADMIITEKLGGIYIPDGIYVHVERIDG
RASMENGI IAVDRNNHPALLAGLEIMHTKFDADPYSBGVCNGIRKHFNYS
LNEDYNSFCDFIEFKHDNIIMNTSQFTQSSWARHVQ