

		βA3	H1	βA2	H2	H3	
AOX	<i>Candida boidinii</i>	MAIPEEFDVIVCGGGSTGCVIAGRLANVDE-NLKVLLIENGENN-LNNPWVYLPGIY	55				
AOX	<i>P. angusta</i>	MAIPDEFDIIIVVGGGSTGCCIAAGRLANLDDQNLTVALI EGGENN-INNPWVYLPGVY	56				
AOX	<i>K. capsulata</i>	MAIPDEFDIIIVAGGGSAGCCIAAGRLANLDP-ELKVCLIEAGENN-LNNPWVYLPGIY	55				
AOX	alcohol oxidase <i>Pichia pastoris</i>	MAIPEEFDILVLGGSSGSCIAAGRLANLDH-SLKVGLIEAGENN-LNNPWVYLPGIY	55				
AAOX	aryl-alcohol oxidase <i>Pleurotus eryngii</i>	ADFVYVVVGAGNAGNVVAARLTE-DP-DVSVLVL EAGVSD-ENVLGAEAPLLA	50				
CHOX	choline oxidase <i>Arthrobacter globiformis</i>	MHIDNIENLSDREFDYIVVGGGSAGAAVAARLSE-DP-AVSVVALV EAGPDD-RGVPEVLQLDRW	61				
GLOX	glucose oxidase <i>Aspergillus niger</i>	SNGIEASLLTDPKDVSGRVTDYIIAGGLTGLTTAARLTE-NP-NISVLVIESSGYESDRGPIIEDLNAY	68				
		<u>D.iv.GgG..G...A.RL.....V.liE.G.....p.....y</u>					

		H4	H5	H6 (3 ₁₀)	H7	H8	βB1	
Cb	56	PRNMRLLDSKTATFYNSRPSKHLNGRRRAIVPQANILGGSSINFMMYTRASASDYDDWES---EGWTTDELLPLMKKFETYQRP-----CNNRDL	141					
Pa	57	PRNMRLLDSKTATFYSSRPSKALNGRRRAIVPCANILGGSSINFLMYTRASASDYDDWES---EGWSTDELLPLIKKIETYQRP-----CNNRDL	142					
Kc	56	PRNMQLDSKTATFYTAEPSPHLNGRRRAIVPCANILGGSSINFMMYTRGSASDYDDWET---EGWTTKDLLPLMKKTEETYQRA-----CNNRDI	141					
AOX	56	PRNMKLDSTASFYTSNPSPHLNGRRRAIVPCANVGGSSINFMMYTRGSASDYDDFQA---EGWTKDLLPLMKKTEETYQRA-----CNPDI	141					
AAOX	51	PGD-VPNSIFDWNYTSTAQAGYNGRSIAYPRGRMLGGSSSVHYMVMRGS TEDFDRYAAVTGDEGNWDNIQQFVRKNE MV--VPPADNHNTSGEFIPAV	147					
CHOX	62	ME--LLESGYDWDYPIEPQENGN-SFMRHARAKVMGGCSSHNSCIAFWAPREDLDEWEAKYGATGWNAAEAAPLYKRL ETN-----EDAGPDAPH	148					
GLOX	69	GD--IFGSSVDHAYETVELATNN-QTALIRSGNGLGGSTLVNGGTWTRPHKAQVDSWETVFGNEGWNWDNVAAYS LQAERA-RAPNAKQIAAGHYFNASC	164					
		<u>.....S.....Y.....N.....an.lGGsss.n....r....d.D.we.....eGW.....l.kk.E.....</u>						

		βB2	H9	βC1	H10	βA1	βD1	
Cb	142	HGFDGPIKVSFGNYTY---PQCQDFLRACETQGI---PYVDDLEDLTTSHGAEQWLKWINRDLGRSDTAHAFIHSTMRNKENLFLLTNTKVDKVIEI-	233					
Pa	143	HGFDGPIKVSFGNYTY---PTCQDFLRAAESQGI---PVVDDLEDLDFKTSHGAEHWLKWIRNDRGRSDSAHAYVHPTMRNKQSLFLITSTKCDKVIIE-	234					
Kc	142	HGFEGPIKVSFGNYTY---DNCQDFLRAAESQGI---PVVDDLEDLVTAGAEHWLKWIRNDRGRSDSAHAFIHSTMRNKDNLFVLTSTKIDKIIIVE-	233					
AOX	142	HGFEGPIKVSFGNYTY---PVCQDFLRASESQGI---PYVDDLEDLVTAGAEHWLKWIRNDRGRSDSAHAFVHSTMRNHDNLYLICNTKVDKIIVE-	233					
AAOX	148	HGTNGSVSISLPGFPPT---PLDDRVLATTOEQSEEFFNPDMGHGH---PLGISWSIASVNGG--QRSSSTAYLRPAQ-SRPNLSVLINAQVTKLVNSG	238					
CHOX	149	HGDSGPVHLMNVPPKD---PTGVALLDACEQAGI---PRAKFNTGTTVVNGANFFQINRRADG-TRSSSSVSYIHP IV-EQENFTLLTGLRARQLVFDA	239					
GLOX	165	HGVNGTVHAGPRDGTDDYSPIVKALMSAVEDRGV---PTKKDF-GCGDPHGVSMPNTLHEDQ-VRSDAAREWLLPNY-QRPNLQVLTGQYVGVKVLVLSQ	257					
		<u>HG..Gpv.....p.....l.a.e..q.....HG...w.....RS.sa..y.....nl.ll.....k....</u>						

		βD2	βD3	βA4	H11	H12	βC5	H13	
Cb	234	----NGRAVAVRTVPSKPIGDSK-VSRTFKARKQIVVSCGTISSPMVLQRSIGIGESKLRAAGVKPIVEVPGVGNFQDHYCYFVPYRIKHDSSESDFDAFV	328						
Pa	235	----DGKAVAVRTVPMKPLNPKKPVSRFTFRARKQIVISCGTISSPVLVQRSIGIGAHHLSVGVKPIVDLPGVGENFQDHYCFFTPYVVKPDVPTDFDFV	330						
Kc	234	----DGRAVGVKTVPSKPLDPKNPKTRTFRARKQIVLSCGTVSSPMVLQRSIGFGDPQKLRAAGVKPLVNLPGVGRNFQDHYCFFTPYRIKPHLESDFDFV	329						
AOX	234	----DGRAAAVRTVPSKPLNPKKPSHKIYRARKQIVLSCGTISSPMVLVQRSIGFGDPIKLRAAGVKPLVNLPGVGRNFQDHYCFFSPYRIKPYESDFDFV	329						
AAOX	239	TTNGLPAFRCVEYAEQE----GAPTTTVC AKKEVVL SAGSVGTPILLQLSGIGDENDLSSVGIDTIVNNSVGRNLS DHLLLPAAFFVNSN-QTFDNIF	332						
CHOX	240	----DRRCTGV DIVDSA----FGHTRHRTARNEVVLSTGAIDTPKLLMLSGIGPAAHLAEHGIEVLVDS PGVGEHLQDHPEGVVQFEA-----	319						
GLOX	258	-NGTTPRAVGV EFGTHK-----GNTHNVYAKHEVLLAAGSAVSP TILEYS GIGMKSILEPLGIDTVVDLP-VGLNLQDQTTATVRSRITSAG-----	341						
		<u>...V....Ar.evvlsaG.i.sP.vL..SGiG....L...G...lV..P.VG.n.qDh.....i.</u>							

