Supplementary figure S1.

A:

```
Conf: 904799999999989887899888988899999998799999999999998787499997332123789999998538889999986788789999999999996289
Pred: CHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCC
  AA: GMMIMEEILREIVKAERLAEERIEAAKVEAKKIIQNAREEAKKLEEEILKKAEEEGKRIIESKKAEGEQEAKKIREEGEKEIEELKVKAEEKFETAVSECLRIIRGV
              10        20        30        40        50        60        70        80        90       100
```

B:

```
MEM : ------------------------------------------------------------------------------------------------------------------------
Conf: 997755208999978577999999998479589997686767544510589999999999999999999865221267621110556755202133878999999987889899999999
Pred: CCCCCCCCEEEEEEEHHHHHHHHHHHHCCCCEEEEECCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHCCCCCHHHCCCCCCCCCEECCCCCCHHHHHHHHHHHHHHHHHHHHHHHHH
  AA: MFKPEEMVKIELISLARYRDIIMTYLHERGVVQLEEVPIEDIQHDAPNEYYRKATSYSITMGRLVDTLKGFLPPRKTSIKEFIFPKEREKRVYTYRGIEDLVKDVEKFLSEVEPKIREVE
              10        20        30        40        50        60        70        80        90       100       110       120

MEM : ------------------------------------------------------------------------------------------------------------------------
Conf: 999999999999999999854312388786782378836999999618889999999985439829999951796199999871357999999998569869856898875799999999
Pred: HHHHHHHHHHHHHHHHHHHHHHHCCCCCCHHHHCCCCCCEEEEEEEECHHHHHHHHHHHHHCCCCEEEEEEECCCCEEEEEEEEHHHHHHHHHHHHCCCCEEEECCCCCCCCHHHHHHHHH
  AA: TQLTAINNRIANIREIINTLELLSSLNIEIEYLIPGSFLAIEVGKIERERVEKLIGELKNELGDKVFILRRDLGTISLLVVVTLKEFQGKLTSILAKYGFEKVEIPRERGHPRELIPKYN
             130       140       150       160       170       180       190       200       210       220       230       240

MEM : ------------------------------------------------------------------------------------------------------------------------
Conf: 999999999999999999999999999899999999999999999863410597899998714777899999998606897349997256888878982401852002687899860789 8
Pred: HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCEEEEEEEEHHHHHHHHHHHHHCCCCCCEEEEECCCCCCCCCCCCCCCCCCCCHHHHHHHHHCCCC
  AA: ELLKEEMKKLEEIRKKGREFAEKYYEDLVFYKELMDNERDKANYLSYLARTELTVALVGWLPKKNVEEVVEGIKNLTGGKVYINIREPEPNEIEEVPVKLKNPEFISQFEMLTEMYGVPK
             250       260       270       280       290       300       310       320       330       340       350       360

MEM : --------------OOOOOOOXXXXXXXXXXXXXXIIIIIII++++++++++IIIIIIXXXXXXXXXXXXXOOOOOO-----------------OOOOOOOXXXXXXXXXXXXXXIIIII
Conf: 899884678999999999999999899999999999999984374435676279999999899999998742120252234530022012401143321356640253897522156778 8
Pred: CCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCHHCHHHHHHHHHHCCHHHHHCHHHHHHHH
  AA: YNELDPTPILAFTYSFFFGFMLTDFMYGLLLGIVSALLVKGHSKMKDGTWKFAKIMLWSSVFTMLLGALFGSYFGNALDMAGFKVPRIMDAMEEALTVLIIALAIGLGHLFTGYVLGFIV
             370       380       390       400       410       420       430       440       450       460       470       480

MEM : II+++++IIIIIIXXXXXXXXXXXXXOOOOOO-------------------------------OOOOOXXXXXXXXXXIIIII++IIIIIXXXXXXXXXXOOOOO------------OOOOXXXXX
Conf: 622577111243112299999999897740346663579999720356753013445240678998998999898879999999999986078999999999998313566573146899 9
Pred: HHHCCCCHHHHHHCCHHHHHHHHHHHHHHCCCCCCCHHHHHHHHHHHHHHHHCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCHHHHHHHHHHHHHHCCCCCCCCCCHHHHH
  AA: KWKNGDKVGAILDQLSWILIILGVTLFAISSRIDLPKLAWMSVFGAGAVLFIIGEFKNNGLMALLLVISDFFGFVGNWLSYARLMALALATAGIALVINIMVQMIWGFKIGPVPLGIIVG
             490       500       510       520       530       540       550       560       570       580       590       600

MEM : XXXXXIIIII++IIIIIXXXXXXXXXXXXXOOOOO------------------------------
Conf: 999999999999975578889999999999761521305976006546013321011347789 9
Pred: HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCEECCCCEECCCCCHHHHHHCCCCCCCCCC
  AA: AIVFIGGHIFSTAINALGAFVHALRLHYVEFFGTFYSGEGRRFEPFAARREISELKIEKPGGE
             610       620       630       640       650       660
```

C:

```
Conf: 934888789999999999999999999999999999999999999999999999999999999999999999999999999999999999999999993168345999999999999999
Pred: CCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHH
  AA: MEERKMNGAQVIIQEINREAEQKIKYILDEARKEAEKIKEEARKRGESRAEWILRKAKTQAELEKQRIIATARLEVRRKKLSLQEEYISRVLKEVTSRLSNLSEDEYLETVLALLKEALK
              10        20        30        40        50        60        70        80        90       100       110       120

Conf: 61898168987777899999999999987388618966875446717688479846485559999999999857999986379
Pred: HHCCCCEEEEECHHHHHHHHHHHHHHHHHHCCCEEEECCCCCCCCEEEEEECCCCEEEECCHHHHHHHHHHHHHHHHHHHHCC
  AA: ELDVKEIRVHSNEKTLALISSRIEEIRRELGDVSIEIGSPIQTIGGVIVETKDGNMRVDNTFEARMARLESELRSKIAEILFG
             130       140       150       160       170       180       190       200
```

Figure S1.
Secondary structure prediction of *P. furiosus* subunits, carried out with PSIPRED (Bryson et al., 2005; Jones, 1999). Conf.: confidence level (0=low, 9=high), Pred.: predicted secondary structure (H=helix, E=strand, C=coil), AA: amino acid sequence, MEM: transmembrane helix prediction with MEMSAT3 (Jones, 2007; Jones et al., 1994). High-confidence β-strands are highlighted in pink, α-helices in yellow, and transmembrane helices in green. A: the H subunit, B: the *a* subunit, C: the E subunit.

Supplementary references:

Bryson K, McGuffin LJ, Marsden RL, Ward JJ, Sodhi JS, Jones DT (2005) Protein structure prediction servers at University College London. *Nucl Acids Res* **33**: W36-38

Jones DT (1999) Protein secondary structure prediction based on position-specific scoring matrices. *J Mol Biol* **292**: 195-202

Jones DT (2007) Improving the accuracy of transmembrane protein topology prediction using evolutionary information. *Bioinformatics* **23**: 538-544

Jones DT, Taylor WR, Thornton JM (1994) A model recognition approach to the prediction of all-helical membrane protein structure and topology. *Biochemistry* **33**: 3038-3049