Supplementary Figure 1

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Query Sat_Feb_14_18:33:14_+0100_2009 (seq=MGNCHTVGPN...LIKKATGVQV Len=428 Neff=7.8  Nseqs=302)
Parameters  score SS:yes search:local realign with MAP:yes MAP threshold=0.0

   No Hit                             Prob E-value P-value  Score    SS Cols Query HMM  Template HMM
  1 1win_A Flotillin 2; BAND 7 dom  99.8 4.3E-20 2.2E-24  203.8   6.9  143   17-178     1-143 (143)
  2 3bk6_A PH stomatin; archaea, t  99.7 1.6E-15 8.3E-20  161.4  15.6  188   37-266     1-188 (188)
  3 2zuo_A MVP, major vault protei  99.6 2.6E-11 1.4E-15  122.2  32.7  365    1-408   456-861 (861)
  4 2zuo_A MVP, major vault protei  95.7    0.16   8E-06   31.5  19.6  398    1-422   320-861 (861)
  5 3etk_A Uncharacterized metal-d  50.9     7.8  0.0004   15.7   3.1  356    1-427    42-534 (534)
  6 2k5c_A Uncharacterized protein  28.4      16  0.0008   12.9   3.3   89   67-193     1-95  (95)
  7 1vq8_T 50S ribosomal protein L  18.0      23  0.0012   11.3   2.0   73    1-98     38-120 (120)
  8 2p9x_A Hypothetical protein PH  16.8      24  0.0013   11.1   3.5   86   78-198     1-99  (99)
  9 3ecf_A NTF2-like protein; YP_3  15.8      25  0.0013   11.0   0.4   86    1-120    20-130 (130)
 10 1vpr_A Luciferase; beta barrel  13.5      29  0.0015   10.4   0.6  110    1-119   212-374 (374)

    No 1

1win_A Flotillin 2; BAND 7 domain, structural genomics, riken structural genomics/proteomics initiative, RSGI; NMR
  {Mus musculus} SCOP: d.43.2.1
  Probab=99.80  E-value=4.3e-20  Score=203.78  Aligned_cols=143  Identities=93%  Similarity=1.248  Sum_probs=128.9

  Q ss_pred             ECCCCCCCCEEEECCEEEEEEEEEEEEEEEECEEEEEECCCCCEECCCCEEEEEEEEEEEEECCCHHHHHHHHHHHHCCCH
  Q ss_conf             44557988759977929999976778999966589970688633513992899999999999789799999999998827889
  Q Sat_Feb_14_18:   17 GGCCGSDYKQYVFGGWAWAWWCISDTQRISLEIMTLQPRCEDVETAEGVALTVTGVAQVKIMTEKELLAVACEQFLGKNV   96 (428)
  Q Consensus        17 g~~~g~~~~kvv~~g~~~v~P~~~~~~~~~l~~~~i~v~~~~~~t~d~i~~~v~a~~~~~V~~~~~~i~~Aa~~~l~~~~   96 (428)
                        |.            .|         -...+|||+.++++++.++++|+||++++|+++++|||.++++.+.+|+++||+++.
  T Consensus         1 ~~------------~~---------~~~~rv~l~~~~l~~~~q~v~TkD~v~i~V~av~~~rI~d~~~~i~~A~~rfl~~~~   61 (143)
  T 1win_A           1 GS-----------SG--------SSGQRISLEIMTLQPRCEDVETAEGVALTVTGVAQVKIMTEKELLAVACEQFLGKNV   61 (143)
  T ss_dssp             CC-----------CC--------CCCCSCCCSCEEECCCEEEEECSSSCEEEECCEEEEEECCCSSCCHHHHHHHSSSCH
  T ss_pred             CC-----------CC--------CCCEEEEEEEEEECCCCCEEECCCCCEEEEEEEEEEEEECCHHHHHHHHHHHCCCCH
  T ss_conf             99-----------88--------7306711068974588806785799689999999999991576999999988606988


  Q ss_pred             HHHHHHHHHHHHHHHHHHHHHCCHHHHHHHHHHHHHHHHHHHHHHHHHHHCCEEEEEEEEEECCCCHHHHHHHHHHHHHHHH
  Q ss_conf             9999999999999999999656799998639999999999999998637279999998761369555789999999999999
  Q Sat_Feb_14_18:   97 QDIKNVVLQTLEGHLRSILGTLTVEQIYQDRDQFAKLVREVAAPDVGRMGIEILSFTIKDVYDKVDYLSSLGKTQTAVVQ  176 (428)
  Q Consensus        97 ~~i~~~~~~~~~g~lR~v~~~~t~eei~~~R~~f~~~v~~~v~~dl~~~Gl~l~~~~i~di~d~~~~~~a~g~~~~ae~~  176 (428)
                        +++...+..+++++||+++|+||+++++++|+.|...|.+.+..++.+||++|+++.|+||.+|++|+++||++++|---
  T Consensus        62 ~~~~~~i~~~~~~~lR~vig~~tl~ei~~~R~~i~~~i~~~i~~~l~~~GieV~~v~I~dI~~~~~~~~~al~~~~~A~~~  141 (143)
  T 1win_A          62 QDIKNVVLQTLEGHLRSILGTLTVEQIYQDRDQFAKLVREVAAPDVGRMGIEILSFTIKDVYDKVDYLSSLGKTQTSGPS  141 (143)
  T ss_dssp             HHHHHHHHHHHHHHHHHHHHHHSCHHHHHHTHHHHHHHHHHHHHHHHTTTTEEEEEEECCCEECTTCHHHHHCCCCCCCCC
  T ss_pred             HHHHHHHHHHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHCCEEEEEEEEEECCCCHHHHHHHHHHHHHCCC
  T ss_conf             8999999999999999999700529999753999999999999999998578799999998637849999999999984664


  Q ss_pred             HH
  Q ss_conf             99
  Q Sat_Feb_14_18:  177 RD  178 (428)
  Q Consensus       177 r~  178 (428)
                        .-
  T Consensus       142 ~~  143 (143)
  T 1win_A         142 SG  143 (143)
  T ss_dssp             CC
  T ss_pred             CC
  T ss_conf             88


    No 2

3bk6_A PH stomatin; archaea, trimer, coiled- coil, flotillin, SPFH, membrane fusion, trafficking, transmembrane,
  membrane protein; 3.20A {Pyrococcus horikoshii}
  Probab=99.68  E-value=1.6e-15  Score=161.39  Aligned_cols=188  Identities=19%  Similarity=0.294  Sum_probs=130.6

  Q ss_pred             EEEEEEEEEECEEEEEECCCCCEECCCCEEEEEEEEEEEEECCCHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHH
  Q ss_conf             76778999966589970688633513992899999999999789799999999998827889999999999999999999996
  Q Sat_Feb_14_18:   37 WCISDTQRISLEIMTLQPRCEDVETAEGVALTVTGVAQVKIMTEKELLAVACEQFLGKNVQDIKNVVLQTLEGHLRSILG  116 (428)
  Q Consensus        37 P~~~~~~~~~l~~~~i~v~~~~~~t~d~i~~~v~a~~~~~V~~~~~~i~~Aa~~~l~~~~~~i~~~~~~~~~g~lR~v~~  116 (428)
                        -+|+++.++|+++++++++.++++|+||++++|+++++|||.++...+.+          ..+....+...+.+.||.++|
  T Consensus         1 ~i~~~~~vd~r~~~~~i~~q~vlT~D~~~V~v~~~v~yrV~d~~~~~~~~---------~~~~~~~~l~~~~~~~lR~~i~   71 (188)
  T 3bk6_A           1 MIFEKAVIVDLRTQVLDVPVQETITKDNVPVRVNAVVYFRVVDPVKAVTQ---------VKNYIMATSQISQTTLRSVIG   71 (188)
  T ss_dssp             CCEEECCCCCSSCEEEEEEEEEEECTTSCEEEEEEEEEEEESCHHHHHHS---------SSCHHHHHHHHHHHHHHHHH
  T ss_pred             CEEEEEEEEEEEEEEEECCCCCEEECCCCCEEEEEEEEEEEEECCCHHHHHH---------CCCCCHHHHHHHHHHHHHHHH
  T ss_conf             958886999805787627975446268989999989999997654888871---------05710467999999999999997


  Q ss_pred             HCCHHHHHHHHHHHHHHHHHHHHHHHHHCCEEEEEEEEEECCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
  Q ss_conf             567999986399999999999999986372799999987613695557899999999999999999999999887678998 8
  Q Sat_Feb_14_18:  117 TLTVEQIYQDRDQFAKLVREVAAPDVGRMGIEILSFTIKDVYDKVDYLSSLGKTQTAVVQRDADIGVAEAERDAGIREAE  196 (428)
  Q Consensus       117 ~~t~eei~~~R~~f~~~v~~~v~~dl~~~Gl~l~~~~i~di~d~~~~~~a~g~~~~ae~~r~A~ia~aeaerea~i~eAe  196 (428)
                        ++++++++++|..|...+.+.+..++.+||++|+++.|+||.+|.++.+++.++..++..+++.+..|++++++....++
  T Consensus        72 ~~~~~ei~~~r~~~~~~~i~~~l~~~~~~~~Gi~I~~v~i~~i~~p~~v~~a~~~~~~Ae~~~~a~~~~Ae~e~~aa~~~~e  151 (188)
  T 3bk6_A          72 QAHLDELLSERDKLNMQLQRIIDEATDPWGIKVTAVEIKDVELPAGMQKAMARQAEAERERRARITLAEAERQAAEKLRE  151 (188)
  T ss_dssp             TSCHHHHHHCHHHHHHHHHHHHHHTGGGTEEEEEEEEEEEEEETTHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
  T ss_pred             HCCHHHHHCCHHHHHHHHHHHHHCCCCCCEEEEEEEECCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
  T ss_conf             1559875264788999999999872464574478998863679988999999999999999999999999999999999


  Q ss_pred             HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCHHHHCCCHHHHHHHHHHHHHHH
  Q ss_conf             88887778999999998887778878989999999999985320010100331210566799999999986
  Q Sat_Feb_14_18:  197 CKKEMLDVKFMADTKIADSKRAFELQKSAFSEEVNIKTAEAQLAYELQGAREQQKIRQEEIEIEVVQRKK  266 (428)
  Q Consensus       197 ae~e~~~a~~~ae~eiae~~~~~e~~~a~~~~e~~~~~aeae~a~e~~~a~~~~~~~~~e~e~e~~~~~~  266 (428)
                        +.      +.     +++......++           ..++-    ........      ..+-...-.
  T Consensus       152 aa------~~------~~e~~~a~~~r-----------~~e~~-------~~i~~~~n-----~~~~~~~~~~~~~  188 (188)
  T 3bk6_A         152 AA------EI-----ISEHPMALQLR-----------TLQTI-----SDVAGDKS------NLEHHHHHH  188 (188)
  T ss_dssp             HH------HH-----HHHCTTHHHHH-----------HTTC--------------------------
  T ss_pred             HH------HH-----HHHHHHHHHHH-----------HHHHH-----HHHHHCCC------CCCCCCCCC
  T ss_conf             99------99-----98659999999-----------99999-----99974725------432144679
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  No 3

  protein; 3.50A {Rattus norvegicus} PDB: 2zv4_N 2zv5_a 2qzv_A 1y7x_A
/g; # link to PDB 2zv5_a 2qzv_A 1y7x_A
>2zuo_A MVP, major vault protein; repeat domains, protein-protein complex, cytoplasm, ribonucleoprotein, structural
  Probab=99.64  E-value=2.6e-11  Score=122.23  Aligned_cols=365  Identities=16%  Similarity=0.116  Sum_probs=160.3

  Q ss_pred             CCCEEEECCCEEEEEEECCCCCCCCEEEECCEEEEEEEEEEEEEEECE-----------EEEEECCCC------CEECCC
  Q ss_conf             996389579848999944557988759977929999767789999665-----------899706886------335139
  Q Sat_Feb_14_18:    1 MGNCHTVGPNEALVVSGGCCGSDYKQYVFGGWAWAWWCISDTQRISLE-----------IMTLQPRCE------DVETAE   63 (428)
  Q Consensus         1 ~~~~~~~~p~e~lvitg~~~g~~~~kvv~~g~~~v~P~~~~~~~~~l~-------------~~~i~v~~~~~~~~~~~t~d   63 (428)
                        ..=-|-||+|-+.-||-.+  .+..|||.|.-.+.++.-+.++.++|+           +..|.+...      .+-|+|
  T Consensus       456 r~v~~~vp~n~avqvy~~~~~~~~~rvv~GP~~v~L~pde~ft~lsLS~g~pK~~~~i~~l~L~lgp~~~tD~i~veT~D  533 (861)
  T 2zuo_A          456 RVVSYRVPHNAAVQVYDYR--AKRARVVFGPELVTLDPEEQFTVLSLSAGRPKRPHARRALCLLLGPDFFTDVITIETAD  533 (861)
  T ss_dssp             BCCEEECCTTEEEEEECSS--SCCEEEECSSCEEECCSSCEECCEEECCSSSCCTTSEEESSEECSSCEEEEEEEECTT
  T ss_pred             EEEEEECCCCCEEEEEECC--CCCEEEEECCCEEEECCCCEEEEEEECCCCCCCCCCEEEEEEECCCCCEEEEEEECC
  T ss_conf             589998898179999878--884799988267877876168999528998999844799997448730589999971 5


  Q ss_pred             CEEEEEEEEEEEECC-CHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHCCHHHHHHHHHHHHHHHHHHHH-
  Q ss_conf             928999999999789-79999999998827889999999999999999965679999863999999999999999-
  Q Sat_Feb_14_18:   64 GVALTVTGVAQVKIMT-EKELLAVACEQFLGKNVQDIKNVVLQTLEGHLRSILGTLTVEQIYQDRDQFAKLVREVAAPD-  141 (428)
  Q Consensus        64 ~i~~~v~a~~~~~V~~~~~~i~~Aa~~~l~~~~~~i~~~~~~~~~g~lR~v~~~~t~eei~~~R~~f~~~v~~~v~~d-  141 (428)
                        ..++.+...++|-..- ++.+...++.-| + ..|-|..+.+.+ .+.+|.++++|+++++|.++..|.....-.+...
  T Consensus       534 harl~l~lsynw~F~~~~~~~~~~~~~~F~~v~DfVgdack~I-aSrIR~AVAs~tFeEfhknsakiIR~aVfgv~e~~  610 (861)
  T 2zuo_A          534 HARLQLQLAYNWHFELKNRNDPAEAAKLF-S-VPDFVGDACKAI-ASRVRGAVASVTFDDFHKNSARIIRMAVFGFEMSE  610 (861)
  T ss_dssp             CCEEEEEEEEEEECCTTTTCHHHHHGGG-S-SSSHHHHHHHH-HHHHHHHHTTSCHHHHHHHHHHHHHSSCCC---
  T ss_pred             CCEEEEEEEEEEEECCCCCCHHHHHHHH-C-CCCHHHHHHHH-HHHHHHHHHCCHHHHHHHHHHHHHHHCCCHHH
  T ss_conf             406899899999997268788125788 73-7-974899999999-999999986456998850299999998714356 77


  Q ss_pred             -----------------HHHCCEEEEEEEEEEC-CCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
  Q ss_conf             -----------------863727999998761 36-955578999999999999999999999988767899888888777
  Q Sat_Feb_14_18:  142 -----------------VGRMGIEILSFTIKDVY-DKVDYLSSLGKTQTAVVQRDADIGVAEAERDAGIREAECKKEMLD  203 (428)
  Q Consensus       142 -----------------l~~~Gl~l~~~~i~di~~d~~~~~~a~g~~~~ae~~r~A~ia~aeaerea~i~eAeae~e~~~  203 (428)
                                                  ...+|+.+.++.++.+- -+..+.+++.+.....+...+...+++++++++..+.++.....
  T Consensus       611 ~~~~d~ti~~~ire~~rF~angl~itsvdvQsiE~~D~ktrdaLaKsvq~AiEItTqsqEAeAr~eA~~lEqEAr~~LEr  690 (861)
  T 2zuo_A          611 DTGPDGTLLPKARDQAVFPQNGLVVSSVDVQSVEPVDQRTRDALQRSVQLAIEITTNSQEAAAKHEAQRLEQEARGRLER  690 (861)
  T ss_dssp             ----------CCCSCEECTTTCEEEEEEEEEEEESSHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
  T ss_pred             HHHHHHHHHCCCHHHHHHCCCEEHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
  T ss_conf             654444444035434578865983225577653688899999998999999999988899999999998889999999 9


  Q ss_pred             HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
  Q ss_conf             899999999888777887898999999999985320010100331210566799999999986999999999999999
  Q Sat_Feb_14_18:  204 VKFMADTKIADSKRAFELQKSAFSEEVNIKTAEAQLAYELQGAREEQQKIRQEEIEIEVVQRKKQIAVEAQEILRTDKELI  283 (428)
  Q Consensus       204 a~~~ae~eiae~~~~e~~~a~~~~e~~~~~aeae~a~e~~~a~~~~~~~~~e~e~e~~~~~~q~~~e~~e~~~~e~e~~  283 (428)
                        .+...+.+...+++.....++...+.....++++                +.+.+.+..+.+.+.+..+..
  T Consensus       691 QkledEaeae~ark~lleaqA~saAve~~aka~A----------------EaeaeaEaariEaEaeieqAk---------  745 (861)
  T 2zuo_A          691 QKILDQSEAEKARKELLELEAMSMAVESTGNAKA----------------EAESRAEAARIEGEGSVLQAK---------  745 (861)
  T ss_dssp             HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH----------------HHHHHHHHHHHHHHHHHHH---------
  T ss_pred             HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH----------------HHHHHHHHHHHHHHHHHHH---------
  T ss_conf             989999999999999999999999999999999----------------99999999999999999998---------


  Q ss_pred             HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
  Q ss_conf             999879999999999999999999999999999999975799999999999999999999998715999999999999
  Q Sat_Feb_14_18:  284 ATVRRPAEAEAHRIQQIAEGEKVKQVLLAQAEAEKIRKIGEAEAAVIEAMGKAEAERMKLKAEAYQKYGDAAKMALVLEA  363 (428)
  Q Consensus       284 a~~~~~AEaE~~~~e~~Aeae~~~~~~~aeaeae~~r~~~eaeA~~~~~~~~AeAe~~~~~aeA~~~~~~aa~~~~~~e~  363 (428)
                          .    .++....+.+|+.+..+  ...+++.+..+.+.+.+.+...+.+.+|++..+.+.+|.+.   ..+. -+...
  T Consensus       746 --l----KaeAl~ie~EAEle~lk~~~rE~Ele~~~aq~elEieKaK~lAeiEa~kf~a~vEAig~---eti~~aiA~A  813 (861)
  T 2zuo_A          746 --L----KAQALAIETEAELERVK--KVREMELIYARAQLELEVSKAQQLANVEAKKFKEMTEALGP---GTIR-DLAVA  813 (861)
  T ss_dssp             --H----HHHHHHHHHHHHHHHH--HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHSCT---THHH-HTGGG
  T ss_pred             --H----HHHHHHHHHHHHHHHH--HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCH---HHHH-HHHHH
  T ss_conf             --8----999999999999999999--99999999999999999999999988999999999997689---9999-99974


  Q ss_pred             HHHHHHHHHHHHCCCCEEEEECCC----HHHHHHHHHHHHHHHHHH
  Q ss_conf             999999999998659967999599 7----246699999998689999 9
  Q Sat_Feb_14_18:  364 LPQIAAKIAAPLTKVDEIVVLSGDN----SKVTSEVNRLLAELPASVHA  408 (428)
  Q Consensus       364 lpei~~~~~~p~~~id~i~v~~~~~~~~~~~~v~~~~~~l~~~i~~  408 (428)
                        -|++.++..+.| .+..-.|.||.+    -++++.+.++..+.+|.+++
  T Consensus       814 g~ElqAKLL~~L~gLk~~liTdGktpinLf~tA~gl~G~~~~~p~~~~  861 (861)
  T 2zuo_A          814 GPEMQVKLLQSL-GLKSTLITDGSSPINLFSTAFGLLGLGSDGQPPAQK  861 (861)
  T ss_dssp             CC----------------------------------------------
  T ss_pred             CHHHHHHHHHC-CCCEEEEECCCCHHHHHHHHHHCCCCCCCCCCCCCC
  T ss_conf             789999998607-984478607987788888887874557789999999


    No 4

  protein; 3.50A {Rattus norvegicus} PDB: 2zv4_N 2zv5_a 2qzv_A 1y7x_A
/g; # link to PDB 2zv5_a 2qzv_A 1y7x_A
>2zuo_A MVP, major vault protein; repeat domains, protein-protein complex, cytoplasm, ribonucleoprotein, structural
  Probab=95.67  E-value=0.16  Score=31.51  Aligned_cols=398  Identities=16%  Similarity=0.112  Sum_probs=75.7

  Q ss_pred             CCCEEEECCCEEEEEEECCCC---CC---------CCEEEECCEEEEEEEEEEEEEEEECC-CCCEECCCCEEE
  Q ss_conf             996389579848999944557---98---------875997792999976778999966589970 68-863351399289
  Q Sat_Feb_14_18:    1 MGNCHTVGPNEALVVSGGCCG---SD---------YKQYVFGGWAWAWWCISDTQRISLEIMTLQPR-CEDVETAEGVAL   67 (428)
  Q Consensus         1 ~~~~~~~~p~e~lvitg~~~g---~~~~~~~~~~~~~~kvv~~g~~~v~P~~~~~~~~~l~~~~i~v~~~~~~t~d~i~~   67 (428)
                        +-++|+.++||+|++.-...+   ++         ..=+|+|...|+-|.-..+.   -+-..|.++ .+++|-.|.-.-
  T Consensus       320 i~~~yvL~e~eaL~l~a~~~f~d~~~~~~~~r~~Gdrw~irGp~~yiP~~~veV~~~~~r~ai~L~~neGiYVrd~~TG  396 (861)
  T 2zuo_A          320 IQDVYVLSEQQGLLLKALQPLEEGESEEKVSHQAGDCWLIRGPLEYVPSAKVEVV---EERQAIPLDQNEGIYVQDVKTG  396 (861)
  T ss_dssp             SCBCEECCEEEEEEEEEESSCBSSCSTTCCCBCTTCCEEEEESCEECCCTTEEEE---EEEECBCCCTTCEEEEETTTC
  T ss_pred             CEEEEEECCCCEEEEEEEEEEECCCCCCEEECCCCEEEEECCCCCCCCCCEEEE---EEEEECCCCCCEEEEEECCEE
  T ss_conf             357676257865899996457727998754766886899988132388527997---653210258885389996640 1


  Q ss_pred             EEEEEEEEEECCCHHHHHHHHHHCCC-HHHHHHHHHHHHHHHHHHHHCCHHHH--HHHHHHHH-------------
  Q ss_conf             999999999789799999999988 2788-99999999999999999999965679999--86399999-------------
  Q Sat_Feb_14_18:   68 TVTGVAQVKIMTEKELLAVACEQFLGKN-VQDIKNVVLQTLEGHLRSILGTLTVEQI--YQDRDQFA-------------  131 (428)
  Q Consensus        68 ~v~a~~~~~V~~~~~i~~Aa~~~l~~~~~~~i~~~~~~~~~g~lR~v~~~~t~eei--~~~R~~f~-------------  131 (428)
                        .|.++    .+++  .+...-+.+-.+. ...++.+.. ..-+.|+.....+-..+  +..|+.-.
  T Consensus       397 ~vR~v----~G~~~ymL~~~Eelwek~l~~~ve~ll~~~~~~~~~~~~~~~~~~~~~~~r~~~r~v~~~vp~n~avq  469 (861)
  T 2zuo_A          397 KVRAV----IGST--YMLTQDEVLWEKELPSGVEELLN-LGHDPLADRGQKGTAKPLQPSAPRNKTRVVSYRVPHNAAVQ  469 (861)
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 T ss_dssp              CEEEE----ESSC--BCCCTTEEECCCCCTTHHHHHTC---------------------CCCCCTTBCCEEECCTTEEEE
 T ss_pred              EEEEE----ECCC--CCCCCCCEEEECCCCCCHHHHHH-CCCCHHHHHCCCCCCCCCCCCCCCCCCEEEEEECCCCCEEE
 T ss_conf              69999----6772--11677525542458801699985-56523233202368776677888787458999888981799


 Q ss_pred              ------HHHHHHHHHHHHHCC----EEEEEEE---------------------EE-----------------------EC
 Q ss_conf              ------999999999986372----7999998---------------------76-----------------------13
 Q Sat_Feb_14_18:  132 ------KLVREVAAPDVGRMG----IEILSFT---------------------IK-----------------------DV  157 (428)
 Q Consensus       132 ------~~v~~~v~~dl~~~G----l~l~~~~---------------------i~-----------------------di  157 (428)
                          .+-+-..++++--+|    |.+.+++                     .+                       |+
 T Consensus       470 vy~~~~~~~rvv~GP~~v~L~pde~ft~lsLS~g~pK~~~~i~~l~L~lgp~~~tD~i~veT~Dharl~l~lsynw~F~~  549 (861)
 T 2zuo_A          470 VYDYRAKRARVVFGPELVTLDPEEQFTVLSLSAGRPKRPHARRALCLLLGPDFFTDVITIETADHARLQLQLAYNWHFEL  549 (861)
 T ss_dssp              EECSSSCCEEEECSSCEEECCSSCEECCEEECCSSSCCTTSEEESSEECSSCEEEEEEEEECTTCCEEEEEEEEEEEECC
 T ss_pred              EEECCCCCEEEEECCCEEEECCCCEEEEEEECCCCCCCCCEEEEEEEECCCCCEEEEEEEECCCCEEEEEEEEEEEEEC
 T ss_conf              99878884799988826787787616899952899899984479999744873058999997154068998999999972


 Q ss_pred              CCCHHHH---------HHHHH--HHHHHHHHHH----HHHHHHHHHHHHHHHHHH---H--------------HHH----
 Q ss_conf              6955578---------99999--9999999999----999999988767899888---8--------------887----
 Q Sat_Feb_14_18:  158 YDKVDYL---------SSLGK--TQTAVVQRDA----DIGVAEAERDAGIREAEC---K--------------KEM----  201 (428)
 Q Consensus       158 ~d~~~~~---------~a~g~------ae~~r~A----~ia~aeaerea~i~eAea---e--------------~e~-----  201 (428)
                        .|+++.-          |.+|-  +.++...|.+    .+.+....+..-++.+-.   .              +..
 T Consensus       550 ~~~~~~~~~~~~F~v~DfVgdack~IaSrIR~AVAs~tFeEfhknsakiIR~aVfgv~e~~~~~~d~ti~~~ire~~rF~  629 (861)
 T 2zuo_A          550 KNRNDPAEAAKLFSVPDFVGDACKAIASRVRGAVASVTFDDFHKNSARIIRMAVFGFEMSEDTGPDGTLLPKARDQAVFP  629 (861)
 T ss_dssp              TTTTCHHHHHGGGSSSSHHHHHHHHHHHHHHHHHTTSCHHHHHHHHHHHHHHHSSCCC-------------CCCSCEECT
 T ss_pred              CCCCCHHHHHHHHCCCCHHHHHHHHHHHHHHHHHHHHCCHHHHHHHHHHHHHHHHHCCCHHHHHHHHHHHHHCCCHHHHHH
 T ss_conf              68788125788737974899999999999999998645699885029999999871435677654444440354345788


 Q ss_pred              --------------H-HHHHHHHHHHHHHH--HHHHHHHHHHHHHHHHHHHHHHHCCCCCCHHHHCCCHHHHHHHHHHHHH
 Q ss_conf              --------------7-78999999998887--77887898999999999998532001010033121056679999999999
 Q Sat_Feb_14_18:  202 --------------L-DVKFMADTKIADSK--RAFELQKSAFSEEVNIKTAEAQLAYELQGAREQQKIRQEEIEIEVVQR  264 (428)
 Q Consensus       202 --------------~-~a~~~ae~eiae~~--~~~~e~~~a~~~~e~~~~~aeae~a~e~~~a~~~~~~~~~e~e~e~~~~  264 (428)
                                   + ..+...+......+  .+...+.++..++.+.+..+.+       +..+......+.+.+....
 T Consensus       630 angl~itsvdvQsiE~~D~ktrdaLaKsvq~AiEItTqsqEAeAr~eA~~lEqE-------Ar~~LErQkledEaeae~a  702 (861)
 T 2zuo_A          630 QNGLVVSSVDVQSVEPVDQRTRDALQRSVQLAIEITTNSQEAAAKHEAQRLEQE-------ARGRLERQKILDQSEAEKA  702 (861)
 T ss_dssp              TTCEEEEEEEEEEEEESSHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------HHHHHHHHHHHHHHHHHHH
 T ss_pred              HCCCEEHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------HHHHHHHHHHHHHHHHHHH
 T ss_conf              6598322557765368889999999899999999999888999999999988999-------9999999989999999999


 Q ss_pred              HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
 Q ss_conf              869999999999999999999987999999999999999-----99999999999999999999975799999999999999
 Q Sat_Feb_14_18:  265 KKQIAVEAQEILRTDKELIATVRRPAEAEAHRIQQIAE-----GEKVKQVLLAQAEAEKIRKIGEAEAAVIEAMGKAEAE  339 (428)
 Q Consensus       265 ~~q~~~e~~e~~~~e~e~~a~~~~~AEaE~~~~e~~Ae-----ae~~~~~~~aeaeae~~r~~~eaeA~~~~~~~~~AeAe  339 (428)
                       ++.....+......+....+.....++++..+++..++     .+........+++.+..+...+++.+...++...+.+
 T Consensus       703 rk~lleaqA~saAve~~aka~AEaeaeaEaariEaEaeieqAklKaeAl~ie~EAEle~lk~~rE~Ele~~~aq~elEie  782 (861)
 T 2zuo_A          703 RKELLELEAMSMAVESTGNAKAEAESRAEAARIEGEGSVLQAKLKAQALAIETEAELERVKKVREMELIYARAQLELEVS  782 (861)
 T ss_dssp              HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
 T ss_pred              HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
 T ss_conf              99999999999999999999999999999999999999999999999988999999999999999999999999999999


 Q ss_pred              HHHHHHHHHHHHHHHHHHHHHHHHHH-HHHHHHHHHHHHCCCCEEEEECCCHHHHHHHH--HHHHHHHHHHHHHHCCCHHH
 Q ss_conf              999999999871599999999999999-999999999986599679999599724669999--99998689999985998767
 Q Sat_Feb_14_18:  340 RMKLKAEAYQKYGDAAKMALVLEAL-PQIAAKIAAPLTKVDEIVVLSGDNSKVTSEVN--RLLAELPASVHALTGVDLSK  416 (428)
 Q Consensus       340 ~~~~~aeA~~~~~~aa~~~~~~e~l-pei~~~~~~p~~~id~i~v~~~~~~~~~~~~~v~--~~~~~~l~~~i~~~~Gvdl~~  416 (428)
                       ..+.++++     ++.....+++.+ |+.+.++++.-... .-..+++.|-+.+- ++  +..-.|..+-..++|.--+-
 T Consensus       783 KaK~lAei-----Ea~kf~a~vEAig~eti~aiA~Ag~El-qAKLL~~LgLk~~l-iTdGktpinLf~tA~gl~G~~~~~  855 (861)
 T 2zuo_A          783 KAQQLANV-----EAKKFKEMTEALGPGTIRDLAVAGPEM-QVKLLQSLGLKSTL-ITDGSSPINLFSTAFGLLGLGSDG  855 (861)
 T ss_dssp              HHHHHHHH-----HHHHHHHHHHHSCTTHHHHTGGGCC-----------------------------------------
 T ss_pred              HHHHHHHH-----HHHHHHHHHHHHCHHHHHHHHHHCHHH-HHHHHHHCCCCEEE-EECCCCHHHHHHHHHHHHCCCCCC
 T ss_conf              99999998-----89999999997689999999997478 99-99998607984478-607987788888887874557789


 Q ss_pred              HHHHCC
 Q ss_conf              676376
 Q Sat_Feb_14_18:  417 IPLIKK  422 (428)
 Q Consensus       417 ~~~~~~  422 (428)
                    =|-.++
 T Consensus       856 ~p~~~~  861 (861)
 T 2zuo_A          856 QPPAQK  861 (861)
 T ss_dssp              ------
 T ss_pred              CCCCCC
 T ss_conf              999999


   No 5

3etk_A Uncharacterized metal-dependent hydrolase; structural genomics, unknown function, PSI-2, protein structure
 initiative; 2.10A {Pyrococcus furiosus}
 Probab=50.87  E-value=7.8  Score=15.73  Aligned_cols=356  Identities=12%  Similarity=0.106  Sum_probs=53.4

 Q ss_pred              CCCEEEECC----CEEEEEEECCC---CC----------CCCEEEECCEEEEEEEEEEEEE-EECE---EEEEECCC-C-
 Q ss_conf              996389579----84899994455---79----------8875997792999976778999-9665---89970688-6-
 Q Sat_Feb_14_18:    1 MGNCHTVGP----NEALVVSGGCC---GS----------DYKQYVFGGWAWAWWCISDTQR-ISLE---IMTLQPRC-E-   57 (428)
 Q Consensus         1 ~~~~~~~~p----~e~lvitg~~~~---g~----------~~~kvv~~g~~~v~P~~~~~~~~~~l~---~~~i~v~~-~-   57 (428)
                   =|+|||+..    +++++|.|++.   |.          .+.+||..+|.+|+|.|=....  ++..   ....+... .
 T Consensus        42 Ng~i~t~~~~~~~~~~ai~I~~gkI~~vG~~~~~~~~~~~~~~gaeVIDa~Gk~V~PGfID~H~H~~~~~~~~~~~~~~~~~~~~s  121 (534)
 T 3etk_A           42 NGTIYTSFSPVKKVSGLVISNERVLYAGDSSTALRIAELAGGEIIDLKGKFVMPAFFDSHLHLDELGMSLEMVDLRGVKS  121 (534)
 T ss_dssp              SSEEEEEETTEEEESEEEEETTEEEEEECHHHHHHHHHHTCEEEECTTCEEEECEEEEEECHHHHHHHHTSEECTTCCS
 T ss_pred              CCEEEECCCCCCEEEEEEEECCEEEEECCHHHHHHHHCCCCCEEEECCCCEEECCCCHHHHHHHHHHCCCCCCCCCCCC
 T ss_conf              5688976799856899999867878996795899985079996589667887806721211226554110035675 6779


 Q ss_pred              --CE---E----------------------------CCCCEEEEEEEEEEEEEECCCHHHHHHHHHHHHHCCC---------
 Q ss_conf              --33---5----------------------------13992899999999997897999999999882788---------
 Q Sat_Feb_14_18:   58 --DV---E----------------------------TAEGVALTVTGVAQVKIMTEKELLAVACEQFLGKN---------   95 (428)
 Q Consensus        58 --~~---~----------------------------t~d~i~~~v~a~~~~~V~~~~~~~i~~Aa~~~l~~~----------   95 (428)
                     .+   +                            ..................  .    .+.  ...+..
 T Consensus       122 ~~~~~~~i~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-----~a~~~~~g~~~~~~~~~~~~  195 (534)
 T 3etk_A          122 MEELVERVKKGRGRIIFGFGWDQDELGRWPTREDLDVIDRPVFLYRRCFHVAVMN-S----KMI-DLLNLKPSKDFDEST  195 (534)
 T ss_dssp              HHHHHHHHHTCCSSSEEEEEECHHHHTSCCCHHHHTTSSSCEEEEETTSSEEEEC-H----HHH-HHHCCCCCTTEETTT
 T ss_pred              HHHHHHHHHCCCCCEEEECCCCHHHCCCCCCHHHHHHHCCHHHHHHHHHHHHHHHH-H----HHH-HHCCCCCCCCCCCHH
 T ss_conf              8999999843577378720145012034443145554101021122233456655-5----555-531577442100001
```

```
Q ss_pred            ---HHHHHHHHHHHHHHHHHHHHCCHHHHHHHHHHHHHHHHHHHHHHCCEEEEEEEEECCCCHHHHHHHHHHH
Q ss_conf            ---99999999999999999999656799998639999999999999986372799999987613695557899999999
Q Sat_Feb_14_18:   96 ---VQDIKNVVLQTLEGHLRSILGTLTVEQIYQDRDQFAKLVREVAAPDVGRMGIEILSFTIKDVYDKVDYLSSLGKTQT  172 (428)
Q Consensus        96 ---~~~i~~~~~~~~~g~lR~v~~~~t~eei~~~R~~f~~~v~~~v~~dl~~~Gl~l~~~~i~di~d~~~~~~a~g~~~~  172 (428)
                       .......+        ...+...     ......+.. ............+..........   +.. ....
T Consensus       196 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  252 (534)
T 3etk_A          196 GIVRERALEES--------RKIINEK-----ILTVKDYKH-YIESAQEHLLSLGVHSVGFMSVG---EKA-LKAL-----  252 (534)
T ss_dssp            TEEEHHHHHHH--------HHHHHHT-----TSCHHHHHH-HHHHHHHHHHTTEEEEEEEEEC---HHH-HHHH-----
T ss_pred            HHHHHHCCHHH--------HHHHHHH-----HHHHHHHHH-HHHHHHHHHHCCCCCCCCCCCC---HHH-HHHH-----
T ss_conf            10111000023--------5665443-----102578999-999988763200011233211 11---356-7899-----


Q ss_pred            HHHHHHHHHHH-HHHHHHHHHHHHHHHHH-------------------------------------------HHHHHH
Q ss_conf            99999999999-999887678998888887-------------------------------------------778999
Q Sat_Feb_14_18:  173 AVVQRDADIGV-AEAERDAGIREAECKKEM-------------------------------------------LDVKFM  207 (428)
Q Consensus       173 ae~~r~A~ia~~aeaerea~i~eAeae~e-------------------------------------------~~a~~~  207 (428)
                      .+..+...... .-................                                            ......
T Consensus       253 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  332 (534)
T 3etk_A          253 FELEREGRLKMNVFAYLSPELLDKLEELNLGKFEGRRLRIWGVKLFVDGSLGARTALLSEPYTDNPTTSGELVMNKDEIV  332 (534)
T ss_dssp            HHHHHTTCCCSEEEEEECGGGHHHHHHTCCSEECSSEEEEEEEEESCCCTTTTCSCCSSCBTTBTTCCCCCSSCHHHHH
T ss_pred            HHHHHHCCCCCEEEEECCHHHHHHHHHHHHHHHHHCCCCHHHEECCCHHHHHHHHHHHHHCCCCCHHHHHHHHHH
T ss_conf            99986325750455401323688999876322100011014301000011013456665344310001000122467887


Q ss_pred            HHHHHHHHHH-HH---HHHHHHHHHHHHHHHHHCCCCCCHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
Q ss_conf            9999988877-78---8788999999999985320010100331210566799999999986999999999999999
Q Sat_Feb_14_18:  208 ADTKIADSKR-AF---ELQKSAFSEEVNIKTAEAQLAYELQGAREQQKIRQEEIEIEVVQRKKQIAVEAQEILRTDKELI  283 (428)
Q Consensus       208 ae~eiae~~~~~~~~e~~~a~~~~e~~~~~aeae~a~e~~~a~~~~~~~~~e~e~e~~~~~~q~~~e~~e~~~~e~e~~  283 (428)
                      .......... ..   ........... ...............   ............. ..........
T Consensus       333 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  395 (534)
T 3etk_A          333 EVIERAKPLGLDVAVHAIGDKAVDVAL-DAFEEAEFSGRIEH---ASLVRDDQLERI-KELKVRISAQ------------  395 (534)
T ss_dssp            HHHHHHGGGTCEEEEEECSHHHHHHHH-HHHHHTTCCCEEEE---CCBCCHHHHHHH-HHHTCEEEEC------------
T ss_pred            HHHHHHHHHHHHHHHHHHHHHHHHHHH-HHHHHHHHHHHHH---HHCCCHHHHHHH-HHHCCCHHCC------------
T ss_conf            66655445555443100013578888 8-76542101123443---203786787677-6412100000------------


Q ss_pred            HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------HHHHHHHHHHHHHHHHHHHHHH--HHHHH
Q ss_conf            9998799999999999999999999999999999999997-------579999999999999999999998--71599
Q Sat_Feb_14_18:  284 ATVRRPAEAEAHRIQQIAEGEKVKQVLLAQAEAEKIRKIGEA-------EAAVIEAMGKAEAERMKLKAEAYQ--KYGDA  354 (428)
Q Consensus       284 a~~~~~AEaE~~~~e~~Aeae~~~~~~~aeaeae~~r~~~ea-------eA~~~~~~~~AeAe~~~~~aeA~~~~~~~a  354 (428)
                         ....-........... ++.        ..+.........       ++-..      --.-......+..  .+...
T Consensus       396 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  458 (534)
T 3etk_A          396 ---PHFIVSDWWIVNRVGE-ERA-------KWAYRLKTLSSITKLGFSTDSPIE------PADPWVSIDAAVNRYVVDPG  458 (534)
T ss_dssp            ---THHHHHCTTHHHHHHH-HHG-------GGBCCHHHHHHHSCEEECCTTTTS------CCCHHHHHHHHHCCSSCGG
T ss_pred            ---CCHHCCCCHHHHHHHH-HHH-------HHCHHHHHHCCCCEEEECCCCCC------CCCHHHHHHHHHHHHCCC
T ss_conf            ---0000022024555547-765-------100079998659819974578888------600799999998765404 34


Q ss_pred            HHHHHHHHHHHHHHHHHHHH-----H-----CCCCEEEEECCCHHHHHHHHHHHHHHHHHHHHCCCHHHHH-HHCCC
Q ss_conf            99999999999999999998-----6-----5996799959972466999999986899999859987676 7-63766
Q Sat_Feb_14_18:  355 AKMALVLEALPQIAAKIAAPL-----T-----KVDEIVVLSGDNSKVTSEVNRLLAELPASVHALTGVDLSKIP-LIKKA  423 (428)
Q Consensus       355 a~~~~~~e~lpei~~~~~~p~~~~~~~~~~~id~i~v~~~~~~~~~~v~~~~~~l~~~i~~~~Gvdl~~~~~~~~~  423 (428)
                      . .+-+.+.+..+-...++.+     .     +.=.|.|||++--.   .+.++. .+   .-+-.++++..+. -++.-
T Consensus       459 ~~~ls~~eai~~~T~~~A~~~g~~~~G~I~~G~~ADlvI~D~dPl~~~~i~~i~~~v~~~~~d~~~~~~~~v~~~~~~~  530 (534)
T 3etk_A          459 E-RVSREEALHLYTHGSAQVTLAEDLGKLERGFRAEYIILDRDPLK---EMKGII-TI---TTDPNSSSVDKLAAALEHH  530 (534)
T ss_dssp            G-CCCHHHHHHHTTHHHHHHTTCTTCSCCSTTSBCCEEEESSCTTC--------------------------------
T ss_pred            C-CCCHHHHHHHHHHHHHHHCCCCCCEECCCCCCCCEEEECCCHHH---HHHCCE-EE---EECCCCEEEEEEEEECCCC
T ss_conf            5-7798999999854489982778851352457306788868802 0---020372-78---8516755888887510000


Q ss_pred            CCCC
Q ss_conf            7998
Q Sat_Feb_14_18:  424 TGVQ  427 (428)
Q Consensus       424 ~~~~  427 (428)
                      .+-.
T Consensus       531 ~~~~  534 (534)
T 3etk_A          531 HHHH  534 (534)
T ss_dssp            ----
T ss_pred            CCCC
T ss_conf            2579
```

No 6

2k5c_A Uncharacterized protein PF0385; structural genomics, PSI-2, protein structure initiative, northeast structural genomics consortium, NESG; NMR {Pyrococcus furiosus}

Probab=28.42 E-value=16 Score=12.94 Aligned_cols=89 Identities=16% Similarity=0.187 Sum_probs=21.3

```
Q ss_pred            EEEEEEEEEEECCCHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHC----CHHHHHHHHHHHHHHHHHHHHH
Q ss_conf            9999999999789799999999988278899999999999999999999656----79999863999999999999998
Q Sat_Feb_14_18:   67 LTVTGVAQVKIMTEKELLAVACEQFLGKNVQDIKNVVLQTLEGHLRSILGTL----TVEQIYQDRDQFAKLVREVAAPDV  142 (428)
Q Consensus         67 ~~v~a~~~~~V~~~~~~i~~Aa~~~l~~~~~~i~~~~~~~~~g~lR~v~~~~~~~t~eei~~~R~~f~~~v~~~v~~dl  142 (428)
                       ..-.---.-+-            -..|.+ -+            -|..+.+|    ..++|++||+.|...+.+-+-.--
T Consensus          1 ~~~~~~~MAkC-------------P~CG~~-Ld-------------W~eLI~qML~~en~~eifkDre~Fl~~~~~F~FKCP   55 (95)
T 2k5c_A             1 AHHHHHHMAKC-------------PICGSP-LK-------------WEELIEEMLIIENFEEIVKDRERFLAQVEEFVFKCP   55 (95)
T ss_dssp            -------CEEC-------------SSSCCE-EC-------------HHHHHHHSTTCSTHHHHTTCHHHHHHHHHSEEECT
T ss_pred            CCCCHHHHHCC-------------CCCCCC-CC-------------HHHHHHHHHHHHHHHHCCHHHHHHHHHHEEECC
T ss_conf            95312134148-------------867883-67-------------99999999853009998714999999985126458 9


Q ss_pred            HHCCEEEEEEEEECCC--CHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
Q ss_conf            6372799999876136 9--555789999999999999999999998876789
Q Sat_Feb_14_18:  143 GRMGIEILSFTIKDVYD--KVDYLSSLGKTQTAVVQRDADIGVAEAERDAGIR  193 (428)
Q Consensus       143 ~~~Gl~l~~~~i~di~d--~~~~~~~a~g~~~~ae~~r~A~ia~aeaerea~i~  193 (428)
                       --|=+..-   +.+..  ...+|+-++-=.-       .|+--.  +..+++
T Consensus        56 -~CGEEF~G---k~LP~~E~EKVFeLLNdFKG-------sIDWen--kkVrlr   95 (95)
T 2k5c_A           56 -VCGEEFYG---KTLPRREAEKVFELLNDFKG-------GIDWEN--KRVKLK   95 (95)
T ss_dssp            -TTCCEEET---TSSCTTTHHHHHHHHSCSS-------SCBTTT--TBCCCC
T ss_pred            -CCCHHHHC---CCCCHHHHHHHHHHHCCC-------CCCCCC--CEEECC
T ss_conf            -77678863---5688478999999998625 7-------756443--434249
```

No 7

b.34.5.1 PDB: b.34.5.1 PDB: " target="_blank" title="PDB"> peptidyl transferase reaction; HET: 1MA OMU OMG UR3 PSU SPS; 2.20A {Haloarcula marismortui} SCOP: b.34.5.1 PDB: 1vq4_T* 1vq5_T* 1vq6_T* 1vq7_T* 1s72_T* 1vq9_T* 1vqk_T* 1vql_T* 1vqm_T* 1vqn_T* 1vqo_T* 1vqp_T* 1yhq_T* 1yi2_T* 1yij_T* 1yit_T* 1yj9_T* 1yjn_T* 1yjw_T* 2otj_T* ...
/g; # link to PDB 1vq5_T* 1vq6_T* 1vq7_T* 1s72_T* 1vq9_T* 1vqk_T* 1vql_T* 1vqm_T* 1vqn_T* 1vqo_T* 1vqp_T* 1yhq_T* 1yi2_T* 1yij_T* 1yit_T* 1yj9_T* 1yjn_T* 1yjw_T* 2otj_T* ...
>1vq8_T 50S ribosomal protein L24P; ribosome 50S, protein-protein complex, RNA-RNA complex, protein-RNA complex,
Probab=17.96 E-value=23 Score=11.31 Aligned_cols=73 Identities=11% Similarity=0.007 Sum_probs=26.9

```
Q ss_pred             CCCEEEECCCEEEEEEECCCCCCC---------CEEEECCEEEEEEEEEEEEEEECEEEEECCCCCEECCCCEEEEEEE
Q ss_conf             9963895798489999445579 88---------75997792999976778999966589970688633513992899999
Q Sat_Feb_14_18:    1 MGNCHTVGPNEALVVSGGCCGSDY---------KQYVFGGWAWAWWCISDTQRISLEIMTLQPRCEDVETAEGVALTVTG   71 (428)
Q Consensus         1 ~~~~~~~~p~e~lvitg~~~g~~~~~~~~~~~~kvv~~g~~~v~P~~~~~~~~~l~~~~i~v~~~~~~t~d~i~~~v~a   71 (428)
                      ++++.+..-|++.|++|...|..+         .+|+..|....-        -+-++....|             .+.-
T Consensus        38 ~r~~~IkkGD~V~Vi~G~~KGk~GkV~~V~~k~~rV~Vegvn~~k---------~~g~~~~~pI-------------h~SN   96 (120)
T 1vq8_T           38 QRNVRVNAGDTVEVLRGDFAGEEGEVINVDLDKAVIHVEDVTLEK--------TDGEEVPRPL-------------DTSN   96 (120)
T ss_dssp             CSEEECCTTCEEEECSSTTTTCEEEEEEEETTTTEEEETTCEEEC--------SSSCEEECCB-------------CGGG
T ss_pred             CCCCCEECCCEEEEEECCCCCCCCEEEEEEECCCCEEEEECEEEEE--------CCCCEEECCC-------------CHHH
T ss_conf             8456055599999975678997303999988799999959389 96--------5885276136-------------5488
```

```
Q ss_pred             EEEEEECCC-HHHHHHHHHHHCCCHHH
Q ss_conf             999997897-999999999882788999
Q Sat_Feb_14_18:   72 VAQVKIMTE-KELLAVACEQFLGKNVQD   98 (428)
Q Consensus        72 ~~~~~V~~~~~~i~~Aa~~~l~~~~~~   98 (428)
                      +..+....+ +.-+..    +-..+.+.
T Consensus        97 v~i~~~~~~~~~R~~~~~~~~~kd~s~  120 (120)
T 1vq8_T           97 VRVTDLDLEDEKREAR----LESEDDSA  120 (120)
T ss_dssp             EEEEECCCCCHHHHHH----HHCSSCCC
T ss_pred             EEEEECCCCCHHHHHH----HHCCCCCC
T ss_conf             7999377895466445----53334689
```

No 8

2p9x_A Hypothetical protein PH0832; pyrococcus horikoshii OT3, NPPSFA, national project on protein structural and functional analyses; 1.65A {Pyrococcus horikoshii}
Probab=16.80 E-value=24 Score=11.10 Aligned_cols=86 Identities=19% Similarity=0.295 Sum_probs=38.0

```
Q ss_pred             CCCHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHCCHHHHHHHHHHHHHHHHHHHHHH-------------H
Q ss_conf             897999999999882788999999999999999999965679999863999999999999986-------------3
Q Sat_Feb_14_18:   78 MTEKELLAVACEQFLGKNVQDIKNVVLQTLEGHLRSILGTLTVEQIYQDRDQFAKLVREVAAPDVG-------------R  144 (428)
Q Consensus        78 ~~~~~~i~~Aa~~~l~~~~~~i~~~~~~~~~g~lR~v~~~~t~eei~~~R~~f~~~v~~~v~~dl~-------------~  144 (428)
                      .++.++|..++-..+   ..+...-+..+++.+||+..++ +++=.++|..+|.+.|.+..++--.             +
T Consensus         1 ms~~rdiiv~t~~a---l~~~~P~l~~~LEahLrat~n~-g~ElAyeDP~kFkeAVskLFGEysarllem~iis~~k~~   76 (99)
T 2p9x_A            1 MSKGRDILTKTIILA---LREVAPGLEAVLEAHLRATLNS-GIELAYDDPQKFKEAVSKLFGEYSARLLEMVIISKLKGR   76 (99)
T ss_dssp             -CHHHHHHHHHHHH---HHHHCTTHHHHHHHHHHHHSC-CTTHHHHCHHHHHHHHHHHCHHHHHHHHHHHHHHHHHH
T ss_pred             CCCHHHHHHHHHHH---HHHHCCCHHHHHHHHHHHHCC-CEEECCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
T ss_conf             971899999999999---998582139999999999987477-6032046989999999999988789999999999999
```

```
Q ss_pred             CCEEEEEEEEEECCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
Q ss_conf             727999998761369555789999999999999999999999887678998888
Q Sat_Feb_14_18:  145 MGIEILSFTIKDVYDKVDYLSSLGKTQTAVVQRDADIGVAEAERDAGIREAECK  198 (428)
Q Consensus       145 ~Gl~l~~~~i~di~d~~~~~~a~g~~~~ae~~r~A~ia~aeaerea~i~eAeae  198 (428)
                      .|+.+.   +.|+.+-.            .++++--                .+
T Consensus        77 ~g~~~~---~~~le~lv-----------~~ikkiy-----------------ge   99 (99)
T 2p9x_A           77 LGEDIE---ANSLEELV-----------SEIRKIY-----------------GE   99 (99)
T ss_dssp             SCTTCC---CSSHHHHH-----------HHHHHHH-----------------TC
T ss_pred             HCCCCC---HHHHHHHH-----------HHHHHHC-----------------CC
T ss_conf             674011---60199999-----------9999883-----------------79
```

No 9

3ecf_A NTF2-like protein; YP_324687.1, structural genomics, joint center for structural genomics, JCSG, protein structure initiative; 1.90A {Anabaena variabilis atcc 29413}
Probab=15.77 E-value=25 Score=10.96 Aligned_cols=86 Identities=15% Similarity=0.132 Sum_probs=30.9

```
Q ss_pred             CC---------CEEEECCCEEEEEEECCCCCCCCEEEECCEEEEEEEE----EEEEEEECEEEEECCCCC---------
Q ss_conf             99---------63895798489999445579887599779299997 67----789999665899706886 3---------
Q Sat_Feb_14_18:    1 MG---------NCHTVGPNEALVVSGGCCGSDYKQYVFGGWAWAWWCI----SDTQRISLEIMTLQPRCED---------   58 (428)
Q Consensus         1 ~~----------------p~e~lvitg~~~g~~~~kvv~~g~~~v~P~~~~~~~~~~~~l~~~~i~v~~~~~~~~~~~~   58 (428)
                      -|         |+....|     |+|     .   .+ .|---|+|++    -++.-|++...+++.++-+
T Consensus        20 tGdFS~VQFS~~~qFlSP-----I~~~~~~~~~t~~G~e~v~~Fl~gV~tRvaeVni~s~tveYPrASgvwqmrTTK   85 (130)
T 3ecf_A           20 TGDFSQVQFSCNLEFLSP-----ISG-----N---TL-KGTEEVIPFLKGVTTRVAEVNIMSTTVEYPRASGVWQMRTTK   85 (130)
T ss_dssp             HCCCTTSCEEEEEEECCT-----TCS-----S---CE-ESHHHHHHHHHHTTEEEEEEEEEEETTEEEEEEEEEETT
T ss_pred             CCCEEEEEEECCCEEECC-----CCC-----C---CC-CCHHHHHHHHCHHHHEEEEEEEEEEECCCCCCEEEEEECC
T ss_conf             5880268750473676 56-----668-----8---74-4778898874242221245674675541467642278874 26
```

```
Q ss_pred             --EECC-CCEEEEEEEEEEEECCCHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHCCH
Q ss_conf             --3513-99289999999999789799999999988278899999999999999999965679
Q Sat_Feb_14_18:   59 --VETA-EGVALTVTGVAQVKIMTEKELLAVACEQFLGKNVQDIKNVVLQTLEGHLRSILGTLTV  120 (428)
Q Consensus        59 --~~t~-d~i~~~v~a~~~~~V~~~~~~i~~Aa~~~l~~~~~~i~~~~~~~~~g~lR~v~~~~t~  120 (428)
                        ++|- |.-++|=.+..|+-..=||+.+..--+++        -....    |.=        +
T Consensus        86 G~lytlhnfFrlDEeGi~yiWPmfDPKa~i~dpdaL--------~qwLT----G~~--------Y  130 (130)
T 3ecf_A           86 GTLYTLHNFFRLDEEGIVYVWPMFDPKAVMENPDAL--------IQWLT----GKD--------Y  130 (130)
T ss_dssp             SCEEEEEEEEEETTEEEEEECCBCHHHHHHCHHHH--------HHHHH----CTT--------C
T ss_pred             CEEEEEEEEEECCCCEEEEECCCHHHHHCCHHHH--------HHHHH----CCC--------C
T ss_conf             2489773000436467389974268777642967 88--------88860----699--------9
```

No 10

1vpr_A Luciferase; beta barrel, fatty acid binding protein, lipocalin, PH regulation; 1.80A {Lingulodinium polyedrum} SCOP: b.60.1.7
Probab=13.54 E-value=29 Score=10.43 Aligned_cols=110 Identities=19% Similarity=0.171 Sum_probs=29.4

```
Q ss_pred              CCCEEEECCCEEEEEEECCCCCCC----CEEEECC---EEEEEEEEEEEEEE----EC---EEEEEE-----CCCCCEEC
Q ss_conf              9963895798489999445579888----7599779---29999767789999----66---589970-----68863351
Q Sat_Feb_14_18:    1 MGNCHTVGPNEALVVSGGCCGSDY----KQYVFGG---WAWAWWCISDTQRI----SL---EIMTLQ-----PRCEDVET   61 (428)
Q Consensus         1 ~~~~~~~~~p~e~lvitg~~~g~~~~~~----~kvv~~g---~~~~v~P~~~~~~~~~~~~---~l---~~~~~i~------v~~~~~~t   61 (428)
                       .|..+||..+-+----..|++..+    --.|.||   |.||+|  +.+.++    .|   +-+.|+     +..-- +-
T Consensus       212 ~gd~ctvdasvak~arakrtwksghyfyeplvsggnllgvwvlp--eeyrkigffwemesg~cfrierraf~~~~~m-~l  288 (374)
T 1vpr_A          212 FGDVCTVDASVAKFARAKRTWKSGHYFYEPLVSGGNLLGVWVLP--EEYRKIGFFWEMESGRCFRIERRAFPVGPYT-FM  288 (374)
T ss_dssp              ETTEEEEECCTTTBSBSEEEEETTCEEEEEBTTSCEEEEEEEECC--SSSEEEEEEEEETTTTEEEEEEEEEEEEETTEE-EE
T ss_pred              CCCEEEEEHHHHHHHHHHCCCCCCCEEECCCCCCCCEEEEEECH--HHHHHCCEEEEECCCCEEEEEECCCCCCCEE-EE
T ss_conf              7977675157888887650113674132023357835789856 1--674101058871378378776102455875 8-98


Q ss_pred              CCC--EEEEEEEEEEEEEECCCHHHH--------HHHHH------HHHCCC---------------H---HHHHHHHHHHH
Q ss_conf              399--28999999999997897999 9--------99999------882788---------------9---99999999999
Q Sat_Feb_14_18:   62 AEG--VALTVTGVAQVKIMTEKELL--------AVACE------QFLGKN---------------V---QDIKNVVLQTL  107 (428)
Q Consensus        62 ~d~--i~~~v~a~~~~~~V~~~~~~~~i----------~Aa~~--------~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~  107 (428)
                 ++-  +.=.|.-+|||+|+.||++-         ++|--       .-||+.               +   .+-+.++.
T Consensus       289 rq~tev~gkisfvfyvkvsndp~s~~ip~qsrdytalag~dn~pdnlg~pyp~takdld~p~krdtwld~n~~~m~~---  365 (374)
T 1vpr_A          289 RQATEVGGKISFVFYVKVSNDPESDPIPLQSRDYTALAGRDNAPTNLGKPYPTLAKDLDYPKKRDGWLEKNEKEMLR---  365 (374)
T ss_dssp              EEEEEETTEEEEEEEEEEEESCCCSCCCCCCCCHHHHTTTCTTCBBTTSCBCCCCSSCTTTTCCBC---------------
T ss_pred              EECHHCCCEEEEEEEEEEECCCCCCCCCCCCCCHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHCCHHHHHH---
T ss_conf              63000165689999999836898888546545630766178777555799877731027876323302116889998 7---


Q ss_pred              HHHHHHHHHHCC
Q ss_conf              999999996567
Q Sat_Feb_14_18:  108 EGHLRSILGTLT  119 (428)
Q Consensus       108 ~g~lR~v~~~~~t  119 (428)
                    -|.++++--
T Consensus       366 ---qr~~v~~~f  374 (374)
T 1vpr_A          366 ---QRNIVSSTF  374 (374)
T ss_dssp              ------------
T ss_pred              ---HHHHHCCCC
T ss_conf              ---642110469
```

Done!

Please cite as appropriate:

***HHpred*: Söding, J. (2005) Protein homology detection by HMM-HMM comparison. Bioinformatics 21: 951-960.**

PSIPRED: Jones, D.T. (1999) Protein secondary structure prediction based on position-specific scoring matrices. JMB 292: 195-202.

PDB: Bourne, PE. *et al.* (2004) The distribution and query systems of the RCSB Protein Data Bank. NAR 32: D223.