Phyre2

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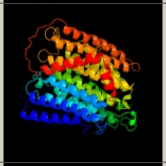
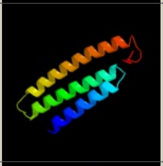
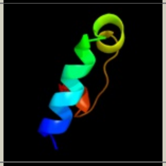
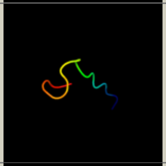
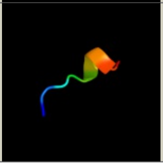
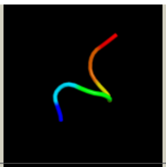
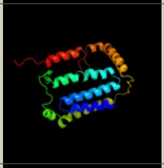
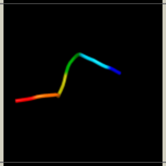
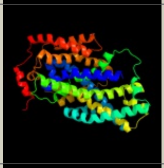
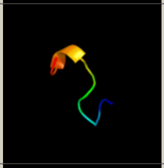
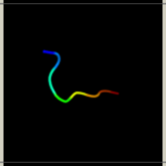
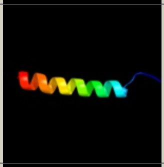
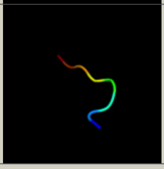
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoM_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**nadh-quinone oxidoreductase subunit m; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
2	c3rkoL_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**nadh-quinone oxidoreductase subunit l; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
3	c3rkoN_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**nadh-quinone oxidoreductase subunit n; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
4	c3rkoK_	Alignment		47.0	13	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**nadh-quinone oxidoreductase subunit k; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
5	c2l3iA_	Alignment		28.1	58	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**aoxki4a, antimicrobial peptide in spider venom; **PDBTitle:** oxki4a, spider derived antimicrobial peptide
6	d1a6qa1	Alignment		26.4	6	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
7	d1o8bb1	Alignment		21.0	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
8	d1s1qa_	Alignment		16.6	31	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
9	d1r6ra_	Alignment		16.6	15	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
10	c1r6rA_	Alignment		16.6	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** solution structure of dengue virus capsid protein reveals a2 new fold
11	c3r24A_	Alignment		16.5	33	**PDB header:**transferase, viral protein **Chain:** A: **PDB Molecule:**2'-o-methyl transferase; **PDBTitle:** crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible

12	c3c25A_	Alignment		14.8	83	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**noti restriction endonuclease; **PDBTitle:** crystal structure of noti restriction endonuclease bound to cognate2 dna
13	c3na2C_	Alignment		14.6	33	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from mine drainage2 metagenome leptospirillum rubarum
14	c3rkoF_	Alignment		14.4	9	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
15	c2kwtA_	Alignment		14.4	50	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protease ns2-3; **PDBTitle:** solution structure of ns2 [27-59]
16	c2jlnA_	Alignment		14.3	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
17	c3mesB_	Alignment		13.8	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline kinase; **PDBTitle:** crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
18	d1n9wa2	Alignment		13.3	63	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
19	d1xmec1	Alignment		13.1	26	**Fold:**Single transmembrane helix **Superfamily:**Bacterial ba3 type cytochrome c oxidase subunit IIa **Family:**Bacterial ba3 type cytochrome c oxidase subunit IIa
20	c1n9wA_	Alignment		13.1	63	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2; **PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
21	c2latA_	Alignment	not modelled	13.0	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** solution structure of a human minimembrane protein ost4
22	c2kncA_	Alignment	not modelled	12.8	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
23	c3bjuB_	Alignment	not modelled	12.8	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
24	c2p04B_	Alignment	not modelled	12.1	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**signal transduction histidine kinase; **PDBTitle:** 2.1 ang structure of the dimerized pas domain of signal transduction2 histidine kinase from nostoc punctiforme pcc 73102 with homology to3 the h-noxa/h-noba domain of the soluble guanylyl cyclase
25	d1iwga7	Alignment	not modelled	12.1	13	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
26	c1b8aB_	Alignment	not modelled	11.9	63	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
27	d3d37a2	Alignment	not modelled	11.8	57	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
28	c1wydB_	Alignment	not modelled	11.7	50	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase;

28	c1wydB_	Alignment	not modelled	11.7	30	**PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
29	c2re3A_	Alignment	not modelled	11.7	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
30	d2pila_	Alignment	not modelled	11.5	18	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
31	c2voyK_	Alignment	not modelled	11.5	27	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
32	c1x55A_	Alignment	not modelled	11.4	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase; **PDBTitle:** crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
33	c1e22A_	Alignment	not modelled	11.3	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
34	c2xgtB_	Alignment	not modelled	11.3	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
35	c2pjmA_	Alignment	not modelled	11.2	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
36	c3m6jD_	Alignment	not modelled	11.1	32	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of unknown function protein from leptospirillum2 rubarum
37	c1ar1B_	Alignment	not modelled	11.0	16	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
38	c1qleB_	Alignment	not modelled	11.0	16	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
39	c1asyA_	Alignment	not modelled	11.0	25	**PDB header:**complex (aminoacyl-trna synthase/trna) **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
40	d1sfka_	Alignment	not modelled	10.9	10	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
41	d1fftb2	Alignment	not modelled	10.9	12	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
42	d2gf4a1	Alignment	not modelled	10.8	13	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Vng1086c-like **Family:**Vng1086c-like
43	c3sokB_	Alignment	not modelled	10.5	18	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
44	c3e9hB_	Alignment	not modelled	10.5	63	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
45	d2cosa1	Alignment	not modelled	10.4	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
46	d1iapa_	Alignment	not modelled	10.4	5	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
47	c3rpfC_	Alignment	not modelled	10.4	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**molybdopterin converting factor, subunit 1 (moad); **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
48	c1efwA_	Alignment	not modelled	10.3	38	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
49	c3m4qA_	Alignment	not modelled	10.3	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
50	d1sfkb_	Alignment	not modelled	10.1	10	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
51	c3jzdA_	Alignment	not modelled	10.1	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
						Fold:PAP/OAS1 substrate-binding domain

52	d1r89a1	Alignment	not modelled	10.1	31	**Superfamily:**PAP/OAS1 substrate-binding domain **Family:**Archaeal tRNA CCA-adding enzyme substrate-binding domain
53	d1lgha_	Alignment	not modelled	9.9	26	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
54	c2cosA_	Alignment	not modelled	9.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase lats2; **PDBTitle:** solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
55	c3kdpH_	Alignment	not modelled	9.8	25	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
56	c3kdpG_	Alignment	not modelled	9.8	25	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
57	c1lk5C_	Alignment	not modelled	9.8	11	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
58	c1ceuA_	Alignment	not modelled	9.8	17	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hiv-1 regulatory protein n-terminal **PDBTitle:** nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
59	c2i3fA_	Alignment	not modelled	9.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycolipid transfer-like protein; **PDBTitle:** crystal structure of a glycolipid transfer-like protein2 from galdieria sulphuraria
60	c1m0sA_	Alignment	not modelled	9.8	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
61	d2f05a1	Alignment	not modelled	9.7	33	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
62	c2kluA_	Alignment	not modelled	9.7	19	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
63	d1iwga8	Alignment	not modelled	9.7	17	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
64	c1m93A_	Alignment	not modelled	9.6	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**serine proteinase inhibitor 2; **PDBTitle:** 1.65 a structure of cleaved viral serpin crma
65	c1lkzB_	Alignment	not modelled	9.6	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
66	c4a1cK_	Alignment	not modelled	9.6	0	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l27a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
67	c2q1kA_	Alignment	not modelled	9.6	44	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**asce; **PDBTitle:** cyrstal structure of asce from aeromonas hydrophilla
68	d1oqwa_	Alignment	not modelled	9.4	21	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
69	d3c07a2	Alignment	not modelled	9.4	15	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
70	c3kwmC_	Alignment	not modelled	9.4	25	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
71	d1p9qc3	Alignment	not modelled	9.3	22	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**Hypothetical protein AF0491, C-terminal domain
72	c1m57H_	Alignment	not modelled	9.3	16	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
73	c2k21A_	Alignment	not modelled	9.3	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
74	c2hfvA_	Alignment	not modelled	9.3	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa1041; **PDBTitle:** solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
75	d1l0wa3	Alignment	not modelled	9.2	38	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
76	d1swxa_	Alignment	not modelled	9.1	38	**Fold:**Glycolipid transfer protein, GLTP **Superfamily:**Glycolipid transfer protein, GLTP **Family:**Glycolipid transfer protein, GLTP
77	d1zvpa1	Alignment	not modelled	9.1	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like

78	d3dtub2	Alignment	not modelled	9.1	16	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
79	d1ej5a_	Alignment	not modelled	9.1	29	**Fold:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Superfamily:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Family:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
80	c3cu4A_	Alignment	not modelled	9.1	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
81	d2hfva1	Alignment	not modelled	9.1	4	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**RPA1041-like
82	d1t95a3	Alignment	not modelled	9.1	22	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**Hypothetical protein AF0491, C-terminal domain
83	c3m8jA_	Alignment	not modelled	9.1	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**focb protein; **PDBTitle:** crystal structure of e.coli focb at 1.4 a resolution
84	c1uj6A_	Alignment	not modelled	9.1	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
85	c3pisA_	Alignment	not modelled	9.0	31	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kazal-type serine protease inhibitor spi-1; **PDBTitle:** crystal structure of carcinoscorpius rotundicauda serine protease2 inhibitor domain 1
86	d1c0aa3	Alignment	not modelled	9.0	25	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
87	d1c8sa_	Alignment	not modelled	9.0	4	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like
88	c3i7fA_	Alignment	not modelled	8.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
89	c1eqrC_	Alignment	not modelled	8.9	25	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
90	c2kseA_	Alignment	not modelled	8.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein qsec; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor qsec, center for structures of3 membrane proteins (csmp) target 4311c
91	c2fxpA_	Alignment	not modelled	8.8	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**spike glycoprotein; **PDBTitle:** solution structure of the sars-coronavirus hr2 domain
92	c2k1aA_	Alignment	not modelled	8.8	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
93	d1b8aa2	Alignment	not modelled	8.8	63	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
94	d2b1xa1	Alignment	not modelled	8.7	80	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
95	c1w2lA_	Alignment	not modelled	8.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
96	d1oedb_	Alignment	not modelled	8.7	15	**Fold:**Neurotransmitter-gated ion-channel transmembrane pore **Superfamily:**Neurotransmitter-gated ion-channel transmembrane pore **Family:**Neurotransmitter-gated ion-channel transmembrane pore
97	c3bs7A_	Alignment	not modelled	8.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
98	d1vzva_	Alignment	not modelled	8.6	33	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
99	d1eova2	Alignment	not modelled	8.6	25	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain