Phyre^2

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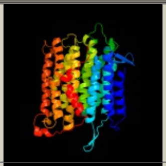
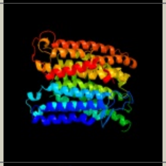
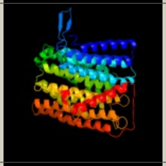
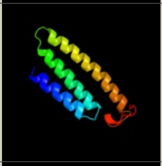
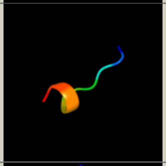
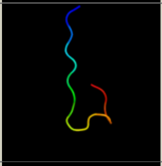
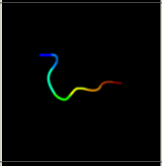
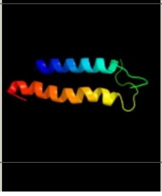
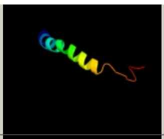
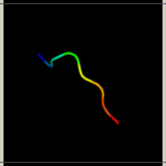
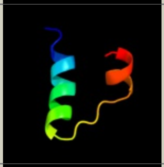
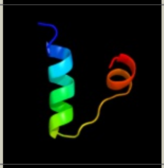
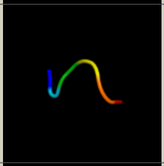
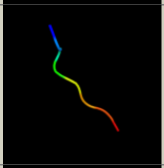
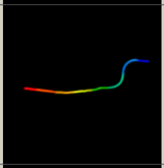
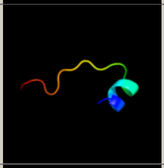
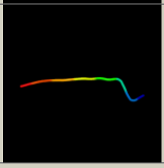
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoL_	Alignment		100.0	32	**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
2	c3rkoM_	Alignment		100.0	19	**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
3	c3rkoN_	Alignment		100.0	19	**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		61.3	20	**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		33.3	50	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**aoxki4a, antimicrobial peptide in spider venom; **PDBTitle:** oxki4a, spider derived antimicrobial peptide
6	d1a6qa1	Alignment		24.6	26	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
7	c3r24A_	Alignment		14.9	22	**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
8	d1s1qa_	Alignment		14.6	31	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
9	d1n9wa2	Alignment		14.5	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
10	c1n9wA_	Alignment		14.5	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
11	c2kseA_	Alignment		14.0	19	**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

12	c2k21A_	Alignment		13.9	28	**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
13	c3bjuB_	Alignment		13.8	50	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
14	d1r6ra_	Alignment		13.7	30	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
15	c1r6rA_	Alignment		13.7	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** solution structure of dengue virus capsid protein reveals a2 new fold
16	c3c25A_	Alignment		13.4	50	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**noti restriction endonuclease; **PDBTitle:** crystal structure of noti restriction endonuclease bound to cognate2 dna
17	c1b8aB_	Alignment		12.9	63	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
18	c1wydB_	Alignment		12.6	63	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
19	c3fq6A_	Alignment		12.5	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
20	c1x55A_	Alignment		12.4	50	**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
21	c1e22A_	Alignment	not modelled	12.3	50	**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
22	c2xgtB_	Alignment	not modelled	12.3	38	**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
23	c2kncA_	Alignment	not modelled	11.8	0	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
24	d1o8bb1	Alignment	not modelled	11.7	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
25	c1asyA_	Alignment	not modelled	11.6	50	**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
26	c3e9hB_	Alignment	not modelled	11.0	50	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
27	c3m4qA_	Alignment	not modelled	10.8	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
28	c1efwA_	Alignment	not modelled	10.8	50	**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
29	d2gf4a1	Alignment	not modelled	10.2	17	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Vng1086c-like **Family:**Vng1086c-like
30	c3mesB_	Alignment	not modelled	10.2	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline kinase; **PDBTitle:** crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
31	c1ceuA_	Alignment	not modelled	9.9	25	**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
32	c2voyK_	Alignment	not modelled	9.7	14	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
33	d1l0wa3	Alignment	not modelled	9.7	50	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
34	d1c0aa3	Alignment	not modelled	9.4	50	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
35	c2i3fA_	Alignment	not modelled	9.4	13	**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
36	d3d37a2	Alignment	not modelled	9.4	36	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
37	c1eqrC_	Alignment	not modelled	9.2	50	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
38	d1b8aa2	Alignment	not modelled	9.2	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
39	d1eova2	Alignment	not modelled	9.1	50	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
40	c3i7fA_	Alignment	not modelled	9.1	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
41	c2ejbA_	Alignment	not modelled	9.0	40	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
42	d1lgha_	Alignment	not modelled	9.0	29	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
43	c2re3A_	Alignment	not modelled	9.0	27	**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
44	c3rpfC_	Alignment	not modelled	8.9	50	**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
45	c2hg5D_	Alignment	not modelled	8.8	10	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**kcsa channel; **PDBTitle:** cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
46	c3na2C_	Alignment	not modelled	8.8	25	**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
47	d1sfka_	Alignment	not modelled	8.7	19	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
48	d1sfkb_	Alignment	not modelled	8.7	19	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
49	c2uwjG_	Alignment	not modelled	8.7	32	**PDB header:**chaperone **Chain:** G: **PDB Molecule:**type iii export protein pscg; **PDBTitle:** structure of the heterotrimeric complex which regulates2 type iii secretion needle formation
50	d1unca_	Alignment	not modelled	8.6	33	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
51	c2jwaA_	Alignment	not modelled	8.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
52	d1yu8x1	Alignment	not modelled	8.5	33	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
53	c2p04B_	Alignment	not modelled	8.4	14	**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

54	d1unda_	Alignment	not modelled	8.3	33	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
55	c3g1zB_	Alignment	not modelled	8.1	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative lysyl-trna synthetase; **PDBTitle:** structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
56	c1m93A_	Alignment	not modelled	8.1	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**serine proteinase inhibitor 2; **PDBTitle:** 1.65 a structure of cleaved viral serpin crma
57	d1swxa_	Alignment	not modelled	8.0	13	**Fold:**Glycolipid transfer protein, GLTP **Superfamily:**Glycolipid transfer protein, GLTP **Family:**Glycolipid transfer protein, GLTP
58	d1sbza_	Alignment	not modelled	7.9	40	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
59	d2axth1	Alignment	not modelled	7.9	10	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II 10 kDa phosphoprotein PsbH **Family:**PsbH-like
60	d2axti1	Alignment	not modelled	7.8	17	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
61	c2pjmA_	Alignment	not modelled	7.8	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
62	d1oqwa_	Alignment	not modelled	7.8	20	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
63	d1r89a1	Alignment	not modelled	7.8	15	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**Archaeal tRNA CCA-adding enzyme substrate-binding domain
64	d2q7ra1	Alignment	not modelled	7.6	21	**Fold:**MAPEG domain-like **Superfamily:**MAPEG domain-like **Family:**MAPEG domain
65	d1nnha_	Alignment	not modelled	7.5	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
66	d2b1xa1	Alignment	not modelled	7.4	40	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
67	d2f05a1	Alignment	not modelled	7.4	30	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
68	d1qzpa_	Alignment	not modelled	7.4	21	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
69	c3kv0A_	Alignment	not modelled	7.3	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**het-c2; **PDBTitle:** crystal structure of het-c2: a fungal glycolipid transfer protein2 (gltp)
70	c2l3xA_	Alignment	not modelled	7.3	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ablim2 protein; **PDBTitle:** villin head piece domain of human ablim2
71	d2qam31	Alignment	not modelled	7.2	9	**Fold:**L35p-like **Superfamily:**L35p-like **Family:**Ribosomal protein L35p
72	d1m0sa1	Alignment	not modelled	7.2	45	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
73	c3zquA_	Alignment	not modelled	7.2	30	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
74	c2zylA_	Alignment	not modelled	7.1	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible oxidoreductase; **PDBTitle:** crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
75	d1zvpa1	Alignment	not modelled	7.0	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
76	c2k6nA_	Alignment	not modelled	7.0	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**supervillin; **PDBTitle:** solution structure of human supervillin headpiece, minimized2 average
77	c2qieB_	Alignment	not modelled	7.0	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
78	c3cu4A_	Alignment	not modelled	6.9	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
79	d2cosa1	Alignment	not modelled	6.9	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
						PDB header:isomerase

80	c1m0sA_	Alignment	not modelled	6.9	28	**Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
81	c1lkzB_	Alignment	not modelled	6.9	19	**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.
82	c2kwtA_	Alignment	not modelled	6.9	27	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protease ns2-3; **PDBTitle:** solution structure of ns2 [27-59]
83	d1jhda1	Alignment	not modelled	6.9	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
84	d1yu5x1	Alignment	not modelled	6.8	33	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
85	c3bs7A_	Alignment	not modelled	6.8	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
86	d1p9qc3	Alignment	not modelled	6.8	33	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**Hypothetical protein AF0491, C-terminal domain
87	d1o7na1	Alignment	not modelled	6.8	20	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
88	d1ulia1	Alignment	not modelled	6.7	20	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
89	d1wqla1	Alignment	not modelled	6.7	20	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
90	d1fm0d_	Alignment	not modelled	6.7	50	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
91	d2ha9a1	Alignment	not modelled	6.7	23	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**SP0239-like
92	c3gteB_	Alignment	not modelled	6.7	20	**PDB header:**electron transport, oxidoreductase **Chain:** B: **PDB Molecule:**ddmc; **PDBTitle:** crystal structure of dicamba monooxygenase with non-heme2 iron
93	c2q1kA_	Alignment	not modelled	6.6	44	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**asce; **PDBTitle:** cyrstal structure of asce from aeromonas hydrophilla
94	d1gdva_	Alignment	not modelled	6.6	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
95	d1ujsa_	Alignment	not modelled	6.6	11	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
96	c3acgA_	Alignment	not modelled	6.6	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-1,4-endoglucanase; **PDBTitle:** crystal structure of carbohydrate-binding module family 282 from clostridium josui cel5a in complex with cellobiose
97	c1w2lA_	Alignment	not modelled	6.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
98	c3gkqB_	Alignment	not modelled	6.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a- **PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 novosphingobium sp. ka1
99	d1vzva_	Alignment	not modelled	6.5	29	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin