Phyre2

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Description	P23482
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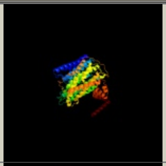
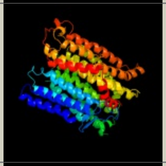
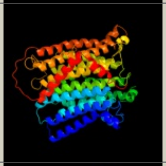
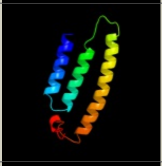
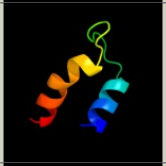
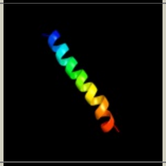
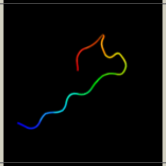
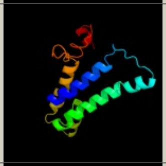
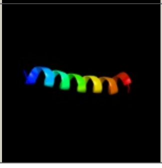
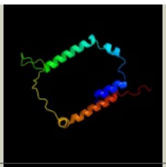
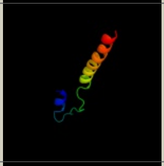
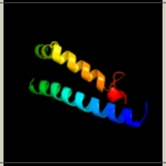
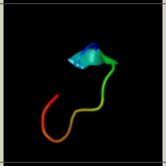
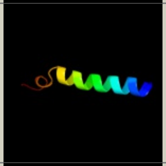
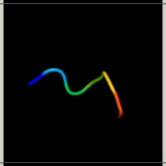
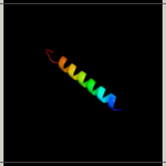
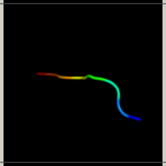
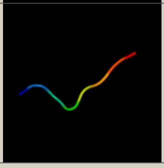
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoL_	Alignment		100.0	23	**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	24	**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		80.5	17	**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	d1a6qa1	Alignment		31.6	11	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
6	c2l3iA_	Alignment		28.2	50	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**aoxki4a, antimicrobial peptide in spider venom; **PDBTitle:** oxki4a, spider derived antimicrobial peptide
7	d2gf4a1	Alignment		18.7	23	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Vng1086c-like **Family:**Vng1086c-like
8	d1o8bb1	Alignment		17.2	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
9	d1s1qa_	Alignment		15.3	31	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
10	d1j4na_	Alignment		15.1	17	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
11	c1iijA_	Alignment		13.5	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**erbb-2 receptor protein-tyrosine kinase; **PDBTitle:** solution structure of the neu/erbb-2 membrane spanning2 segment

12	c3rkoF_	Alignment		13.2	16	**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
13	d2q7ra1	Alignment		12.8	11	**Fold:**MAPEG domain-like **Superfamily:**MAPEG domain-like **Family:**MAPEG domain
14	d1nekd_	Alignment		12.8	16	**Fold:**Heme-binding four-helical bundle **Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
15	c3na2C_	Alignment		12.7	58	**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
16	d2axti1	Alignment		12.6	7	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
17	d3d37a2	Alignment		12.4	57	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
18	d1lgha_	Alignment		12.2	29	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
19	d1n9wa2	Alignment		10.5	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
20	c1n9wA_	Alignment		10.4	50	**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	c2p64B_	Alignment	not modelled	10.4	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**f-box/wd repeat protein 1a; **PDBTitle:** d domain of b-trcp
22	c1r6rA_	Alignment	not modelled	10.0	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** solution structure of dengue virus capsid protein reveals a2 new fold
23	d1r6ra_	Alignment	not modelled	10.0	30	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
24	c3bjuB_	Alignment	not modelled	9.6	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
25	c3r24A_	Alignment	not modelled	9.5	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
26	c2voyK_	Alignment	not modelled	9.4	18	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
27	c2kncA_	Alignment	not modelled	9.2	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
28	c2yvxD_	Alignment	not modelled	9.2	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte

29	c3c25A_	Alignment	not modelled	9.2	67	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**noti restriction endonuclease; **PDBTitle:** crystal structure of noti restriction endonuclease bound to cognate2 dna
30	c1b8aB_	Alignment	not modelled	9.2	50	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
31	d1bcce2	Alignment	not modelled	9.1	8	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
32	c2pjmA_	Alignment	not modelled	9.0	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
33	d1fftb2	Alignment	not modelled	9.0	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
34	c1wydB_	Alignment	not modelled	9.0	50	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
35	c3rpfC_	Alignment	not modelled	8.7	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
36	c2xgtB_	Alignment	not modelled	8.6	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
37	d2f05a1	Alignment	not modelled	8.5	33	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
38	c2hg5D_	Alignment	not modelled	8.4	13	**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
39	c1x55A_	Alignment	not modelled	8.4	38	**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
40	d2uuia1	Alignment	not modelled	8.4	12	**Fold:**MAPEG domain-like **Superfamily:**MAPEG domain-like **Family:**MAPEG domain
41	c2pnoL_	Alignment	not modelled	8.4	12	**PDB header:**lyase **Chain:** L: **PDB Molecule:**leukotriene c4 synthase; **PDBTitle:** crystal structure of human leukotriene c4 synthase
42	c2p63D_	Alignment	not modelled	8.3	33	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**cell division control protein 4; **PDBTitle:** suprafacial orientation of the scfcdc4 dimer accommodates multiple2 geometries for substrate ubiquitination
43	c1asyA_	Alignment	not modelled	8.3	38	**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
44	c1e22A_	Alignment	not modelled	8.1	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
45	c2bg9B_	Alignment	not modelled	8.0	12	**PDB header:**ion channel/receptor **Chain:** B: **PDB Molecule:**acetylcholine receptor protein, beta chain; **PDBTitle:** refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
46	c4a1cK_	Alignment	not modelled	7.9	27	**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.
47	d1ppje2	Alignment	not modelled	7.9	11	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
48	c3gm1A_	Alignment	not modelled	7.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein tyrosine kinase 2 beta; **PDBTitle:** crystal structure of the focal adhesion targeting (fat)2 domain of pyk2 in complex with paxillin ld4 motif-derived3 peptides
49	c3m4qA_	Alignment	not modelled	7.6	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
50	c2kwtA_	Alignment	not modelled	7.6	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protease ns2-3; **PDBTitle:** solution structure of ns2 [27-59]
51	c1efwA_	Alignment	not modelled	7.6	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
52	d1h2sb_	Alignment	not modelled	7.6	27	**Fold:**Transmembrane helix hairpin **Superfamily:**Htr2 transmembrane domain-like **Family:**Htr2 transmembrane domain-like

53	c1h2sB_	Alignment	not modelled	7.6	27	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**sensory rhodopsin ii transducer; **PDBTitle:** molecular basis of transmenbrane signalling by sensory2 rhodopsin ii-transducer complex
54	c3swyB_	Alignment	not modelled	7.5	25	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cyclic nucleotide-gated cation channel alpha-3; **PDBTitle:** cnga3 626-672 containing clz domain
55	c2ojmA_	Alignment	not modelled	7.5	22	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**moronecidin; **PDBTitle:** solution structure and cell selectivity of piscidin 1 and2 its analogues
56	d1k04a_	Alignment	not modelled	7.4	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**FAT domain of focal adhesion kinase **Family:**FAT domain of focal adhesion kinase
57	c3mesB_	Alignment	not modelled	7.3	46	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline kinase; **PDBTitle:** crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
58	c3kdpG_	Alignment	not modelled	7.3	52	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
59	c3kdpH_	Alignment	not modelled	7.3	52	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
60	c3e9hB_	Alignment	not modelled	7.2	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
61	c2uwjG_	Alignment	not modelled	7.2	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
62	c2kseA_	Alignment	not modelled	7.1	13	**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
63	d1oqwa_	Alignment	not modelled	7.1	28	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
64	c1uj6A_	Alignment	not modelled	7.1	19	**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
65	c2bg9A_	Alignment	not modelled	7.0	10	**PDB header:**ion channel/receptor **Chain:** A: **PDB Molecule:**acetylcholine receptor protein, alpha chain; **PDBTitle:** refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
66	c1ceuA_	Alignment	not modelled	7.0	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
67	c3kwmC_	Alignment	not modelled	6.9	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
68	d2qam31	Alignment	not modelled	6.8	9	**Fold:**L35p-like **Superfamily:**L35p-like **Family:**Ribosomal protein L35p
69	c3cu4A_	Alignment	not modelled	6.8	8	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
70	d1zvpa1	Alignment	not modelled	6.8	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
71	d1unca_	Alignment	not modelled	6.8	21	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
72	d1ty9a_	Alignment	not modelled	6.8	43	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
73	c2y0nE_	Alignment	not modelled	6.6	29	**PDB header:**transcription **Chain:** E: **PDB Molecule:**male-specific lethal 1 homolog; **PDBTitle:** crystal structure of the complex between dosage2 compensation factors msl1 and msl3
74	d1vzva_	Alignment	not modelled	6.6	33	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
75	d1l0wa3	Alignment	not modelled	6.5	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
76	d1sfkb_	Alignment	not modelled	6.5	22	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
77	c2qieB_	Alignment	not modelled	6.5	67	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
78	c1m93A_	Alignment	not modelled	6.5	4	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**serine proteinase inhibitor 2;

						PDBTitle: 1.65 a structure of cleaved viral serpin crma
79	d1b8aa2	Alignment	not modelled	6.4	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
80	d1c0aa3	Alignment	not modelled	6.4	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
81	d1unda_	Alignment	not modelled	6.4	14	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
82	d1ubdc4	Alignment	not modelled	6.3	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
83	c2eiuE_	Alignment	not modelled	6.3	67	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**hypothetical protein aq_1627; **PDBTitle:** crystal structure of a putative protein (aq1627) from aquifex aeolicus
84	d3cx5c2	Alignment	not modelled	6.3	7	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
85	c1lkzB_	Alignment	not modelled	6.2	20	**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.
86	c2jttD_	Alignment	not modelled	6.2	38	**PDB header:**calcium binding protein/antitumor protei **Chain:** D: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of calcium loaded s100a6 bound to c-2 terminal siah-1 interacting protein
87	c1eqrC_	Alignment	not modelled	6.2	38	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
88	c2hfvA_	Alignment	not modelled	6.2	14	**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.
89	d2hfva1	Alignment	not modelled	6.2	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**RPA1041-like
90	c1w3zA_	Alignment	not modelled	6.2	45	**PDB header:**complement regulator **Chain:** A: **PDB Molecule:**bbcrasp-1; **PDBTitle:** semet derivative of bbcrasp-1 from borrelia burgdorferi
91	d1fm0d_	Alignment	not modelled	6.2	50	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
92	c3oqvA_	Alignment	not modelled	6.2	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**albc; **PDBTitle:** albc, a cyclodipeptide synthase from streptomyces noursei
93	d1eova2	Alignment	not modelled	6.2	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
94	d1yu8x1	Alignment	not modelled	6.2	22	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
95	c1zp0D_	Alignment	not modelled	6.2	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**small cytochrome binding protein; **PDBTitle:** crystal structure of mitochondrial respiratory complex ii2 bound with 3-nitropropionate and 2-thenoyltrifluoroacetone
96	c3i7fA_	Alignment	not modelled	6.2	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
97	c2lkjA_	Alignment	not modelled	6.2	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-m; **PDBTitle:** structures and interaction analyses of the integrin alpha-m beta-22 cytoplasmic tails
98	d1r89a1	Alignment	not modelled	6.1	15	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**Archaeal tRNA CCA-adding enzyme substrate-binding domain
99	d1iega_	Alignment	not modelled	6.1	14	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin