Phyre^2

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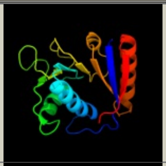
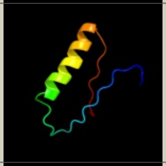
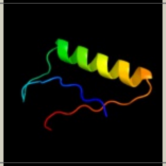
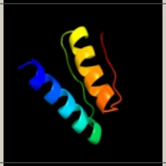
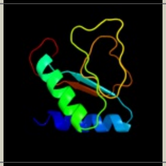
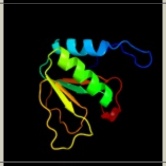
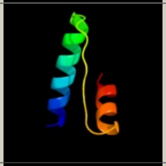
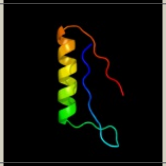
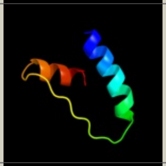
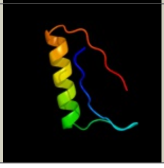
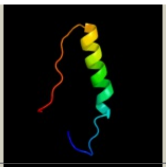
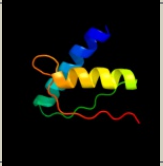
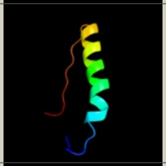
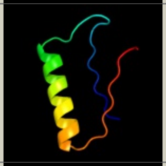
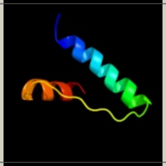
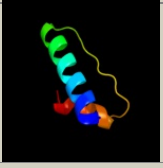
Unique Job ID	e89ec7e33ff802e3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1em8a_	Alignment		100.0	100	**Fold:**DNA polymerase III chi subunit **Superfamily:**DNA polymerase III chi subunit **Family:**DNA polymerase III chi subunit
2	d1c4oa2	Alignment		80.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
3	c2j17A_	Alignment		80.2	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase yil113w; **PDBTitle:** ptyr bound form of sdp-1
4	c2imgA_	Alignment		78.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 23; **PDBTitle:** crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
5	d1tf5a4	Alignment		78.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
6	d1t5la2	Alignment		77.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
7	d1fuka_	Alignment		76.2	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
8	d1nkta4	Alignment		69.0	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
9	c3rgqA_	Alignment		67.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine phosphatase mitochondrial 1; **PDBTitle:** crystal structure of ptpmt1 in complex with pi(5)p
10	c3hgtA_	Alignment		62.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hda1 complex subunit 3; **PDBTitle:** structural and functional studies of the yeast class ii hda12 hdac complex
11	c1fpzF_	Alignment		62.0	10	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cyclin-dependent kinase inhibitor 3; **PDBTitle:** crystal structure analysis of kinase associated phosphatase2 (kap) with a substitution of the catalytic site cysteine3 (cys140) to a serine

12	c2p4dA_	Alignment		61.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** structure-assisted discovery of variola major h12 phosphatase inhibitors
13	c1nl3B_	Alignment		61.0	25	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase seca 1 subunit; **PDBTitle:** crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
14	c2esbA_	Alignment		57.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 18; **PDBTitle:** crystal structure of human dusp18
15	d1fpza_	Alignment		56.5	10	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
16	d1t5ia_	Alignment		53.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
17	c1yz4A_	Alignment		52.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase-like 15 isoform a; **PDBTitle:** crystal structure of dusp15
18	c3dl8B_	Alignment		49.5	20	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
19	d1gm5a4	Alignment		49.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
20	c1tf2A_	Alignment		49.1	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of seca:adp in an open conformation from2 bacillus subtilis
21	d2eyqa2	Alignment	not modelled	48.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
22	c2vdaA_	Alignment	not modelled	45.9	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**translocase subunit seca; **PDBTitle:** solution structure of the seca-signal peptide complex
23	c2vbcA_	Alignment	not modelled	45.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
24	c2hcmA_	Alignment	not modelled	45.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural genomics3 consortium
25	c2hk8B_	Alignment	not modelled	44.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
26	d1oywa3	Alignment	not modelled	44.1	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
27	c1wrmA_	Alignment	not modelled	41.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 22; **PDBTitle:** crystal structure of jsp-1
28	c3juxA_	Alignment	not modelled	41.7	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the translocation atpase seca from thermotoga2 maritima

29	c2oudA_	Alignment	not modelled	41.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the catalytic domain of human mkp5
30	c3dinB_	Alignment	not modelled	36.5	18	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
31	d1jr6a_	Alignment	not modelled	35.6	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
32	c2jmkA_	Alignment	not modelled	35.4	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein ta0956; **PDBTitle:** solution structure of ta0956
33	c1zzwA_	Alignment	not modelled	34.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of catalytic domain of human map kinase2 phosphatase 5
34	c1p74B_	Alignment	not modelled	34.6	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
35	c3dmdA_	Alignment	not modelled	34.6	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
36	c3i32A_	Alignment	not modelled	34.5	14	**PDB header:**rna binding protein,hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
37	c1ii0A_	Alignment	not modelled	33.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of the escherichia coli arsenite-translocating2 atpase
38	d1ihua1	Alignment	not modelled	33.5	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
39	c2wv9A_	Alignment	not modelled	32.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns2b regulatory subunit, flavivirin **PDBTitle:** crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
40	c2wgpA_	Alignment	not modelled	32.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 14; **PDBTitle:** crystal structure of human dual specificity phosphatase 14
41	c2eyqA_	Alignment	not modelled	32.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
42	c2qeqA_	Alignment	not modelled	31.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns3 catalytic subunit; **PDBTitle:** crystal structure of kunjin virus ns3 helicase
43	d1m3ga_	Alignment	not modelled	30.8	22	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
44	c3emuA_	Alignment	not modelled	30.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine rich repeat and phosphatase domain **PDBTitle:** crystal structure of a leucine rich repeat and phosphatase2 domain containing protein from entamoeba histolytica
45	d1t5la1	Alignment	not modelled	29.9	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
46	d1mkpa_	Alignment	not modelled	29.1	14	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
47	c2nt2C_	Alignment	not modelled	28.5	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein phosphatase slingshot homolog 2; **PDBTitle:** crystal structure of slingshot phosphatase 2
48	c3nmeA_	Alignment	not modelled	27.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase
49	c2fsgA_	Alignment	not modelled	26.5	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** complex seca:atp from escherichia coli
50	d1xo1a2	Alignment	not modelled	25.6	10	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
51	c2g6zB_	Alignment	not modelled	25.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 5; **PDBTitle:** crystal structure of human dusp5
52	c3d4oA_	Alignment	not modelled	24.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
53	c3e59A_	Alignment	not modelled	24.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyoverdine biosynthesis protein pvca; **PDBTitle:** crystal structure of the pvca (pa2254) protein from pseudomonas2 aeruginosa
						Fold:P-loop containing nucleoside triphosphate hydrolases

54	d2eyqa5	Alignment	not modelled	24.0	21	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
55	c2j37W_	Alignment	not modelled	22.7	22	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
56	d1tfra2	Alignment	not modelled	22.4	15	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
57	c1gl9B_	Alignment	not modelled	21.5	13	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
58	c2iy3A_	Alignment	not modelled	20.4	16	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
59	d1fx0a3	Alignment	not modelled	20.4	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
60	d2g2ja1	Alignment	not modelled	20.2	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
61	c2r0bA_	Alignment	not modelled	19.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine/tyrosine-interacting protein; **PDBTitle:** crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
62	c3dm5A_	Alignment	not modelled	19.0	19	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
63	c1rrzA_	Alignment	not modelled	18.9	16	**PDB header:**structural genomics,biosynthetic protein **Chain:** A: **PDB Molecule:**glycogen synthesis protein glgs; **PDBTitle:** solution structure of glgs protein from e. coli
64	d1rrza_	Alignment	not modelled	18.9	16	**Fold:**Spectrin repeat-like **Superfamily:**Glycogen synthesis protein GlgS **Family:**Glycogen synthesis protein GlgS
65	d2jdia3	Alignment	not modelled	18.1	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
66	c2z83A_	Alignment	not modelled	17.6	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**helicase/nucleoside triphosphatase; **PDBTitle:** crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
67	d1z5za1	Alignment	not modelled	17.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
68	d2p6ra4	Alignment	not modelled	17.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
69	c2cnwF_	Alignment	not modelled	17.0	16	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
70	d1cmwa2	Alignment	not modelled	16.5	16	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
71	d1j8yf2	Alignment	not modelled	16.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
72	c1gm5A_	Alignment	not modelled	15.6	14	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
73	d2j0sa2	Alignment	not modelled	14.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
74	d2a90a1	Alignment	not modelled	14.9	5	**Fold:**WWE domain **Superfamily:**WWE domain **Family:**WWE domain
75	c2x0dA_	Alignment	not modelled	14.7	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
76	d1pjca1	Alignment	not modelled	14.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
77	d1z3ix1	Alignment	not modelled	13.8	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
78	c1zu4A_	Alignment	not modelled	13.6	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
79	c1vmaA_	Alignment	not modelled	13.5	22	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution

80	c2ihnA_	Alignment	not modelled	13.5	15	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
81	c2pqmA_	Alignment	not modelled	13.5	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
82	c2j7pA_	Alignment	not modelled	13.4	16	**PDB header:**signal recognition **Chain:** A: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
83	d1hv8a2	Alignment	not modelled	13.3	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
84	c3ia7A_	Alignment	not modelled	13.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
85	c2hjvB_	Alignment	not modelled	12.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase dbpa; **PDBTitle:** structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein
86	c2ipcB_	Alignment	not modelled	12.3	25	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
87	c1j8yF_	Alignment	not modelled	12.1	16	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
88	d1b74a1	Alignment	not modelled	12.0	16	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
89	c2v6jA_	Alignment	not modelled	11.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna helicase; **PDBTitle:** kokobera virus helicase: mutant met47thr
90	d1skyb3	Alignment	not modelled	11.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
91	d2b2na1	Alignment	not modelled	11.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
92	d2pd4a1	Alignment	not modelled	11.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	c3bxzA_	Alignment	not modelled	11.4	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**preprotein translocase subunit seca; **PDBTitle:** crystal structure of the isolated dead motor domains from2 escherichia coli seca
94	c1zq1B_	Alignment	not modelled	11.0	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
95	c2qsdB_	Alignment	not modelled	11.0	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of a protein il1583 from idiomarina loihiensis
96	d1t6t1_	Alignment	not modelled	10.8	9	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
97	c3u62A_	Alignment	not modelled	10.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from thermotoga maritima
98	c3b9qA_	Alignment	not modelled	10.4	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
99	c3fshC_	Alignment	not modelled	10.1	55	**PDB header:**ligase **Chain:** C: **PDB Molecule:**autocrine motility factor receptor, isoform 2; **PDBTitle:** crystal structure of the ubiquitin conjugating enzyme2 ube2g2 bound to the g2br domain of ubiquitin ligase gp78