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Description	P0A7I0
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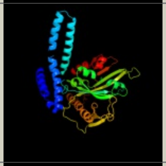
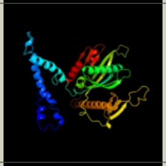
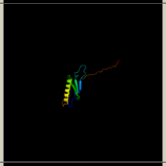
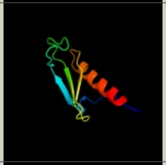
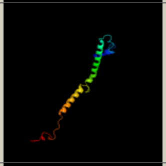
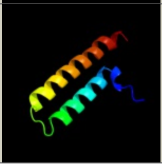
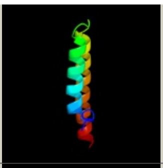
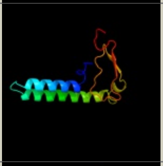
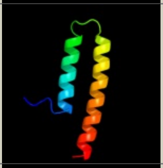
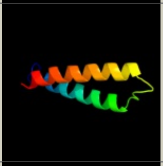
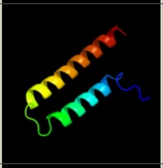
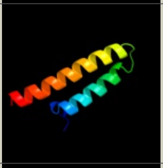
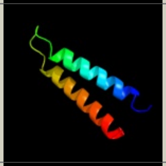
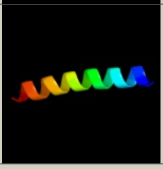
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d5cX_	Alignment		100.0	48	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
2	d1gqea_	Alignment		100.0	38	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
3	c2ihr1_	Alignment		100.0	35	**PDB header:**translation **Chain:** 1: **PDB Molecule:**peptide chain release factor 2; **PDBTitle:** rf2 of thermus thermophilus
4	d1rq0a_	Alignment		100.0	45	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
5	c1zbtA_	Alignment		100.0	44	**PDB header:**translation **Chain:** A: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** crystal structure of peptide chain release factor 1 (rf-1) (smu.1085)2 from streptococcus mutans at 2.34 a resolution
6	d2b3tb1	Alignment		100.0	99	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
7	c2jy9A_	Alignment		99.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative trna hydrolase domain; **PDBTitle:** nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220
8	c2jvaA_	Alignment		99.8	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase domain protein; **PDBTitle:** nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
9	d1j26a_	Alignment		99.8	30	**Fold:**dsRBD-like **Superfamily:**Peptidyl-tRNA hydrolase domain-like **Family:**Peptidyl-tRNA hydrolase domain
10	c3errB_	Alignment		82.9	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fusion protein of microtubule binding domain from **PDBTitle:** microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase
11	c3cx3A_	Alignment		56.1	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure analysis of the streptococcus pneumoniae2 adcaii protein

12	d1xvla1	Alignment		49.9	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
13	c3hjtB_	Alignment		46.1	19	**PDB header:**cell adhesion, transport protein **Chain:** B: **PDB Molecule:**lmb; **PDBTitle:** structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
14	d1pq4a_	Alignment		45.4	22	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
15	c1f8sA_	Alignment		44.6	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
16	c3sjaG_	Alignment		44.3	13	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
17	c2ps3A_	Alignment		44.2	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
18	c3mfqB_	Alignment		42.4	17	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
19	c3layF_	Alignment		41.6	20	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**zinc resistance-associated protein; **PDBTitle:** alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
20	c3ci9B_	Alignment		41.6	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
21	c1wpaA_	Alignment	not modelled	40.1	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** 1.5 angstrom crystal structure of human occludin fragment2 413-522
22	c2ogwB_	Alignment	not modelled	38.0	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua **PDBTitle:** structure of abc type zinc transporter from e. coli
23	c1wleB_	Alignment	not modelled	37.6	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
24	c1toaA_	Alignment	not modelled	37.1	14	**PDB header:**binding protein **Chain:** A: **PDB Molecule:**protein (periplasmic binding protein troa); **PDBTitle:** periplasmic zinc binding protein troa from treponema pallidum
25	d1toaa_	Alignment	not modelled	37.1	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
26	c2ov3A_	Alignment	not modelled	36.6	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein component of an abc **PDBTitle:** crystal structure of 138-173 znua deletion mutant plus zinc2 bound
27	c2e1mA_	Alignment	not modelled	36.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
						PDB header:ribosome **Chain:** I: **PDB Molecule:**40s ribosomal protein s16;

28	c1s1hl_	Alignment	not modelled	35.5	16	**PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
29	c1xawA_	Alignment	not modelled	35.1	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** crystal structure of the cytoplasmic distal c-terminal2 domain of occludin
30	c2jyaA_	Alignment	not modelled	34.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
31	c3qo8A_	Alignment	not modelled	34.2	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
32	d2ctka1	Alignment	not modelled	33.9	14	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
33	c2zkrv_	Alignment	not modelled	31.6	12	**PDB header:**ribosomal protein/rna **Chain:** V: **PDB Molecule:**rna expansion segment es9 part2; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
34	c3pdgA_	Alignment	not modelled	30.5	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
35	d1ivsa1	Alignment	not modelled	30.3	16	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
36	d2vqei1	Alignment	not modelled	30.0	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
37	d2gy9i1	Alignment	not modelled	28.8	32	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
38	c3bbnl_	Alignment	not modelled	27.8	21	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein s9; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
39	c2o1eB_	Alignment	not modelled	27.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ycdh; **PDBTitle:** crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
40	c2fsgA_	Alignment	not modelled	27.0	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** complex seca:atp from escherichia coli
41	c1i4wA_	Alignment	not modelled	25.3	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mitochondrial replication protein mtf1; **PDBTitle:** the crystal structure of the transcription factor sc-mttfb2 offers intriguing insights into mitochondrial transcription
42	d1i4wa_	Alignment	not modelled	25.3	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
43	c2r60A_	Alignment	not modelled	24.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
44	d1sd4a_	Alignment	not modelled	24.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
45	c2zkqi_	Alignment	not modelled	22.4	23	**PDB header:**ribosomal protein/rna **Chain:** I: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
46	c2lf0A_	Alignment	not modelled	21.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yibl; **PDBTitle:** solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scatting, nesg4 target sfr339/ocsp target sf3636
47	c2vvlD_	Alignment	not modelled	21.6	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**monoamine oxidase n; **PDBTitle:** the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
48	d1nj1a3	Alignment	not modelled	21.5	10	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
49	d1psza_	Alignment	not modelled	20.3	18	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
50	d2foka1	Alignment	not modelled	20.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Restriction endonuclease FokI, N-terminal (recognition) domain
51	d2pc6a2	Alignment	not modelled	19.8	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
52	c2yg4B_	Alignment	not modelled	19.5	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putrescine oxidase; **PDBTitle:** structure-based redesign of cofactor binding in

						putrescine2 oxidase: wild type bound to putrescine
53	d2axya1	Alignment	not modelled	19.0	16	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
54	c2xzml_	Alignment	not modelled	18.8	23	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**rps16e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
55	c1sezA_	Alignment	not modelled	18.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase, mitochondrial; **PDBTitle:** crystal structure of protoporphyrinogen ix oxidase
56	d2fgca2	Alignment	not modelled	18.8	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
57	c1xvlC_	Alignment	not modelled	18.4	13	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**mn transporter; **PDBTitle:** the three-dimensional structure of mntc from synechocystis2 6803
58	c3pdyB_	Alignment	not modelled	18.2	21	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**plectin; **PDBTitle:** structure of the third and fourth spectrin repeats of the plakin2 domain of plectin
59	d1m0da_	Alignment	not modelled	17.1	17	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
60	c2bbjB_	Alignment	not modelled	17.0	10	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
61	c3sjbC_	Alignment	not modelled	16.4	12	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
62	d2f1fa1	Alignment	not modelled	16.3	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
63	d2ctla1	Alignment	not modelled	15.7	12	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
64	d2ctea1	Alignment	not modelled	14.9	16	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
65	c3rhaA_	Alignment	not modelled	14.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putrescine oxidase; **PDBTitle:** the crystal structure of oxidoreductase from arthrobacter aurescens
66	c1s3bB_	Alignment	not modelled	14.7	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amine oxidase [flavin-containing] b; **PDBTitle:** crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
67	c3nrxB_	Alignment	not modelled	14.6	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**protein regulator of cytokinesis 1; **PDBTitle:** insights into anti-parallel microtubule crosslinking by prc1, a2 conserved non-motor microtubule binding protein
68	c2b7fD_	Alignment	not modelled	14.5	40	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**htlv protease; **PDBTitle:** crystal structure of human t-cell leukemia virus protease, a novel2 target for anti-cancer design
69	d1lp1a_	Alignment	not modelled	14.5	24	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
70	d1nj8a3	Alignment	not modelled	13.9	14	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
71	d1s05a_	Alignment	not modelled	13.2	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
72	c3neaA_	Alignment	not modelled	12.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
73	d1djqa3	Alignment	not modelled	12.9	34	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
74	c3s2xB_	Alignment	not modelled	12.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
75	c3h0gA_	Alignment	not modelled	12.7	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb1; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
76	d1vqov1	Alignment	not modelled	12.5	18	**Fold:**Long alpha-hairpin **Superfamily:**Ribosomal protein L29 (L29p) **Family:**Ribosomal protein L29 (L29p)
77	c3g5rA_	Alignment	not modelled	12.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)- **PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
78	d2g5ca1	Alignment	not modelled	12.2	12	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like

						Family: TyrA dimerization domain-like
79	c2z2jA_	Alignment	not modelled	12.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
80	c1ztgD_	Alignment	not modelled	11.4	16	**PDB header:**dna, rna binding protein/dna **Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1; **PDBTitle:** human alpha polyc binding protein kh1
81	c2p90B_	Alignment	not modelled	11.3	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
82	c2dq3A_	Alignment	not modelled	11.3	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
83	d3lada1	Alignment	not modelled	11.2	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
84	d1dtja_	Alignment	not modelled	11.2	21	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
85	c2pc6C_	Alignment	not modelled	11.1	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
86	d2asba3	Alignment	not modelled	11.0	22	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
87	d1n4ka2	Alignment	not modelled	10.9	32	**Fold:**beta-Trefoil **Superfamily:**MIR domain **Family:**MIR domain
88	d1r73a_	Alignment	not modelled	10.8	16	**Fold:**Long alpha-hairpin **Superfamily:**Ribosomal protein L29 (L29p) **Family:**Ribosomal protein L29 (L29p)
89	c3v2iA_	Alignment	not modelled	10.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis
90	d1wvna1	Alignment	not modelled	10.7	20	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
91	c2ftcB_	Alignment	not modelled	10.6	23	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**mitochondrial ribosomal protein l2; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
92	d2ho2a1	Alignment	not modelled	10.6	57	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
93	c3on7C_	Alignment	not modelled	10.6	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, iron/ascorbate family; **PDBTitle:** crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution
94	d1hh2p3	Alignment	not modelled	10.5	25	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
95	c2z9fC_	Alignment	not modelled	10.4	19	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**cellulose synthase operon protein d; **PDBTitle:** crystal structure of axcesd protein from acetobacter xylinum
96	c2fgcA_	Alignment	not modelled	10.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
97	c2b9yA_	Alignment	not modelled	10.3	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aminooxidase; **PDBTitle:** crystal structure of cla-producing fatty acid isomerase2 from p. acnes
98	d1vk8a_	Alignment	not modelled	10.3	6	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
99	d1s35a1	Alignment	not modelled	10.3	9	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat