Phyre2

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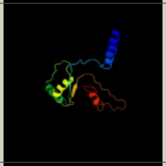
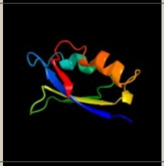
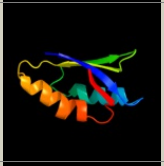
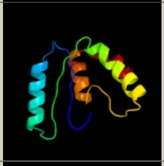
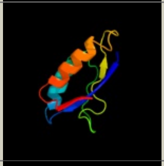
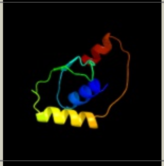
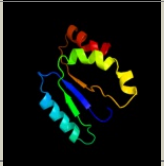
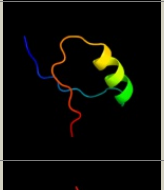
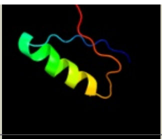
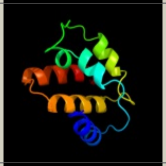
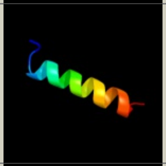
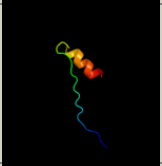
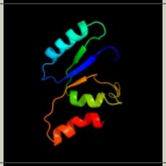
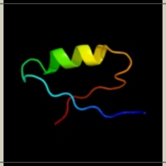
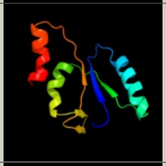
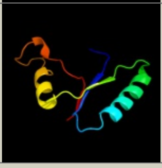
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k07A_	Alignment		94.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
2	c1oy8A_	Alignment		90.1	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
3	d2cyya2	Alignment		78.2	23	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
4	d2cg4a2	Alignment		77.9	19	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
5	c2e1aD_	Alignment		73.5	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
6	c2zbcH_	Alignment		64.2	19	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
7	c3iouB_	Alignment		59.5	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**maltose-binding protein, huntingtin fusion **PDBTitle:** huntingtin amino-terminal region with 17 gln residues -2 crystal c94
8	c2e1cA_	Alignment		55.4	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
9	c1tkeA_	Alignment		53.1	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
10	c3py7A_	Alignment		52.1	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,paxillin ld1,protein e6 **PDBTitle:** crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
11	d2cfxa2	Alignment		52.0	9	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain

12	c2djwF_	Alignment		51.1	12	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
13	c3ibwA_	Alignment		47.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
14	c1ciiA_	Alignment		46.6	10	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
15	c2voyG_	Alignment		41.5	24	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
16	d1z1za1	Alignment		41.5	14	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**Lambda phage gpU-like
17	c3dm0A_	Alignment		40.9	11	**PDB header:**sugar binding protein,signaling protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein fused with **PDBTitle:** maltose binding protein fusion with rack1 from a. thaliana
18	d1i1ga2	Alignment		40.2	12	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
19	c3c4mA_	Alignment		36.8	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fusion protein of maltose-binding periplasmic protein and **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
20	c3ob4A_	Alignment		32.8	13	**PDB header:**allergen **Chain:** A: **PDB Molecule:**maltose abc transporter periplasmic protein, arah 2; **PDBTitle:** mbp-fusion protein of the major peanut allergen ara h 2
21	c1hsjA_	Alignment	not modelled	32.3	13	**PDB header:**transcription/sugar binding protein **Chain:** A: **PDB Molecule:**fusion protein consisting of staphylococcus **PDBTitle:** sarr mbp fusion structure
22	c2nvuB_	Alignment	not modelled	30.8	11	**PDB header:**protein turnover, ligase **Chain:** B: **PDB Molecule:**maltose binding protein/nedd8-activating enzyme **PDBTitle:** structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
23	c2kjwA_	Alignment	not modelled	30.8	19	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55
24	c3f5fA_	Alignment	not modelled	30.4	13	**PDB header:**transport, transferase **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, heparan **PDBTitle:** crystal structure of heparan sulfate 2-o-sulfotransferase2 from gallus gallus as a maltose binding protein fusion.
25	d1vq3a_	Alignment	not modelled	29.8	23	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
26	d1nnfa_	Alignment	not modelled	29.3	26	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
27	c3osrA_	Alignment	not modelled	29.3	13	**PDB header:**fluorescent protein, transport protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, green fluorescent **PDBTitle:** maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 311
						Fold: PurS-like

28	d1gtda_	Alignment	not modelled	29.0	22	**Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
29	c3bn7A_	Alignment	not modelled	27.1	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ferredoxin-like protein; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein (cc_2267) from2 caulobacter crescentus cb15 at 1.64 a resolution
30	d1xc1a_	Alignment	not modelled	27.0	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
31	d1iwga3	Alignment	not modelled	26.6	19	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
32	d1t4aa_	Alignment	not modelled	25.7	21	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
33	d1laxa_	Alignment	not modelled	25.5	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
34	d1q35a_	Alignment	not modelled	25.4	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
35	d1ygya3	Alignment	not modelled	25.4	23	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
36	d1v4pa_	Alignment	not modelled	24.5	18	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**AlaX-like
37	c1svxB_	Alignment	not modelled	23.3	12	**PDB header:**de novo protein/sugar binding protein **Chain:** B: **PDB Molecule:**maltose-binding periplasmic protein; **PDBTitle:** crystal structure of a designed selected ankyrin repeat2 protein in complex with the maltose binding protein
38	c3bb5B_	Alignment	not modelled	22.7	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**stress responsive alpha-beta protein; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution
39	d1xvxa_	Alignment	not modelled	22.7	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
40	c3oaiB_	Alignment	not modelled	22.1	13	**PDB header:**membrane protein, cell adhesion **Chain:** B: **PDB Molecule:**maltose-binding periplasmic protein, myelin protein p0; **PDBTitle:** crystal structure of the extra-cellular domain of human myelin protein2 zero
41	c2zw2B_	Alignment	not modelled	22.0	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
42	c3oq2A_	Alignment	not modelled	21.9	16	**PDB header:**immune system **Chain:** A: **PDB Molecule:**crispr-associated protein cas2; **PDBTitle:** structure of a crispr associated protein cas2 from desulfovibrio2 vulgaris
43	c1t3gB_	Alignment	not modelled	21.8	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**x-linked interleukin-1 receptor accessory **PDBTitle:** crystal structure of the toll/interleukin-1 receptor (tir)2 domain of human il-1rapl
44	c1r6zA_	Alignment	not modelled	21.8	12	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**chimera of maltose-binding periplasmic protein and **PDBTitle:** the crystal structure of the argonaute2 paz domain (as a mbp fusion)
45	c2yx5A_	Alignment	not modelled	21.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
46	c3h4zC_	Alignment	not modelled	21.3	13	**PDB header:**allergen **Chain:** C: **PDB Molecule:**maltose-binding periplasmic protein fused with allergen **PDBTitle:** crystal structure of an mbp-der p 7 fusion protein
47	c3bdeA_	Alignment	not modelled	20.6	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**mll5499 protein; **PDBTitle:** crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from mesorhizobium loti maff303099 at 1.79 a resolution
48	c1mh3A_	Alignment	not modelled	20.4	14	**PDB header:**sugar binding, dna binding protein **Chain:** A: **PDB Molecule:**maltose binding-a1 homeodomain protein chimera; **PDBTitle:** maltose binding-a1 homeodomain protein chimera, crystal2 form i
49	d2csfa1	Alignment	not modelled	20.2	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
50	c2dgbA_	Alignment	not modelled	20.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
51	d1ryla_	Alignment	not modelled	19.9	14	**Fold:**Hypothetical protein yfbM **Superfamily:**Hypothetical protein yfbM **Family:**Hypothetical protein yfbM
52	d1sc6a3	Alignment	not modelled	19.9	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain

53	c3bguA_	Alignment	not modelled	19.8	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ferredoxin-like protein of unknown function; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein of unknown2 function (tfu_0763) from thermobifida fusca yx at 1.50 a resolution
54	d1zpwx1	Alignment	not modelled	19.7	13	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
55	c3mp6A_	Alignment	not modelled	19.1	12	**PDB header:**histone binding protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, linker, saga- **PDBTitle:** complex structure of sgf29 and dimethylated h3k4
56	c2p6tH_	Alignment	not modelled	17.8	14	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
57	c2qycA_	Alignment	not modelled	17.7	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ferredoxin-like protein; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
58	d2qfia1	Alignment	not modelled	17.3	20	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
59	c2ew9A_	Alignment	not modelled	16.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
60	c1i1gA_	Alignment	not modelled	16.4	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
61	c3o3uN_	Alignment	not modelled	16.3	11	**PDB header:**transport protein, signaling protein **Chain:** N: **PDB Molecule:**maltose-binding periplasmic protein, advanced glycosylation **PDBTitle:** crystal structure of human receptor for advanced glycation endproducts2 (rage)
62	c3gr1A_	Alignment	not modelled	15.8	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
63	c3k5pA_	Alignment	not modelled	15.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
64	c3gr0D_	Alignment	not modelled	15.7	9	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**protein prgh; **PDBTitle:** periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
65	c2yy3B_	Alignment	not modelled	15.6	6	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 1-beta; **PDBTitle:** crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii
66	d1kn0a_	Alignment	not modelled	14.3	17	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**The homologous-pairing domain of Rad52 recombinase
67	c2pt1A_	Alignment	not modelled	14.2	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron transport protein; **PDBTitle:** futa1 synechocystis pcc 6803
68	c2rf4B_	Alignment	not modelled	14.1	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
69	d1nyra3	Alignment	not modelled	14.0	11	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
70	c2pc6C_	Alignment	not modelled	14.0	16	**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
71	c3ftjA_	Alignment	not modelled	13.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrolide export atp-binding/permease protein **PDBTitle:** crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
72	c2jo1A_	Alignment	not modelled	13.7	8	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
73	c2vgqA_	Alignment	not modelled	13.6	15	**PDB header:**immune system/transport **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, **PDBTitle:** crystal structure of human ips-1 card
74	c3hzpA_	Alignment	not modelled	13.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 natl2a at 1.40 a resolution
75	c2jp3A_	Alignment	not modelled	13.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
76	c3csgA_	Alignment	not modelled	13.2	13	**PDB header:**de novo protein, sugar binding protein **Chain:** A: **PDB Molecule:**maltose-binding protein monobody ys1 fusion;

						PDBTitle: crystal structure of monobody ys1(mbp-74)/maltose binding2 protein fusion complex
77	d2e74d2	Alignment	not modelled	13.2	18	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
78	d2rh3a1	Alignment	not modelled	13.1	21	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VirC2-like
79	c2f1fA_	Alignment	not modelled	13.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
80	c2cfxD_	Alignment	not modelled	12.9	9	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
81	c1h2iG_	Alignment	not modelled	12.9	17	**PDB header:**dna-binding protein **Chain:** G: **PDB Molecule:**dna repair protein rad52 homolog; **PDBTitle:** human rad52 protein, n-terminal domain
82	d1tr0a_	Alignment	not modelled	12.3	3	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Plant stress-induced protein
83	c1nyqA_	Alignment	not modelled	12.1	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
84	d1qupa2	Alignment	not modelled	12.1	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
85	c1qupA_	Alignment	not modelled	11.9	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
86	c1jk9D_	Alignment	not modelled	11.7	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
87	c3d4cA_	Alignment	not modelled	11.5	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, linker, zona pellucida **PDBTitle:** zp-n domain of mammalian sperm receptor zp3 (crystal form i)
88	c2jsxA_	Alignment	not modelled	11.3	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd
89	d1r8ja1	Alignment	not modelled	11.2	11	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
90	c1om8A_	Alignment	not modelled	11.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serralysin; **PDBTitle:** crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallyzed with 10 mm edta
91	d1sata2	Alignment	not modelled	11.1	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
92	d1tkea2	Alignment	not modelled	10.9	18	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
93	d1y4ta_	Alignment	not modelled	10.8	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
94	d1hyua3	Alignment	not modelled	10.7	4	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
95	d1g9ka2	Alignment	not modelled	10.7	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
96	c2z56B_	Alignment	not modelled	10.6	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tk-subtilisin; **PDBTitle:** crystal structure of g56s-propeptide:s324a-subtilisin complex
97	c3lqbA_	Alignment	not modelled	10.5	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
98	d1v5ib1	Alignment	not modelled	10.3	17	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
99	d1osce_	Alignment	not modelled	10.1	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)