
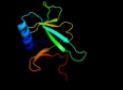





















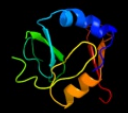





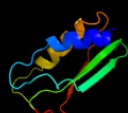


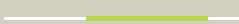
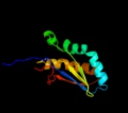







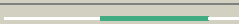

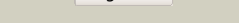
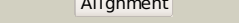
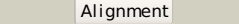


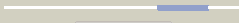


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2k4zA_</a>	 Alignment		100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dsrrr; <b>PDBTitle:</b> solution nmr structure of allochromatium vinosum dsrrr:2 northeast structural genomics consortium target op5
2	<a href="#">dlveha_</a>	 Alignment		100.0	29	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like
3	<a href="#">dlxhja_</a>	 Alignment		100.0	31	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like
4	<a href="#">dls98a_</a>	 Alignment		100.0	26	<b>Fold:</b> HesB-like domain <b>Superfamily:</b> HesB-like domain <b>Family:</b> HesB-like domain
5	<a href="#">c2d2aA_</a>	 Alignment		99.9	21	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> sufa protein; <b>PDBTitle:</b> crystal structure of escherichia coli sufa involved in2 biosynthesis of iron-sulfur clusters
6	<a href="#">dlnwba_</a>	 Alignment		99.9	26	<b>Fold:</b> HesB-like domain <b>Superfamily:</b> HesB-like domain <b>Family:</b> HesB-like domain
7	<a href="#">c1x0gA_</a>	 Alignment		99.9	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> isca; <b>PDBTitle:</b> crystal structure of isca with the [2fe-2s] cluster
8	<a href="#">c2jnvA_</a>	 Alignment		99.9	34	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> nifu-like protein 1, chloroplast; <b>PDBTitle:</b> solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
9	<a href="#">c2apnA_</a>	 Alignment		99.9	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein hi1723; <b>PDBTitle:</b> hi1723 solution structure
10	<a href="#">c2z51A_</a>	 Alignment		99.9	35	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> nifu-like protein 2, chloroplast; <b>PDBTitle:</b> crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis
11	<a href="#">d1th5a1</a>	 Alignment		99.8	25	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like

12	<a href="#">d2p2ea1</a>	 Alignment		97.7	16	<b>Fold:</b> HesB-like domain <b>Superfamily:</b> HesB-like domain <b>Family:</b> HesB-like domain
13	<a href="#">c2qgoA</a>	 Alignment		97.6	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative fe-s biosynthesis protein; <b>PDBTitle:</b> crystal structure of a putative fe-s biosynthesis protein from2 lactobacillus acidophilus
14	<a href="#">c3lnoA</a>	 Alignment		96.1	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of domain of unknown function duf59 from2 bacillus anthracis
15	<a href="#">d2cu6a1</a>	 Alignment		93.9	19	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
16	<a href="#">d1uwda</a>	 Alignment		91.4	14	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
17	<a href="#">c3qauA</a>	 Alignment		63.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxy-3-methylglutaryl-coenzyme a reductase; <b>PDBTitle:</b> 3-hydroxy-3-methylglutaryl-coenzyme a reductase from streptococcus2 pneumoniae
18	<a href="#">c1r7iB</a>	 Alignment		59.5	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxy-3-methylglutaryl-coenzyme a reductase; <b>PDBTitle:</b> hmg-coa reductase from p. mevalonii, native structure at 2.2 angstroms2 resolution.
19	<a href="#">d2c42a2</a>	 Alignment		56.1	25	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR PP module
20	<a href="#">d1xg8a</a>	 Alignment		50.6	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> YuzD-like
21	<a href="#">d1t82a</a>	 Alignment	not modelled	43.6	22	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
22	<a href="#">c3lwaA</a>	 Alignment	not modelled	40.2	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted thiol-disulfide isomerase; <b>PDBTitle:</b> the crystal structure of a secreted thiol-disulfide2 isomerase from corynebacterium glutamicum to 1.75a
23	<a href="#">c2c3yA</a>	 Alignment	not modelled	33.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
24	<a href="#">d2a0sa1</a>	 Alignment	not modelled	32.5	16	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> 6-pyruvoyl tetrahydropterin synthase
25	<a href="#">d1xn7a</a>	 Alignment	not modelled	31.6	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein YhgG
26	<a href="#">d1wp0a1</a>	 Alignment	not modelled	29.4	8	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
27	<a href="#">d1qxha</a>	 Alignment	not modelled	29.2	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
28	<a href="#">c2rmlA</a>	 Alignment	not modelled	28.3	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting p-type atpase copa; <b>PDBTitle:</b> solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
29	<a href="#">c1virA</a>	 Alignment	not modelled	26.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1;

29	<a href="#">c1y1rA_</a>	Alignment	not modelled	20.0	32	<b>PDBTitle:</b> solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
30	<a href="#">d1e2ya_</a>	Alignment	not modelled	22.9	7	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
31	<a href="#">d1y13a_</a>	Alignment	not modelled	21.7	15	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> 6-pyruvoyl tetrahydropterin synthase
32	<a href="#">d1j2ga2</a>	Alignment	not modelled	20.4	24	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> Urate oxidase (uricase)
33	<a href="#">c1bcrA_</a>	Alignment	not modelled	20.1	13	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine carboxypeptidase ii; <b>PDBTitle:</b> complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature
34	<a href="#">c2dhmA_</a>	Alignment	not modelled	19.7	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein bola; <b>PDBTitle:</b> solution structure of the bola protein from escherichia coli
35	<a href="#">d1s6ua_</a>	Alignment	not modelled	19.7	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
36	<a href="#">c2rogA_</a>	Alignment	not modelled	19.1	35	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal binding protein; <b>PDBTitle:</b> solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
37	<a href="#">c3e8pA_</a>	Alignment	not modelled	18.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the protein q8e9m7 from shewanella2 oneidensis related to thioesterase superfamily. northeast3 structural genomics consortium target sor246.
38	<a href="#">d2ibaa2</a>	Alignment	not modelled	18.6	20	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> Urate oxidase (uricase)
39	<a href="#">c3ixrA_</a>	Alignment	not modelled	18.2	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein; <b>PDBTitle:</b> crystal structure of xylella fastidiosa prqx c47s mutant
40	<a href="#">c2rliA_</a>	Alignment	not modelled	17.7	8	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> sco2 protein homolog, mitochondrial; <b>PDBTitle:</b> solution structure of cu(i) human sco2
41	<a href="#">c2k5eA_</a>	Alignment	not modelled	16.8	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
42	<a href="#">c1y8oA_</a>	Alignment	not modelled	16.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; <b>PDBTitle:</b> crystal structure of the pdk3-l2 complex
43	<a href="#">d2yzca2</a>	Alignment	not modelled	15.7	12	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> Urate oxidase (uricase)
44	<a href="#">c1g1vA_</a>	Alignment	not modelled	15.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [3-methyl-2-oxobutanoate dehydrogenase <b>PDBTitle:</b> branched-chain alpha-ketoacid dehydrogenase kinase (bck)2 complexed with atp-gamma-s
45	<a href="#">c2npbA_</a>	Alignment	not modelled	15.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> selenoprotein w; <b>PDBTitle:</b> nmr solution structure of mouse selw
46	<a href="#">c1gxsc_</a>	Alignment	not modelled	14.8	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> p-(s)-hydroxymandelonitrile lyase chain a; <b>PDBTitle:</b> crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme
47	<a href="#">c2kt2A_</a>	Alignment	not modelled	14.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
48	<a href="#">c2q8fA_</a>	Alignment	not modelled	14.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; <b>PDBTitle:</b> structure of pyruvate dehydrogenase kinase isoform 1
49	<a href="#">d1r9fa_</a>	Alignment	not modelled	13.8	21	<b>Fold:</b> Tombusvirus P19 core protein, VP19 <b>Superfamily:</b> Tombusvirus P19 core protein, VP19 <b>Family:</b> Tombusvirus P19 core protein, VP19
50	<a href="#">d1q8la_</a>	Alignment	not modelled	13.7	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
51	<a href="#">c2b7kD_</a>	Alignment	not modelled	13.6	11	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> sco1 protein; <b>PDBTitle:</b> crystal structure of yeast sco1
52	<a href="#">d2b7ka1</a>	Alignment	not modelled	13.4	8	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
53	<a href="#">c2k53A_</a>	Alignment	not modelled	13.2	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> a3dk08 protein; <b>PDBTitle:</b> nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
54	<a href="#">d1rpua_</a>	Alignment	not modelled	13.0	21	<b>Fold:</b> Tombusvirus P19 core protein, VP19 <b>Superfamily:</b> Tombusvirus P19 core protein, VP19 <b>Family:</b> Tombusvirus P19 core protein, VP19

55	<a href="#">c1rpuA</a>	Alignment	not modelled	13.0	21	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> 19 kda protein; <b>PDBTitle:</b> crystal structure of cirv p19 bound to sirna
56	<a href="#">c3lgbB</a>	Alignment	not modelled	12.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna primase large subunit; <b>PDBTitle:</b> crystal structure of the fe-s domain of the yeast dna primase
57	<a href="#">c3cynC</a>	Alignment	not modelled	12.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> probable glutathione peroxidase 8; <b>PDBTitle:</b> the structure of human gpx8
58	<a href="#">c1j2gC</a>	Alignment	not modelled	12.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> uricase; <b>PDBTitle:</b> crystal structure of urate oxidase from bacillus sp. tb-90 co-2 crystallized with 8-azaxanthine
59	<a href="#">c2jszA</a>	Alignment	not modelled	12.6	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> solution structure of tpx in the reduced state
60	<a href="#">c2v1mA</a>	Alignment	not modelled	12.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase; <b>PDBTitle:</b> crystal structure of schistosoma mansoni glutathione2 peroxidase
61	<a href="#">d1lowa</a>	Alignment	not modelled	12.2	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
62	<a href="#">c3gknA</a>	Alignment	not modelled	12.1	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein; <b>PDBTitle:</b> insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
63	<a href="#">c1zyeL</a>	Alignment	not modelled	12.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> thioredoxin-dependent peroxide reductase; <b>PDBTitle:</b> crystal strucutre analysis of bovine mitochondrial peroxiredoxin iii
64	<a href="#">c3qq5A</a>	Alignment	not modelled	12.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> small gtp-binding protein; <b>PDBTitle:</b> crystal structure of the [fefe]-hydrogenase maturation protein hydf
65	<a href="#">c1r56H</a>	Alignment	not modelled	11.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> uricase; <b>PDBTitle:</b> uncomplexed urate oxidase from aspergillus flavus
66	<a href="#">c2yzbA</a>	Alignment	not modelled	11.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uricase; <b>PDBTitle:</b> crystal structure of uricase from arthrobacter globiformis2 in complex with uric acid (substrate)
67	<a href="#">d1q98a</a>	Alignment	not modelled	11.5	6	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
68	<a href="#">d1afia</a>	Alignment	not modelled	11.1	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
69	<a href="#">d1o73a</a>	Alignment	not modelled	10.5	31	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
70	<a href="#">d2aw0a</a>	Alignment	not modelled	10.4	35	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
71	<a href="#">c2gvsA</a>	Alignment	not modelled	10.2	21	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemosensory protein csp-sg4; <b>PDBTitle:</b> nmr solution structure of cspsg4
72	<a href="#">d1kx9b</a>	Alignment	not modelled	9.9	17	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Chemosensory protein Csp2 <b>Family:</b> Chemosensory protein Csp2
73	<a href="#">c3me5A</a>	Alignment	not modelled	9.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosine-specific methyltransferase; <b>PDBTitle:</b> crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 301
74	<a href="#">c2kyzA</a>	Alignment	not modelled	9.7	30	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal binding protein; <b>PDBTitle:</b> nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
75	<a href="#">c2ga7A</a>	Alignment	not modelled	9.6	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
76	<a href="#">d2cx4a1</a>	Alignment	not modelled	9.4	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
77	<a href="#">d2ggpb1</a>	Alignment	not modelled	9.3	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
78	<a href="#">d1n8va</a>	Alignment	not modelled	9.2	17	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Chemosensory protein Csp2 <b>Family:</b> Chemosensory protein Csp2
79	<a href="#">d1osda</a>	Alignment	not modelled	9.1	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
80	<a href="#">d2a4va1</a>	Alignment	not modelled	9.1	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
						<b>PDB header:</b> oxidoreductase

81	<a href="#">c3dwvB</a>	Alignment	not modelled	9.0	12	<b>Chain:</b> B: <b>PDB Molecule:</b> glutathione peroxidase-like protein; <b>PDBTitle:</b> glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
82	<a href="#">d1dosa</a>	Alignment	not modelled	8.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
83	<a href="#">d1xzoa1</a>	Alignment	not modelled	8.6	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
84	<a href="#">d1gpla</a>	Alignment	not modelled	8.5	8	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
85	<a href="#">d1p6ta1</a>	Alignment	not modelled	8.3	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
86	<a href="#">d1rutx3</a>	Alignment	not modelled	8.2	43	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
87	<a href="#">c219wA</a>	Alignment	not modelled	7.8	12	<b>PDB header:</b> splicing, rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> u4/u6 snrna-associated-splicing factor prp24; <b>PDBTitle:</b> solution structure of the c-terminal domain of prp24
88	<a href="#">c2ywiA</a>	Alignment	not modelled	7.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
89	<a href="#">c2he3A</a>	Alignment	not modelled	7.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 2; <b>PDBTitle:</b> crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gpx2)
90	<a href="#">d1u9ya1</a>	Alignment	not modelled	7.6	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
91	<a href="#">d1yexa1</a>	Alignment	not modelled	7.6	8	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
92	<a href="#">c3kebB</a>	Alignment	not modelled	7.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> thiol peroxidase from chromobacterium violaceum
93	<a href="#">c3l9qB</a>	Alignment	not modelled	7.3	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna primase large subunit; <b>PDBTitle:</b> crystal structure of human polymerase alpha-primase p58 iron-sulfur2 cluster domain
94	<a href="#">c2gcfA</a>	Alignment	not modelled	7.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cation-transporting atpase pacs; <b>PDBTitle:</b> solution structure of the n-terminal domain of the copppe(r)i atpase2 pacs in its apo form
95	<a href="#">c3i24B</a>	Alignment	not modelled	7.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hit family hydrolase; <b>PDBTitle:</b> crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176
96	<a href="#">c3dxsX</a>	Alignment	not modelled	7.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> copper-transporting atpase ran1; <b>PDBTitle:</b> crystal structure of a copper binding domain from hma7, a p-2 type atpase
97	<a href="#">c3ha9A</a>	Alignment	not modelled	7.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized thioredoxin-like protein; <b>PDBTitle:</b> the 1.7a crystal structure of a thioredoxin-like protein from2 aeropyrum pernix
98	<a href="#">d1xvwa1</a>	Alignment	not modelled	7.0	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
99	<a href="#">c3eurA</a>	Alignment	not modelled	6.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of uncharacterized protein2 from bacteroides fragilis nctc 9343