
























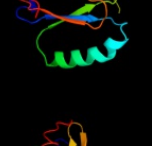
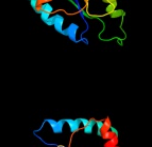



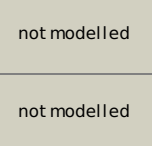



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2hyxA</a>	 Alignment		99.7	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein dipz; <b>PDBTitle:</b> structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
2	<a href="#">dlz5ye1</a>	 Alignment		99.6	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
3	<a href="#">c2l57A</a>	 Alignment		99.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of an uncharacterized thioredoxin-like protein from2 clostridium perfringens
4	<a href="#">dlzmaa1</a>	 Alignment		99.6	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
5	<a href="#">dlj08a2</a>	 Alignment		99.6	11	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
6	<a href="#">c2pptA</a>	 Alignment		99.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-2; <b>PDBTitle:</b> crystal structure of thioredoxin-2
7	<a href="#">dlknga</a>	 Alignment		99.5	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
8	<a href="#">d2b5xa1</a>	 Alignment		99.5	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
9	<a href="#">d1a8la2</a>	 Alignment		99.5	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
10	<a href="#">c3f9uA</a>	 Alignment		99.5	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported cytochrome c biogenesis-related protein; <b>PDBTitle:</b> crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
11	<a href="#">d2fy6a1</a>	 Alignment		99.5	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like

12	<a href="#">dli5ga_</a>	Alignment		99.5	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
13	<a href="#">c3p2aB_</a>	Alignment		99.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thioredoxin-like protein; <b>PDBTitle:</b> crystal structure of thioredoxin 2 from yersinia pestis
14	<a href="#">c3p2aA_</a>	Alignment		99.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin-like protein; <b>PDBTitle:</b> crystal structure of thioredoxin 2 from yersinia pestis
15	<a href="#">d1o8xa_</a>	Alignment		99.5	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
16	<a href="#">c2I5IA_</a>	Alignment		99.5	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution structure of thioredoxin from bacteroides vulgatus
17	<a href="#">c2I6dA_</a>	Alignment		99.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
18	<a href="#">c3hypB_</a>	Alignment		99.5	19	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of bacteroides fragilis trxp_s105g mutant
19	<a href="#">c3emxB_</a>	Alignment		99.5	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from aeropyrum pernix
20	<a href="#">d1o73a_</a>	Alignment		99.5	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
21	<a href="#">c3qdnA_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin protein; <b>PDBTitle:</b> putative thioredoxin protein from salmonella typhimurium
22	<a href="#">d2fwha1</a>	Alignment	not modelled	99.5	11	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
23	<a href="#">c3ul3A_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
24	<a href="#">c1xbsA_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> transcription, cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dim1-like protein; <b>PDBTitle:</b> crystal structure of human dim2: a dim1-like protein
25	<a href="#">c3kh7A_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
26	<a href="#">c3erwG_</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> sporulation thiol-disulfide oxidoreductase a; <b>PDBTitle:</b> crystal structure of stoa from bacillus subtilis
27	<a href="#">c3lorB_</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol-disulfide isomerase and thioredoxins; <b>PDBTitle:</b> the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
28	<a href="#">c2b1kA_</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of e. coli ccmg protein

29	<a href="#">dlzooa1</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
30	<a href="#">c2vocA</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> thioredoxin a active site mutants form mixed disulfide2 dimers that resemble enzyme-substrate reaction3 intermediate
31	<a href="#">d1hyua4</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
32	<a href="#">c2i1uA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> mycobacterium tuberculosis thioredoxin c
33	<a href="#">d1dbya</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
34	<a href="#">c3dxbE</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> splicing, transcription <b>Chain:</b> E: <b>PDB Molecule:</b> thioredoxin n-terminally fused to puf60(uhm); <b>PDBTitle:</b> structure of the uhm domain of puf60 fused to thioredoxin
35	<a href="#">c3hz4A</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from methanosarcina mazei
36	<a href="#">d1qgva</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> spliceosomal protein U5-15Kd
37	<a href="#">d1thxa</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
38	<a href="#">c3eytA</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein spoa0173; <b>PDBTitle:</b> crystal structure of thioredoxin-like superfamily protein spoa0173
39	<a href="#">c2ju5A</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin disulfide isomerase; <b>PDBTitle:</b> dsbh oxidoreductase
40	<a href="#">c3d22A</a>	Alignment		99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin h-type; <b>PDBTitle:</b> crystal structure of a poplar thioredoxin h mutant,2 ptrxh4c61s
41	<a href="#">c1w89E</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> electron transport <b>Chain:</b> E: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structure of the reduced form of human thioredoxin 2
42	<a href="#">c1v98A</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure analysis of thioredoxin from thermus thermophilus
43	<a href="#">c2i4aA</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from the acidophile2 acetobacter aceti
44	<a href="#">c3gnjD</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin domain protein; <b>PDBTitle:</b> the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
45	<a href="#">c3ia1A</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thio-disulfide isomerase/thioredoxin; <b>PDBTitle:</b> crystal structure of thio-disulfide isomerase from thermus2 thermophilus
46	<a href="#">c2diyA</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-like protein 2; <b>PDBTitle:</b> the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2
47	<a href="#">c2xbqB</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
48	<a href="#">c2f51B</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structure of trichomonas vaginalis thioredoxin
49	<a href="#">c2kucA</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative disulphide-isomerase; <b>PDBTitle:</b> solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
50	<a href="#">d1ep7a</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
51	<a href="#">d1xwaa</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
52	<a href="#">c3lwaA</a>	Alignment	not modelled	99.4	9	<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
53	<a href="#">d1m7ta</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
54	<a href="#">c2vimA</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin;

					<b>PDBTitle:</b> x-ray structure of fasciola hepatica thioredoxin
55	<a href="#">c2o7kA</a>	Alignment	not modelled	99.4	17 <b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> s. aureus thioredoxin
56	<a href="#">c3hcZA</a>	Alignment	not modelled	99.4	15 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible thiol-disulfide isomerase; <b>PDBTitle:</b> the crystal structure of a domain of possible thiol-disulfide2 isomerase from cytophaga hutchinsonii atcc 33406.
57	<a href="#">c2e0qA</a>	Alignment	not modelled	99.4	16 <b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of k53e thioredoxin from sulfobolus2 tokodaii strain7
58	<a href="#">d1lu4a</a>	Alignment	not modelled	99.4	15 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
59	<a href="#">c1t00A</a>	Alignment	not modelled	99.4	15 <b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> the structure of thioredoxin from s. coelicolor
60	<a href="#">d1gh2a</a>	Alignment	not modelled	99.4	11 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
61	<a href="#">c2vlvA</a>	Alignment	not modelled	99.4	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin h isoform 2.; <b>PDBTitle:</b> crystal structure of barley thioredoxin h isoform 2 in2 partially radiation-reduced state
62	<a href="#">c2fgxA</a>	Alignment	not modelled	99.4	11 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
63	<a href="#">c2qsiB</a>	Alignment	not modelled	99.4	14 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydrogenase expression/formation protein hupg; <b>PDBTitle:</b> crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
64	<a href="#">d1syra</a>	Alignment	not modelled	99.4	21 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
65	<a href="#">c3gl3D</a>	Alignment	not modelled	99.4	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative thiol:disulfide interchange protein <b>PDBTitle:</b> crystal structure of a putative thiol:disulfide interchange2 protein dsbe from chlorobium tepidum
66	<a href="#">d1fb6a</a>	Alignment	not modelled	99.4	14 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
67	<a href="#">c2wz9A</a>	Alignment	not modelled	99.4	14 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-3; <b>PDBTitle:</b> crystal structure of the thioredoxin domain of human txnl2
68	<a href="#">d1f9ma</a>	Alignment	not modelled	99.3	12 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
69	<a href="#">c1x5dA</a>	Alignment	not modelled	99.3	22 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide-isomerase a6; <b>PDBTitle:</b> the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase a6
70	<a href="#">c3razA</a>	Alignment	not modelled	99.3	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-related protein; <b>PDBTitle:</b> the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
71	<a href="#">d1j08a1</a>	Alignment	not modelled	99.3	15 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
72	<a href="#">d1nw2a</a>	Alignment	not modelled	99.3	16 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
73	<a href="#">c3or5A</a>	Alignment	not modelled	99.3	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein, thioredoxin family <b>PDBTitle:</b> crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from chlorobium tepidum t1s
74	<a href="#">d1xfla</a>	Alignment	not modelled	99.3	13 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
75	<a href="#">d1a8la1</a>	Alignment	not modelled	99.3	16 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
76	<a href="#">c3tcoA</a>	Alignment	not modelled	99.3	12 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin (trxa-1); <b>PDBTitle:</b> crystallographic and spectroscopic characterization of sulfobolus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
77	<a href="#">d1ti3a</a>	Alignment	not modelled	99.3	16 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
78	<a href="#">c2yzuA</a>	Alignment	not modelled	99.3	14 <b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
79	<a href="#">d2ifqa1</a>	Alignment	not modelled	99.3	16 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase

80	<a href="#">c2vm2C_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin h isoform 1.; <b>PDBTitle:</b> crystal structure of barley thioredoxin h isoform 12 crystallized using peg as precipitant
81	<a href="#">c3ed3A_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide-isomerase mpd1; <b>PDBTitle:</b> crystal structure of the yeast dithiol/disulfide2 oxidoreductase mpd1p
82	<a href="#">c1zypB_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf
83	<a href="#">c3ewlA_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein bf1870; <b>PDBTitle:</b> crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
84	<a href="#">c2r2jA_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin domain-containing protein 4; <b>PDBTitle:</b> crystal structure of human erp44
85	<a href="#">d1st9a_</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
86	<a href="#">c2dmlA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide-isomerase a6; <b>PDBTitle:</b> the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a6
87	<a href="#">d1r26a_</a>	Alignment	not modelled	99.3	11	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
88	<a href="#">c2ywiA_</a>	Alignment	not modelled	99.3	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="#">c3ha9A_</a>	Alignment	not modelled	99.3	18	<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
90	<a href="#">d2trxa_</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
91	<a href="#">d2cvba1</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
92	<a href="#">c2l5oA_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> solution structure of a putative thioredoxin from neisseria2 meningitidis
93	<a href="#">c3dmlA_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
94	<a href="#">c2albA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide-isomerase a3; <b>PDBTitle:</b> nmr structure of the n-terminal domain a of the2 glycoprotein chaperone erp57
95	<a href="#">c2oe0B_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin-3; <b>PDBTitle:</b> crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
96	<a href="#">d1v9wa_</a>	Alignment	not modelled	99.3	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Txn15-like
97	<a href="#">c3fk8A_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> disulphide isomerase; <b>PDBTitle:</b> the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
98	<a href="#">d2f8aa1</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
99	<a href="#">c2j23A_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> immune protein <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> cross-reactivity and crystal structure of malassezia2 sympodialis thioredoxin (mala s 13), a member of a new pan-3 allergen family
100	<a href="#">c3fkfC_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol-disulfide oxidoreductase; <b>PDBTitle:</b> thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
101	<a href="#">c3cmiA_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxiredoxin hyr1; <b>PDBTitle:</b> crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
102	<a href="#">d1jfua_</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
103	<a href="#">c3apsA_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily c member 10; <b>PDBTitle:</b> crystal structure of trx4 domain of erdj5
104	<a href="#">c3cynC_</a>	Alignment	not modelled	99.2	9	<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
105	<a href="#">c2dizA_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin domain-containing protein 5; <b>PDBTitle:</b> the solution structure of the third thioredoxin domain of2 human thioredoxin domain-containing protein 5

106	<a href="#">d1woua_</a>	Alignment	not modelled	99.2	11	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Txnl5-like
107	<a href="#">c1j08A_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-like protein; <b>PDBTitle:</b> crystal structure of glutaredoxin-like protein from2 pyrococcus horikoshii
108	<a href="#">d1fo5a_</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
109	<a href="#">d2b5ea4</a>	Alignment	not modelled	99.2	11	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
110	<a href="#">c3fw2A_</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol-disulfide oxidoreductase; <b>PDBTitle:</b> c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
111	<a href="#">d1gp1a_</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
112	<a href="#">d1uula_</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
113	<a href="#">c2dj0A_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-related transmembrane protein 2; <b>PDBTitle:</b> the solution structure of the thioredoxin domain of human2 thioredoxin-related transmembrane protein 2
114	<a href="#">c3kcmC_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> the crystal structure of thioredoxin protein from geobacter2 metallireducens
115	<a href="#">c3cxgA_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> crystal structure of plasmodium falciparum thioredoxin, pfi0790w
116	<a href="#">c3f8uA_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> immune system/isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide-isomerase a3erp57; <b>PDBTitle:</b> tapasin/erp57 heterodimer
117	<a href="#">d1nhoa_</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
118	<a href="#">c2he3A_</a>	Alignment	not modelled	99.1	8	<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 glutathione peroxidase 2 (gpx2)
119	<a href="#">c2p5qA_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 5; <b>PDBTitle:</b> crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
120	<a href="#">c3dwvB_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione peroxidase-like protein; <b>PDBTitle:</b> glutathione peroxidase-type trypanothione peroxidase,2 oxidized form