Phyre2

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Description	P0AEG4
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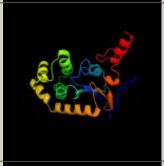
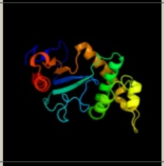
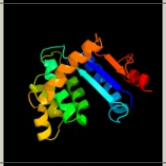
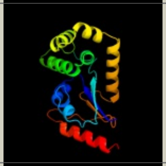
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fvka_	Alignment		100.0	100	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
2	c3l9vE_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
3	c3h93A_	Alignment		100.0	31	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of pseudomonas aeruginosa dsba
4	d1beda_	Alignment		100.0	41	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
5	c3dvwA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of reduced dsba1 from neisseria2 meningitidis
6	c3hd5A_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
7	c2remB_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**disulfide oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase dsba from xylella2 fastidiosa
8	c3feuA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
9	c3c7mB_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thiol:disulfide interchange protein dsba-like; **PDBTitle:** crystal structure of reduced dsbl
10	c2znmA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** oxidoreductase nmdsba3 from neisseria meningitidis
11	c3f4tA_	Alignment		100.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a

12	c3ghaA_	Alignment		99.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond formation protein d; **PDBTitle:** crystal structure of etda-treated bdbd (reduced)
13	c3bciA_	Alignment		99.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond protein a; **PDBTitle:** crystal structure of staphylococcus aureus dsba
14	c3gykC_	Alignment		99.9	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**27kda outer membrane protein; **PDBTitle:** the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3
15	c3gmfA_	Alignment		99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein-disulfide isomerase; **PDBTitle:** crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
16	c3kzqE_	Alignment		99.9	10	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**putative uncharacterized protein vp2116; **PDBTitle:** the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
17	c3gn3B_	Alignment		99.9	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative protein-disulfide isomerase; **PDBTitle:** crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.
18	c2in3A_	Alignment		99.9	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
19	d1z6ma1	Alignment		99.9	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
20	c3gl5A_	Alignment		99.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dsba oxidoreductase sco1869; **PDBTitle:** crystal structure of probable dsba oxidoreductase sco1869 from2 streptomyces coelicolor
21	d1un2a_	Alignment	not modelled	99.8	97	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
22	c2imeA_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-hydroxychromene-2-carboxylate isomerase; **PDBTitle:** 2-hydroxychromene-2-carboxylate isomerase: a kappa class glutathione-2 s-transferase from pseudomonas putida
23	c3fz5C_	Alignment	not modelled	99.8	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**possible 2-hydroxychromene-2-carboxylate isomerase; **PDBTitle:** crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
24	d1r4wa_	Alignment	not modelled	99.7	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
25	d1v58a1	Alignment	not modelled	99.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
26	d1eeja1	Alignment	not modelled	99.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
27	c1yzxB_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase kappa 1; **PDBTitle:** crystal structure of human kappa class glutathione2 transferase
28	d1t3ba1	Alignment	not modelled	99.7	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like

29	c3gv1A_	Alignment	not modelled	99.6	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
30	c1v57A_	Alignment	not modelled	99.6	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbg; **PDBTitle:** crystal structure of the disulfide bond isomerase dsbg
31	c1jzdA_	Alignment	not modelled	99.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
32	c1t3bA_	Alignment	not modelled	99.6	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
33	c2l57A_	Alignment	not modelled	98.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
34	d1j08a2	Alignment	not modelled	98.3	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
35	c1v98A_	Alignment	not modelled	98.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
36	c3emxB_	Alignment	not modelled	98.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
37	c3p2aB_	Alignment	not modelled	98.2	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
38	c2l5lA_	Alignment	not modelled	98.2	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus
39	c2pptA_	Alignment	not modelled	98.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
40	d1v9wa_	Alignment	not modelled	98.1	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
41	c3hypB_	Alignment	not modelled	98.1	29	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
42	c1zypB_	Alignment	not modelled	98.1	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf
43	c2ju5A_	Alignment	not modelled	98.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
44	d1a8la2	Alignment	not modelled	98.1	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
45	c2l6dA_	Alignment	not modelled	98.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
46	c3p2aA_	Alignment	not modelled	98.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
47	c3dxbE_	Alignment	not modelled	98.0	25	**PDB header:**splicing, transcription **Chain:** E: **PDB Molecule:**thioredoxin n-terminally fused to puf60(uhm); **PDBTitle:** structure of the uhm domain of puf60 fused to thioredoxin
48	d1dbya_	Alignment	not modelled	98.0	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
49	d1zmaa1	Alignment	not modelled	98.0	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
50	c3gnjD_	Alignment	not modelled	98.0	25	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**thioredoxin domain protein; **PDBTitle:** the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
51	c3ul3A_	Alignment	not modelled	98.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
52	d2fwha1	Alignment	not modelled	98.0	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
53	d1nhoa_	Alignment	not modelled	97.9	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
54	d1thxa_	Alignment	not modelled	97.9	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
55	c1t00A_	Alignment	not modelled	97.9	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor

56	c2hyxA_	Alignment	not modelled	97.9	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
57	c2r2jA_	Alignment	not modelled	97.9	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 4; **PDBTitle:** crystal structure of human erp44
58	c2hlsB_	Alignment	not modelled	97.9	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
59	c2i4aA_	Alignment	not modelled	97.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from the acidophile2 acetobacter aceti
60	d1hyua4	Alignment	not modelled	97.9	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
61	d1woua_	Alignment	not modelled	97.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
62	d1ep7a_	Alignment	not modelled	97.8	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
63	c1xbsA_	Alignment	not modelled	97.8	27	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
64	c3tcoA_	Alignment	not modelled	97.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin (trxa-1); **PDBTitle:** crystallographic and spectroscopic characterization of sulfolobus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
65	c2i1uA_	Alignment	not modelled	97.8	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** mycobacterium tuberculosis thioredoxin c
66	d1gh2a_	Alignment	not modelled	97.8	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
67	c2dj1A_	Alignment	not modelled	97.8	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a4
68	d1xwaa_	Alignment	not modelled	97.8	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
69	d1f9ma_	Alignment	not modelled	97.8	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
70	c3hz4A_	Alignment	not modelled	97.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
71	c2kucA_	Alignment	not modelled	97.7	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
72	c2e0qA_	Alignment	not modelled	97.7	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
73	c2vocA_	Alignment	not modelled	97.7	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** thioredoxin a active site mutants form mixed disulfide2 dimers that resemble enzyme-substrate reaction3 intermediate
74	c1w89E_	Alignment	not modelled	97.7	30	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
75	d1ti3a_	Alignment	not modelled	97.7	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
76	d1r26a_	Alignment	not modelled	97.7	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
77	c2yzuA_	Alignment	not modelled	97.7	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
78	c3dmlA_	Alignment	not modelled	97.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
79	c2diyA_	Alignment	not modelled	97.6	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**thioredoxin-like protein 2; **PDBTitle:** the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2
80	c1x5dA_	Alignment	not modelled	97.6	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase a6
81	c2o7kA_	Alignment	not modelled	97.6	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** s. aureus thioredoxin
						Fold: Thioredoxin fold

82	d1qgva_	Alignment	not modelled	97.6	20	**Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
83	c2aytB_	Alignment	not modelled	97.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aquifex aeolicus
84	d1j08a1	Alignment	not modelled	97.6	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
85	c3qdnA_	Alignment	not modelled	97.6	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
86	d1syra_	Alignment	not modelled	97.6	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
87	d1a8la1	Alignment	not modelled	97.5	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
88	d1fo5a_	Alignment	not modelled	97.5	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
89	c3d22A_	Alignment	not modelled	97.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
90	d2trxa_	Alignment	not modelled	97.5	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
91	c2wz9A_	Alignment	not modelled	97.5	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
92	d1nw2a_	Alignment	not modelled	97.5	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
93	c2dizA_	Alignment	not modelled	97.5	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 5; **PDBTitle:** the solution structure of the third thioredoxin domain of2 human thioredoxin domain-containing protein 5
94	c2dj2A_	Alignment	not modelled	97.4	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the second thioredoxin domain of2 mouse protein disulfide-isomerase a4
95	d1m7ta_	Alignment	not modelled	97.4	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
96	c2xbqB_	Alignment	not modelled	97.4	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
97	c3apsA_	Alignment	not modelled	97.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of trx4 domain of erdj5
98	d2b5xa1	Alignment	not modelled	97.4	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
99	c2vlvA_	Alignment	not modelled	97.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h isoform 2.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 2 in2 partially radiation-reduced state
100	d1xfla_	Alignment	not modelled	97.4	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
101	d1i5ga_	Alignment	not modelled	97.3	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
102	c2f51B_	Alignment	not modelled	97.3	23	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of trichomonas vaginalis thioredoxin
103	c3f9uA_	Alignment	not modelled	97.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported cytochrome c biogenesis-related protein; **PDBTitle:** crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
104	c3cxgA_	Alignment	not modelled	97.3	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** crystal structure of plasmodium falciparum thioredoxin, pfi0790w
105	c3f8uA_	Alignment	not modelled	97.3	19	**PDB header:**immune system/isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3erp57; **PDBTitle:** tapasin/erp57 heterodimer
106	c2vimA_	Alignment	not modelled	97.3	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
107	c2oe0B_	Alignment	not modelled	97.2	22	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin-3; **PDBTitle:** crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
108	c2vm2C_	Alignment	not modelled	97.2	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin h isoform 1.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 12

						crystallized using peg as precipitant
109	d2cvba1	Alignment	not modelled	97.2	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
110	c2j23A_	Alignment	not modelled	97.2	26	**PDB header:**immune protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** cross-reactivity and crystal structure of malassezia2 sympodialis thioredoxin (mala s 13), a member of a new pan-3 allergen family
111	d1o73a_	Alignment	not modelled	97.2	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
112	c1j08A_	Alignment	not modelled	97.2	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** crystal structure of glutaredoxin-like protein from2 pyrococcus horikoshii
113	c3kh7A_	Alignment	not modelled	97.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
114	c2ywiA_	Alignment	not modelled	97.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
115	d1knga_	Alignment	not modelled	97.2	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
116	d1z5ye1	Alignment	not modelled	97.1	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
117	d1fb6a_	Alignment	not modelled	97.1	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
118	c2b1kA_	Alignment	not modelled	97.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
119	c2qsiB_	Alignment	not modelled	97.1	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
120	c2fgxA_	Alignment	not modelled	97.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.