Phyre²

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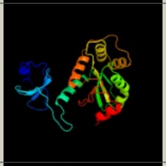
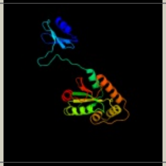
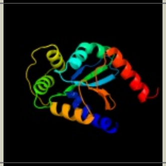
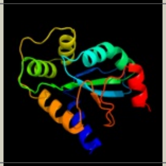
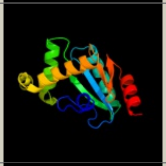
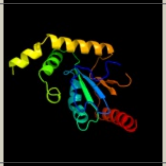
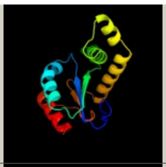
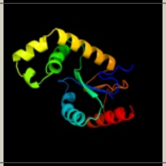
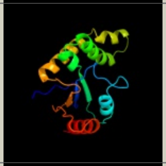
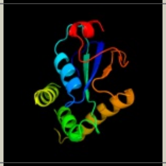
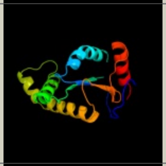
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1jzdA_	Alignment		100.0	99	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
2	c1t3bA_	Alignment		100.0	45	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
3	c1v57A_	Alignment		100.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbg; **PDBTitle:** crystal structure of the disulfide bond isomerase dsbg
4	d1eeja1	Alignment		100.0	100	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
5	d1t3ba1	Alignment		100.0	49	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
6	c3gv1A_	Alignment		100.0	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
7	d1v58a1	Alignment		100.0	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
8	c3gykC_	Alignment		99.9	22	**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
9	d1z6ma1	Alignment		99.9	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
10	c3f4tA_	Alignment		99.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a
11	c3ghaA_	Alignment		99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond formation protein d; **PDBTitle:** crystal structure of etda-treated bdbd (reduced)

12	c2remB_	Alignment		99.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**disulfide oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase dsba from xylella2 fastidiosa
13	c3h93A_	Alignment		99.9	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of pseudomonas aeruginosa dsba
14	c3hd5A_	Alignment		99.9	14	**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
15	c3dvwA_	Alignment		99.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of reduced dsba1 from neisseria2 meningitidis
16	c2znmA_	Alignment		99.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** oxidoreductase nmdsba3 from neisseria meningitidis
17	c3gn3B_	Alignment		99.8	21	**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	c3gmfA_	Alignment		99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein-disulfide isomerase; **PDBTitle:** crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
19	d1beda_	Alignment		99.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
20	c3feuA_	Alignment		99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
21	c3bciA_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond protein a; **PDBTitle:** crystal structure of staphylococcus aureus dsba
22	c3l9vE_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
23	c3c7mB_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thiol:disulfide interchange protein dsba-like; **PDBTitle:** crystal structure of reduced dsbl
24	d1fvka_	Alignment	not modelled	99.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
25	c3kzqE_	Alignment	not modelled	99.6	19	**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
26	c2in3A_	Alignment	not modelled	99.6	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
27	c3gl5A_	Alignment	not modelled	99.6	24	**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
28	c3fz5C_	Alignment	not modelled	99.6	20	**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
29	c2imeA_	Alignment	not modelled	99.5	14	**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
30	c2iyjA_	Alignment	not modelled	99.4	100	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol disulfide interchange protein dsbc; **PDBTitle:** crystal structure of the n-terminal dimer domain of e.coli2 dsbc
31	d1eeja2	Alignment	not modelled	99.3	100	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
32	d1t3ba2	Alignment	not modelled	99.3	37	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
33	d1r4wa_	Alignment	not modelled	99.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
34	c1yzxB_	Alignment	not modelled	99.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase kappa 1; **PDBTitle:** crystal structure of human kappa class glutathione2 transferase
35	d1hyua4	Alignment	not modelled	98.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
36	c2l57A_	Alignment	not modelled	98.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
37	d1zmaa1	Alignment	not modelled	98.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
38	d1j08a2	Alignment	not modelled	98.8	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
39	c1zypB_	Alignment	not modelled	98.8	16	**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
40	c2l6dA_	Alignment	not modelled	98.7	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
41	d1a8la2	Alignment	not modelled	98.7	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
42	d2fwha1	Alignment	not modelled	98.6	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
43	c3gnjD_	Alignment	not modelled	98.6	15	**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
44	c2i4aA_	Alignment	not modelled	98.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from the acidophile2 acetobacter aceti
45	c3emxB_	Alignment	not modelled	98.6	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
46	d1a8la1	Alignment	not modelled	98.6	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
47	c2l5lA_	Alignment	not modelled	98.6	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus
48	d1nhoa_	Alignment	not modelled	98.6	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
49	c3hz4A_	Alignment	not modelled	98.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
50	c2e0qA_	Alignment	not modelled	98.5	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
51	c3p2aB_	Alignment	not modelled	98.5	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
52	c1v98A_	Alignment	not modelled	98.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
53	c2hyxA_	Alignment	not modelled	98.5	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
54	c1t00A_	Alignment	not modelled	98.5	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
						Fold: Thioredoxin fold

55	d1dbya_	Alignment	not modelled	98.5	13	**Superfamily:**Thioredoxin-like **Family:**Thioltransferase
56	c3ul3A_	Alignment	not modelled	98.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
57	d1un2a_	Alignment	not modelled	98.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
58	c2pptA_	Alignment	not modelled	98.5	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
59	c3p2aA_	Alignment	not modelled	98.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
60	d1j08a1	Alignment	not modelled	98.5	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
61	d1z5ye1	Alignment	not modelled	98.5	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
62	d1zzoa1	Alignment	not modelled	98.4	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
63	c3dxbE_	Alignment	not modelled	98.4	19	**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
64	d1thxa_	Alignment	not modelled	98.4	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
65	d1r26a_	Alignment	not modelled	98.4	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
66	c3dmlA_	Alignment	not modelled	98.4	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
67	c1w89E_	Alignment	not modelled	98.4	33	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
68	c2aytB_	Alignment	not modelled	98.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aquifex aeolicus
69	c2vlvA_	Alignment	not modelled	98.3	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
70	d1syra_	Alignment	not modelled	98.3	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
71	d2b5xa1	Alignment	not modelled	98.3	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
72	c2vocA_	Alignment	not modelled	98.3	19	**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
73	c3hypB_	Alignment	not modelled	98.3	21	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
74	d1fo5a_	Alignment	not modelled	98.3	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
75	d1ti3a_	Alignment	not modelled	98.3	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
76	d1gh2a_	Alignment	not modelled	98.3	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
77	c2diyA_	Alignment	not modelled	98.3	23	**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
78	c2yzuA_	Alignment	not modelled	98.3	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
79	d2trxa_	Alignment	not modelled	98.3	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
80	c3ic4A_	Alignment	not modelled	98.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
81	d1f9ma_	Alignment	not modelled	98.3	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase

82	c2fgxA_	Alignment	not modelled	98.2	18	**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.
83	c2hlsB_	Alignment	not modelled	98.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
84	c2vimA_	Alignment	not modelled	98.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
85	c3tcoA_	Alignment	not modelled	98.2	22	**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
86	c3kh7A_	Alignment	not modelled	98.2	22	**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
87	c3d22A_	Alignment	not modelled	98.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
88	d1m7ta_	Alignment	not modelled	98.2	34	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
89	c2ju5A_	Alignment	not modelled	98.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
90	c2o7kA_	Alignment	not modelled	98.2	29	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** s. aureus thioredoxin
91	c1x5dA_	Alignment	not modelled	98.2	16	**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
92	d1fb6a_	Alignment	not modelled	98.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
93	d1xfla_	Alignment	not modelled	98.2	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
94	c2i1uA_	Alignment	not modelled	98.2	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** mycobacterium tuberculosis thioredoxin c
95	d1ep7a_	Alignment	not modelled	98.2	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
96	c3erwG_	Alignment	not modelled	98.2	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**sporulation thiol-disulfide oxidoreductase a; **PDBTitle:** crystal structure of stoa from bacillus subtilis
97	d1nw2a_	Alignment	not modelled	98.2	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
98	d2fy6a1	Alignment	not modelled	98.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
99	d1xwaa_	Alignment	not modelled	98.1	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
100	c2dizA_	Alignment	not modelled	98.1	19	**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
101	c2r2jA_	Alignment	not modelled	98.1	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 4; **PDBTitle:** crystal structure of human erp44
102	c1xbsA_	Alignment	not modelled	98.1	18	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
103	c3nznA_	Alignment	not modelled	98.1	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
104	c3lorB_	Alignment	not modelled	98.1	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**thiol-disulfide isomerase and thioredoxins; **PDBTitle:** the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
105	d1r7ha_	Alignment	not modelled	98.1	32	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
106	c2kucA_	Alignment	not modelled	98.1	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
107	c2b1kA_	Alignment	not modelled	98.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
						PDB header:protein binding

108	c2wz9A_	Alignment	not modelled	98.1	17	**Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
109	c2klxA_	Alignment	not modelled	98.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
110	d1st9a_	Alignment	not modelled	98.1	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
111	d1knga_	Alignment	not modelled	98.1	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
112	c3qdnA_	Alignment	not modelled	98.1	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
113	c3razA_	Alignment	not modelled	98.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-related protein; **PDBTitle:** the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
114	c2oe0B_	Alignment	not modelled	98.0	25	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin-3; **PDBTitle:** crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
115	c2vm2C_	Alignment	not modelled	98.0	27	**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
116	c2ht9A_	Alignment	not modelled	98.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
117	c2albA_	Alignment	not modelled	98.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3; **PDBTitle:** nmr structure of the n-terminal domain a of the2 glycoprotein chaperone erp57
118	c3or5A_	Alignment	not modelled	98.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein, thioredoxin family **PDBTitle:** crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from chlorobium tepidum tls
119	d1egoa_	Alignment	not modelled	98.0	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
120	c3f9uA_	Alignment	not modelled	98.0	18	**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