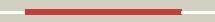
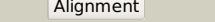
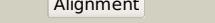
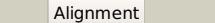
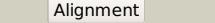


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD2969c_(-)_3323719_3324486
Date	Thu Aug 8 16:20:13 BST 2019
Unique Job ID	45d09606c5a6a194

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4jr6A</a>			100.0	98	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> possible conserved membrane or secreted protein; <b>PDBTitle:</b> crystal structure of dsba from mycobacterium tuberculosis (reduced)
2	<a href="#">c4pwoA</a>			100.0	21	<b>PDB header:</b> structural genomics <b>Chain:</b> A; <b>PDB Molecule:</b> dsba; <b>PDBTitle:</b> crystal structure of dsba from the gram positive bacterium2 corynebacterium diphtheriae
3	<a href="#">c6bo0A</a>			100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> mdba protein; <b>PDBTitle:</b> mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 matruchotii
4	<a href="#">c5c00B</a>			100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> mdba protein; <b>PDBTitle:</b> mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 diphtheriae
5	<a href="#">c4z7xA</a>			100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> mdba; <b>PDBTitle:</b> mdba protein, a thiol-disulfide oxidoreductase from actinomyces oris.
6	<a href="#">c5kbcA</a>			100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dsba; <b>PDBTitle:</b> crystal structure of chlamydia trachomatis dsba
7	<a href="#">c3f4tA</a>			100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of wolbachia pipiensis alpha-dsba1 c97a/c146a
8	<a href="#">c4xvwK</a>			100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> K; <b>PDB Molecule:</b> dsba-like protein; <b>PDBTitle:</b> crystal structure of proteus mirabilis scsc in a compact conformation
9	<a href="#">c3ghaA</a>			100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> disulfide bond formation protein d; <b>PDBTitle:</b> crystal structure of etda-treated bdbd (reduced)
10	<a href="#">d1z6ma1</a>			100.0	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
11	<a href="#">c3dvwA</a>			100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of reduced dsba1 from neisseria meningitidis

12	<a href="#">c2remB</a>			100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase dsba from xylella fastidiosa	
13	<a href="#">c3bciA</a>			100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide bond protein a; <b>PDBTitle:</b> crystal structure of staphylococcus aureus dsba	
14	<a href="#">c3gmfA</a>			100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-disulfide isomerase; <b>PDBTitle:</b> crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans	
15	<a href="#">c4gxzB</a>			100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> suppression of copper sensitivity protein; <b>PDBTitle:</b> crystal structure of a periplasmic thioredoxin-like protein from2 salmonella enterica serovar typhimurium	
16	<a href="#">c6eezC</a>			99.9	21	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> dsba-like disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of the thiol-disulfide exchange protein alpha-dsba22 from wolbachia pipiensis	
17	<a href="#">c3gykC</a>			99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 27kda outer membrane protein; <b>PDBTitle:</b> the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3	
18	<a href="#">c3h93A</a>			99.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa dsba	
19	<a href="#">c4k2dA</a>			99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> crystal structure of burkholderia pseudomallei dsba	
20	<a href="#">c3gn3B</a>			99.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative protein-disulfide isomerase; <b>PDBTitle:</b> crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.	
21	<a href="#">c4p3yB</a>		Alignment	not modelled	99.9	21	<b>PDB header:</b> translation/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> crystal structure of acinetobacter baumannii dsba in complex with ef-2 tu
22	<a href="#">c4jrrC</a>		Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of disulfide bond oxidoreductase dsba1 from2 legionella pneumophila
23	<a href="#">c3hd5A</a>		Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
24	<a href="#">c4od7A</a>		Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> complex structure of proteus mirabilis dsba (c30s) with a non-2 covalently bound peptide pwatcds
25	<a href="#">c3c7mB</a>		Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba-like; <b>PDBTitle:</b> crystal structure of reduced dsbl
26	<a href="#">d1beda</a>		Alignment	not modelled	99.9	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
27	<a href="#">c4n30A</a>		Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide isomerase; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa dsba2
28	<a href="#">c6dxnC</a>		Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> 1.95 angstrom resolution crystal structure of dsba disulfide2 interchange protein from klebsiella pneumoniae. <b>PDB header:</b> oxidoreductase

29	<a href="#">c3l9vE</a>	Alignment	not modelled	99.9	17	<b>Chain:</b> E: <b>PDB Molecule:</b> putative thiol-disulfide isomerase or thioredoxin; <b>PDBTitle:</b> crystal structure of salmonella enterica serovar typhimurium srga
30	<a href="#">c2znmA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> oxidoreductase nmdsba3 from neisseria meningitidis
31	<a href="#">c6ghbB</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> upf0413 protein gk0824; <b>PDBTitle:</b> crystal structure of spx in complex with yjbh (oxidized)
32	<a href="#">d1fvka</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
33	<a href="#">c3feuA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
34	<a href="#">d1v58a1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
35	<a href="#">c5cohA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> frne protein; <b>PDBTitle:</b> crystal structure of a novel disulfide oxidoreductase from deinococcus2 radiodurans crystallized in presence of beta-mercaptoethanol
36	<a href="#">c1v57A</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbg; <b>PDBTitle:</b> crystal structure of the disulfide bond isomerase dsbg
37	<a href="#">c4nxIB</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> rv2466c mediates the activation of tp053 to kill replicating and non-2 replicating mycobacterium tuberculosis
38	<a href="#">c3fz5C</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> possible 2-hydroxychromene-2-carboxylate isomerase; <b>PDBTitle:</b> crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
39	<a href="#">d1t3ba1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
40	<a href="#">c3kzqE</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> putative uncharacterized protein vp2116; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimb 2210633
41	<a href="#">d1eeja1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
42	<a href="#">c3gl5A</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative dsba oxidoreductase sco1869; <b>PDBTitle:</b> crystal structure of probable dsba oxidoreductase sco1869 from2 streptomyces coelicolor
43	<a href="#">c1t3bA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbc; <b>PDBTitle:</b> x-ray structure of dsbc from haemophilus influenzae
44	<a href="#">c1jzdA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbc; <b>PDBTitle:</b> dsbc-dsbdalpha complex
45	<a href="#">c2in3A</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
46	<a href="#">c4npbA</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide isomerase ii; <b>PDBTitle:</b> the crystal structure of thiol:disulfide interchange protein dsbc from2 yersinia pestis co92
47	<a href="#">c3gv1A</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide interchange protein; <b>PDBTitle:</b> crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
48	<a href="#">c2imeA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxychromene-2-carboxylate isomerase; <b>PDBTitle:</b> 2-hydroxychromene-2-carboxylate isomerase: a kappa class glutathione-2-s-transferase from pseudomonas putida
49	<a href="#">c4ml1D</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> dsbp; <b>PDBTitle:</b> disulfide isomerase (dsbp) from multidrug resistance inca/c2 transferable plasmid in oxidized state (p212121 space group)
50	<a href="#">d1r4wa</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
51	<a href="#">c5hf1A</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein, cytosolic disulfide reductase <b>PDBTitle:</b> cytosolic disulfide reductase dsbm from pseudomonas aeruginosa with2 gsh
52	<a href="#">c1yzxB</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase kappa 1; <b>PDBTitle:</b> crystal structure of human kappa class glutathione transferase
53	<a href="#">c5h29A</a>	Alignment	not modelled	99.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase/glutathione-related protein; <b>PDBTitle:</b> crystal structure of the ntd_n/c domain of alkylhydroperoxide2 reductase ahpf from enterococcus faecalis (v583)

54	<a href="#">d1un2a</a>	Alignment	not modelled	98.6	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
55	<a href="#">d1j08a2</a>	Alignment	not modelled	98.3	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
56	<a href="#">d1a8la2</a>	Alignment	not modelled	97.8	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
57	<a href="#">d1zmaa1</a>	Alignment	not modelled	97.6	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
58	<a href="#">d1hyua4</a>	Alignment	not modelled	97.6	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
59	<a href="#">c2hlsB</a>	Alignment	not modelled	97.5	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein disulfide oxidoreductase; <b>PDBTitle:</b> the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
60	<a href="#">d1nhoa</a>	Alignment	not modelled	97.5	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
61	<a href="#">c3dmIA</a>	Alignment	not modelled	97.5	33	<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 from paracoccus2 pantotrophus (reduced form)
62	<a href="#">c2hyxA</a>	Alignment	not modelled	97.4	13	<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
63	<a href="#">c2diyA</a>	Alignment	not modelled	97.4	32	<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
64	<a href="#">c5e37A</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ef-hand domain-containing thioredoxin; <b>PDBTitle:</b> redox protein from chlamydomonas reinhardtii
65	<a href="#">c1zyPb</a>	Alignment	not modelled	97.4	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 ahfp
66	<a href="#">c5dbqA</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of insect thioredoxin at 1.95 angstroms
67	<a href="#">c2ywIA</a>	Alignment	not modelled	97.3	14	<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
68	<a href="#">c2pptA</a>	Alignment	not modelled	97.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-2; <b>PDBTitle:</b> crystal structure of thioredoxin-2
69	<a href="#">c3dxbE</a>	Alignment	not modelled	97.3	17	<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
70	<a href="#">d1fo5a</a>	Alignment	not modelled	97.2	27	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
71	<a href="#">c2lrcA</a>	Alignment	not modelled	97.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable thioredoxin; <b>PDBTitle:</b> structure of thioredoxin 2 from pseudomonas aeruginosa pao1 in its2 reduced form
72	<a href="#">c3or5A</a>	Alignment	not modelled	97.2	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 tis
73	<a href="#">c6g61A</a>	Alignment	not modelled	97.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin o1, mitochondrial; <b>PDBTitle:</b> crystal structure of thioredoxin o1 from arabidopsis thaliana in2 oxidized state
74	<a href="#">c2aytB</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin-like protein; <b>PDBTitle:</b> the crystal structure of a protein disulfide oxidoreductase from2 aquifex aeolicus
75	<a href="#">c1v98A</a>	Alignment	not modelled	97.2	20	<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
76	<a href="#">c1x5dA</a>	Alignment	not modelled	97.2	17	<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
77	<a href="#">c4kndA</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> thioredoxin from anaeromyxobacter dehalogenans.
78	<a href="#">c3s9fA</a>	Alignment	not modelled	97.1	24	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> tryparedoxin; <b>PDBTitle:</b> the structure of tryparedoxin i from leishmania major
79	<a href="#">c6ckpA</a>	Alignment	not modelled	97.1	22	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of a thioredoxin domain 2 from brucella melitensis2 at 1.15 angstrom resolution
						<b>Fold:</b> Thioredoxin fold

80	<a href="#">d1i5ga</a>	Alignment	not modelled	97.1	20	<b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
81	<a href="#">c1t00A</a>	Alignment	not modelled	97.1	24	<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
82	<a href="#">c2i57A</a>	Alignment	not modelled	97.1	20	<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
83	<a href="#">c3emxB</a>	Alignment	not modelled	97.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from aeropyrum pernix
84	<a href="#">d1f9ma</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
85	<a href="#">c3d22A</a>	Alignment	not modelled	97.1	25	<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, pptrxh4c61s
86	<a href="#">c6bkvB</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from helicobacter pylori (strain g27)
87	<a href="#">d1gh2a</a>	Alignment	not modelled	97.1	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
88	<a href="#">c3ul3A</a>	Alignment	not modelled	97.1	27	<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
89	<a href="#">c2mcsA</a>	Alignment	not modelled	97.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution nmr structure of a putative thioredoxin (ech_0218) in the2 reduced state from ehrlichia chaffeensis, the etiological agent3 responsible for human monocytic ehrlichiosis. seattle structural4 genomics center for infectious disease target ehcha.00546.a
90	<a href="#">c3hz4A</a>	Alignment	not modelled	97.1	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from methanosa
91	<a href="#">c2i4aa</a>	Alignment	not modelled	97.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from the acidophile acetobacter aceti
92	<a href="#">c2lqoA</a>	Alignment	not modelled	97.1	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glutaredoxin rv3198.1/mt3292; <b>PDBTitle:</b> mrx1 reduced
93	<a href="#">d2b5xa1</a>	Alignment	not modelled	97.1	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
94	<a href="#">c3p2aB</a>	Alignment	not modelled	97.1	19	<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
95	<a href="#">c1xbxA</a>	Alignment	not modelled	97.1	24	<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
96	<a href="#">d1dbya</a>	Alignment	not modelled	97.0	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
97	<a href="#">c2i5IA</a>	Alignment	not modelled	97.0	23	<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
98	<a href="#">c6mzaA</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution nmr structure of a putative thioredoxin (trxa) in the reduced2 state from rickettsia prowazekii, the etiological agent responsible3 for typhus. seattle structural genomics center for infectious disease4 target ripra.00029.a
99	<a href="#">c3p2aA</a>	Alignment	not modelled	97.0	19	<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
100	<a href="#">d1ep7a</a>	Alignment	not modelled	97.0	28	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
101	<a href="#">c6dnub</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbd; <b>PDBTitle:</b> crystal structure of neisseria meningitidis dsbd c-terminal domain in2 the oxidised form
102	<a href="#">c3hypB</a>	Alignment	not modelled	97.0	21	<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
103	<a href="#">d1thxa</a>	Alignment	not modelled	97.0	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
104	<a href="#">d2fwha1</a>	Alignment	not modelled	97.0	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
105	<a href="#">c4yodA</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-like protein; <b>PDBTitle:</b> crystal structure of a thioredoxin-like protein (baccac_02376) from2 bacteroides caccae atcc 43185 at 1.90 a

					resolution	
106	<a href="#">d2fy6a1</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
107	<a href="#">d1j08a1</a>	Alignment	not modelled	96.9	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
108	<a href="#">c3fkfC</a>	Alignment	not modelled	96.9	15	<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 ntc 9343
109	<a href="#">c4cw9A</a>	Alignment	not modelled	96.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> entamoeba histolytica thioredoxin c34s mutant
110	<a href="#">d1xwaa</a>	Alignment	not modelled	96.9	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
111	<a href="#">c2qsiB</a>	Alignment	not modelled	96.9	38	<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
112	<a href="#">c1w89E</a>	Alignment	not modelled	96.9	33	<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
113	<a href="#">c2e0qA</a>	Alignment	not modelled	96.9	28	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of k53e thioredoxin from sulfolobus tokodaii strain7
114	<a href="#">d1syra</a>	Alignment	not modelled	96.8	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
115	<a href="#">c2yoia</a>	Alignment	not modelled	96.8	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> leca thioredoxin; <b>PDBTitle:</b> crystal structure of ancestral thioredoxin relative to last eukaryotes2 common ancestor (leca) from the precambrian period
116	<a href="#">c2l6dA</a>	Alignment	not modelled	96.8	27	<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
117	<a href="#">c6iblB</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin 1,beta-1 adrenergic receptor; <b>PDBTitle:</b> activated turkey beta1 adrenoceptor with bound agonist formoterol and2 nanobody nb80
118	<a href="#">c3ic4A</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin (grx-1); <b>PDBTitle:</b> the crystal structure of the glutaredoxin(grx-1) from archaeoglobus fulgidus
119	<a href="#">c6esxC</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin 1; <b>PDBTitle:</b> caulobacter crescentus trx1
120	<a href="#">c3wgD</a>	Alignment	not modelled	96.8	21	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin domain-containing protein 5; <b>PDBTitle:</b> crystal structure of erp46 trx1