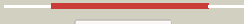



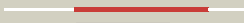



















# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0816c\_(thiX)\_909614\_910036  
 Date Fri Jul 26 01:50:40 BST 2019  
 Unique Job ID 1e53cdb09d154e61

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2pptA_</a>	 Alignment		99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-2; <b>PDBTitle:</b> crystal structure of thioredoxin-2
2	<a href="#">c6ib1B_</a>	 Alignment		99.9	19	<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
3	<a href="#">c5e37A_</a>	 Alignment		99.9	23	<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
4	<a href="#">c2I57A_</a>	 Alignment		99.9	16	<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
5	<a href="#">c3p2aB_</a>	 Alignment		99.9	24	<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
6	<a href="#">c2I6dA_</a>	 Alignment		99.9	20	<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
7	<a href="#">c2IrcA_</a>	 Alignment		99.9	28	<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
8	<a href="#">c3p2aA_</a>	 Alignment		99.9	24	<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
9	<a href="#">c6gc1A_</a>	 Alignment		99.9	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nhl repeat-containing protein 2; <b>PDBTitle:</b> crystal structure of trx-like and nhl repeat containing domains of2 human nhlc2
10	<a href="#">c6ckpA_</a>	 Alignment		99.9	26	<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
11	<a href="#">c3d22A_</a>	 Alignment		99.9	15	<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

12	<a href="#">c3hypB_</a>	Alignment		99.9	22	<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
13	<a href="#">d1xfla_</a>	Alignment		99.9	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
14	<a href="#">c2vlvA_</a>	Alignment		99.9	24	<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 in partially2 radiation-reduced state
15	<a href="#">c3qdnA_</a>	Alignment		99.9	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
16	<a href="#">c3hz4A_</a>	Alignment		99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from methanosarcina mazei
17	<a href="#">c3dxbE_</a>	Alignment		99.9	22	<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
18	<a href="#">c2i5IA_</a>	Alignment		99.9	22	<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
19	<a href="#">d2trxa_</a>	Alignment		99.9	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
20	<a href="#">c3gnjD_</a>	Alignment		99.9	17	<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
21	<a href="#">c2nbsA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> e_1r26; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for designed2 protein e_1r26
22	<a href="#">d1gh2a_</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
23	<a href="#">c2hyxA_</a>	Alignment	not modelled	99.9	19	<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
24	<a href="#">c2diyA_</a>	Alignment	not modelled	99.9	22	<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
25	<a href="#">c3ul3A_</a>	Alignment	not modelled	99.9	25	<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
26	<a href="#">d1thxA_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
27	<a href="#">c2i1uA_</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> mycobacterium tuberculosis thioredoxin c
28	<a href="#">d1m7ta_</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c1v98A</a>	Alignment	not modelled	99.8	32	<b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure analysis of thioredoxin from thermophilus
30	<a href="#">d1ti3a</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
31	<a href="#">d1dbya</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
32	<a href="#">c2e0qA</a>	Alignment	not modelled	99.8	30	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of k53e thioredoxin from sulfolobus2 tokodail strain7
33	<a href="#">d1ep7a</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
34	<a href="#">d1r26a</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
35	<a href="#">c5nymA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-like protein 2.1; <b>PDBTitle:</b> crystal structure of the atypical poplar thioredoxin-like2.1 in2 reduced state
36	<a href="#">c2vm2C</a>	Alignment	not modelled	99.8	17	<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 1 crystallized using2 peg as precipitant
37	<a href="#">d1j08a2</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
38	<a href="#">d1a8la2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
39	<a href="#">c5zf2A</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin (h-type,trx-h); <b>PDBTitle:</b> crystal structure of trxp from edwardsiella tarda eib202
40	<a href="#">c3vfiA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of a metagenomic thioredoxin
41	<a href="#">c1t00A</a>	Alignment	not modelled	99.8	22	<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
42	<a href="#">c4kndA</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> thioredoxin from anaeromyxobacter dehalogenans.
43	<a href="#">c2vocA</a>	Alignment	not modelled	99.8	24	<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 disulfide dimers that2 resemble enzyme-substrate reaction intermediate
44	<a href="#">c1w89E</a>	Alignment	not modelled	99.8	24	<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
45	<a href="#">c2f51B</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structure of trichomonas vaginalis thioredoxin
46	<a href="#">c6mzaA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution nmr rickettsia prowazekii, the etiological agent responsible3 for typhus. seattle structural genomics center for infectious disease4 target ripra.00029.a
47	<a href="#">c6g61A</a>	Alignment	not modelled	99.8	21	<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
48	<a href="#">c6bkvB</a>	Alignment	not modelled	99.8	26	<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)
49	<a href="#">d1fb6a</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
50	<a href="#">c2i4aA</a>	Alignment	not modelled	99.8	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
51	<a href="#">d2ifqa1</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
52	<a href="#">c4fybA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein (dsbc); <b>PDBTitle:</b> structural and functional characterizations of a thioredoxin-fold2 protein from helicobacter pylori
53	<a href="#">d1qgva</a>	Alignment	not modelled	99.8	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> spliceosomal protein U5-15Kd
54	<a href="#">c4ruvA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325
55	<a href="#">c2wz9A</a>	Alignment	not modelled	99.8	22	<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
56	<a href="#">c6gd1B_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin 1,elav-like protein 1; <b>PDBTitle:</b> structure of hur rrm3
57	<a href="#">c2yoiA_</a>	Alignment	not modelled	99.8	22 <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
58	<a href="#">d1xwaa_</a>	Alignment	not modelled	99.8	23 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
59	<a href="#">d1z5ye1</a>	Alignment	not modelled	99.8	23 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
60	<a href="#">c5dbqA_</a>	Alignment	not modelled	99.8	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
61	<a href="#">d1syra_</a>	Alignment	not modelled	99.8	19 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
62	<a href="#">c2xbqB_</a>	Alignment	not modelled	99.8	21 <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
63	<a href="#">d1f9ma_</a>	Alignment	not modelled	99.8	19 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
64	<a href="#">c6esxC_</a>	Alignment	not modelled	99.8	23 <b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin 1; <b>PDBTitle:</b> caulobacter crescentum trx1
65	<a href="#">c3zzxB_</a>	Alignment	not modelled	99.8	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystallographic structure of thioredoxin from litopenaeus vannamei
66	<a href="#">c6dnuB_</a>	Alignment	not modelled	99.8	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thio:disulfide interchange protein dsbd; <b>PDBTitle:</b> crystal structure of neisseria meningitidis dsbd c-terminal domain in2 the oxidised form
67	<a href="#">c2kucA_</a>	Alignment	not modelled	99.8	17 <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
68	<a href="#">c3tcoA_</a>	Alignment	not modelled	99.8	25 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin (trxa-1); <b>PDBTitle:</b> crystallographic and spectroscopic characterization of sulfolobus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
69	<a href="#">d2fwha1</a>	Alignment	not modelled	99.8	23 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
70	<a href="#">d1nw2a_</a>	Alignment	not modelled	99.8	24 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
71	<a href="#">c2oe0B_</a>	Alignment	not modelled	99.8	21 <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
72	<a href="#">c2vimA_</a>	Alignment	not modelled	99.8	29 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> x-ray structure of fasciola hepatica thioredoxin
73	<a href="#">c4cw9A_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> entamoeba histolytica thioredoxin c34s mutant
74	<a href="#">c4xhmB_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin (trx-3); <b>PDBTitle:</b> archaeoglobus fulgidus thioredoxin 3 m60h
75	<a href="#">c3emxB_</a>	Alignment	not modelled	99.8	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from aeropyrum pernix
76	<a href="#">c2j23A_</a>	Alignment	not modelled	99.8	21 <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
77	<a href="#">c2mcsA_</a>	Alignment	not modelled	99.8	16 <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
78	<a href="#">d1oaza_</a>	Alignment	not modelled	99.8	21 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
79	<a href="#">c2yj7A_</a>	Alignment	not modelled	99.8	25 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lpbca thioredoxin; <b>PDBTitle:</b> crystal structure of a hyperstable protein from the precambrian2 period
80	<a href="#">c2yzuA_</a>	Alignment	not modelled	99.8	24 <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 <b>PDB header:</b> oxidoreductase

81	<a href="#">c5jy5A_</a>	Alignment	not modelled	99.8	22	<b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin 1 from cryptococcus neoformans at 1.82 angstroms resolution
82	<a href="#">c1x5dA_</a>	Alignment	not modelled	99.8	21	<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
83	<a href="#">c2o7kA_</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> s. aureus thioredoxin
84	<a href="#">c3f9uA_</a>	Alignment	not modelled	99.8	16	<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
85	<a href="#">c6i1cB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin f2; <b>PDBTitle:</b> crystal structure of chlamydomonas reinhardtii thioredoxin f2
86	<a href="#">c1xbsA_</a>	Alignment	not modelled	99.8	18	<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
87	<a href="#">c2qsiB_</a>	Alignment	not modelled	99.8	13	<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 rhodospseudomonas palustris cga009
88	<a href="#">c6gn9A_</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of a thioredoxin from clostridium acetobutylicum at2 1.75 a resolution
89	<a href="#">d1knga_</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
90	<a href="#">c3dmlA_</a>	Alignment	not modelled	99.8	20	<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)
91	<a href="#">c4euyA_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of thioredoxin-like protein bce_0499 from bacillus2 cereus atcc 10987
92	<a href="#">c2dmlA_</a>	Alignment	not modelled	99.8	19	<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
93	<a href="#">c5ganD_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> spliceosomal protein dib1; <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
94	<a href="#">c4i8bA_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from schistosoma japonicum
95	<a href="#">c2i9hA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin i; <b>PDBTitle:</b> nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)
96	<a href="#">c3wgdD_</a>	Alignment	not modelled	99.8	23	<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
97	<a href="#">d1a8la1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
98	<a href="#">c2dj0A_</a>	Alignment	not modelled	99.8	20	<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
99	<a href="#">c2albA_</a>	Alignment	not modelled	99.8	25	<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
100	<a href="#">c3razA_</a>	Alignment	not modelled	99.8	19	<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
101	<a href="#">d1fo5a_</a>	Alignment	not modelled	99.8	28	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
102	<a href="#">d2b5xa1</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
103	<a href="#">c3wgeA_</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin domain-containing protein 5; <b>PDBTitle:</b> crystal structure of erp46 trx2
104	<a href="#">d1j08a1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
105	<a href="#">c3cxgA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> crystal structure of plasmodium falciparum thioredoxin, pf10790w
						<b>PDB header:</b> oxidoreductase

106	<a href="#">c2b1kA_</a>	Alignment	not modelled	99.7	19	<b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of e. coli ccmg protein
107	<a href="#">c4tr3A_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> type iii iodothyronine deiodinase; <b>PDBTitle:</b> mouse iodothyronine deiodinase 3 catalytic core, semet-labeled active2 site mutant secys->cys
108	<a href="#">d2fy6a1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
109	<a href="#">c2lstA_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution structure of a thioredoxin from thermus thermophilus
110	<a href="#">c4pq1B_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative electron transport related protein; <b>PDBTitle:</b> crystal structure and functional implications of a dsbf homologue from2 corynebacterium diphtheriae
111	<a href="#">d1zooa1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
112	<a href="#">c3lwaA_</a>	Alignment	not modelled	99.7	14	<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-disulfide isomerase from2 corynebacterium glutamicum to 1.75a
113	<a href="#">c4tw5A_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> eps1p; <b>PDBTitle:</b> structure of the first two thioredoxin domains of saccharomyces2 cerevisiae eps1p
114	<a href="#">c2k8vA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin domain-containing protein 12; <b>PDBTitle:</b> solution structure of oxidised erp18
115	<a href="#">c4tveA_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> naumovozyma dairenensis eps1p; <b>PDBTitle:</b> structure of the first two thioredoxin domains of naumovozyma2 dairenensis eps1p
116	<a href="#">c2dizA_</a>	Alignment	not modelled	99.7	19	<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
117	<a href="#">c4ka0C_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative thiol-disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative thiol-disulfide oxidoreductase from2 bacteroides vulgatus (target nysgrc-011676), space group p21221
118	<a href="#">c3apsA_</a>	Alignment	not modelled	99.7	19	<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
119	<a href="#">c4evmA_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of soluble domain of membrane-anchored2 thioredoxin family protein from streptococcus pneumoniae strain3 canada mdr_19a
120	<a href="#">c2ju5A_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin disulfide isomerase; <b>PDBTitle:</b> dsbh oxidoreductase