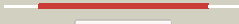












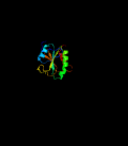











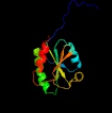







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1324 (-)_1487167_1488081
Date	Wed Jul 31 22:05:42 BST 2019
Unique Job ID	cbb2732d0d82bad9

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qdnA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
2	c6ib1B_	 Alignment		99.9	22	PDB header: immune system Chain: B: PDB Molecule: thioredoxin 1,beta-1 adrenergic receptor; PDBTitle: activated turkey beta1 adrenoceptor with bound agonist formoterol and2 nanobody nb80
3	c2pptA_	 Alignment		99.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
4	c3p2aB_	 Alignment		99.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis
5	c3p2aA_	 Alignment		99.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis
6	c3dxbE_	 Alignment		99.9	23	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
7	c5e37A_	 Alignment		99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ef-hand domain-containing thioredoxin; PDBTitle: redox protein from chlamydomonas reinhardtii
8	c6ckpA_	 Alignment		99.9	26	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a thioredoxin domain 2 from brucella melitensis2 at 1.15 angstrom resolution
9	c3hz4A_	 Alignment		99.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from methanosarcina mazei
10	c2mcsA_	 Alignment		99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: 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
11	c6bkbB_	 Alignment		99.9	29	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from helicobacter pylori (strain g27)

12	c3gnjD_	Alignment		99.9	16	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
13	c2l5lA_	Alignment		99.9	23	PDB header: transport protein Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution structure of thioredoxin from bacteroides vulgatus
14	c6mzaA_	Alignment		99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: 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
15	c2diyA_	Alignment		99.9	21	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
16	c6gd1B_	Alignment		99.9	23	PDB header: rna binding protein Chain: B: PDB Molecule: thioredoxin 1,elav-like protein 1; PDBTitle: structure of hur rrm3
17	d1thxa_	Alignment		99.9	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
18	c2albA_	Alignment		99.9	22	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
19	c2i1uA_	Alignment		99.9	26	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: mycobacterium tuberculosis thioredoxin c
20	c2i4aA_	Alignment		99.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from the acidophile acetobacter aceti
21	d2trxa_	Alignment	not modelled	99.9	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
22	c3hypB_	Alignment	not modelled	99.9	25	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of bacteroides fragilis trxp_s105g mutant
23	d1dbya_	Alignment	not modelled	99.9	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
24	c3vfiA_	Alignment	not modelled	99.9	17	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a metagenomic thioredoxin
25	c2vocA_	Alignment	not modelled	99.9	23	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: thioredoxin a active site mutants form mixed disulfide dimers that2 resemble enzyme-substrate reaction intermediate
26	c1t00A_	Alignment	not modelled	99.9	23	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: the structure of thioredoxin from s. coelicolor
27	d1ep7a_	Alignment	not modelled	99.9	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
28	c4kndA_	Alignment	not modelled	99.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: thioredoxin from anaeromyxobacter dehalogenans.
29	c1w89E_	Alignment	not modelled	99.9	33	PDB header: electron transport Chain: E: PDB Molecule: thioredoxin;

					PDBTitle: structure of the reduced form of human thioredoxin 2
30	c6esxC_	Alignment	not modelled	99.9	26 PDB header: cell cycle Chain: C: PDB Molecule: thioredoxin 1; PDBTitle: caulobacter crescentum trx1
31	c2l6dA_	Alignment	not modelled	99.9	20 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
32	d1xwaa_	Alignment	not modelled	99.9	18 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
33	c1x5dA_	Alignment	not modelled	99.9	23 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
34	d1fb6a_	Alignment	not modelled	99.9	28 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
35	c2o7kA_	Alignment	not modelled	99.9	29 PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: s. aureus thioredoxin
36	c3tcoA_	Alignment	not modelled	99.9	27 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin (trxa-1); PDBTitle: crystallographic and spectroscopic characterization of sulfobolus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
37	c5dbqA_	Alignment	not modelled	99.9	19 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of insect thioredoxin at 1.95 angstroms
38	c4xhmB_	Alignment	not modelled	99.9	27 PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin (trx-3); PDBTitle: archaeoglobus fulgidus thioredoxin 3 m60h
39	c3wgeA_	Alignment	not modelled	99.9	21 PDB header: isomerase Chain: A: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: crystal structure of erp46 trx2
40	c3f8uA_	Alignment	not modelled	99.9	22 PDB header: immune system/isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a3erp57; PDBTitle: tapasin/erp57 heterodimer
41	c6gn9A_	Alignment	not modelled	99.9	32 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a thioredoxin from clostridium acetobutylicum at2 1.75 a resolution
42	c2xbqB_	Alignment	not modelled	99.9	16 PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
43	c2yzuA_	Alignment	not modelled	99.9	27 PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
44	c5zf2A_	Alignment	not modelled	99.9	24 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin (h-type,trx-h); PDBTitle: crystal structure of trxlp from edwardsiella tarda eib202
45	c2yoiA_	Alignment	not modelled	99.9	20 PDB header: oxidoreductase Chain: A: PDB Molecule: leca thioredoxin; PDBTitle: crystal structure of ancestral thioredoxin relative to last eukaryotes2 common ancestor (leca) from the precambrian period
46	d1f9ma_	Alignment	not modelled	99.9	19 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
47	d1m7ta_	Alignment	not modelled	99.9	22 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
48	d1qgva_	Alignment	not modelled	99.9	13 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: spliceosomal protein U5-15Kd
49	d1nw2a_	Alignment	not modelled	99.9	30 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
50	c2wz9A_	Alignment	not modelled	99.9	22 PDB header: protein binding Chain: A: PDB Molecule: glutaredoxin-3; PDBTitle: crystal structure of the thioredoxin domain of human txn12
51	c1xbsA_	Alignment	not modelled	99.9	19 PDB header: transcription, cell cycle Chain: A: PDB Molecule: dim1-like protein; PDBTitle: crystal structure of human dim2: a dim1-like protein
52	d1xfla_	Alignment	not modelled	99.9	21 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
53	c2e0qA_	Alignment	not modelled	99.9	24 PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
54	c2yj7A_	Alignment	not modelled	99.9	34 PDB header: oxidoreductase Chain: A: PDB Molecule: lpbca thioredoxin; PDBTitle: crystal structure of a hyperstable protein from the precambrian2 period
55	d2ifqa1	Alignment	not modelled	99.9	21 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
					Fold: Thioredoxin fold

56	d1gh2a_	Alignment	not modelled	99.9	17	Superfamily: Thioredoxin-like Family: Thioltransferase
57	c5nymA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-like protein 2.1; PDBTitle: crystal structure of the atypical poplar thioredoxin-like2.1 in2 reduced state
58	c3zzxB_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystallographic structure of thioredoxin from litopenaeus vannamei
59	c2vm2C_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: C: PDB Molecule: thioredoxin h isoform 1.; PDBTitle: crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant
60	c2dj0A_	Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: thioredoxin-related transmembrane protein 2; PDBTitle: the solution structure of the thioredoxin domain of human2 thioredoxin-related transmembrane protein 2
61	d1ti3a_	Alignment	not modelled	99.9	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
62	c3emxB_	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix
63	c3d22A_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h-type; PDBTitle: crystal structure of a poplar thioredoxin h mutant, pptrxh4c61s
64	c3apsA_	Alignment	not modelled	99.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of trx4 domain of erdj5
65	c2v1vA_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h isoform 2.; PDBTitle: crystal structure of barley thioredoxin h isoform 2 in partially2 radiation-reduced state
66	c2r2jA_	Alignment	not modelled	99.9	15	PDB header: chaperone Chain: A: PDB Molecule: thioredoxin domain-containing protein 4; PDBTitle: crystal structure of human erp44
67	c5ganD_	Alignment	not modelled	99.9	13	PDB header: transcription Chain: D: PDB Molecule: spliceosomal protein dib1; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
68	c1v98A_	Alignment	not modelled	99.9	27	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure analysis of thioredoxin from thermus thermophilus
69	d1r26a_	Alignment	not modelled	99.9	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
70	c6g61A_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin o1, mitochondrial; PDBTitle: crystal structure of thioredoxin o1 from arabidopsis thaliana in2 oxidized state
71	c3ul3A_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
72	c2vimA_	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: x-ray structure of fasciola hepatica thioredoxin
73	c2dizA_	Alignment	not modelled	99.9	23	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
74	d1oaza_	Alignment	not modelled	99.9	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
75	c4tw5A_	Alignment	not modelled	99.9	14	PDB header: isomerase Chain: A: PDB Molecule: eps1p; PDBTitle: structure of the first two thioredoxin domains of saccharomyces2 cerevisiae eps1p
76	c6i1cB_	Alignment	not modelled	99.9	15	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin f2; PDBTitle: crystal structure of chlamydomonas reinhardtii thioredoxin f2
77	d1j08a2	Alignment	not modelled	99.9	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
78	c2dm1A_	Alignment	not modelled	99.9	25	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a6; PDBTitle: the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a6
79	c2b5eA_	Alignment	not modelled	99.9	12	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: crystal structure of yeast protein disulfide isomerase
80	c4ruvA_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325
81	c2j23A_	Alignment	not modelled	99.9	22	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
						PDB header: structural genomics, unknown function

82	c2qsiB	Alignment	not modelled	99.9	21	Chain: B: PDB Molecule: putative hydrogenase expression/formation protein hupg; PDBTitle: crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodospseudomonas palustris cga009
83	c3ed3A	Alignment	not modelled	99.9	15	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase mpd1; PDBTitle: crystal structure of the yeast dithio/disulfide2 oxidoreductase mpd1p
84	c3wgdD	Alignment	not modelled	99.9	24	PDB header: isomerase Chain: D: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: crystal structure of erp46 trx1
85	d1a8la2	Alignment	not modelled	99.9	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
86	c4i8bA	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from schistosoma japonicum
87	c2oe0B	Alignment	not modelled	99.9	23	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin-3; PDBTitle: crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
88	c2lrcA	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: probable thioredoxin; PDBTitle: structure of thioredoxin 2 from pseudomonas aeruginosa pao1 in its2 reduced form
89	c2i57A	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of an uncharacterized thioredoxin-like protein from2 clostridium perfringens
90	c4cw9A	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: entamoeba histolytica thioredoxin c34s mutant
91	c2dj1A	Alignment	not modelled	99.8	22	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
92	c1sjiA	Alignment	not modelled	99.8	17	PDB header: metal binding protein Chain: A: PDB Molecule: calsequestrin, cardiac muscle isoform; PDBTitle: comparing skeletal and cardiac calsequestrin structures and their2 calcium binding: a proposed mechanism for coupled calcium binding and3 protein polymerization
93	d1syra	Alignment	not modelled	99.8	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
94	c1a8yA	Alignment	not modelled	99.8	17	PDB header: calcium-binding protein Chain: A: PDB Molecule: calsequestrin; PDBTitle: crystal structure of calsequestrin from rabbit skeletal muscle2 sarcoplasmic reticulum at 2.4 a resolution
95	c1x5eA	Alignment	not modelled	99.8	17	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin domain containing protein 1; PDBTitle: the solution structure of the thioredoxin-like domain of2 human thioredoxin-related transmembrane protein
96	c5xf7A	Alignment	not modelled	99.8	17	PDB header: chaperone Chain: A: PDB Molecule: protein disulfide-isomerase-like protein of2 the testis; PDBTitle: crystal structure of human protein disulfide isomerase-like protein of2 the testis
97	c4tveA	Alignment	not modelled	99.8	15	PDB header: isomerase Chain: A: PDB Molecule: naumovozyma dairenensis eps1p; PDBTitle: structure of the first two thioredoxin domains of naumovozyma2 dairenensis eps1p
98	c2vafA	Alignment	not modelled	99.8	19	PDB header: metal binding protein Chain: A: PDB Molecule: calsequestrin-2; PDBTitle: crystal structure of human cardiac calsequestrin
99	c2dbcA	Alignment	not modelled	99.8	18	PDB header: signaling protein Chain: A: PDB Molecule: unnamed protein product; PDBTitle: solution structure of the thioredoxin-like domain of2 phosducin-like protein 2(pdcl2)
100	d2b5ea4	Alignment	not modelled	99.8	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
101	c3qd9D	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: D: PDB Molecule: qsox from trypanosoma brucei (tbqsox); PDBTitle: c72s/c353s mutant of trypanosoma brucei qsox containing an interdomain2 disulfide
102	c5yryA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 5'-adenylylsulfate reductase 1, chloroplastic; PDBTitle: crystal structure of c-terminal redox domain of apr1 from arabidopsis2 thaliana
103	c5jy5A	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 1 from cryptococcus neoformans at 1.82 angstroms resolution
104	c3q6oA	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfhydryl oxidase 1; PDBTitle: oxidoreductase fragment of human qsox1
105	c2nbsA	Alignment	not modelled	99.8	20	PDB header: unknown function Chain: A: PDB Molecule: e_1r26; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for designed2 protein e_1r26
106	c2qc7A	Alignment	not modelled	99.8	11	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic reticulum protein erp29; PDBTitle: crystal structure of the protein-disulfide isomerase related chaperone2 erp29
						PDB header: oxidoreductase

107	c3t59D_	Alignment	not modelled	99.8	17	Chain: D: PDB Molecule: sulfhydryl oxidase 1; PDBTitle: c76a/c455s mutant of mouse qsox1 containing an interdomain disulfide
108	c3apoA_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of full-length erdj5
109	c2f51B_	Alignment	not modelled	99.8	19	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: structure of trichomonas vaginalis thioredoxin
110	c2dj2A_	Alignment	not modelled	99.8	19	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
111	d1a8ya1	Alignment	not modelled	99.8	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Calsequestrin
112	d1zmaa1	Alignment	not modelled	99.8	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
113	c4e1A_	Alignment	not modelled	99.8	22	PDB header: chaperone Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: crystal structure of oxidized hpdi (abb'xa')
114	c3h79A_	Alignment	not modelled	99.8	24	PDB header: unknown function Chain: A: PDB Molecule: thioredoxin-like protein; PDBTitle: crystal structure of trypanosoma cruzi thioredoxin-like hypothetical2 protein q4dv70
115	d2hfda1	Alignment	not modelled	99.8	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: HyaE-like
116	c2dj3A_	Alignment	not modelled	99.8	21	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a4; PDBTitle: the solution structure of the third thioredoxin domain of2 mouse protein disulfide-isomerase a4
117	c2hyxA_	Alignment	not modelled	99.8	15	PDB header: unknown function Chain: A: PDB Molecule: protein dipz; PDBTitle: structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
118	c1x5cA_	Alignment	not modelled	99.8	18	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase
119	d1meka_	Alignment	not modelled	99.8	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
120	c4m90A_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: tumor suppressor candidate 3; PDBTitle: crystal structure of oxidized hn33/tusc3