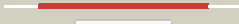



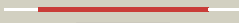



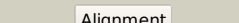
























Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3914_(trxC)_4402909_4403259
 Date Sat Aug 10 22:05:10 BST 2019
 Unique Job ID 899754627c203750

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ibB_	Alignment 		100.0	48	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
2	c3dxbE_	Alignment 		100.0	50	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
3	c2i1uA_	Alignment 		100.0	100	PDB header: electron transport Chain: A; PDB Molecule: thioredoxin; PDBTitle: mycobacterium tuberculosis thioredoxin c
4	c3hz4A_	Alignment 		99.9	31	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from methanosarcina mazei
5	c2pptA_	Alignment 		99.9	31	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
6	c6mzaA_	Alignment 		99.9	41	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
7	c3p2aB_	Alignment 		99.9	32	PDB header: oxidoreductase Chain: B; PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis
8	c2i4aA_	Alignment 		99.9	50	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from the acidophile acetobacter aceti
9	c6gd1B_	Alignment 		99.9	49	PDB header: rna binding protein Chain: B; PDB Molecule: thioredoxin 1,elav-like protein 1; PDBTitle: structure of hur rrm3
10	d1thxa_	Alignment 		99.9	38	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
11	c3p2aA_	Alignment 		99.9	31	PDB header: oxidoreductase Chain: A; PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis

12	c6ckpA_	Alignment		99.9	49	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
13	d2trxa_	Alignment		99.9	50	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
14	c3qdnA_	Alignment		99.9	30	PDB header: oxidoreductase Chain: A; PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
15	c2vocA_	Alignment		99.9	48	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
16	c1t00A_	Alignment		99.9	51	PDB header: electron transport Chain: A; PDB Molecule: thioredoxin; PDBTitle: the structure of thioredoxin from s. coelicolor
17	c6esxC_	Alignment		99.9	49	PDB header: cell cycle Chain: C; PDB Molecule: thioredoxin 1; PDBTitle: caulobacter crescentus trx1
18	c3gnjD_	Alignment		99.9	23	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
19	c6bkvB_	Alignment		99.9	39	PDB header: electron transport Chain: B; PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from helicobacter pylori (strain g27)
20	c3f8uA_	Alignment		99.9	29	PDB header: immune system/isomerase Chain: A; PDB Molecule: protein disulfide-isomerase a3erp57; PDBTitle: tapasin/erp57 heterodimer
21	d1dbya_	Alignment	not modelled	99.9	42	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
22	c4kndA_	Alignment	not modelled	99.9	40	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin; PDBTitle: thioredoxin from anaeromyxobacter dehalogenans.
23	c3vfiA_	Alignment	not modelled	99.9	26	PDB header: electron transport Chain: A; PDB Molecule: thioredoxin; PDBTitle: crystal structure of a metagenomic thioredoxin
24	c2l5lA_	Alignment	not modelled	99.9	32	PDB header: transport protein Chain: A; PDB Molecule: thioredoxin; PDBTitle: solution structure of thioredoxin from bacteroides vulgatus
25	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
26	c2yj7A_	Alignment	not modelled	99.9	52	PDB header: oxidoreductase Chain: A; PDB Molecule: lpbca thioredoxin; PDBTitle: crystal structure of a hyperstable protein from the precambrian2 period
27	c4xhmB_	Alignment	not modelled	99.9	44	PDB header: oxidoreductase Chain: B; PDB Molecule: thioredoxin (trx-3); PDBTitle: archaeoglobus fulgidus thioredoxin 3 m60h
28	c3ed3A_	Alignment	not modelled	99.9	21	PDB header: isomerase Chain: A; PDB Molecule: protein disulfide-isomerase mpd1; PDBTitle: crystal structure of the yeast dithiol/disulfide2 oxidoreductase mpd1p
						Fold: Thioredoxin fold

29	d1fb6a_	Alignment	not modelled	99.9	41	Superfamily: Thioredoxin-like Family: Thioltransferase
30	c1x5dA_	Alignment	not modelled	99.9	26	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
31	c2yoiA_	Alignment	not modelled	99.9	38	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
32	c3apoA_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of full-length erdj5
33	c2o7kA_	Alignment	not modelled	99.9	55	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: s. aureus thioredoxin
34	c2albA_	Alignment	not modelled	99.9	31	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
35	c4tw5A_	Alignment	not modelled	99.9	19	PDB header: isomerase Chain: A: PDB Molecule: eps1p; PDBTitle: structure of the first two thioredoxin domains of saccharomyces2 cerevisiae eps1p
36	c3apsA_	Alignment	not modelled	99.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of trx4 domain of erdj5
37	c2dmlA_	Alignment	not modelled	99.9	23	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
38	c3tcoA_	Alignment	not modelled	99.9	32	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
39	c2r2jA_	Alignment	not modelled	99.9	22	PDB header: chaperone Chain: A: PDB Molecule: thioredoxin domain-containing protein 4; PDBTitle: crystal structure of human erp44
40	c1sjjA_	Alignment	not modelled	99.9	14	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
41	c2b5eA_	Alignment	not modelled	99.9	26	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: crystal structure of yeast protein disulfide isomerase
42	d1oaza_	Alignment	not modelled	99.9	42	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
43	c4tveA_	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: A: PDB Molecule: naumovozya dairenensis eps1p; PDBTitle: structure of the first two thioredoxin domains of naumovozya2 dairenensis eps1p
44	c2vafA_	Alignment	not modelled	99.9	11	PDB header: metal binding protein Chain: A: PDB Molecule: calsequestrin-2; PDBTitle: crystal structure of human cardiac calsequestrin
45	c2mcsA_	Alignment	not modelled	99.9	31	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
46	d1nw2a_	Alignment	not modelled	99.9	57	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
47	c2yzuA_	Alignment	not modelled	99.9	54	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
48	c1a8yA_	Alignment	not modelled	99.9	14	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
49	c3hypB_	Alignment	not modelled	99.9	41	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of bacteroides fragilis trxp_s105g mutant
50	d1ep7a_	Alignment	not modelled	99.9	31	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
51	c3q6oA_	Alignment	not modelled	99.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfhydryl oxidase 1; PDBTitle: oxidoreductase fragment of human qsox1
52	c3wqeA_	Alignment	not modelled	99.9	25	PDB header: isomerase Chain: A: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: crystal structure of erp46 trx2
53	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
54	c5e37A_	Alignment	not modelled	99.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ef-hand domain-containing thioredoxin; PDBTitle: redox protein from chlamydomonas reinhardtii

55	c6gn9A	Alignment	not modelled	99.9	37	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a thioredoxin from clostridium acetobutylicum at2 1.75 a resolution
56	c2e0qA	Alignment	not modelled	99.9	37	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
57	c2wz9A	Alignment	not modelled	99.9	25	PDB header: protein binding Chain: A: PDB Molecule: glutaredoxin-3; PDBTitle: crystal structure of the thioredoxin domain of human txn2
58	d1r26a	Alignment	not modelled	99.9	28	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
59	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
60	c5xf7A	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: A: PDB Molecule: protein disulfide-isomerase-like protein of the testis; PDBTitle: crystal structure of human protein disulfide isomerase-like protein of2 the testis
61	c2diyA	Alignment	not modelled	99.9	25	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
62	c3t59D	Alignment	not modelled	99.9	29	PDB header: oxidoreductase Chain: D: PDB Molecule: sulfhydryl oxidase 1; PDBTitle: c76a/c455s mutant of mouse qsox1 containing an interdomain disulfide
63	c4cw9A	Alignment	not modelled	99.9	37	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: entamoeba histolytica thioredoxin c34s mutant
64	c2j23A	Alignment	not modelled	99.9	31	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
65	d1a8ya1	Alignment	not modelled	99.9	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Calsequestrin
66	d1xfla	Alignment	not modelled	99.9	28	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
67	c6ilcB	Alignment	not modelled	99.9	24	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin f2; PDBTitle: crystal structure of chlamydomonas reinhardtii thioredoxin f2
68	c4e11A	Alignment	not modelled	99.9	25	PDB header: chaperone Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: crystal structure of oxidized hpdi (abb'xa')
69	d1f9ma	Alignment	not modelled	99.9	26	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
70	c1x5cA	Alignment	not modelled	99.9	20	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
71	c3d22A	Alignment	not modelled	99.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h-type; PDBTitle: crystal structure of a poplar thioredoxin h mutant, ptxrh4c61s
72	d2b5ea1	Alignment	not modelled	99.9	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
73	c2v1vA	Alignment	not modelled	99.9	31	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
74	c5zf2A	Alignment	not modelled	99.9	34	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin (h-type,trx-h); PDBTitle: crystal structure of trxlp from edwardsiella tarda eib202
75	c3ul3A	Alignment	not modelled	99.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
76	c2xbqB	Alignment	not modelled	99.9	36	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
77	c5dbqA	Alignment	not modelled	99.9	32	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of insect thioredoxin at 1.95 angstroms
78	c2dj1A	Alignment	not modelled	99.9	30	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
79	c2oe0B	Alignment	not modelled	99.9	36	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin-3; PDBTitle: crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
80	d1ti3a	Alignment	not modelled	99.9	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase

81	d1xwaa	Alignment	not modelled	99.9	32	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
82	d1gh2a	Alignment	not modelled	99.9	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
83	c1x5eA	Alignment	not modelled	99.9	25	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
84	c3qd9D	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: D: PDB Molecule: qsox from trypanosoma brucei (tbqsox); PDBTitle: c72s/c353s mutant of trypanosoma brucei qsox containing an interdomain2 disulfide
85	d1qgva	Alignment	not modelled	99.9	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: spliceosomal protein U5-15Kd
86	c3wgdD	Alignment	not modelled	99.9	27	PDB header: isomerase Chain: D: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: crystal structure of erp46 trx1
87	c4ruvA	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325
88	c2dj3A	Alignment	not modelled	99.9	25	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
89	c3zzxB	Alignment	not modelled	99.9	36	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystallographic structure of thioredoxin from litopenaeus vannamei
90	c4i8bA	Alignment	not modelled	99.9	37	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from schistosoma japonicum
91	c1v98A	Alignment	not modelled	99.9	43	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure analysis of thioredoxin from thermus thermophilus
92	d2b5ea4	Alignment	not modelled	99.9	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
93	d1m7ta	Alignment	not modelled	99.9	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
94	c3h79A	Alignment	not modelled	99.9	15	PDB header: unknown function Chain: A: PDB Molecule: thioredoxin-like protein; PDBTitle: crystal structure of trypanosoma cruzi thioredoxin-like hypothetical2 protein q4dv70
95	c2dj0A	Alignment	not modelled	99.9	21	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
96	c2nbsA	Alignment	not modelled	99.9	21	PDB header: unknown function Chain: A: PDB Molecule: e_1r26; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for designed2 protein e_1r26
97	d1syra	Alignment	not modelled	99.9	34	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
98	d1mekA	Alignment	not modelled	99.9	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
99	d1j08a2	Alignment	not modelled	99.9	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
100	c2dmmA	Alignment	not modelled	99.9	24	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a3; PDBTitle: the solution structure of the second thioredoxin domain of2 human protein disulfide-isomerase a3
101	c2dj2A	Alignment	not modelled	99.9	29	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
102	c6g61A	Alignment	not modelled	99.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin o1, mitochondrial; PDBTitle: crystal structure of thioredoxin o1 from arabidopsis thaliana in2 oxidized state
103	c5jy5A	Alignment	not modelled	99.9	29	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 1 from cryptococcus neoformans at 1.82 angstroms resolution
104	c2vm2C	Alignment	not modelled	99.9	32	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
105	c2lrcA	Alignment	not modelled	99.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: probable thioredoxin; PDBTitle: structure of thioredoxin 2 from pseudomonas aeruginosa pao1 in its2 reduced form
106	c5nymA	Alignment	not modelled	99.9	24	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
						Fold: Thioredoxin fold

107	d2ifqa1	Alignment	not modelled	99.9	32	Superfamily: Thioredoxin-like Family: Thioltransferase
108	c5yryA	Alignment	not modelled	99.9	18	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
109	c3emxB	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix
110	d1a8la2	Alignment	not modelled	99.9	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
111	c2vimA	Alignment	not modelled	99.9	35	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: x-ray structure of fasciola hepatica thioredoxin
112	c1xbsA	Alignment	not modelled	99.9	18	PDB header: transcription, cell cycle Chain: A: PDB Molecule: dim1-like protein; PDBTitle: crystal structure of human dim2: a dim1-like protein
113	c2qc7A	Alignment	not modelled	99.8	24	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic reticulum protein erp29; PDBTitle: crystal structure of the protein-disulfide isomerase related chaperone2 erp29
114	c3cxgA	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin; PDBTitle: crystal structure of plasmodium falciparum thioredoxin, pfi0790w
115	c2f51B	Alignment	not modelled	99.8	31	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: structure of trichomonas vaginalis thioredoxin
116	c3idvA	Alignment	not modelled	99.8	32	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a4; PDBTitle: crystal structure of the a0a fragment of erp72
117	c5ganD	Alignment	not modelled	99.8	14	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
118	c3apqB	Alignment	not modelled	99.8	23	PDB header: oxidoreductase Chain: B: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of j-trx1 fragment of erdj5
119	c2qsiB	Alignment	not modelled	99.8	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative hydrogenase expression/formation protein hupg; PDBTitle: crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodospseudomonas palustris cga009
120	c2i9hA	Alignment	not modelled	99.8	38	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin i; PDBTitle: nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)