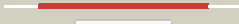



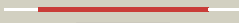




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1471_(trxB1)_1659376_1659747
Date	Fri Aug 2 13:30:05 BST 2019
Unique Job ID	6b5e35dade2bb9d5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pptA_	 Alignment		99.9	33	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
2	c6ib1B_	 Alignment		99.9	30	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	c3p2aB_	 Alignment		99.9	38	PDB header: oxidoreductase Chain: B: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis
4	c6gd1B_	 Alignment		99.9	32	PDB header: rna binding protein Chain: B: PDB Molecule: thioredoxin 1,elav-like protein 1; PDBTitle: structure of hur rrm3
5	c3dxbE_	 Alignment		99.9	30	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
6	c3p2aA_	 Alignment		99.9	38	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis
7	c2l6dA_	 Alignment		99.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
8	c2e0qA_	 Alignment		99.9	30	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
9	c6ckpA_	 Alignment		99.9	39	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
10	c2r2jA_	 Alignment		99.9	26	PDB header: chaperone Chain: A: PDB Molecule: thioredoxin domain-containing protein 4; PDBTitle: crystal structure of human erp44
11	c5zf2A_	 Alignment		99.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin (h-type,trx-h); PDBTitle: crystal structure of trxlp from edwardsiella tarda eib202

12	c3hz4A_	Alignment		99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from methanosarcina mazei
13	c6bkvB_	Alignment		99.9	34	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from helicobacter pylori (strain g27)
14	c3gnjD_	Alignment		99.9	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: thioredoxin domain protein; PDBTitle: the crystal structure of a thioredoxin-related protein from <i>Desulfotobacterium hafniense</i> dcb
15	c3tcoA_	Alignment		99.9	33	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin (trxa-1); PDBTitle: crystallographic and spectroscopic characterization of <i>Sulfolobus solfataricus</i> trxa1 provide insights into the determinants of thioredoxin fold stability
16	c2vocA_	Alignment		99.9	30	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: thioredoxin active site mutants form mixed disulfide dimers that resemble enzyme-substrate reaction intermediate
17	c4tw5A_	Alignment		99.9	15	PDB header: isomerase Chain: A: PDB Molecule: eps1p; PDBTitle: structure of the first two thioredoxin domains of <i>Saccharomyces cerevisiae</i> eps1p
18	d1dbya_	Alignment		99.9	37	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
19	d1gh2a_	Alignment		99.9	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
20	c3vfiA_	Alignment		99.9	25	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a metagenomic thioredoxin
21	c2o7kA_	Alignment	not modelled	99.9	30	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: s. aureus thioredoxin
22	c2i4aA_	Alignment	not modelled	99.9	36	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from the acidophile acetobacter aceti
23	c4cw9A_	Alignment	not modelled	99.9	27	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: entamoeba histolytica thioredoxin c34s mutant
24	c4xhmB_	Alignment	not modelled	99.9	35	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin (trx-3); PDBTitle: archaeoglobus fulgidus thioredoxin 3 m60h
25	c6mzaA_	Alignment	not modelled	99.9	32	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution nmr structure of a putative thioredoxin (trxa) in the reduced state from <i>Rickettsia prowazekii</i> , the etiological agent responsible for typhus. seattle structural genomics center for infectious disease target ripra.00029.a
26	c3qdnA_	Alignment	not modelled	99.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
27	c2vafA_	Alignment	not modelled	99.9	14	PDB header: metal binding protein Chain: A: PDB Molecule: calsequestrin-2; PDBTitle: crystal structure of human cardiac calsequestrin
28	c6gn9A_	Alignment	not modelled	99.9	31	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a thioredoxin from clostridium acetobutylicum at 2.175 Å resolution

29	c6esxC	Alignment	not modelled	99.9	35	PDB header: cell cycle Chain: C: PDB Molecule: thioredoxin 1; PDBTitle: caulobacter crescentus trx1
30	c2dj1A	Alignment	not modelled	99.9	23	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
31	c1a8yA	Alignment	not modelled	99.9	13	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
32	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 txn12
33	d1nw2a	Alignment	not modelled	99.9	39	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
34	c4ruvA	Alignment	not modelled	99.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325
35	c3wgeA	Alignment	not modelled	99.9	27	PDB header: isomerase Chain: A: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: crystal structure of erp46 trx2
36	c4tveA	Alignment	not modelled	99.9	16	PDB header: isomerase Chain: A: PDB Molecule: naumovozyma dairenensis eps1p; PDBTitle: structure of the first two thioredoxin domains of naumovozyma2 dairenensis eps1p
37	c5jy5A	Alignment	not modelled	99.9	38	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 1 from cryptococcus neoformans at 1.82 angstroms resolution
38	c2yzuA	Alignment	not modelled	99.9	32	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
39	c1x5dA	Alignment	not modelled	99.9	25	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
40	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
41	c2b5eA	Alignment	not modelled	99.9	25	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: crystal structure of yeast protein disulfide isomerase
42	d1fb6a	Alignment	not modelled	99.9	32	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
43	c2oe0B	Alignment	not modelled	99.9	31	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin-3; PDBTitle: crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
44	d2trxa	Alignment	not modelled	99.9	32	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
45	c1sjjA	Alignment	not modelled	99.9	19	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
46	c4kndA	Alignment	not modelled	99.9	33	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: thioredoxin from anaeromyxobacter dehalogenans.
47	d1thxa	Alignment	not modelled	99.9	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
48	d1m7ta	Alignment	not modelled	99.9	32	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
49	d1syra	Alignment	not modelled	99.9	31	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
50	d1r26a	Alignment	not modelled	99.9	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
51	c3apoA	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of full-length erdj5
52	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
53	c1t00A	Alignment	not modelled	99.9	30	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: the structure of thioredoxin from s. coelicolor
54	c3f8uA	Alignment	not modelled	99.9	21	PDB header: immune system/isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a3erp57; PDBTitle: tapasin/erp57 heterodimer
55	c2vz9C	Alignment	not modelled	99.9	27	PDB header: oxidoreductase Chain: C: PDB Molecule: thioredoxin h isoform 1.;

55	c2vnr2C_	Alignment	not modelled	99.9	47	PDBTitle: crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant
56	c2i1uA_	Alignment	not modelled	99.9	37	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: mycobacterium tuberculosis thioredoxin c
57	c3zzxB_	Alignment	not modelled	99.9	33	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystallographic structure of thioredoxin from litopenaeus vannamei
58	c2diyA_	Alignment	not modelled	99.9	27	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
59	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
60	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
61	d1ep7a_	Alignment	not modelled	99.9	31	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
62	d1ti3a_	Alignment	not modelled	99.9	34	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
63	c2vimA_	Alignment	not modelled	99.9	35	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: x-ray structure of fasciola hepatica thioredoxin
64	d1oaza_	Alignment	not modelled	99.9	29	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
65	c2v1vA_	Alignment	not modelled	99.9	30	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	c3wgdD_	Alignment	not modelled	99.9	32	PDB header: isomerase Chain: D: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: crystal structure of erp46 trx1
67	c2lrcA_	Alignment	not modelled	99.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: probable thioredoxin; PDBTitle: structure of thioredoxin 2 from pseudomonas aeruginosa pao1 in its2 reduced form
68	c2albA_	Alignment	not modelled	99.9	25	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
69	c2l5lA_	Alignment	not modelled	99.9	34	PDB header: transport protein Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution structure of thioredoxin from bacteroides vulgatus
70	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
71	d1xfla_	Alignment	not modelled	99.9	38	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
72	c2mcsA_	Alignment	not modelled	99.9	30	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
73	c2yoiA_	Alignment	not modelled	99.9	35	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
74	c2yj7A_	Alignment	not modelled	99.9	37	PDB header: oxidoreductase Chain: A: PDB Molecule: lpbca thioredoxin; PDBTitle: crystal structure of a hyperstable protein from the precambrian2 period
75	c5dbqA_	Alignment	not modelled	99.9	27	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of insect thioredoxin at 1.95 angstroms
76	d1f9ma_	Alignment	not modelled	99.9	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
77	c3d22A_	Alignment	not modelled	99.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h-type; PDBTitle: crystal structure of a poplar thioredoxin h mutant, ptxrh4c61s
78	c4el1A_	Alignment	not modelled	99.9	25	PDB header: chaperone Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: crystal structure of oxidized hpdi (abb'xa')
79	c3hypB_	Alignment	not modelled	99.9	31	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of bacteroides fragilis trxp_s105g mutant
80	d2ifqa1	Alignment	not modelled	99.9	30	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase

81	d1a8ya1	Alignment	not modelled	99.9	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Caesquestrin
82	c5e37A	Alignment	not modelled	99.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: ef-hand domain-containing thioredoxin; PDBTitle: redox protein from chlamydomonas reinhardtii
83	c2dizA	Alignment	not modelled	99.9	33	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
84	d1a8la2	Alignment	not modelled	99.9	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
85	c2i9hA	Alignment	not modelled	99.9	31	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin i; PDBTitle: nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)
86	d1qgva	Alignment	not modelled	99.9	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: spliceosomal protein U5-15Kd
87	d1j08a2	Alignment	not modelled	99.9	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
88	c6g61A	Alignment	not modelled	99.9	29	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin o1, mitochondrial; PDBTitle: crystal structure of thioredoxin o1 from arabidopsis thaliana in2 oxidized state
89	d1xwaa	Alignment	not modelled	99.9	30	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
90	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
91	c4i6xA	Alignment	not modelled	99.9	12	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a5; PDBTitle: crystal structure of non-catalytic domain of protein disulfide2 isomerase-related (pdir) protein
92	d2b5ea4	Alignment	not modelled	99.9	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
93	c1x5eA	Alignment	not modelled	99.9	22	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
94	c2xbqB	Alignment	not modelled	99.9	33	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
95	c5nymA	Alignment	not modelled	99.9	18	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
96	c2dj2A	Alignment	not modelled	99.9	25	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
97	d1mekA	Alignment	not modelled	99.9	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
98	c4i8bA	Alignment	not modelled	99.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from schistosoma japonicum
99	c2dm1A	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
100	c6i1cB	Alignment	not modelled	99.8	24	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin f2; PDBTitle: crystal structure of chlamydomonas reinhardtii thioredoxin f2
101	c1xbsA	Alignment	not modelled	99.8	16	PDB header: transcription, cell cycle Chain: A: PDB Molecule: dim1-like protein; PDBTitle: crystal structure of human dim2: a dim1-like protein
102	c1v98A	Alignment	not modelled	99.8	32	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure analysis of thioredoxin from thermus thermophilus
103	c3ul3A	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
104	c3t59D	Alignment	not modelled	99.8	26	PDB header: oxidoreductase Chain: D: PDB Molecule: sulfhydryl oxidase 1; PDBTitle: c76a/c455s mutant of mouse qsox1 containing an interdomain disulfide
105	c3emxB	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix
106	c3apsA	Alignment	not modelled	99.8	29	PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of trx4 domain of erdj5
						Fold: Thioredoxin fold

107	d1zmaa1	Alignment	not modelled	99.8	12	Superfamily: Thioredoxin-like Family: Thioltransferase
108	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
109	c3q6oA	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfhydryl oxidase 1; PDBTitle: oxidoreductase fragment of human qsox1
110	c2f51B	Alignment	not modelled	99.8	29	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: structure of trichomonas vaginalis thioredoxin
111	c2qc7A	Alignment	not modelled	99.8	21	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic reticulum protein erp29; PDBTitle: crystal structure of the protein-disulfide isomerase related chaperone2 erp29
112	c3qd9D	Alignment	not modelled	99.8	23	PDB header: oxidoreductase Chain: D: PDB Molecule: qsox from trypanosoma brucei (tbqsox); PDBTitle: c 72s/c353s mutant of trypanosoma brucei qsox containing an interdomain2 disulfide
113	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)
114	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
115	c3idvA	Alignment	not modelled	99.8	25	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a4; PDBTitle: crystal structure of the a0a fragment of erp72
116	c5ganD	Alignment	not modelled	99.8	12	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
117	c2l57A	Alignment	not modelled	99.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
118	c2qsiB	Alignment	not modelled	99.8	19	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 rhodopseudomonas palustris cga009
119	c3h79A	Alignment	not modelled	99.8	20	PDB header: unknown function Chain: A: PDB Molecule: thioredoxin-like protein; PDBTitle: crystal structure of trypanosoma cruzi thioredoxin-like hypothetical2 protein q4dv70
120	c5yryA	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 5'-adenylsulfate reductase 1, chloroplastic; PDBTitle: crystal structure of c-terminal redox domain of apr1 from arabidopsis2 thaliana