Phyre^2

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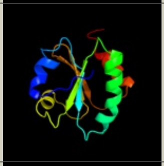
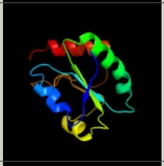
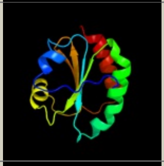
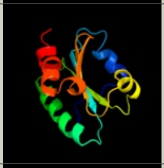
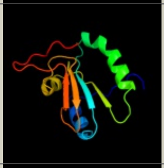
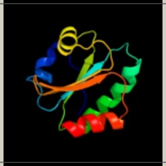
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qdnA_	Alignment		100.0	93	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
2	c2pptA_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
3	c2r5sB_	Alignment		99.9	45	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp0806; **PDBTitle:** the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
4	c3dxbE_	Alignment		99.9	28	**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
5	c3p2aB_	Alignment		99.9	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
6	c3p2aA_	Alignment		99.9	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
7	c3hz4A_	Alignment		99.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
8	c3f8uA_	Alignment		99.9	23	**PDB header:**immune system/isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3erp57; **PDBTitle:** tapasin/erp57 heterodimer
9	c2i1uA_	Alignment		99.9	30	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** mycobacterium tuberculosis thioredoxin c
10	c2diyA_	Alignment		99.9	16	**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
11	c2l5lA_	Alignment		99.9	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus

12	c2i4aA_	Alignment		99.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from the acidophile2 acetobacter aceti
13	d1f9ma_	Alignment		99.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
14	c3gnjD_	Alignment		99.9	19	**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
15	d1dbya_	Alignment		99.9	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
16	c2albA_	Alignment		99.9	24	**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
17	c2dj0A_	Alignment		99.9	20	**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
18	c3ed3A_	Alignment		99.9	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase mpd1; **PDBTitle:** crystal structure of the yeast dithiol/disulfide2 oxidoreductase mpd1p
19	d1thxa_	Alignment		99.9	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
20	d1xwaa_	Alignment		99.9	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
21	c2wz9A_	Alignment	not modelled	99.9	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
22	d2trxa_	Alignment	not modelled	99.9	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
23	d1ep7a_	Alignment	not modelled	99.9	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
24	c3hypB_	Alignment	not modelled	99.9	23	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
25	c2vlvA_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h isoform 2.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 2 in2 partially radiation-reduced state
26	c3tcoA_	Alignment	not modelled	99.9	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin (trxa-1); **PDBTitle:** crystallographic and spectroscopic characterization of sulfolobus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
27	c2vocA_	Alignment	not modelled	99.9	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** thioredoxin a active site mutants form mixed disulfide2 dimers that resemble enzyme-substrate reaction3 intermediate
28	c1w89E_	Alignment	not modelled	99.9	32	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2

29	c1t00A_	Alignment	not modelled	99.9	28	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
30	c2xbqB_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
31	c2o7kA_	Alignment	not modelled	99.9	36	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** s. aureus thioredoxin
32	d1xfla_	Alignment	not modelled	99.9	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
33	c2l6dA_	Alignment	not modelled	99.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
34	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
35	d1fb6a_	Alignment	not modelled	99.9	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
36	c2vimA_	Alignment	not modelled	99.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
37	c1x5dA_	Alignment	not modelled	99.9	20	**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
38	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
39	c2r2jA_	Alignment	not modelled	99.9	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 4; **PDBTitle:** crystal structure of human erp44
40	d1ti3a_	Alignment	not modelled	99.9	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
41	d1qgva_	Alignment	not modelled	99.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
42	d1gh2a_	Alignment	not modelled	99.9	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
43	d1m7ta_	Alignment	not modelled	99.9	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
44	c2b5eA_	Alignment	not modelled	99.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** crystal structure of yeast protein disulfide isomerase
45	c1a8yA_	Alignment	not modelled	99.9	20	**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
46	c1sjiA_	Alignment	not modelled	99.9	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calsequestrin, cardiac muscle isoform; **PDBTitle:** comparing skeletal and cardiac calsequestrin structures and2 their calcium binding: a proposed mechanism for coupled3 calcium binding and protein polymerization
47	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
48	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
49	c3d22A_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
50	c2e0qA_	Alignment	not modelled	99.9	35	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
51	c2vm2C_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin h isoform 1.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 12 crystallized using peg as precipitant
52	c2vafA_	Alignment	not modelled	99.9	20	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**calsequestrin-2; **PDBTitle:** crystal structure of human cardiac calsequestrin
53	c2yzuA_	Alignment	not modelled	99.9	37	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
54	d1nw2a_	Alignment	not modelled	99.9	35	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
55	d2ifqa1	Alignment	not modelled	99.8	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase

56	c2qc7A_	Alignment	not modelled	99.8	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmic reticulum protein erp29; **PDBTitle:** crystal structure of the protein-disulfide isomerase related chaperone2 erp29
57	d1syra_	Alignment	not modelled	99.8	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
58	c3emxB_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
59	c3apoA_	Alignment	not modelled	99.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of full-length erdj5
60	c2l57A_	Alignment	not modelled	99.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
61	d1r26a_	Alignment	not modelled	99.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
62	c2oe0B_	Alignment	not modelled	99.8	21	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin-3; **PDBTitle:** crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
63	c2qsiB_	Alignment	not modelled	99.8	20	**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
64	c1x5eA_	Alignment	not modelled	99.8	23	**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
65	d2b5ea4	Alignment	not modelled	99.8	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
66	c3h79A_	Alignment	not modelled	99.8	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein; **PDBTitle:** crystal structure of trypanosoma cruzi thioredoxin-like hypothetical2 protein q4dv70
67	d1j08a2	Alignment	not modelled	99.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
68	c2i9hA_	Alignment	not modelled	99.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin i; **PDBTitle:** nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)
69	d1oaza_	Alignment	not modelled	99.8	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
70	c2dj1A_	Alignment	not modelled	99.8	26	**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
71	c3ul3A_	Alignment	not modelled	99.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
72	c2j23A_	Alignment	not modelled	99.8	26	**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
73	d1a8la2	Alignment	not modelled	99.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
74	d1a8ya1	Alignment	not modelled	99.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin
75	c1v98A_	Alignment	not modelled	99.8	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
76	c3cxgA_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** crystal structure of plasmodium falciparum thioredoxin, pfi0790w
77	c2f51B_	Alignment	not modelled	99.8	25	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of trichomonas vaginalis thioredoxin
78	c2dj2A_	Alignment	not modelled	99.8	22	**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
79	c3idvA_	Alignment	not modelled	99.8	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** crystal structure of the a0a fragment of erp72
80	d1zmaa1	Alignment	not modelled	99.8	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
81	c2dbcA_	Alignment	not modelled	99.8	19	**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)
82	c3apqB_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
83	c1ovnA_	Alignment	not modelled	99.8	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**windbeutel; **PDBTitle:** crystal structure and functional analysis of drosophila2 wind-- a pdi-related protein
84	d1meka_	Alignment	not modelled	99.8	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
85	c3d6iB_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**monothiol glutaredoxin-3; **PDBTitle:** structure of the thioredoxin-like domain of yeast2 glutaredoxin 3
86	c2dj3A_	Alignment	not modelled	99.8	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
87	d2hfda1	Alignment	not modelled	99.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
88	c1x5cA_	Alignment	not modelled	99.8	17	**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
89	d1g7ea_	Alignment	not modelled	99.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ERP29 N domain-like
90	d1v9wa_	Alignment	not modelled	99.7	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
91	d1woua_	Alignment	not modelled	99.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
92	d2b5ea1	Alignment	not modelled	99.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
93	c3pe3D_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
94	d1fo5a_	Alignment	not modelled	99.7	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
95	c1b9xC_	Alignment	not modelled	99.7	16	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**protein (phosducin); **PDBTitle:** structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin
96	d2c0ga2	Alignment	not modelled	99.7	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ERP29 N domain-like
97	d1a8la1	Alignment	not modelled	99.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
98	c2dmmA_	Alignment	not modelled	99.7	17	**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
99	c3g9bA_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide-protein **PDBTitle:** crystal structure of reduced ost6l
100	d2fwha1	Alignment	not modelled	99.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
101	d2djja1	Alignment	not modelled	99.7	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
102	d1j08a1	Alignment	not modelled	99.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
103	c3uemA_	Alignment	not modelled	99.7	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** crystal structure of human pdi bb'a' domains
104	d2trcp_	Alignment	not modelled	99.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Phosducin
105	c1j08A_	Alignment	not modelled	99.7	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** crystal structure of glutaredoxin-like protein from2 pyrococcus horikoshii
106	c2fgxA_	Alignment	not modelled	99.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
107	c2kucA_	Alignment	not modelled	99.7	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
						Fold: Thioredoxin fold

108	d1a0rp_	Alignment	not modelled	99.7	17	**Superfamily:**Thioredoxin-like **Family:**Phosducin
109	c1zypB_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf
110	c3kp8A_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
111	c3dmlA_	Alignment	not modelled	99.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
112	d1nhoa_	Alignment	not modelled	99.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
113	c2hlsB_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
114	d1hyua4	Alignment	not modelled	99.6	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
115	c2aytB_	Alignment	not modelled	99.5	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aquifex aeolicus
116	c2hyxA_	Alignment	not modelled	99.5	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
117	c3f9uA_	Alignment	not modelled	99.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported cytochrome c biogenesis-related protein; **PDBTitle:** crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
118	d1z5ye1	Alignment	not modelled	99.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
119	c3fk8A_	Alignment	not modelled	99.4	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**disulphide isomerase; **PDBTitle:** the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
120	c1fchB_	Alignment	not modelled	99.4	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**peroxisomal targeting signal 1 receptor; **PDBTitle:** crystal structure of the pts1 complexed to the tpr region2 of human pex5