Phyre²

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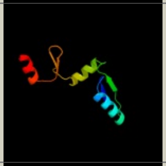
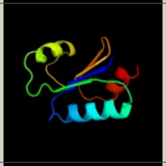
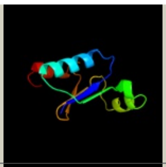
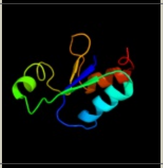
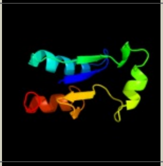
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1h75a_	Alignment		99.9	100	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
2	d1r7ha_	Alignment		99.8	41	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
3	c3ic4A_	Alignment		99.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
4	d1fova_	Alignment		99.7	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
5	c1nm3B_	Alignment		99.7	23	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**protein hi0572; **PDBTitle:** crystal structure of heamophilus influenza hybrid-prx5
6	c2khpA_	Alignment		99.7	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from brucella melitensis
7	c2klxA_	Alignment		99.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
8	d1nm3a1	Alignment		99.7	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
9	c3nznA_	Alignment		99.7	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
10	c3lgcA_	Alignment		99.7	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glutaredoxin 1; **PDBTitle:** crystal structure of glutaredoxin 1 from francisella2 tularensis
11	c2e7pC_	Alignment		99.6	17	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides

12	c3fzaA_	Alignment		99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
13	c1ykaA_	Alignment		99.6	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin ydhd; **PDBTitle:** solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
14	d1wika_	Alignment		99.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
15	d1egoa_	Alignment		99.6	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
16	c2ht9A_	Alignment		99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
17	c3h8qB_	Alignment		99.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
18	d1t1va_	Alignment		99.5	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
19	c2hzfA_	Alignment		99.5	16	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes
20	d1ktea_	Alignment		99.5	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
21	c3ipzA_	Alignment	not modelled	99.5	14	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
22	d1jhba_	Alignment	not modelled	99.5	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
23	c2wulB_	Alignment	not modelled	99.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin related protein 5; **PDBTitle:** crystal structure of the human glutaredoxin 5 with bound2 glutathione in an fes cluster
24	c3gx8A_	Alignment	not modelled	99.5	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-5, mitochondrial; **PDBTitle:** structural and biochemical characterization of yeast2 monothiol glutaredoxin grx5
25	c3l4nA_	Alignment	not modelled	99.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-6; **PDBTitle:** crystal structure of yeast monothiol glutaredoxin grx6
26	d1abaa_	Alignment	not modelled	99.5	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
27	c2jacA_	Alignment	not modelled	99.5	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** glutaredoxin grx1p c30s mutant from yeast
28	c3d5jB_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2, mitochondrial; **PDBTitle:** structure of yeast grx2-c30s mutant with glutathionyl mixed2 disulfide

29	c3c1sA_	Alignment	not modelled	99.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structure of grx1 in glutathionylated form
30	c2jadA_	Alignment	not modelled	99.4	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**yellow fluorescent protein glutaredoxin fusion **PDBTitle:** yellow fluorescent protein - glutaredoxin fusion protein
31	c2ct6A_	Alignment	not modelled	99.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
32	c2kokA_	Alignment	not modelled	99.2	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a.
33	c1u6tA_	Alignment	not modelled	99.2	15	**PDB header:**protein binding, signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** crystal structure of the human sh3 binding glutamic-rich2 protein like
34	c3f0iA_	Alignment	not modelled	99.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** arsenate reductase from vibrio cholerae.
35	d1wjka_	Alignment	not modelled	98.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
36	d1ttza_	Alignment	not modelled	98.9	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
37	d1rw1a_	Alignment	not modelled	98.9	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
38	c3gkxB_	Alignment	not modelled	98.8	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
39	d1z3ea1	Alignment	not modelled	98.8	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
40	c3rdwB_	Alignment	not modelled	98.8	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** putative arsenate reductase from yersinia pestis
41	c2fgxA_	Alignment	not modelled	98.8	26	**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.
42	d1iloa_	Alignment	not modelled	98.7	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
43	c3l78A_	Alignment	not modelled	98.7	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
44	d1z9ha2	Alignment	not modelled	98.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
45	c1z9hB_	Alignment	not modelled	98.6	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**membrane-associated prostaglandin e synthase-2; **PDBTitle:** microsomal prostaglandin e synthase type-2
46	d1hyua4	Alignment	not modelled	98.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
47	d1g7oa2	Alignment	not modelled	98.6	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
48	c1zypB_	Alignment	not modelled	98.5	14	**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
49	d1k0ma2	Alignment	not modelled	98.5	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
50	d1eema2	Alignment	not modelled	98.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
51	d1oyja2	Alignment	not modelled	98.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
52	c3lykA_	Alignment	not modelled	98.5	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**stringent starvation protein a homolog; **PDBTitle:** structure of stringent starvation protein a homolog from2 haemophilus influenzae
53	d1j9ba_	Alignment	not modelled	98.4	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
54	d1gwca2	Alignment	not modelled	98.4	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain

55	c1g7oA_	Alignment	not modelled	98.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin 2; **PDBTitle:** nmr solution structure of reduced e. coli glutaredoxin 2
56	c1k0nB_	Alignment	not modelled	98.3	13	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 1; **PDBTitle:** chloride intracellular channel 1 (clic1) complexed with glutathione
57	c3kp8A_	Alignment	not modelled	98.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
58	d1e6ba2	Alignment	not modelled	98.3	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
59	c2aheA_	Alignment	not modelled	98.3	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**chloride intracellular channel protein 4; **PDBTitle:** crystal structure of a soluble form of clic4. intercellular2 chloride ion channel
60	c1oyjC_	Alignment	not modelled	98.2	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
61	d1nhoa_	Alignment	not modelled	98.2	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
62	c3ic8D_	Alignment	not modelled	98.2	11	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized gst-like proteinprotein; **PDBTitle:** the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
63	d1ljra2	Alignment	not modelled	98.2	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
64	c1hyuA_	Alignment	not modelled	98.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf
65	c3fz4A_	Alignment	not modelled	98.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** the crystal structure of a possible arsenate reductase from2 streptococcus mutans ua159
66	c1yy7A_	Alignment	not modelled	98.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stringent starvation protein a; **PDBTitle:** crystal structure of stringent starvation protein a (sspa),2 an rna polymerase-associated transcription factor
67	d1v2aa2	Alignment	not modelled	98.2	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
68	c2l6dA_	Alignment	not modelled	98.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
69	c3kp9A_	Alignment	not modelled	98.1	14	**PDB header:**blood coagulation,oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** structure of a bacterial homolog of vitamin k epoxide reductase
70	d1a8la2	Alignment	not modelled	98.1	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
71	c2vlvA_	Alignment	not modelled	98.1	16	**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
72	d1j08a2	Alignment	not modelled	98.1	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
73	c1ljrB_	Alignment	not modelled	98.1	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** glutathione transferase (hgst t2-2) from human
74	c1gwcC_	Alignment	not modelled	98.1	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase tsi-1; **PDBTitle:** the structure of a tau class glutathione s-transferase from2 wheat, active in herbicide detoxification
75	c3rbtD_	Alignment	not modelled	98.1	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione transferase o1; **PDBTitle:** crystal structure of glutathione s-transferase omega 3 from the2 silkworm bombyx mori
76	c3fy7B_	Alignment	not modelled	98.1	23	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 3; **PDBTitle:** crystal structure of homo sapiens clic3
77	c2v6oA_	Alignment	not modelled	98.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin glutathione reductase; **PDBTitle:** structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
78	c2vo4A_	Alignment	not modelled	98.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,4-d inducible glutathione s-transferase; **PDBTitle:** glutathione transferase from glycine max
79	c2r4vA_	Alignment	not modelled	98.0	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**chloride intracellular channel protein 2; **PDBTitle:** structure of human clic2, crystal form a
80	d1pn9a2	Alignment	not modelled	98.0	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
81	d1k0da2	Alignment	not modelled	98.0	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain

82	c1eemA_	Alignment	not modelled	98.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione-s-transferase; **PDBTitle:** glutathione transferase from homo sapiens
83	c3lypA_	Alignment	not modelled	98.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stringent starvation protein a; **PDBTitle:** structure of stringent starvation protein a homolog from pseudomonas2 fluorescens
84	c2hlsB_	Alignment	not modelled	97.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
85	d1fw1a2	Alignment	not modelled	97.9	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
86	d1r26a_	Alignment	not modelled	97.9	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
87	c2aytB_	Alignment	not modelled	97.9	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aquifex aeolicus
88	c2oe0B_	Alignment	not modelled	97.9	17	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin-3; **PDBTitle:** crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
89	d1ep7a_	Alignment	not modelled	97.9	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
90	d1xfla_	Alignment	not modelled	97.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
91	c3m3mA_	Alignment	not modelled	97.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure of glutathione s-transferase from pseudomonas2 fluorescens [pf-5]
92	d1j08a1	Alignment	not modelled	97.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
93	d1k0dd2	Alignment	not modelled	97.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
94	d1axda2	Alignment	not modelled	97.8	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
95	c3m0fA_	Alignment	not modelled	97.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein gst_n; **PDBTitle:** crystal structure of glutathione s transferase in complex2 with glutathione from pseudomonas fluorescens
96	c2wz9A_	Alignment	not modelled	97.8	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
97	c3bbyA_	Alignment	not modelled	97.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized gst-like protein yfcf; **PDBTitle:** crystal structure of glutathione s-transferase (np_416804.1) from2 escherichia coli k12 at 1.85 a resolution
98	d1jlwa2	Alignment	not modelled	97.8	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
99	c1k0dB_	Alignment	not modelled	97.8	18	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ure2 protein; **PDBTitle:** ure2p in complex with glutathione
100	d1ti3a_	Alignment	not modelled	97.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
101	c1zl9A_	Alignment	not modelled	97.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 5; **PDBTitle:** crystal structure of a major nematode c.elegans specific gst (ce01613)
102	d1gnwa2	Alignment	not modelled	97.8	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
103	c2vimA_	Alignment	not modelled	97.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
104	c3nivD_	Alignment	not modelled	97.8	22	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** the crystal structure of glutathione s-transferase from legionella2 pneumophila
105	d1zmaa1	Alignment	not modelled	97.8	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
106	c2f51B_	Alignment	not modelled	97.8	20	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of trichomonas vaginalis thioredoxin
107	c1jzdA_	Alignment	not modelled	97.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
108	d1aw9a2	Alignment	not modelled	97.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain

109	d1syra_	Alignment	not modelled	97.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
110	c2diyA_	Alignment	not modelled	97.7	12	**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
111	c2xbqB_	Alignment	not modelled	97.7	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
112	c2j23A_	Alignment	not modelled	97.7	19	**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
113	d1jlva2	Alignment	not modelled	97.7	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
114	c2l57A_	Alignment	not modelled	97.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
115	d1tu7a2	Alignment	not modelled	97.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
116	d2ifqa1	Alignment	not modelled	97.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
117	c3lxzD_	Alignment	not modelled	97.7	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione s-transferase family protein; **PDBTitle:** structure of probable glutathione s-transferase(pp0183) from2 pseudomonas putida
118	c3f6fA_	Alignment	not modelled	97.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cg18548-pa (ip02196p) (ip02193p); **PDBTitle:** crystal structure of glutathione transferase dmgstd10 from2 drosophila melanogaster
119	c3cbuB_	Alignment	not modelled	97.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable gst-related protein; **PDBTitle:** crystal structure of a putative glutathione s-transferase (reut_a1011)2 from ralstonia eutropha jmp134 at 2.05 a resolution
120	d1xwaa_	Alignment	not modelled	97.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase