Phyre^2

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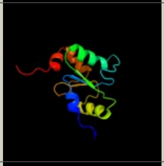
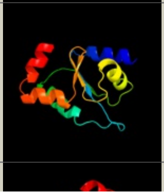
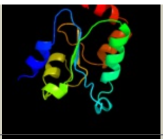
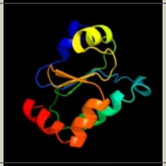
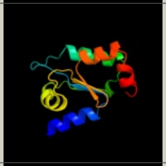
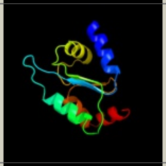
Description	P0AC69
Date	Thu Jan 5 11:17:25 GMT 2012
Unique Job ID	705c441946b6a2d8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ykaA_	Alignment		100.0	100	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin ydhd; **PDBTitle:** solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
2	c2wulB_	Alignment		100.0	36	**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
3	c3ipzA_	Alignment		100.0	38	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
4	c3gx8A_	Alignment		100.0	36	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-5, mitochondrial; **PDBTitle:** structural and biochemical characterization of yeast2 monothiol glutaredoxin grx5
5	d1wika_	Alignment		100.0	36	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
6	c2e7pC_	Alignment		100.0	26	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
7	c3fzaA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
8	c2ht9A_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
9	c2jadA_	Alignment		99.9	28	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**yellow fluorescent protein glutaredoxin fusion **PDBTitle:** yellow fluorescent protein - glutaredoxin fusion protein
10	c3h8qB_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
11	c3l4nA_	Alignment		99.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-6; **PDBTitle:** crystal structure of yeast monothiol glutaredoxin grx6
						

12	c2hzfA_	Alignment		99.9	21	**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
13	d1jhba_	Alignment		99.9	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
14	d1ktea_	Alignment		99.9	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
15	c3c1sA_	Alignment		99.9	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structure of grx1 in glutathionylated form
16	c2jacA_	Alignment		99.9	32	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** glutaredoxin grx1p c30s mutant from yeast
17	c3d5jB_	Alignment		99.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2, mitochondrial; **PDBTitle:** structure of yeast grx2-c30s mutant with glutathionyl mixed2 disulfide
18	c2khpA_	Alignment		99.9	32	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from brucella melitensis
19	c2klxA_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
20	d1fova_	Alignment		99.9	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
21	d1t1va_	Alignment	not modelled	99.8	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
22	c3lgcA_	Alignment	not modelled	99.8	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glutaredoxin 1; **PDBTitle:** crystal structure of glutaredoxin 1 from francisella2 tularensis
23	c2ct6A_	Alignment	not modelled	99.8	20	**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
24	c1nm3B_	Alignment	not modelled	99.8	25	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**protein hi0572; **PDBTitle:** crystal structure of heamophilus influenza hybrid-prx5
25	c1u6tA_	Alignment	not modelled	99.8	20	**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
26	d1nm3a1	Alignment	not modelled	99.8	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
27	d1abaa_	Alignment	not modelled	99.7	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
28	d1egoa_	Alignment	not modelled	99.7	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
						PDB header:oxidoreductase

29	c3ic4A_	Alignment	not modelled	99.6	20	**Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
30	c3nznA_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
31	d1r7ha_	Alignment	not modelled	99.6	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
32	d1h75a_	Alignment	not modelled	99.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
33	c2v6oA_	Alignment	not modelled	99.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin glutathione reductase; **PDBTitle:** structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
34	d1hyua4	Alignment	not modelled	98.5	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
35	d1oyja2	Alignment	not modelled	98.4	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
36	d1wjka_	Alignment	not modelled	98.4	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
37	c1zypB_	Alignment	not modelled	98.4	24	**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
38	d1g7oa2	Alignment	not modelled	98.3	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
39	d1k0ma2	Alignment	not modelled	98.2	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
40	d1gwca2	Alignment	not modelled	98.2	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
41	d1eema2	Alignment	not modelled	98.1	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
42	c1k0nB_	Alignment	not modelled	98.1	18	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 1; **PDBTitle:** chloride intracellular channel 1 (clic1) complexed with glutathione
43	c3ic8D_	Alignment	not modelled	98.0	14	**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
44	c1g7oA_	Alignment	not modelled	98.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin 2; **PDBTitle:** nmr solution structure of reduced e. coli glutaredoxin 2
45	c3lykA_	Alignment	not modelled	98.0	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**stringent starvation protein a homolog; **PDBTitle:** structure of stringent starvation protein a homolog from2 haemophilus influenzae
46	c1hyuA_	Alignment	not modelled	98.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf
47	c2aheA_	Alignment	not modelled	98.0	19	**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
48	c1oyjC_	Alignment	not modelled	98.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
49	c1z9hB_	Alignment	not modelled	97.8	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**membrane-associated prostaglandin e synthase-2; **PDBTitle:** microsomal prostaglandin e synthase type-2
50	c2fgxA_	Alignment	not modelled	97.8	17	**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.
51	c3fy7B_	Alignment	not modelled	97.8	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 3; **PDBTitle:** crystal structure of homo sapiens clic3
52	d1e6ba2	Alignment	not modelled	97.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
53	c2vo4A_	Alignment	not modelled	97.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,4-d inducible glutathione s-transferase; **PDBTitle:** glutathione transferase from glycine max
54	c1gwcC_	Alignment	not modelled	97.8	18	**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
55	c2r4vA_	Alignment	not modelled	97.7	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**chloride intracellular channel protein 2; **PDBTitle:** structure of human clic2, crystal form a

56	c1yy7A_	Alignment	not modelled	97.6	20	**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
57	d1pn9a2	Alignment	not modelled	97.6	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
58	d1fw1a2	Alignment	not modelled	97.6	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
59	d1z9ha2	Alignment	not modelled	97.6	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
60	c3kp8A_	Alignment	not modelled	97.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
61	d1v2aa2	Alignment	not modelled	97.5	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
62	d1aw9a2	Alignment	not modelled	97.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
63	d1axda2	Alignment	not modelled	97.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
64	d1zmaa1	Alignment	not modelled	97.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
65	c3kp9A_	Alignment	not modelled	97.5	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
66	d1ljra2	Alignment	not modelled	97.4	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
67	d1rk4a2	Alignment	not modelled	97.4	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
68	d1k0da2	Alignment	not modelled	97.4	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
69	c1xbsA_	Alignment	not modelled	97.4	16	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
70	d1nhoa_	Alignment	not modelled	97.4	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
71	d1ttza_	Alignment	not modelled	97.3	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
72	d1gnwa2	Alignment	not modelled	97.3	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
73	c1k0dB_	Alignment	not modelled	97.3	14	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ure2 protein; **PDBTitle:** ure2p in complex with glutathione
74	c3l78A_	Alignment	not modelled	97.3	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
75	d1j08a1	Alignment	not modelled	97.3	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
76	c3bbyA_	Alignment	not modelled	97.3	23	**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
77	c1eemA_	Alignment	not modelled	97.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione-s-transferase; **PDBTitle:** glutathione transferase from homo sapiens
78	d1z3ea1	Alignment	not modelled	97.2	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
79	d1j08a2	Alignment	not modelled	97.1	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
80	c1byeA_	Alignment	not modelled	97.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (glutathione s-transferase); **PDBTitle:** glutathione s-transferase i from mais in complex with2 atrazine glutathione conjugate
81	d1k0dd2	Alignment	not modelled	97.1	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
82	c2l6dA_	Alignment	not modelled	97.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form

83	d1jlva2	Alignment	not modelled	97.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
84	c2l57A_	Alignment	not modelled	97.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
85	c3rbtD_	Alignment	not modelled	97.1	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione transferase o1; **PDBTitle:** crystal structure of glutathione s-transferase omega 3 from the2 silkworm bombyx mori
86	c3lypA_	Alignment	not modelled	97.1	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stringent starvation protein a; **PDBTitle:** structure of stringent starvation protein a homolog from pseudomonas2 fluorescens
87	c3nivD_	Alignment	not modelled	97.1	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** the crystal structure of glutathione s-transferase from legionella2 pneumophila
88	c1r5aA_	Alignment	not modelled	97.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase; **PDBTitle:** glutathione s-transferase
89	c3gkxB_	Alignment	not modelled	97.0	17	**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
90	d1iloa_	Alignment	not modelled	97.0	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
91	d1jlwa2	Alignment	not modelled	97.0	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
92	c3fz4A_	Alignment	not modelled	97.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** the crystal structure of a possible arsenate reductase from2 streptococcus mutans ua159
93	c1zl9A_	Alignment	not modelled	97.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 5; **PDBTitle:** crystal structure of a major nematode c.elegans specific gst (ce01613)
94	d1woua_	Alignment	not modelled	96.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
95	c2hlsB_	Alignment	not modelled	96.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
96	c2jl4A_	Alignment	not modelled	96.9	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**maleylpyruvate isomerase; **PDBTitle:** holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
97	d1r26a_	Alignment	not modelled	96.9	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
98	c2vm2C_	Alignment	not modelled	96.9	19	**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
99	d1a8la2	Alignment	not modelled	96.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
100	c3lxzD_	Alignment	not modelled	96.8	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione s-transferase family protein; **PDBTitle:** structure of probable glutathione s-transferase(pp0183) from2 pseudomonas putida
101	d2ifqa1	Alignment	not modelled	96.8	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
102	c2kokA_	Alignment	not modelled	96.8	16	**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.
103	d1a8la1	Alignment	not modelled	96.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
104	c1ljrB_	Alignment	not modelled	96.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** glutathione transferase (hgst t2-2) from human
105	d1r5aa2	Alignment	not modelled	96.8	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
106	d1fo5a_	Alignment	not modelled	96.8	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
107	c2kucA_	Alignment	not modelled	96.8	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
108	c2vimA_	Alignment	not modelled	96.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
109	d2trcp_	Alignment	not modelled	96.7	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like

						Family: Phosducin
110	c2c3nB_	Alignment	not modelled	96.7	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase theta 1; **PDBTitle:** human glutathione-s-transferase t1-1, apo form
111	c2vlvA_	Alignment	not modelled	96.7	12	**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
112	d1v9wa_	Alignment	not modelled	96.7	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
113	c2cz2A_	Alignment	not modelled	96.7	22	**PDB header:**isomerase, transferase **Chain:** A: **PDB Molecule:**maleylacetoacetate isomerase; **PDBTitle:** crystal structure of glutathione transferase zeta 1-12 (maleylacetoacetate isomerase) from mus musculus (form-1 crystal)
114	d1ep7a_	Alignment	not modelled	96.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
115	c1v2aD_	Alignment	not modelled	96.7	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione transferase gst1-6; **PDBTitle:** glutathione s-transferase 1-6 from anopheles dirus species b
116	c1gnwA_	Alignment	not modelled	96.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structure of glutathione s-transferase
117	c1aw9A_	Alignment	not modelled	96.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase iii; **PDBTitle:** structure of glutathione s-transferase iii in apo form
118	c3f0iA_	Alignment	not modelled	96.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** arsenate reductase from vibrio cholerae.
119	c2j23A_	Alignment	not modelled	96.6	14	**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
120	d1syra_	Alignment	not modelled	96.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase