Phyre2

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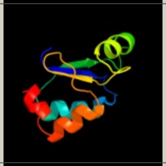
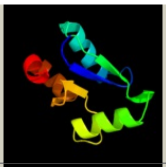
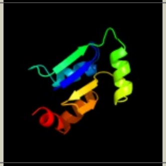
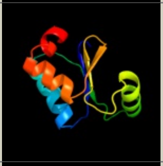
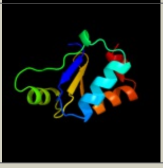
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2khpA_	Alignment		99.9	58	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from brucella melitensis
2	d1fova_	Alignment		99.9	99	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
3	c2klxA_	Alignment		99.9	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
4	c3qmxA_	Alignment		99.9	61	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin a; **PDBTitle:** x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
5	c3fzaA_	Alignment		99.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
6	c2e7pC_	Alignment		99.9	37	**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	c2ht9A_	Alignment		99.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
8	c3h8qB_	Alignment		99.9	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
9	d1wika_	Alignment		99.9	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
10	c1ykaA_	Alignment		99.9	32	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin ydhd; **PDBTitle:** solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
11	c2hzfA_	Alignment		99.9	30	**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

12	d1t1va_	Alignment		99.9	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
13	d1jhba_	Alignment		99.9	37	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
14	c2jadA_	Alignment		99.9	35	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**yellow fluorescent protein glutaredoxin fusion **PDBTitle:** yellow fluorescent protein - glutaredoxin fusion protein
15	d1ktea_	Alignment		99.9	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
16	c3l4nA_	Alignment		99.9	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-6; **PDBTitle:** crystal structure of yeast monothiol glutaredoxin grx6
17	c3ipzA_	Alignment		99.9	26	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
18	c3d5jB_	Alignment		99.9	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2, mitochondrial; **PDBTitle:** structure of yeast grx2-c30s mutant with glutathionyl mixed2 disulfide
19	c3c1sA_	Alignment		99.9	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structure of grx1 in glutathionylated form
20	c2jacA_	Alignment		99.9	34	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** glutaredoxin grx1p c30s mutant from yeast
21	c2wulB_	Alignment	not modelled	99.9	26	**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
22	c3gx8A_	Alignment	not modelled	99.9	29	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-5, mitochondrial; **PDBTitle:** structural and biochemical characterization of yeast2 monothiol glutaredoxin grx5
23	c3lgcA_	Alignment	not modelled	99.8	43	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glutaredoxin 1; **PDBTitle:** crystal structure of glutaredoxin 1 from francisella2 tularensis
24	c1nm3B_	Alignment	not modelled	99.8	47	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**protein hi0572; **PDBTitle:** crystal structure of heamophilus influenza hybrid-prx5
25	d1nm3a1	Alignment	not modelled	99.8	47	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
26	c3ic4A_	Alignment	not modelled	99.8	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
27	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
28	d1egoa_	Alignment	not modelled	99.8	39	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase

29	d1h75a_	Alignment	not modelled	99.7	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
30	c1u6tA_	Alignment	not modelled	99.7	23	**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
31	d1abaa_	Alignment	not modelled	99.7	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
32	d1r7ha_	Alignment	not modelled	99.7	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
33	c3nznA_	Alignment	not modelled	99.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
34	d1wjka_	Alignment	not modelled	98.9	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
35	c2v6oA_	Alignment	not modelled	98.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin glutathione reductase; **PDBTitle:** structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
36	d1oyja2	Alignment	not modelled	98.8	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
37	d1g7oa2	Alignment	not modelled	98.8	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
38	d1k0ma2	Alignment	not modelled	98.7	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
39	d1hyua4	Alignment	not modelled	98.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
40	c3ic8D_	Alignment	not modelled	98.7	16	**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
41	c3lykA_	Alignment	not modelled	98.7	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
42	d1gwca2	Alignment	not modelled	98.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
43	c2fgxA_	Alignment	not modelled	98.6	24	**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.
44	d1eema2	Alignment	not modelled	98.6	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
45	c1zypB_	Alignment	not modelled	98.6	19	**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
46	c1k0nB_	Alignment	not modelled	98.6	21	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 1; **PDBTitle:** chloride intracellular channel 1 (clic1) complexed with glutathione
47	d1e6ba2	Alignment	not modelled	98.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
48	c1z9hB_	Alignment	not modelled	98.6	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**membrane-associated prostaglandin e synthase-2; **PDBTitle:** microsomal prostaglandin e synthase type-2
49	d1k0da2	Alignment	not modelled	98.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
50	c1g7oA_	Alignment	not modelled	98.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin 2; **PDBTitle:** nmr solution structure of reduced e. coli glutaredoxin 2
51	d1ttza_	Alignment	not modelled	98.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
52	d1v2aa2	Alignment	not modelled	98.5	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
53	c2aheA_	Alignment	not modelled	98.5	21	**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
54	d1ljra2	Alignment	not modelled	98.5	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
55	c1oyjC_	Alignment	not modelled	98.5	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase;

55	c1oyjC_	Alignment	not modelled	98.5	9	**PDBTitle:** crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
56	c2vo4A_	Alignment	not modelled	98.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,4-d inducible glutathione s-transferase; **PDBTitle:** glutathione transferase from glycine max
57	d1pn9a2	Alignment	not modelled	98.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
58	d1z3ea1	Alignment	not modelled	98.5	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
59	c2kokA_	Alignment	not modelled	98.4	21	**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.
60	d1z9ha2	Alignment	not modelled	98.4	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
61	d1k0dd2	Alignment	not modelled	98.4	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
62	c1k0dB_	Alignment	not modelled	98.4	13	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ure2 protein; **PDBTitle:** ure2p in complex with glutathione
63	c3l78A_	Alignment	not modelled	98.4	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
64	c3kp9A_	Alignment	not modelled	98.4	23	**PDB header:**blood coagulation,oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** structure of a bacterial homolog of vitamin k epoxide reductase
65	d1fw1a2	Alignment	not modelled	98.4	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
66	c1yy7A_	Alignment	not modelled	98.4	15	**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	c1gwcC_	Alignment	not modelled	98.3	12	**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
68	c3qagA_	Alignment	not modelled	98.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase omega-2; **PDBTitle:** human glutathione transferase o2 with glutathione -new crystal form
69	d1axda2	Alignment	not modelled	98.3	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
70	c1zl9A_	Alignment	not modelled	98.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 5; **PDBTitle:** crystal structure of a major nematode c.elegans specific gst (ce01613)
71	c3fy7B_	Alignment	not modelled	98.3	25	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 3; **PDBTitle:** crystal structure of homo sapiens clic3
72	d1aw9a2	Alignment	not modelled	98.3	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
73	d1gnwa2	Alignment	not modelled	98.3	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
74	d1nhoa_	Alignment	not modelled	98.3	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
75	c1ljrB_	Alignment	not modelled	98.2	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** glutathione transferase (hgst t2-2) from human
76	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
77	d1jlva2	Alignment	not modelled	98.2	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
78	d1iloa_	Alignment	not modelled	98.2	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
79	d1jlwa2	Alignment	not modelled	98.2	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
80	c2r4vA_	Alignment	not modelled	98.2	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**chloride intracellular channel protein 2; **PDBTitle:** structure of human clic2, crystal form a
81	c2jl4A_	Alignment	not modelled	98.2	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**maleylpyruvate isomerase; **PDBTitle:** holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
						PDB header:transcription

82	c3lypA_	Alignment	not modelled	98.2	19	**Chain:** A: **PDB Molecule:**stringent starvation protein a; **PDBTitle:** structure of stringent starvation protein a homolog from pseudomonas2 fluorescens
83	c3kp8A_	Alignment	not modelled	98.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
84	c3gkxB_	Alignment	not modelled	98.1	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
85	c1hyuA_	Alignment	not modelled	98.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf
86	c2cz2A_	Alignment	not modelled	98.1	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)
87	d1r5aa2	Alignment	not modelled	98.1	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
88	c3rbtD_	Alignment	not modelled	98.1	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione transferase o1; **PDBTitle:** crystal structure of glutathione s-transferase omega 3 from the2 silkworm bombyx mori
89	c1r5aA_	Alignment	not modelled	98.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase; **PDBTitle:** glutathione s-transferase
90	c1v2aD_	Alignment	not modelled	98.0	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione transferase gst1-6; **PDBTitle:** glutathione s-transferase 1-6 from anopheles dirus species b
91	c1eemA_	Alignment	not modelled	98.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione-s-transferase; **PDBTitle:** glutathione transferase from homo sapiens
92	c3lxzD_	Alignment	not modelled	98.0	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione s-transferase family protein; **PDBTitle:** structure of probable glutathione s-transferase(pp0183) from2 pseudomonas putida
93	c2c3nB_	Alignment	not modelled	98.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase theta 1; **PDBTitle:** human glutathione-s-transferase t1-1, apo form
94	c1gnwA_	Alignment	not modelled	98.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structure of glutathione s-transferase
95	c2imiA_	Alignment	not modelled	98.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**epsilon-class glutathione s-transferase; **PDBTitle:** structures of an insect epsilon-class glutathione s-2 transferase from the malaria vector anopheles gambiae:3 evidence for high ddt-detoxifying activity
96	c3bbyA_	Alignment	not modelled	98.0	25	**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
97	c3nivD_	Alignment	not modelled	98.0	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** the crystal structure of glutathione s-transferase from legionella2 pneumophila
98	d1rk4a2	Alignment	not modelled	98.0	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
99	d1rw1a_	Alignment	not modelled	98.0	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
100	d1pd212	Alignment	not modelled	98.0	5	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
101	c1byeA_	Alignment	not modelled	97.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (glutathione s-transferase); **PDBTitle:** glutathione s-transferase i from mais in complex with2 atrazine glutathione conjugate
102	c3f6fA_	Alignment	not modelled	97.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cg18548-pa (ip02196p) (ip02193p); **PDBTitle:** crystal structure of glutathione transferase dmgstd10 from2 drosophila melanogaster
103	c3f0iA_	Alignment	not modelled	97.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** arsenate reductase from vibrio cholerae.
104	c1jlvA_	Alignment	not modelled	97.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase gst1-3; **PDBTitle:** anopheles dirus species b glutathione s-transferases 1-3
105	c3rdwB_	Alignment	not modelled	97.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** putative arsenate reductase from yersinia pestis
106	c1oktA_	Alignment	not modelled	97.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** x-ray structure of glutathione s-transferase from the2 malarial parasite plasmodium falciparum
107	c2on7A_	Alignment	not modelled	97.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**na glutathione s-transferase 1; **PDBTitle:** structure of nagst-1
108	c3ergA_	Alignment	not modelled	97.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 2; **PDBTitle:** crystal structure of gtt2 from saccharomyces cerevisiae

						in complex2 with glutathione sulfnate
109	d1zmaa1	Alignment	not modelled	97.9	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
110	c1vf1A_	Alignment	not modelled	97.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 3; **PDBTitle:** cgsta1-1 in complex with glutathione
111	c3m3mA_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure of glutathione s-transferase from pseudomonas2 fluorescens [pf-5]
112	c3cbuB_	Alignment	not modelled	97.8	15	**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
113	c2l6dA_	Alignment	not modelled	97.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
114	d1j9ba_	Alignment	not modelled	97.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
115	c3m0fA_	Alignment	not modelled	97.8	13	**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
116	c1aw9A_	Alignment	not modelled	97.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase iii; **PDBTitle:** structure of glutathione s-transferase iii in apo form
117	c2on5E_	Alignment	not modelled	97.8	7	**PDB header:**transferase **Chain:** E: **PDB Molecule:**na glutathione s-transferase 2; **PDBTitle:** structure of nagst-2
118	c2ws2B_	Alignment	not modelled	97.8	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** the 2 angstrom structure of a nu-class gst from haemonchus contortus
119	c1iyiA_	Alignment	not modelled	97.8	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hematopoietic prostagladin d synthase; **PDBTitle:** crystal structure of hematopoietic prostaglandin d synthase
120	c2hnlB_	Alignment	not modelled	97.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase 1; **PDBTitle:** structure of the prostaglandin d synthase from the parasitic nematode2 onchocerca volvulus