

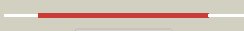





















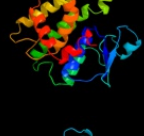


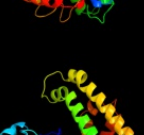
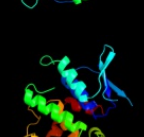

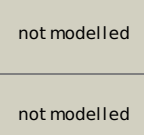


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1g7oA_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin 2; PDBTitle: nmr solution structure of reduced e. coli glutaredoxin 2
2	c3c8eB_	 Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: yghu, glutathione s-transferase homologue; PDBTitle: crystal structure analysis of yghu from e. coli
3	c1ljrB_	 Alignment		100.0	12	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: glutathione transferase (hgst t2-2) from human
4	c3m0fA_	 Alignment		100.0	14	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
5	c3lykA_	 Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: stringent starvation protein a homolog; PDBTitle: structure of stringent starvation protein a homolog from2 haemophilus influenzae
6	c1oyjC_	 Alignment		100.0	12	PDB header: transferase Chain: C: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
7	c2hnlB_	 Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase 1; PDBTitle: structure of the prostaglandin d synthase from the parasitic nematode2 onchocerca volvulus
8	c3m3mA_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of glutathione s-transferase from pseudomonas2 fluorescens [pf-5]
9	c3ergA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase 2; PDBTitle: crystal structure of gtt2 from saccharomyces cerevisiae in complex2 with glutathione sulfinate
10	c3ic8D_	 Alignment		100.0	13	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
11	c3nivD_	 Alignment		100.0	18	PDB header: isomerase Chain: D: PDB Molecule: glutathione s-transferase; PDBTitle: the crystal structure of glutathione s-transferase from legionella2 pneumophila

12	c1yq1A_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: structural genomics of caenorhabditis elegans: glutathione2 s-transferase
13	c3lxzD_	Alignment		100.0	14	PDB header: transferase Chain: D: PDB Molecule: glutathione s-transferase family protein; PDBTitle: structure of probable glutathione s-transferase(pp0183) from2 pseudomonas putida
14	c2jl4A_	Alignment		100.0	12	PDB header: isomerase Chain: A: PDB Molecule: maleylpyruvate isomerase; PDBTitle: holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
15	c1gwcC_	Alignment		100.0	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
16	c1eemA_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: glutathione-s-transferase; PDBTitle: glutathione transferase from homo sapiens
17	c2pmtA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: glutathione transferase; PDBTitle: glutathione transferase from proteus mirabilis
18	c1zl9A_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase 5; PDBTitle: crystal structure of a major nematode c.elegans specific gst (ce01613)
19	c3bbyA_	Alignment		100.0	20	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
20	c3uarA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of glutathione transferase (target efi-501774) from2 methylococcus capsulatus str. bath with gsh bound
21	c1n2aB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of a bacterial glutathione transferase2 from escherichia coli with glutathione sulfonate in the3 active site
22	c1tu8A_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase 2; PDBTitle: structure of onchoverca volvulus pi-class glutathione s-2 transferase with its kompetitive inhibitor s-hexyl-gsh
23	c1m0uB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: gst2 gene product; PDBTitle: crystal structure of the drosophila glutathione s-2 transferase-2 in complex with glutathione
24	c1f2eB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: structure of sphingomonad, glutathione s-transferase complexed with2 glutathione
25	c2vo4A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: 2,4-d inducible glutathione s-transferase; PDBTitle: glutathione transferase from glycine max
26	c1yy7A_	Alignment	not modelled	100.0	17	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
27	c2x64A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: glutathione-s-transferase; PDBTitle: glutathione-s-transferase from xylella fastidiosa
28	c2gsqA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: glutathione s-transferase from squid digestive gland complexed with s-2 (3-iodobenzyl)glutathione
						PDB header: transferase

29	c3rbtD_	Alignment	not modelled	100.0	18	Chain: D: PDB Molecule: glutathione transferase o1; PDBTitle: crystal structure of glutathione s-transferase omega 3 from the2 silkworm bombyx mori
30	c1k3yB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase a1; PDBTitle: crystal structure analysis of human glutathione s-transferase with s-2 hexyl glutatione and glycerol at 1.3 angstrom
31	c2ws2B_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: the 2 angstrom structure of a nu-class gst from haemonchus contortus
32	c2on5E_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: E: PDB Molecule: na glutathione s-transferase 2; PDBTitle: structure of nagst-2
33	c2c3nB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase theta 1; PDBTitle: human glutathione-s-transferase t1-1, apo form
34	c1z9hB_	Alignment	not modelled	100.0	14	PDB header: isomerase Chain: B: PDB Molecule: membrane-associated prostaglandin e synthase-2; PDBTitle: microsomal prostaglandin e synthase type-2
35	c2on7A_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: na glutathione s-transferase 1; PDBTitle: structure of nagst-1
36	c2aheA_	Alignment	not modelled	100.0	14	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
37	c1iyiA_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: A: PDB Molecule: hematopoietic prostagladin d synthase; PDBTitle: crystal structure of hematopoietic prostaglandin d synthase
38	c1oktA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: x-ray structure of glutathione s-transferase from the2 malarial parasite plasmodium falciparum
39	c1r5aA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: glutathione transferase; PDBTitle: glutathione s-transferase
40	c2gdrA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of a bacterial glutathione transferase
41	c1jlvA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: glutathione transferase gst1-3; PDBTitle: anopheles dirus species b glutathione s-transferases 1-3
42	c1k0dB_	Alignment	not modelled	100.0	12	PDB header: gene regulation Chain: B: PDB Molecule: ure2 protein; PDBTitle: ure2p in complex with glutathione
43	c1vf1A_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase 3; PDBTitle: cgsta1-1 in complex with glutathione
44	c1k0nB_	Alignment	not modelled	100.0	17	PDB header: metal transport Chain: B: PDB Molecule: chloride intracellular channel protein 1; PDBTitle: chloride intracellular channel 1 (clic1) complexed with glutathione
45	c3lypA_	Alignment	not modelled	100.0	17	PDB header: transcription Chain: A: PDB Molecule: stringent starvation protein a; PDBTitle: structure of stringent starvation protein a homolog from pseudomonas2 fluorescens
46	c2ntoA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: structure of the glutathione transferase from ochrobactrum anthropi in2 complex with glutathione
47	c2r4vA_	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A: PDB Molecule: chloride intracellular channel protein 2; PDBTitle: structure of human clic2, crystal form a
48	c3f6fA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: cg18548-pa (ip02196p) (ip02193p); PDBTitle: crystal structure of glutathione transferase dmgstd10 from2 drosophila melanogaster
49	c1gnwA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: structure of glutathione s-transferase
50	c3lg6B_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: putative glutathione transferase; PDBTitle: crystal structure of putative glutathione transferase from2 coccidioides immitis
51	c1byeA_	Alignment	not modelled	99.9	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
52	c1ua5A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: non-fusion gst from s. japonicum in complex with glutathione
53	c2imiA_	Alignment	not modelled	99.9	13	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
54	c1v2aD_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: D: PDB Molecule: glutathione transferase gst1-6; PDBTitle: glutathione s-transferase 1-6 from anopheles dirus species b
						PDB header: transport protein

55	c3fy7B_	Alignment	not modelled	99.9	17	Chain: B: PDB Molecule: chloride intracellular channel protein 3; PDBTitle: crystal structure of homo sapiens clic3
56	c2wb9A_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: glutathione transferase sigma class; PDBTitle: fasciola hepatica sigma class gst
57	c3h1nA_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: probable glutathione s-transferase; PDBTitle: crystal structure of probable glutathione s-transferase from2 bordetella bronchiseptica rb50
58	c2cz2A_	Alignment	not modelled	99.9	18	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)
59	c3gx0A_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: gst-like protein yfcg; PDBTitle: crystal structure of gsh-dependent disulfide bond2 oxidoreductase
60	c1gumA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: protein (glutathione transferase a4-4); PDBTitle: human glutathione transferase a4-4 without ligands
61	c3cbuB_	Alignment	not modelled	99.9	17	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
62	c1b48A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: protein (glutathione s-transferase); PDBTitle: crystal structure of mgsta4-4 in complex with gsh conjugate2 of 4-hydroxynonenal in one subunit and gsh in the other:3 evidence of signaling across dimer interface in mgsta4-4
63	c1c72A_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: protein (glutathione s-transferase); PDBTitle: tyr115, gln165 and trp209 contribute to the 1,2-epoxy-3-(p-2 nitrophenoxy)propane conjugating activities of glutathione3 s-transferase cgstm1-1
64	c3csiA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase p; PDBTitle: crystal structure of the glutathione transferase pi allelic variant*c,2 i104v/a113v, in complex with the chlorambucil-glutathione conjugate
65	c1gtuB_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: ligand-free human glutathione s-transferase m1a-1a
66	c3ppuB_	Alignment	not modelled	99.9	23	PDB header: transferase Chain: B: PDB Molecule: glutathione-s-transferase; PDBTitle: crystal structure of the glutathione-s-transferase xi from2 phanerochaete chrysosporium
67	c2yv7A_	Alignment	not modelled	99.9	16	PDB header: metal transport Chain: A: PDB Molecule: cg10997-pa; PDBTitle: crystal structure of the clic homolog from drosophila2 melanogaster
68	c3m8nA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: possible glutathione s-transferase; PDBTitle: crystal structure of a possible glutathione s-transferase from2 rhodopseudomonas palustris
69	c2fheA_	Alignment	not modelled	99.9	11	PDB header: transferase/substrate Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: fasciola hepatica glutathione s-transferase isoform 1 in complex with2 glutathione
70	c1nhya_	Alignment	not modelled	99.9	14	PDB header: translation Chain: A: PDB Molecule: elongation factor 1-gamma 1; PDBTitle: crystal structure of the gst-like domain of elongation2 factor 1-gamma from saccharomyces cerevisiae.
71	c1j1wA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: glutathione transferase gst1-4; PDBTitle: anopheles dirus species b glutathione s-transferases 1-4
72	c1aw9A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase iii; PDBTitle: structure of glutathione s-transferase iii in apo form
73	c2yv9B_	Alignment	not modelled	99.9	18	PDB header: metal transport Chain: B: PDB Molecule: chloride intracellular channel exc-4; PDBTitle: crystal structure of the clic homologue exc-4 from c.2 elegans
74	c1tw9C_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: C: PDB Molecule: glutathione s-transferase 2; PDBTitle: glutathione transferase-2, apo form, from the nematode heligmosomoides2 polygyrus
75	c3isoB_	Alignment	not modelled	99.9	9	PDB header: transferase Chain: B: PDB Molecule: putative glutathione transferase; PDBTitle: crystal structure of 26 kda gst of clonorchis sinensis in p32212 symmetry
76	c3m1gC_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: C: PDB Molecule: putative glutathione s-transferase; PDBTitle: the structure of a putative glutathione s-transferase from2 corynebacterium glutamicum
77	c3touB_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase protein; PDBTitle: crystal structure of glutathione transferase (target efi-501058) from2 ralstonia solanacearum gmi1000 with gsh bound
78	c2c8uA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase 28 kda; PDBTitle: structure of r21q mutant of sh28gst
79	c3lszA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of glutathione s-transferase from2 rhodobacter sphaeroides
80	c3lq7B_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of glutathione s-transferase from2

						agrobacterium tumefaciens str. c58
81	c1b8xA	Alignment	not modelled	99.9	13	PDB header: signal protein Chain: A: PDB Molecule: protein (aml-1b); PDBTitle: glutathione s-transferase fused with the nuclear matrix targeting2 signal of the transcription factor aml-1
82	c3ay8A	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: glutathione s-transferase unclassified 2 from bombyx mori
83	c1bg5A	Alignment	not modelled	99.9	14	PDB header: ankyrin binding Chain: A: PDB Molecule: fusion protein of alpha-na,k-atpase with PDBTitle: crystal structure of the ankyrin binding domain of alpha-na,2 k-atpase as a fusion protein with glutathione s-transferase
84	c2fnoB	Alignment	not modelled	99.9	11	PDB header: transferase Chain: B: PDB Molecule: agr_pat_752p; PDBTitle: crystal structure of a glutathione s-transferase (atu5508) from2 agrobacterium tumefaciens str. c58 at 2.00 a resolution
85	c1e6bA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of a zeta class glutathione s-transferase2 from arabidopsis thaliana
86	d1g7oa2	Alignment	not modelled	99.8	100	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
87	d1v2aa2	Alignment	not modelled	99.8	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
88	c2uz8A	Alignment	not modelled	99.8	17	PDB header: rna-binding protein Chain: A: PDB Molecule: eukaryotic translation elongation factor 1 PDBTitle: the crystal structure of p18, human translation elongation2 factor 1 epsilon 1
89	d1g7oa1	Alignment	not modelled	99.8	100	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
90	d1eema2	Alignment	not modelled	99.8	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
91	d1pn9a2	Alignment	not modelled	99.7	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
92	d1jlwa2	Alignment	not modelled	99.7	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
93	d1e6ba2	Alignment	not modelled	99.7	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
94	d1gwca2	Alignment	not modelled	99.7	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
95	d1k0ma2	Alignment	not modelled	99.7	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
96	d1oyja2	Alignment	not modelled	99.7	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
97	d1k0da2	Alignment	not modelled	99.7	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
98	d1ljra2	Alignment	not modelled	99.7	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
99	d1gnwa2	Alignment	not modelled	99.7	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
100	d1jlva2	Alignment	not modelled	99.7	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
101	d1z9ha2	Alignment	not modelled	99.7	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
102	d1k0dd2	Alignment	not modelled	99.7	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
103	d1axda2	Alignment	not modelled	99.7	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
104	d1aw9a2	Alignment	not modelled	99.7	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
105	d1fw1a2	Alignment	not modelled	99.7	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
106	d1n2aa2	Alignment	not modelled	99.7	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
107	d1r5aa2	Alignment	not modelled	99.6	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain

108	d1rk4a2	Alignment	not modelled	99.6	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
109	d1f2ea2	Alignment	not modelled	99.6	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
110	d1pmta2	Alignment	not modelled	99.6	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
111	d1tu7a2	Alignment	not modelled	99.6	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
112	d2gsra2	Alignment	not modelled	99.6	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
113	d1tw9a2	Alignment	not modelled	99.6	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
114	d1m0ua2	Alignment	not modelled	99.6	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
115	d2cvda2	Alignment	not modelled	99.5	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
116	d2gsqa2	Alignment	not modelled	99.5	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
117	d1pd212	Alignment	not modelled	99.5	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
118	d1gula2	Alignment	not modelled	99.5	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
119	d1okta2	Alignment	not modelled	99.5	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
120	d1glqa2	Alignment	not modelled	99.5	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain