Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P77544
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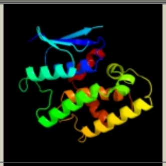
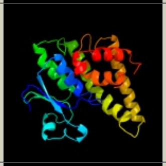
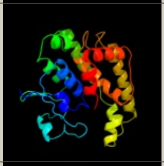
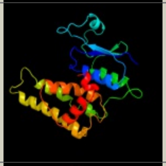
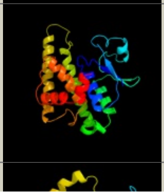
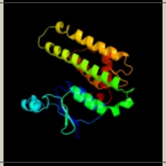
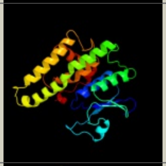
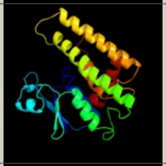
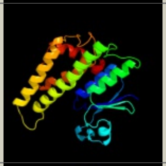
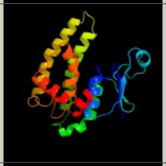
Unique Job ID	945a2e9446a84244

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bbyA_	Alignment		100.0	98	**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
2	c3c8eB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**yghu, glutathione s-transferase homologue; **PDBTitle:** crystal structure analysis of yghu from e. coli
3	c3lykA_	Alignment		100.0	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
4	c1ljrB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** glutathione transferase (hgst t2-2) from human
5	c3lxzD_	Alignment		100.0	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione s-transferase family protein; **PDBTitle:** structure of probable glutathione s-transferase(pp0183) from2 pseudomonas putida
6	c2aheA_	Alignment		100.0	18	**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
7	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 sulfnate
8	c1yy7A_	Alignment		100.0	22	**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
9	c3lg6B_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glutathione transferase; **PDBTitle:** crystal structure of putative glutathione transferase from2 coccidioides immitis
10	c2jl4A_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**maleylpyruvate isomerase; **PDBTitle:** holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
11	c2x64A_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione-s-transferase; **PDBTitle:** glutathione-s-transferase from xylella fastidiosa
						

12	c1c72A_	Alignment		100.0	11	**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
13	c1yq1A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structural genomics of caenorhabditis elegans: glutathione2 s-transferase
14	c3qagA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase omega-2; **PDBTitle:** human glutathione transferase o2 with glutathione -new crystal form
15	c3gx0A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gst-like protein yfcg; **PDBTitle:** crystal structure of gsh-dependent disulfide bond2 oxidoreductase
16	c1k0dB_	Alignment		100.0	20	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ure2 protein; **PDBTitle:** ure2p in complex with glutathione
17	c2gsqA_	Alignment		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
18	c3nivD_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** the crystal structure of glutathione s-transferase from legionella2 pneumophila
19	c3csiA_	Alignment		100.0	12	**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
20	c1ua5A_	Alignment		100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** non-fusion gst from s. japonicum in complex with glutathione
21	c1byeA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (glutathione s-transferase); **PDBTitle:** glutathione s-transferase i from mais in complex with2 atrazine glutathione conjugate
22	c1oktA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** x-ray structure of glutathione s-transferase from the2 malarial parasite plasmodium falciparum
23	c1zl9A_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 5; **PDBTitle:** crystal structure of a major nematode c.elegans specific gst (ce01613)
24	c3m0fA_	Alignment	not modelled	100.0	18	**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
25	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
26	c3h1nA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable glutathione s-transferase; **PDBTitle:** crystal structure of probable glutathione s-transferase from2 bordetella bronchiseptica rb50
27	c3m3mA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure of glutathione s-transferase from pseudomonas2 fluorescens [pf-5]
28	c1k3yB_	Alignment	not modelled	100.0	18	**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
						PDB header:transferase

29	c1gwcC_	Alignment	not modelled	100.0	18	**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
30	c1vf1A_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 3; **PDBTitle:** cgsta1-1 in complex with glutathione
31	c2pmtA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase; **PDBTitle:** glutathione transferase from proteus mirabilis
32	c3isoB_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glutathione transferase; **PDBTitle:** crystal structure of 26 kda gst of clonorchis sinensis in p32212 symmetry
33	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
34	c1oyjC_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
35	c1f2eB_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structure of sphingomonad, glutathione s-transferase complexed with2 glutathione
36	c2vo4A_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,4-d inducible glutathione s-transferase; **PDBTitle:** glutathione transferase from glycine max
37	c1gnwA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structure of glutathione s-transferase
38	c3lszA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure of glutathione s-transferase from2 rhodobacter sphaeroides
39	c2on5E_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** E: **PDB Molecule:**na glutathione s-transferase 2; **PDBTitle:** structure of nagst-2
40	c1gtuB_	Alignment	not modelled	100.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** ligand-free human glutathione s-transferase m1a-1a
41	c1jlvA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase gst1-3; **PDBTitle:** anopheles dirus species b glutathione s-transferases 1-3
42	c2on7A_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**na glutathione s-transferase 1; **PDBTitle:** structure of nagst-1
43	c1r5aA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase; **PDBTitle:** glutathione s-transferase
44	c3uarA_	Alignment	not modelled	100.0	18	**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
45	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
46	c1tu8A_	Alignment	not modelled	100.0	11	**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
47	c2fheA_	Alignment	not modelled	100.0	14	**PDB header:**transferase/substrate **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** fasciola hepatica glutathione s-transferase isoform 1 in complex with2 glutathione
48	c3fy7B_	Alignment	not modelled	100.0	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 3; **PDBTitle:** crystal structure of homo sapiens clic3
49	c2gdrA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure of a bacterial glutathione transferase
50	c1m0uB_	Alignment	not modelled	100.0	12	**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
51	c1g7oA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin 2; **PDBTitle:** nmr solution structure of reduced e. coli glutaredoxin 2
52	c3lypA_	Alignment	not modelled	100.0	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stringent starvation protein a; **PDBTitle:** structure of stringent starvation protein a homolog from pseudomonas2 fluorescens
53	c2hnlB_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase 1; **PDBTitle:** structure of the prostaglandin d synthase from the parasitic nematode2 onchocerca volvulus
54	c1b8xA_	Alignment	not modelled	100.0	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
55	c3ic8D_	Alignment	not modelled	100.0	20	**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

56	c2c3nB_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase theta 1; **PDBTitle:** human glutathione-s-transferase t1-1, apo form
57	c1gumA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (glutathione transferase a4-4); **PDBTitle:** human glutathione transferase a4-4 without ligands
58	c1aw9A_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase iii; **PDBTitle:** structure of glutathione s-transferase iii in apo form
59	c1b48A_	Alignment	not modelled	100.0	18	**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
60	c2yv9B_	Alignment	not modelled	100.0	13	**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
61	c1nhyA_	Alignment	not modelled	100.0	15	**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.
62	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
63	c3cbuB_	Alignment	not modelled	100.0	21	**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
64	c1n2aB_	Alignment	not modelled	100.0	21	**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
65	c2cz2A_	Alignment	not modelled	100.0	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)
66	c2yv7A_	Alignment	not modelled	100.0	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cg10997-pa; **PDBTitle:** crystal structure of the clic homolog from drosophila2 melanogaster
67	c1eemA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione-s-transferase; **PDBTitle:** glutathione transferase from homo sapiens
68	c3f6fA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cg18548-pa (ip02196p) (ip02193p); **PDBTitle:** crystal structure of glutathione transferase dmgstd10 from2 drosophila melanogaster
69	c1v2aD_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione transferase gst1-6; **PDBTitle:** glutathione s-transferase 1-6 from anopheles dirus species b
70	c2wb9A_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase sigma class; **PDBTitle:** fasciola hepatica sigma class gst
71	c3lq7B_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure of glutathione s-transferase from2 agrobacterium tumefaciens str. c58
72	c2imiA_	Alignment	not modelled	100.0	19	**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
73	c1jlwA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase gst1-4; **PDBTitle:** anopheles dirus species b glutathione s-transferases 1-4
74	c3rbtD_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione transferase o1; **PDBTitle:** crystal structure of glutathione s-transferase omega 3 from the2 silkworm bombyx mori
75	c3ppuB_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione-s-transferase; **PDBTitle:** crystal structure of the glutathione-s-transferase xi from2 phanerochaete chrysosporium
76	c2ws2B_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** the 2 angstrom structure of a nu-class gst from haemonchus contortus
77	c2fnoB_	Alignment	not modelled	100.0	17	**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
78	c1tw9C_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase 2; **PDBTitle:** glutathione transferase-2, apo form, from the nematode heligmosomoides2 polygyrus
79	c3touB_	Alignment	not modelled	99.9	18	**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
80	c3ay8A_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** glutathione s-transferase unclassified 2 from bombyx mori
81	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
82	c3m8nA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible glutathione s-transferase; **PDBTitle:** crystal structure of a possible gutathione s-tranferase from2 rhodopseudomonas palustris
83	c2c8uA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 28 kda; **PDBTitle:** structure of r21q mutant of sh28gst
84	c3m1gC_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative glutathione s-transferase; **PDBTitle:** the structure of a putative glutathione s-transferase from2 corynebacterium glutamicum
85	c1z9hB_	Alignment	not modelled	99.9	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**membrane-associated prostaglandin e synthase-2; **PDBTitle:** microsomal prostaglandin e synthase type-2
86	c1e6bA_	Alignment	not modelled	99.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure of a zeta class glutathione s-transferase2 from arabidopsis thaliana
87	c2uz8A_	Alignment	not modelled	99.8	16	**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
88	d1k0ma2	Alignment	not modelled	99.8	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
89	d1e6ba2	Alignment	not modelled	99.8	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
90	d1ljra2	Alignment	not modelled	99.8	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
91	d1pn9a2	Alignment	not modelled	99.7	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
92	d1gnwa2	Alignment	not modelled	99.7	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
93	d1axda2	Alignment	not modelled	99.7	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
94	d1v2aa2	Alignment	not modelled	99.7	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
95	d1aw9a2	Alignment	not modelled	99.7	34	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
96	d1r5aa2	Alignment	not modelled	99.7	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
97	d1jlva2	Alignment	not modelled	99.7	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
98	d1fw1a2	Alignment	not modelled	99.7	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
99	d1k0da2	Alignment	not modelled	99.7	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
100	d1k0dd2	Alignment	not modelled	99.7	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
101	d1jlwa2	Alignment	not modelled	99.7	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
102	d1oyja2	Alignment	not modelled	99.7	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
103	d1gwca2	Alignment	not modelled	99.7	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
104	d1eema2	Alignment	not modelled	99.6	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
105	d1n2aa2	Alignment	not modelled	99.6	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
106	d1axda1	Alignment	not modelled	99.6	15	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
107	d1n2aa1	Alignment	not modelled	99.6	13	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
108	d1aw9a1	Alignment	not modelled	99.6	16	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain

109	d1k0da1	Alignment	not modelled	99.6	15	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
110	d1g7oa2	Alignment	not modelled	99.6	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
111	d1rk4a2	Alignment	not modelled	99.6	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
112	d1f2ea2	Alignment	not modelled	99.6	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
113	d1pmta2	Alignment	not modelled	99.6	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
114	d2gsra2	Alignment	not modelled	99.6	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
115	c2hsmA_	Alignment	not modelled	99.6	11	**PDB header:**ligase/rna binding protein **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase, cytoplasmic; **PDBTitle:** structural basis of yeast aminoacyl-trna synthetase complex2 formation revealed by crystal structures of two binary sub-3 complexes
116	d1okta2	Alignment	not modelled	99.6	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
117	d1glqa2	Alignment	not modelled	99.6	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
118	d1f2ea1	Alignment	not modelled	99.6	20	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
119	d1pmta1	Alignment	not modelled	99.6	16	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
120	d2gsqa2	Alignment	not modelled	99.6	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain