







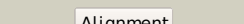
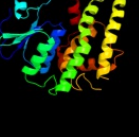
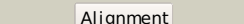

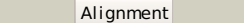

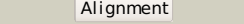

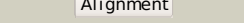

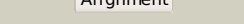

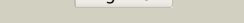
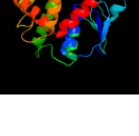





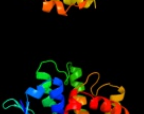





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1yy7A_</a>	 Alignment		100.0	83	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> stringent starvation protein a; <b>PDBTitle:</b> crystal structure of stringent starvation protein a (sspa),2 an rna polymerase-associated transcription factor
2	<a href="#">c3lykA_</a>	 Alignment		100.0	60	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> stringent starvation protein a homolog; <b>PDBTitle:</b> structure of stringent starvation protein a homolog from2 haemophilus influenzae
3	<a href="#">c3qagA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase omega-2; <b>PDBTitle:</b> human glutathione transferase o2 with glutathione -new crystal form
4	<a href="#">c3c8eB_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> yghu, glutathione s-transferase homologue; <b>PDBTitle:</b> crystal structure analysis of yghu from e. coli
5	<a href="#">c1eemA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione-s-transferase; <b>PDBTitle:</b> glutathione transferase from homo sapiens
6	<a href="#">c2vo4A_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-d inducible glutathione s-transferase; <b>PDBTitle:</b> glutathione transferase from glycine max
7	<a href="#">c2aheA_</a>	 Alignment		100.0	19	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloride intracellular channel protein 4; <b>PDBTitle:</b> crystal structure of a soluble form of clic4. intercellular2 chloride ion channel
8	<a href="#">c1gwcC_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione s-transferase tsi-1; <b>PDBTitle:</b> the structure of a tau class glutathione s-transferase from2 wheat, active in herbicide detoxification
9	<a href="#">c1oyiC_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
10	<a href="#">c3rbtD_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutathione transferase o1; <b>PDBTitle:</b> crystal structure of glutathione s-transferase omega 3 from2 silkworm bombyx mori
11	<a href="#">c3lxzD_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutathione s-transferase family protein; <b>PDBTitle:</b> structure of probable glutathione s-transferase(pp0183) from2 pseudomonas putida

12	<a href="#">c1k0nB_</a>	Alignment		100.0	18	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> chloride intracellular channel protein 1; <b>PDBTitle:</b> chloride intracellular channel 1 (clic1) complexed with glutathione
13	<a href="#">c3lypA_</a>	Alignment		100.0	55	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> stringent starvation protein a; <b>PDBTitle:</b> structure of stringent starvation protein a homolog from pseudomonas2 fluorescens
14	<a href="#">c3m0fA_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein gst_n; <b>PDBTitle:</b> crystal structure of glutathione s transferase in complex2 with glutathione from pseudomonas fluorescens
15	<a href="#">c1ljrB_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> glutathione transferase (hgst t2-2) from human
16	<a href="#">c2jl4A_</a>	Alignment		100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> maleylpyruvate isomerase; <b>PDBTitle:</b> holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
17	<a href="#">c3ergA_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase 2; <b>PDBTitle:</b> crystal structure of gtt2 from saccharomyces cerevisiae in complex2 with glutathione sulfnate
18	<a href="#">c1c72A_</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione s-transferase); <b>PDBTitle:</b> tyr115, gln165 and trp209 contribute to the 1,2-epoxy-3-(p-2 nitrophenoxy)propane conjugating activities of glutathione3 s-transferase cgstm1-1
19	<a href="#">c3touB_</a>	Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase protein; <b>PDBTitle:</b> crystal structure of glutathione transferase (target efi-501058) from2 ralstonia solanacearum gmi1000 with gsh bound
20	<a href="#">c3nivD_</a>	Alignment		100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> the crystal structure of glutathione s-transferase from legionella2 pneumophila
21	<a href="#">c2x64A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione-s-transferase; <b>PDBTitle:</b> glutathione-s-transferase from xylella fastidiosa
22	<a href="#">c3m3mA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure of glutathione s-transferase from pseudomonas2 fluorescens [pf-5]
23	<a href="#">c2cz2A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> isomerase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maleylacetoacetate isomerase; <b>PDBTitle:</b> crystal structure of glutathione transferase zeta 1-12 (maleylacetoacetate isomerase) from mus musculus (form-1 crystal)
24	<a href="#">c3csiA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase p; <b>PDBTitle:</b> crystal structure of the glutathione transferase pi allelic variant*c,2 i104v/a113v, in complex with the chlorambucil-glutathione conjugate
25	<a href="#">c1byeA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione s-transferase); <b>PDBTitle:</b> glutathione s-transferase i from mais in complex with2 atrazine glutathione conjugate
26	<a href="#">c1yq1A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> structural genomics of caenorhabditis elegans: glutathione2 s-transferase
27	<a href="#">c1iyiA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> hematopietic prostagladin d synthase; <b>PDBTitle:</b> crystal structure of hematopietic prostagladin d synthase
28	<a href="#">c3lg6B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glutathione transferase; <b>PDBTitle:</b> crystal structure of putative glutathione transferase from2 coccidioides immitis

29	<a href="#">c3cbuB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable gst-related protein; <b>PDBTitle:</b> crystal structure of a putative glutathione s-transferase (reut a1011)2 from ralstonia eutropha jmp134 at 2.05 a resolution
30	<a href="#">c3gx0A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gst-like protein yfcg; <b>PDBTitle:</b> crystal structure of gsh-dependent disulfide bond2 oxidoreductase
31	<a href="#">c1f2eB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> structure of sphingomonad, glutathione s-transferase complexed with2 glutathione
32	<a href="#">c1jlvA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione transferase gst1-3; <b>PDBTitle:</b> anopheles dirus species b glutathione s-transferases 1-3
33	<a href="#">c2gdrA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure of a bacterial glutathione transferase
34	<a href="#">c1ua5A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> non-fusion gst from s. japonicum in complex with glutathione
35	<a href="#">c2fheA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase/substrate <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> fasciola hepatica glutathione s-transferase isoform 1 in complex with2 glutathione
36	<a href="#">c1v2aD</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutathione transferase gst1-6; <b>PDBTitle:</b> glutathione s-transferase 1-6 from anopheles dirus species b
37	<a href="#">c1gnwA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> structure of glutathione s-transferase
38	<a href="#">c2gsqA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> glutathione s-transferase from squid digestive gland complexed with s-2 (3-iodobenzyl)glutathione
39	<a href="#">c3f6fA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cg18548-pa (ip02196p) (ip02193p); <b>PDBTitle:</b> crystal structure of glutathione transferase dmgstd10 from2 drosophila melanogaster
40	<a href="#">c1k3yB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase a1; <b>PDBTitle:</b> crystal structure analysis of human glutathione s-transferase with s-2 hexyl glutathione and glycerol at 1.3 angstrom
41	<a href="#">c1vf1A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase 3; <b>PDBTitle:</b> cgsta1-1 in complex with glutathione
42	<a href="#">c1gtuB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> ligand-free human glutathione s-transferase m1a-1a
43	<a href="#">c1m0uB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> gst2 gene product; <b>PDBTitle:</b> crystal structure of the drosophila glutathione s-2 transferase-2 in complex with glutathione
44	<a href="#">c2imiA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> epsilon-class glutathione s-transferase; <b>PDBTitle:</b> structures of an insect epsilon-class glutathione s-2 transferase from the malaria vector anopheles gambiae:3 evidence for high ddt-detoxifying activity
45	<a href="#">c1tu8A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase 2; <b>PDBTitle:</b> structure of onchoverca volvulus pi-class glutathione s-2 transferase with its kompetitive inhibitor s-hexyl-gsh
46	<a href="#">c3uarA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure of glutathione transferase (target efi-501774) from2 methylococcus capsulatus str. bath with gsh bound
47	<a href="#">c1r5aA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione transferase; <b>PDBTitle:</b> glutathione s-transferase
48	<a href="#">c2pmtA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione transferase; <b>PDBTitle:</b> glutathione transferase from proteus mirabilis
49	<a href="#">c1zl9A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase 5; <b>PDBTitle:</b> crystal structure of a major nematode c.elegans specific gst (ce01613)
50	<a href="#">c2c3nB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase theta 1; <b>PDBTitle:</b> human glutathione-s-transferase t1-1, apo form
51	<a href="#">c3bbyA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized gst-like protein yfcf; <b>PDBTitle:</b> crystal structure of glutathione s-transferase (np_416804.1) from2 escherichia coli k12 at 1.85 a resolution
52	<a href="#">c1k0dB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> ure2 protein; <b>PDBTitle:</b> ure2p in complex with glutathione
53	<a href="#">c1oktA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> x-ray structure of glutathione s-transferase from the2 malarial parasite plasmodium falciparum
54	<a href="#">c2r4vA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chloride intracellular channel protein 2; <b>PDBTitle:</b> structure of human clic2, crystal form a
						<b>PDB header:</b> transferase

55	<a href="#">c3ay8A_</a>	Alignment	not modelled	100.0	16	<b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> glutathione s-transferase unclassified 2 from bombyx mori
56	<a href="#">c1b8xA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> signal protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (aml-1b); <b>PDBTitle:</b> glutathione s-transferase fused with the nuclear matrix targeting2 signal of the transcription factor aml-1
57	<a href="#">c3isoB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glutathione transferase; <b>PDBTitle:</b> crystal structure of 26 kda gst of clonorchis sinensis in p32212 symmetry
58	<a href="#">c2yv7A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> cg10997-pa; <b>PDBTitle:</b> crystal structure of the clic homolog from drosophila2 melanogaster
59	<a href="#">c1aw9A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase iii; <b>PDBTitle:</b> structure of glutathione s-transferase iii in apo form
60	<a href="#">c3m8nA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible glutathione s-transferase; <b>PDBTitle:</b> crystal structure of a possible glutathione s-transferase from2 rhodopseudomonas palustris
61	<a href="#">c3lszA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure of glutathione s-transferase from2 rhodobacter sphaeroides
62	<a href="#">c3fy7B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride intracellular channel protein 3; <b>PDBTitle:</b> crystal structure of homo sapiens clic3
63	<a href="#">c1b48A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione s-transferase); <b>PDBTitle:</b> 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
64	<a href="#">c1gumA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione transferase a4-4); <b>PDBTitle:</b> human glutathione transferase a4-4 without ligands
65	<a href="#">c2hnlB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase 1; <b>PDBTitle:</b> structure of the prostaglandin d synthase from the parasitic nematode2 onchocerca volvulus
66	<a href="#">c2on5E_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> na glutathione s-transferase 2; <b>PDBTitle:</b> structure of nagst-2
67	<a href="#">c3ic8D_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized gst-like proteinprotein; <b>PDBTitle:</b> the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
68	<a href="#">c2ntoA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> structure of the glutathione transferase from ochrobactrum anthropi in2 complex with glutathione
69	<a href="#">c2on7A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> na glutathione s-transferase 1; <b>PDBTitle:</b> structure of nagst-1
70	<a href="#">c3h1nA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutathione s-transferase; <b>PDBTitle:</b> crystal structure of probable glutathione s-transferase from2 bordetella bronchiseptica rb50
71	<a href="#">c1g7oA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin 2; <b>PDBTitle:</b> nmr solution structure of reduced e. coli glutaredoxin 2
72	<a href="#">c2wb9A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione transferase sigma class; <b>PDBTitle:</b> fasciola hepatica sigma class gst
73	<a href="#">c3ppuB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione-s-transferase; <b>PDBTitle:</b> crystal structure of the glutathione-s-transferase xi from2 phanerochaete chrysosporium
74	<a href="#">c1n2aB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure of a bacterial glutathione transferase2 from escherichia coli with glutathione sulfonate in the3 active site
75	<a href="#">c2yv9B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> chloride intracellular channel exc-4; <b>PDBTitle:</b> crystal structure of the clic homologue exc-4 from c.2 elegans
76	<a href="#">c1e6bA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure of a zeta class glutathione s-transferase2 from arabidopsis thaliana
77	<a href="#">c1nhya_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-gamma 1; <b>PDBTitle:</b> crystal structure of the gst-like domain of elongation2 factor 1-gamma from saccharomyces cerevisiae.
78	<a href="#">c1tw9C_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione s-transferase 2; <b>PDBTitle:</b> glutathione transferase-2, apo form, from the nematode heligmosomoides2 polygyrus
79	<a href="#">c2c8uA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase 28 kda; <b>PDBTitle:</b> structure of r21q mutant of sh28gst
80	<a href="#">c1j1wA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione transferase gst1-4; <b>PDBTitle:</b> anopheles dirus species b glutathione s-transferases 1-4
						<b>PDB header:</b> ankyrin binding

81	<a href="#">c1bg5A_</a>	Alignment	not modelled	100.0	16	<b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of alpha-na,k-ase with <b>PDBTitle:</b> crystal structure of the ankyrin binding domain of alpha-na,2 k-ase as a fusion protein with glutathione s-transferase
82	<a href="#">c2ws2B_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> the 2 angstrom structure of a nu-class gst from haemonchus contortus
83	<a href="#">c3lq7B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure of glutathione s-transferase from2 agrobacterium tumefaciens str. c58
84	<a href="#">c3m1gC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative glutathione s-transferase; <b>PDBTitle:</b> the structure of a putative glutathione s-transferase from2 corynebacterium glutamicum
85	<a href="#">c2fnoB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> agr_pat_752p; <b>PDBTitle:</b> crystal structure of a glutathione s-transferase (atu5508) from2 agrobacterium tumefaciens str. c58 at 2.00 a resolution
86	<a href="#">c1z9hB_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> membrane-associated prostaglandin e synthase-2; <b>PDBTitle:</b> microsomal prostaglandin e synthase type-2
87	<a href="#">c2uz8A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation elongation factor 1 <b>PDBTitle:</b> the crystal structure of p18, human translation elongation2 factor 1 epsilon 1
88	<a href="#">d1eema1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
89	<a href="#">d1gwca1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
90	<a href="#">d1n2aa1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
91	<a href="#">d1axda1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
92	<a href="#">d1aw9a1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
93	<a href="#">d1loyja1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
94	<a href="#">d1nhya1</a>	Alignment	not modelled	99.7	10	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
95	<a href="#">d1gnwa1</a>	Alignment	not modelled	99.7	9	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
96	<a href="#">d1pmta1</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
97	<a href="#">c2hsmA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> ligase/rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> structural basis of yeast aminoacyl-trna synthetase complex2 formation revealed by crystal structures of two binary sub-3 complexes
98	<a href="#">d3gtub1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
99	<a href="#">d1xw6a1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
100	<a href="#">d4gtua1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
101	<a href="#">d1f2ea1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
102	<a href="#">d2gsta1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
103	<a href="#">d2fhea1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
104	<a href="#">d1b4pa1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
105	<a href="#">d1fw1a1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
106	<a href="#">d1duga1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
107	<a href="#">d2c4ja1</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
						<b>Fold:</b> GST C-terminal domain-like



108	<a href="#">div2aa1</a>	Alignment	not modelled	99.7	14	<b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
109	<a href="#">dlglqa1</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
110	<a href="#">dlgnea1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
111	<a href="#">dlgsua1</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
112	<a href="#">dloyja2</a>	Alignment	not modelled	99.6	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
113	<a href="#">dlb48a1</a>	Alignment	not modelled	99.6	9	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
114	<a href="#">d2cvda1</a>	Alignment	not modelled	99.6	7	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
115	<a href="#">d2gsra1</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
116	<a href="#">dlgwca2</a>	Alignment	not modelled	99.6	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
117	<a href="#">dlpd211</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
118	<a href="#">dlk0da1</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
119	<a href="#">dl1bka1</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
120	<a href="#">dlfhea1</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain