Phyre^2

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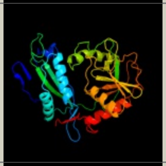
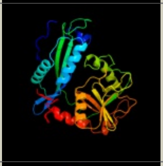
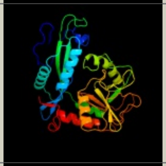
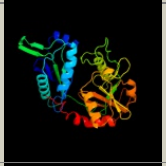
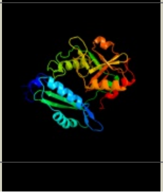
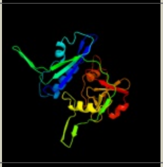
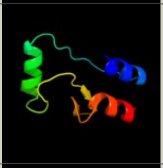
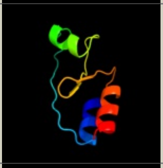
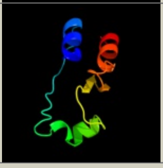
Description	P0AB80
Date	Thu Jan 5 11:14:50 GMT 2012
Unique Job ID	63269aa27c2b8f71

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1iyea_	Alignment		100.0	100	**Fold:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Superfamily:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Family:**D-aminoacid aminotransferase-like PLP-dependent enzymes
2	c1wrvB_	Alignment		100.0	48	**PDB header:**transferase **Chain:** B: **PDB Molecule:**branched-chain amino acid aminotransferase; **PDBTitle:** crystal structure of t.th.hb8 branched-chain amino acid2 aminotransferase
3	c3dtfB_	Alignment		100.0	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**branched-chain amino acid aminotransferase; **PDBTitle:** structural analysis of mycobacterial branched chain aminotransferase-2 implications for inhibitor design
4	d2a1ha1	Alignment		100.0	28	**Fold:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Superfamily:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Family:**D-aminoacid aminotransferase-like PLP-dependent enzymes
5	c2abjG_	Alignment		100.0	28	**PDB header:**transferase **Chain:** G: **PDB Molecule:**branched-chain-amino-acid aminotransferase, cytosolic; **PDBTitle:** crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
6	d1daaa_	Alignment		100.0	29	**Fold:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Superfamily:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Family:**D-aminoacid aminotransferase-like PLP-dependent enzymes
7	c3cswB_	Alignment		100.0	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative branched-chain-amino-acid aminotransferase; **PDBTitle:** crystal structure of a putative branched-chain amino acid2 aminotransferase (tm0831) from thermotoga maritima at 2.15 a3 resolution
8	c2xpfB_	Alignment		100.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**4-amino-4-deoxychorismate lyase; **PDBTitle:** crystal structure of putative aminodeoxychorismate lyase2 from pseudomonas aeruginosa
9	d1i2ka_	Alignment		100.0	21	**Fold:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Superfamily:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Family:**D-aminoacid aminotransferase-like PLP-dependent enzymes
10	c3lulA_	Alignment		100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-amino-4-deoxychorismate lyase; **PDBTitle:** crystal structure of putative 4-amino-4-deoxychorismate lyase.2 (yp_094631.1) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 1.78 a resolution
11	c2zgiA_	Alignment		100.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative 4-amino-4-deoxychorismate lyase; **PDBTitle:** crystal structure of putative 4-amino-4-deoxychorismate lyase

12	c3snoA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical aminotransferase; **PDBTitle:** crystal structure of a hypothetical aminotransferase (ncgl2491) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.60 a resolution
13	c3qqmD_	Alignment		100.0	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**mlr3007 protein; **PDBTitle:** crystal structure of a putative amino-acid aminotransferase2 (np_104211.1) from mesorhizobium loti at 2.30 a resolution
14	c3cebA_	Alignment		100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-aminoacid aminotransferase-like plp-dependent enzyme; **PDBTitle:** crystal structure of a putative 4-amino-4-deoxychorismate lyase2 (hs_0128) from haemophilus somnus 129pt at 2.40 a resolution
15	d1ljra2	Alignment		71.0	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
16	d1jlva2	Alignment		69.3	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
17	d1k3ya2	Alignment		69.0	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
18	d1axda2	Alignment		68.4	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
19	d1aw9a2	Alignment		68.1	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
20	d1r5aa2	Alignment		67.9	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
21	d1pn9a2	Alignment	not modelled	67.2	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
22	d1gnwa2	Alignment	not modelled	67.0	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
23	d1oyja2	Alignment	not modelled	64.7	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
24	d1e6ba2	Alignment	not modelled	59.2	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
25	d1ev4a2	Alignment	not modelled	58.0	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
26	d1v2aa2	Alignment	not modelled	56.0	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
27	d2r48a1	Alignment	not modelled	54.1	16	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
28	d2c4ja2	Alignment	not modelled	53.3	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
29	c3h1nA_	Alignment	not modelled	53.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable glutathione s-transferase; **PDBTitle:** crystal structure of probable glutathione s-transferase from2 bordetella bronchiseptica rb50

30	d2gsta2	Alignment	not modelled	52.4	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
31	d2gsqa2	Alignment	not modelled	51.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
32	d1glqa2	Alignment	not modelled	50.3	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
33	d1ml6a2	Alignment	not modelled	50.0	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
34	d1xw6a2	Alignment	not modelled	48.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
35	d1tu7a2	Alignment	not modelled	48.4	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
36	d1gwca2	Alignment	not modelled	47.6	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
37	d1tw9a2	Alignment	not modelled	47.3	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
38	d2gsra2	Alignment	not modelled	47.0	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
39	d1gula2	Alignment	not modelled	46.4	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
40	d2a2ra2	Alignment	not modelled	46.0	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
41	d1b48a2	Alignment	not modelled	45.3	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
42	c1ua5A_	Alignment	not modelled	44.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** non-fusion gst from s. japonicum in complex with glutathione
43	d1fhea2	Alignment	not modelled	43.5	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
44	d2fnoa2	Alignment	not modelled	41.9	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
45	d2r4qa1	Alignment	not modelled	39.5	21	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
46	d1k0da2	Alignment	not modelled	37.9	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
47	c1gumA_	Alignment	not modelled	36.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (glutathione transferase a4-4); **PDBTitle:** human glutathione transferase a4-4 without ligands
48	d1duga2	Alignment	not modelled	35.3	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
49	c2cb1A_	Alignment	not modelled	35.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
50	c1vf1A_	Alignment	not modelled	34.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 3; **PDBTitle:** cgsta1-1 in complex with glutathione
51	d2fhea2	Alignment	not modelled	34.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
52	c1tw9C_	Alignment	not modelled	34.0	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase 2; **PDBTitle:** glutathione transferase-2, apo form, from the nematode heligmosomoides2 polygyrus
53	d1m0ua2	Alignment	not modelled	33.5	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
54	c3ic4A_	Alignment	not modelled	33.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
55	d1k0dd2	Alignment	not modelled	33.0	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
56	d1fw1a2	Alignment	not modelled	32.4	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
57	d1pd212	Alignment	not modelled	32.0	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like

						Family: Glutathione S-transferase (GST), N-terminal domain
58	d1jlwa2	Alignment	not modelled	31.6	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
59	d1k0ma2	Alignment	not modelled	29.4	5	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
60	c2kyrA_	Alignment	not modelled	28.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
61	c2gsqA_	Alignment	not modelled	27.9	16	**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
62	d1nm3a1	Alignment	not modelled	26.3	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
63	d1t1va_	Alignment	not modelled	25.3	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
64	c1k3yB_	Alignment	not modelled	25.0	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
65	c1m0uB_	Alignment	not modelled	24.9	17	**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
66	c1ljrB_	Alignment	not modelled	24.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** glutathione transferase (hgst t2-2) from human
67	c1zl9A_	Alignment	not modelled	24.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 5; **PDBTitle:** crystal structure of a major nematode c.elegans specific gst (ce01613)
68	c3csiA_	Alignment	not modelled	24.3	15	**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
69	c2jl4A_	Alignment	not modelled	23.2	5	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**maleylpyruvate isomerase; **PDBTitle:** holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
70	d1okta2	Alignment	not modelled	23.0	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
71	c1gtuB_	Alignment	not modelled	22.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** ligand-free human glutathione s-transferase m1a-1a
72	c1k0nB_	Alignment	not modelled	22.1	4	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 1; **PDBTitle:** chloride intracellular channel 1 (clic1) complexed with glutathione
73	d1gsua2	Alignment	not modelled	21.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
74	c1jlvA_	Alignment	not modelled	21.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase gst1-3; **PDBTitle:** anopheles dirus species b glutathione s-transferases 1-3
75	d1r7ha_	Alignment	not modelled	21.3	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
76	c3ic8D_	Alignment	not modelled	21.1	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
77	d1oe8a2	Alignment	not modelled	20.9	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
78	d2cvda2	Alignment	not modelled	20.1	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
79	c2vo4A_	Alignment	not modelled	19.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,4-d inducible glutathione s-transferase; **PDBTitle:** glutathione transferase from glycine max
80	c2aheA_	Alignment	not modelled	19.2	5	**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
81	d1rk4a2	Alignment	not modelled	18.8	5	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
82	c2fheA_	Alignment	not modelled	18.8	17	**PDB header:**transferase/substrate **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** fasciola hepatica glutathione s-transferase isoform 1 in complex with2 glutathione
						PDB header:transferase

83	c2fnoB_	Alignment	not modelled	18.2	9	**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
84	c3isoB_	Alignment	not modelled	17.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glutathione transferase; **PDBTitle:** crystal structure of 26 kda gst of clonorchis sinensis in p32212 symmetry
85	d2ftsa3	Alignment	not modelled	15.7	9	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
86	c3lykA_	Alignment	not modelled	15.6	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**stringent starvation protein a homolog; **PDBTitle:** structure of stringent starvation protein a homolog from2 haemophilus influenzae
87	d1fova_	Alignment	not modelled	15.4	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
88	c3ipzA_	Alignment	not modelled	15.3	11	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
89	c1gnwA_	Alignment	not modelled	15.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structure of glutathione s-transferase
90	c2x64A_	Alignment	not modelled	15.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione-s-transferase; **PDBTitle:** glutathione-s-transferase from xylella fastidiosa
91	c2klxA_	Alignment	not modelled	14.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
92	c2on7A_	Alignment	not modelled	14.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**na glutathione s-transferase 1; **PDBTitle:** structure of nagst-1
93	c2ws2B_	Alignment	not modelled	13.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** the 2 angstrom structure of a nu-class gst from haemonchus contortus
94	c1tu8A_	Alignment	not modelled	13.4	10	**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
95	c1oyjC_	Alignment	not modelled	13.1	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
96	d1rxxa_	Alignment	not modelled	13.1	20	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Arginine deiminase
97	c2hnlB_	Alignment	not modelled	13.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase 1; **PDBTitle:** structure of the prostaglandin d synthase from the parasitic nematode2 onchocerca volvulus
98	d1dzfa1	Alignment	not modelled	13.0	9	**Fold:**Restriction endonuclease-like **Superfamily:**Eukaryotic RPB5 N-terminal domain **Family:**Eukaryotic RPB5 N-terminal domain
99	d1n2aa2	Alignment	not modelled	12.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain