Phyre^{2}

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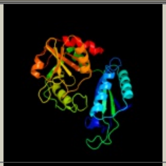
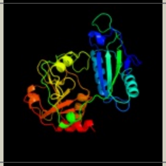
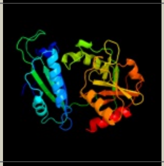
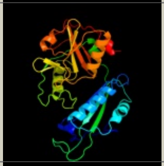
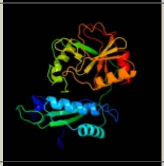
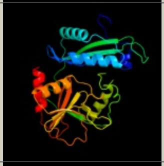
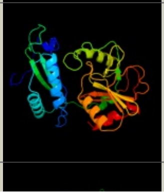
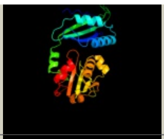
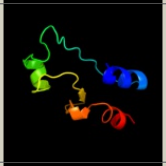
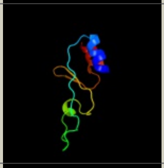
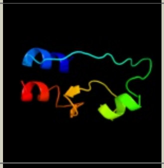
Description	P28305
Date	Thu Jan 5 11:44:41 GMT 2012
Unique Job ID	24586e651ac21f8d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i2ka_	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	c2xpfB_	Alignment		100.0	33	**PDB header:**lyase **Chain:** B: **PDB Molecule:**4-amino-4-deoxychorismate lyase; **PDBTitle:** crystal structure of putative aminodeoxychorismate lyase2 from pseudomonas aeruginosa
3	c1wrvB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**branched-chain amino acid aminotransferase; **PDBTitle:** crystal structure of t.th.hb8 branched-chain amino acid2 aminotransferase
4	d1iyea_	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
5	d1daaa_	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
6	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
7	c3cswB_	Alignment		100.0	22	**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	c3dtfB_	Alignment		100.0	18	**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
9	d2a1ha1	Alignment		100.0	15	**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	c2zgiA_	Alignment		100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative 4-amino-4-deoxychorismate lyase; **PDBTitle:** crystal structure of putative 4-amino-4-deoxychorismate lyase
11	c2abjG_	Alignment		100.0	15	**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.

12	c3snoA_	Alignment		100.0	19	**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	18	**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		64.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
16	d1jlva2	Alignment		54.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
17	d1oyja2	Alignment		53.5	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
18	d1aw9a2	Alignment		52.4	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
19	d1axda2	Alignment		44.1	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
20	d1r5aa2	Alignment		41.9	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
21	d1pn9a2	Alignment	not modelled	38.2	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
22	c2klxA_	Alignment	not modelled	36.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
23	d1gnwa2	Alignment	not modelled	33.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
24	d1e6ba2	Alignment	not modelled	32.8	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
25	d1k3ya2	Alignment	not modelled	32.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
26	d1v2aa2	Alignment	not modelled	27.1	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
27	c2cb1A_	Alignment	not modelled	27.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
28	d1rxxa_	Alignment	not modelled	22.0	18	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Arginine deiminase
29	d2fnoa2	Alignment	not modelled	22.0	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain

30	d1tw9a2	Alignment	not modelled	20.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
31	d1fhea2	Alignment	not modelled	18.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
32	d1ev4a2	Alignment	not modelled	18.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
33	c8jdwA_	Alignment	not modelled	17.9	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (l-arginine:glycine amidinotransferase); **PDBTitle:** crystal structure of human l-arginine:glycine2 amidinotransferase in complex with l-alanine
34	d1jdwa_	Alignment	not modelled	16.9	5	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Amidinotransferase
35	c1jdwA_	Alignment	not modelled	16.9	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-arginine\:glycine amidinotransferase; **PDBTitle:** crystal structure and mechanism of l-arginine: glycine2 amidinotransferase: a mitochondrial enzyme involved in3 creatine biosynthesis
36	d1tu7a2	Alignment	not modelled	16.9	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
37	d1gwca2	Alignment	not modelled	16.4	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
38	c3kgkA_	Alignment	not modelled	15.8	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**arsenical resistance operon trans-acting repressor arsd; **PDBTitle:** crystal structure of arsd
39	d2gk3a1	Alignment	not modelled	15.8	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**STM3548-like
40	d1pd212	Alignment	not modelled	15.4	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
41	c3ktbD_	Alignment	not modelled	15.4	7	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
42	d1r7ha_	Alignment	not modelled	15.0	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
43	d1nm3a1	Alignment	not modelled	14.6	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
44	d2gsta2	Alignment	not modelled	14.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
45	d1jlwa2	Alignment	not modelled	14.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
46	d1h75a_	Alignment	not modelled	14.0	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
47	d1xw6a2	Alignment	not modelled	13.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
48	c3h1nA_	Alignment	not modelled	13.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable glutathione s-transferase; **PDBTitle:** crystal structure of probable glutathione s-transferase from2 bordetella bronchiseptica rb50
49	d1t1va_	Alignment	not modelled	13.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
50	c3ndnC_	Alignment	not modelled	13.1	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**o-succinylhomoserine sulfhydrylase; **PDBTitle:** crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
51	d1fw1a2	Alignment	not modelled	12.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
52	d1glqa2	Alignment	not modelled	12.6	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
53	d2fhea2	Alignment	not modelled	12.2	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
54	d1duga2	Alignment	not modelled	11.4	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
55	d1bwda_	Alignment	not modelled	11.0	21	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Amidinotransferase
						PDB header:dna binding protein

56	c2hueB_	Alignment	not modelled	10.8	9	**Chain:** B: **PDB Molecule:**histone h3; **PDBTitle:** structure of the h3-h4 chaperone asf1 bound to histones h3 and h4
57	d2c4ja2	Alignment	not modelled	10.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
58	d2nv0a1	Alignment	not modelled	10.5	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
59	c2nmpC_	Alignment	not modelled	10.4	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine gamma-lyase; **PDBTitle:** crystal structure of human cystathionine gamma lyase
60	d1rk4a2	Alignment	not modelled	10.1	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
61	d1s9ra_	Alignment	not modelled	9.9	11	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Arginine deiminase
62	d2ftsa3	Alignment	not modelled	9.8	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
63	d2a2ra2	Alignment	not modelled	9.7	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
64	d2gsqa2	Alignment	not modelled	9.5	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
65	c1ua5A_	Alignment	not modelled	9.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** non-fusion gst from s. japonicum in complex with glutathione
66	d2f99a1	Alignment	not modelled	9.0	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
67	d1kx5a_	Alignment	not modelled	9.0	7	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
68	d1k0da2	Alignment	not modelled	9.0	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
69	d1p3ie_	Alignment	not modelled	8.8	9	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
70	c1ibjC_	Alignment	not modelled	8.7	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
71	c2c5sA_	Alignment	not modelled	8.7	15	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
72	c2jl4A_	Alignment	not modelled	8.6	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**maleylpyruvate isomerase; **PDBTitle:** holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
73	d2c5sa1	Alignment	not modelled	8.5	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
74	d2cvda2	Alignment	not modelled	8.0	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
75	d2gsra2	Alignment	not modelled	7.9	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
76	d1dzfa1	Alignment	not modelled	7.9	5	**Fold:**Restriction endonuclease-like **Superfamily:**Eukaryotic RPB5 N-terminal domain **Family:**Eukaryotic RPB5 N-terminal domain
77	d1b48a2	Alignment	not modelled	7.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
78	c1y1yE_	Alignment	not modelled	7.8	6	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** E: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 27 **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
79	d1m0ua2	Alignment	not modelled	7.7	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
80	c3b4oB_	Alignment	not modelled	7.7	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**phenazine biosynthesis protein a/b; **PDBTitle:** crystal structure of phenazine biosynthesis protein phza/b2 from burkholderia cepacia r18194, apo form
81	c1htmB_	Alignment	not modelled	7.4	50	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin ha2 chain; **PDBTitle:** structure of influenza haemagglutinin at the ph of membrane2 fusion
82	d1eqzg_	Alignment	not modelled	7.4	9	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones

83	d1k0dd2	Alignment	not modelled	7.2	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
84	d1ng7a_	Alignment	not modelled	6.8	8	**Fold:**Soluble domain of poliovirus core protein 3a **Superfamily:**Soluble domain of poliovirus core protein 3a **Family:**Soluble domain of poliovirus core protein 3a
85	c2kppA_	Alignment	not modelled	6.7	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0431 protein; **PDBTitle:** solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
86	c3ff0A_	Alignment	not modelled	6.6	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**phenazine biosynthesis protein phzb 2; **PDBTitle:** crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
87	c1tw9C_	Alignment	not modelled	6.6	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase 2; **PDBTitle:** glutathione transferase-2, apo form, from the nematode heligmosomoides2 polygyrus
88	d1ibja_	Alignment	not modelled	6.5	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
89	c3lkxA_	Alignment	not modelled	6.5	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**transcription factor btf3; **PDBTitle:** human nac dimerization domain
90	d1ygya4	Alignment	not modelled	6.4	18	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Serine metabolism enzymes domain **Family:**SerA intervening domain-like
91	c2k6tA_	Alignment	not modelled	6.2	21	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin-like 3 a chain; **PDBTitle:** solution structure of the relaxin-like factor
92	d1id3a_	Alignment	not modelled	6.2	6	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
93	d1gula2	Alignment	not modelled	6.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
94	d2hqya2	Alignment	not modelled	6.1	7	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
95	d1tzyc_	Alignment	not modelled	6.0	7	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
96	c1gumA_	Alignment	not modelled	6.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (glutathione transferase a4-4); **PDBTitle:** human glutathione transferase a4-4 without ligands
97	d1vk9a_	Alignment	not modelled	5.9	11	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Hypothetical protein TM1506
98	d1vbka1	Alignment	not modelled	5.8	6	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
99	d2a1ja1	Alignment	not modelled	5.8	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like