Phyre^2

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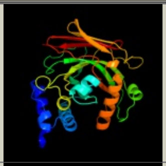
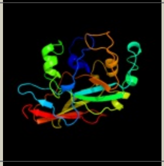
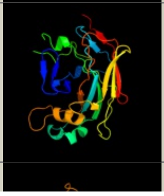
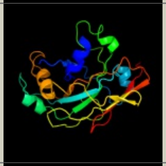
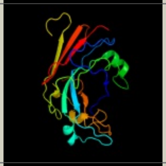
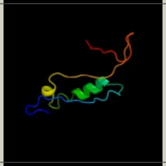
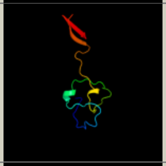
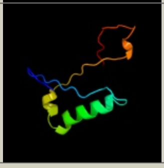
Description	P77608
Date	Thu Jan 5 12:30:59 GMT 2012
Unique Job ID	f51f8aef79b431fd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sv6a_	Alignment		100.0	100	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
2	c2eb5D_	Alignment		100.0	35	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2-oxo-hept-3-ene-1,7-dioate hydratase; **PDBTitle:** crystal structure of hpcg complexed with oxalate
3	c3qdfA_	Alignment		100.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; **PDBTitle:** crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
4	d1sawa_	Alignment		100.0	16	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
5	c3l53F_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative fumarylacetoacetate isomerase/hydrolase; **PDBTitle:** crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
6	d1gtta1	Alignment		100.0	18	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
7	c1wzoC_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hpce; **PDBTitle:** crystal structure of the hpce from thermus thermophilus hb8
8	d1gtta2	Alignment		100.0	17	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
9	d1nr9a_	Alignment		100.0	15	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
10	c1i7oC_	Alignment		100.0	20	**PDB header:**isomerase, lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate degradation bifunctional **PDBTitle:** crystal structure of hpce
11	c3r6oA_	Alignment		100.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; **PDBTitle:** crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus

12	c2dfuB_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; **PDBTitle:** crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
13	d1nkqa_	Alignment		100.0	19	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
14	c3lzkC_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
15	c2q1dX_	Alignment		100.0	16	**PDB header:**lyase **Chain:** X: **PDB Molecule:**2-keto-3-deoxy-d-arabinonate dehydratase; **PDBTitle:** 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate
16	d1hyoa2	Alignment		100.0	17	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
17	c1hyoB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fumarylacetoacetate hydrolase; **PDBTitle:** crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic3 acid
18	d1t8sa_	Alignment		65.1	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
19	c3frnA_	Alignment		41.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flga; **PDBTitle:** crystal structure of flagellar protein flga from thermotoga maritima2 msb8
20	d1ybfa_	Alignment		38.9	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
21	c3qrqA_	Alignment	not modelled	30.3	17	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**putative uncharacterized protein tthb192; **PDBTitle:** structure of thermus thermophilus cse3 bound to an rna representing a2 pre-cleavage complex
22	c3pcoD_	Alignment	not modelled	28.7	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylalanyl-trna synthetase, beta chain; **PDBTitle:** crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
23	c3m9bK_	Alignment	not modelled	23.3	17	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
24	d1m1la_	Alignment	not modelled	22.1	20	**Fold:**Suppressor of Fused, N-terminal domain **Superfamily:**Suppressor of Fused, N-terminal domain **Family:**Suppressor of Fused, N-terminal domain
25	c3mb8A_	Alignment	not modelled	21.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from toxoplasma2 gondii in complex with immucillin-h
26	c2zy3A_	Alignment	not modelled	21.1	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
27	c3butA_	Alignment	not modelled	19.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0446; **PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus
28	d1q1ga_	Alignment	not modelled	18.3	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
						PDB header:transferase

29	c1nw4C_	Alignment	not modelled	18.3	15	**Chain:** C: **PDB Molecule:**uridine phosphorylase, putative; **PDBTitle:** crystal structure of plasmodium falciparum purine nucleoside2 phosphorylase in complex with immh and sulfate
30	c3f6tA_	Alignment	not modelled	17.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
31	d1d4oa_	Alignment	not modelled	14.8	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
32	d1g7sa1	Alignment	not modelled	14.0	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
33	c1yycA_	Alignment	not modelled	13.5	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative late embryogenesis abundant protein; **PDBTitle:** solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
34	c1pt9B_	Alignment	not modelled	12.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
35	d2f4la1	Alignment	not modelled	11.8	30	**Fold:**CUB-like **Superfamily:**Acetamidase/Formamidase-like **Family:**Acetamidase/Formamidase-like
36	d3dm8a1	Alignment	not modelled	11.4	35	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rpa4348-like
37	c1z34A_	Alignment	not modelled	11.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
38	d1k9sa_	Alignment	not modelled	11.0	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
39	d2qamc2	Alignment	not modelled	10.9	38	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
40	d1rl2a2	Alignment	not modelled	9.3	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
41	c3b9tD_	Alignment	not modelled	9.3	41	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of predicted acetamidase/formamidase (yp_546212.1)2 from methylobacillus flagellatus kt at 1.58 a resolution
42	d2j5wa4	Alignment	not modelled	9.1	30	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
43	c3qpbB_	Alignment	not modelled	8.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine phosphorylase; **PDBTitle:** crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
44	d2djia1	Alignment	not modelled	7.9	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
45	c3qo6B_	Alignment	not modelled	7.9	19	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**protease do-like 1, chloroplastic; **PDBTitle:** crystal structure analysis of the plant protease deg1
46	d2j5wa3	Alignment	not modelled	7.8	30	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
47	d1pnoa_	Alignment	not modelled	7.7	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
48	d1vhwa_	Alignment	not modelled	7.7	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
49	d2j5wa1	Alignment	not modelled	7.3	35	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
50	d1pj3a1	Alignment	not modelled	7.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
51	c3icaB_	Alignment	not modelled	7.1	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** the crystal structure of the beta subunit of a phenylalanyl-trna2 synthetase from porphyromonas gingivalis w83
52	d1sdda1	Alignment	not modelled	6.9	37	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
53	c1gr3A_	Alignment	not modelled	6.6	9	**PDB header:**collagen **Chain:** A: **PDB Molecule:**collagen x; **PDBTitle:** structure of the human collagen x nc1 trimer
54	d1gr3a_	Alignment	not modelled	6.6	9	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like

55	c3ggsA_	Alignment	not modelled	6.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
56	c3khsB_	Alignment	not modelled	6.2	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
57	c2csdB_	Alignment	not modelled	6.2	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
58	d1c3ha_	Alignment	not modelled	6.1	9	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
59	c1sddA_	Alignment	not modelled	5.9	35	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
60	d3bgsa1	Alignment	not modelled	5.7	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
61	c2p4sA_	Alignment	not modelled	5.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
62	d1hfua1	Alignment	not modelled	5.4	30	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
63	d1vmka_	Alignment	not modelled	5.2	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
64	d1xo8a_	Alignment	not modelled	5.2	6	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
65	d1odka_	Alignment	not modelled	5.2	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases