Phyre²

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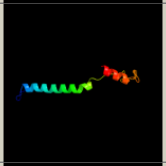
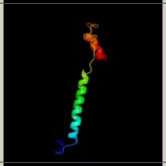
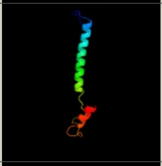
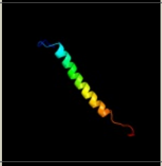
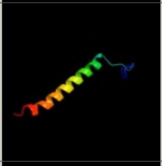
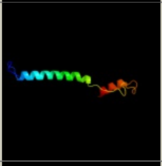
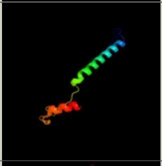
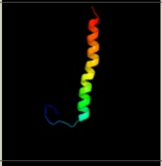
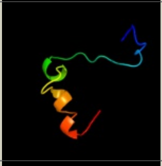
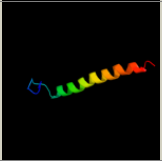
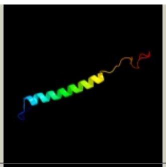
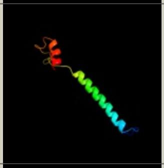
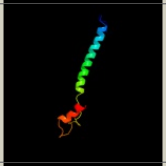
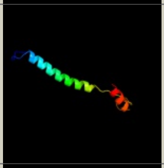
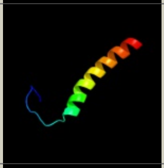
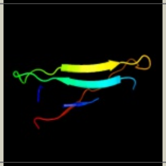
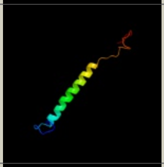
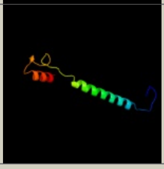
Description	P39375
Date	Wed Jan 25 15:20:53 GMT 2012
Unique Job ID	0c8fb13a0fdeca10

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ia7a1	Alignment		99.5	15	**Fold:**gpW/gp25-like **Superfamily:**gpW/gp25-like **Family:**gpW/gp25-like
2	d1re5a_	Alignment		39.5	14	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
3	c2fenA_	Alignment		33.8	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**3-carboxy-cis,cis-muconate lactonizing enzyme; **PDBTitle:** 3-carboxy-cis,cis-muconate lactonizing enzyme from agrobacterium2 radiobacter s2
4	d1hy0a_	Alignment		24.2	17	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
5	d1tjva_	Alignment		22.5	21	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
6	d1fuoa_	Alignment		22.3	20	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
7	c3c8tA_	Alignment		22.1	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fumarate lyase; **PDBTitle:** crystal structure of fumarate lyase from mesorhizobium sp. bnc1
8	d1q5na_	Alignment		21.9	20	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
9	c3ocfB_	Alignment		21.3	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fumarate lyase:delta crystallin; **PDBTitle:** crystal structure of fumarate lyase:delta crystallin from brucella2 melitensis in native form
10	c3chgB_	Alignment		19.9	13	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**glycine betaine-binding protein; **PDBTitle:** the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
11	d1jswa_	Alignment		19.1	15	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase

12	d1k62a_	Alignment		18.2	17	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
13	c2lhuA_	Alignment		17.1	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
14	d1tj7a_	Alignment		16.8	14	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
15	d1i0aa_	Alignment		16.1	18	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
16	c2pfmA_	Alignment		15.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
17	c1yisA_	Alignment		14.6	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** structural genomics of caenorhabditis elegans: adenylosuccinate lyase
18	d1h3ga1	Alignment		14.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
19	c2e9fC_	Alignment		13.9	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**argininosuccinate lyase; **PDBTitle:** crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine
20	d1dofa_	Alignment		13.5	11	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
21	d1f1oa_	Alignment	not modelled	13.0	10	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
22	c3tl8K_	Alignment	not modelled	11.6	16	**PDB header:**transferase/ligase **Chain:** K: **PDB Molecule:**effector protein hopab2; **PDBTitle:** the avrptob-bak1 complex reveals two structurally similar2 kinaseinteracting domains in a single type iii effector
23	c3tqmD_	Alignment	not modelled	10.7	5	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** structure of an ribosomal subunit interface protein from coxiella2 burnetii
24	c3e04C_	Alignment	not modelled	10.6	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fumarate hydratase; **PDBTitle:** crystal structure of human fumarate hydratase
25	c2vd6B_	Alignment	not modelled	9.9	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** human adenylosuccinate lyase in complex with its substrate2 n6-(1,2-dicarboxyethyl)-amp, and its products amp and3 fumarate.
26	d1c3ca_	Alignment	not modelled	9.6	13	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
27	c2rqlA_	Alignment	not modelled	9.2	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable sigma-54 modulation protein; **PDBTitle:** solution structure of the e. coli ribosome hibernation2 promoting factor hpf
28	c3bhgA_	Alignment	not modelled	8.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of adenylosuccinate lyase from legionella2 pneumophila

29	d1bg4a_	Alignment	not modelled	8.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
30	c1h6wA_	Alignment	not modelled	8.2	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**bacteriophage t4 short tail fibre; **PDBTitle:** crystal structure of a heat- and protease-stable fragment2 of the bacteriophage t4 short fibre
31	d1ddwa_	Alignment	not modelled	7.5	14	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Enabled/VASP homology 1 domain (EVH1 domain)
32	c2fyzC_	Alignment	not modelled	6.9	18	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structural of mumps virus fusion protein core
33	d1ft8e_	Alignment	not modelled	6.9	21	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Non-canonical RBD domain
34	d2arha1	Alignment	not modelled	6.9	10	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Aq 1966-like
35	c2ptsA_	Alignment	not modelled	6.7	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of wild type escherichia coli adenylosuccinate lyase
36	d1tm0a_	Alignment	not modelled	6.0	9	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Proline racemase
37	c3juaB_	Alignment	not modelled	5.9	63	**PDB header:**transcription **Chain:** B: **PDB Molecule:**65 kda yes-associated protein; **PDBTitle:** structural basis of yap recognition by tead4 in the hippo pathway
38	d2i8da1	Alignment	not modelled	5.8	10	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
39	c3pt1A_	Alignment	not modelled	5.7	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0364 protein ymr027w; **PDBTitle:** structure of duf89 from saccharomyces cerevisiae co-crystallized with2 f6p.
40	d2oc6a1	Alignment	not modelled	5.7	13	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
41	c3hfdA_	Alignment	not modelled	5.5	9	**PDB header:**chaperone, protein transport **Chain:** A: **PDB Molecule:**nucleosome assembly protein 1; **PDBTitle:** nucleosome assembly protein 1 from plasmodium knowlesi
42	d2ywqa1	Alignment	not modelled	5.4	16	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
43	d1j3ua_	Alignment	not modelled	5.4	14	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
44	c3gtdB_	Alignment	not modelled	5.2	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fumarate hydratase class ii; **PDBTitle:** 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
45	d1rhoa_	Alignment	not modelled	5.2	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like