Phyre2

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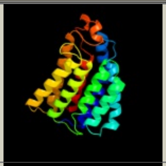
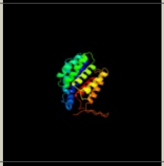
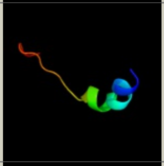
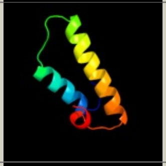
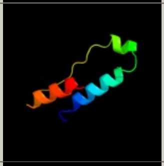
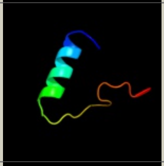
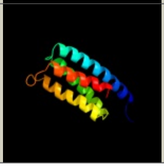
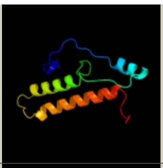
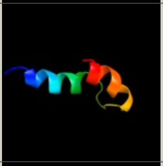
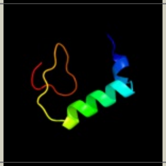
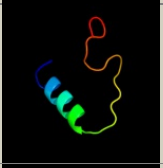
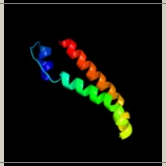
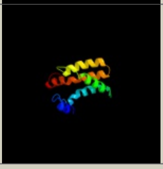
Description	P76014
Date	Thu Jan 5 12:17:24 GMT 2012
Unique Job ID	6209e43972609c5a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2btdA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts-dependent dihydroxyacetone kinase; **PDBTitle:** crystal structure of dhal from e. coli
2	d3cr3a1	Alignment		100.0	35	**Fold:**DhaL-like **Superfamily:**DhaL-like **Family:**DhaL-like
3	d1un8a1	Alignment		100.0	25	**Fold:**DhaL-like **Superfamily:**DhaL-like **Family:**DhaL-like
4	c1un9B_	Alignment		100.0	26	**PDB header:**kinase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
5	d2r6gf1	Alignment		40.0	9	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
6	d1a6db1	Alignment		33.1	17	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**Group II chaperonin (CCT, TRIC), ATPase domain
7	d2hh6a1	Alignment		21.4	8	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
8	d1f61a_	Alignment		21.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
9	d2ax3a2	Alignment		14.0	16	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
10	c2dg2D_	Alignment		12.6	17	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**apolipoprotein a-i binding protein; **PDBTitle:** crystal structure of mouse apolipoprotein a-i binding2 protein
11	c2lchA_	Alignment		11.2	9	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or38; **PDBTitle:** solution nmr structure of a protein with a redesigned hydrophobic2 core, northeast structural genomics consortium target or38

12	d1rvga_	Alignment		10.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
13	c2r5rA_	Alignment		9.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0343 protein ne1163; **PDBTitle:** the crystal structure of duf198 from nitrosomonas europaea2 atcc 19718
14	d2g3qa1	Alignment		9.3	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
15	c3d3kD_	Alignment		9.2	11	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
16	d1ifya_	Alignment		8.4	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
17	c2ax3A_	Alignment		7.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein tm0922; **PDBTitle:** crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
18	d2choa1	Alignment		7.6	16	**Fold:**Hyaluronidase domain-like **Superfamily:**Hyaluronidase post-catalytic domain-like **Family:**Hyaluronidase post-catalytic domain-like
19	c2kddB_	Alignment		7.0	20	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**borealin; **PDBTitle:** solution structure of the conserved c-terminal dimerization2 domain of borealin
20	d1q3qa1	Alignment		7.0	16	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**Group II chaperonin (CCT, TRIC), ATPase domain
21	c3d3jA_	Alignment	not modelled	6.8	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
22	d1wgwa_	Alignment	not modelled	6.6	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
23	d1asha_	Alignment	not modelled	6.5	6	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
24	d1xo3a_	Alignment	not modelled	6.3	40	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
25	d1x6aa2	Alignment	not modelled	6.1	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
26	d2o3la1	Alignment	not modelled	6.0	6	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
27	d1x62a1	Alignment	not modelled	5.9	43	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
28	d1igwa_	Alignment	not modelled	5.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
29	c3d2oB_	Alignment	not modelled	5.6	10	**PDB header:**hydrolase, biosynthetic protein **Chain:** B: **PDB Molecule:**upf0343 protein ngo0387; **PDBTitle:** crystal structure of manganese-metallated gtp

						cyclohydrolase2 type ib
30	c1p58C_	Alignment	not modelled	5.6	22	**PDB header:**virus **Chain:** C: **PDB Molecule:**major envelope protein e; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
31	d1oqya1	Alignment	not modelled	5.5	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
32	c3pm6B_	Alignment	not modelled	5.3	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr