Phyre2

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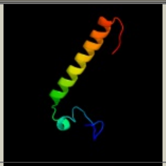
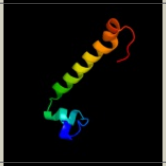
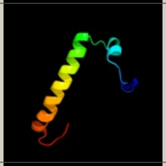
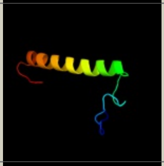
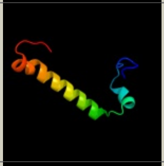
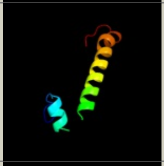
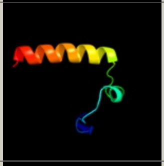
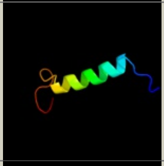
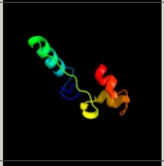
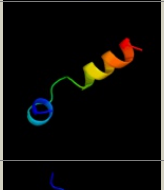
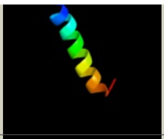
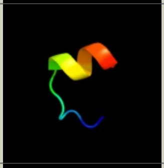
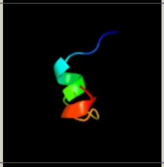
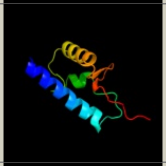
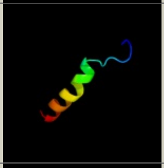
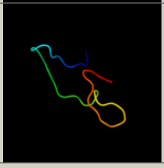
Description	P39283
Date	Thu Jan 5 11:58:53 GMT 2012
Unique Job ID	6ff5fb1865af2c66

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1kuta_	Alignment		69.7	14	**Fold:**SAICAR synthase-like **Superfamily:**SAICAR synthase-like **Family:**SAICAR synthase
2	c2ywvB_	Alignment		65.5	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole succinocarboxamide synthetase; **PDBTitle:** crystal structure of saicar synthetase from geobacillus kaustophilus
3	c3kreA_	Alignment		64.2	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide synthase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from ehrlichia chaffeensis at 1.8a resolution
4	c2h31A_	Alignment		63.0	22	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
5	c2gqsA_	Alignment		60.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide **PDBTitle:** saicar synthetase complexed with cair-mg2+ and adp
6	c2z02A_	Alignment		43.1	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide **PDBTitle:** crystal structure of2 phosphoribosylaminoimidazolesuccinocarboxamide synthase3 wit atp from methanocaldococcus jannaschii
7	c3nuaB_	Alignment		37.1	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide synthase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from clostridium perfringens
8	c3dukD_	Alignment		26.9	13	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
9	c3noyA_	Alignment		18.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
10	d2rgqa1	Alignment		18.2	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rv3472-like
11	d1whra_	Alignment		16.5	30	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain

12	c3fkaD_	Alignment		14.7	12	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized ntf-2 like protein; **PDBTitle:** crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
13	d1x4ta1	Alignment		12.5	29	**Fold:**Long alpha-hairpin **Superfamily:**ISY1 domain-like **Family:**ISY1 N-terminal domain-like
14	d1h8ba_	Alignment		12.3	24	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
15	c2plyB_	Alignment		11.2	14	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
16	d1zk8a2	Alignment		8.6	4	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
17	d1k9vf_	Alignment		7.4	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
18	d1ofcx1	Alignment		6.6	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
19	d1xlya_	Alignment		6.5	4	**Fold:**RNA-binding protein She2p **Superfamily:**RNA-binding protein She2p **Family:**RNA-binding protein She2p
20	d1ogyb_	Alignment		6.5	28	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
21	c2jpmA_	Alignment	not modelled	6.0	19	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**bacteriocin lactococcin-g subunit beta; **PDBTitle:** lactococcin g-b in tfe
22	c1y32A_	Alignment	not modelled	5.8	71	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**humanin; **PDBTitle:** nmr structure of humanin in 30% tfe solution
23	d1o98a1	Alignment	not modelled	5.6	20	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
24	d1ycya1	Alignment	not modelled	5.6	47	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**PF1955-like