Phyre2

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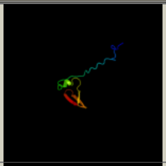
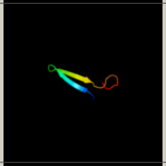
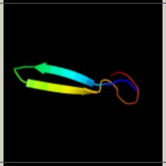
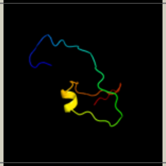
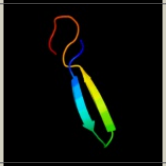
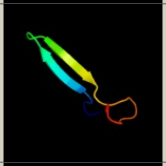
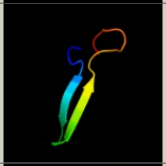
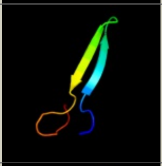
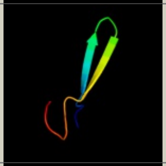
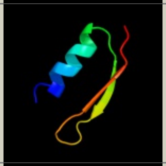
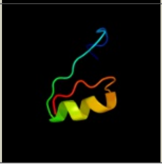
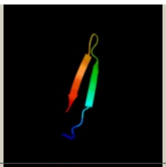
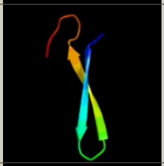
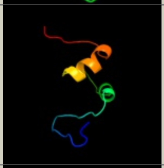
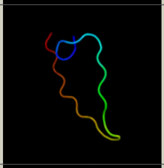
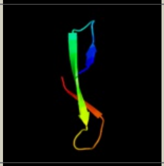
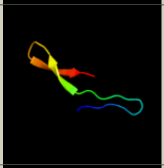
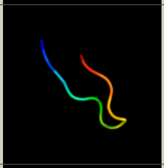
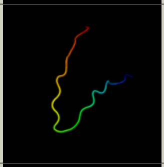
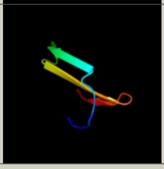
Description	P0ACX9
Date	Thu Jan 5 11:19:22 GMT 2012
Unique Job ID	29e0096d7847767e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jraB_	Alignment		99.8	32	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein rpa2121; **PDBTitle:** a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
2	d1t1ua1	Alignment		29.5	16	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
3	d1xl7a1	Alignment		28.7	12	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
4	d1qqra_	Alignment		22.7	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
5	c1q6xA_	Alignment		17.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline o-acetyltransferase; **PDBTitle:** crystal structure of rat choline acetyltransferase
6	d1nm8a1	Alignment		14.4	21	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
7	c1t7qA_	Alignment		12.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine acetyltransferase; **PDBTitle:** crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
8	d1ndba1	Alignment		12.3	21	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
9	c1xl8B_	Alignment		10.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**peroxisomal carnitine o-octanoyltransferase; **PDBTitle:** crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
10	d1dcja_	Alignment		9.8	19	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
11	c3tq8A_	Alignment		9.6	22	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** structure of the dihydrofolate reductase (fola) from coxiella burnetii2 in complex with trimethoprim

12	c3lydA_	Alignment		9.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative uncharacterized protein from jonesia2 denitrificans
13	c2fy2A_	Alignment		9.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline o-acetyltransferase; **PDBTitle:** structures of ligand bound human choline acetyltransferase2 provide insight into regulation of acetylcholine synthesis
14	c3f0uX_	Alignment		8.5	10	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**trimethoprim-sensitive dihydrofolate reductase; **PDBTitle:** staphylococcus aureus f98y mutant dihydrofolate reductase2 complexed with nadph and 2,4-diamino-5-[3-(3-methoxy-5-3 phenylphenyl)but-1-ynyl]-6-methylpyrimidine
15	d1kv7a2	Alignment		8.1	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
16	c2xzmW_	Alignment		8.1	16	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**40s ribosomal protein s4; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
17	c3iz6D_	Alignment		7.5	24	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
18	d2zjr31	Alignment		7.0	27	**Fold:**L35p-like **Superfamily:**L35p-like **Family:**Ribosomal protein L35p
19	d1v10a2	Alignment		6.5	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
20	c2hsiB_	Alignment		5.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23; **PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
21	d1u0la1	Alignment	not modelled	5.9	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	c3ia5A_	Alignment	not modelled	5.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** moritella profunda dihydrofolate reductase (dhfr)