Phyre2

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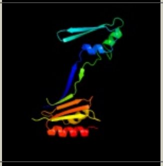
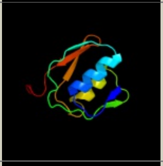
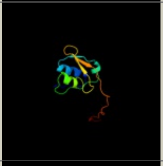
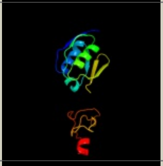
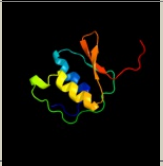
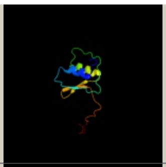
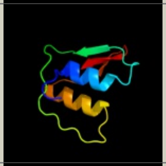
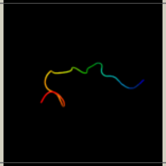
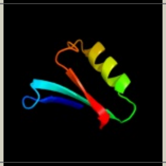
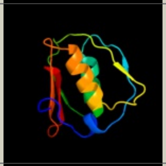
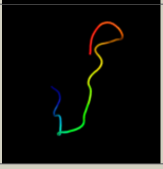
Description	P45758
Date	Thu Jan 5 12:03:35 GMT 2012
Unique Job ID	a697e370707bcc55

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ezjA_	Alignment		100.0	51	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**general secretion pathway protein gspd; **PDBTitle:** crystal structure of the n-terminal domain of the secretin gspd from2 etec determined with the assistance of a nanobody
2	c3ossD_	Alignment		100.0	43	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**type 2 secretion system, secretin gspd; **PDBTitle:** the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
3	c3gr5A_	Alignment		99.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**escc; **PDBTitle:** periplasmic domain of the outer membrane secretin escc from2 enteropathogenic e.coli (epec)
4	c2y9kG_	Alignment		99.9	11	**PDB header:**protein transport **Chain:** G: **PDB Molecule:**protein invg; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
5	c2y3mA_	Alignment		99.8	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein hofq; **PDBTitle:** structure of the extra-membranous domain of the secretin2 hofq from actinobacillus actinomycetemcomitans
6	c2a02A_	Alignment		98.0	11	**PDB header:**membrane protein, metal transport **Chain:** A: **PDB Molecule:**ferric-pseudobactin 358 receptor; **PDBTitle:** solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter pupa from3 pseudomonas putida.
7	c1zzvA_	Alignment		97.0	21	**PDB header:**membrane protein, metal transport **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca; **PDBTitle:** solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter feca from3 escherichia coli.
8	c2d1uA_	Alignment		96.7	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca; **PDBTitle:** solution strcuture of the periplasmic signaling domain of2 feca from escherichia coli
9	c2iahA_	Alignment		96.5	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine.
10	c3cddD_	Alignment		94.2	17	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**prophage muso2, 43 kda tail protein; **PDBTitle:** crystal structure of prophage muso2, 43 kda tail protein from2 shewanella oneidensis
11	d3cdda2	Alignment		94.1	17	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like

12	c3d37A_	Alignment		86.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tail protein, 43 kda; **PDBTitle:** the crystal structure of the tail protein from neisseria meningitidis2 mc58
13	c1wruA_	Alignment		84.7	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**43 kda tail protein; **PDBTitle:** structure of central hub elucidated by x-ray analysis of gene product2 44; baseplate component of bacteriophage mu
14	d3d37a1	Alignment		80.9	10	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
15	d1wrua2	Alignment		74.9	14	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
16	c1b35D_	Alignment		45.9	26	**PDB header:**virus **Chain:** D: **PDB Molecule:**protein (cricket paralysis virus, vp4); **PDBTitle:** cricket paralysis virus (crpv)
17	d3proc2	Alignment		26.7	23	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
18	c4proD_	Alignment		17.7	21	**PDB header:**serine protease **Chain:** D: **PDB Molecule:**alpha-lytic protease; **PDBTitle:** alpha-lytic protease complexed with pro region
19	c3adyA_	Alignment		13.2	14	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**dotd; **PDBTitle:** crystal structure of dotd from legionella
20	c3ec1A_	Alignment		12.6	29	**PDB header:**hydrolase, signaling protein **Chain:** A: **PDB Molecule:**yqeh gtpase; **PDBTitle:** structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnos1 / atnoa1 ortholog)
21	c3h2yA_	Alignment	not modelled	12.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtpase family protein; **PDBTitle:** crystal structure of yqeh gtpase from bacillus anthracis with dgdp2 bound
22	d2ctfa1	Alignment	not modelled	10.7	12	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
23	d2dy1a4	Alignment	not modelled	7.0	17	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
24	c2ehoL_	Alignment	not modelled	6.7	23	**PDB header:**replication **Chain:** L: **PDB Molecule:**gins complex subunit 3; **PDBTitle:** crystal structure of human gins complex
25	d2jnaa1	Alignment	not modelled	6.5	13	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
26	d2ahua2	Alignment	not modelled	5.7	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
27	d1mlaa2	Alignment	not modelled	5.2	11	**Fold:**Ferredoxin-like **Superfamily:**Probable ACP-binding domain of malonyl-CoA ACP transacylase **Family:**Probable ACP-binding domain of malonyl-CoA ACP transacylase
28	c3rrlC_	Alignment	not modelled	5.2	42	**PDB header:**transferase **Chain:** C: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; **PDBTitle:** complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695