Phyre2

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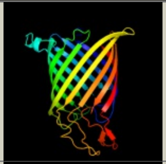
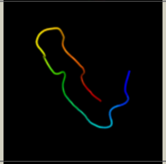
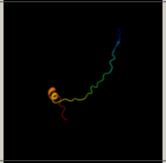
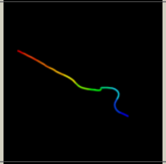
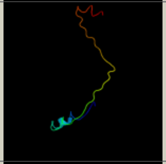
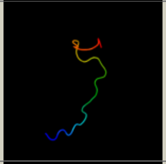
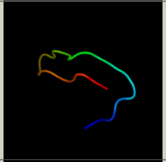
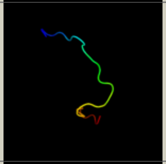
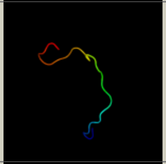
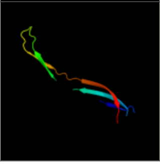
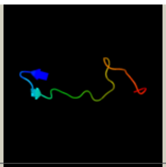
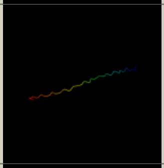
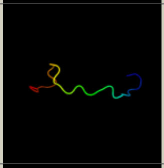
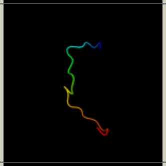
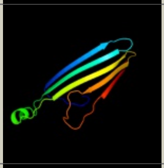
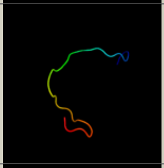
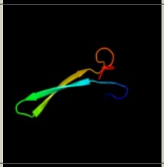
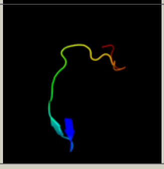
Description	P0A927
Date	Thu Jan 5 11:09:14 GMT 2012
Unique Job ID	b8a24512c3d908f0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tlya_	Alignment		100.0	100	**Fold:**Transmembrane beta-barrels **Superfamily:**Tsx-like channel **Family:**Tsx-like channel
2	d2e9xb2	Alignment		20.4	41	**Fold:**GINS/PriA/YqbF domain **Superfamily:**PriA/YqbF domain **Family:**PSF2 N-terminal domain-like
3	d2jnaa1	Alignment		20.3	39	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
4	c3epzA_	Alignment		20.2	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 1; **PDBTitle:** structure of the replication foci-targeting sequence of human dna2 cytosine methyltransferase dnmt1
5	c3f09B_	Alignment		18.9	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** 1.82 angstrom resolution crystal structure of holo-(acyl-carrier-2 protein) synthase (acps) from staphylococcus aureus
6	c1u8cB_	Alignment		17.7	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** a novel adaptation of the integrin psi domain revealed from its2 crystal structure
7	c3n6rK_	Alignment		16.7	25	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
8	c2e9xF_	Alignment		15.5	41	**PDB header:**replication **Chain:** F: **PDB Molecule:**dna replication complex gins protein psf2; **PDBTitle:** the crystal structure of human gins core complex
9	d2j9ga3	Alignment		14.0	29	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
10	c3u9sE_	Alignment		13.7	33	**PDB header:**ligase **Chain:** E: **PDB Molecule:**methylcrotonyl-coa carboxylase, alpha-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
11	c2x27X_	Alignment		13.1	17	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa

12	c3g8cB_	Alignment		12.5	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
13	c2k3aA_	Alignment		12.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chap domain protein; **PDBTitle:** nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
14	d1w96a3	Alignment		12.0	24	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
15	d1gsoa3	Alignment		10.0	35	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
16	c2qdzA_	Alignment		9.3	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**tpsb transporter fhac; **PDBTitle:** structure of the membrane protein fhac: a member of the2 omp85/tpsb transporter family
17	c2vpqA_	Alignment		7.6	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
18	c3bg5C_	Alignment		7.6	25	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
19	c2pvpB_	Alignment		7.5	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
20	c2gpwC_	Alignment		7.3	27	**PDB header:**ligase **Chain:** C: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
21	c2hjwA_	Alignment	not modelled	7.2	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2
22	c1w96B_	Alignment	not modelled	7.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
23	d1iu4a_	Alignment	not modelled	6.5	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Microbial transglutaminase
24	d1ev11_	Alignment	not modelled	6.4	19	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
25	c3iu0A_	Alignment	not modelled	6.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** structural basis for zymogen activation and substrate binding of2 transglutaminase from streptomyces mobaraense
26	c3lyvF_	Alignment	not modelled	5.8	24	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
27	c3k6sB_	Alignment	not modelled	5.8	15	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
28	c2ktlA_	Alignment	not modelled	5.7	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of c-terminal domain from mttyrrs of a.

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29	d1vkza3	Alignment	not modelled	5.6	25	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
30	c2k0lA_	Alignment	not modelled	5.6	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
31	c3ouzA_	Alignment	not modelled	5.5	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
32	c2q5xA_	Alignment	not modelled	5.5	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** crystal structure of the c-terminal domain of hnup98
33	c2jmmA_	Alignment	not modelled	5.3	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr solution structure of a minimal transmembrane beta-2 barrel platform protein
34	d1jyaa_	Alignment	not modelled	5.2	19	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone