Phyre^2

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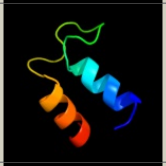
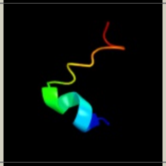
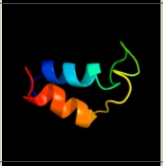
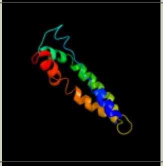
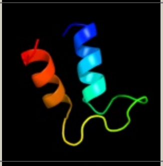
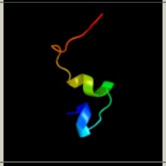
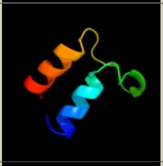
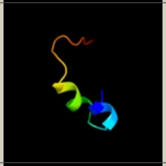
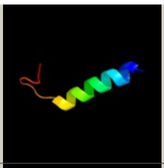
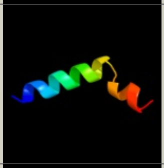
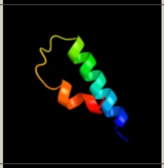
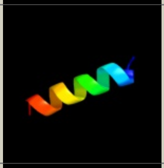
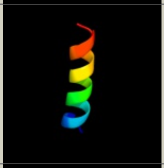
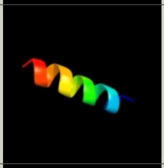
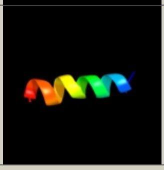
Description	P21345
Date	Thu Jan 5 11:38:04 GMT 2012
Unique Job ID	6d69d8d5fdc8356f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2nwwa1	Alignment		100.0	36	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
2	d1a77a1	Alignment		48.3	21	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
3	c1dpqA_	Alignment		28.8	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib subunit; **PDBTitle:** solution structure of the constitutively active mutant of2 the integrin alpha iib cytoplasmic domain.
4	d1mc8a1	Alignment		28.5	18	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
5	d1iwga8	Alignment		26.8	5	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
6	d1b43a1	Alignment		21.4	18	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
7	c3ah5E_	Alignment		18.4	12	**PDB header:**transferase **Chain:** E: **PDB Molecule:**thymidylate synthase thyx; **PDBTitle:** crystal structure of flavin dependent thymidylate synthase thyx from2 helicobacter pylori complexed with fad and dump
8	d1ul1x1	Alignment		18.3	16	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
9	d1rxwa1	Alignment		18.2	24	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
10	d1o26a_	Alignment		15.7	16	**Fold:**Thymidylate synthase-complementing protein Thy1 **Superfamily:**Thymidylate synthase-complementing protein Thy1 **Family:**Thymidylate synthase-complementing protein Thy1
11	d1xo1a1	Alignment		12.9	21	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain

12	c2klzA_	Alignment		11.3	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ataxin-3; **PDBTitle:** solution structure of the tandem uim domain of ataxin-3 complexed with2 ubiquitin
13	d1fp1d1	Alignment		8.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Plant O-methyltransferase, N-terminal domain
14	c2vy8A_	Alignment		8.6	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** the 627-domain from influenza a virus polymerase pb22 subunit with glu-627
15	d2e74e1	Alignment		7.8	24	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
16	c2e75E_	Alignment		7.8	24	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
17	c2e76E_	Alignment		7.8	24	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
18	c2e74E_	Alignment		7.8	24	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
19	c1vf5R_	Alignment		7.7	22	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
20	c1vf5E_	Alignment		7.7	22	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
21	d1iwga7	Alignment	not modelled	7.5	8	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
22	c2c9kA_	Alignment	not modelled	7.4	11	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidal crystal protein cry4aa; **PDBTitle:** structure of the functional form of the mosquito-larvicidal2 cry4aa toxin from bacillus thuringiensis at 2.8 a3 resolution
23	d1kyza1	Alignment	not modelled	7.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Plant O-methyltransferase, N-terminal domain
24	c2izoA_	Alignment	not modelled	6.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** structure of an archaeal pcna1-pcna2-fen1 complex
25	c3h3mB_	Alignment	not modelled	6.5	17	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**flagellar protein flit; **PDBTitle:** crystal structure of flagellar protein flit from bordetella2 bronchiseptica
26	d1cmwa1	Alignment	not modelled	6.2	22	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
27	c2cfaB_	Alignment	not modelled	5.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate synthase; **PDBTitle:** structure of viral flavin-dependant thymidylate synthase2 thyx
28	c1rxvA_	Alignment	not modelled	5.7	24	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** crystal structure of a. fulgidus fen-1 bound to dna

29	d2z1ca1	Alignment	not modelled	5.2	12	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
30	c3d9sB_	Alignment	not modelled	5.2	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
31	c2zt9E_	Alignment	not modelled	5.1	27	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
32	c2jwaA_	Alignment	not modelled	5.1	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure