Phyre^2

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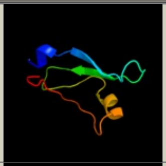
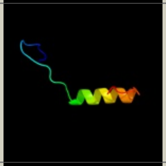
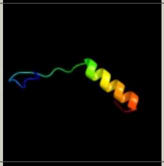
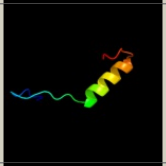
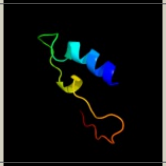
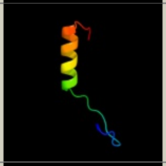
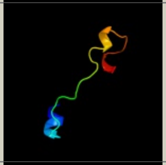
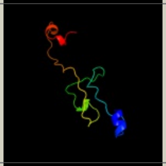
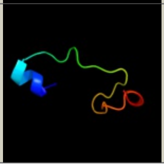
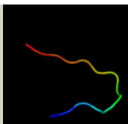
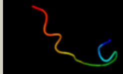
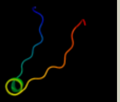
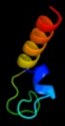
Description	P75737
Date	Thu Jan 5 12:13:36 GMT 2012
Unique Job ID	40c12eecaa3f5d6e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jiwi_	Alignment		54.9	25	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
2	c3ko7E_	Alignment		51.6	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase; **PDBTitle:** dtd from plasmodium falciparum in complex with d-lysine
3	d2f2ab2	Alignment		38.0	21	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
4	c3h0mE_	Alignment		36.8	32	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
5	c2g5iB_	Alignment		36.3	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
6	d1j7ga_	Alignment		31.3	29	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
7	c3al0B_	Alignment		27.5	29	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
8	c2xuvB_	Alignment		27.5	33	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hdeb; **PDBTitle:** the structure of hdeb
9	c2xi1A_	Alignment		23.5	42	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nef; **PDBTitle:** crystal structure of the hiv-1 nef sequenced from a patient's sample
10	c3rbbA_	Alignment		21.1	23	**PDB header:**viral protein, protein binding **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** hiv-1 nef protein in complex with engineered hck sh3 domain
11	d2nefa_	Alignment		20.5	38	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef

12	d1jkea_	Alignment		16.3	29	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
13	c2okvC_	Alignment		13.8	43	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable d-tyrosyl-trna(tyr) deacylase 1; **PDBTitle:** c-myc dna unwinding element binding protein
14	c2dboA_	Alignment		13.7	57	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase; **PDBTitle:** crystal structure of d-tyr-trna(tyr) deacylase from aquifex aeolicus
15	d1f3va_	Alignment		13.2	39	**Fold:**Ferredoxin-like **Superfamily:**TRADD, N-terminal domain **Family:**TRADD, N-terminal domain
16	d2pifa1	Alignment		12.1	32	**Fold:**PSTPO5379-like **Superfamily:**PSTPO5379-like **Family:**PSTPO5379-like
17	c2yrcA_	Alignment		11.4	31	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec23a; **PDBTitle:** solution structure of the zf-sec23_sec24 from human sec23a
18	d1w0na_	Alignment		10.5	41	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
19	c3nymA_	Alignment		9.4	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of functionally unknown protein from neisseria2 meningitidis mc58
20	c1yodB_	Alignment		8.7	77	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**water-solublized phospholamban; **PDBTitle:** crystal structure of a water soluble analog of phospholamban
21	d1tc5a_	Alignment	not modelled	8.6	22	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
22	c3ho6B_	Alignment	not modelled	8.6	16	**PDB header:**toxin **Chain:** B: **PDB Molecule:**toxin a; **PDBTitle:** structure-function analysis of inositol hexakisphosphate-2 induced autoprocessing in clostridium difficile toxin a
23	c2p22D_	Alignment	not modelled	8.1	38	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**hypothetical 12.0 kda protein in ade3-ser2 **PDBTitle:** structure of the yeast escrt-i heterotetramer core
24	d1zxqa2	Alignment	not modelled	7.9	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
25	d1efnb_	Alignment	not modelled	7.9	32	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
26	c1yodA_	Alignment	not modelled	7.8	77	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**water-solublized phospholamban; **PDBTitle:** crystal structure of a water soluble analog of phospholamban
27	c3ik5A_	Alignment	not modelled	6.8	37	**PDB header:**viral protein/signaling protein **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** sivmac239 nef in complex with tcr zeta itam 1 polypeptide2 (a63-r80)
28	d2qtva5	Alignment	not modelled	6.6	16	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24
						Fold: Acyl carrier protein-like

29	d1a8oa_	Alignment	not modelled	6.5	43	**Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
30	d1ny722	Alignment	not modelled	6.4	29	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
31	d1smpi_	Alignment	not modelled	6.3	19	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
32	c2bfuL_	Alignment	not modelled	6.2	29	**PDB header:**virus **Chain:** L: **PDB Molecule:**cowpea mosaic virus, large (l) subunit; **PDBTitle:** x-ray structure of cpmv top component
33	d1pgl22	Alignment	not modelled	6.2	35	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
34	d2ysca1	Alignment	not modelled	6.1	83	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
35	d1jmxa5	Alignment	not modelled	5.9	33	**Fold:**Streptavidin-like **Superfamily:**Quinohemoprotein amine dehydrogenase A chain, domain 3 **Family:**Quinohemoprotein amine dehydrogenase A chain, domain 3
36	d2oa4a1	Alignment	not modelled	5.8	60	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
37	c2opkC_	Alignment	not modelled	5.5	56	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
38	c3r47I_	Alignment	not modelled	5.4	100	**PDB header:**de novo protein **Chain:** I: **PDB Molecule:**coiled coil helix l24h; **PDBTitle:** crystal structure of a 6-helix coiled coil cc-hex-h24
39	c3r47J_	Alignment	not modelled	5.4	100	**PDB header:**de novo protein **Chain:** J: **PDB Molecule:**coiled coil helix l24h; **PDBTitle:** crystal structure of a 6-helix coiled coil cc-hex-h24
40	c3r47B_	Alignment	not modelled	5.4	100	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coiled coil helix l24h; **PDBTitle:** crystal structure of a 6-helix coiled coil cc-hex-h24
41	c3fzyA_	Alignment	not modelled	5.3	50	**PDB header:**toxin **Chain:** A: **PDB Molecule:**rtx toxin rtxa; **PDBTitle:** crystal structure of pre-cleavage form of cysteine protease domain2 from vibrio cholerae rtxa toxin
42	c3eebB_	Alignment	not modelled	5.2	50	**PDB header:**toxin **Chain:** B: **PDB Molecule:**rtx toxin rtxa; **PDBTitle:** structure of the v. cholerae rtx cysteine protease domain
43	c2re3A_	Alignment	not modelled	5.2	58	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
44	c1bmv2_	Alignment	not modelled	5.1	35	**PDB header:**virus/rna **Chain:** 2: **PDB Molecule:**protein (icosahedral virus - b and c domain); **PDBTitle:** protein-rna interactions in an icosahedral virus at 3.02 angstroms resolution
45	c2xxzA_	Alignment	not modelled	5.1	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of the human jmjd3 jumonji domain
46	c3r47L_	Alignment	not modelled	5.1	100	**PDB header:**de novo protein **Chain:** L: **PDB Molecule:**coiled coil helix l24h; **PDBTitle:** crystal structure of a 6-helix coiled coil cc-hex-h24
47	c3r47M_	Alignment	not modelled	5.1	100	**PDB header:**de novo protein **Chain:** M: **PDB Molecule:**coiled coil helix l24h; **PDBTitle:** crystal structure of a 6-helix coiled coil cc-hex-h24
48	c3r47F_	Alignment	not modelled	5.1	100	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**coiled coil helix l24h; **PDBTitle:** crystal structure of a 6-helix coiled coil cc-hex-h24