Phyre2

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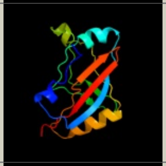
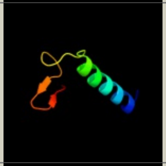
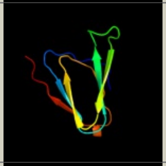
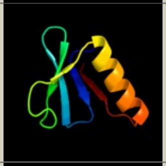
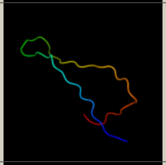
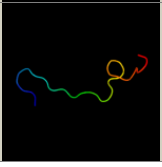
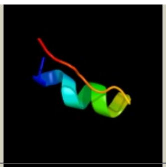
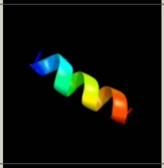
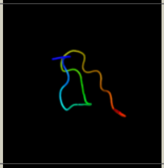
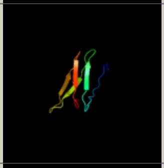
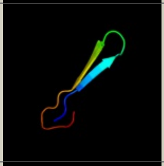
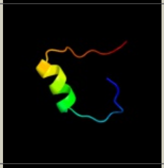
Description	C3UPD1
Date	Thu Jan 5 10:56:22 GMT 2012
Unique Job ID	9481017d6fde861c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1p6va_	Alignment		100.0	50	**Fold:**Small protein B (SmpB) **Superfamily:**Small protein B (SmpB) **Family:**Small protein B (SmpB)
2	c1p6vC_	Alignment		100.0	50	**PDB header:**rna binding protein/rna **Chain:** C: **PDB Molecule:**ssra-binding protein; **PDBTitle:** crystal structure of the trna domain of transfer-messenger2 rna in complex with smpb
3	c1j1hA_	Alignment		100.0	46	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**small protein b; **PDBTitle:** solution structure of a tmrna-binding protein, smpb, from2 thermus thermophilus
4	d1wjxa_	Alignment		100.0	51	**Fold:**Small protein B (SmpB) **Superfamily:**Small protein B (SmpB) **Family:**Small protein B (SmpB)
5	d2ipqx1	Alignment		34.1	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**STY4665 C-terminal domain-like
6	c2qnkA_	Alignment		32.5	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyanthranilate 3,4-dioxygenase; **PDBTitle:** crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
7	c2agaA_	Alignment		23.3	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**machado-joseph disease protein 1; **PDBTitle:** de-ubiquitinating function of ataxin-3: insights from the2 solution structure of the josephin domain
8	d1yfua1	Alignment		18.0	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
9	d1sdwa2	Alignment		17.0	15	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**PHM/PNGase F **Family:**Peptidylglycine alpha-hydroxylating monooxygenase, PHM
10	c1wqsA_	Alignment		16.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3c-like protease; **PDBTitle:** crystal structure of norovirus 3c-like protease
11	d1g31a_	Alignment		14.1	36	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES

12	c3jsbA_	Alignment		11.9	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-directed rna polymerase; **PDBTitle:** crystal structure of the n-terminal domain of the lymphocytic2 choriomeningitis virus l protein
13	c1hf9B_	Alignment		11.5	21	**PDB header:**atpase inhibitor **Chain:** B: **PDB Molecule:**atpase inhibitor (mitochondrial); **PDBTitle:** c-terminal coiled-coil domain from bovine if1
14	d2qfaa1	Alignment		11.4	27	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
15	d1zvfa1	Alignment		10.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
16	c2quoA_	Alignment		10.0	27	**PDB header:**toxin **Chain:** A: **PDB Molecule:**heat-labile enterotoxin b chain; **PDBTitle:** crystal structure of c terminal fragment of clostridium2 perfringens enterotoxin
17	c2w3zA_	Alignment		8.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
18	c2oa9B_	Alignment		8.7	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**r.mvai; **PDBTitle:** restriction endonuclease mvai in the absence of dna
19	d2raxa1	Alignment		8.3	27	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
20	d2nlya1	Alignment		7.8	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
21	d2c1ia1	Alignment	not modelled	7.7	24	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
22	d1m4ma_	Alignment	not modelled	7.7	27	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
23	d2qqra1	Alignment	not modelled	7.6	31	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
24	d1d1na_	Alignment	not modelled	7.4	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
25	d2cc0a1	Alignment	not modelled	7.4	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
26	c3mjdA_	Alignment	not modelled	6.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
27	c2ylaA_	Alignment	not modelled	6.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
28	d1im3d_	Alignment	not modelled	6.3	28	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Cytomegalovirus protein US2
29	d8ohma2	Alignment	not modelled	6.2	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate

29		Alignment	not modelled	6.2	24	hydrolases **Family:**RNA helicase
30	d1kk1a1	Alignment	not modelled	6.1	36	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
31	c2z59A_	Alignment	not modelled	6.0	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein adrm1; **PDBTitle:** complex structures of mouse rpn13 (22-130aa) and ubiquitin
32	c2r2yA_	Alignment	not modelled	6.0	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein adrm1; **PDBTitle:** crystal structure of the proteasomal rpn13 pru-domain
33	d1jd5a_	Alignment	not modelled	5.9	26	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
34	d2ieca1	Alignment	not modelled	5.7	71	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
35	c2crvA_	Alignment	not modelled	5.5	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
36	d2gjxa1	Alignment	not modelled	5.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
37	d2i52a1	Alignment	not modelled	5.4	71	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
38	d1jaka1	Alignment	not modelled	5.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
39	d1yhta1	Alignment	not modelled	5.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
40	d1mkya3	Alignment	not modelled	5.2	9	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Probable GTPase Der, C-terminal domain **Family:**Probable GTPase Der, C-terminal domain
41	c2elvA_	Alignment	not modelled	5.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 6th c2h2 zinc finger of human2 zinc finger protein 406
42	c2ogfD_	Alignment	not modelled	5.1	57	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0408; **PDBTitle:** crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372