Phyre2

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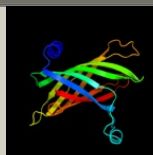
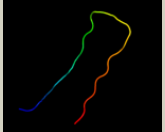
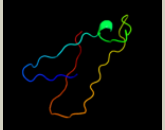
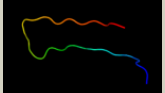
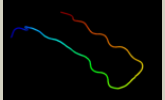
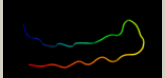
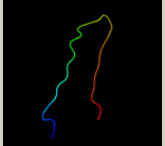
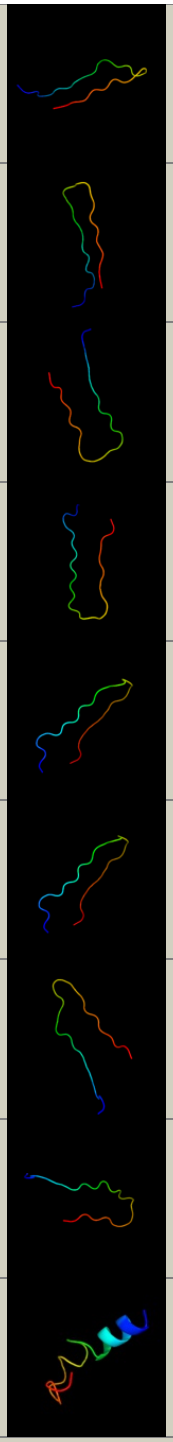
Description	P37001
Date	Thu Jan 5 11:54:10 GMT 2012
Unique Job ID	8340449e0b2aa36e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1thqa_	Alignment		100.0	99	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane enzyme PagP
2	d1c8na_	Alignment		42.4	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
3	c4sbvC_	Alignment		42.0	27	**PDB header:**virus **Chain:** C: **PDB Molecule:**southern bean mosaic virus coat protein; **PDBTitle:** the refinement of southern bean mosaic virus in reciprocal2 space
4	d4sbvc_	Alignment		42.0	27	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
5	d4sbva_	Alignment		40.0	27	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
6	d1f2nc_	Alignment		39.9	21	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
7	d2vq0a1	Alignment		38.2	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
8	c1x35C_	Alignment		35.0	23	**PDB header:**virus **Chain:** C: **PDB Molecule:**coat protein; **PDBTitle:** recombinant t=3 capsid of a site specific mutant of semv cp
9	d1smva_	Alignment		34.3	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
10	c2izwC_	Alignment		31.7	31	**PDB header:**virus **Chain:** C: **PDB Molecule:**ryegrass mottle virus coat protein; **PDBTitle:** crystal structure of ryegrass mottle virus
11	c1c8nC_	Alignment		30.5	23	**PDB header:**virus **Chain:** C: **PDB Molecule:**coat protein; **PDBTitle:** tobacco necrosis virus

12	d1c8nc_	Alignment		30.5	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
13	c1f2nA_	Alignment		30.5	15	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** rice yellow mottle virus
14	d1f2na_	Alignment		30.5	15	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
15	d1ng0c_	Alignment		29.1	19	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
16	d1ng0a_	Alignment		26.8	19	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
17	c1ng0A_	Alignment		26.8	19	**PDB header:**virus **Chain:** A: **PDB Molecule:**coat protein; **PDBTitle:** the three-dimensional structure of cocksfoot mottle virus2 at 2.7a resolution
18	d1smvc_	Alignment		24.7	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
19	d2tbvc_	Alignment		24.3	29	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
20	d2axtz1	Alignment		19.7	33	**Fold:**Transmembrane helix hairpin **Superfamily:**PsbZ-like **Family:**PsbZ-like
21	c2zahC_	Alignment	not modelled	16.6	38	**PDB header:**virus **Chain:** C: **PDB Molecule:**coat protein; **PDBTitle:** x-ray structure of melon necrotic spot virus
22	d1m3ya1	Alignment	not modelled	15.5	38	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Major capsid protein vp54
23	d1opoa_	Alignment	not modelled	12.2	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
24	c1opoB_	Alignment	not modelled	12.2	23	**PDB header:**virus **Chain:** B: **PDB Molecule:**coat protein; **PDBTitle:** the structure of carnation mottle virus
25	d1bev1_	Alignment	not modelled	12.2	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
26	d1cov1_	Alignment	not modelled	10.7	22	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
27	d1igqa_	Alignment	not modelled	9.7	26	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
28	c1m4xC_	Alignment	not modelled	8.3	38	**PDB header:**virus **Chain:** C: **PDB Molecule:**pbcv-1 virus capsid; **PDBTitle:** pbcv-1 virus capsid, quasi-atomic model
29	d1p2za1	Alignment	not modelled	8.3	26	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP

						Family: Adenovirus hexon
30	c1j5qB_	Alignment	not modelled	8.3	38	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**major capsid protein; **PDBTitle:** the structure and evolution of the major capsid protein of a large,2 lipid-containing, dna virus.
31	d2d8za2	Alignment	not modelled	8.1	56	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
32	d1igub_	Alignment	not modelled	7.8	26	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
33	d2gr8a1	Alignment	not modelled	7.8	29	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
34	d1txna_	Alignment	not modelled	7.0	29	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
35	d1lrwb_	Alignment	not modelled	6.9	50	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Methanol dehydrogenase subunit **Family:**Methanol dehydrogenase subunit
36	c3hdfA_	Alignment	not modelled	6.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of truncated endolysin r21 from phage 21
37	c2c1lA_	Alignment	not modelled	6.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease; **PDBTitle:** structure of the bfii restriction endonuclease
38	d1qjpa_	Alignment	not modelled	6.2	25	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
39	c2inyA_	Alignment	not modelled	6.0	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hexon protein; **PDBTitle:** nanoporous crystals of chicken embryo lethal orphan (celo) adenovirus2 major coat protein, hexon
40	c3c5yD_	Alignment	not modelled	5.9	43	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
41	c2ppwA_	Alignment	not modelled	5.9	43	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
42	d1aa7a_	Alignment	not modelled	5.8	20	**Fold:**Influenza virus matrix protein M1 **Superfamily:**Influenza virus matrix protein M1 **Family:**Influenza virus matrix protein M1
43	c3l4cB_	Alignment	not modelled	5.7	28	**PDB header:**cell adhesion, cell invasion, apoptosis **Chain:** B: **PDB Molecule:**dedicator of cytokinesis protein 1; **PDBTitle:** structural basis of membrane-targeting by dock180
44	d1qj8a_	Alignment	not modelled	5.7	20	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
45	d1t23a_	Alignment	not modelled	5.7	46	**Fold:**Chromosomal protein MC1 **Superfamily:**Chromosomal protein MC1 **Family:**Chromosomal protein MC1
46	c2bviK_	Alignment	not modelled	5.6	26	**PDB header:**virus **Chain:** K: **PDB Molecule:**hexon protein; **PDBTitle:** the quasi-atomic model of human adenovirus type 52 capsid (part 2)
47	d1xmeb2	Alignment	not modelled	5.6	50	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
48	d1y60a_	Alignment	not modelled	5.6	33	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Formaldehyde-activating enzyme, FAE
49	c3onoA_	Alignment	not modelled	5.5	57	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
50	c3rpjA_	Alignment	not modelled	5.5	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**curlin genes transcriptional regulator; **PDBTitle:** structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.
51	d2hepa1	Alignment	not modelled	5.4	29	**Fold:**Long alpha-hairpin **Superfamily:**YnzC-like **Family:**YznC-like
52	c2hepA_	Alignment	not modelled	5.4	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** solution nmr structure of the upf0291 protein ynzc from2 bacillus subtilis. northeast structural genomics target3 sr384.
53	d1ncqa_	Alignment	not modelled	5.1	13	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
54	c2kebA_	Alignment	not modelled	5.1	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit