Phyre2

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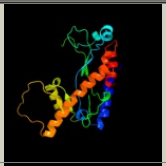
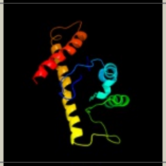
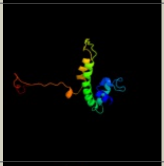
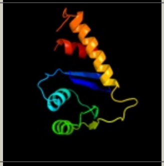
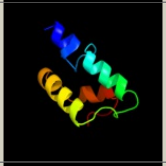
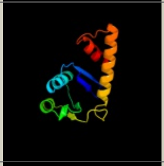
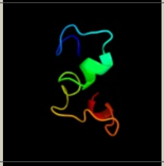
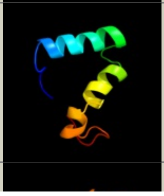
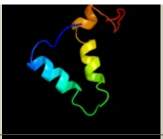
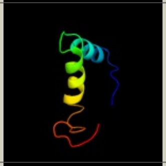
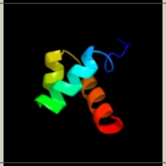
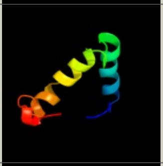
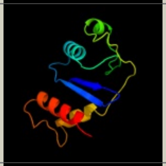
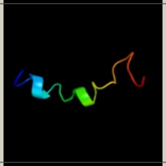
Description	P0CE49
Date	Wed Jan 25 15:20:36 GMT 2012
Unique Job ID	4761ea2154e3d457

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	Alignment		98.2	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	Alignment		97.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
3	d1cxqa_	Alignment		84.2	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
4	c3hefB_	Alignment		79.7	14	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
5	d1asua_	Alignment		70.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
6	c3nf9A_	Alignment		47.7	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
7	d1a9xa1	Alignment		39.7	16	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
8	d1c0ma2	Alignment		35.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
9	c1c0mA_	Alignment		30.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase
10	d1slma1	Alignment		29.6	27	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
11	c3ohwB_	Alignment		22.4	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**phycobilisome lcm core-membrane linker polypeptide; **PDBTitle:** x-ray structure of phycobilisome lcm core-membrane linker polypeptide2 (fragment 721-860) from synechocystis sp. pcc 6803, northeast3 structural genomics consortium target sgr209e

12	c2ky4A_	Alignment		22.4	16	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycobilisome linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
13	c2l3wA_	Alignment		20.8	20	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycobilisome rod linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker domain of phycobilisome rod2 linker polypeptide from synechococcus elongatus, northeast structural3 genomics consortium target snr168a
14	d1k78a1	Alignment		19.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
15	c3pruD_	Alignment		19.4	13	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**phycobilisome 32.1 kda linker polypeptide, phycocyanin- **PDBTitle:** crystal structure of phycobilisome 32.1 kda linker polypeptide,2 phycocyanin-associated, rod 1 (fragment 14-158) from synechocystis3 sp. pcc 6803, northeast structural genomics consortium target sgr182a
16	c2l06A_	Alignment		18.7	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phycobilisome lcm core-membrane linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker polypeptide domain (fragment2 254-400) of phycobilisome linker protein apce from synechocystis sp.3 pcc 6803. northeast structural genomics consortium target sgr209c
17	d1hyva_	Alignment		18.2	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
18	c1q2iA_	Alignment		17.8	28	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**pnc27; **PDBTitle:** nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
19	d1exqa_	Alignment		16.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
20	c3pvpA_	Alignment		15.9	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
21	c3f9kV_	Alignment	not modelled	15.1	14	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
22	d1su3a1	Alignment	not modelled	14.8	28	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
23	c2o8kA_	Alignment	not modelled	14.2	27	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
24	c3u1nC_	Alignment	not modelled	14.2	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** structure of the catalytic core of human samhd1
25	c1k6yB_	Alignment	not modelled	12.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase
26	c1x6iB_	Alignment	not modelled	12.2	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ygfy; **PDBTitle:** crystal structure of ygfy from escherichia coli
27	c1bg1A_	Alignment	not modelled	10.9	11	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex
28	d2fug11	Alignment	not modelled	9.9	19	**Fold:**Bromodomain-like **Superfamily:**Nqo1C-terminal domain-like **Family:**Nqo1C-terminal domain-like
29	d1nkua_	Alignment	not modelled	9.1	13	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase I (Tag)

30	d2d1ha1	Alignment	not modelled	8.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
31	c3iwfA_	Alignment	not modelled	8.3	4	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
32	c2kvcA_	Alignment	not modelled	8.2	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
33	d1sfka_	Alignment	not modelled	7.6	19	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
34	d1s1ma2	Alignment	not modelled	7.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
35	d1c6va_	Alignment	not modelled	7.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
36	d1vcoa2	Alignment	not modelled	6.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
37	d1r6ra_	Alignment	not modelled	5.9	10	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
38	c1r6rA_	Alignment	not modelled	5.9	10	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** solution structure of dengue virus capsid protein reveals a2 new fold
39	c1yvlB_	Alignment	not modelled	5.7	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1
40	c1ud0B_	Alignment	not modelled	5.6	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**70 kda heat-shock-like protein; **PDBTitle:** crystal structure of the c-terminal 10-kda subdomain of hsc70
41	d1h3fa1	Alignment	not modelled	5.6	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
42	c2vkpA_	Alignment	not modelled	5.6	12	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**btb/poz domain-containing protein 6; **PDBTitle:** crystal structure of btb domain from btbd6
43	c3d3kD_	Alignment	not modelled	5.4	12	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
44	c1m6vE_	Alignment	not modelled	5.4	16	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
45	d1j1va_	Alignment	not modelled	5.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
46	c2lkyA_	Alignment	not modelled	5.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b