Phyre2

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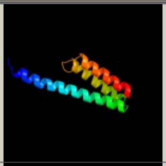
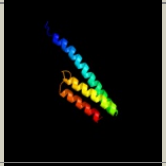
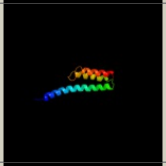
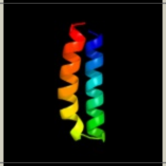
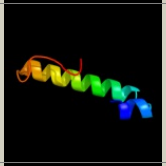
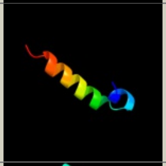
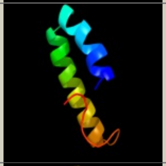
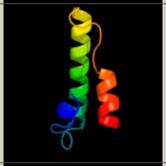
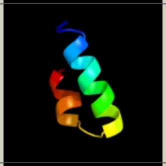
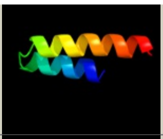
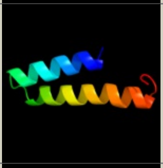
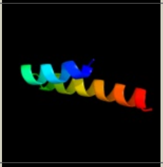
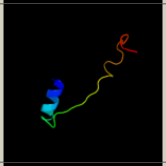
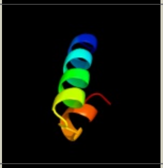
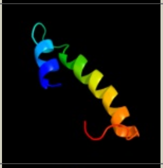
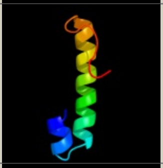
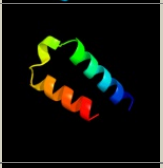
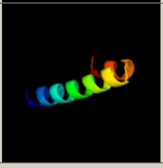
Description	P0A7U7
Date	Wed Jan 25 15:20:18 GMT 2012
Unique Job ID	80cea54fa2c74294

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gy9t1	Alignment		100.0	100	**Fold:**Spectrin repeat-like **Superfamily:**Ribosomal protein S20 **Family:**Ribosomal protein S20
2	d2uubt1	Alignment		100.0	33	**Fold:**Spectrin repeat-like **Superfamily:**Ribosomal protein S20 **Family:**Ribosomal protein S20
3	c3bbnT_	Alignment		100.0	35	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**ribosomal protein s20; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
4	d1h6qa_	Alignment		26.7	14	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Translationally controlled tumor protein TCTP (histamine-releasing factor)
5	d1txja_	Alignment		24.4	9	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Translationally controlled tumor protein TCTP (histamine-releasing factor)
6	c2oxoA_	Alignment		21.7	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
7	c3dzaB_	Alignment		19.8	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized putative membrane protein; **PDBTitle:** crystal structure of a putative membrane protein of unknown function2 (yfdx) from klebsiella pneumoniae subsp. at 1.65 a resolution
8	c2khvA_	Alignment		18.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
9	c2kj8A_	Alignment		18.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative prophage cps-53 integrase; **PDBTitle:** nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
10	d2k54a1	Alignment		17.8	23	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0742-like
11	d1yz1a1	Alignment		17.2	7	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Translationally controlled tumor protein TCTP (histamine-releasing factor)

12	c3k1sE_	Alignment		16.3	18	**PDB header:**transferase **Chain:** E: **PDB Molecule:**pts system, cellobiose-specific iia component; **PDBTitle:** crystal structure of the pts cellobiose specific enzyme iia2 from bacillus anthracis
13	d2oo2a1	Alignment		13.6	16	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**AF1782-like **Family:**AF1782-like
14	c2dl1A_	Alignment		13.2	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**spartin; **PDBTitle:** solution structure of the mit domain from human spartin
15	c1xb2B_	Alignment		13.1	28	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor ts, mitochondrial; **PDBTitle:** crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex
16	d3en8a1	Alignment		12.9	24	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rpa4348-like
17	c3lysC_	Alignment		12.9	10	**PDB header:**recombination **Chain:** C: **PDB Molecule:**prophage pi2 protein 01, integrase; **PDBTitle:** crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
18	c2kj9A_	Alignment		10.3	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
19	d1h7ca_	Alignment		10.0	8	**Fold:**Spectrin repeat-like **Superfamily:**Tubulin chaperone cofactor A **Family:**Tubulin chaperone cofactor A
20	c3soyA_	Alignment		9.5	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ntf2-like superfamily protein; **PDBTitle:** nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
21	c2khqA_	Alignment	not modelled	9.1	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
22	c3kspA_	Alignment	not modelled	7.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**calcium/calmodulin-dependent kinase ii association domain; **PDBTitle:** crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution
23	d1ohpa1	Alignment	not modelled	7.3	28	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ketosteroid isomerase-like
24	c3l8rA_	Alignment	not modelled	6.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative pts system, cellobiose-specific iia **PDBTitle:** the crystal structure of ptca from s. mutans
25	d2a15a1	Alignment	not modelled	6.7	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ketosteroid isomerase-like
26	d1u00a1	Alignment	not modelled	6.6	15	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Heat shock protein 70kD (HSP70), C-terminal subdomain **Family:**Heat shock protein 70kD (HSP70), C-terminal subdomain
27	c2odmA_	Alignment	not modelled	6.6	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**upf0358 protein mw0995; **PDBTitle:** crystal structure of s. aureus ylan, an essential leucine rich protein2 involved in the control of cell shape
28	d2f86b1	Alignment	not modelled	6.2	10	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent

						protein kinase type II alpha subunit, CAMK2A
29	c1wcrA_	Alignment	not modelled	6.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, n, n'-diacetylchitobiose-specific **PDBTitle:** trimeric structure of the enzyme iia from escherichia coli2 phosphotransferase system specific for n,n'-3 diacetylchitobiose
30	c3kh1B_	Alignment	not modelled	5.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**predicted metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of predicted metal-dependent2 phosphohydrolase (zp_00055740.2) from magnetospirillum3 magnetotacticum ms-1 at 1.37 a resolution
31	c2kkvA_	Alignment	not modelled	5.5	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of an integrase domain from protein2 spa4288 from salmonella enterica, northeast structural3 genomics consortium target slr105h
32	d2ux0a1	Alignment	not modelled	5.3	23	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
33	d1aipc1	Alignment	not modelled	5.2	29	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
34	c3i0yC_	Alignment	not modelled	5.2	24	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution