Phyre^2

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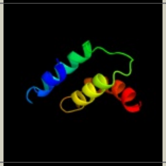
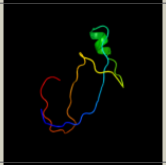
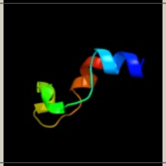
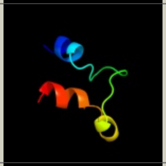
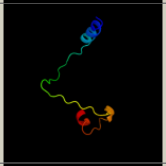
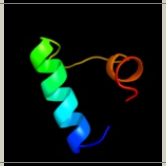
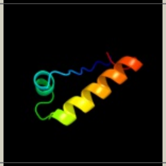
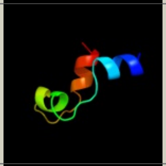
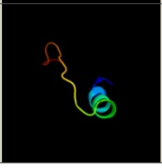
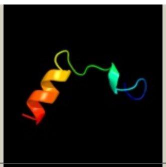
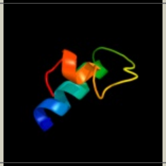
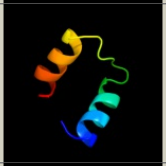
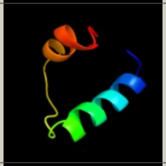
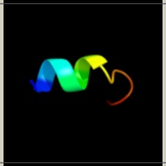
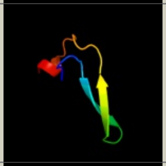
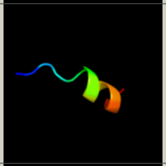
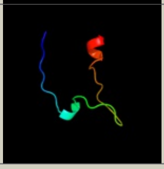
Description	P39336
Date	Thu Jan 5 11:59:27 GMT 2012
Unique Job ID	f4d7d81ed7f3e669

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qzaA_	Alignment		95.3	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of salmonella effector protein sopa
2	c3nb2B_	Alignment		94.6	31	**PDB header:**ligase **Chain:** B: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of e. coli o157:h7 effector protein nleI
3	d1qcsa2	Alignment		24.9	21	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
4	d1vmja_	Alignment		19.3	24	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
5	c1ve0A_	Alignment		18.3	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein (st2072); **PDBTitle:** crystal structure of uncharacterized protein st2072 from sulfolobus2 tokodaii
6	d1vpha_	Alignment		18.0	24	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
7	c2w8dB_	Alignment		17.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid synthase 2; **PDBTitle:** distinct and essential morphogenic functions for wall- and2 lipo-teichoic acids in bacillus subtilis
8	c3ik5A_	Alignment		16.9	33	**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)
9	d1s4ka_	Alignment		16.6	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**YdiL-like
10	c2p6cB_	Alignment		15.9	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**aq_2013 protein; **PDBTitle:** crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
11	d2py5a1	Alignment		14.9	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease

12	c2jynA_	Alignment		14.2	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0368 protein ypl225w; **PDBTitle:** a novel solution nmr structure of protein yst0336 from2 saccharomyces cerevisiae. northeast structural genomics3 consortium target yt51/ontario centre for structural4 proteomics target yst0336
13	c2xi1A_	Alignment		14.2	39	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nef; **PDBTitle:** crystal structure of the hiv-1 nef sequenced from a patient's sample
14	d1efnb_	Alignment		13.4	33	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
15	c3rbbA_	Alignment		12.4	39	**PDB header:**viral protein, protein binding **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** hiv-1 nef protein in complex with engineered hck sh3 domain
16	d2nefa_	Alignment		12.1	33	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
17	c3ebcA_	Alignment		11.9	62	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**type-2 restriction enzyme hincii; **PDBTitle:** structure of n141a hincii with cognate dna
18	d1bf4a_	Alignment		11.8	42	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
19	c1p82A_	Alignment		11.6	62	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**10 kda chaperonin; **PDBTitle:** nmr structure of 1-25 fragment of mycobacterium2 tuberculosis cpn10
20	d2pgca1	Alignment		11.5	56	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Marine metagenome family DABB3
21	d1tx3a1	Alignment	not modelled	11.3	62	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease HincII
22	d1vj0a1	Alignment	not modelled	10.9	20	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
23	c2xrhA_	Alignment	not modelled	10.8	32	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein hp0721; **PDBTitle:** crystal structure of the truncated form of hp0721
24	c2elpA_	Alignment	not modelled	9.0	55	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
25	d1alqa_	Alignment	not modelled	8.9	22	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
26	d1ug7a_	Alignment	not modelled	8.6	20	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain from hypothetical 2610208m17rik protein **Family:**Domain from hypothetical 2610208m17rik protein
27	c2qyxB_	Alignment	not modelled	8.3	31	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein mj0159; **PDBTitle:** crystal structure of uncharacterized protein mj0159 from2 methanocaldococcus jannaschii
28	c2jvfA_	Alignment	not modelled	8.1	32	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
29	c1qysA_	Alignment	not modelled	7.9	29	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7;

29	c1qysA_	Alignment	not modelled	7.9	29	**PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
30	c2ejsA_	Alignment	not modelled	7.9	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**autocrine motility factor receptor, isoform 2; **PDBTitle:** solution structure of ruh-076, a human cue domain
31	d1y14a_	Alignment	not modelled	7.8	12	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNA polymerase II subunit RBP4 (RpoF)
32	c2r8rB_	Alignment	not modelled	7.7	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
33	c3lgeG_	Alignment	not modelled	7.3	47	**PDB header:**lyase/protein binding **Chain:** G: **PDB Molecule:**sorting nexin-9; **PDBTitle:** crystal structure of rabbit muscle aldolase-snx9 lc4 complex
34	c3lgeF_	Alignment	not modelled	7.3	47	**PDB header:**lyase/protein binding **Chain:** F: **PDB Molecule:**sorting nexin-9; **PDBTitle:** crystal structure of rabbit muscle aldolase-snx9 lc4 complex
35	c3h0gP_	Alignment	not modelled	6.9	21	**PDB header:**transcription **Chain:** P: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb4; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
36	c3l76B_	Alignment	not modelled	6.7	42	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
37	c1qdnA_	Alignment	not modelled	6.6	21	**PDB header:**fusion protein **Chain:** A: **PDB Molecule:**protein (n-ethylmaleimide sensitive fusion **PDBTitle:** amino terminal domain of the n-ethylmaleimide sensitive2 fusion protein (nsf)
38	c2klqA_	Alignment	not modelled	6.5	29	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication licensing factor mcm6; **PDBTitle:** the solution structure of cbd of human mcm6
39	d1vmfa_	Alignment	not modelled	6.1	23	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
40	d2qrdb1	Alignment	not modelled	6.0	44	**Fold:**AMPKBI-like **Superfamily:**AMPKBI-like **Family:**AMPKBI-like
41	d1p2fa1	Alignment	not modelled	5.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
42	c3fo8D_	Alignment	not modelled	5.9	43	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**tail sheath protein gp18; **PDBTitle:** crystal structure of the bacteriophage t4 tail sheath2 protein, protease resistant fragment gp18pr
43	c2ex3I_	Alignment	not modelled	5.9	33	**PDB header:**transferase/replication **Chain:** I: **PDB Molecule:**dna polymerase; **PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein
44	c2wzpR_	Alignment	not modelled	5.8	28	**PDB header:**viral protein **Chain:** R: **PDB Molecule:**lactococcal phage p2 orf16; **PDBTitle:** structures of lactococcal phage p2 baseplate shed light on2 a novel mechanism of host attachment and activation in3 siphoviridae
45	c3gpkA_	Alignment	not modelled	5.8	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ppic-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
46	c2k0mA_	Alignment	not modelled	5.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43
47	d1gado1	Alignment	not modelled	5.6	58	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	d1ggaa1	Alignment	not modelled	5.6	58	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	d2qlvb2	Alignment	not modelled	5.5	44	**Fold:**AMPKBI-like **Superfamily:**AMPKBI-like **Family:**AMPKBI-like
50	d2nn4a1	Alignment	not modelled	5.4	37	**Fold:**YqgQ-like **Superfamily:**YqgQ-like **Family:**YqgQ-like
51	c3jszA_	Alignment	not modelled	5.4	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** legionella pneumophila glucosyltransferase lgt1 n293a with udp-glc
52	d2v8qb1	Alignment	not modelled	5.3	44	**Fold:**AMPKBI-like **Superfamily:**AMPKBI-like **Family:**AMPKBI-like
53	c2qdjA_	Alignment	not modelled	5.2	11	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**retinoblastoma-associated protein; **PDBTitle:** crystal structure of the retinoblastoma protein n-domain2 provides insight into tumor suppression, ligand3 interaction and holoprotein architecture
						PDB header:protein binding

54	c2cp8A_	 Alignment	not modelled	5.2	31	**Chain:** A: **PDB Molecule:**next to brca1 gene 1 protein; **PDBTitle:** solution structure of the rsgi ruh-046, a uba domain from2 human next to brca1 gene 1 protein (kiaa0049 protein)3 r923h variant
55	c2cu5C_	 Alignment	not modelled	5.2	27	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved hypothetical protein tt1486; **PDBTitle:** crystal structure of the conserved hypothetical protein tt1486 from2 thermus thermophilus hb8
56	c1zk6A_	 Alignment	not modelled	5.1	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** nmr solution structure of b. subtilis prsa ppiase