Phyre^2

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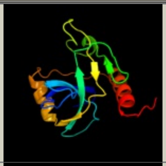
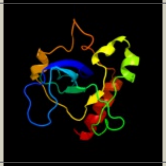
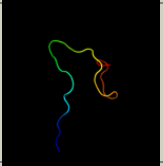
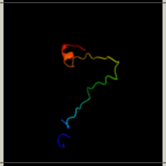
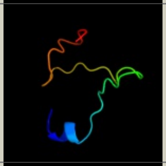
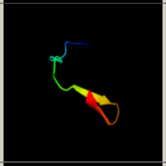
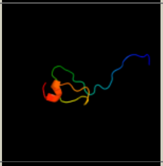
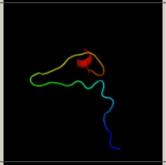
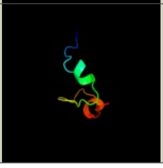
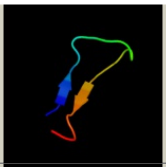
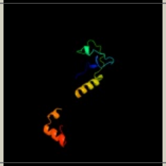
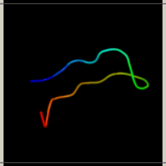
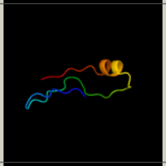
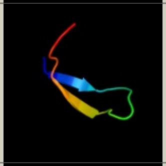
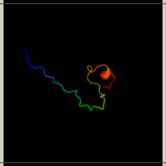
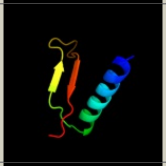
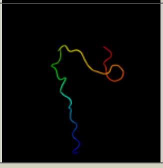
Description	P56259
Date	Thu Jan 5 12:06:21 GMT 2012
Unique Job ID	ce6bc104702e7f54

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ne8a_	Alignment		99.6	16	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
2	d1m1fa_	Alignment		99.5	18	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
3	d1ub4a_	Alignment		99.3	27	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
4	c1ym7C_	Alignment		56.4	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**beta-adrenergic receptor kinase 1; **PDBTitle:** g protein-coupled receptor kinase 2 (grk2)
5	c3e7eA_	Alignment		54.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mitotic checkpoint serine/threonine-protein kinase bub1; **PDBTitle:** structure and substrate recruitment of the human spindle checkpoint2 kinase bub
6	c3qa8A_	Alignment		38.9	18	**PDB header:**immune system, signaling protein **Chain:** A: **PDB Molecule:**mgc80376 protein; **PDBTitle:** crystal structure of inhibitor of kappa b kinase beta
7	c2kytA_	Alignment		37.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
8	c3pfqA_	Alignment		35.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c beta type; **PDBTitle:** crystal structure and allosteric activation of protein kinase c beta2 ii
9	c3c4yA_	Alignment		33.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodopsin kinase; **PDBTitle:** crystal structure of apo form of g protein coupled receptor kinase 12 at 7.51a
10	d1kjwa2	Alignment		25.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
11	c2a1aB_	Alignment		24.2	16	**PDB header:**protein synthesis/transferase **Chain:** B: **PDB Molecule:**interferon-induced, double-stranded rna-activated protein **PDBTitle:** pkr kinase domain-eif2alpha complex

12	c3iz5N_	Alignment		15.9	30	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
13	d1fn9a_	Alignment		15.9	23	**Fold:**Outer capsid protein sigma 3 **Superfamily:**Outer capsid protein sigma 3 **Family:**Outer capsid protein sigma 3
14	c3izcN_	Alignment		14.8	25	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
15	c2jqmA_	Alignment		12.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**envelope protein e; **PDBTitle:** yellow fever envelope protein domain iii nmr structure2 (s288-k398)
16	c4a19F_	Alignment		12.7	25	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl14; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
17	c2qg5D_	Alignment		12.7	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**calcium/calmodulin-dependent protein kinase; **PDBTitle:** cryptosporidium parvum calcium dependent protein kinase cgd7_1840
18	d1qb5d_	Alignment		12.5	24	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
19	d1x6oa1	Alignment		11.8	25	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
20	c3dzoA_	Alignment		11.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhoptry kinase domain; **PDBTitle:** crystal structure of a rhoptry kinase from toxoplasma gondii
21	c3byvA_	Alignment	not modelled	10.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhoptry kinase; **PDBTitle:** crystal structure of toxoplasma gondii specific rhoptry2 antigen kinase domain
22	c1kjwA_	Alignment	not modelled	10.4	14	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**postsynaptic density protein 95; **PDBTitle:** sh3-guanylate kinase module from psd-95
23	c3q60A_	Alignment	not modelled	9.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rop5b; **PDBTitle:** crystal structure of virulent allele rop5b pseudokinase domain bound2 to atp
24	d2je6i1	Alignment	not modelled	9.6	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
25	d2joya1	Alignment	not modelled	9.6	30	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L14e
26	c2acxB_	Alignment	not modelled	8.9	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**g protein-coupled receptor kinase 6; **PDBTitle:** crystal structure of g protein coupled receptor kinase 6 bound to2 amppnp
27	d1qcfa3	Alignment	not modelled	8.7	16	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
28	c3nahC_	Alignment	not modelled	8.6	5	**PDB header:**transferase **Chain:** C: **PDB Molecule:**rna dependent rna polymerase; **PDBTitle:** crystal structures and functional analysis of murine norovirus rna-2 dependent rna polymerase
						PDB header:ribosome

29	c4a18N_	Alignment	not modelled	8.6	21	**Chain:** N: **PDB Molecule:**rpl27; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
30	c3ayhB_	Alignment	not modelled	8.4	36	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc8; **PDBTitle:** crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
31	c2vwiC_	Alignment	not modelled	8.3	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine/threonine-protein kinase osr1; **PDBTitle:** structure of the osr1 kinase, a hypertension drug target
32	d2g4ca1	Alignment	not modelled	8.1	12	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
33	c2b43D_	Alignment	not modelled	8.1	4	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**non-structural polyprotein; **PDBTitle:** crystal structure of the norwalk virus rna dependent rna polymerase2 from strain hu/nlv/dresden174/1997/ge
34	d1k8ib2	Alignment	not modelled	7.7	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
35	c2cgvA_	Alignment	not modelled	7.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase chk1; **PDBTitle:** identification of chemically diverse chk1 inhibitors by2 receptor-based virtual screening
36	c1khiA_	Alignment	not modelled	7.4	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hex1; **PDBTitle:** crystal structure of hex1
37	d1qpca_	Alignment	not modelled	7.4	13	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
38	d1u09a_	Alignment	not modelled	7.3	9	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
39	c2pziA_	Alignment	not modelled	7.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable serine/threonine-protein kinase pkng; **PDBTitle:** crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
40	c3egpA_	Alignment	not modelled	7.1	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure analysis of dengue-1 envelope protein2 domain iii
41	c1imhD_	Alignment	not modelled	7.1	16	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**nuclear factor of activated t cells 5; **PDBTitle:** tonebp/dna complex
42	c2ckzB_	Alignment	not modelled	7.1	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase iii 25 kd **PDBTitle:** x-ray structure of rna polymerase iii subcomplex c17-c25.
43	c3ckxA_	Alignment	not modelled	7.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase 24; **PDBTitle:** crystal structure of sterile 20-like kinase 3 (mst3, stk24)2 in complex with staurosporine
44	c1zp9A_	Alignment	not modelled	6.8	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rio1 kinase; **PDBTitle:** crystal structure of full-legnth a.fulgidus rio1 serine kinase bound2 to atp and mn2+ ions.
45	c2uutA_	Alignment	not modelled	6.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase; **PDBTitle:** the 2.4 angstrom resolution structure of the d346g mutant2 of the sapporo virus rdrp polymerase
46	c3uatA_	Alignment	not modelled	6.5	15	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**disks large homolog 1; **PDBTitle:** guanylate kinase domains of the maguk family scaffold proteins as2 specific phospho-protein binding modules
47	c3lijA_	Alignment	not modelled	6.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calcium/calmodulin dependent protein kinase with **PDBTitle:** crystal structure of full length cpcdpk3 (cgd5_820) in2 complex with ca2+ and amppnp
48	c2ux8G_	Alignment	not modelled	6.4	13	**PDB header:**transferase **Chain:** G: **PDB Molecule:**glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
49	d1nsca_	Alignment	not modelled	6.3	31	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
50	c3f6kA_	Alignment	not modelled	6.2	50	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sortilin; **PDBTitle:** crystal structure of the vps10p domain of human sortilin/nts3 in2 complex with neurotensin
51	c2fo0A_	Alignment	not modelled	6.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase abl1 (1b isoform); **PDBTitle:** organization of the sh3-sh2 unit in active and inactive forms of the2 c-abl tyrosine kinase
52	c3er0A_	Alignment	not modelled	6.1	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of the full length eif5a from2 saccharomyces cerevisiae
						PDB header:transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase i subunit

53	c2rf4A_	Alignment	not modelled	5.6	36	rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
54	d1umga_	Alignment	not modelled	5.3	19	**Fold:**Sulfolobus fructose-1,6-bisphosphatase-like **Superfamily:**Sulfolobus fructose-1,6-bisphosphatase-like **Family:**Sulfolobus fructose-1,6-bisphosphatase-like
55	c2htuA_	Alignment	not modelled	5.2	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**neuraminidase; **PDBTitle:** n8 neuraminidase in complex with peramivir
56	d1unaa_	Alignment	not modelled	5.2	39	**Fold:**RNA bacteriophage capsid protein **Superfamily:**RNA bacteriophage capsid protein **Family:**RNA bacteriophage capsid protein
57	c2b8kG_	Alignment	not modelled	5.1	36	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii