Phyre^2

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Description	P0A763
Date	Wed Jan 25 15:20:17 GMT 2012
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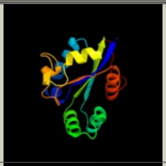
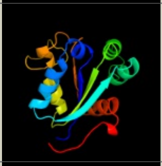
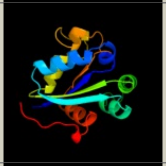
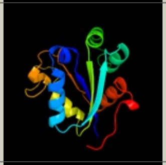
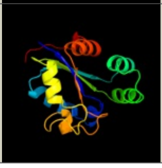
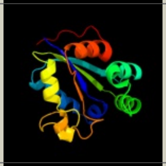
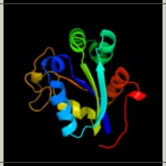
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hurF_	Alignment		100.0	100	**PDB header:**signaling protein,transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** escherichia coli nucleoside diphosphate kinase
2	d1s57a_	Alignment		100.0	40	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
3	d1ehwa_	Alignment		100.0	39	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
4	d1w7wa_	Alignment		100.0	42	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
5	c3js9A_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase family protein; **PDBTitle:** crystal structure of nucleoside diphosphate kinase family protein from2 babesia bovis
6	c2vu5A_	Alignment		100.0	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of pndk from bacillus anthracis
7	c1w7wF_	Alignment		100.0	42	**PDB header:**transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure and mutational analysis of a plant mitochondrial2 nucleoside diphosphate kinase: identification of residues3 involved in serine phosphorylation and oligomerization.
8	d3bbba1	Alignment		100.0	42	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
9	d1xiqa_	Alignment		100.0	39	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
10	d1nhkl_	Alignment		100.0	57	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
11	c3q89H_	Alignment		100.0	45	**PDB header:**transferase **Chain:** H: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of staphylococcus aureus nucleoside diphosphate2 kinase complexed with cdp

12	d1nb2a_	Alignment		100.0	47	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
13	d1ucna_	Alignment		100.0	42	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
14	c3mpdA_	Alignment		100.0	39	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of nucleoside diphosphate kinase from2 encephalitozoon cuniculi, cubic form, apo
15	d2dyaa1	Alignment		100.0	47	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
16	d1be4a_	Alignment		100.0	43	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
17	d1u8wa_	Alignment		100.0	43	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
18	d1hlwa_	Alignment		100.0	45	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
19	c3ngtJ_	Alignment		100.0	51	**PDB header:**transferase **Chain:** J: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure of leishmania ndkb complexed with amp.
20	d1zs6a1	Alignment		100.0	45	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
21	d1wkja1	Alignment	not modelled	100.0	50	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
22	d1pkua1	Alignment	not modelled	100.0	42	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
23	d2az3a1	Alignment	not modelled	100.0	47	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
24	d1xqia1	Alignment	not modelled	100.0	44	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
25	d1nsqa_	Alignment	not modelled	100.0	46	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
26	d1k44a_	Alignment	not modelled	100.0	46	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
27	c2az1B_	Alignment	not modelled	100.0	45	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure of a halophilic nucleoside diphosphate kinase2 from halobacterium salinarum
28	c3b54A_	Alignment	not modelled	100.0	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** saccharomyces cerevisiae nucleoside diphosphate kinase
29	d2b8qa1	Alignment	not modelled	100.0	37	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK

						Family: Nucleoside diphosphate kinase, NDK
30	c3b6bF_	Alignment	not modelled	100.0	37	**PDB header:**transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of acanthamoeba polyphaga mimivirus2 nucleoside diphosphate kinase complexed with dgdp
31	c3r9lA_	Alignment	not modelled	100.0	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of nucleoside diphosphate kinase from giardia2 lamblia featuring a disordered dinucleotide binding site
32	c2bx6A_	Alignment	not modelled	98.4	18	**PDB header:**transduction protein **Chain:** A: **PDB Molecule:**xrp2 protein; **PDBTitle:** crystal structure of the human retinitis pigmentosa2 protein 2 (rp2)
33	c3bqsB_	Alignment	not modelled	36.9	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
34	c3p04A_	Alignment	not modelled	35.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
35	c1y7pB_	Alignment	not modelled	22.5	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
36	d2fi0a1	Alignment	not modelled	17.5	29	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
37	c2qgqF_	Alignment	not modelled	15.0	19	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**protein tm_1862; **PDBTitle:** crystal structure of tm_1862 from thermotoga maritima.2 northeast structural genomics consortium target vr77
38	d1ywxa1	Alignment	not modelled	11.4	12	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
39	d2g7oa1	Alignment	not modelled	11.3	27	**Fold:**TraM-like **Superfamily:**TraM-like **Family:**TraM-like
40	c3odnA_	Alignment	not modelled	10.0	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dally-like protein; **PDBTitle:** the crystal structure of drosophila dally-like protein core domain
41	d1xn9a_	Alignment	not modelled	9.8	6	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
42	c3iz6U_	Alignment	not modelled	9.7	8	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**40s ribosomal protein s24 (s24e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
43	d1wdcc_	Alignment	not modelled	9.2	22	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
44	c1kxfA_	Alignment	not modelled	9.1	43	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sindbis virus capsid protein; **PDBTitle:** sindbis virus capsid, (wild-type) residues 1-264,2 tetragonal crystal form (form ii)
45	d1ep5a_	Alignment	not modelled	9.0	43	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
46	d1kvka2	Alignment	not modelled	9.0	16	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate kinase
47	c3ceuA_	Alignment	not modelled	7.8	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268
48	d1wyka_	Alignment	not modelled	7.8	43	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
49	d1vcpa_	Alignment	not modelled	7.7	48	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
50	d2f06a1	Alignment	not modelled	7.5	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
51	c3zvrA_	Alignment	not modelled	6.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of dynamin
52	d1ufza_	Alignment	not modelled	6.9	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**HBS1-like domain **Family:**HBS1-like domain
53	c3grzA_	Alignment	not modelled	6.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
54	d2g1da1	Alignment	not modelled	6.0	12	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
55	d1whza_	Alignment	not modelled	5.9	18	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like

56	d1ul7a_	Alignment	not modelled	5.7	21	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Kinase associated domain 1, KA1
57	c2vldA_	Alignment	not modelled	5.5	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
58	c3ebhA_	Alignment	not modelled	5.4	15	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**m1 family aminopeptidase; **PDBTitle:** structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
59	d2v94a1	Alignment	not modelled	5.3	8	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
60	c2o01J_	Alignment	not modelled	5.3	36	**PDB header:**photosynthesis **Chain:** J: **PDB Molecule:**photosystem i reaction center subunit ix; **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
61	d1d02a_	Alignment	not modelled	5.2	30	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease MunI