Phyre2

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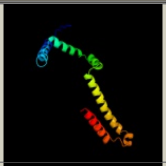
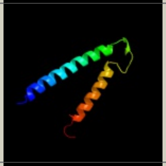
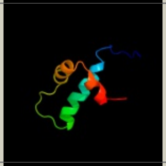
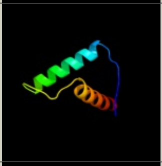
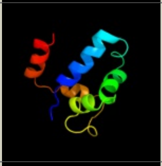
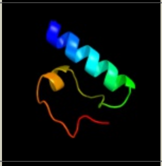
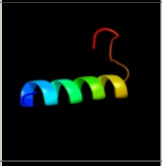
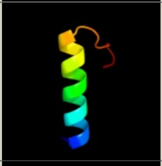
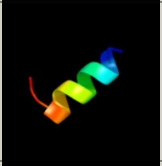
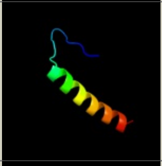
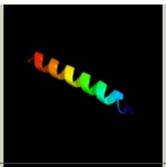
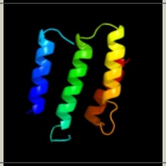
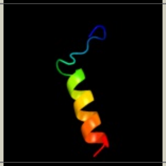
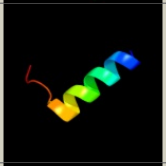
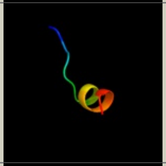
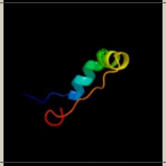
Description	P10026
Date	Thu Jan 5 11:31:57 GMT 2012
Unique Job ID	a527fa44fb29cb5d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3on0D_	Alignment		100.0	39	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**protein tram; **PDBTitle:** crystal structure of the ped208 tram-sbma complex
2	d2g7oa1	Alignment		99.9	100	**Fold:**TraM-like **Superfamily:**TraM-like **Family:**TraM-like
3	d1dp3a_	Alignment		99.9	64	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**DNA-binding domain (fragment?) of the TraM protein
4	c3omyB_	Alignment		99.9	48	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**protein tram; **PDBTitle:** crystal structure of the ped208 tram n-terminal domain
5	d1tlha_	Alignment		42.5	15	**Fold:**Anti-sigma factor AsiA **Superfamily:**Anti-sigma factor AsiA **Family:**Anti-sigma factor AsiA
6	c2qwtA_	Alignment		23.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of the tetr transcription regulatory2 protein from mycobacterium vanbaalenii
7	c2jvdA_	Alignment		15.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynzc from bacillus subtilis. northeast3 structural genomics target sr384-1-46
8	c3bhpA_	Alignment		14.7	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** crystal structure of upf0291 protein ynzc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
9	c2l53B_	Alignment		14.4	36	**PDB header:**ca-binding protein/proton transport **Chain:** B: **PDB Molecule:**voltage-gated sodium channel type v alpha isoform b **PDBTitle:** solution nmr structure of apo-calmodulin in complex with the iq motif2 of human cardiac sodium channel nav1.5
10	d1oysa2	Alignment		13.2	25	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
11	d1x2la1	Alignment		11.5	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain

12	c3bpqC_	Alignment		11.1	32	**PDB header:**toxin **Chain:** C: **PDB Molecule:**antitoxin relb3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
13	c2r17C_	Alignment		10.8	14	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vacuolar protein sorting-associated protein 35; **PDBTitle:** functional architecture of the retromer cargo-recognition complex
14	c3r9lA_	Alignment		10.4	13	**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
15	d2v7qi1	Alignment		10.2	23	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Epsilon subunit of mitochondrial F1F0-ATP synthase **Family:**Epsilon subunit of mitochondrial F1F0-ATP synthase
16	c2jdqB_	Alignment		9.9	25	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**importin alpha-1 subunit; **PDBTitle:** c-terminal domain of influenza a virus polymerase pb22 subunit in complex with human importin alpha5
17	c2cp8A_	Alignment		8.4	29	**PDB header:**protein binding **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
18	d1zkda1	Alignment		8.4	28	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**RPA4359-like
19	d1l7da2	Alignment		7.3	16	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
20	c2kxwB_	Alignment		7.2	36	**PDB header:**calcium-binding protein/metal transport **Chain:** B: **PDB Molecule:**sodium channel protein type 2 subunit alpha; **PDBTitle:** structure of the c-domain fragment of apo calmodulin bound to the iq2 motif of nav1.2
21	c3mtuE_	Alignment	not modelled	7.1	28	**PDB header:**contractile protein **Chain:** E: **PDB Molecule:**head morphogenesis protein, tropomyosin alpha-1 chain; **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
22	d1f7ca_	Alignment	not modelled	6.9	14	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
23	c1f7cA_	Alignment	not modelled	6.9	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rhogap protein; **PDBTitle:** crystal structure of the bh domain from graf, the gtpase2 regulator associated with focal adhesion kinase
24	c3izcR_	Alignment	not modelled	6.4	24	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**60s ribosomal protein rpl18 (l18e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
25	d1nhkl_	Alignment	not modelled	6.2	25	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
26	c3pk1A_	Alignment	not modelled	6.2	20	**PDB header:**apoptosis/apoptosis regulator **Chain:** A: **PDB Molecule:**induced myeloid leukemia cell differentiation protein mcl- **PDBTitle:** crystal structure of mcl-1 in complex with the baxbh3 domain
27	d1kx5b_	Alignment	not modelled	6.0	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
28	d2o4aa1	Alignment	not modelled	6.0	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains

						Family:CUT domain
29	d1xiqa_	Alignment	not modelled	6.0	13	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
30	c2hurF_	Alignment	not modelled	5.9	27	**PDB header:**signaling protein,transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** escherichia coli nucleoside diphosphate kinase
31	c2imuA_	Alignment	not modelled	5.8	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**structural polyprotein (pp) p1; **PDBTitle:** nmr structure of pep46 from the infectious bursal disease2 virus (ibdv) in dodecylphosphocholin (dpc).
32	d1ehwa_	Alignment	not modelled	5.7	20	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
33	c3knyA_	Alignment	not modelled	5.5	39	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt_3535; **PDBTitle:** crystal structure of a two domain protein with unknown function2 (bt_3535) from bacteroides thetaiotaomicron vpi-5482 at 2.60 a3 resolution
34	c2o01J_	Alignment	not modelled	5.4	63	**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