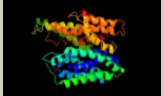
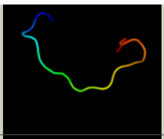
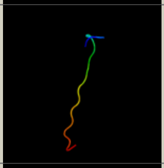
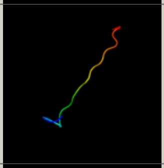
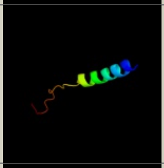
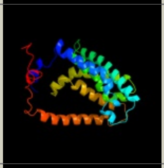
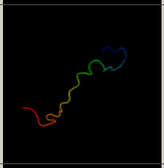
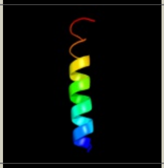
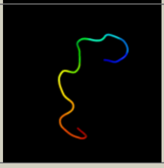
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P37758
Date	Thu Jan 5 11:57:30 GMT 2012
Unique Job ID	73d681bc0941543d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	Alignment		100.0	12	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
2	c3o7pA_	Alignment		100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
3	d1pv7a_	Alignment		100.0	12	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
4	c2gfpA_	Alignment		100.0	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
5	c2xutC_	Alignment		99.9	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	c3b9yA_	Alignment		55.5	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
7	c2bbjB_	Alignment		34.2	10	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
8	c3obhA_	Alignment		26.4	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
9	c3db3A_	Alignment		26.1	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhrf1 in complex with trimethylated histone h3-k93 peptide
10	c3metB_	Alignment		23.6	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**saga-associated factor 29 homolog; **PDBTitle:** crystal structure of sgf29 in complex with h3k4me2
11	c2l92A_	Alignment		20.6	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**histone family protein nucleoid-structuring protein h-ns; **PDBTitle:** solution structure of the c-terminal domain of h-ns like protein bv3f

12	c3pm7A_	Alignment		18.6	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184
13	c1hw4A_	Alignment		17.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate synthase; **PDBTitle:** structure of thymidylate synthase suggests advantages of chemotherapy2 with noncompetitive inhibitors
14	c1hw3A_	Alignment		14.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate synthase; **PDBTitle:** structure of human thymidylate synthase suggests advantages of2 chemotherapy with noncompetitive inhibitors
15	c2kncA_	Alignment		14.6	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
16	c3hd6A_	Alignment		12.3	13	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
17	c2kz7C_	Alignment		11.9	27	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**leucine-rich repeat-containing protein 16a; **PDBTitle:** solution structure of the carmil cah3a/b domain bound to capping2 protein (cp)
18	d2iuba2	Alignment		11.6	17	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
19	c2g9pA_	Alignment		11.5	14	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
20	c3dgpB_	Alignment		8.4	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rna polymerase ii transcription factor b subunit 5; **PDBTitle:** crystal structure of the complex between tfb5 and the c-terminal2 domain of tfb2
21	c3ke2A_	Alignment	not modelled	8.1	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_928783.1; **PDBTitle:** crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
22	c3mkuA_	Alignment	not modelled	7.9	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
23	d1sv0c_	Alignment	not modelled	7.7	33	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
24	d1sxda_	Alignment	not modelled	7.5	33	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
25	c2dkxA_	Alignment	not modelled	7.2	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam pointed domain-containing ets transcription **PDBTitle:** solution structure of the sam_pnt-domain of ets2 transcription factor pdef (prostate ets)
26	d1hnra_	Alignment	not modelled	7.1	18	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
27	d1bcoa1	Alignment	not modelled	7.0	7	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
28	d1sv0a_	Alignment	not modelled	6.1	33	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain

29	c1y6gB_	Alignment	not modelled	6.1	33	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna alpha-glucosyltransferase; **PDBTitle:** alpha-glucosyltransferase in complex with udp and a 13_mer2 dna containing a hmu base at 2.8 a resolution
30	d1vbva1	Alignment	not modelled	6.1	22	**Fold:**SH3-like barrel **Superfamily:**YccV-like **Family:**YccV-like
31	d1bqva_	Alignment	not modelled	5.9	33	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
32	d1jb0a_	Alignment	not modelled	5.9	20	**Fold:**Photosystem I subunits PsaA/PsaB **Superfamily:**Photosystem I subunits PsaA/PsaB **Family:**Photosystem I subunits PsaA/PsaB
33	d2z15a1	Alignment	not modelled	5.7	50	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
34	d3e9va1	Alignment	not modelled	5.6	50	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
35	c2h31A_	Alignment	not modelled	5.6	12	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
36	d1jb0b_	Alignment	not modelled	5.5	16	**Fold:**Photosystem I subunits PsaA/PsaB **Superfamily:**Photosystem I subunits PsaA/PsaB **Family:**Photosystem I subunits PsaA/PsaB
37	c2k9pA_	Alignment	not modelled	5.5	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pheromone alpha factor receptor; **PDBTitle:** structure of tm1_tm2 in lppg micelles
38	c2o8kA_	Alignment	not modelled	5.5	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
39	c2yh6C_	Alignment	not modelled	5.5	25	**PDB header:**lipid binding protein **Chain:** C: **PDB Molecule:**lipoprotein 34; **PDBTitle:** structure of the n-terminal domain of bamc from e. coli
40	c3hftA_	Alignment	not modelled	5.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wbms, polysaccharide deacetylase involved in o-antigen **PDBTitle:** crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution
41	c3ehuC_	Alignment	not modelled	5.4	27	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**corticoliberin; **PDBTitle:** crystal structure of the extracellular domain of human corticotropin2 releasing factor receptor type 1 (crfr1) in complex with crf
42	c3ehuD_	Alignment	not modelled	5.4	27	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**corticoliberin; **PDBTitle:** crystal structure of the extracellular domain of human corticotropin2 releasing factor receptor type 1 (crfr1) in complex with crf
43	c3jyvT_	Alignment	not modelled	5.4	16	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**s19e protein; **PDBTitle:** structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
44	d1sxea_	Alignment	not modelled	5.2	33	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
45	d1hdmb2	Alignment	not modelled	5.2	29	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
46	c2ytuA_	Alignment	not modelled	5.1	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**friend leukemia integration 1 transcription **PDBTitle:** solution structure of the sam_pnt-domain of the human2 friend leukemiaintegration 1 transcription factor