Phyre2

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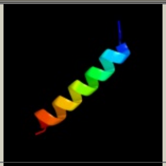
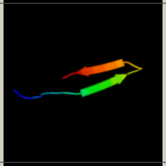
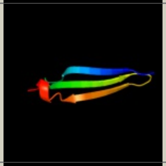
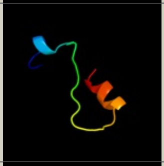
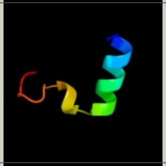
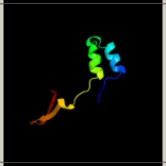
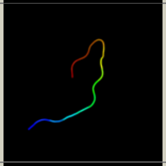
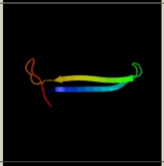
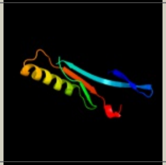
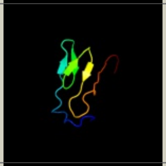
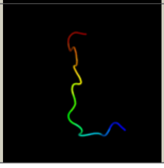
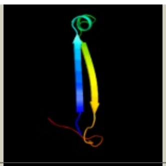
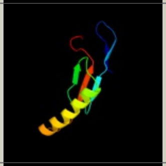
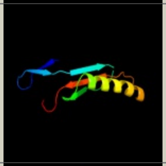
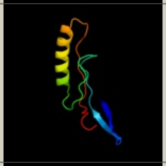
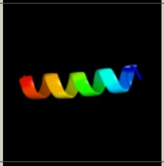
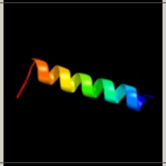
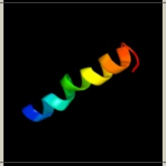
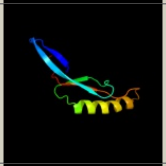
Description	P52645
Date	Thu Jan 5 12:05:58 GMT 2012
Unique Job ID	4de6e716f4db8da3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xmec1	Alignment		32.1	30	**Fold:**Single transmembrane helix **Superfamily:**Bacterial ba3 type cytochrome c oxidase subunit IIa **Family:**Bacterial ba3 type cytochrome c oxidase subunit IIa
2	d1im3d_	Alignment		29.1	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Cytomegalovirus protein US2
3	d1e50b_	Alignment		19.9	26	**Fold:**Core binding factor beta, CBF **Superfamily:**Core binding factor beta, CBF **Family:**Core binding factor beta, CBF
4	c3ghfA_	Alignment		19.9	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the septum site-determining protein2 minc from salmonella typhimurium
5	d2isya2	Alignment		18.5	17	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
6	c2im5C_	Alignment		18.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of nicotinate phosphoribosyltransferase2 from porphyromonas gingivalis
7	d2nwaa1	Alignment		16.4	44	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YtmB-like
8	d1gl4a1	Alignment		14.6	18	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Domain G2 of nidogen-1
9	d1b26a2	Alignment		11.8	13	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
10	c2cg5A_	Alignment		11.4	12	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**l-aminoadipate-semialdehyde dehydrogenase- **PDBTitle:** structure of aminoadipate-semialdehyde dehydrogenase-2 phosphopantetheinyl transferase in complex with cytosolic3 acyl carrier protein and coenzyme a
11	c3db3A_	Alignment		11.2	25	**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

12	c1h4uA_	Alignment		8.7	18	**PDB header:**extracellular matrix protein **Chain:** A: **PDB Molecule:**nidogen-1; **PDBTitle:** domain g2 of mouse nidogen-1
13	d1v9la2	Alignment		8.3	14	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
14	d1hwxa2	Alignment		8.1	14	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
15	d1bgva2	Alignment		8.0	16	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
16	c1piqA_	Alignment		8.0	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein (general control protein gcn4-piq); **PDBTitle:** crystal structure of gcn4-piq, a trimeric coiled coil with buried2 polar residues
17	d1jb0j_	Alignment		7.3	17	**Fold:**Single transmembrane helix **Superfamily:**Subunit IX of photosystem I reaction centre, PsaJ **Family:**Subunit IX of photosystem I reaction centre, PsaJ
18	c2o01J_	Alignment		7.3	17	**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
19	d1euza2	Alignment		7.1	13	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
20	d1xo8a_	Alignment		6.9	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
21	d1bvua2	Alignment	not modelled	6.7	9	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
22	c1v9lA_	Alignment	not modelled	6.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
23	c2e6gI_	Alignment	not modelled	6.2	32	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of the stationary phase survival protein sure from2 thermus thermophilus hb8 in complex with phosphate
24	d1ikta_	Alignment	not modelled	6.1	16	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
25	c2wpzA_	Alignment	not modelled	6.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
26	d1g3wa2	Alignment	not modelled	5.8	17	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
27	c2wpzB_	Alignment	not modelled	5.8	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
28	c2wpzC_	Alignment	not modelled	5.6	16	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
						Fold: SurE-like

29	d1l5xa_	Alignment	not modelled	5.6	12	**Superfamily:**SurE-like **Family:**SurE-like
30	c3aogA_	Alignment	not modelled	5.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
31	c2ccfA_	Alignment	not modelled	5.3	24	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel configuration of pli e20s
32	d1gtma2	Alignment	not modelled	5.3	12	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
33	c1unyB_	Alignment	not modelled	5.2	24	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
34	c1gcmA_	Alignment	not modelled	5.1	18	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
35	c1uo0B_	Alignment	not modelled	5.1	24	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
36	c1uo0A_	Alignment	not modelled	5.1	24	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
37	c1uo1B_	Alignment	not modelled	5.1	24	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
38	c1uo1A_	Alignment	not modelled	5.1	24	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
39	c1unwB_	Alignment	not modelled	5.1	24	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
40	c1gclD_	Alignment	not modelled	5.0	24	**PDB header:**leucine zipper **Chain:** D: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
41	c1gclB_	Alignment	not modelled	5.0	24	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
42	c1gclC_	Alignment	not modelled	5.0	24	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
43	c1gclA_	Alignment	not modelled	5.0	24	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li