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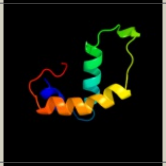
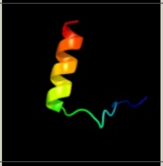
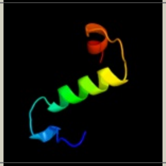
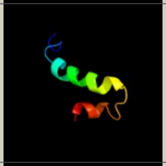
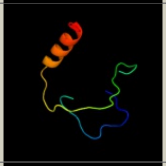
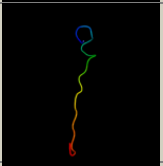
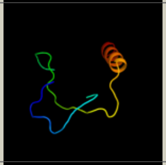
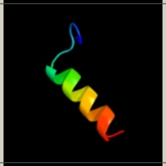
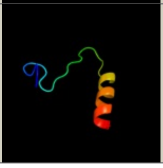
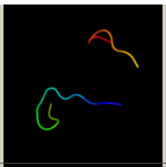
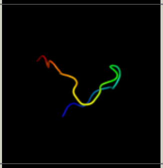
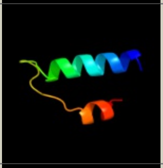
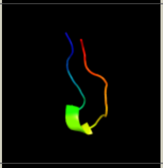
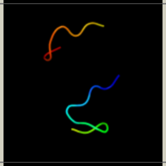
Description	P0AET2
Date	Thu Jan 5 11:24:10 GMT 2012
Unique Job ID	b261290cdd78e992

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xuvB_	Alignment		100.0	90	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hdeb; **PDBTitle:** the structure of hdeb
2	d1dj8a_	Alignment		96.5	18	**Fold:**Protein HNS-dependent expression A; HdeA **Superfamily:**Protein HNS-dependent expression A; HdeA **Family:**Protein HNS-dependent expression A; HdeA
3	d2dk8a1	Alignment		29.9	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RPO3F domain-like
4	d1fs1b2	Alignment		29.2	32	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
5	d1t3wa_	Alignment		26.3	9	**Fold:**DNA primase DnaG, C-terminal domain **Superfamily:**DNA primase DnaG, C-terminal domain **Family:**DNA primase DnaG, C-terminal domain
6	d2ezwa1	Alignment		19.6	9	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
7	d2pi2e1	Alignment		18.4	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
8	c3kwrA_	Alignment		17.1	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**putative rna-binding protein; **PDBTitle:** crystal structure of putative rna-binding protein (np_785364.1) from2 lactobacillus plantarum at 1.45 a resolution
9	c2pqaB_	Alignment		16.5	14	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer
10	d1nexa2	Alignment		16.3	19	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
11	d1hv2a_	Alignment		12.9	23	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain

12	c2dadA_	Alignment		12.8	20	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**absent in melanoma 1 protein; **PDBTitle:** solution structure of the fifth crystall domain of the non-2 lens protein, absent in melanoma 1
13	c3iuwA_	Alignment		12.1	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**activating signal cointegrator; **PDBTitle:** crystal structure of activating signal cointegrator (np_814290.1) from2 enterococcus faecalis v583 at 1.58 a resolution
14	c2kddB_	Alignment		10.7	28	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**borealin; **PDBTitle:** solution structure of the conserved c-terminal dimerization2 domain of borealin
15	d1vqoq1	Alignment		9.2	20	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
16	c3iz6M_	Alignment		9.1	24	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**40s ribosomal protein s18 (s13p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
17	d1bc9a_	Alignment		8.7	18	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
18	c3dkqB_	Alignment		8.7	41	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pkhd-type hydroxylase sbal_3634; **PDBTitle:** crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
19	d1zira2	Alignment		8.6	32	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
20	c3knyA_	Alignment		8.5	20	**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
21	c2zkrq_	Alignment	not modelled	8.5	50	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
22	d1elpa1	Alignment	not modelled	8.3	37	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
23	d2b50a1	Alignment	not modelled	8.2	14	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
24	c2ovqA_	Alignment	not modelled	8.2	32	**PDB header:**transcription/cell cycle **Chain:** A: **PDB Molecule:**s-phase kinase-associated protein 1a; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
25	c1s1iQ_	Alignment	not modelled	7.9	60	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l21-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
26	d2c9wc1	Alignment	not modelled	7.8	24	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
27	c3drzE_	Alignment	not modelled	7.3	25	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**btb/poz domain-containing protein kctd5; **PDBTitle:** x-ray crystal structure of the n-terminal btb domain of human kctd52 protein
28	c2hdeA_	Alignment	not modelled	7.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap18;

						PDBTitle: solution structure of human sap18
29	c2vx6A_	Alignment	not modelled	6.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellvibrio japonicus mannanase cjman26c; **PDBTitle:** cellvibrio japonicus mannanase cjman26c gal1man4-bound form
30	c2dbiA_	Alignment	not modelled	6.5	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ybiu; **PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli
31	c3g36D_	Alignment	not modelled	6.4	10	**PDB header:**nuclear protein **Chain:** D: **PDB Molecule:**protein dpy-30 homolog; **PDBTitle:** crystal structure of the human dpy-30-like c-terminal domain
32	d1qcsa1	Alignment	not modelled	6.3	36	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
33	c1wd6B_	Alignment	not modelled	6.3	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydhr; **PDBTitle:** crystal structure of jw1657 from escherichia coli
34	d2eyqa1	Alignment	not modelled	6.2	22	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
35	d2csga1	Alignment	not modelled	6.0	27	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YbiU-like
36	c4a1aP_	Alignment	not modelled	5.9	50	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l21; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
37	c1okiB_	Alignment	not modelled	5.8	26	**PDB header:**eye lens protein **Chain:** B: **PDB Molecule:**beta crystallin b1; **PDBTitle:** crystal structure of truncated human beta-b1-crystallin
38	c2ddxA_	Alignment	not modelled	5.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-1,3-xylanase; **PDBTitle:** crystal structure of beta-1,3-xylanase from vibrio sp. ax-4
39	c3gf8A_	Alignment	not modelled	5.7	36	**PDB header:**carbohydrate binding protein **Chain:** A: **PDB Molecule:**putative polysaccharide binding proteins (duf1812); **PDBTitle:** crystal structure of putative polysaccharide binding proteins2 (duf1812) (np_809975.1) from bacteroides thetaiotaomicron vpi-5482 at3 2.20 a resolution
40	c2bv2B_	Alignment	not modelled	5.7	16	**PDB header:**crystallin **Chain:** B: **PDB Molecule:**ciona betagamma-crystallin; **PDBTitle:** beta gamma crystallin from ciona intestinalis
41	d1nhya2	Alignment	not modelled	5.7	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
42	d1vj1a1	Alignment	not modelled	5.5	17	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
43	c3ogiC_	Alignment	not modelled	5.5	100	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative esat-6-like protein 6; **PDBTitle:** crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
44	d1okia1	Alignment	not modelled	5.5	26	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
45	c3izcU_	Alignment	not modelled	5.4	60	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein rpl21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
46	d1pbva_	Alignment	not modelled	5.3	12	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
47	c2zkqm_	Alignment	not modelled	5.3	23	**PDB header:**ribosomal protein/rna **Chain:** M: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
48	d2hiqa1	Alignment	not modelled	5.2	25	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YdhR
49	d1pvda3	Alignment	not modelled	5.1	24	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
50	c2oaxC_	Alignment	not modelled	5.1	33	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mineralocorticoid receptor; **PDBTitle:** crystal structure of the s810l mutant mineralocorticoid2 receptor associated with sc9420