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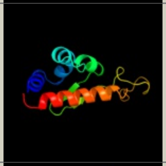
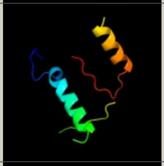
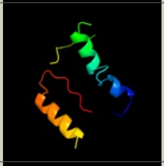
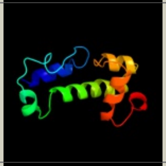
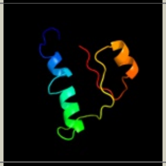
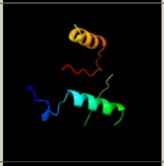
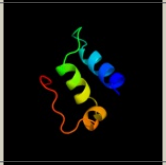
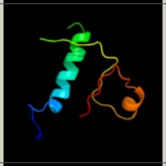
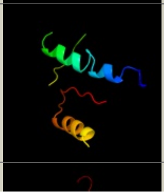
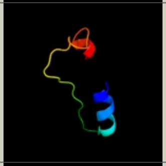
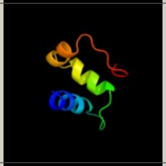
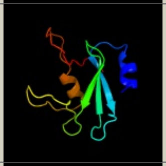
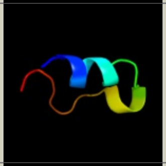
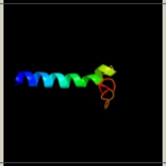
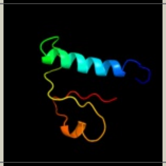
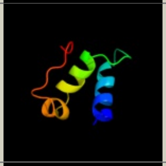
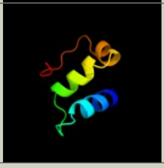
Description	P30192
Date	Thu Jan 5 11:46:17 GMT 2012
Unique Job ID	9b84ce7843cf72bb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	Alignment		98.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	Alignment		97.3	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
3	d1yoca1	Alignment		49.5	22	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
4	d1wb9a2	Alignment		46.7	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
5	c3thxB_	Alignment		32.6	18	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein msh3; **PDBTitle:** human mutsbeta complexed with an idl of 3 bases (loop3) and adp
6	c1d5yD_	Alignment		26.2	20	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**rob transcription factor; **PDBTitle:** crystal structure of the e. coli rob transcription factor2 in complex with dna
7	c1ewqA_	Alignment		20.7	21	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure taq muts complexed with a heteroduplex2 dna at 2.2 a resolution
8	c1wbdA_	Alignment		16.6	27	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of e. coli dna mismatch repair enzyme2 muts, e38q mutant, in complex with a g.t mismatch
9	d1u35c1	Alignment		12.2	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
10	c2o8bA_	Alignment		12.0	18	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein msh2; **PDBTitle:** human mutsalpha (msh2/msh6) bound to adp and a g t mispair
11	c2o8dB_	Alignment		11.6	21	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein msh6; **PDBTitle:** human mutsalpha (msh2/msh6) bound to adp and a g du mispair

12	c3pcoD_	Alignment		11.2	26	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylalanyl-trna synthetase, beta chain; **PDBTitle:** crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
13	d2jfga2	Alignment		10.7	14	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
14	c2f8nK_	Alignment		8.9	17	**PDB header:**structural protein/dna **Chain:** K: **PDB Molecule:**histone h2a type 1; **PDBTitle:** 2.9 angstrom x-ray structure of hybrid macroh2a nucleosomes
15	c2hmhA_	Alignment		8.8	11	**PDB header:**cytokine regulator **Chain:** A: **PDB Molecule:**suppressor of cytokine signaling 3; **PDBTitle:** crystal structure of socs3 in complex with gp130(ptyr757)2 phosphopeptide.
16	c3czpA_	Alignment		8.8	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
17	d1k8ke_	Alignment		8.8	24	**Fold:**Arp2/3 complex 21 kDa subunit ARPC3 **Superfamily:**Arp2/3 complex 21 kDa subunit ARPC3 **Family:**Arp2/3 complex 21 kDa subunit ARPC3
18	d1ewqa2	Alignment		8.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
19	d1id3c_	Alignment		7.7	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
20	d1eqza_	Alignment		7.7	15	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
21	c3btpA_	Alignment	not modelled	7.6	20	**PDB header:**dna binding protein, chaperone **Chain:** A: **PDB Molecule:**single-strand dna-binding protein; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
22	c3tdqB_	Alignment	not modelled	7.6	36	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**pily2 protein; **PDBTitle:** crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution
23	c2vzaD_	Alignment	not modelled	7.4	18	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**cell filamentation protein; **PDBTitle:** type iv secretion system effector protein bepa
24	d1tzya_	Alignment	not modelled	7.0	15	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
25	d1dk7a_	Alignment	not modelled	6.9	43	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
26	d1sjpa2	Alignment	not modelled	6.6	57	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
27	c3rhfB_	Alignment	not modelled	6.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative polyphosphate kinase 2 family protein; **PDBTitle:** crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1
28	d1srva_	Alignment	not modelled	6.4	57	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain

29	d1ioka2	Alignment	not modelled	6.2	43	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
30	d1aoic_	Alignment	not modelled	6.1	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
31	d1ikpa3	Alignment	not modelled	6.0	69	**Fold:**Toxins' membrane translocation domains **Superfamily:**Exotoxin A, middle domain **Family:**Exotoxin A, middle domain
32	c2vifA_	Alignment	not modelled	6.0	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**suppressor of cytokine signalling 6; **PDBTitle:** crystal structure of socs6 sh2 domain in complex with a c-kit2 phosphopeptide
33	c3ld9D_	Alignment	not modelled	5.9	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase from ehrlichia chaffeensis at2 2.15a resolution
34	d1oela2	Alignment	not modelled	5.7	43	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
35	d1kx3c_	Alignment	not modelled	5.7	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
36	c3pjvD_	Alignment	not modelled	5.5	50	**PDB header:**lyase **Chain:** D: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd periplasmic domain
37	d1pvda3	Alignment	not modelled	5.5	2	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
38	d1sjpa3	Alignment	not modelled	5.3	0	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**GroEL-like chaperone, intermediate domain