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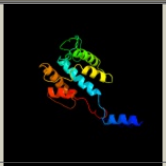
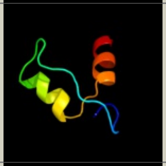
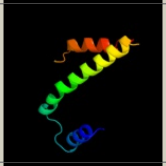
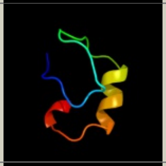
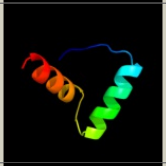
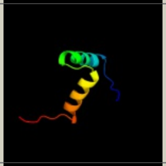
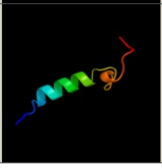
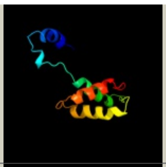
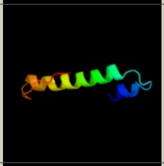
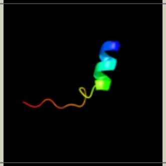
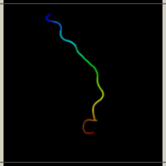
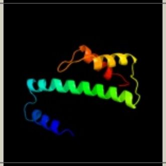
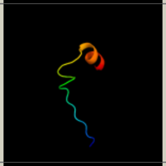
Description	Q9S4X5
Date	Thu Jan 5 12:38:29 GMT 2012
Unique Job ID	10d4c1a69bfba01a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ijra1	Alignment		100.0	31	**Fold:**Api92-like **Superfamily:**Api92-like **Family:**Api92-like
2	d1xs8a_	Alignment		58.2	21	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
3	d1t07a_	Alignment		54.8	21	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
4	c1ec8B_	Alignment		37.6	31	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glucarate dehydratase; **PDBTitle:** e. coli glucarate dehydratase bound to product 2,3-2 dihydroxy-5-oxo-hexanedioate
5	c1tndA_	Alignment		26.8	16	**PDB header:**binding protein(gtp) **Chain:** A: **PDB Molecule:**transducin; **PDBTitle:** the 2.2 angstroms crystal structure of transducin-alpha complexed with2 gtp gamma s
6	c2xtzB_	Alignment		22.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein alpha-1 subunit; **PDBTitle:** crystal structure of the g alpha protein atgpa1 from2 arabidopsis thaliana
7	d1saza1	Alignment		22.2	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
8	d2bj7a1	Alignment		20.4	13	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
9	c2ca9B_	Alignment		20.4	13	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
10	c1zcbA_	Alignment		18.4	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**g alpha i/13; **PDBTitle:** crystal structure of g alpha 13 in complex with gdp
11	c3n6jA_	Alignment		16.8	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from actinobacillus succinogenes 130z

12	c1tl7C_	Alignment		14.5	23	**PDB header:**lyase **Chain:** C: **PDB Molecule:**guanine nucleotide-binding protein g(s), alpha **PDBTitle:** complex of gs- with the catalytic domains of mammalian2 adenylyl cyclase: complex with 2'(3')-o-(n-3 methylanthraniloyl)-guanosine 5'-triphosphate and mn
13	c3ijmA_	Alignment		13.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized restriction endonuclease-like fold **PDBTitle:** the structure of a restriction endonuclease-like fold superfamily2 protein from spirosoma linguale.
14	d2ihoa2	Alignment		12.9	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**MOA C-terminal domain-like
15	d2a90a2	Alignment		12.2	18	**Fold:**WWE domain **Superfamily:**WWE domain **Family:**WWE domain
16	c1cipA_	Alignment		12.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (guanine nucleotide-binding protein **PDBTitle:** gi-alpha-1 subunit of guanine nucleotide-binding protein2 complexed with a gtp analogue
17	c3ue9A_	Alignment		12.1	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of adenylosuccinate synthetase (ampsase) (pura) from2 burkholderia thailandensis
18	d1osce_	Alignment		11.8	23	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
19	d1iwea_	Alignment		11.6	36	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
20	c1iweB_	Alignment		11.4	36	**PDB header:**ligase **Chain:** B: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** imp complex of the recombinant mouse-muscle2 adenylosuccinate synthetase
21	d1ngka_	Alignment	not modelled	10.6	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
22	c3cx6A_	Alignment	not modelled	10.3	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**guanine nucleotide-binding protein alpha-13 **PDBTitle:** crystal structure of pdzrhogef rgrgs domain in a complex2 with galpha-13 bound to gdp
23	d2ozka1	Alignment	not modelled	10.0	56	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Nsp15 N-terminal domain-like
24	c2bcjQ_	Alignment	not modelled	9.9	12	**PDB header:**transferase/hydrolase **Chain:** Q: **PDB Molecule:**g alpha i1, guanine nucleotide-binding protein g(q), alpha **PDBTitle:** crystal structure of g protein-coupled receptor kinase 2 in complex2 with galpha-q and gbetagamma subunits
25	d2guka1	Alignment	not modelled	9.5	27	**Fold:**PG1857-like **Superfamily:**PG1857-like **Family:**PG1857-like
26	c3iuzA_	Alignment	not modelled	9.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative glyoxalase superfamily protein; **PDBTitle:** crystal structure of putative glyoxalase superfamily protein2 (yp_299723.1) from ralstonia eutropha jmp134 at 1.90 a resolution
27	d2gqfa2	Alignment	not modelled	8.9	3	**Fold:**HI0933 insert domain-like **Superfamily:**HI0933 insert domain-like **Family:**HI0933 insert domain-like
28	d1jdfa1	Alignment	not modelled	8.9	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like

						Family:D-glucarate dehydratase-like
29	d2h85a1	Alignment	not modelled	8.6	56	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Nsp15 N-terminal domain-like
30	c1sxjB_	Alignment	not modelled	8.1	22	**PDB header:**replication **Chain:** B: **PDB Molecule:**activator 1 37 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
31	d1p9ba_	Alignment	not modelled	8.1	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
32	d1ac5a_	Alignment	not modelled	8.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Serine carboxypeptidase-like
33	d1sxjc2	Alignment	not modelled	7.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
34	c3thgA_	Alignment	not modelled	7.8	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase activase 1, **PDBTitle:** crystal structure of the creosote rubisco activase c-domain
35	d2bcjq1	Alignment	not modelled	7.6	11	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
36	c2d7uA_	Alignment	not modelled	7.6	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of hypothetical adenylosuccinate synthetase, ph04382 from pyrococcus horikoshii ot3
37	c1iqpF_	Alignment	not modelled	7.5	25	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
38	c3gnzP_	Alignment	not modelled	7.3	25	**PDB header:**toxin **Chain:** P: **PDB Molecule:**25 kda protein elicitor; **PDBTitle:** toxin fold for microbial attack and plant defense
39	c2zzxD_	Alignment	not modelled	7.3	32	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc transporter, solute-binding protein; **PDBTitle:** crystal structure of a periplasmic substrate binding protein in2 complex with lactate
40	c1rrzA_	Alignment	not modelled	7.2	33	**PDB header:**structural genomics,biosynthetic protein **Chain:** A: **PDB Molecule:**glycogen synthesis protein glgs; **PDBTitle:** solution structure of glgs protein from e. coli
41	d1rrza_	Alignment	not modelled	7.2	33	**Fold:**Spectrin repeat-like **Superfamily:**Glycogen synthesis protein GlgS **Family:**Glycogen synthesis protein GlgS
42	c2xykB_	Alignment	not modelled	7.0	13	**PDB header:**oxygen storage/transport **Chain:** B: **PDB Molecule:**2-on-2 hemoglobin; **PDBTitle:** group ii 2-on-2 hemoglobin from the plant pathogen2 agrobacterium tumefaciens
43	d2ixma1	Alignment	not modelled	7.0	19	**Fold:**PTPA-like **Superfamily:**PTPA-like **Family:**PTPA-like
44	d1zcaa1	Alignment	not modelled	6.8	23	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
45	d1dj2a_	Alignment	not modelled	6.6	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
46	d2hzaa1	Alignment	not modelled	6.5	13	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
47	d1nmla2	Alignment	not modelled	5.8	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
48	d2ixoa1	Alignment	not modelled	5.8	25	**Fold:**PTPA-like **Superfamily:**PTPA-like **Family:**PTPA-like
49	c2bj3D_	Alignment	not modelled	5.5	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
50	c2chgB_	Alignment	not modelled	5.5	22	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c domains 1 and 2
51	d1pyla_	Alignment	not modelled	5.3	12	**Fold:**Microbial ribonucleases **Superfamily:**Microbial ribonucleases **Family:**Bacterial ribonucleases
52	c2a3zC_	Alignment	not modelled	5.2	57	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** ternary complex of the wh2 domain of wasp with actin-dnase i
53	c3d33B_	Alignment	not modelled	5.2	33	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**domain of unknown function with an immunoglobulin-like **PDBTitle:** crystal structure of a duf3244 family protein with an immunoglobulin-2 like beta-sandwich fold (bvu_0276) from bacteroides vulgatus atcc3 8482 at 1.70 a resolution
						PDB header:hydrolase activator

54	c2g62A_	Alignment	not modelled	5.2	25	**Chain:** A: **PDB Molecule:**protein phosphatase 2a, regulatory subunit b' (pr 53); **PDBTitle:** crystal structure of human ptpa
55	c2rhbD_	Alignment	not modelled	5.1	56	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**uridylate-specific endoribonuclease; **PDBTitle:** crystal structure of nsp15-h234a mutant- hexamer in2 asymmetric unit
56	d1sxjb2	Alignment	not modelled	5.1	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
57	c2nz7A_	Alignment	not modelled	5.1	21	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**caspase recruitment domain-containing protein 4; **PDBTitle:** crystal structure analysis of caspase-recruitment domain2 (card) of nod1
58	c1z7s1_	Alignment	not modelled	5.0	38	**PDB header:**virus **Chain:** 1: **PDB Molecule:**human coxsackievirus a21; **PDB Fragment:**viral protein 1; **PDBTitle:** the crystal structure of coxsackievirus a21