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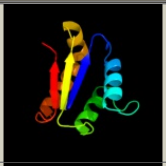
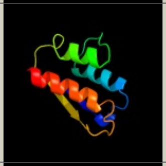
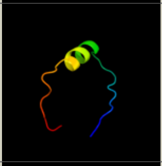
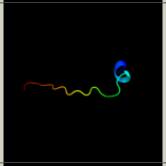
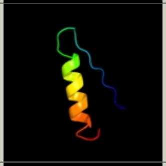
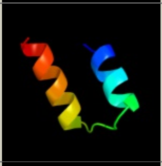
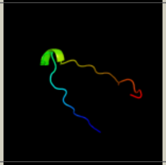
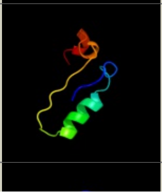
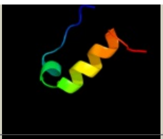
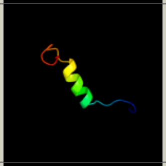
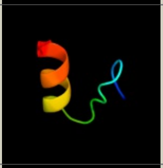
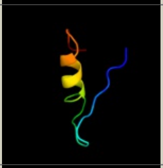
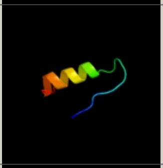
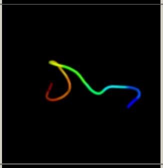
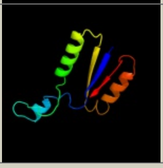
Description	P64616
Date	Thu Jan 5 12:09:57 GMT 2012
Unique Job ID	5e7b7d0afaf7f00e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cx6a1	Alignment		100.0	98	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
2	d1ay7b_	Alignment		99.9	24	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
3	c1sb7A_	Alignment		68.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase d; **PDBTitle:** crystal structure of the e.coli pseudouridine synthase trud
4	d1szwa_	Alignment		68.2	16	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**tRNA pseudouridine synthase TruD
5	c3nmeA_	Alignment		24.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase
6	d2ahob1	Alignment		23.6	6	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like
7	d1nksa_	Alignment		21.2	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
8	c2c0kB_	Alignment		18.9	10	**PDB header:**oxygen transport **Chain:** B: **PDB Molecule:**hemoglobin; **PDBTitle:** the structure of hemoglobin from the botfly gasterophilus2 intestinalis
9	c1z2zB_	Alignment		18.5	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**probable trna pseudouridine synthase d; **PDBTitle:** crystal structure of the putative trna pseudouridine2 synthase d (trud) from methanosarcina mazei, northeast3 structural genomics target mar1
10	c3da5A_	Alignment		18.5	45	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**argonaute; **PDBTitle:** crystal structure of piwi/argonaute/zwille(paz) domain from2 thermococcus thioreducens
11	d1vpya_	Alignment		17.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**TM1631-like **Family:**TM1631-like

12	c2dnfA_	Alignment		17.4	4	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**doublecortin domain-containing protein 2; **PDBTitle:** solution structure of rsgi ruh-062, a dcx domain from human
13	c3f1xA_	Alignment		16.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
14	c2zpmA_	Alignment		14.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
15	d2hgaa1	Alignment		12.7	5	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**MTH1368 C-terminal domain-like
16	c2k5cA_	Alignment		12.5	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
17	d1gg3a3	Alignment		12.2	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
18	c2grjH_	Alignment		11.7	4	**PDB header:**transferase **Chain:** H: **PDB Molecule:**dephospho-coa kinase; **PDBTitle:** crystal structure of dephospho-coa kinase (ec 2.7.1.24)2 (dephosphocoenzyme a kinase) (tm1387) from thermotoga maritima at3 2.60 a resolution
19	d1y14b2	Alignment		11.6	0	**Fold:**Dodecin subunit-like **Superfamily:**N-terminal, heterodimerisation domain of RBP7 (RpoE) **Family:**N-terminal, heterodimerisation domain of RBP7 (RpoE)
20	d2c4va1	Alignment		10.4	15	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
21	d1sota1	Alignment	not modelled	9.6	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
22	d1ky9b2	Alignment	not modelled	9.5	5	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
23	d1wuda1	Alignment	not modelled	9.3	11	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
24	d2ciwa2	Alignment	not modelled	9.1	11	**Fold:**EF Hand-like **Superfamily:**Cloroperoxidase **Family:**Cloroperoxidase
25	c3q3uA_	Alignment	not modelled	9.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lignin peroxidase; **PDBTitle:** trametes cervina lignin peroxidase
26	d2zpya3	Alignment	not modelled	8.9	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
27	c2p3wB_	Alignment	not modelled	8.4	5	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**probable serine protease htra3; **PDBTitle:** crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
28	c2xxsA_	Alignment	not modelled	8.4	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein mxig; **PDBTitle:** solution structure of the n-terminal domain of the shigella2 type iii secretion protein mxig
29	c3i18A_	Alignment	not modelled	7.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2051 protein; **PDBTitle:** crystal structure of the pdz domain of the sdrc-like protein2 (lmo2051) from listeria monocytogenes, northeast

						structural3 genomics consortium target lmr166b
30	d2e1fa1	Alignment	not modelled	7.6	6	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
31	c2kl1A_	Alignment	not modelled	7.5	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ylbl protein; **PDBTitle:** solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
32	c2x7jA_	Alignment	not modelled	7.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene **PDBTitle:** structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
33	d1ni2a3	Alignment	not modelled	7.1	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
34	d2z9ia1	Alignment	not modelled	6.9	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
35	c2o42B_	Alignment	not modelled	6.9	19	**PDB header:**apoptosis inhibitor **Chain:** B: **PDB Molecule:**m11l protein; **PDBTitle:** crystal structure of m11l, bcl-2 homolog from myxoma virus
36	c3bq9A_	Alignment	not modelled	6.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
37	d1itha_	Alignment	not modelled	6.6	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
38	d1ef1a3	Alignment	not modelled	6.6	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
39	c1yz7A_	Alignment	not modelled	6.6	9	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 alpha **PDBTitle:** crystal structure of a c-terminal segment of the alpha2 subunit of aif2 from pyrococcus abyssi
40	d1sxja1	Alignment	not modelled	6.5	0	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
41	d1ukza_	Alignment	not modelled	6.5	0	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
42	d2r8oa2	Alignment	not modelled	6.5	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
43	c3u8zD_	Alignment	not modelled	5.8	17	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**merlin; **PDBTitle:** human merlin ferm domain
44	c2joaA_	Alignment	not modelled	5.8	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**serine protease htra1; **PDBTitle:** htra1 bound to an optimized peptide: nmr assignment of pdz2 domain and ligand resonances
45	c2q9rA_	Alignment	not modelled	5.7	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** crystal structure of a duf416 family protein (sbal_3149) from2 shewanella baltica os155 at 1.91 a resolution
46	d1yyda1	Alignment	not modelled	5.5	17	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
47	d2e39a1	Alignment	not modelled	5.5	22	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
48	d1tw9a2	Alignment	not modelled	5.4	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
49	d1orjb_	Alignment	not modelled	5.2	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**Flagellar export chaperone FliS **Family:**Flagellar export chaperone FliS
50	d2i6va1	Alignment	not modelled	5.2	5	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
51	d3c8ya2	Alignment	not modelled	5.1	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
52	c2vvyC_	Alignment	not modelled	5.1	32	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**protein b15; **PDBTitle:** structure of vaccinia virus protein b14
53	d1glqa2	Alignment	not modelled	5.0	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
54	c2z5sN_	Alignment	not modelled	5.0	8	**PDB header:**cell cycle **Chain:** N: **PDB Molecule:**mdm4 protein; **PDBTitle:** molecular basis for the inhibition of p53 by mdmx