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Description	P52123
Date	Thu Jan 5 12:05:26 GMT 2012
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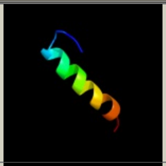
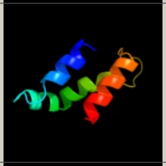
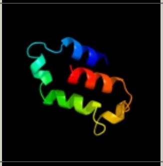
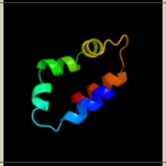
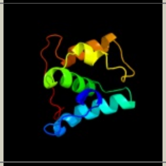
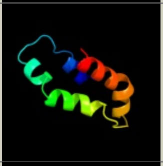
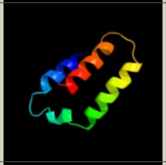
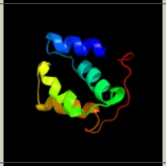
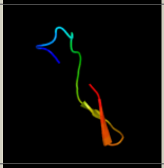
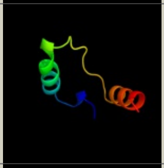
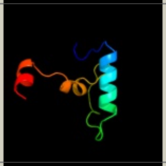
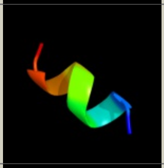
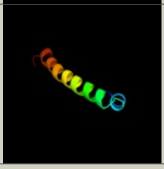
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k19A_	Alignment		29.8	22	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**putative piscicolin 126 immunity protein; **PDBTitle:** nmr solution structure of pisi
2	c3rruA_	Alignment		27.0	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tom1l1 protein; **PDBTitle:** x-ray crystal structure of the vhs domain of human tom1-like protein,2 northeast structural genomics consortium target hr3050e
3	d1mhqa_	Alignment		26.9	18	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
4	d1ujka_	Alignment		26.1	20	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
5	d1wh4a_	Alignment		24.3	27	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
6	d1dvpa1	Alignment		23.7	8	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
7	c1iqrA_	Alignment		23.7	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**photolyase; **PDBTitle:** crystal structure of dna photolyase from thermus2 thermophilus
8	d1elka_	Alignment		21.4	21	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
9	c1x5bA_	Alignment		19.7	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2; **PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
10	d1u3da1	Alignment		18.6	12	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
11	d1dnpa1	Alignment		18.2	12	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain

12	c3fefB_	Alignment		17.1	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glucosidase lpld; **PDBTitle:** crystal structure of putative glucosidase lpld from2 bacillus subtilis
13	d2bvca2	Alignment		16.4	43	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamine synthetase catalytic domain
14	c3lo0A_	Alignment		15.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis
15	c3nj2B_	Alignment		15.5	6	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**duf269-containing protein; **PDBTitle:** crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
16	c2jqeA_	Alignment		15.3	56	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** soution structure of af54 m-domain
17	d2ffha2	Alignment		15.1	56	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
18	d1qb2a_	Alignment		14.8	56	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
19	c2j4dA_	Alignment		12.7	16	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**cryptochrome dash; **PDBTitle:** cryptochrome 3 from arabidopsis thaliana
20	c3fvyA_	Alignment		12.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl-peptidase 3; **PDBTitle:** crystal structure of human dipeptidyl peptidase iii
21	d1w7pd1	Alignment	not modelled	12.1	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
22	d1v66a_	Alignment	not modelled	12.1	20	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
23	d2ebfx1	Alignment	not modelled	11.5	7	**Fold:**PMT central region-like **Superfamily:**PMT central region-like **Family:**PMT central region-like
24	c2gjhA_	Alignment	not modelled	11.4	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
25	c1dvpA_	Alignment	not modelled	11.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
26	c1u3cA_	Alignment	not modelled	11.1	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cryptochrome 1 apoprotein; **PDBTitle:** crystal structure of the phr domain of cryptochrome 1 from2 arabidopsis thaliana
27	d1r76a_	Alignment	not modelled	11.0	26	**Fold:**alpha/alpha toroid **Superfamily:**Family 10 polysaccharide lyase **Family:**Family 10 polysaccharide lyase
28	c1oefA_	Alignment	not modelled	10.8	33	**PDB header:**apolipoprotein **Chain:** A: **PDB Molecule:**apolipoprotein e; **PDBTitle:** peptide of human apoe residues 263-286, nmr, 5 structures2 at ph 4.8, 37 degrees celsius and peptide:sds mole

						ratio3 of 1:90
29	d2h80a1	Alignment	not modelled	10.5	22	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Variant SAM domain
30	d2dkya1	Alignment	not modelled	10.5	33	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Variant SAM domain
31	c1dnpA_	Alignment	not modelled	10.4	12	**PDB header:**lyase (carbon-carbon) **Chain:** A: **PDB Molecule:**dna photolyase; **PDBTitle:** structure of deoxyribodipyrimidine photolyase
32	d1u5tb1	Alignment	not modelled	10.3	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
33	c2qqoB_	Alignment	not modelled	10.1	44	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**neuropilin-2; **PDBTitle:** crystal structure of the a2b1b2 domains from human neuropilin-2
34	d1vyva2	Alignment	not modelled	9.8	37	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
35	d1qzxa2	Alignment	not modelled	9.3	50	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
36	d2sh1a_	Alignment	not modelled	9.0	42	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
37	c3s90D_	Alignment	not modelled	8.9	55	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**talin-1; **PDBTitle:** human vinculin head domain vh1 (residues 1-252) in complex with murine2 talin (vbs33; residues 1512-1546)
38	c1htoB_	Alignment	not modelled	8.6	43	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
39	c3g7pA_	Alignment	not modelled	8.4	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**nitrogen fixation protein; **PDBTitle:** crystal structure of a nifx-associated protein of unknown function2 (afe_1514) from acidithiobacillus ferrooxidans atcc at 2.00 a3 resolution
40	d1f52a2	Alignment	not modelled	8.2	33	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamine synthetase catalytic domain
41	c1s6yA_	Alignment	not modelled	8.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phospho-beta-glucosidase; **PDBTitle:** 2.3a crystal structure of phospho-beta-glucosidase
42	c2qqmA_	Alignment	not modelled	8.1	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**neuropilin-1; **PDBTitle:** crystal structure of the a2b1b2 domains from human neuropilin-1
43	c2jxfA_	Alignment	not modelled	8.0	27	**PDB header:**viral protein, membrane protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** the solution structure of hcv ns4b(40-69)
44	c1np7A_	Alignment	not modelled	7.9	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dna photolyase; **PDBTitle:** crystal structure analysis of synechocystis sp. pcc6803 cryptochrome
45	c1u8xX_	Alignment	not modelled	7.8	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**maltose-6'-phosphate glucosidase; **PDBTitle:** crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
46	c2iunD_	Alignment	not modelled	7.8	30	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**avian adenovirus celo long fibre; **PDBTitle:** structure of the c-terminal head domain of the avian2 adenovirus celo long fibre (p21 crystal form)
47	c3c8zB_	Alignment	not modelled	7.7	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
48	c1fpyE_	Alignment	not modelled	7.5	33	**PDB header:**ligase **Chain:** E: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
49	c2hfzA_	Alignment	not modelled	7.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase(ns5); **PDBTitle:** crystal structure of rna dependent rna polymerase domain2 from west nile virus
50	c1zzpA_	Alignment	not modelled	7.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase abl1; **PDBTitle:** solution structure of the f-actin binding domain of bcr-2 abl/c-abl
51	c1vjtA_	Alignment	not modelled	7.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
52	d1np7a1	Alignment	not modelled	7.1	14	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
53	c2eodA_	Alignment	not modelled	7.0	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 4; **PDBTitle:** solution structure of traf-type zinc finger domains (190-2 248) from human tnf receptor-associated factor 4
54	c3zxpC_	Alignment	not modelled	6.9	15	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**bro1 domain-containing protein brox; **PDBTitle:** structural and functional analyses of the bro1 domain

						protein brox
55	d1enwa_	Alignment	not modelled	6.8	10	**Fold:**RuvA C-terminal domain-like **Superfamily:**Elongation factor TFIIS domain 2 **Family:**Elongation factor TFIIS domain 2
56	c3r9mA_	Alignment	not modelled	6.8	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bro1 domain-containing protein brox; **PDBTitle:** crystal structure of the brox bro1 domain
57	c1tezB_	Alignment	not modelled	6.8	11	**PDB header:**lyase/dna **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** complex between dna and the dna photolyase from anacystis nidulans
58	c1oegA_	Alignment	not modelled	6.7	37	**PDB header:**apolipoprotein **Chain:** A: **PDB Molecule:**apolipoprotein e; **PDBTitle:** peptide of human apoe residues 267-289, nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:sds mole ratio3 of 1:90
59	d1t3la2	Alignment	not modelled	6.6	53	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
60	d1t0hb_	Alignment	not modelled	6.5	47	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
61	d1vyua2	Alignment	not modelled	6.5	47	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
62	d1aq0a_	Alignment	not modelled	6.4	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
63	c3juaB_	Alignment	not modelled	6.3	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**65 kda yes-associated protein; **PDBTitle:** structural basis of yap recognition by tead4 in the hippo pathway
64	c2entA_	Alignment	not modelled	6.0	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**krueppel-like factor 15; **PDBTitle:** solution structure of the second c2h2-type zinc finger2 domain from human krueppel-like factor 15
65	d1bvp11	Alignment	not modelled	5.9	23	**Fold:**A virus capsid protein alpha-helical domain **Superfamily:**A virus capsid protein alpha-helical domain **Family:**Orbivirus capsid
66	c1up6F_	Alignment	not modelled	5.9	22	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**6-phospho-beta-glucosidase; **PDBTitle:** structure of the 6-phospho-beta glucosidase from thermotoga2 maritima at 2.55 angstrom resolution in the tetragonal form3 with manganese, nad+ and glucose-6-phosphate
67	d1oqva_	Alignment	not modelled	5.7	31	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**TcpA-like pilin
68	d2bo9b1	Alignment	not modelled	5.6	17	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Latexin-like
69	c3mkqB_	Alignment	not modelled	5.6	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
70	c2kk1A_	Alignment	not modelled	5.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase abl2; **PDBTitle:** solution structure of c-terminal domain of tyrosine-protein2 kinase abl2 from homo sapiens, northeast structural3 genomics consortium (nesg) target hr5537a
71	c3cskA_	Alignment	not modelled	5.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidyl-peptidase 3; **PDBTitle:** structure of dpp iii from saccharomyces cerevisiae
72	d1hn6a_	Alignment	not modelled	5.2	30	**Fold:**Apical membrane antigen 1 **Superfamily:**Apical membrane antigen 1 **Family:**Apical membrane antigen 1
73	c2v0xB_	Alignment	not modelled	5.2	21	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**lamina-associated polypeptide 2 isoforms **PDBTitle:** the dimerization domain of lap2alpha
74	c3fkyD_	Alignment	not modelled	5.2	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
75	c2w2uA_	Alignment	not modelled	5.1	27	**PDB header:**hydrolase/transport **Chain:** A: **PDB Molecule:**hypothetical p60 katanin; **PDBTitle:** structural insight into the interaction between archaeal2 escrt-iii and aaa-atpase
76	d1czsa_	Alignment	not modelled	5.0	42	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Discoidin domain (FA58C, coagulation factor 5/8 C-terminal domain)
77	c2l5rA_	Alignment	not modelled	5.0	50	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide alyteserin-1c; **PDBTitle:** conformational and membrane interactins studies of antimicrobial2 peptide alyteserin-1c