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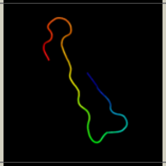
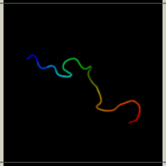
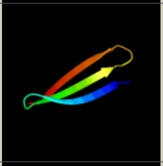
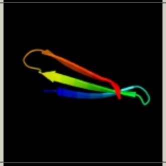
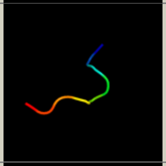
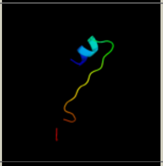
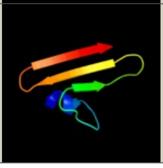
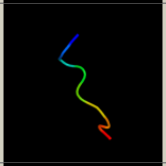
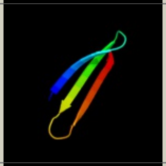
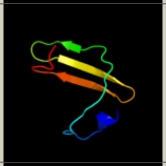
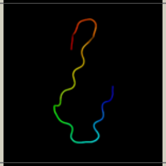
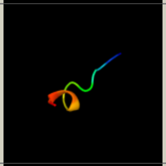
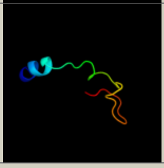
Description	P0AE98
Date	Thu Jan 5 11:22:50 GMT 2012
Unique Job ID	6f764af51a014979

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hc5a1	Alignment		45.5	8	**Fold:**FlaG-like **Superfamily:**FlaG-like **Family:**FlaG-like
2	c3sd2A_	Alignment		44.1	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative member of duf3244 protein family; **PDBTitle:** crystal structure of a putative member of duf3244 protein family2 (bt_3571) from bacteroides thetaiotaomicron vpi-5482 at 1.40 a3 resolution
3	c2hzsH_	Alignment		41.6	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**rna polymerase ii mediator complex subunit 18; **PDBTitle:** structure of the mediator head submodule med8c/18/20
4	d1dkza2	Alignment		28.3	23	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
5	d1u00a2	Alignment		24.6	30	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
6	c3dqgC_	Alignment		20.5	24	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock 70 kda protein f; **PDBTitle:** peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from caenorhabditis elegans.
7	c1m8oB_	Alignment		16.6	33	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**platele integrin beta3 subunit: cytoplasmic **PDBTitle:** platelet integrin alfaiib-beta3 cytoplasmic domain
8	c3ieiD_	Alignment		15.5	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**leucine carboxyl methyltransferase 1; **PDBTitle:** crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
9	c3fcgB_	Alignment		13.4	14	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** crystal structure analysis of the middle domain of the2 caf1a usher
10	c1s4xA_	Alignment		12.4	33	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** nmr structure of the integrin b3 cytoplasmic domain in dpc2 micelles
11	c2jpiA_	Alignment		12.0	10	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa

12	c1hznA_	Alignment		11.7	26	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**cholecystokinin type a receptor; **PDBTitle:** nmr solution structure of the third extracellular loop of2 the cholecystokinin a receptor
13	c2kncB_	Alignment		11.5	33	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
14	c1u00A_	Alignment		10.7	31	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
15	d2oq0a1	Alignment		10.6	8	**Fold:**OB-fold **Superfamily:**HIN-2000 domain-like **Family:**HIN-200/IF120x domain
16	c3d33B_	Alignment		10.6	21	**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
17	c3dpqE_	Alignment		10.5	23	**PDB header:**chaperone, peptide binding protein **Chain:** E: **PDB Molecule:**chaperone protein dnak; **PDBTitle:** crystal structure of the substrate binding domain of e.2 coli dnak in complex with a long pyrrhocoricin-derived3 inhibitor peptide (form b)
18	d1ddwa_	Alignment		10.4	29	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Enabled/VASP homology 1 domain (EVH1 domain)
19	c3rj1S_	Alignment		9.7	20	**PDB header:**transcription **Chain:** S: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 18; **PDBTitle:** architecture of the mediator head module
20	d5csma_	Alignment		9.6	18	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Allosteric chorismate mutase
21	d2fwua1	Alignment	not modelled	9.2	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
22	d1y71a1	Alignment	not modelled	8.0	26	**Fold:**SH3-like barrel **Superfamily:**Kinase-associated protein B-like **Family:**Kinase-associated protein B-like
23	c3hftA_	Alignment	not modelled	7.9	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wbms, polysaccharide deacetylase involved in o-antigen **PDBTitle:** crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution
24	c3l9fD_	Alignment	not modelled	7.2	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative uncharacterized protein smu.1604c; **PDBTitle:** the crystal structure of smu.1604c from streptococcus mutans ua159
25	d1gcya1	Alignment	not modelled	6.7	21	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
26	d1egxa_	Alignment	not modelled	6.3	27	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Enabled/VASP homology 1 domain (EVH1 domain)
27	c2op6A_	Alignment	not modelled	5.9	19	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**heat shock 70 kda protein d; **PDBTitle:** peptide-binding domain of heat shock 70 kda protein d precursor from2 c.elegans
						PDB header:hydrolase **Chain:** B: **PDB Molecule:**infectious bronchitis virus (ibv) main

28	c2q6fB_	Alignment	not modelled	5.9	42	protease; **PDBTitle:** crystal structure of infectious bronchitis virus (ibv) main2 protease in complex with a michael acceptor inhibitor n3
29	c3e9uA_	Alignment	not modelled	5.9	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of calx cbd2 domain
30	d1j7na2	Alignment	not modelled	5.8	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
31	d1lvoa_	Alignment	not modelled	5.8	42	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
32	d1jb0d_	Alignment	not modelled	5.8	40	**Fold:**Photosystem I subunit PsaD **Superfamily:**Photosystem I subunit PsaD **Family:**Photosystem I subunit PsaD
33	c3nztA_	Alignment	not modelled	5.8	5	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase; **PDBTitle:** 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 ftom francisella tularensis in complex with amp
34	c3d23A_	Alignment	not modelled	5.7	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3c-like proteinase; **PDBTitle:** main protease of hcov-hku1
35	c3cu2A_	Alignment	not modelled	5.7	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribulose-5-phosphate 3-epimerase; **PDBTitle:** crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
36	c2j3mA_	Alignment	not modelled	5.5	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
37	d1qc6a_	Alignment	not modelled	5.5	12	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Enabled/VASP homology 1 domain (EVH1 domain)
38	d2duca1	Alignment	not modelled	5.4	33	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
39	c2oq0D_	Alignment	not modelled	5.4	8	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**gamma-interferon-inducible protein ifi-16; **PDBTitle:** crystal structure of the first hin-200 domain of interferon-inducible2 protein 16
40	c3n8eA_	Alignment	not modelled	5.3	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stress-70 protein, mitochondrial; **PDBTitle:** substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
41	c3fyfA_	Alignment	not modelled	5.2	55	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein bvu-3222; **PDBTitle:** crystal structure of uncharacterized protein bvu_3222 from2 bacteroides vulgatus
42	d1g5ga1	Alignment	not modelled	5.2	22	**Fold:**Head and neck region of the ectodomain of NDV fusion glycoprotein **Superfamily:**Head and neck region of the ectodomain of NDV fusion glycoprotein **Family:**Head and neck region of the ectodomain of NDV fusion glycoprotein
43	c2cblA_	Alignment	not modelled	5.1	23	**PDB header:**complex (proto-oncogene/peptide) **Chain:** A: **PDB Molecule:**proto-oncogene cbl; **PDBTitle:** n-terminal domain of cbl in complex with its binding site2 on zap-70