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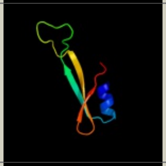
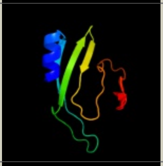
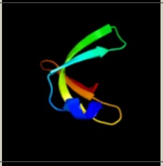
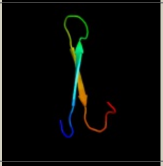
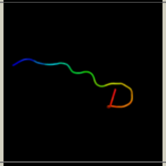
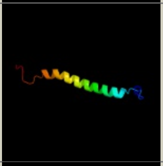
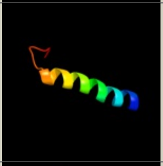
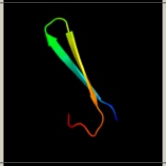
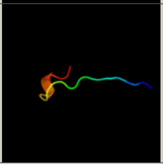
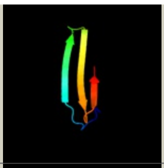
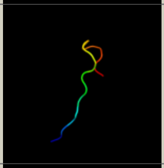
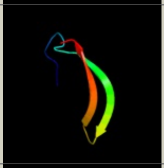
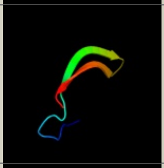
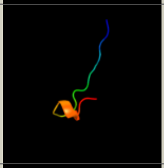
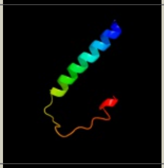
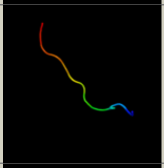
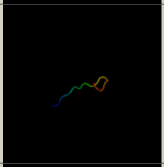
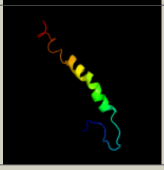
Description	P22586
Date	Thu Jan 5 11:39:00 GMT 2012
Unique Job ID	7a4a98cd69a2b3ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fqmA_	Alignment		39.8	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural protein 5a; **PDBTitle:** crystal structure of a novel dimeric form of hcv ns5a domain i protein
2	d1e2ta_	Alignment		33.5	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
3	c2pfrB_	Alignment		25.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arylamine n-acetyltransferase 2; **PDBTitle:** human n-acetyltransferase 2
4	c3lnbA_	Alignment		24.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase family protein; **PDBTitle:** crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
5	c2qtxL_	Alignment		22.3	16	**PDB header:**rna binding protein **Chain:** L: **PDB Molecule:**uncharacterized protein mj1435; **PDBTitle:** crystal structure of an hfq-like protein from methanococcus2 jannaschii
6	c1j3wB_	Alignment		20.4	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**giding protein-mglb; **PDBTitle:** structure of gliding protein-mglb from thermus thermophilus hb8
7	c3hh1D_	Alignment		19.9	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**tetrapyrrole methylase family protein; **PDBTitle:** the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum tls
8	c2kncA_	Alignment		18.4	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
9	c2l2tA_	Alignment		16.6	32	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
10	d1j3wa_	Alignment		16.3	22	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
11	d1pjqa2	Alignment		15.8	24	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase

12	c3e19D_	Alignment		14.1	19	**PDB header:**transcription regulator, metal binding p **Chain:** D: **PDB Molecule:**feoa; **PDBTitle:** crystal structure of iron uptake regulatory protein (feoa) solved by2 sulfur sad in a monoclinic space group
13	c2e0kA_	Alignment		13.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
14	c1xe1A_	Alignment		13.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf0907; **PDBTitle:** hypothetical protein from pyrococcus furiosus pfu-880080-001
15	d1xe1a_	Alignment		13.1	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
16	d1ve2a1	Alignment		12.8	18	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
17	c1v55B_	Alignment		12.8	0	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** bovine heart cytochrome c oxidase at the fully reduced state
18	c3gztF_	Alignment		12.6	50	**PDB header:**virus **Chain:** F: **PDB Molecule:**outer capsid glycoprotein vp7; **PDBTitle:** vp7 recoated rotavirus dlp
19	c3kwpA_	Alignment		12.5	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**predicted methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase from lactobacillus2 brevis
20	d1fftb2	Alignment		12.5	19	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
21	c1afoB_	Alignment	not modelled	12.4	25	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
22	c3nutC_	Alignment	not modelled	12.2	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**precorrin-3 methylase; **PDBTitle:** crystal structure of the methyltransferase cobj
23	d1va0a1	Alignment	not modelled	12.2	24	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
24	c2zvbA_	Alignment	not modelled	12.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-3 c17-methyltransferase; **PDBTitle:** crystal structure of tt0207 from thermus thermophilus hb8
25	c2qbuA_	Alignment	not modelled	11.7	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 methyltransferase; **PDBTitle:** crystal structure of methanothermobacter thermautotrophicus cbil
26	c2jwaA_	Alignment	not modelled	11.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
27	c2ks1B_	Alignment	not modelled	11.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
28	d1q18a1	Alignment	not modelled	10.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
						PDB header:transferase/oxidoreductase/lyase

29	c1pjtB_	Alignment	not modelled	10.8	24	**Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
30	c2yboA_	Alignment	not modelled	10.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
31	d1s4da_	Alignment	not modelled	9.7	24	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
32	c1cbfA_	Alignment	not modelled	9.5	18	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**cobalt-precorrin-4 transmethylase; **PDBTitle:** the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
33	d1cbfa_	Alignment	not modelled	9.5	18	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
34	d1ppjd2	Alignment	not modelled	9.2	17	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
35	d1vdda_	Alignment	not modelled	9.1	23	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
36	c3q1jA_	Alignment	not modelled	8.5	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 1 of human phd finger protein 20
37	c3kdpG_	Alignment	not modelled	8.5	33	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
38	c3kdpH_	Alignment	not modelled	8.5	33	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
39	c3sftA_	Alignment	not modelled	8.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
40	c2i2rK_	Alignment	not modelled	8.3	18	**PDB header:**transport protein **Chain:** K: **PDB Molecule:**potassium voltage-gated channel subfamily d member 3; **PDBTitle:** crystal structure of the kchip1/kv4.3 t1 complex
41	d3cx5d2	Alignment	not modelled	8.1	13	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
42	d2ftwa1	Alignment	not modelled	7.6	25	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
43	c2fynH_	Alignment	not modelled	7.5	24	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
44	c2r6fA_	Alignment	not modelled	7.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
45	c2l34A_	Alignment	not modelled	7.4	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer
46	c2l34B_	Alignment	not modelled	7.2	26	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer
47	d1w4ta1	Alignment	not modelled	6.6	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
48	d2bsza1	Alignment	not modelled	6.4	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
49	c2l35A_	Alignment	not modelled	6.4	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dap12-nkg2c_tm; **PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer
50	c2kpeA_	Alignment	not modelled	6.4	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
51	c2kpeB_	Alignment	not modelled	6.4	29	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
52	c3cwbQ_	Alignment	not modelled	6.2	10	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
53	c2npnA_	Alignment	not modelled	6.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative cobalamin synthesis related protein;

						PDBTitle: crystal structure of putative cobalamin synthesis related protein2 (cobf) from corynebacterium diphtheriae
54	c2rmzA_	 Alignment	not modelled	5.7	32	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** bicelle-embedded integrin beta3 transmembrane segment
55	c2k21A_	 Alignment	not modelled	5.7	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
56	c2yiuE_	 Alignment	not modelled	5.6	24	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
57	c3nd1B_	 Alignment	not modelled	5.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-6a synthase/cobf protein; **PDBTitle:** crystal structure of precorrin-6a synthase from rhodobacter capsulatus
58	d2j01v1	 Alignment	not modelled	5.4	6	**Fold:**L21p-like **Superfamily:**L21p-like **Family:**Ribosomal protein L21p
59	c2rddB_	 Alignment	not modelled	5.4	13	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
60	c1vddC_	 Alignment	not modelled	5.1	23	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
61	c1p84D_	 Alignment	not modelled	5.1	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex