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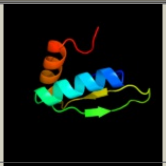
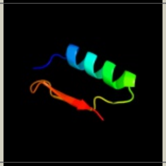
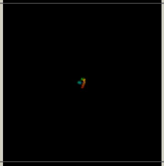
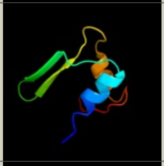
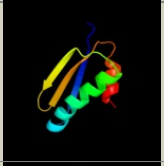
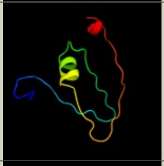
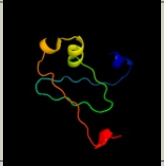
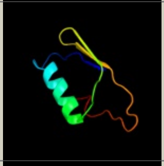
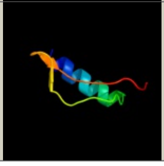
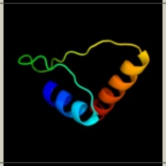
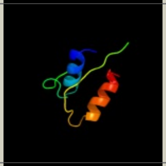
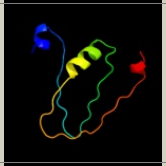
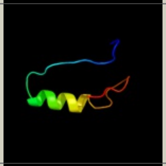
Description	P42615
Date	Thu Jan 5 12:01:49 GMT 2012
Unique Job ID	985276605896ab17

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yj7A_	Alignment		58.8	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
2	c3aqoD_	Alignment		53.8	10	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** structure and function of a membrane component secdf that enhances2 protein export
3	d1t1ea2	Alignment		41.1	21	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
4	c2y9jt_	Alignment		40.6	21	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**protein prgh; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
5	c3mahA_	Alignment		36.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
6	d2f06a1	Alignment		31.6	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
7	c2re1A_	Alignment		31.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase, alpha and beta subunits; **PDBTitle:** crystal structure of aspartokinase alpha and beta subunits
8	c2os2A_	Alignment		30.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 3a; **PDBTitle:** crystal structure of jmjd2a complexed with histone h3 peptide2 trimethylated at lys36
9	c2w2iC_	Alignment		27.9	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate oxygenase; **PDBTitle:** crystal structure of the human 2-oxoglutarate oxygenase2 loc390245
10	d2j0wa2	Alignment		27.0	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
11	c1zswA_	Alignment		26.6	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family

12	c2dnrA_	Alignment		26.0	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**synaptojanin-1; **PDBTitle:** solution structure of rna binding domain in synaptojanin 1
13	c3ftbA_	Alignment		25.1	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
14	c2rrnA_	Alignment		24.0	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** solution structure of secdf periplasmic domain p4
15	d2cdqa2	Alignment		23.1	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
16	c2q8eB_	Alignment		22.6	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** specificity and mechanism of jmjd2a, a trimethyllysine-2 specific histone demethylase
17	c2k42B_	Alignment		22.3	38	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**espfu; **PDBTitle:** solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
18	c2zhoB_	Alignment		21.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
19	c2wbrA_	Alignment		20.1	18	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**gw182; **PDBTitle:** the rrm domain in gw182 proteins contributes to mirna-2 mediated gene silencing
20	d1vbka2	Alignment		18.6	24	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
21	c3ktbD_	Alignment	not modelled	18.3	21	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
22	c3eucB_	Alignment	not modelled	17.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase 2; **PDBTitle:** crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution
23	c2f06B_	Alignment	not modelled	16.6	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
24	d1uv7a_	Alignment	not modelled	16.1	10	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**General secretion pathway protein M, EpsM **Family:**General secretion pathway protein M, EpsM
25	c1uv7A_	Alignment	not modelled	16.1	10	**PDB header:**transport **Chain:** A: **PDB Molecule:**general secretion pathway protein m; **PDBTitle:** periplasmic domain of epsm from vibrio cholerae
26	c3ffhA_	Alignment	not modelled	15.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
27	d2i8ga1	Alignment	not modelled	15.7	15	**Fold:**Mog1p/PsbP-like **Superfamily:**Mog1p/PsbP-like **Family:**DIP2269-like
28	c3kgkA_	Alignment	not modelled	15.1	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**arsenical resistance operon trans-acting repressor arsd;

						PDBTitle: crystal structure of arsd
29	d1gtda_	Alignment	not modelled	14.6	23	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
30	c2kyzA_	Alignment	not modelled	13.8	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
31	c2yx5A_	Alignment	not modelled	13.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
32	d2f06a2	Alignment	not modelled	12.1	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
33	d1vkpa_	Alignment	not modelled	11.7	26	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
34	d1b5pa_	Alignment	not modelled	11.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
35	c1t1eA_	Alignment	not modelled	10.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kumamolisin; **PDBTitle:** high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp)
36	c3edyA_	Alignment	not modelled	10.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1; **PDBTitle:** crystal structure of the precursor form of human tripeptidyl-peptidase2 1
37	c3ffrA_	Alignment	not modelled	9.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase serc; **PDBTitle:** crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
38	c1vbkA_	Alignment	not modelled	9.4	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
39	d1zswa2	Alignment	not modelled	9.2	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**BC1024-like
40	c3getA_	Alignment	not modelled	9.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
41	d1t4aa_	Alignment	not modelled	8.6	15	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
42	d2zkmx4	Alignment	not modelled	8.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
43	c3p1tB_	Alignment	not modelled	7.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
44	c2qqzB_	Alignment	not modelled	7.6	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase family protein, putative; **PDBTitle:** crystal structure of putative glyoxalase family protein from bacillus2 anthracis
45	c3cnrA_	Alignment	not modelled	7.5	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**type iv fimbriae assembly protein; **PDBTitle:** crystal structure of pilz (xac1133) from xanthomonas2 axonopodis pv citri
46	c2dgbA_	Alignment	not modelled	7.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
47	d2cmua1	Alignment	not modelled	6.9	24	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
48	d1qasa3	Alignment	not modelled	6.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
49	d2hmfa3	Alignment	not modelled	6.8	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
50	c3c0uA_	Alignment	not modelled	6.8	60	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yaeq; **PDBTitle:** crystal structure of e.coli yaeq protein
51	c3h96B_	Alignment	not modelled	6.7	19	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**f420-h2 dependent reductase a; **PDBTitle:** msmeg_3358 f420 reductase
52	c2zw2B_	Alignment	not modelled	6.6	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
53	c1oy8A_	Alignment	not modelled	6.5	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the

						acrb2 multidrug efflux pump
54	d2ot9a1	Alignment	not modelled	6.4	40	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**YaeQ-like
55	d1vhqa_	Alignment	not modelled	6.4	10	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
56	d2g3wa1	Alignment	not modelled	6.3	40	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**YaeQ-like
57	d1vq3a_	Alignment	not modelled	6.2	10	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
58	c3oajA_	Alignment	not modelled	6.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative ring-cleaving dioxygenase mhqo; **PDBTitle:** crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168
59	c3fwzA_	Alignment	not modelled	5.9	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein ybal; **PDBTitle:** crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
60	d2op5a1	Alignment	not modelled	5.7	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Marine metagenome family DABB1
61	c3ly1C_	Alignment	not modelled	5.6	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
62	d1iuga_	Alignment	not modelled	5.6	4	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
63	d1o4sa_	Alignment	not modelled	5.6	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like