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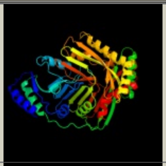
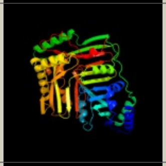
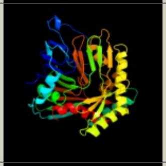
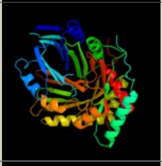
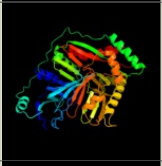
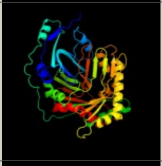
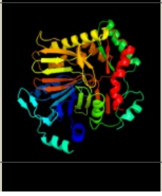
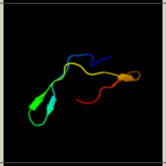
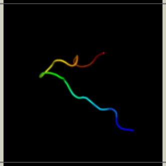
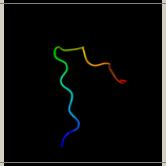
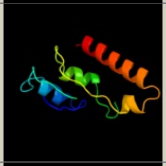
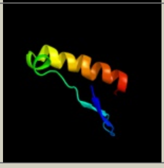
Description	P38051
Date	Thu Jan 5 11:57:52 GMT 2012
Unique Job ID	8118ec9c8f21e963

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3bzna1	Alignment		100.0	100	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
2	c3gseA_	Alignment		100.0	53	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**menaquinone-specific isochorismate synthase; **PDBTitle:** crystal structure of menaquinone-specific isochorismate synthase from2 yersinia pestis co92
3	c3hwoB_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**isochorismate synthase entc; **PDBTitle:** crystal structure of escherichia coli enterobactin-specific2 isochorismate synthase entc in complex with isochorismate
4	d2g5fa1	Alignment		100.0	23	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
5	d1qdla_	Alignment		100.0	23	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
6	c3os6A_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isochorismate synthase dhbc; **PDBTitle:** crystal structure of putative 2,3-dihydroxybenzoate-specific2 isochorismate synthase, dhbc from bacillus anthracis.
7	d2fn0a1	Alignment		100.0	25	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
8	d1i1qa_	Alignment		100.0	21	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
9	d1i7qa_	Alignment		100.0	22	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
10	c2i6yA_	Alignment		100.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**anthranilate synthase component i, putative; **PDBTitle:** structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbti
11	c3h9mA_	Alignment		100.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**p-aminobenzoate synthetase, component i; **PDBTitle:** crystal structure of para-aminobenzoate synthetase,2 component i from cytophaga hutchinsonii

12	c3r74B_	Alignment		100.0	19	**PDB header:**lyase, biosynthetic protein **Chain:** B: **PDB Molecule:**anthranilate/para-aminobenzoate synthases component i; **PDBTitle:** crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
13	d1k0ga_	Alignment		100.0	19	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
14	c3nqkA_	Alignment		30.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a structural genomics, unknown function2 (bacova_03322) from bacteroides ovatus at 2.61 a resolution
15	d1eyba_	Alignment		19.2	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
16	c1ey2A_	Alignment		19.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
17	d1hxra_	Alignment		18.7	29	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
18	d2fu5a1	Alignment		17.9	29	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
19	d2ffca1	Alignment		17.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
20	c3fuyC_	Alignment		14.2	36	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative integron gene cassette protein; **PDBTitle:** structure from the mobile metagenome of cole harbour salt2 marsh: integron cassette protein hfx_cass1
21	d2nwua1	Alignment	not modelled	12.7	12	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**SSO1042-like
22	d1d5ta2	Alignment	not modelled	11.6	36	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GDI-like
23	c3ci9B_	Alignment	not modelled	10.3	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
24	d1ji8a_	Alignment	not modelled	9.7	26	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
25	c1wxnA_	Alignment	not modelled	9.2	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin apetx2; **PDBTitle:** solution structure of apetx2, a specific peptide inhibitor2 of asic3 proton-gated channels
26	c2km1A_	Alignment	not modelled	8.7	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein dre2; **PDBTitle:** solution structure of the n-terminal domain of the yeast protein dre2
27	c3c66B_	Alignment	not modelled	8.7	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** yeast poly(a) polymerase in complex with fip1 residues 80-105
28	d1aopa2	Alignment	not modelled	8.7	13	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
29	c3ol4B_	Alignment	not modelled	8.6	38	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein

						from2 mycobacterium smegmatis, an ortholog of rv0543c
30	d2ch5a2	Alignment	not modelled	8.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
31	c2z1tA_	Alignment	not modelled	7.9	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hydrogenase maturation protein hype
32	c1wqkA_	Alignment	not modelled	7.9	54	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin apetx1; **PDBTitle:** solution structure of apetx1, a specific peptide inhibitor2 of human ether-a-go-go-related gene potassium channels3 from the venom of the sea anemone anthopleura4 elegantissima: a new fold for an herg toxin
33	c2zkrf_	Alignment	not modelled	7.4	20	**PDB header:**ribosomal protein/rna **Chain:** F: **PDB Molecule:**rna expansion segment es7 part iii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
34	c3rpdB_	Alignment	not modelled	7.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methionine synthase (b12-independent); **PDBTitle:** the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.
35	c1s1iG_	Alignment	not modelled	6.9	16	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein l8-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
36	d2bcgg3	Alignment	not modelled	6.8	21	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GDI-like
37	c3izcH_	Alignment	not modelled	6.1	16	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein rpl8 (l7ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
38	c3rrrB_	Alignment	not modelled	6.0	45	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the rsv f protein in the post-fusion conformation
39	c3t6mA_	Alignment	not modelled	6.0	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of the catalytic domain of dape protein from2 v.cholerea in the zn bound form
40	c4a1eF_	Alignment	not modelled	5.7	22	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl7a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
41	d2c1wa1	Alignment	not modelled	5.6	50	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Eukaryotic EndoU ribonuclease
42	c3dwlG_	Alignment	not modelled	5.6	14	**PDB header:**structural protein **Chain:** G: **PDB Molecule:**actin-related protein 2/3 complex subunit 5; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
43	c3fhdA_	Alignment	not modelled	5.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**orf 37; **PDBTitle:** crystal structure of the shutoff and exonuclease protein from kaposis2 sarcoma associated herpesvirus
44	d2fkia1	Alignment	not modelled	5.5	14	**Fold:**Secretion chaperone-like **Superfamily:**YjbR-like **Family:**YjbR-like
45	d1ydua1	Alignment	not modelled	5.1	7	**Fold:**At5g01610-like **Superfamily:**At5g01610-like **Family:**At5g01610-like
46	c2kvcA_	Alignment	not modelled	5.1	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a