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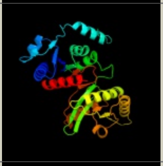
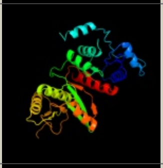
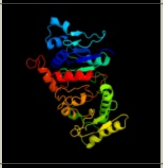
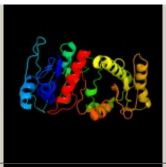
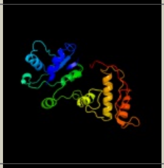
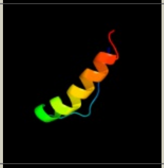
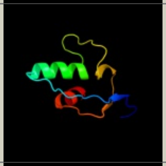
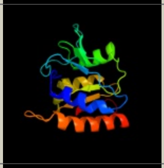
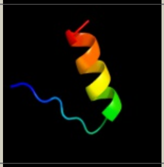
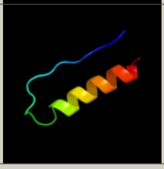
Description	P27247
Date	Thu Jan 5 11:43:26 GMT 2012
Unique Job ID	13addc5eb3f6a62d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1u7na_	Alignment		100.0	37	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
2	d1vi1a_	Alignment		100.0	36	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
3	d1xcoa_	Alignment		100.0	22	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
4	d2af4c1	Alignment		100.0	19	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
5	d1r5ja_	Alignment		100.0	22	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
6	c1ycoA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**branched-chain phosphotransacylase; **PDBTitle:** crystal structure of a branched-chain phosphotransacylase from2 enterococcus faecalis v583
7	c3tngA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lmo1369 protein; **PDBTitle:** the crystal structure of a possible phosphate acetyl/butaryl2 transferase from listeria monocytogenes egd-e.
8	d1vmia_	Alignment		100.0	19	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
9	c1vmiA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphate acetyltransferase; **PDBTitle:** crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
10	d1ptma_	Alignment		100.0	16	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
11	c1yxoB_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593

12	d1r8ka_	Alignment		100.0	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
13	c2hi1A_	Alignment		98.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 2; **PDBTitle:** the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
14	d1qgoa_	Alignment		74.7	12	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Cobalt chelatase CbiK
15	d1gmla_	Alignment		64.9	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
16	c2phjA_	Alignment		56.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of sure protein from aquifex aeolicus
17	c3qd5B_	Alignment		56.0	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
18	c3lyhB_	Alignment		55.8	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cobalamin (vitamin b12) biosynthesis cbix protein; **PDBTitle:** crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
19	c3gdwA_	Alignment		53.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
20	d1tjna_	Alignment		52.2	23	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**CbiX-like
21	c1tjnA_	Alignment	not modelled	52.2	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase; **PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
22	c2pjuD_	Alignment	not modelled	52.0	21	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
23	d1kzyc2	Alignment	not modelled	48.1	29	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**53BP1
24	c2ja9A_	Alignment	not modelled	46.9	14	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the n-terminal deletion of yeast exosome2 component rrp40
25	d1q3qa3	Alignment	not modelled	43.6	19	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**Group II chaperonin (CCT, TRIC), intermediate domain
26	d1j9ja_	Alignment	not modelled	43.5	16	**Fold:**SurE-like **Superfamily:**SurE-like **Family:**SurE-like
27	d1wu2a3	Alignment	not modelled	42.9	33	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
28	c2v4oB_	Alignment	not modelled	42.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**multifunctional protein sur e; **PDBTitle:** crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form

29	c2xvzA_	Alignment	not modelled	40.6	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**chelatase, putative; **PDBTitle:** cobalt chelatase cbik (periplasmatic) from desulvobrio2 vulgaris hildenborough (co-crystallized with cobalt)
30	d1y5ea1	Alignment	not modelled	39.5	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
31	d2pjua1	Alignment	not modelled	38.5	22	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
32	d1fuia2	Alignment	not modelled	38.3	14	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
33	d2ja9a2	Alignment	not modelled	38.2	15	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
34	d2ftsa3	Alignment	not modelled	36.8	45	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
35	c3gx1A_	Alignment	not modelled	35.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1832 protein; **PDBTitle:** crystal structure of a domain of lin1832 from listeria innocua
36	d3ct6a1	Alignment	not modelled	35.2	29	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
37	d1uz5a3	Alignment	not modelled	34.8	45	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
38	c3k93A_	Alignment	not modelled	31.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phage related exonuclease; **PDBTitle:** crystal structure of phage related exonuclease (yp_719632.1) from2 haemophilus somnus 129pt at 2.15 a resolution
39	d3b48a1	Alignment	not modelled	30.1	24	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
40	c3imkA_	Alignment	not modelled	29.7	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative molybdenum carrier protein; **PDBTitle:** crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
41	d1pkpa1	Alignment	not modelled	28.9	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
42	d2uube1	Alignment	not modelled	28.3	24	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
43	d1iowa1	Alignment	not modelled	28.0	21	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
44	c3se7A_	Alignment	not modelled	26.7	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**vana; **PDBTitle:** ancient vana
45	c3lkzB_	Alignment	not modelled	24.6	23	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**non-structural protein 5; **PDBTitle:** structural and functional analyses of a conserved hydrophobic pocket2 of flavivirus methyltransferase
46	d1jlja_	Alignment	not modelled	22.9	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
47	d1su1a_	Alignment	not modelled	21.8	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
48	c1su1A_	Alignment	not modelled	21.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce; **PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
49	c1p6gE_	Alignment	not modelled	21.6	15	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**30s ribosomal protein s5; **PDBTitle:** real space refined coordinates of the 30s subunit fitted2 into the low resolution cryo-em map of the ef-g.gtp state3 of e. coli 70s ribosome
50	c1jqsB_	Alignment	not modelled	21.3	50	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**elongation factor g; **PDBTitle:** fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
51	d2qale1	Alignment	not modelled	21.2	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
52	c3i12A_	Alignment	not modelled	20.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
53	d1v4va_	Alignment	not modelled	19.9	21	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
54	d1a6db2	Alignment	not modelled	19.8	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain

55	d1assa_	Alignment	not modelled	17.5	17	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
56	d1iqoa_	Alignment	not modelled	17.2	14	**Fold:**Hypothetical protein MTH1880 **Superfamily:**Hypothetical protein MTH1880 **Family:**Hypothetical protein MTH1880
57	c2xcuC_	Alignment	not modelled	17.2	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**3-deoxy-d-manno-2-octulosonic acid transferase; **PDBTitle:** membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, comlex with cmp
58	c2xnkA_	Alignment	not modelled	16.3	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 2-binding protein 1; **PDBTitle:** structure and function of the rad9-binding region of the dna damage2 checkpoint adaptor topbp1
59	c2e6gI_	Alignment	not modelled	16.1	19	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of the stationary phase survival protein sure from2 thermus thermophilus hb8 in complex with phosphate
60	c3qfnA_	Alignment	not modelled	16.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
61	c3af5A_	Alignment	not modelled	15.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
62	d1tqya1	Alignment	not modelled	14.5	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
63	c2nqqA_	Alignment	not modelled	14.0	50	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
64	c3dcjA_	Alignment	not modelled	13.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
65	c2xzmE_	Alignment	not modelled	13.4	20	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**ribosomal protein s5 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
66	c3lfhF_	Alignment	not modelled	13.0	19	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
67	c2fu3A_	Alignment	not modelled	13.0	27	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
68	c2q5cA_	Alignment	not modelled	12.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
69	d1b77a2	Alignment	not modelled	12.5	19	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
70	c3iprC_	Alignment	not modelled	12.5	35	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
71	c3oryA_	Alignment	not modelled	12.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap endonuclease 1; **PDBTitle:** crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
72	c2ow8f_	Alignment	not modelled	12.4	28	**PDB header:**ribosome **Chain:** F: **PDB Molecule:** **PDBTitle:** crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8, contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa.
73	d1lqta1	Alignment	not modelled	12.1	9	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
74	d2nn6g3	Alignment	not modelled	11.5	13	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
75	d1kfia2	Alignment	not modelled	11.3	25	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
76	c3bbnE_	Alignment	not modelled	10.6	31	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**ribosomal protein s5; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
77	d1oaoa_	Alignment	not modelled	10.5	27	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
78	c2yw3E_	Alignment	not modelled	10.5	20	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1

79	d1o6ca_	Alignment	not modelled	10.4	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
80	c2jfsA_	Alignment	not modelled	10.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ser-thr phosphatase mspp; **PDBTitle:** crystal structure of the ppm ser-thr phosphatase mspp from2 mycobacterium smegmatis in complex with cacodylate
81	d2oqea3	Alignment	not modelled	10.4	15	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
82	c1eg0B_	Alignment	not modelled	10.2	22	**PDB header:**ribosome **PDB COMPND:**
83	d1e4ea1	Alignment	not modelled	10.2	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
84	d1o1xa_	Alignment	not modelled	10.0	11	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
85	c2p3qA_	Alignment	not modelled	9.9	22	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**type ii methyltransferase; **PDBTitle:** crystal structure of dengue methyltransferase in complex with gpppg2 and s-adenosyl-l-homocysteine
86	d2bfwa1	Alignment	not modelled	9.9	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
87	c3hp7A_	Alignment	not modelled	9.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
88	c1uz5A_	Alignment	not modelled	9.6	30	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
89	c2kpmA_	Alignment	not modelled	9.6	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein from gene2 locus ne0665 of nitrosomonas europaea. northeast structural3 genomics target ner103a
90	c1wu2B_	Alignment	not modelled	9.6	31	**PDB header:**structural genomics,biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis moea protein; **PDBTitle:** crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
91	c2jh3C_	Alignment	not modelled	9.5	21	**PDB header:**ribosomal protein **Chain:** C: **PDB Molecule:**ribosomal protein s2-related protein; **PDBTitle:** the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
92	c1b43A_	Alignment	not modelled	9.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (fen-1); **PDBTitle:** fen-1 from p. furiosus
93	c2wa1A_	Alignment	not modelled	9.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**non-structural protein 5; **PDBTitle:** structure of the methyltransferase domain from modoc virus,2 a flavivirus with no known vector (nkv)
94	d1xo1a1	Alignment	not modelled	9.1	10	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
95	c3s5pA_	Alignment	not modelled	8.9	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
96	d1p90a_	Alignment	not modelled	8.9	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**Nitrogenase accessory factor
97	d1pdoa_	Alignment	not modelled	8.8	25	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
98	c3mtqA_	Alignment	not modelled	8.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphoenolpyruvate-dependent sugar **PDBTitle:** crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
99	d3pmga2	Alignment	not modelled	8.4	42	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains