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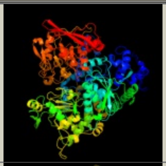
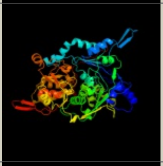
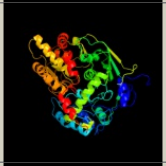
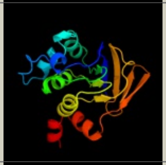
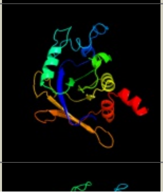
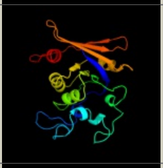
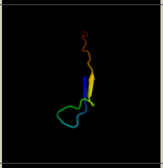
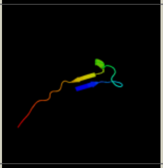
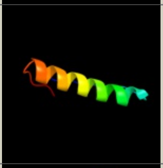
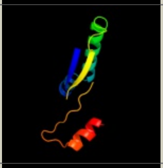
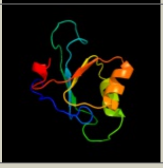
Description	P25516
Date	Thu Jan 5 11:41:52 GMT 2012
Unique Job ID	b6ee1aed79cad8cc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b3yB_	Alignment		100.0	52	**PDB header:**lyase **Chain:** B: **PDB Molecule:**iron-responsive element binding protein 1; **PDBTitle:** structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
2	c5acnA_	Alignment		100.0	29	**PDB header:**lyase(carbon-oxygen) **Chain:** A: **PDB Molecule:**aconitase; **PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
3	d2b3ya2	Alignment		100.0	52	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
4	d1acoa2	Alignment		100.0	29	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
5	d1l5ja3	Alignment		100.0	23	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
6	c1l5jB_	Alignment		100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aconitate hydratase 2; **PDBTitle:** crystal structure of e. coli aconitase b.
7	d2b3ya1	Alignment		100.0	54	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
8	d1acoa1	Alignment		100.0	28	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
9	d1v7la_	Alignment		100.0	35	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
10	c2pkpA_	Alignment		100.0	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
11	d1l5ja2	Alignment		100.0	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like

12	c2hcuA_	Alignment		100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
13	c3q3wB_	Alignment		100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.
14	c3h5jA_	Alignment		100.0	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
15	d1cf1a1	Alignment		71.8	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
16	d1g4ma1	Alignment		69.4	28	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
17	d2r4qa1	Alignment		63.9	35	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
18	c3c52B_	Alignment		59.5	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
19	c2iswB_	Alignment		54.4	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
20	d1t3va_	Alignment		43.3	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
21	d1rdua_	Alignment	not modelled	40.8	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
22	c3elfA_	Alignment	not modelled	40.2	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
23	d1dosa_	Alignment	not modelled	34.8	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
24	d2r48a1	Alignment	not modelled	31.6	39	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
25	d1p90a_	Alignment	not modelled	29.5	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**Nitrogenase accessory factor
26	d1o13a_	Alignment	not modelled	26.4	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
27	c2gp4A_	Alignment	not modelled	25.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
28	c2yx6C_	Alignment	not modelled	24.7	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein ph0822; **PDBTitle:** crystal structure of ph0822
29	d1o60a_	Alignment	not modelled	23.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase

						Family: Class I DAHP synthetase
30	c3bolB_	Alignment	not modelled	23.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
31	c3qm3C_	Alignment	not modelled	23.6	23	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
32	c2wbrA_	Alignment	not modelled	23.5	31	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**gw182; **PDBTitle:** the rrm domain in gw182 proteins contributes to mirna-2 mediated gene silencing
33	c3q94B_	Alignment	not modelled	23.0	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
34	c3l2iB_	Alignment	not modelled	22.7	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
35	d1gvfa_	Alignment	not modelled	22.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
36	d1t0tv_	Alignment	not modelled	22.3	23	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
37	d1rvga_	Alignment	not modelled	21.4	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
38	c3iz5Q_	Alignment	not modelled	19.9	22	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l5 (l18p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
39	c2rhbD_	Alignment	not modelled	19.8	33	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**uridylate-specific endoribonuclease; **PDBTitle:** crystal structure of nsp15-h234a mutant- hexamer in2 asymmetric unit
40	d3bofa2	Alignment	not modelled	19.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
41	d1iuka_	Alignment	not modelled	19.2	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
42	c2kyrA_	Alignment	not modelled	19.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
43	c2wfbA_	Alignment	not modelled	18.7	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein orp; **PDBTitle:** high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
44	d1vdha_	Alignment	not modelled	18.7	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
45	d2aioa1	Alignment	not modelled	18.4	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
46	d1eo1a_	Alignment	not modelled	17.4	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
47	c3c3jA_	Alignment	not modelled	16.7	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
48	c3dmyA_	Alignment	not modelled	16.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein fdra; **PDBTitle:** crystal structure of a predicated acyl-coa synthetase from e.coli
49	d1eg7a_	Alignment	not modelled	16.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
50	c3l4gI_	Alignment	not modelled	16.0	33	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
51	d2ghra1	Alignment	not modelled	16.0	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
52	c2yrvA_	Alignment	not modelled	15.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**at-rich interactive domain-containing protein 4a; **PDBTitle:** solution structure of the rbb1nt domain of human2 rb(retinoblastoma)-binding protein 1
53	c2oxlA_	Alignment	not modelled	15.2	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hypothetical protein ymgb; **PDBTitle:** structure and function of the e. coli protein ymgb: a protein critical2 for biofilm formation and acid resistance
54	d2ac7a1	Alignment	not modelled	15.1	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases

55	d2gp4a2	Alignment	not modelled	14.9	12	**Fold:**IlvD/EDD N-terminal domain-like **Superfamily:**IlvD/EDD N-terminal domain-like **Family:**lvD/EDD N-terminal domain-like
56	d2ieaa3	Alignment	not modelled	14.6	29	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
57	d2zdra1	Alignment	not modelled	14.0	23	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
58	d1jjca_	Alignment	not modelled	13.9	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
59	c2vxhF_	Alignment	not modelled	13.7	9	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**chlorite dismutase; **PDBTitle:** the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
60	c3cf4A_	Alignment	not modelled	13.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
61	c3qpbB_	Alignment	not modelled	13.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine phosphorylase; **PDBTitle:** crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
62	c2o8vA_	Alignment	not modelled	13.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
63	c3mwbA_	Alignment	not modelled	13.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
64	c2jz2A_	Alignment	not modelled	13.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
65	d1k6ka_	Alignment	not modelled	12.9	25	**Fold:**Double Clp-N motif **Superfamily:**Double Clp-N motif **Family:**Double Clp-N motif
66	c2r2dC_	Alignment	not modelled	12.5	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**zn-dependent hydrolases; **PDBTitle:** structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
67	c2w9mB_	Alignment	not modelled	12.5	35	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
68	c1pt1B_	Alignment	not modelled	12.5	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
69	c2ebbA_	Alignment	not modelled	12.4	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
70	d1vjta1	Alignment	not modelled	12.3	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
71	d1ppya_	Alignment	not modelled	11.6	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
72	d1vhwa_	Alignment	not modelled	11.5	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
73	c1z34A_	Alignment	not modelled	11.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
74	c3nn4C_	Alignment	not modelled	11.3	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**chlorite dismutase; **PDBTitle:** structure of chlorite dismutase from candidatus nitrospira defluvii2 r173k mutant
75	c2gacD_	Alignment	not modelled	11.2	30	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glycosylasparaginase; **PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
76	d1lt7a_	Alignment	not modelled	10.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
77	d1p9ea_	Alignment	not modelled	10.9	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Methyl parathion hydrolase
78	c1p9eA_	Alignment	not modelled	10.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methyl parathion hydrolase; **PDBTitle:** crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
79	d1ybfa_	Alignment	not modelled	10.9	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases

80	c2kmfA_	Alignment	not modelled	10.7	28	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kda protein; **PDBTitle:** solution structure of psb27 from cyanobacterial photosystem2 ii
81	c1b70A_	Alignment	not modelled	10.7	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase; **PDBTitle:** phenylalanyl trna synthetase complexed with phenylalanine
82	c3do6B_	Alignment	not modelled	10.6	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**formate--tetrahydrofolate ligase; **PDBTitle:** crystal structure of putative formyltetrahydrofolate2 synthetase (tm1766) from thermotoga maritima at 1.85 a3 resolution
83	d1hyua4	Alignment	not modelled	10.6	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
84	d1uf2c1	Alignment	not modelled	10.4	21	**Fold:**A virus capsid protein alpha-helical domain **Superfamily:**A virus capsid protein alpha-helical domain **Family:**Phytoreovirus capsid
85	d1je0a_	Alignment	not modelled	10.4	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
86	c3fz5C_	Alignment	not modelled	10.3	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**possible 2-hydroxychromene-2-carboxylate isomerase; **PDBTitle:** crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
87	d1umya_	Alignment	not modelled	10.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
88	c2nu8D_	Alignment	not modelled	10.2	18	**PDB header:**ligase **Chain:** D: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase
89	c1p0yA_	Alignment	not modelled	10.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulose-1,5 bisphosphate carboxylase/oxygenase **PDBTitle:** crystal structure of the set domain of lsmt bound to2 melysine and adohcy
90	c3r2nC_	Alignment	not modelled	9.9	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium leprae
91	d3c8ya1	Alignment	not modelled	9.8	17	**Fold:**Fe-only hydrogenase **Superfamily:**Fe-only hydrogenase **Family:**Fe-only hydrogenase
92	d2pt0a1	Alignment	not modelled	9.8	13	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Myo-inositol hexaphosphate phosphohydrolase (phytase) PhyA
93	c2v4oB_	Alignment	not modelled	9.6	29	**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
94	c3bjeA_	Alignment	not modelled	9.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside phosphorylase, putative; **PDBTitle:** crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
95	d1th7a1	Alignment	not modelled	9.1	23	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
96	c3oqhB_	Alignment	not modelled	8.9	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein yvmc; **PDBTitle:** crystal structure of b. licheniformis cdps yvmc-blic
97	c2phjA_	Alignment	not modelled	8.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of sure protein from aquifex aeolicus
98	c3bl5E_	Alignment	not modelled	8.9	19	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec; **PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
99	d1pvda3	Alignment	not modelled	8.7	23	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module