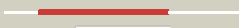








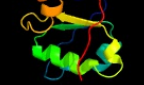
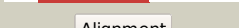

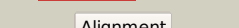

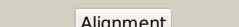

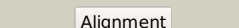

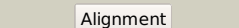
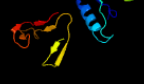



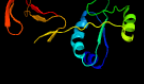

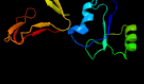



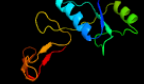
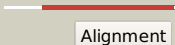
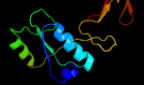
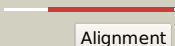
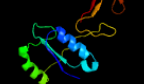
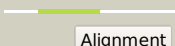


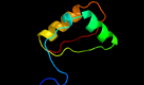


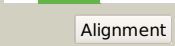
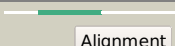
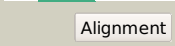
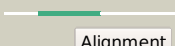
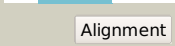
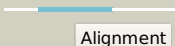





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0358 (-) _436861_437508
Date	Tue Jul 23 14:50:42 BST 2019
Unique Job ID	7bd26422fcc8126c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jgra1	 Alignment		99.7	13	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
2	c2bonB	 Alignment		99.7	14	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
3	d2bona1	 Alignment		99.7	14	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
4	c2qv7A	 Alignment		99.6	17	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
5	c3s40C	 Alignment		99.6	14	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
6	d2p1ra1	 Alignment		99.6	14	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
7	d2qv7a1	 Alignment		99.6	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
8	c4werA	 Alignment		99.6	14	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase catalytic domain protein; PDBTitle: crystal structure of diacylglycerol kinase catalytic domain protein2 from enterococcus faecalis v583
9	c3vzdB	 Alignment		99.5	18	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
10	d1u0ta	 Alignment		97.8	12	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
11	c3afoB	 Alignment		97.2	14	PDB header: transferase Chain: B: PDB Molecule: nadh kinase pos5; PDBTitle: crystal structure of yeast nadh kinase complexed with nadh

12	c2an1D	 Alignment		97.1	19	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
13	c1yt5A	 Alignment		97.1	15	PDB header: transferase Chain: A: PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima
14	c3pfnB	 Alignment		96.8	12	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
15	d1z0sa1	 Alignment		92.6	13	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
16	c1z0zC	 Alignment		92.6	13	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
17	c2i2aA	 Alignment		92.6	9	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes
18	c3opyE	 Alignment		64.0	11	PDB header: transferase Chain: E: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
19	c3opyG	 Alignment		63.2	11	PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
20	d2f48a1	 Alignment		54.5	20	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
21	c1zxxA	 Alignment	not modelled	52.7	14	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
22	d2a0ma1	 Alignment	not modelled	44.3	22	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
23	c2qipA	 Alignment	not modelled	41.8	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function vpa0982; PDBTitle: crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
24	c3o8oC	 Alignment	not modelled	40.9	8	PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
25	c2fu3A	 Alignment	not modelled	39.7	21	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
26	d2fts3	 Alignment	not modelled	39.7	21	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
27	c5zeeA	 Alignment	not modelled	36.6	21	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: arginase; PDBTitle: crystal structure of entamoeba histolytica arginase in complex with2 n(omega)-hydroxy-l-arginine (noha) at 1.74 a
28	c3o8nA	 Alignment	not modelled	35.8	14	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
		 Alignment				Fold: Triple-stranded beta-helix

29	d1v0ea2	Alignment	not modelled	35.4	27	Superfamily: Phage fibre proteins Family: Endo-alpha-sialidase
30	c3o8oB	Alignment	not modelled	32.1	13	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
31	c4dz4D	Alignment	not modelled	31.8	20	PDB header: hydrolase Chain: D: PDB Molecule: agmatinase; PDBTitle: x-ray crystal structure of a hypothetical agmatinase from burkholderia2 thailandensis
32	c4rhjE	Alignment	not modelled	31.5	15	PDB header: unknown function Chain: E: PDB Molecule: arginase; PDBTitle: crystal structure of wild-type t. brucei arginase-like protein in a2 reduced form
33	c5xoeA	Alignment	not modelled	30.1	15	PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus phosphofructokinase
34	c4bgaB	Alignment	not modelled	29.5	15	PDB header: transferase Chain: B: PDB Molecule: predicted molecular chaperone distantly related to PDBTitle: nucleotide-bound open form of a putative sugar kinase2 mk0840 from methanopyrus kandleri
35	c3k2qA	Alignment	not modelled	29.1	13	PDB header: transferase Chain: A: PDB Molecule: pyrophosphate-dependent phosphofructokinase; PDBTitle: crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
36	d4pfka	Alignment	not modelled	28.6	15	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
37	c2kimA	Alignment	not modelled	27.9	15	PDB header: transferase Chain: A: PDB Molecule: o6-methylguanine-dna methyltransferase; PDBTitle: 1.7-mm microcryoprobe solution nmr structure of an o6-methylguanine2 dna methyltransferase family protein from vibrio parahaemolyticus.3 northeast structural genomics consortium target vpr247.
38	c4kdiC	Alignment	not modelled	26.8	20	PDB header: signaling protein/hydrolase Chain: C: PDB Molecule: ubiquitin thioesterase otu1; PDBTitle: crystal structure of p97/vcp n in complex with otu1 ubxl
39	c2higA	Alignment	not modelled	26.6	29	PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
40	c3opyB	Alignment	not modelled	26.5	15	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
41	c3opyH	Alignment	not modelled	26.5	15	PDB header: transferase Chain: H: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
42	c2ogxA	Alignment	not modelled	25.0	17	PDB header: metal binding protein Chain: A: PDB Molecule: molybdenum storage protein subunit alpha; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
43	c3nioF	Alignment	not modelled	21.6	18	PDB header: hydrolase Chain: F: PDB Molecule: guanidinobutyrase; PDBTitle: crystal structure of pseudomonas aeruginosa guanidinobutyrase
44	d1pfka	Alignment	not modelled	20.5	15	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
45	d1woha	Alignment	not modelled	20.5	24	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
46	d1qnta1	Alignment	not modelled	17.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
47	c3gx4X	Alignment	not modelled	16.9	15	PDB header: dna binding protein/dna Chain: X: PDB Molecule: alkyltransferase-like protein 1; PDBTitle: crystal structure analysis of s. pombe atl in complex with dna
48	c1wx4B	Alignment	not modelled	16.3	25	PDB header: oxidoreductase/metal transport Chain: B: PDB Molecule: melc; PDBTitle: crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of dithiothreitol
49	c5ynlA	Alignment	not modelled	16.0	13	PDB header: hydrolase Chain: A: PDB Molecule: arginase; PDBTitle: crystal structure of a cold-adapted arginase from psychrophilic yeast,2 gliaciozyma antarctica
50	c3louB	Alignment	not modelled	15.7	19	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
51	c4au1A	Alignment	not modelled	15.1	16	PDB header: isomerase Chain: A: PDB Molecule: precorrin-8x methylmutase; PDBTitle: crystal structure of cobh (precorrin-8x methyl mutase)2 complexed with c5 desmethyl-hba
52	d1zpd3	Alignment	not modelled	15.1	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
						Fold: Thiamin diphosphate-binding fold (THDP-binding)

53	d1ozha3	Alignment	not modelled	15.0	16	Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
54	c4g3hC	Alignment	not modelled	14.5	9	PDB header: hydrolase Chain: C: PDB Molecule: arginase (rocF); PDBTitle: crystal structure of helicobacter pylori arginase
55	c3o1B	Alignment	not modelled	14.1	21	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
56	d1gr0a1	Alignment	not modelled	14.1	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
57	d1sfea1	Alignment	not modelled	13.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
58	c4f6tA	Alignment	not modelled	13.5	17	PDB header: metal binding protein Chain: A: PDB Molecule: molybdenum storage protein subunit alpha; PDBTitle: the crystal structure of the molybdenum storage protein (mosto) from2 azotobacter vinelandii loaded with various polyoxometalates
59	d1ybha3	Alignment	not modelled	13.3	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
60	c1v0eB	Alignment	not modelled	13.0	27	PDB header: hydrolase Chain: B: PDB Molecule: endo-alpha-sialidase; PDBTitle: endosialidase of bacteriophage k1f
61	c3iauA	Alignment	not modelled	11.9	13	PDB header: lyase Chain: A: PDB Molecule: threonine deaminase; PDBTitle: the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
62	d2djia3	Alignment	not modelled	11.8	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
63	d1jsca3	Alignment	not modelled	11.6	25	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
64	d2ez9a3	Alignment	not modelled	11.5	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
65	d1t9ba3	Alignment	not modelled	11.3	24	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
66	d2ihta3	Alignment	not modelled	11.2	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
67	d1lovma3	Alignment	not modelled	11.1	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
68	c4gr5B	Alignment	not modelled	10.8	20	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
69	d1vhva	Alignment	not modelled	10.2	15	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
70	c1sfeA	Alignment	not modelled	9.9	22	PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
71	d2cvea2	Alignment	not modelled	9.7	30	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: YigZ C-terminal domain-like
72	c1uz5A	Alignment	not modelled	9.3	8	PDB header: molybdopterin biosynthesis Chain: A: PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
73	d1ou0a	Alignment	not modelled	9.1	13	Fold: Flavodoxin-like Superfamily: Precorrin-8X methylmutase CbiC/CobH Family: Precorrin-8X methylmutase CbiC/CobH
74	d1q6za3	Alignment	not modelled	8.6	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
75	c3mmrA	Alignment	not modelled	8.5	10	PDB header: hydrolase Chain: A: PDB Molecule: arginase; PDBTitle: structure of plasmodium falciparum arginase in complex with abh
76	c4iu1A	Alignment	not modelled	8.5	13	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: arginase; PDBTitle: crystal structure of leishmania mexicana arginase in complex with2 inhibitor nor-noha
77	c3n0vD	Alignment	not modelled	8.0	28	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
78	c4bhCA	Alignment	not modelled	7.9	19	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of the m. tuberculosis o6-

						methylguanine2 methyltransferase r37l variant
79	c3qk9B_	Alignment	not modelled	7.7	38	PDB header: protein transport Chain: B: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: yeast tim44 c-terminal domain complexed with cymal-3
80	c3w7bB_	Alignment	not modelled	7.5	21	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
81	c2e0kA_	Alignment	not modelled	7.5	14	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
82	d2ceva_	Alignment	not modelled	7.4	20	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
83	c6n2oB_	Alignment	not modelled	7.2	25	PDB header: oxidoreductase Chain: B: PDB Molecule: pyruvate ferredoxin/ferredoxin oxidoreductase, beta PDBTitle: 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound
84	c5b46B_	Alignment	not modelled	7.1	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase beta subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus tokodai - ligand2 free form
85	d2fgca2	Alignment	not modelled	6.9	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
86	c3m1rF_	Alignment	not modelled	6.9	11	PDB header: hydrolase Chain: F: PDB Molecule: formimidoylglutamase; PDBTitle: the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
87	c3nrB_	Alignment	not modelled	6.7	33	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
88	d1l9xa_	Alignment	not modelled	6.7	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
89	c1l9xA_	Alignment	not modelled	6.7	20	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
90	c1t39A_	Alignment	not modelled	6.6	22	PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
91	d1ep3b2	Alignment	not modelled	6.6	23	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Dihydroorotate dehydrogenase B, PyrK subunit
92	c2mdpA_	Alignment	not modelled	6.3	40	PDB header: viral protein Chain: A: PDB Molecule: gene 1.2 protein; PDBTitle: the bacteriophage t7 encoded inhibitor (gp1.2) of e. coli dgtp2 triphosphohydrolase
93	c5d5pC_	Alignment	not modelled	6.0	13	PDB header: transferase Chain: C: PDB Molecule: hcgB; PDBTitle: hcgB from methanococcus maripaludis
94	c2l8bA_	Alignment	not modelled	6.0	25	PDB header: hydrolase Chain: A: PDB Molecule: protein trai; PDBTitle: trai (381-569)
95	c3l3bA_	Alignment	not modelled	5.7	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
96	c5wmmA_	Alignment	not modelled	5.5	29	PDB header: biosynthetic protein Chain: A: PDB Molecule: nrps; PDBTitle: crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
97	c2pc6C_	Alignment	not modelled	5.5	22	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
98	d2ji7a3	Alignment	not modelled	5.4	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
99	d1f2da_	Alignment	not modelled	5.3	10	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes