

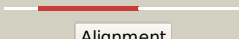

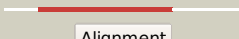














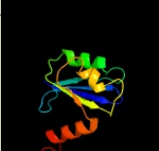

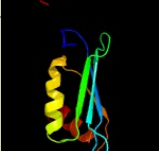








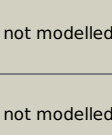


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3348 (-)_3753936_3754427
Date	Thu Aug 8 16:20:56 BST 2019
Unique Job ID	6dcdfc6c1d8b8995

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5m1oA	 Alignment		96.9	8	PDB header: viral protein Chain: A: PDB Molecule: phage terminase large subunit; PDBTitle: crystal structure of the large terminase nuclease from thermophilic2 phage g20c with bound cobalt
2	c3c6aA	 Alignment		96.7	18	PDB header: viral protein Chain: A: PDB Molecule: terminase large subunit; PDBTitle: crystal structure of the rb49 gp17 nuclease domain
3	d1hjra	 Alignment		96.6	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
4	c4ep5A	 Alignment		96.3	19	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure
5	c2e2pA	 Alignment		96.1	14	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
6	d1xc3a1	 Alignment		95.2	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
7	d2ap1a2	 Alignment		94.5	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
8	c2ap1A	 Alignment		94.2	15	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
9	c3psfA	 Alignment		94.2	7	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
10	c1xc3A	 Alignment		94.2	18	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
11	c3ezkB	 Alignment		94.0	15	PDB header: hydrolase Chain: B: PDB Molecule: dna packaging protein gp17; PDBTitle: bacteriophage t4 gp17 motor assembly based on crystal structures and2 cryo-em reconstructions

12	d1z05a3	Alignment		93.9	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
13	c3eo3B_	Alignment		93.9	16	PDB header: isomerase, transferase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
14	d3bzka5	Alignment		93.6	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
15	d2gupa1	Alignment		92.7	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
16	c1zc6A_	Alignment		92.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable n-acetylglucosamine kinase; PDBTitle: crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
17	c2gupA_	Alignment		90.4	19	PDB header: transferase Chain: A: PDB Molecule: rok family protein; PDBTitle: structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
18	c4ijaA_	Alignment		90.2	9	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecR2
19	c3htvA_	Alignment		90.1	13	PDB header: transferase Chain: A: PDB Molecule: d-allose kinase; PDBTitle: crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
20	c3h1qB_	Alignment		89.9	19	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrus hydrogenoformans
21	c4db3A_	Alignment	not modelled	89.4	16	PDB header: transferase Chain: A: PDB Molecule: n-acetyl-d-glucosamine kinase; PDBTitle: 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus.
22	c2ch5D_	Alignment	not modelled	88.8	14	PDB header: transferase Chain: D: PDB Molecule: magk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
23	c4htIA_	Alignment	not modelled	87.5	14	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
24	d2aa4a1	Alignment	not modelled	87.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
25	c3vovC_	Alignment	not modelled	86.7	16	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
26	c2aa4B_	Alignment	not modelled	86.6	16	PDB header: transferase Chain: B: PDB Molecule: putative n-acetylmannosamine kinase; PDBTitle: crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
27	c5nckA_	Alignment	not modelled	85.8	14	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
28	c5f7pA_	Alignment	not modelled	85.6	11	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes

29	d1g8ma1	Alignment	not modelled	85.6	20	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
30	c2w40C_	Alignment	not modelled	85.1	11	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
31	c6nkoA_	Alignment	not modelled	84.6	18	PDB header: unknown function Chain: A: PDB Molecule: forh; PDBTitle: crystal structure of forh
32	d2ch5a2	Alignment	not modelled	84.5	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
33	c3gbtA_	Alignment	not modelled	84.5	23	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
34	d1zcza1	Alignment	not modelled	84.1	11	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
35	c2qm1D_	Alignment	not modelled	83.4	20	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
36	d1z6ra2	Alignment	not modelled	83.4	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
37	d1nu0a_	Alignment	not modelled	83.1	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
38	c1zcza_	Alignment	not modelled	83.0	11	PDB header: transferase/hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
39	d1pkxa1	Alignment	not modelled	82.2	18	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
40	d1zc6a1	Alignment	not modelled	82.1	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
41	c1z05A_	Alignment	not modelled	82.0	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, rok family; PDBTitle: crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
42	d1woqa1	Alignment	not modelled	81.7	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
43	c3lm2B_	Alignment	not modelled	81.7	14	PDB header: transferase Chain: B: PDB Molecule: putative kinase; PDBTitle: crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
44	c4ehtA_	Alignment	not modelled	81.5	17	PDB header: electron transport Chain: A: PDB Molecule: activator of 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
45	c1thzA_	Alignment	not modelled	81.4	20	PDB header: transferase, hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
46	d2p3ra1	Alignment	not modelled	81.4	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
47	c5f7rA_	Alignment	not modelled	81.1	9	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
48	c4a1oB_	Alignment	not modelled	80.3	18	PDB header: transferase-hydrolase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
49	c3wxiB_	Alignment	not modelled	80.0	20	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
50	c6gmhM_	Alignment	not modelled	78.4	18	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
51	c3ifrB_	Alignment	not modelled	77.7	18	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
52	c3g25B_	Alignment	not modelled	76.6	15	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
53	c2nlxA_	Alianment	not modelled	76.4	17	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase;

						PDBTitle: crystal structure of the apo e. coli xylulose kinase
54	c5m45K_	Alignment	not modelled	76.1	24	PDB header: ligase Chain: K; PDB Molecule: acetone carboxylase beta subunit; PDBTitle: structure of acetone carboxylase purified from xanthobacter2 autotrophicus
55	c5vm1A_	Alignment	not modelled	76.0	12	PDB header: transferase Chain: A; PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xylolose kinase from brucella ovis
56	c5htxA_	Alignment	not modelled	75.6	15	PDB header: transferase Chain: A; PDB Molecule: putative xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp
57	d2ews1_	Alignment	not modelled	75.6	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
58	d1huxa_	Alignment	not modelled	73.8	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
59	c2hoeA_	Alignment	not modelled	73.6	8	PDB header: transferase Chain: A; PDB Molecule: n-acetylglucosamine kinase; PDBTitle: crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
60	c3hz6A_	Alignment	not modelled	73.3	20	PDB header: transferase Chain: A; PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
61	c3flcX_	Alignment	not modelled	72.5	20	PDB header: transferase Chain: X; PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
62	c2duwA_	Alignment	not modelled	72.2	8	PDB header: ligand binding protein Chain: A; PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
63	c3t69A_	Alignment	not modelled	72.0	12	PDB header: transferase Chain: A; PDB Molecule: putative 2-dehydro-3-deoxygalactonokinase; PDBTitle: crystal structure of a putative 2-dehydro-3-deoxygalactonokinase2 protein from sinorhizobium meliloti
64	d1q18a1_	Alignment	not modelled	71.9	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
65	c3r8eA_	Alignment	not modelled	71.4	14	PDB header: transferase Chain: A; PDB Molecule: hypothetical sugar kinase; PDBTitle: crystal structure of a putative sugar kinase (chu_1875) from cytophaga2 hutchinsonii atcc 33406 at 1.65 a resolution
66	d1vhxa_	Alignment	not modelled	70.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
67	c5ya2A_	Alignment	not modelled	70.2	21	PDB header: structural protein Chain: A; PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
68	c2oceA_	Alignment	not modelled	70.0	12	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
69	d1y81a1_	Alignment	not modelled	69.7	4	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
70	c2d4wA_	Alignment	not modelled	69.4	19	PDB header: transferase Chain: A; PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
71	d2pgda2_	Alignment	not modelled	69.3	5	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
72	c4c23A_	Alignment	not modelled	68.7	14	PDB header: transferase Chain: A; PDB Molecule: l-fucose kinase fuck; PDBTitle: l-fucose kinase
73	c1woqB_	Alignment	not modelled	68.7	28	PDB header: transferase Chain: B; PDB Molecule: inorganic polyphosphate/atp-glucomannokinase; PDBTitle: crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
74	c3ff4A_	Alignment	not modelled	68.2	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
75	c4bc2A_	Alignment	not modelled	68.2	19	PDB header: transferase Chain: A; PDB Molecule: xylulose kinase; PDBTitle: crystal structure of human d-xylulokinase in complex with d-2 xylulose and adenosine diphosphate
76	d2d59a1_	Alignment	not modelled	67.6	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
77	c4e1jA_	Alignment	not modelled	67.4	16	PDB header: transferase Chain: A; PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
78	c5hv7A_	Alignment	not modelled	66.9	21	PDB header: transferase Chain: A; PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
79	c3nciA_	Alignment	not modelled	65.2	6	PDB header: transcription Chain: A; PDB Molecule: transcription elongation factor spt6;

79	c3ps1A_	Alignment	not modelled	63.2	0	PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
80	d2hoea3	Alignment	not modelled	64.9	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
81	c3vgkB_	Alignment	not modelled	64.2	19	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
82	c1glbG_	Alignment	not modelled	64.1	18	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiglc with2 glycerol kinase
83	c3mcpA_	Alignment	not modelled	62.9	13	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
84	d1iv0a_	Alignment	not modelled	62.0	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
85	c3h6eB_	Alignment	not modelled	61.5	21	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
86	c3ezwD_	Alignment	not modelled	61.0	14	PDB header: transferase Chain: D: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
87	c1z6rC_	Alignment	not modelled	60.3	19	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
88	c4ehiB_	Alignment	not modelled	58.3	13	PDB header: hydrolase,transferase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: an x-ray crystal structure of a putative bifunctional2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
89	d1iuKa_	Alignment	not modelled	58.2	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
90	c2dnpB_	Alignment	not modelled	58.1	17	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
91	d1r59o1	Alignment	not modelled	57.0	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
92	c2rkbE_	Alignment	not modelled	55.9	6	PDB header: lyase Chain: E: PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells
93	c3gg4B_	Alignment	not modelled	55.7	23	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
94	c3i8bA_	Alignment	not modelled	54.5	15	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
95	c3fwzA_	Alignment	not modelled	53.9	12	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
96	c2zf5O_	Alignment	not modelled	53.8	15	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
97	c2cgkB_	Alignment	not modelled	52.8	12	PDB header: transferase Chain: B: PDB Molecule: l-rhamnulose kinase; PDBTitle: crystal structure of l-rhamnulose kinase from escherichia coli in an2 open uncomplexed conformation.
98	d1yt8a4	Alignment	not modelled	52.4	11	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
99	c6hulB_	Alignment	not modelled	49.9	4	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase beta chain 1; PDBTitle: sulfolobus solfataricus tryptophan synthase ab complex
100	d1pwHa_	Alignment	not modelled	49.7	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
101	c5j9wb_	Alignment	not modelled	49.5	21	PDB header: ligase Chain: B: PDB Molecule: acetophenone carboxylase gamma subunit; PDBTitle: crystal structure of the apc core complex
102	d1gsoa2	Alignment	not modelled	49.4	15	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
103	c1xupO_	Alignment	not modelled	48.5	23	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
104	c3od1A_	Alignment	not modelled	47.5	12	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase regulatory subunit; PDBTitle: the crystal structure of an atp phosphoribosyltransferase

						regulatory2 subunit/histidyl-trna synthetase from bacillus halodurans c
105	c2d1fA_	Alignment	not modelled	46.8	13	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
106	c6cggA_	Alignment	not modelled	45.3	15	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
107	c5ybwA_	Alignment	not modelled	44.5	13	PDB header: isomerase Chain: A: PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyridoxal 5'-phosphate-dependent aspartate2 racemase
108	d1java_	Alignment	not modelled	43.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
109	d1f0ya2	Alignment	not modelled	43.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
110	d1v7ca_	Alignment	not modelled	42.7	13	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
111	c3nglA_	Alignment	not modelled	42.3	16	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
112	c4a26B_	Alignment	not modelled	41.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative c-1-tetrahydrofolate synthase, cytoplasmic; PDBTitle: the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
113	d2csua1	Alignment	not modelled	40.9	0	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
114	d1a9xa2	Alignment	not modelled	40.4	17	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
115	c5i4aC_	Alignment	not modelled	39.7	22	PDB header: rna binding protein/rna Chain: C: PDB Molecule: argonaute protein; PDBTitle: x-ray crystal structure of marinitoga piezophila argonaute in complex2 with 5' oh guide rna
116	c4negA_	Alignment	not modelled	39.2	6	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: the crystal structure of tryptophan synthase subunit beta from2 bacillus anthracis str. 'ames ancestor'
117	d1b0aa1	Alignment	not modelled	38.4	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
118	c2o2jA_	Alignment	not modelled	38.4	6	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: mycobacterium tuberculosis tryptophan synthase beta chain dimer2 (apofom)
119	c4j7cA_	Alignment	not modelled	38.1	5	PDB header: transport protein Chain: A: PDB Molecule: ktr system potassium uptake protein a; PDBTitle: ktrab potassium transporter from bacillus subtilis
120	c1np3B_	Alignment	not modelled	38.0	8	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetoxy acid isomeroreductase from2 pseudomonas aeruginosa