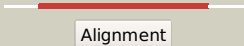

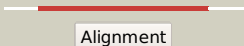

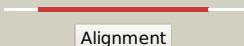







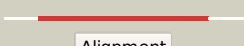
















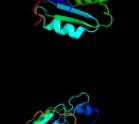



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3029c_(fixA)_3388081_3388881
Date	Thu Aug 8 16:20:20 BST 2019
Unique Job ID	9e15109b08e285a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fahB_	 Alignment		100.0	34	PDB header: flavoprotein Chain: B: PDB Molecule: caffeyl-coa reductase-etf complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
2	c5ol2E_	 Alignment		100.0	34	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
3	c4kpuB_	 Alignment		100.0	33	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein alpha/beta-subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
4	d1efvb_	 Alignment		100.0	30	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
5	c5ow0B_	 Alignment		100.0	28	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
6	d3clsc1	 Alignment		100.0	29	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
7	d1efpb_	 Alignment		100.0	33	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
8	d1o94c_	 Alignment		100.0	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
9	c1o94D_	 Alignment		99.9	15	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
10	d3clsd1	 Alignment		99.9	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
11	c3clrD_	 Alignment		99.9	16	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein subunit alpha; PDBTitle: crystal structure of the r236a etf mutant from m. methylotrophus

12	c3ih5A_	Alignment		99.9	16	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: crystal structure of electron transfer flavoprotein alpha-subunit from2 bacteroides thetaiotaomicron
13	c4l2iA_	Alignment		99.9	17	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
14	c5ol2D_	Alignment		99.9	11	PDB header: flavoprotein Chain: D: PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
15	c1efvA_	Alignment		99.8	17	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein; PDBTitle: three-dimensional structure of human electron transfer2 flavoprotein to 2.1 a resolution
16	c6fahE_	Alignment		99.8	15	PDB header: flavoprotein Chain: E: PDB Molecule: caffeoyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeoyl-coa2 reductase reaction
17	d1efva1	Alignment		99.8	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
18	c1t9gR_	Alignment		99.7	17	PDB header: oxidoreductase, electron transport Chain: R: PDB Molecule: electron transfer flavoprotein alpha-subunit, PDBTitle: structure of the human mcad:etf complex
19	c5ow0A_	Alignment		99.5	22	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein, alpha subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
20	d1efpa1	Alignment		99.5	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
21	c1efpC_	Alignment	not modelled	99.4	20	PDB header: electron transport Chain: C: PDB Molecule: protein (electron transfer flavoprotein); PDBTitle: electron transfer flavoprotein (etf) from paracoccus2 denitrificans
22	c3fetA_	Alignment	not modelled	99.4	12	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein subunit alpha related PDBTitle: crystal structure of the electron transfer flavoprotein subunit alpha2 related protein ta0212 from thermoplasma acidophilum
23	d1q77a_	Alignment	not modelled	87.3	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
24	c4r2lB_	Alignment	not modelled	86.5	15	PDB header: unknown function Chain: B: PDB Molecule: universal stress protein f; PDBTitle: crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
25	c3fh0A_	Alignment	not modelled	83.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative universal stress protein kpn_01444; PDBTitle: crystal structure of putative universal stress protein kpn_01444 -2 atpase
26	d2z3va1	Alignment	not modelled	83.1	22	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
27	c4r2jA_	Alignment	not modelled	82.7	14	PDB header: metal binding protein, unknown function Chain: A: PDB Molecule: universal stress protein e; PDBTitle: crystal structure of ydaa (universal stress protein e) from salmonella2 typhimurium
28	d1znaa1	Alignment	not modelled	82.3	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like

29	c2pfsA	Alignment	not modelled	81.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
30	c3mt0A	Alignment	not modelled	80.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1789; PDBTitle: the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
31	c4wnyA	Alignment	not modelled	79.6	20	PDB header: signaling protein Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei
32	c1znnF	Alignment	not modelled	79.6	19	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
33	c2c4kD	Alignment	not modelled	79.6	12	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase-associated protein PDBTitle: crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39)
34	c1dkrB	Alignment	not modelled	78.6	16	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
35	c3hgmD	Alignment	not modelled	77.6	15	PDB header: signaling protein Chain: D: PDB Molecule: universal stress protein tead; PDBTitle: universal stress protein tead from the trap transporter teaabc of2 halomonas elongata
36	d2hk6a1	Alignment	not modelled	77.1	10	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
37	d1w0ma	Alignment	not modelled	76.2	18	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
38	c5t3oB	Alignment	not modelled	75.6	17	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase ii2 from thermus thermophilus
39	d1iowa1	Alignment	not modelled	73.7	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
40	d1tq8a	Alignment	not modelled	72.3	27	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
41	c3fg9B	Alignment	not modelled	71.8	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
42	d1ozha1	Alignment	not modelled	71.0	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
43	d2ji7a1	Alignment	not modelled	69.0	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
44	c5j6qA	Alignment	not modelled	66.4	25	PDB header: cell adhesion Chain: A: PDB Molecule: cell wall binding protein cwp8; PDBTitle: cwp8 from clostridium difficile
45	d2iyva1	Alignment	not modelled	66.1	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
46	c3cgxA	Alignment	not modelled	65.3	23	PDB header: transferase Chain: A: PDB Molecule: putative nucleotide-diphospho-sugar transferase; PDBTitle: crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
47	d1to6a	Alignment	not modelled	65.2	26	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
48	d1uana	Alignment	not modelled	64.7	30	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
49	c5gk2A	Alignment	not modelled	63.4	11	PDB header: transferase Chain: A: PDB Molecule: ketosynthase stld; PDBTitle: the structure of the h302a mutant of stld
50	c2ixdB	Alignment	not modelled	61.6	24	PDB header: hydrolase Chain: B: PDB Molecule: lmbE-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from bacillus2 cereus
51	c2vu2D	Alignment	not modelled	61.3	23	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: biosynthetic thiolase from z. ramigera. complex with s-pantetheine-11-2 pivalate.
52	d2djia1	Alignment	not modelled	60.8	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
53	c4zhtB	Alignment	not modelled	60.6	17	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcnaC 2-epimerase
54	c2zhtB	Alignment	not modelled	60.5	16	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs;

54	c2z0tB	Alignment	not modelled	60.5	10	PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8 PDB header: transferase
55	c3s29C	Alignment	not modelled	60.5	30	Chain: C; PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
56	c3vaaC	Alignment	not modelled	59.0	15	PDB header: transferase Chain: C; PDB Molecule: shikimate kinase; PDBTitle: 1.7 angstrom resolution crystal structure of shikimate kinase from2 bacteroides thetaiotaomicron
57	d2ihta1	Alignment	not modelled	58.9	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
58	d1zpdA1	Alignment	not modelled	57.7	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
59	c2yzzB	Alignment	not modelled	57.1	14	PDB header: lyase Chain: B; PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii
60	c3rggD	Alignment	not modelled	57.0	9	PDB header: lyase Chain: D; PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
61	c3cwcB	Alignment	not modelled	56.4	26	PDB header: transferase Chain: B; PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
62	d1kaga	Alignment	not modelled	56.3	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
63	c2v4wB	Alignment	not modelled	55.5	13	PDB header: transferase Chain: B; PDB Molecule: hydroxymethylglutaryl-coa synthase, PDBTitle: crystal structure of human mitochondrial 3-hydroxy-3-2 methylglutaryl-coenzyme a synthase 2 (hmgcs2)
64	c1zuiA	Alignment	not modelled	54.4	21	PDB header: transferase Chain: A; PDB Molecule: shikimate kinase; PDBTitle: structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
65	c2ebdB	Alignment	not modelled	54.4	13	PDB header: transferase Chain: B; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase iii2 from aquifex aeolicus vf5
66	c3efhB	Alignment	not modelled	54.4	20	PDB header: transferase Chain: B; PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
67	d1rkba	Alignment	not modelled	54.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
68	d1lbqa	Alignment	not modelled	54.3	15	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
69	c2nv2U	Alignment	not modelled	53.9	18	PDB header: lyase/transferase Chain: U; PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
70	d1ovma1	Alignment	not modelled	53.8	8	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
71	c4lzaB	Alignment	not modelled	53.4	24	PDB header: transferase Chain: B; PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 thermoanaerobacter pseudethanolicus atcc 33223, nysgrc target 029700.
72	c2z1dA	Alignment	not modelled	53.2	19	PDB header: metal binding protein Chain: A; PDB Molecule: hydrogenase expression/formation protein hypd; PDBTitle: crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
73	d2gx8a1	Alignment	not modelled	51.8	19	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
74	c4adsF	Alignment	not modelled	51.6	14	PDB header: transferase/transferase Chain: F; PDB Molecule: pyridoxine biosynthetic enzyme pdx1 homologue, putative; PDBTitle: crystal structure of plasmodial plp synthase complex
75	c4o9cC	Alignment	not modelled	51.5	28	PDB header: transferase Chain: C; PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of beta-ketothiolase (phaa) from ralstonia eutropha2 h16
76	c3loqA	Alignment	not modelled	51.4	15	PDB header: structure genomics, unknown function Chain: A; PDB Molecule: universal stress protein; PDBTitle: the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
77	c2gx8B	Alignment	not modelled	50.0	20	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: nif3-related protein; PDBTitle: the crystal structure of bacillus cereus protein related to nif3
78	c3jyfB	Alignment	not modelled	49.7	20	PDB header: hydrolase Chain: B; PDB Molecule: 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- PDBTitle: the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578

79	c2iikA_	Alignment	not modelled	49.7	18	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase, peroxisomal; PDBTitle: crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaal1)
80	d1viaa_	Alignment	not modelled	49.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
81	c5n6yD_	Alignment	not modelled	49.4	13	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase vanadium-iron protein alpha chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
82	d1hg3a_	Alignment	not modelled	49.0	17	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
83	c3femB_	Alignment	not modelled	48.7	15	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
84	d1e6ca_	Alignment	not modelled	47.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
85	d1zq1a2	Alignment	not modelled	47.7	30	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
86	c6bn2A_	Alignment	not modelled	47.4	27	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of acetyl-coa acetyltransferase from elizabethkingia2 anophelis nuhp1
87	c4eunA_	Alignment	not modelled	47.1	18	PDB header: transferase Chain: A: PDB Molecule: thermoreistant glucokinase; PDBTitle: crystal structure of a sugar kinase (target efi-502144 from janibacter2 sp. htcc2649), unliganded structure
88	c4wysB_	Alignment	not modelled	46.8	23	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of thiolase from escherichia coli
89	c4dfeB_	Alignment	not modelled	46.6	19	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase iii2 from burkholderia xenovorans
90	c4dd5A_	Alignment	not modelled	46.5	24	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: biosynthetic thiolase (thla1) from clostridium difficile
91	c3fdiA_	Alignment	not modelled	45.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from eubacterium2 ventriosum atcc 27560.
92	c1zq1B_	Alignment	not modelled	45.8	22	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
93	d1s3ga1	Alignment	not modelled	44.4	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
94	d2gnpa1	Alignment	not modelled	44.4	8	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
95	c3s3tD_	Alignment	not modelled	44.2	14	PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
96	d2ocda1	Alignment	not modelled	43.9	21	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
97	d1jlja_	Alignment	not modelled	43.8	12	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
98	d1zn7a1	Alignment	not modelled	43.5	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
99	c6hxgE_	Alignment	not modelled	43.2	13	PDB header: plant protein Chain: E: PDB Molecule: pyridoxal 5'-phosphate synthase-like subunit pdx1.2; PDBTitle: pdx1.2/pdx1.3 complex (intermediate)
100	c2pt5D_	Alignment	not modelled	43.2	15	PDB header: transferase Chain: D: PDB Molecule: shikimate kinase; PDBTitle: crystal structure of shikimate kinase (aq_2177) from aquifex aeolicus2 vf5
101	c5g3yA_	Alignment	not modelled	42.9	21	PDB header: transferase Chain: A: PDB Molecule: adenylate kinase; PDBTitle: crystal structure of adenylyate kinase ancestor 1 with zn and adp bound
102	c2eu8B_	Alignment	not modelled	42.7	25	PDB header: transferase Chain: B: PDB Molecule: adenylate kinase; PDBTitle: crystal structure of a thermostable mutant of bacillus2 subtilis adenylyate kinase (q199r)
103	d1zfa1	Alignment	not modelled	42.6	18	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
104	d2cdna1	Alignment	not modelled	42.4	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
						PDB header: structural genomics, unknown function

105	c3hdtB_	Alignment	not modelled	42.3	26	Chain: B: PDB Molecule: putative kinase; PDBTitle: crystal structure of putative kinase from clostridium symbiosum atcc2 14940
106	c2h92C_	Alignment	not modelled	42.2	11	PDB header: transferase Chain: C: PDB Molecule: cytidylate kinase; PDBTitle: crystal structure of staphylococcus aureus cytidine2 monophosphate kinase in complex with cytidine-5'-3 monophosphate
107	c6aqpA_	Alignment	not modelled	41.8	25	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: aspergillus fumigatus cytosolic thiolase: acetylated enzyme in complex2 with coa and potassium ions
108	c4n45B_	Alignment	not modelled	41.5	23	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of reduced form of thiolase from clostridium2 acetobutylicum
109	c5bz4K_	Alignment	not modelled	41.4	27	PDB header: transferase Chain: K: PDB Molecule: beta-ketothiolase; PDBTitle: crystal structure of a t1-like thiolase (coa-complex) from2 mycobacterium smegmatis
110	c4q0mA_	Alignment	not modelled	41.4	22	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of pyrococcus furiosus l-asparaginase
111	d1g8fa3	Alignment	not modelled	41.4	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ATP sulfurylase C-terminal domain
112	c4rbnD_	Alignment	not modelled	41.3	31	PDB header: transferase Chain: D: PDB Molecule: sucrose synthase:glycosyl transferases group 1; PDBTitle: the crystal structure of nitrosomonas europaea sucrose synthase:2 insights into the evolutionary origin of sucrose metabolism in3 prokaryotes
113	c4pzcC_	Alignment	not modelled	40.5	11	PDB header: transferase Chain: C: PDB Molecule: adenylate kinase; PDBTitle: the crystal structure of adenylate kinase from francisella tularensis2 subsp. tularensis schu s4
114	d2fywa1	Alignment	not modelled	40.4	10	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
115	c3dloC_	Alignment	not modelled	40.3	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus
116	d1nmpa_	Alignment	not modelled	40.1	19	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
117	c3ss6B_	Alignment	not modelled	39.8	17	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
118	c1ub7A_	Alignment	not modelled	39.7	21	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] synthase; PDBTitle: the crystal analysis of beta-keroacyl-[acyl carrier protein] synthase2 iii (fabh)from thermus thermophilus.
119	c2ar7A_	Alignment	not modelled	39.7	32	PDB header: transferase Chain: A: PDB Molecule: adenylate kinase 4; PDBTitle: crystal structure of human adenylate kinase 4, ak4
120	c3be4A_	Alignment	not modelled	39.5	21	PDB header: transferase Chain: A: PDB Molecule: adenylate kinase; PDBTitle: crystal structure of cryptosporidium parvum adenylate kinase cgd5_3360