

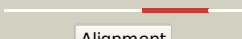

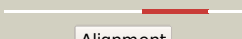











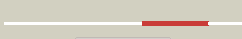






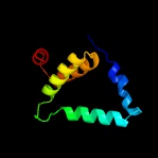
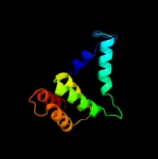
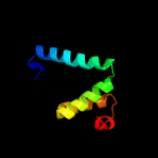



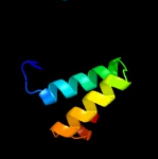



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3327_(-)_3711920_3713632
Date	Thu Aug 8 16:20:54 BST 2019
Unique Job ID	a8fd90960cccafd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2prra1	 Alignment		100.0	19	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
2	c6ohiA_	 Alignment		100.0	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: debrominase bmp8; PDBTitle: crystal structure of the debrominase bmp8 (apo)
3	d2oyoa1	 Alignment		100.0	24	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
4	c3lvyB_	 Alignment		100.0	15	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family; PDBTitle: crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
5	c3c1B_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative antioxidant defense protein mlr4105; PDBTitle: crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
6	d2pfxa1	 Alignment		100.0	15	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
7	d2gmya1	 Alignment		100.0	22	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
8	d2o4da1	 Alignment		100.0	24	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
9	d2ouwa1	 Alignment		99.7	19	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
10	c5dj4D_	 Alignment		99.5	17	PDB header: signaling protein Chain: D: PDB Molecule: sestrin-2; PDBTitle: leucine-bound sestrin2 from homo sapiens
11	c2qeua_	 Alignment		99.2	16	PDB header: lyase Chain: A: PDB Molecule: putative carboxymuconolactone decarboxylase; PDBTitle: crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution

12	d2cwqa1	Alignment		99.0	20	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
13	c5dipB	Alignment		98.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide reductase ahpd; PDBTitle: crystal structure of lpg0406 in reduced form from legionella2 pneumophila
14	d1vkea	Alignment		98.8	15	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
15	c3beyC	Alignment		98.7	13	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: conserved protein o27018; PDBTitle: crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
16	c1p8cD	Alignment		98.7	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of tm1620 (apc4843) from thermotoga2 maritima
17	c3d7iB	Alignment		98.4	13	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family protein; PDBTitle: crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
18	c5gzxD	Alignment		98.4	11	PDB header: hydrolase Chain: D: PDB Molecule: (r)-2-haloacid dehalogenase; PDBTitle: the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
19	d1knca	Alignment		98.4	26	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
20	d2q0ta1	Alignment		98.4	11	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
21	d1vkeb	Alignment	not modelled	98.3	12	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
22	c2oceA	Alignment	not modelled	97.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
23	c4g9qA	Alignment	not modelled	97.3	15	PDB header: lyase Chain: A: PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase
24	c3psfA	Alignment	not modelled	97.1	15	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)
25	c4ep5A	Alignment	not modelled	97.0	17	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure
26	d1hjra	Alignment	not modelled	96.7	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
27	c2nnwC	Alignment	not modelled	96.7	16	PDB header: transferase Chain: C: PDB Molecule: nop5/nop56 related protein; PDBTitle: alternative conformations of nop56/58-fibrillar complex and2 implication for induced-fit assenly of box c/d rnps
28	d2af7a1	Alignment	not modelled	96.6	11	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
						PDB header: transferase

29	c2e2pA	Alignment	not modelled	96.5	22	Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
30	c3eo3B	Alignment	not modelled	96.2	14	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
31	c5nckA	Alignment	not modelled	96.1	14	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
32	c3c6aA	Alignment	not modelled	95.8	13	PDB header: viral protein Chain: A: PDB Molecule: terminase large subunit; PDBTitle: crystal structure of the rb49 gp17 nuclease domain
33	d2ozbb1	Alignment	not modelled	95.7	17	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
34	c3id5E	Alignment	not modelled	95.5	15	PDB header: transferase/ribosomal protein/rna Chain: E: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarln, l7ae and a split half c/d rna
35	c4n2xF	Alignment	not modelled	95.3	21	PDB header: hydrolase Chain: F: PDB Molecule: dl-2-haloacid dehalogenase; PDBTitle: crystal structure of dl-2-haloacid dehalogenase
36	c5ganF	Alignment	not modelled	95.1	15	PDB header: transcription Chain: F: PDB Molecule: pre-mrna-processing factor 31; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
37	c5m1oA	Alignment	not modelled	95.1	14	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
38	c1xc3A	Alignment	not modelled	94.9	11	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
39	d1iv0a	Alignment	not modelled	94.9	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
40	c6nd4a	Alignment	not modelled	94.7	18	PDB header: ribosome Chain: A: PDB Molecule: mpp10; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
41	c6gmhM	Alignment	not modelled	94.5	13	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
42	d3bzka5	Alignment	not modelled	94.4	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
43	c5o9zH	Alignment	not modelled	94.3	19	PDB header: splicing Chain: H: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp31; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
44	c3psiA	Alignment	not modelled	94.3	12	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
45	c3icxB	Alignment	not modelled	94.3	15	PDB header: rna binding protein Chain: B: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus nop5 (135-380)
46	c4ehtA	Alignment	not modelled	94.3	20	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
47	c3h1qB	Alignment	not modelled	94.2	18	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrmus hydrogenoformans
48	c6nd4b	Alignment	not modelled	94.0	19	PDB header: ribosome Chain: B: PDB Molecule: PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
49	c2ap1A	Alignment	not modelled	93.8	18	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
50	c3hz6A	Alignment	not modelled	93.7	9	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
51	c2ch5D	Alignment	not modelled	93.5	17	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
52	c2gupA	Alignment	not modelled	93.5	8	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
53	c4db3A	Alignment	not modelled	93.4	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.
						Fold: Ribonuclease H-like motif

54	d2ap1a2	Alignment	not modelled	93.4	20	Superfamily: Actin-like ATPase domain Family: ROK
55	d1xc3a1	Alignment	not modelled	93.3	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
56	c2h5xA	Alignment	not modelled	93.1	15	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
57	c1rrqA	Alignment	not modelled	92.9	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
58	c1zc6A	Alignment	not modelled	92.8	16	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.
59	c3vovC	Alignment	not modelled	92.8	24	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
60	d1huxa	Alignment	not modelled	92.8	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
61	d1rrqa1	Alignment	not modelled	92.7	12	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
62	c5ya2A	Alignment	not modelled	92.6	17	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of Isrk-hpr complex with adp
63	c2aa4B	Alignment	not modelled	92.5	10	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
64	d1vhxa	Alignment	not modelled	92.5	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
65	c3bjxB	Alignment	not modelled	92.3	13	PDB header: hydrolase Chain: B: PDB Molecule: halocarboxylic acid dehalogenase dehi; PDBTitle: structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
66	d1cuka2	Alignment	not modelled	92.2	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
67	d1nu0a	Alignment	not modelled	92.1	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
68	d2a1jb1	Alignment	not modelled	92.1	10	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
69	c2mutA	Alignment	not modelled	91.9	10	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
70	d1keaa	Alignment	not modelled	91.8	12	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
71	c1d8IA	Alignment	not modelled	91.7	21	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
72	d2bgwa1	Alignment	not modelled	91.6	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
73	d1pu6a	Alignment	not modelled	91.6	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
74	c5f7rA	Alignment	not modelled	91.5	16	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
75	d2aa4a1	Alignment	not modelled	91.4	7	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
76	d1ixra1	Alignment	not modelled	91.4	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
77	d1bvsa2	Alignment	not modelled	91.3	28	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
78	c3g25B	Alignment	not modelled	91.3	13	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.
79	c2dpnB	Alignment	not modelled	91.3	20	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
80	c2g7kB	Alignment	not modelled	91.3	14	PDB header: hydrolase Chain: B: PDB Molecule: dna packaging protein gp17;

80	c0e2kb_	Alignment	not modelled	91.3	14	PDBTitle: bacteriophage t4 gp17 motor assembly based on crystal structures and2 cryo-em reconstructions
81	d2aq0a1	Alignment	not modelled	91.2	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
82	d2p3ra1	Alignment	not modelled	91.2	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
83	c5hv7A_	Alignment	not modelled	91.2	18	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
84	c4ijaA_	Alignment	not modelled	91.1	7	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecR2
85	c3htvA_	Alignment	not modelled	91.1	18	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
86	c3gbtA_	Alignment	not modelled	91.0	12	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
87	c4b24A_	Alignment	not modelled	90.9	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: probable dna-3-methyladenine glycosylase 2; PDBTitle: unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
88	d1z05a3	Alignment	not modelled	90.8	7	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
89	c2d4wA_	Alignment	not modelled	90.6	16	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
90	c1z05A_	Alignment	not modelled	90.4	7	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.
91	d1x2ia1	Alignment	not modelled	90.4	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
92	c1ixrA_	Alignment	not modelled	90.3	22	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
93	c2nrzB_	Alignment	not modelled	90.3	19	PDB header: hydrolase Chain: B: PDB Molecule: uvrbc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrC bound to its2 catalytic divalent cation
94	c1ixrB_	Alignment	not modelled	90.2	22	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
95	c3fhgA_	Alignment	not modelled	90.0	9	PDB header: dna repair, hydrolase, lyase Chain: A: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: crystal structure of sulfolobus solfataricus 8-oxoguanine dna2 glycosylase (ssogg)
96	c4htlA_	Alignment	not modelled	90.0	7	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
97	c5f7pA_	Alignment	not modelled	89.8	16	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes
98	c1glbG_	Alignment	not modelled	89.8	16	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiiiglc with2 glycerol kinase
99	c3ficX_	Alignment	not modelled	89.7	19	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
100	d1ul1x1	Alignment	not modelled	89.7	13	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
101	d1nt2b_	Alignment	not modelled	89.6	17	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
102	c5htxA_	Alignment	not modelled	89.5	19	PDB header: transferase Chain: A: PDB Molecule: putative xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp
103	c4e1jA_	Alignment	not modelled	89.5	13	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
104	c1kftA_	Alignment	not modelled	89.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc subunit c; PDBTitle: solution structure of the c-terminal domain of uvrC from e-2 coli
105	d1kfta_	Alignment	not modelled	89.4	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
106	d2ch5a2	Alignment	not modelled	89.3	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like

107	c3ifrB_	Alignment	not modelled	89.3	16	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
108	c2nlxA_	Alignment	not modelled	89.1	22	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
109	d1orna_	Alignment	not modelled	89.0	20	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
110	c3n0uB_	Alignment	not modelled	88.9	14	PDB header: hydrolase, lyase Chain: B: PDB Molecule: probable n-glycosylase/dna lyase; PDBTitle: crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima
111	d1rxwa1	Alignment	not modelled	88.9	13	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
112	c3ezwD_	Alignment	not modelled	88.9	16	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
113	d1ngna_	Alignment	not modelled	88.4	6	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
114	c3jvpA_	Alignment	not modelled	88.2	18	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
115	d3bzka1	Alignment	not modelled	88.2	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
116	c5vm1A_	Alignment	not modelled	88.2	16	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xyloyle kinase from brucella ovis
117	c3s6iA_	Alignment	not modelled	88.2	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-3-methyladenine glycosylase 1; PDBTitle: schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
118	c3gg4B_	Alignment	not modelled	88.1	25	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
119	d2edua1	Alignment	not modelled	88.0	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
120	c3wxiB_	Alignment	not modelled	88.0	28	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)