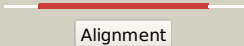

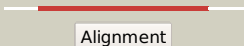

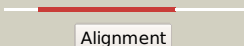







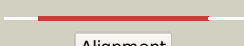


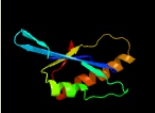








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2554c (-)_2873268_2873780
Date	Wed Aug 7 12:50:19 BST 2019
Unique Job ID	4f74f956ce6c4444

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vhxa_	 Alignment		100.0	34	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
2	d1nu0a_	 Alignment		100.0	29	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
3	d1iv0a_	 Alignment		100.0	31	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
4	d3bzka5	 Alignment		99.1	23	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
5	c2oceA_	 Alignment		98.2	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
6	c3psfA_	 Alignment		98.0	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)
7	c4ep5A_	 Alignment		98.0	18	PDB header: hydrolase Chain: A; PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure
8	d1hjra_	 Alignment		97.9	11	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
9	c3psiA_	 Alignment		97.7	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(239-1451)
10	c6gmhM_	 Alignment		97.4	25	PDB header: transcription Chain: M; PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf- spt6
11	c1xc3A_	 Alignment		96.9	10	PDB header: transferase Chain: A; PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis

12	c3vovC_	Alignment		96.5	21	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermophilus
13	d1xc3a1	Alignment		96.5	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
14	d2hoea3	Alignment		96.2	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
15	d2ap1a2	Alignment		96.2	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
16	c4htiA_	Alignment		96.1	18	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
17	d2gupa1	Alignment		96.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
18	c3htvA_	Alignment		95.9	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
19	d2aa4a1	Alignment		95.8	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
20	c4ijaA_	Alignment		95.7	13	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mec2
21	d1z6ra2	Alignment	not modelled	95.2	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
22	d1z05a3	Alignment	not modelled	95.0	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
23	d1jcea1	Alignment	not modelled	94.8	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
24	c1z6rC_	Alignment	not modelled	94.6	15	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
25	c3vpzA_	Alignment	not modelled	94.5	11	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
26	d1woqa1	Alignment	not modelled	94.2	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
27	c1woqB_	Alignment	not modelled	94.2	21	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
28	c2qm1D_	Alignment	not modelled	94.2	17	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis

29	c2hoeA	Alignment	not modelled	94.0	15	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
30	d1sz2a1	Alignment	not modelled	93.9	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
31	c3r8eA	Alignment	not modelled	93.7	13	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
32	c3eo3B	Alignment	not modelled	93.6	19	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
33	c5nckA	Alignment	not modelled	93.6	16	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
34	d1q18a1	Alignment	not modelled	93.5	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
35	c1z05A	Alignment	not modelled	93.4	16	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.
36	c2e2pA	Alignment	not modelled	93.3	18	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
37	c2gupA	Alignment	not modelled	93.0	18	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
38	d2ch5a2	Alignment	not modelled	92.9	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
39	c3h1qB	Alignment	not modelled	92.8	19	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrus hydrogenoformans
40	c4db3A	Alignment	not modelled	92.7	18	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.
41	c3mcpA	Alignment	not modelled	92.7	17	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
42	c6fpeG	Alignment	not modelled	92.4	16	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
43	c5f7rA	Alignment	not modelled	92.4	13	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
44	d1okja1	Alignment	not modelled	92.3	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
45	c2ap1A	Alignment	not modelled	91.9	22	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
46	c5f7pA	Alignment	not modelled	91.9	14	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes
47	d1bupa1	Alignment	not modelled	91.5	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
48	c5br9C	Alignment	not modelled	91.0	20	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein with similarity to2 peptidase yeaz from pseudomonas aeruginosa
49	d2nu7b1	Alignment	not modelled	90.7	14	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
50	c1okjB	Alignment	not modelled	90.7	19	PDB header: hydrolase Chain: B: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab; PDBTitle: crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
51	d2e8aa1	Alignment	not modelled	90.1	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
52	c3c7nB	Alignment	not modelled	89.9	26	PDB header: chaperone/chaperone Chain: B: PDB Molecule: heat shock cognate; PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex
53	c3vgkB	Alignment	not modelled	89.8	18	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
54	c2v7zA	Alignment	not modelled	89.2	25	PDB header: chaperone Chain: A: PDB Molecule: heat shock cognate 71 kda protein; PDBTitle: crystal structure of the 70-kda heat shock cognate

						protein2 from rattus norvegicus in post-atp hydrolysis state
55	d1dkgd1	Alignment	not modelled	89.1	33	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
56	c3lm2B	Alignment	not modelled	87.7	18	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
57	c1hpmA	Alignment	not modelled	87.1	29	PDB header: hydrolase (acting on acid anhydrides) Chain: A: PDB Molecule: 44k atpase fragment (n-terminal) of 70 kd heat- PDBTitle: how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
58	c5x2hA	Alignment	not modelled	86.9	31	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of campylobacter jejuni cas9 in complex with sgrna2 and target dna (agaaca pam)
59	c2ch5D	Alignment	not modelled	86.9	13	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
60	c3r6mD	Alignment	not modelled	85.3	21	PDB header: hydrolase Chain: D: PDB Molecule: yeaz, resuscitation promoting factor; PDBTitle: crystal structure of vibrio parahaemolyticus yeaz
61	c6da0A	Alignment	not modelled	85.1	21	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (nfhk) from naegleria fowleri
62	c1dkgD	Alignment	not modelled	84.5	33	PDB header: complex (hsp24/hsp70) Chain: D: PDB Molecule: molecular chaperone dnak; PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
63	c2aa4B	Alignment	not modelled	83.7	24	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	c3iucC	Alignment	not modelled	83.5	22	PDB header: chaperone Chain: C: PDB Molecule: heat shock 70kda protein 5 (glucose-regulated PDBTitle: crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
65	c5e84B	Alignment	not modelled	82.9	27	PDB header: chaperone Chain: B: PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: atp-bound state of bip
66	c6melB	Alignment	not modelled	82.6	10	PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta; PDBTitle: succinyl-coa synthase from campylobacter jejuni
67	c4kboA	Alignment	not modelled	80.7	30	PDB header: signaling protein Chain: A: PDB Molecule: stress-70 protein, mitochondrial; PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form
68	d2ewsa1	Alignment	not modelled	79.8	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
69	c5obuA	Alignment	not modelled	79.2	26	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak; PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.
70	c4rtfD	Alignment	not modelled	79.1	29	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv
71	c3wqtB	Alignment	not modelled	78.4	15	PDB header: structural genomics Chain: B: PDB Molecule: cell division protein ftsa; PDBTitle: staphylococcus aureus ftsa complexed with amppnp
72	c5mb9B	Alignment	not modelled	78.0	22	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
73	c2nu9E	Alignment	not modelled	77.5	15	PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
74	c2v7yA	Alignment	not modelled	77.2	27	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
75	c4j8fA	Alignment	not modelled	77.0	21	PDB header: chaperone Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein; PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip
76	c3agjD	Alignment	not modelled	76.4	16	PDB header: translation/hydrolase Chain: D: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
77	c5axwA	Alignment	not modelled	74.5	20	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam)
78	c6gfaA	Alignment	not modelled	74.4	25	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 105 kda; PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed
79	d1kcf2	Alignment	not modelled	73.0	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like

						Family: Mitochondrial resolvase ydc2 catalytic domain
80	d1huxa_	Alignment	not modelled	72.3	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
81	d1yoba1	Alignment	not modelled	72.1	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
82	c6n9aB_	Alignment	not modelled	72.0	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: trna threonylcarbamoyladenosine biosynthesis protein tsab; PDBTitle: crystal structure of thermotoga maritima threonylcarbamoyladenosine2 biosynthesis complex tsab2d2e2 bound to atp and carboxy-amp
83	c2khoA_	Alignment	not modelled	71.6	35	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 70; PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate
84	c4idhA_	Alignment	not modelled	71.1	13	PDB header: viral protein Chain: A: PDB Molecule: gene 2 protein; PDBTitle: crystal structure of the large terminase subunit gp2 of bacterial2 virus sf6
85	c2q2rA_	Alignment	not modelled	70.7	9	PDB header: transferase Chain: A: PDB Molecule: glucokinase 1, putative; PDBTitle: trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
86	c4gniA_	Alignment	not modelled	70.7	23	PDB header: chaperone Chain: A: PDB Molecule: putative heat shock protein; PDBTitle: structure of the ssz1 atpase bound to atp and magnesium
87	d1t6ca1	Alignment	not modelled	70.3	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
88	d3bexa1	Alignment	not modelled	69.5	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
89	c2a6aB_	Alignment	not modelled	68.9	20	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein tm0874; PDBTitle: crystal structure of glycoprotein endopeptidase (tm0874) from2 thermotoga maritima at 2.50 a resolution
90	c1zc6A_	Alignment	not modelled	68.8	13	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.
91	d2fcra_	Alignment	not modelled	68.0	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
92	c4czeA_	Alignment	not modelled	66.6	22	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: c. crescentus mreB, double filament, empty
93	d1oboa_	Alignment	not modelled	66.3	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
94	c3agiB_	Alignment	not modelled	65.6	16	PDB header: translation/hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
95	d1eucb1	Alignment	not modelled	64.8	14	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
96	c5tkyA_	Alignment	not modelled	64.6	30	PDB header: chaperone Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation
97	c6ediA_	Alignment	not modelled	64.6	18	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of leishmania braziliensis glucokinase
98	c4cmqB_	Alignment	not modelled	64.2	26	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
99	c2ychA_	Alignment	not modelled	63.9	14	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilM; PDBTitle: pilM-pilN type iv pilus biogenesis complex
100	c1jcgA_	Alignment	not modelled	63.2	26	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp
101	c3d2fC_	Alignment	not modelled	62.3	18	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
102	d2a6aa1	Alignment	not modelled	62.2	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
103	c5ya2A_	Alignment	not modelled	61.8	13	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
104	d1qopa_	Alignment	not modelled	61.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
105	c6g4qB_	Alignment	not modelled	60.8	10	PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta, PDBTitle: structure of human adp-forming succinyl-coa ligase

						complex suclg1-2 sucla2
106	d1zc6a1	Alignment	not modelled	60.5	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
107	c2ekcA	Alignment	not modelled	58.5	20	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
108	c3djca	Alignment	not modelled	57.6	22	PDB header: transferase Chain: A: PDB Molecule: type iii pantothenate kinase; PDBTitle: crystal structure of pantothenate kinase from legionella pneumophila
109	c3ufxG	Alignment	not modelled	57.3	13	PDB header: ligase Chain: G: PDB Molecule: succinyl-coa synthetase beta subunit; PDBTitle: thermus aquaticus succinyl-coa synthetase in complex with gdp-mn2+
110	d1czna	Alignment	not modelled	56.2	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
111	d2p3ra1	Alignment	not modelled	55.9	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
112	c4ac1X	Alignment	not modelled	55.2	11	PDB header: hydrolase Chain: X: PDB Molecule: endo-n-acetyl-beta-d-glucosaminidase; PDBTitle: the structure of a fungal endo-beta-n-acetylglucosaminidase from2 glycosyl hydrolase family 18, at 1.3a resolution
113	c4ehtA	Alignment	not modelled	53.0	12	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
114	c2w40C	Alignment	not modelled	53.0	17	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
115	c1xupO	Alignment	not modelled	52.8	13	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
116	c5ey5A	Alignment	not modelled	52.0	16	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
117	c3ifrB	Alignment	not modelled	52.0	16	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
118	c2wc1A	Alignment	not modelled	51.5	16	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
119	d2qj2a2	Alignment	not modelled	51.4	14	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: ERF1/Dom34 middle domain-like
120	d1gsoa2	Alignment	not modelled	50.5	17	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like