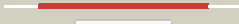



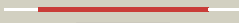








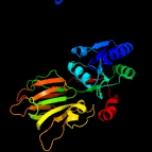



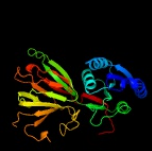










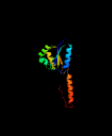

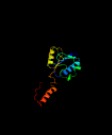


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1695_(ppnK)_1918753_1919676
Date	Fri Aug 2 13:30:29 BST 2019
Unique Job ID	d43ce186db6f4744

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3afoB_	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: nadh kinase pos5; PDBTitle: crystal structure of yeast nadh kinase complexed with nadh
2	c3pfnB_	 Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
3	d1u0ta_	 Alignment		100.0	100	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
4	c2an1D_	 Alignment		100.0	32	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
5	c1yt5A_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima
6	c2i2aA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes
7	d1z0sa1	 Alignment		100.0	28	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
8	c1z0zC_	 Alignment		100.0	28	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
9	d2qv7a1	 Alignment		99.3	13	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
10	c2qv7A_	 Alignment		99.3	14	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
11	c4werA_	 Alignment		99.1	16	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase catalytic domain protein; PDBTitle: crystal structure of diacylglycerol kinase catalytic domain protein2 from enterococcus faecalis v583

12	d2bona1	Alignment		99.1	15	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
13	c3s40C_	Alignment		99.1	17	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
14	c2bonB_	Alignment		99.1	15	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
15	d2p1ra1	Alignment		99.0	15	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
16	d2jgra1	Alignment		98.6	15	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
17	c3vzdB_	Alignment		98.2	14	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
18	c3opyG_	Alignment		95.7	11	PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
19	c1zxxA_	Alignment		95.7	17	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
20	c3opyE_	Alignment		95.4	11	PDB header: transferase Chain: E: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
21	d4pfka_	Alignment	not modelled	95.2	15	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
22	d1vlja_	Alignment	not modelled	95.0	19	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
23	d1pfka_	Alignment	not modelled	94.7	14	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
24	c3okfA_	Alignment	not modelled	94.7	13	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinase synthase2 (arob) from vibrio cholerae
25	c3o8oC_	Alignment	not modelled	94.4	13	PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
26	c5tprB_	Alignment	not modelled	94.3	17	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: desmethyl-4-deoxygadusol synthase from anabaena variabilis (ava_3858)2 with nad+ and zn2+ bound
27	c3opyB_	Alignment	not modelled	94.3	11	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
28	c3opyH_	Alignment	not modelled	94.3	11	PDB header: transferase Chain: H: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
						PDB header: oxidoreductase

29	c3ce9A	Alignment	not modelled	94.3	16	Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
30	c5zxID	Alignment	not modelled	94.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli
31	c3o8nA	Alignment	not modelled	93.9	10	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
32	c4p53A	Alignment	not modelled	93.7	15	PDB header: lyase Chain: A: PDB Molecule: cyclase; PDBTitle: vala (2-epi-5-epi-valiolone synthase) from streptomyces hygrosopicus2 subsp. jinggangensis 5008 with nad+ and zn2+ bound
33	c5eksB	Alignment	not modelled	93.5	13	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from acinetobacter baumannii in2 complex with nad
34	c3ox4D	Alignment	not modelled	93.4	17	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
35	c3qbeA	Alignment	not modelled	93.4	21	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of the 3-dehydroquinase synthase (arob) from2 mycobacterium tuberculosis
36	c3hdvB	Alignment	not modelled	93.3	21	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
37	c6c76A	Alignment	not modelled	93.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: structure of iron containing alcohol dehydrogenase from thermococcus2 thioireducens in an orthorhombic crystal form
38	d1a9xb2	Alignment	not modelled	93.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
39	c1ta9A	Alignment	not modelled	93.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
40	c3r74B	Alignment	not modelled	92.7	21	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
41	d1o1ya	Alignment	not modelled	92.6	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
42	c5xoeA	Alignment	not modelled	92.5	16	PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus phosphofructokinase
43	d1rrma	Alignment	not modelled	92.5	15	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
44	c5yvmA	Alignment	not modelled	92.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
45	c3l7nA	Alignment	not modelled	92.0	13	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
46	d1jq5a	Alignment	not modelled	92.0	14	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
47	c4mcaB	Alignment	not modelled	91.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a
48	d1o2da	Alignment	not modelled	91.4	17	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
49	d1wl8a1	Alignment	not modelled	91.1	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
50	c3jzdA	Alignment	not modelled	90.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
51	c3bfjK	Alignment	not modelled	90.7	17	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
52	c2higA	Alignment	not modelled	90.6	35	PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
53	c3nvaB	Alignment	not modelled	90.4	21	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
54	c3zokB	Alignment	not modelled	90.0	20	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from actinidia chinensis in2 complex with nad

55	d1vhqa_	Alignment	not modelled	89.9	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
56	d2f48a1	Alignment	not modelled	89.6	35	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
57	c1keeH_	Alignment	not modelled	88.6	23	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
58	c2issF_	Alignment	not modelled	88.3	19	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
59	c4fr2A_	Alignment	not modelled	88.1	12	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni
60	d1sg6a_	Alignment	not modelled	87.2	10	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Dehydroquininate synthase, DHQS
61	c3k2qA_	Alignment	not modelled	87.0	23	PDB header: transferase Chain: A: PDB Molecule: pyrophosphate-dependent phosphofructokinase; PDBTitle: crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
62	d1oj7a_	Alignment	not modelled	86.9	20	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Iron-containing alcohol dehydrogenase
63	c5fb3C_	Alignment	not modelled	86.6	25	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerophosphate dehydrogenase in complex with nadph
64	c3hi0B_	Alignment	not modelled	86.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
65	c4o9uB_	Alignment	not modelled	86.1	14	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
66	d2nv0a1	Alignment	not modelled	86.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
67	c2o6lA_	Alignment	not modelled	86.0	12	PDB header: transferase Chain: A: PDB Molecule: udp-glucuronosyltransferase 2b7; PDBTitle: crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
68	d1q7ra_	Alignment	not modelled	85.9	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
69	c3o8oB_	Alignment	not modelled	85.8	23	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
70	c5gqsA_	Alignment	not modelled	85.6	17	PDB header: transport protein Chain: A: PDB Molecule: pts galactitol transporter subunit iib; PDBTitle: nmr based solution structure of pts system, galactitol-specific iib2 component from methicillin resistant staphylococcus aureus
71	d1peya_	Alignment	not modelled	85.3	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
72	c1vcnA_	Alignment	not modelled	84.6	26	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
73	c6qurA_	Alignment	not modelled	84.5	20	PDB header: transferase Chain: A: PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
74	c3l83A_	Alignment	not modelled	84.4	30	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
75	d1i1qb_	Alignment	not modelled	84.4	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
76	c2mswA_	Alignment	not modelled	84.4	17	PDB header: transferase Chain: A: PDB Molecule: response regulator/sensor histidine kinase; PDBTitle: ligand-induced folding of a receiver domain
77	c3zdrA_	Alignment	not modelled	84.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase domain of the bifunctional PDBTitle: structure of the alcohol dehydrogenase (adh) domain of a2 bifunctional adhe dehydrogenase from geobacillus3 thermoglucosidasius ncimb 11955
78	c3d54D_	Alignment	not modelled	84.2	26	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
79	c4nuxA_	Alignment	not modelled	83.6	16	PDB header: immune system Chain: A: PDB Molecule: interleukin-17 receptor a;

						PDBTitle: structure of receptor a
80	c1sy7B_	Alignment	not modelled	83.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
81	d1oi4a1	Alignment	not modelled	83.3	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/PfpI
82	c2zwmA_	Alignment	not modelled	83.2	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
83	d2a9va1	Alignment	not modelled	83.0	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
84	c3a0rB_	Alignment	not modelled	82.9	10	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
85	c3othB_	Alignment	not modelled	82.0	23	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
86	d1k68a_	Alignment	not modelled	82.0	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	c1tvmA_	Alignment	not modelled	82.0	17	PDB header: transferase Chain: A: PDB Molecule: pts system, galactitol-specific iib component; PDBTitle: nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
88	d2c1xa1	Alignment	not modelled	81.9	8	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
89	d1i7qb_	Alignment	not modelled	81.7	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
90	c3nhzA_	Alignment	not modelled	81.4	20	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
91	c2vpiA_	Alignment	not modelled	80.9	18	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
92	d1gpma2	Alignment	not modelled	80.7	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
93	c3d3kD_	Alignment	not modelled	80.1	13	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
94	c6c5cA_	Alignment	not modelled	80.0	15	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: crystal structure of aro1p from candida albicans sc5314 in complex2 with nadh
95	c6jkdD_	Alignment	not modelled	79.9	15	PDB header: oxidoreductase Chain: D: PDB Molecule: methanol dehydrogenase; PDBTitle: crystal structure of sulfoacetaldehyde reductase from bifidobacterium2 kashiwanohense in complex with nad+
96	c4gudA_	Alignment	not modelled	79.8	20	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
97	d1p80a1	Alignment	not modelled	79.7	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
98	c5v2ka_	Alignment	not modelled	78.9	14	PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 74f2; PDBTitle: crystal structure of udp-glycosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid
99	d1pjqa1	Alignment	not modelled	78.8	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
100	d1ujna_	Alignment	not modelled	78.7	18	Fold: Dehydroquinate synthase-like Superfamily: Dehydroquinate synthase-like Family: Dehydroquinate synthase, DHQS
101	c3fniA_	Alignment	not modelled	78.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
102	c3h5iA_	Alignment	not modelled	78.3	15	PDB header: transcription Chain: A: PDB Molecule: response regulator/sensory box protein/ggdef domain PDBTitle: crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from carboxydotherrmus3 hydrogenoformans
103	c3crnA_	Alignment	not modelled	78.3	16	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
104	d1ka9h_	Alignment	not modelled	78.1	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

105	c3lftA_	Alignment	not modelled	78.1	9	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the abc domain in complex with l-trp from 2 streptococcus pneumonia to 1.35a
106	c5lejA_	Alignment	not modelled	77.9	16	PDB header: protein Chain: A: PDB Molecule: sdrG; PDBTitle: solution structure of the bef3-activated conformation of sdrG from 2 pseudomonas melonis fr1
107	c2ad5B_	Alignment	not modelled	77.4	28	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
108	c4ehiB_	Alignment	not modelled	77.4	21	PDB header: hydrolase,transferase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purH; PDBTitle: an x-ray crystal structure of a putative bifunctional 2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
109	c4eukA_	Alignment	not modelled	77.2	16	PDB header: signaling protein Chain: A: PDB Molecule: histidine kinase 5; PDBTitle: crystal structure
110	d1s1ma1	Alignment	not modelled	77.1	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
111	c6csjD_	Alignment	not modelled	76.8	15	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of a bacillus coagulans polyol dehydrogenase double mutant 2 with an acquired d-lactate dehydrogenase activity
112	d1vmea1	Alignment	not modelled	76.4	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
113	c2v4uA_	Alignment	not modelled	76.3	28	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with 2 5-oxo-l-norleucine
114	d1pnoa_	Alignment	not modelled	76.3	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
115	d1qdlb_	Alignment	not modelled	76.2	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
116	c4lzlA_	Alignment	not modelled	76.1	10	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the inactive form of the regulatory domain from the 2 repressor of iron transport regulator (ritr)
117	d1dbwa_	Alignment	not modelled	75.7	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
118	c3lteH_	Alignment	not modelled	74.3	18	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from 2 bermanella marisrubri
119	c5tmdA_	Alignment	not modelled	74.2	12	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase, os79; PDBTitle: crystal structure of os79 from o. sativa in complex with u2f and 2 trichothecene.
120	c4kr3A_	Alignment	not modelled	73.8	14	PDB header: ligase/rna Chain: A: PDB Molecule: glycine--trna ligase; PDBTitle: glycyl-trna synthetase mutant e71g in complex with trna-gly