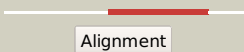
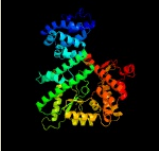
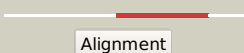





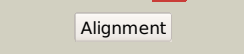
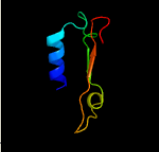




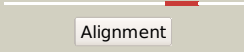

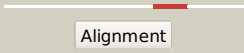
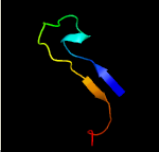
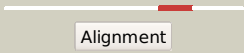
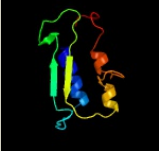
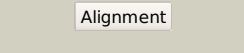
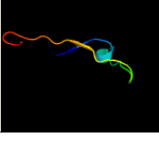
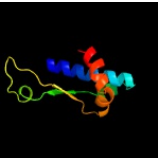

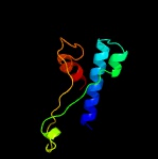


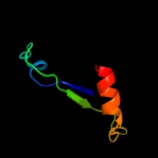


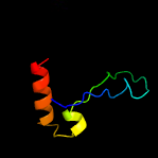


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2221c_glnE_2489377_2492361
Date	Mon Aug 5 13:25:35 BST 2019
Unique Job ID	ba9b76ceceda5bd9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3k7dA</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-ammonia-ligase adenylyltransferase; <b>PDBTitle:</b> c-terminal (adenylation) domain of e.coli glutamine synthetase2 adenylyltransferase
2	<a href="#">c1v4aA</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-ammonia-ligase adenylyltransferase; <b>PDBTitle:</b> structure of the n-terminal domain of escherichia coli2 glutamine synthetase adenylyltransferase
3	<a href="#">d1v4aa2</a>	 Alignment		100.0	23	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> GlnE-like domain
4	<a href="#">d1v4aa1</a>	 Alignment		100.0	27	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Nucleotidyltransferase substrate binding subunit/domain <b>Family:</b> Glutamine synthase adenylyltransferase GlnE, domain 2
5	<a href="#">d1knya2</a>	 Alignment		97.0	20	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
6	<a href="#">c1knyA</a>	 Alignment		96.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> kanamycin nucleotidyltransferase; <b>PDBTitle:</b> kanamycin nucleotidyltransferase
7	<a href="#">c2rffA</a>	 Alignment		96.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of a putative nucleotidyltransferase (np_343093.1)2 from sulfolobus solfataricus at 1.40 a resolution
8	<a href="#">d1vlqa1</a>	 Alignment		95.3	16	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase
9	<a href="#">d1no5a</a>	 Alignment		94.3	20	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase
10	<a href="#">c4cs6A</a>	 Alignment		93.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside adenylyltransferase; <b>PDBTitle:</b> crystal structure of aada - an aminoglycoside adenylyltransferase
11	<a href="#">d1wota</a>	 Alignment		93.5	24	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase

12	<a href="#">c3c66B_</a>	Alignment		92.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> poly(a) polymerase; <b>PDBTitle:</b> yeast poly(a) polymerase in complex with fip1 residues 80-105
13	<a href="#">d2q66a2</a>	Alignment		92.1	15	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly(A) polymerase, PAP, N-terminal domain
14	<a href="#">c1q78A_</a>	Alignment		92.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(a) polymerase alpha; <b>PDBTitle:</b> crystal structure of poly(a) polymerase in complex with 3'-2 datp and magnesium chloride
15	<a href="#">d1q79a2</a>	Alignment		90.8	16	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly(A) polymerase, PAP, N-terminal domain
16	<a href="#">c4ebjB_</a>	Alignment		90.5	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of aminoglycoside 4'-o-adenylyltransferase ant(4')-2 lib, apo
17	<a href="#">c3jz0B_</a>	Alignment		89.3	16	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> lincosamide nucleotidyltransferase; <b>PDBTitle:</b> linb complexed with clindamycin and ampcpp
18	<a href="#">c5z4cA_</a>	Alignment		85.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> terminal uridylyltransferase tailor; <b>PDBTitle:</b> crystal structure of tailor
19	<a href="#">d2fmpa3</a>	Alignment		78.5	17	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
20	<a href="#">c4zr1A_</a>	Alignment		75.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(a) rna polymerase gld-2; <b>PDBTitle:</b> structure of the non canonical poly(a) polymerase complex gld-2 - gld-2 3
21	<a href="#">c2bcuA_</a>	Alignment	not modelled	72.3	19	<b>PDB header:</b> transferase, lyase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase lambda; <b>PDBTitle:</b> dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
22	<a href="#">c4xq7A_</a>	Alignment	not modelled	68.2	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2'-5'-oligoadenylate synthase-like protein; <b>PDBTitle:</b> the crystal structure of the oas-like domain (old) of human oasl
23	<a href="#">c5w0mA_</a>	Alignment	not modelled	67.0	11	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> terminal uridylyltransferase 7; <b>PDBTitle:</b> structure of human tut7 catalytic module (cm) in complex with u5 rna
24	<a href="#">c4ep7A_</a>	Alignment	not modelled	62.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(a) rna polymerase protein cid1; <b>PDBTitle:</b> functional implications from the cid1 poly(u) polymerase crystal2 structure
25	<a href="#">c4e80B_</a>	Alignment	not modelled	61.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> poly(a) rna polymerase protein cid1; <b>PDBTitle:</b> structural basis for the activity of a cytoplasmic rna terminal u-2 transferase
26	<a href="#">c4s3nA_</a>	Alignment	not modelled	54.8	16	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> 2'-5'-oligoadenylate synthase 3; <b>PDBTitle:</b> crystal structure of human oas3 domain i in complex with dsrna
27	<a href="#">d2vana2</a>	Alignment	not modelled	54.3	17	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
28	<a href="#">c2la3A_</a>	Alignment	not modelled	53.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain <b>PDB header:</b> transferase/dna

29	<a href="#">c4p4oA</a>	Alignment	not modelled	51.6	11	<b>Chain:</b> A; <b>PDB Molecule:</b> dna polymerase beta; <b>PDBTitle:</b> crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
30	<a href="#">c4uz0B</a>	Alignment	not modelled	49.8	30	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> nucleolar protein 3; <b>PDBTitle:</b> crystal structure of apoptosis repressor with card (arc)
31	<a href="#">c1sz1A</a>	Alignment	not modelled	49.0	16	<b>PDB header:</b> transferase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> trna nucleotidyltransferase; <b>PDBTitle:</b> mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
32	<a href="#">c3nybA</a>	Alignment	not modelled	48.8	14	<b>PDB header:</b> transferase/rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> poly(a) rna polymerase protein 2; <b>PDBTitle:</b> structure and function of the polymerase core of tramp, a rna2 surveillance complex
33	<a href="#">c5yepA</a>	Alignment	not modelled	46.8	17	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> A; <b>PDB Molecule:</b> toxin-antitoxin system antidote mnt family; <b>PDBTitle:</b> crystal structure of so_3166-so_3165 from shewanella oneidensis
34	<a href="#">d1jmsa4</a>	Alignment	not modelled	39.7	13	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
35	<a href="#">c5m45K</a>	Alignment	not modelled	38.6	25	<b>PDB header:</b> ligase <b>Chain:</b> K; <b>PDB Molecule:</b> acetone carboxylase beta subunit; <b>PDBTitle:</b> structure of acetone carboxylase purified from xanthobacter2 autotrophicus
36	<a href="#">c1kdhA</a>	Alignment	not modelled	35.5	18	<b>PDB header:</b> transferase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> terminal deoxynucleotidyltransferase short <b>PDBTitle:</b> binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
37	<a href="#">c3fioB</a>	Alignment	not modelled	35.4	7	<b>PDB header:</b> nucleotide binding protein, metal bindin <b>Chain:</b> B; <b>PDB Molecule:</b> za cystathionine beta-synthase domain <b>PDBTitle:</b> crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
38	<a href="#">c1x4pA</a>	Alignment	not modelled	35.4	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative splicing factor, arginine/serine-rich <b>PDBTitle:</b> solution structure of surp domain in sfrs14 protei
39	<a href="#">d1r89a2</a>	Alignment	not modelled	33.6	14	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Archaeal tRNA CCA-adding enzyme catalytic domain
40	<a href="#">d1vk2a</a>	Alignment	not modelled	32.2	14	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Mug-like
41	<a href="#">c3db2C</a>	Alignment	not modelled	32.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> putative nadph-dependent oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
42	<a href="#">c1titB</a>	Alignment	not modelled	31.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> putative oxidoreductase (virulence factor mvim homolog); <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
43	<a href="#">c5l9wb</a>	Alignment	not modelled	29.4	13	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
44	<a href="#">d2bcqa3</a>	Alignment	not modelled	28.3	12	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
45	<a href="#">c3o7kA</a>	Alignment	not modelled	26.3	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> ohcu decarboxylase; <b>PDBTitle:</b> crystal structure of 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline2 decarboxylase from klebsiella pneumoniae
46	<a href="#">c3ppq1A</a>	Alignment	not modelled	25.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> poly(a) rna polymerase; <b>PDBTitle:</b> crystal structure of human mitochondrial poly(a) polymerase (papd1)
47	<a href="#">c2a4aB</a>	Alignment	not modelled	25.2	19	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> deoxyribose-phosphate aldolase from p. yoelii
48	<a href="#">c5l3xB</a>	Alignment	not modelled	22.2	20	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> negative elongation factor c/d; <b>PDBTitle:</b> crystal structure of negative elongation factor subcomplex nelf-ac
49	<a href="#">c2jq5A</a>	Alignment	not modelled	22.0	17	<b>PDB header:</b> structural genomics <b>Chain:</b> A; <b>PDB Molecule:</b> sec-c motif; <b>PDBTitle:</b> solution structure of rpa3114, a sec-c motif containing protein from2 rhodopseudomonas palustris; northeast structural genomics consortium3 target rpt5 / ontario center for structural proteomics target rp3097
50	<a href="#">c5l9wB</a>	Alignment	not modelled	21.8	13	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
51	<a href="#">c3ngjC</a>	Alignment	not modelled	21.8	20	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
52	<a href="#">d1vi7a1</a>	Alignment	not modelled	20.2	35	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> YigZ N-terminal domain-like
53	<a href="#">c4hadD</a>	Alignment	not modelled	19.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of probable oxidoreductase protein from

						rhizobium2 etli cfn 42
54	<a href="#">c3qyqC_</a>	Alignment	not modelled	19.6	9	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase, putative; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of a putative deoxyribose-2 phosphate aldolase from toxoplasma gondii me49
55	<a href="#">c3hiyA_</a>	Alignment	not modelled	19.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> minor editosome-associated tutase; <b>PDBTitle:</b> minor editosome-associated tutase 1 with bound utp and mg
56	<a href="#">c3ng3A_</a>	Alignment	not modelled	19.3	37	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
57	<a href="#">c6e0oA_</a>	Alignment	not modelled	19.2	16	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> cgas/dncv-like nucleotidyltransferase in e. coli homolog; <b>PDBTitle:</b> structure of elizabethkingia meningoseptica cdne cyclic dinucleotide2 synthase with pppa[3'-5']pa
58	<a href="#">c4mp6A_</a>	Alignment	not modelled	18.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ornithine cyclodeaminase; <b>PDBTitle:</b> staphyloferrin b precursor biosynthetic enzyme sbnb bound to citrate2 and nad+
59	<a href="#">d1h6da1</a>	Alignment	not modelled	18.4	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
60	<a href="#">d1jqra_</a>	Alignment	not modelled	18.1	26	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
61	<a href="#">c3pq1B_</a>	Alignment	not modelled	17.9	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> poly(a) rna polymerase; <b>PDBTitle:</b> crystal structure of human mitochondrial poly(a) polymerase (papd1)
62	<a href="#">c5wu6B_</a>	Alignment	not modelled	17.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> speckle targeted pip5k1a-regulated poly(a) polymerase; <b>PDBTitle:</b> crystal structure of apo human tut1, form iv
63	<a href="#">c5a2zB_</a>	Alignment	not modelled	17.6	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mitochondrial protein; <b>PDBTitle:</b> crystal structure of mtpap in complex with gtp
64	<a href="#">c6bqiA_</a>	Alignment	not modelled	17.6	19	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> protein impact homolog; <b>PDBTitle:</b> structure of two-domain translational regulator yih1 reveals a2 possible mechanism of action
65	<a href="#">c3ceaA_</a>	Alignment	not modelled	16.6	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
66	<a href="#">d2cvea1</a>	Alignment	not modelled	16.6	44	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> YigZ N-terminal domain-like
67	<a href="#">d1f99a_</a>	Alignment	not modelled	16.3	15	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
68	<a href="#">c8iczA_</a>	Alignment	not modelled	16.3	15	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase beta (e.c.2.7.7.7)); <b>PDBTitle:</b> dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
69	<a href="#">d2nvwa1</a>	Alignment	not modelled	16.0	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
70	<a href="#">c5uibA_</a>	Alignment	not modelled	15.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase protein; <b>PDBTitle:</b> crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
71	<a href="#">c3f2eA_</a>	Alignment	not modelled	15.9	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> svrv coat protein; <b>PDBTitle:</b> crystal structure of yellowstone svrv coat protein c-terminus
72	<a href="#">c2gixD_</a>	Alignment	not modelled	15.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,5-anhydro-d-fructose reductase; <b>PDBTitle:</b> crystal structure analysis of bacterial 1,5-af reductase
73	<a href="#">d1qmga2</a>	Alignment	not modelled	15.1	42	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
74	<a href="#">c3uuwB_</a>	Alignment	not modelled	14.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase with nad(p)-binding rossmann-fold <b>PDBTitle:</b> 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
75	<a href="#">c3nt5B_</a>	Alignment	not modelled	14.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
76	<a href="#">c6ajrA_</a>	Alignment	not modelled	14.5	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uracil dna glycosylase superfamily protein; <b>PDBTitle:</b> complex form of uracil dna glycosylase x and uracil
77	<a href="#">d1r8ka_</a>	Alignment	not modelled	14.3	23	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> PdxA-like
						<b>PDB header:</b> transferase

78	<a href="#">c2q0dA</a>	Alignment	not modelled	13.9	14	<b>Chain:</b> A; <b>PDB Molecule:</b> rna uridylyl transferase; <b>PDBTitle:</b> terminal uridylyl transferase 4 from trypanosoma brucei with bound atp
79	<a href="#">d1p1xa</a>	Alignment	not modelled	13.8	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
80	<a href="#">c5muul</a>	Alignment	not modelled	13.6	17	<b>PDB header:</b> virus <b>Chain:</b> I; <b>PDB Molecule:</b> major outer capsid protein; <b>PDBTitle:</b> dsrna bacteriophage phi6 nucleocapsid
81	<a href="#">c2ihmA</a>	Alignment	not modelled	13.6	14	<b>PDB header:</b> transferase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> dna polymerase mu; <b>PDBTitle:</b> polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
82	<a href="#">c4zbzA</a>	Alignment	not modelled	13.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> family 4 uracil-dna glycosylase from sulfolobus tokodaii (free form, 2 x-ray wavelength=1.5418)
83	<a href="#">d2fi0a1</a>	Alignment	not modelled	13.4	13	<b>Fold:</b> SP0561-like <b>Superfamily:</b> SP0561-like <b>Family:</b> SP0561-like
84	<a href="#">c1evjC</a>	Alignment	not modelled	13.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
85	<a href="#">c4xbsA</a>	Alignment	not modelled	13.0	41	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> 2-deoxyribose-5-phosphate aldolase mutant - e78k
86	<a href="#">c2bn5A</a>	Alignment	not modelled	12.8	26	<b>PDB header:</b> nuclear protein <b>Chain:</b> A; <b>PDB Molecule:</b> psi; <b>PDBTitle:</b> p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
87	<a href="#">d1phna</a>	Alignment	not modelled	12.5	8	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
88	<a href="#">d1jboa</a>	Alignment	not modelled	12.2	16	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
89	<a href="#">c2n5xA</a>	Alignment	not modelled	12.2	50	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> hsp90 co-chaperone cdc37; <b>PDBTitle:</b> c-terminal domain of cdc37 cochaperone
90	<a href="#">c5wu5C</a>	Alignment	not modelled	12.1	19	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> speckle targeted pip5k1a-regulated poly(a) polymerase; <b>PDBTitle:</b> crystal structure of apo human tut1, form iii
91	<a href="#">c2ho3D</a>	Alignment	not modelled	11.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
92	<a href="#">d1cpca</a>	Alignment	not modelled	11.1	14	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
93	<a href="#">c3r66A</a>	Alignment	not modelled	11.0	13	<b>PDB header:</b> viral protein/antiviral protein <b>Chain:</b> A; <b>PDB Molecule:</b> non-structural protein 1; <b>PDBTitle:</b> crystal structure of human isg15 in complex with ns1 n-terminal region2 from influenza virus b, northeast structural genomics consortium3 target ids hx6481, hr2873, and or2
94	<a href="#">d1xeqa1</a>	Alignment	not modelled	10.9	13	<b>Fold:</b> S15/NS1 RNA-binding domain <b>Superfamily:</b> S15/NS1 RNA-binding domain <b>Family:</b> N-terminal, RNA-binding domain of nonstructural protein NS1
95	<a href="#">c5e4rA</a>	Alignment	not modelled	10.8	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of domain-duplicated synthetic class ii ketol-acid2 reductoisomerase 2ia_kari-dd
96	<a href="#">c2bn6A</a>	Alignment	not modelled	10.8	28	<b>PDB header:</b> nuclear protein <b>Chain:</b> A; <b>PDB Molecule:</b> psi; <b>PDBTitle:</b> p-element somatic inhibitor protein
97	<a href="#">c5ncaA</a>	Alignment	not modelled	10.7	33	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> competence protein comgc; <b>PDBTitle:</b> solution structure of comgc from streptococcus pneumoniae
98	<a href="#">d1aora1</a>	Alignment	not modelled	10.5	9	<b>Fold:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains <b>Superfamily:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains <b>Family:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains
99	<a href="#">c3o3nA</a>	Alignment	not modelled	10.4	10	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; <b>PDBTitle:</b> (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa