



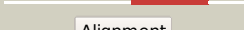

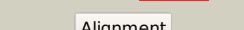




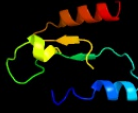


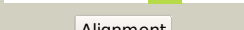

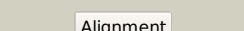
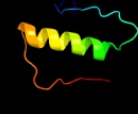
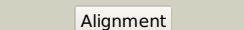




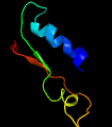





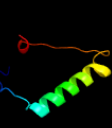



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3081 (-) _3446037_3447275
Date	Thu Aug 8 16:20:25 BST 2019
Unique Job ID	11fff342f79d8916

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5uvdA_</a>	 Alignment		99.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> nucleotidyltransferase-like protein; <b>PDBTitle:</b> crystal structure of an antigenic nucleotidyltransferase-like protein2 from paracoccidioides brasiliensis
2	<a href="#">c4e8iA_</a>	 Alignment		98.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> lincosamide resistance protein; <b>PDBTitle:</b> crystal structure of lincosamide antibiotic adenylyltransferase lina,2 apo
3	<a href="#">c4ok0B_</a>	 Alignment		97.6	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> putative; <b>PDBTitle:</b> crystal structure of putative nucleotidyltransferase from h. pylori
4	<a href="#">c4wqkA_</a>	 Alignment		95.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 2"-aminoglycoside nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of aminoglycoside nucleotidyltransferase ant(2")-2 ia, apo form
5	<a href="#">c3h37B_</a>	 Alignment		78.5	22	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> trna nucleotidyl transferase-related protein; <b>PDBTitle:</b> the structure of cca-adding enzyme apo form i
6	<a href="#">d1ccwa_</a>	 Alignment		73.0	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
7	<a href="#">d1miwa2</a>	 Alignment		68.3	26	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
8	<a href="#">d1ou5a2</a>	 Alignment		65.8	19	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
9	<a href="#">d1ig3a2</a>	 Alignment		62.6	20	<b>Fold:</b> Thiamin pyrophosphokinase, catalytic domain <b>Superfamily:</b> Thiamin pyrophosphokinase, catalytic domain <b>Family:</b> Thiamin pyrophosphokinase, catalytic domain
10	<a href="#">c2yn2A_</a>	 Alignment		62.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein ynl108c; <b>PDBTitle:</b> huf protein - paralogue of the tau55 histidine phosphatase domain
11	<a href="#">c2yn0A_</a>	 Alignment		61.8	30	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcription factor tau 55 kda subunit; <b>PDBTitle:</b> tau55 histidine phosphatase domain

12	<a href="#">c4oi6A_</a>	Alignment		59.4	26	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nickel responsive protein; <b>PDBTitle:</b> crystal structure analysis of nickel-bound form sco4226 from2 streptomyces coelicolor a3(2)
13	<a href="#">c1miyB_</a>	Alignment		55.5	26	<b>PDB header:</b> translation, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna cca-adding enzyme; <b>PDBTitle:</b> crystal structure of bacillus stearothermophilus cca-adding enzyme in2 complex with ctp
14	<a href="#">c2f17A_</a>	Alignment		54.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase 1; <b>PDBTitle:</b> mouse thiamin pyrophosphokinase in a ternary complex with2 pyrithiamin pyrophosphate and amp at 2.5 angstrom
15	<a href="#">c1xrsB_</a>	Alignment		49.6	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-lysine 5,6-aminomutase beta subunit; <b>PDBTitle:</b> crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
16	<a href="#">d2bccqa3</a>	Alignment		49.4	13	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
17	<a href="#">c4q6tA_</a>	Alignment		49.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase, family 18; <b>PDBTitle:</b> the crystal structure of a class v chitinase from pseudomonas2 fluorescens pf-5
18	<a href="#">c2hroA_</a>	Alignment		47.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
19	<a href="#">c3k35D_</a>	Alignment		45.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> crystal structure of human sirt6
20	<a href="#">c2qm3A_</a>	Alignment		44.8	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted methyltransferase; <b>PDBTitle:</b> crystal structure of a predicted methyltransferase from pyrococcus2 furiosus
21	<a href="#">c6q52A_</a>	Alignment	not modelled	44.8	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cca-adding enzyme; <b>PDBTitle:</b> structure of a psychrophilic cca-adding enzyme in complex with cmpcpp2 at room temperature in chipx microfluidic device
22	<a href="#">c1hivA_</a>	Alignment	not modelled	41.5	23	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
23	<a href="#">c4x4wB_</a>	Alignment	not modelled	41.3	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cca trna nucleotidyltransferase 1, mitochondrial; <b>PDBTitle:</b> crystal structure of the full-length human mitochondrial cca-adding2 enzyme
24	<a href="#">d2b4va2</a>	Alignment	not modelled	41.2	15	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> RNA editing terminal uridyl transferase 2, RET2, catalytic domain
25	<a href="#">c5d50I_</a>	Alignment	not modelled	39.9	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> repressor; <b>PDBTitle:</b> crystal structure of rep-ant complex from salmonella-temperate phage
26	<a href="#">d7rega2</a>	Alignment	not modelled	39.2	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
27	<a href="#">c6j27D_</a>	Alignment	not modelled	37.2	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n(4)-bis(aminopropyl)spermidine synthase; <b>PDBTitle:</b> crystal structure of the branched-chain polyamine synthase from2 thermus thermophilus (tth-bpsa) in complex with n4-3 aminopropylspermidine and 5'-methylthioadenosine
						<b>PDB header:</b> translation, transferase

28	<a href="#">c1ou5A_</a>	Alignment	not modelled	36.6	21	<b>Chain:</b> A: <b>PDB Molecule:</b> trna cca-adding enzyme; <b>PDBTitle:</b> crystal structure of human cca-adding enzyme
29	<a href="#">d1vfga2</a>	Alignment	not modelled	36.3	13	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
30	<a href="#">c3e0bA_</a>	Alignment	not modelled	36.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> bacillus anthracis dihydrofolate reductase complexed with nadph and 2,2 4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b)
31	<a href="#">d1wvfa2</a>	Alignment	not modelled	36.0	20	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> FAD-linked oxidases, N-terminal domain
32	<a href="#">c6gioB_</a>	Alignment	not modelled	35.5	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> amino acid amide racemase; <b>PDBTitle:</b> structure of amino acid amide racemase from ochrobactrum anthropi
33	<a href="#">c2hh9A_</a>	Alignment	not modelled	34.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> thiamin pyrophosphokinase from candida albicans
34	<a href="#">c3pkfF_</a>	Alignment	not modelled	34.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> human sirt6 crystal structure in complex with adp ribose
35	<a href="#">c1z7dE_</a>	Alignment	not modelled	33.5	10	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase py00104 from plasmodium yoelii
36	<a href="#">d1rxwa1</a>	Alignment	not modelled	32.8	44	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
37	<a href="#">c3vcoA_</a>	Alignment	not modelled	32.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> schistosoma mansoni dihydrofolate reductase
38	<a href="#">c3aqaA_</a>	Alignment	not modelled	31.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(a) polymerase; <b>PDBTitle:</b> complex structure of bacterial protein (apo form ii)
39	<a href="#">d1p9qc1</a>	Alignment	not modelled	30.9	21	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> Hypothetical protein AF0491, middle domain <b>Family:</b> Hypothetical protein AF0491, middle domain
40	<a href="#">c3c7tB_</a>	Alignment	not modelled	29.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ecdysteroid-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
41	<a href="#">d1jmsa4</a>	Alignment	not modelled	29.8	22	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
42	<a href="#">c5lhaC_</a>	Alignment	not modelled	29.2	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> omega transaminase; <b>PDBTitle:</b> amine transaminase crystal structure from an uncultivated pseudomonas2 species in the pmp-bound form
43	<a href="#">c1sz1A_</a>	Alignment	not modelled	29.2	19	<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
44	<a href="#">d1knva2</a>	Alignment	not modelled	28.7	17	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
45	<a href="#">c2e1mA_</a>	Alignment	not modelled	27.2	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
46	<a href="#">d1xrsb1</a>	Alignment	not modelled	26.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
47	<a href="#">c4a0rB_</a>	Alignment	not modelled	26.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
48	<a href="#">c3wfsC_</a>	Alignment	not modelled	26.5	19	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 3
49	<a href="#">c3jtwB_</a>	Alignment	not modelled	26.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> crystal structure of putative dihydrofolate reductase (yp_805003.1)2 from pediococcus pentosaceus atcc 25745 at 1.90 a resolution
50	<a href="#">c3wfgE_</a>	Alignment	not modelled	26.0	21	<b>PDB header:</b> transferase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 1
51	<a href="#">c3imlB_</a>	Alignment	not modelled	25.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
52	<a href="#">d1mxaa2</a>	Alignment	not modelled	25.6	18	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
53	<a href="#">c2ze5A_</a>	Alignment	not modelled	25.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isopentenyl transferase; <b>PDBTitle:</b> crystal structure of adenosine phosphate-isopentenyltransferase <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylornithine/succinyldiaminopimelate

54	<a href="#">c2pb2B</a>	Alignment	not modelled	25.3	12	aminotransferase; <b>PDBTitle:</b> structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
55	<a href="#">c3wfrF</a>	Alignment	not modelled	25.3	29	<b>PDB header:</b> transferase/rna <b>Chain:</b> F: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
56	<a href="#">d3dfra</a>	Alignment	not modelled	25.1	25	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
57	<a href="#">c3d4iD</a>	Alignment	not modelled	24.9	35	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sts-2 protein; <b>PDBTitle:</b> crystal structure of the 2h-phosphatase domain of sts-2
58	<a href="#">c1qysA</a>	Alignment	not modelled	24.4	25	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> top7; <b>PDBTitle:</b> crystal structure of top7: a computationally designed2 protein with a novel fold
59	<a href="#">c3wfrE</a>	Alignment	not modelled	24.4	25	<b>PDB header:</b> transferase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
60	<a href="#">d1a77a1</a>	Alignment	not modelled	24.1	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
61	<a href="#">c2w8wA</a>	Alignment	not modelled	24.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
62	<a href="#">c2hwgA</a>	Alignment	not modelled	23.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
63	<a href="#">c2rdsA</a>	Alignment	not modelled	23.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- <b>PDBTitle:</b> crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
64	<a href="#">c3ia5A</a>	Alignment	not modelled	23.4	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> moritella profunda dihydrofolate reductase (dhfr)
65	<a href="#">c3wfgH</a>	Alignment	not modelled	23.4	19	<b>PDB header:</b> transferase/rna <b>Chain:</b> H: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 1
66	<a href="#">c3w6kC</a>	Alignment	not modelled	23.4	19	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> scpb; <b>PDBTitle:</b> crystal structure of dimer of scpb n-terminal domain complexed with2 scpa peptide
67	<a href="#">c3wfoB</a>	Alignment	not modelled	23.3	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme (apo form 1)
68	<a href="#">c3wfpA</a>	Alignment	not modelled	23.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme (apo form 2)
69	<a href="#">d1ig0a2</a>	Alignment	not modelled	22.8	21	<b>Fold:</b> Thiamin pyrophosphokinase, catalytic domain <b>Superfamily:</b> Thiamin pyrophosphokinase, catalytic domain <b>Family:</b> Thiamin pyrophosphokinase, catalytic domain
70	<a href="#">c3i5tB</a>	Alignment	not modelled	22.5	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
71	<a href="#">c4iw7A</a>	Alignment	not modelled	22.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-amino-7-oxononanoate synthase; <b>PDBTitle:</b> crystal structure of 8-amino-7-oxononanoate synthase (biof) from2 francisella tularensis.
72	<a href="#">c3dxvA</a>	Alignment	not modelled	22.1	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amino-epsilon-caprolactam racemase; <b>PDBTitle:</b> the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
73	<a href="#">d1wota</a>	Alignment	not modelled	21.9	21	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase
74	<a href="#">c3cseA</a>	Alignment	not modelled	21.6	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> candida glabrata dihydrofolate reductase complexed with nadph and 2,4-2 diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b)
75	<a href="#">c3hjeA</a>	Alignment	not modelled	21.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 704aa long hypothetical glycosyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus tokodaii hypothetical maltooligosyl2 trehalose synthase
76	<a href="#">c2jvfA</a>	Alignment	not modelled	21.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo protein m7; <b>PDBTitle:</b> solution structure of m7, a computationally-designed2 artificial protein
77	<a href="#">d1ohea2</a>	Alignment	not modelled	21.0	22	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
78	<a href="#">c3tq8A</a>	Alignment	not modelled	20.9	26	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> structure of the dihydrofolate reductase (foia) from coxiella burnetii2 in complex with trimethoprim
79	<a href="#">c1vfoB</a>	Alignment	not modelled	20.5	13	<b>PDB header:</b> transferase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> poly a polymerase;

79	<a href="#">c1vlgB_</a>	Alignment	not modelled	20.5	13	<b>PDBTitle:</b> crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog <b>PDB header:</b> ligase
80	<a href="#">c3vmmA_</a>	Alignment	not modelled	20.5	12	<b>Chain:</b> A: <b>PDB Molecule:</b> alanine-anticapsin ligase bacd; <b>PDBTitle:</b> crystal structure of bacd, an l-amino acid dipeptide ligase from2 bacillus subtilis
81	<a href="#">c1ig0A_</a>	Alignment	not modelled	20.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> crystal structure of yeast thiamin pyrophosphokinase
82	<a href="#">c4q2uM_</a>	Alignment	not modelled	19.9	21	<b>PDB header:</b> toxin/toxin repressor <b>Chain:</b> M: <b>PDB Molecule:</b> antitoxin dinj; <b>PDBTitle:</b> crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
83	<a href="#">c2ihmA_</a>	Alignment	not modelled	19.1	11	<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
84	<a href="#">d8dfra_</a>	Alignment	not modelled	19.0	21	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
85	<a href="#">c2bg5C_</a>	Alignment	not modelled	18.8	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoenolpyruvate-protein kinase; <b>PDBTitle:</b> crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
86	<a href="#">d2fmpa3</a>	Alignment	not modelled	18.8	11	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
87	<a href="#">d1fmfa_</a>	Alignment	not modelled	18.5	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
88	<a href="#">c4s3nA_</a>	Alignment	not modelled	18.5	26	<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
89	<a href="#">c3fcrA_</a>	Alignment	not modelled	18.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
90	<a href="#">c3wfsD_</a>	Alignment	not modelled	18.1	15	<b>PDB header:</b> transferase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 3
91	<a href="#">d1e8ga2</a>	Alignment	not modelled	17.6	10	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> FAD-linked oxidases, N-terminal domain
92	<a href="#">c3wfgG_</a>	Alignment	not modelled	17.6	21	<b>PDB header:</b> transferase/rna <b>Chain:</b> G: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 1
93	<a href="#">c3nybA_</a>	Alignment	not modelled	17.4	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
94	<a href="#">c4ky3A_</a>	Alignment	not modelled	17.2	25	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein or327; <b>PDBTitle:</b> three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327
95	<a href="#">c1zdrB_</a>	Alignment	not modelled	17.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> dhfr from bacillus stearothermophilus
96	<a href="#">c2jerG_</a>	Alignment	not modelled	17.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> agmatine deiminase; <b>PDBTitle:</b> agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
97	<a href="#">c1rg9D_</a>	Alignment	not modelled	17.0	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> s-adenosylmethionine synthetase complexed with sam and ppnp
98	<a href="#">c3c37B_</a>	Alignment	not modelled	17.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase, m48 family; <b>PDBTitle:</b> x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
99	<a href="#">c4atpD_</a>	Alignment	not modelled	17.0	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-aminobutyrate transaminase; <b>PDBTitle:</b> structure of gaba-transaminase a1r958 from arthrobacter aureescens in2 complex with plp