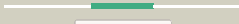
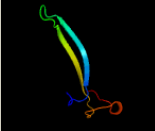
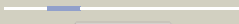




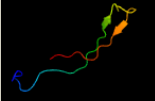







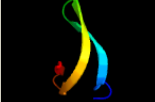









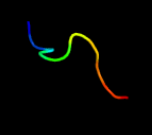




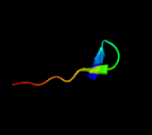


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3243c_(-)_3622246_3623088
Date	Thu Aug 8 16:20:44 BST 2019
Unique Job ID	4b5b8184451b70f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1q42a_	 Alignment		40.6	33	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
2	d1h54a2	 Alignment		27.1	18	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Glycosyltransferase family 36 N-terminal domain
3	c2ka4B_	 Alignment		26.4	67	PDB header: transcription regulator Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: nmr structure of the cbp-taz1/stat2-tad complex
4	c3a10B_	 Alignment		26.0	21	PDB header: ligase/rna Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
5	d1qnia1	 Alignment		25.5	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
6	c2g5iB_	 Alignment		25.1	13	PDB header: ligase Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase PDBTitle: structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
7	d2f2ab2	 Alignment		24.0	13	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: GatB/GatE catalytic domain-like
8	d1n9ra_	 Alignment		19.7	19	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
9	c3iv6C_	 Alignment		17.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: putative zn-dependent alcohol dehydrogenase; PDBTitle: crystal structure of putative zn-dependent alcohol dehydrogenases from2 rhodobacter sphaeroides.
10	c3ip4B_	 Alignment		15.5	30	PDB header: ligase Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: the high resolution structure of gatcab
11	c3h0mE_	 Alignment		15.0	50	PDB header: ligase Chain: E: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus

12	c1wu2B_	Alignment		14.5	17	PDB header: structural genomics,biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis moea protein; PDBTitle: crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
13	c4wj3K_	Alignment		14.1	40	PDB header: ligase/rna Chain: K: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
14	c3kfuL_	Alignment		13.9	40	PDB header: ligase/rna Chain: I: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the transamidosome
15	c4n0iB_	Alignment		13.8	30	PDB header: ligase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit b, PDBTitle: crystal structure of s. cerevisiae mitochondrial gatfab in complex2 with glutamine
16	c4wj3H_	Alignment		13.7	40	PDB header: ligase/rna Chain: H: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
17	c4wj3E_	Alignment		13.7	40	PDB header: ligase/rna Chain: E: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
18	c4wj3B_	Alignment		13.7	40	PDB header: ligase/rna Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
19	c3kfuF_	Alignment		13.4	40	PDB header: ligase/rna Chain: F: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the transamidosome
20	c4wwuD_	Alignment		13.3	29	PDB header: transport protein Chain: D: PDB Molecule: mrna export factor mex67; PDBTitle: structure of mex67:mtr2
21	c5g2rA_	Alignment	not modelled	13.3	21	PDB header: transferase Chain: A: PDB Molecule: molybdopterin biosynthesis protein cnx1; PDBTitle: crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
22	c2ogsA_	Alignment	not modelled	12.8	20	PDB header: hydrolase Chain: A: PDB Molecule: thermostable carboxylesterase est50; PDBTitle: crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2
23	d2d6fc3	Alignment	not modelled	12.2	15	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: GatB/GatE catalytic domain-like
24	c5nbbA_	Alignment	not modelled	12.2	28	PDB header: chaperone Chain: A: PDB Molecule: rna chaperone proq; PDBTitle: structure of the c-terminal domain of the escherichia coli proq rna2 binding protein
25	c1n9sH_	Alignment	not modelled	11.2	17	PDB header: translation Chain: H: PDB Molecule: small nuclear ribonucleoprotein f; PDBTitle: crystal structure of yeast smf in spacegroup p43212
26	d1xi8a3	Alignment	not modelled	10.9	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
27	c2qm3A_	Alignment	not modelled	10.5	19	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of a predicted methyltransferase from pyrococcus2 furiosus
28	d2nqra3	Alignment	not modelled	10.3	28	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
						Fold: Dihydrofolate reductase-like

29	d1j3ka_	Alignment	not modelled	10.3	33	Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
30	c3cseA_	Alignment	not modelled	9.9	47	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: candida glabrata dihydrofolate reductase complexed with nadph and 2,4-2 diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b)
31	c6j9mB_	Alignment	not modelled	9.8	13	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: acriic2; PDBTitle: nmebh+acriic2
32	c1b9uA_	Alignment	not modelled	9.8	50	PDB header: hydrolase Chain: A: PDB Molecule: protein (atp synthase); PDBTitle: membrane domain of the subunit b of the e.coli atp synthase
33	c3rg9A_	Alignment	not modelled	9.6	33	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: trypanosoma brucei dihydrofolate reductase (tdhfr) in complex with2 wr99210
34	c4c92B_	Alignment	not modelled	9.0	24	PDB header: transcription Chain: B: PDB Molecule: u6 snrna-associated sm-like protein lsm2; PDBTitle: crystal structure of the yeast lsm1-7 complex
35	c3dg8B_	Alignment	not modelled	8.9	33	PDB header: oxidoreductase, transferase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: quadruple mutant (n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase (pfdhfr-ts) complexed3 with rjf670, nadph, and dump
36	d1qe3a_	Alignment	not modelled	8.9	33	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
37	c6drsA_	Alignment	not modelled	8.5	27	PDB header: antifungal protein/inhibitor Chain: A: PDB Molecule: dihydrofolate reductase, putative; PDBTitle: dihydrofolate reductase (dhfr) of aspergillus flavus in complex with a2 small molecule inhibitor
38	c2blcA_	Alignment	not modelled	8.4	40	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: sp21 double mutant p. vivax dihydrofolate reductase in complex with2 des-chloropyrimethamine
39	c3dh0B_	Alignment	not modelled	8.1	27	PDB header: transferase Chain: B: PDB Molecule: sam dependent methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 aquifex aeolicus
40	d1zq1c3	Alignment	not modelled	7.9	20	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: GatB/GatE catalytic domain-like
41	c6ghbB_	Alignment	not modelled	7.3	23	PDB header: protein binding Chain: B: PDB Molecule: upf0413 protein gk0824; PDBTitle: crystal structure of spx in complex with yjbh (oxidized)
42	d1ehia1	Alignment	not modelled	7.2	36	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
43	d1gtda_	Alignment	not modelled	7.0	14	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
44	c1z8yE_	Alignment	not modelled	6.8	22	PDB header: virus Chain: E: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
45	c2gidP_	Alignment	not modelled	6.7	21	PDB header: translation Chain: P: PDB Molecule: mitochondrial rna-binding protein 2; PDBTitle: crystal structures of trypanosoma brucei mrp1/mrp2
46	d2giaa1	Alignment	not modelled	6.6	21	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Guide RNA binding protein gBP
47	d1i8fa_	Alignment	not modelled	6.6	29	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
48	c2dgbA_	Alignment	not modelled	6.3	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein purs; PDBTitle: structure of thermus thermophilus purs in the p21 form
49	d1wu2a3	Alignment	not modelled	6.2	21	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
50	c1ld4O_	Alignment	not modelled	6.1	22	PDB header: virus Chain: O: PDB Molecule: spike glycoprotein e1; PDBTitle: placement of the structural proteins in sindbis virus
51	d1t4aa_	Alignment	not modelled	6.0	41	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
52	c2d6fC_	Alignment	not modelled	5.9	14	PDB header: ligase/rna Chain: C: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit e; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
53	c5x7hA_	Alignment	not modelled	5.9	40	PDB header: transferase Chain: A: PDB Molecule: cycloisomaltooligosaccharide glucanotransferase; PDBTitle: crystal structure of paenibacillus sp. 598k2 cycloisomaltooligosaccharide glucanotransferase complexed with3 cycloisomaltoheptaose
						Fold: S-adenosyl-L-methionine-dependent methyltransferases

54	d1p1ca_	Alignment	not modelled	5.9	32	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
55	c2xfbF_	Alignment	not modelled	5.7	12	PDB header: virus Chain: F: PDB Molecule: e1 envelope glycoprotein; PDBTitle: the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map
56	c3n42F_	Alignment	not modelled	5.6	12	PDB header: viral protein Chain: F: PDB Molecule: e1 envelope glycoprotein; PDBTitle: crystal structures of the mature envelope glycoprotein complex (furin2 cleavage) of chikungunya virus.
57	c2xfcD_	Alignment	not modelled	5.5	12	PDB header: virus Chain: D: PDB Molecule: e1 envelope glycoprotein; PDBTitle: the chikungunya e1 e2 envelope glycoprotein complex fit into2 the semliki forest virus cryo-em map
58	c3muwE_	Alignment	not modelled	5.5	22	PDB header: virus Chain: E: PDB Molecule: structural polyprotein; PDBTitle: pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
59	d1e4ea1	Alignment	not modelled	5.5	29	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
60	d1juva_	Alignment	not modelled	5.4	33	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
61	c5cohA_	Alignment	not modelled	5.2	29	PDB header: oxidoreductase Chain: A: PDB Molecule: frne protein; PDBTitle: crystal structure of a novel disulfide oxidoreductase from deinococcus2 radiodurans crystallized in presence of beta-mercaptoethanol
62	c6q2zB_	Alignment	not modelled	5.2	43	PDB header: unknown function Chain: B: PDB Molecule: upf0339 family protein; PDBTitle: nmr solution structure of the hvo_2922 protein from haloferax volcanii
63	c2yx5A_	Alignment	not modelled	5.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0062 protein mj1593; PDBTitle: crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
64	d1fwxa1	Alignment	not modelled	5.0	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin