


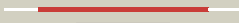

















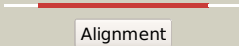

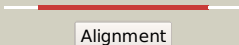


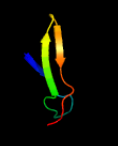
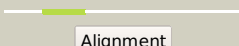

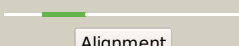

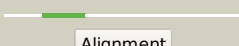

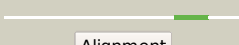
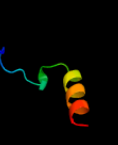



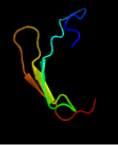




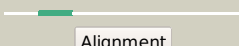
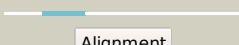
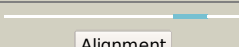



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0357c_purA_435472_436770
Date	Tue Jul 23 14:50:42 BST 2019
Unique Job ID	9b951a72fe81a2a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qf5a_	 Alignment		100.0	51	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
2	d1dj3a_	 Alignment		100.0	46	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
3	d1dj2a_	 Alignment		100.0	44	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
4	d1iwea_	 Alignment		100.0	44	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
5	c1iweB_	 Alignment		100.0	44	PDB header: ligase Chain: B: PDB Molecule: adenylosuccinate synthetase; PDBTitle: imp complex of the recombinant mouse-muscle adenylosuccinate2 synthetase
6	d1p9ba_	 Alignment		100.0	41	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
7	c4m0gB_	 Alignment		100.0	49	PDB header: ligase Chain: B: PDB Molecule: adenylosuccinate synthetase; PDBTitle: the crystal structure of an adenylosuccinate synthetase from bacillus2 anthracis str. ames ancestor.
8	c5i34B_	 Alignment		100.0	43	PDB header: ligase Chain: B: PDB Molecule: adenylosuccinate synthetase; PDBTitle: adenylosuccinate synthetase from cryptococcus neoformans complexed2 with gdp and imp
9	c3ue9A_	 Alignment		100.0	46	PDB header: ligase Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of adenylosuccinate synthetase (ampsase) (pura) from2 burkholderia thailandensis
10	c3r7tA_	 Alignment		100.0	45	PDB header: ligase Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of adenylosuccinate synthetase from campylobacter2 jejuni
11	c6bs7A_	 Alignment		100.0	46	PDB header: ligase Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of adenylosuccinate synthetase from legionella2 pneumophila philadelphia 1

12	c2d7uA_	 Alignment		100.0	43	PDB header: ligase Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of hypothetical adenylosuccinate synthetase, ph04382 from pyrococcus horikoshii ot3
13	c6fm0A_	 Alignment		100.0	27	PDB header: biosynthetic protein Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: deoxyguanylosuccinate synthase (dgss) and atp structure at 1.72 angstrom resolution
14	d1a0ia1	 Alignment		89.4	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
15	c3knuD_	 Alignment		68.1	17	PDB header: transferase Chain: D: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
16	d1p9pa_	 Alignment		59.1	21	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
17	d1uala_	 Alignment		55.8	22	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
18	c1zgxA_	 Alignment		51.3	29	PDB header: hydrolase Chain: A: PDB Molecule: guanyl-specific ribonuclease sa; PDBTitle: crystal structure of ribonuclease mutant
19	d1qwda_	 Alignment		48.1	19	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
20	d2f09a1	 Alignment		45.5	16	Fold: Streptavidin-like Superfamily: YdhA-like Family: YdhA-like
21	c3b9qA_	 Alignment	not modelled	44.6	32	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpfts5 from arabidopsis thaliana
22	c5wyrA_	 Alignment	not modelled	44.1	23	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure and catalytic mechanism of the essential m1g37 trna2 methyltransferase trmd from pseudomonas aeruginosa
23	c4lfmA_	 Alignment	not modelled	42.2	12	PDB header: isomerase Chain: A: PDB Molecule: galactose-6-phosphate isomerase subunit a; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with d-psicose
24	c5knnG_	 Alignment	not modelled	41.8	20	PDB header: ligase Chain: G: PDB Molecule: alanine--trna ligase, cytoplasmic; PDBTitle: evolutionary gain of alanine mischarging to non-cognate trnas with a2 g4:u69 base pair
25	c4txwA_	 Alignment	not modelled	41.2	31	PDB header: carbohydrate-binding module Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure of cbm32-4 from the clostridium perfringens nagh
26	c3ky7A_	 Alignment	not modelled	38.8	19	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mr5a252
27	c5l3sF_	 Alignment	not modelled	38.0	27	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
		 Alignment				PDB header: protein transport

28	c1zu4A_	Alignment	not modelled	37.3	28	Chain: A: PDB Molecule: ftsyl; PDBTitle: crystal structure of ftsyl from mycoplasma mycoides-space2 group p21212
29	c2qy9A_	Alignment	not modelled	36.7	27	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
30	c3dmdA_	Alignment	not modelled	36.1	25	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
31	c1oy5B_	Alignment	not modelled	35.8	16	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
32	d1oy5a_	Alignment	not modelled	35.8	16	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
33	c2og2A_	Alignment	not modelled	35.0	32	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
34	c4ak9A_	Alignment	not modelled	35.0	27	PDB header: protein transport Chain: A: PDB Molecule: cpftsyl; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
35	d1j8yf2	Alignment	not modelled	34.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
36	c2xf4A_	Alignment	not modelled	32.8	16	PDB header: hydrolase Chain: A: PDB Molecule: hydroxyacylglutathione hydrolase; PDBTitle: crystal structure of salmonella enterica serovar2 typhimurium ycb1
37	c3iefA_	Alignment	not modelled	32.2	22	PDB header: transferase, rna binding protein Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna guanine-n1-methyltransferase from bartonella2 henselae using mpcs.
38	c2q9cA_	Alignment	not modelled	31.7	29	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmpnp with mgcl complex
39	c1j8yf_	Alignment	not modelled	31.5	16	PDB header: signaling protein Chain: F: PDB Molecule: signal recognition 54 kda protein; PDBTitle: signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
40	c3opyE_	Alignment	not modelled	31.0	15	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
41	c5mu4A_	Alignment	not modelled	30.3	14	PDB header: viral protein Chain: A: PDB Molecule: tail tubular protein a; PDBTitle: tail tubular protein a of klebsiella pneumoniae bacteriophage kp32
42	c1vmaA_	Alignment	not modelled	29.9	32	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
43	c2yhsA_	Alignment	not modelled	29.5	28	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
44	d2jfga1	Alignment	not modelled	28.7	19	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
45	c6cy1B_	Alignment	not modelled	27.5	26	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
46	c3f6zB_	Alignment	not modelled	27.1	17	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pseudomonas aeruginosa mlic in complex2 with hen egg white lysozyme
47	c2cnwF_	Alignment	not modelled	26.4	30	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases fff and ftsy
48	c5l3rC_	Alignment	not modelled	25.8	35	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
49	d1lt7a_	Alignment	not modelled	25.8	32	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
50	d1iwpG_	Alignment	not modelled	25.4	16	Fold: Open three-helical up-and-down bundle Superfamily: Diol dehydratase, gamma subunit Family: Diol dehydratase, gamma subunit
51	c2qioA_	Alignment	not modelled	25.4	8	PDB header: unknown function Chain: A: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
52	d1oboa_	Alignment	not modelled	25.2	24	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
53	c4zjuA_	Alignment	not modelled	25.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nah]; PDBTitle: structure of a nah-dependent enoyl-acp reductase from

						acinetobacter2 baumannii in complex with nad
54	c3jugA_	Alignment	not modelled	24.9	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-mannanase; PDBTitle: crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
55	c1uc5M_	Alignment	not modelled	24.6	19	PDB header: lyase Chain: M: PDB Molecule: diol dehydrase gamma subunit; PDBTitle: structure of diol dehydratase complexed with (r)-1,2-2 propanediol
56	d1eexg_	Alignment	not modelled	24.6	19	Fold: Open three-helical up-and-down bundle Superfamily: Diol dehydratase, gamma subunit Family: Diol dehydratase, gamma subunit
57	c3ktsA_	Alignment	not modelled	23.6	17	PDB header: transcriptional regulator Chain: A: PDB Molecule: glycerol uptake operon antiterminator regulatory protein; PDBTitle: crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
58	c4adxl_	Alignment	not modelled	22.9	25	PDB header: ribosome Chain: I: PDB Molecule: aif6; PDBTitle: the cryo-em structure of the archaeal 50s ribosomal subunit in complex2 with initiation factor 6
59	d1qyia_	Alignment	not modelled	22.7	24	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
60	c3j4bB_	Alignment	not modelled	22.6	22	PDB header: viral protein Chain: B: PDB Molecule: tail tubular protein a; PDBTitle: structure of t7 gatekeeper protein (gp11)
61	c4dsdA_	Alignment	not modelled	22.2	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of a putative periplasmic protein (bacova_05534)2 from bacteroides ovatus atcc 8483 at 1.75 a resolution
62	c4em8A_	Alignment	not modelled	21.7	20	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
63	d1jsca3	Alignment	not modelled	20.9	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
64	c2px0D_	Alignment	not modelled	20.8	22	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmpnp/mg(2+)
65	d1g7oa1	Alignment	not modelled	19.9	14	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
66	d1lnia_	Alignment	not modelled	19.2	30	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Bacterial ribonucleases
67	d1k1ga_	Alignment	not modelled	19.1	21	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
68	c1uz4A_	Alignment	not modelled	19.1	30	PDB header: hydrolase Chain: A: PDB Molecule: man5a; PDBTitle: common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 itineraries for glucoside and mannoside hydrolysis
69	d1uuqa_	Alignment	not modelled	19.1	30	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
70	c2z2vA_	Alignment	not modelled	18.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
71	c4l6tA_	Alignment	not modelled	18.7	35	PDB header: hydrolase Chain: A: PDB Molecule: ecxa; PDBTitle: gm1 bound form of the ecx ab5 holotoxin
72	d1q44a_	Alignment	not modelled	18.0	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
73	c1yfsB_	Alignment	not modelled	17.9	15	PDB header: ligase Chain: B: PDB Molecule: alanyl-trna synthetase; PDBTitle: the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
74	c3quvB_	Alignment	not modelled	17.6	15	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
75	d1cora_	Alignment	not modelled	17.1	14	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
76	c4h3zA_	Alignment	not modelled	16.8	23	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a symmetric dimer of a trna (guanine-(n(1)-)-2 methyltransferase from burkholderia phymatum bound to s-adenosyl3 homocystein in both half-sites
77	d1fuea_	Alignment	not modelled	16.7	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
78	c3kpgA_	Alignment	not modelled	16.4	42	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfide-quinone reductase, putative; PDBTitle: crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone
79	c5mekA_	Alignment	not modelled	16.4	20	PDB header: transferase Chain: A: PDB Molecule: cytosolic sulfotransferase 18;

79	c1me6A	Alignment	not modelled	16.4	20	PDBTitle: sulphotransferase-18 from arabidopsis thaliana in complex with 3'-2 phosphoadenosine 5'-phosphate (pap)
80	d1msza	Alignment	not modelled	16.4	28	Fold: IF3-like Superfamily: R3H domain Family: R3H domain
81	c1mszA	Alignment	not modelled	16.4	28	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein smubp-2; PDBTitle: solution structure of the r3h domain from human smubp-2
82	c5a9q5	Alignment	not modelled	15.9	10	PDB header: transport protein Chain: 5: PDB Molecule: nuclear pore complex protein nup96; PDBTitle: human nuclear pore complex
83	c2wnfA	Alignment	not modelled	15.7	14	PDB header: transferase Chain: A: PDB Molecule: cmp-n-acetylneuraminate-beta-galactosamide-alpha- PDBTitle: crystal structure of a mammalian sialyltransferase in2 complex with gal-beta-1-3galnac-ortho-nitrophenol
84	c2ixaA	Alignment	not modelled	15.7	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase
85	c4hktA	Alignment	not modelled	15.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol 2-dehydrogenase; PDBTitle: crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
86	c1ujlA	Alignment	not modelled	15.0	25	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h PDBTitle: solution structure of the herg k+ channel s5-p2 extracellular linker
87	c2wfbA	Alignment	not modelled	14.9	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
88	d1y6ia1	Alignment	not modelled	14.8	78	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: GUN4-associated domain
89	d1nh2a1	Alignment	not modelled	14.7	14	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
90	c4js2A	Alignment	not modelled	14.6	22	PDB header: transferase Chain: A: PDB Molecule: beta-galactoside alpha-2,6-sialyltransferase 1; PDBTitle: crystal structure of human beta-galactoside alpha-2,6-2 sialyltransferase 1 in complex with cmp
91	d1qnaa1	Alignment	not modelled	14.6	15	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
92	c5x62A	Alignment	not modelled	14.6	20	PDB header: transferase Chain: A: PDB Molecule: carnosine n-methyltransferase; PDBTitle: crystal structure of a carnosine n-methyltransferase bound by adohcy
93	c2ovfA	Alignment	not modelled	14.6	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stal; PDBTitle: crystal structure of stal-pap complex
94	c2v3cC	Alignment	not modelled	14.5	22	PDB header: signaling protein Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
95	d2rbka1	Alignment	not modelled	14.5	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
96	c4xxlA	Alignment	not modelled	14.4	18	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c class i; PDBTitle: crystal structure of class 1 cytochrome mtod from sideroxydans2 lithotrophicus es-1
97	c6c04j	Alignment	not modelled	14.3	27	PDB header: transcription/dna Chain: J: PDB Molecule: rna polymerase-binding protein rbpa; PDBTitle: mtb rnap holo/rbpa/double fork dna -closed clamp
98	c3u3xl	Alignment	not modelled	14.0	15	PDB header: oxidoreductase Chain: J: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
99	d1fi4a2	Alignment	not modelled	13.8	67	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate 5-diphosphate decarboxylase