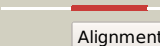









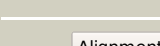

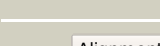
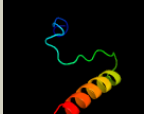
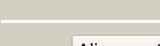









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2482c_(plsB2)_2786924_2789293
Date	Wed Aug 7 12:50:11 BST 2019
Unique Job ID	211154b3546d639e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kymA_	 Alignment		99.7	14	PDB header: transferase Chain: A: PDB Molecule: 1-acyl-sn-glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsc, from thermotoga maritima
2	c5f34A_	 Alignment		97.3	16	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannoside acyltransferase; PDBTitle: crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
3	d1iuqa_	 Alignment		96.5	15	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
4	c3no4A_	 Alignment		84.7	16	PDB header: hydrolase Chain: A: PDB Molecule: creatinine amidohydrolase; PDBTitle: crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
5	c5knkB_	 Alignment		59.4	11	PDB header: transferase Chain: B: PDB Molecule: lipid a biosynthesis lauroyl acyltransferase; PDBTitle: lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
6	d1t3la2	 Alignment		48.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
7	d1vyva2	 Alignment		45.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
8	d1vyua2	 Alignment		44.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
9	c4oydB_	 Alignment		43.1	23	PDB header: viral protein/inhibitor Chain: B: PDB Molecule: computationally designed inhibitor; PDBTitle: crystal structure of a computationally designed inhibitor of an2 epstein-barr viral bcl-2 protein
10	d1t0hb_	 Alignment		38.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
11	c4yyfC_	 Alignment		36.0	17	PDB header: hydrolase Chain: C: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of a glycosyl hydrolase of gh3 family member2 from [mycobacterium smegmatis str. mc2 155

12	d1sr8a_	Alignment		33.8	11	Fold: CbiD-like Superfamily: CbiD-like Family: CbiD-like
13	c3cfyA_	Alignment		33.4	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative luxo repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxo repressor2 protein from vibrio parahaemolyticus
14	c2h09A_	Alignment		33.4	16	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
15	d1wj5a_	Alignment		33.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: An Obfc1 domain
16	c1sfeA_	Alignment		32.8	33	PDB header: dna-binding protein Chain: A; PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
17	c3wo8B_	Alignment		32.8	21	PDB header: hydrolase Chain: B; PDB Molecule: beta-n-acetylglucosaminidase; PDBTitle: crystal structure of the beta-n-acetylglucosaminidase from thermotoga2 maritima
18	c4zyeA_	Alignment		32.3	33	PDB header: transferase Chain: A; PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
19	c1g3wA_	Alignment		31.4	16	PDB header: gene regulation Chain: A; PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
20	c4g6cA_	Alignment		31.3	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-hexosaminidase 1; PDBTitle: crystal structure of beta-hexosaminidase 1 from burkholderia2 cenocepacia j2315
21	c1t39A_	Alignment	not modelled	29.3	33	PDB header: transferase/dna Chain: A; PDB Molecule: methylated-dna--protein-cysteine methyltransferase PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
22	c4bhca_	Alignment	not modelled	28.4	33	PDB header: transferase Chain: A; PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r371 variant
23	c1wrjA_	Alignment	not modelled	28.2	28	PDB header: transferase Chain: A; PDB Molecule: methylated-dna--protein-cysteine methyltransferase PDBTitle: crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
24	c1f5tA_	Alignment	not modelled	27.7	16	PDB header: transcription/dna Chain: A; PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
25	c2it0A_	Alignment	not modelled	26.8	16	PDB header: transcription/dna Chain: A; PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii
26	d2c6ya1	Alignment	not modelled	26.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
27	c3tevA_	Alignment	not modelled	26.1	13	PDB header: hydrolase Chain: A; PDB Molecule: glycosyl hyrolase, family 3; PDBTitle: the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
28	d1sfea1	Alignment	not modelled	25.8	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-

						terminal domain
29	d1mvoa_	Alignment	not modelled	25.1	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
30	c5m5iC_	Alignment	not modelled	24.1	17	PDB header: motor protein Chain: C: PDB Molecule: kinesin-like protein cut7; PDBTitle: pseudo-atomic model of microtubule-bound s.pombe kinesin-5 motor2 domain in the amppnp state (based on cryo-electron microscopy3 experiment): the n-terminus conformation allows formation of a cover4 neck bundle.
31	c2jk1A_	Alignment	not modelled	24.1	12	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein huPr1; PDBTitle: crystal structure of the wild-type huPr receiver domain
32	c2ev5B_	Alignment	not modelled	23.6	14	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
33	c3v32B_	Alignment	not modelled	23.2	22	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
34	c5x2dA_	Alignment	not modelled	23.0	18	PDB header: cell adhesion Chain: A: PDB Molecule: tegumental protein 20.8 kda; PDBTitle: crystal structure of dlc like domain of cstal3 (83-177aa)
35	c3go5A_	Alignment	not modelled	22.9	16	PDB header: gene regulation Chain: A: PDB Molecule: multidomain protein with s1 rna-binding domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
36	c5g1mA_	Alignment	not modelled	22.8	12	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of nagz from pseudomonas aeruginosa
37	c3g73A_	Alignment	not modelled	22.4	13	PDB header: transcription/dna Chain: A: PDB Molecule: forkhead box protein m1; PDBTitle: structure of the foxm1 dna binding
38	c5z2hA_	Alignment	not modelled	22.0	16	PDB header: membrane protein Chain: A: PDB Molecule: dictyostelium discoideum mitochondrial calcium uniporter; PDBTitle: structure of dictyostelium discoideum mitochondrial calcium uniporter2 n-terminal domain(ddmCu-ntd)
39	c5fkzE_	Alignment	not modelled	21.4	13	PDB header: lyase Chain: E: PDB Molecule: lysine decarboxylase, constitutive; PDBTitle: structure of e.coli constitutive lysine decarboxylase
40	d1qnta1	Alignment	not modelled	21.0	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
41	c3hqdB_	Alignment	not modelled	20.8	17	PDB header: motor protein Chain: B: PDB Molecule: kinesin-like protein kif11; PDBTitle: human kinesin eg5 motor domain in complex with amppnp and2 mg2+
42	c3i71B_	Alignment	not modelled	20.8	17	PDB header: unknown function Chain: B: PDB Molecule: ethanolamine utilization protein eutk; PDBTitle: ethanolamine utilization microcompartment shell subunit, eutk c-2 terminal domain
43	d1kcfA2	Alignment	not modelled	20.3	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Mitochondrial resolvase ydc2 catalytic domain
44	d1tr9a_	Alignment	not modelled	20.3	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
45	d2a07f1	Alignment	not modelled	19.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
46	c3kfwX_	Alignment	not modelled	19.4	18	PDB header: structural genomics, unknown function Chain: X: PDB Molecule: uncharacterized protein; PDBTitle: uncharacterized protein rv0674 from mycobacterium tuberculosis
47	d1d5va_	Alignment	not modelled	19.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
48	d1d7ka2	Alignment	not modelled	19.0	10	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
49	d2cqna1	Alignment	not modelled	18.4	18	Fold: Another 3-helical bundle Superfamily: FF domain Family: FF domain
50	c6ncmA_	Alignment	not modelled	18.4	10	PDB header: dna binding protein/dna Chain: A: PDB Molecule: forkhead box protein n3; PDBTitle: crystal structure of the human foxn3 dna binding domain in complex2 with a forkhead-like (fhl) dna sequence
51	c2ctuA_	Alignment	not modelled	18.3	60	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 483; PDBTitle: solution structure of zinc finger domain from human zn2 finger protein 483
52	c2pffB_	Alignment	not modelled	18.2	17	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structural insights of yeast fatty acid synthase
53	c2pffH_	Alignment	not modelled	18.2	17	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structural insights of yeast fatty acid synthase

54	c2pffE_	Alignment	not modelled	18.2	17	PDB header: transferase Chain: E; PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structural insights of yeast fatty acid synthase
55	c2m4eA_	Alignment	not modelled	17.8	22	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution nmr structure of vv2_0175 from vibrio vulnificus, nesg target2 vnr1 and csqid target idp91333
56	c5xcoB_	Alignment	not modelled	17.5	20	PDB header: hydrolase/hydrolase inhibitor Chain: B; PDB Molecule: ace-arg-arg-arg-arg-cys-pro-leu-tyr-ile-ser-tyr-asg-pro- PDBTitle: crystal structure of human k-ras g12d mutant in complex with gdp and2 cyclic inhibitory peptide
57	d1kgsa2	Alignment	not modelled	17.4	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
58	c3u6xU_	Alignment	not modelled	16.6	33	PDB header: viral protein Chain: U; PDB Molecule: orf48; PDBTitle: phage tp901-1 baseplate tripod
59	d1whna_	Alignment	not modelled	16.4	27	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
60	d2dpwa1	Alignment	not modelled	16.3	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
61	d2hfha_	Alignment	not modelled	15.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
62	c2fyuE_	Alignment	not modelled	14.2	27	PDB header: oxidoreductase Chain: E; PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
63	d2doea1	Alignment	not modelled	13.8	26	Fold: Another 3-helical bundle Superfamily: FF domain Family: FF domain
64	c2qzjC_	Alignment	not modelled	13.7	10	PDB header: transcription Chain: C; PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
65	d1vm6a3	Alignment	not modelled	13.6	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	c2g7hA_	Alignment	not modelled	13.5	33	PDB header: transferase Chain: A; PDB Molecule: methylated-dna--protein-cysteine PDBTitle: structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529)
67	d1xhfa1	Alignment	not modelled	13.5	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
68	c3kcnA_	Alignment	not modelled	13.4	11	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodopirellula baltica
69	c1mgtA_	Alignment	not modelled	13.3	16	PDB header: transferase Chain: A; PDB Molecule: protein (o6-methylguanine-dna methyltransferase); PDBTitle: crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
70	c2kiqA_	Alignment	not modelled	13.3	20	PDB header: transcription regulator Chain: A; PDB Molecule: transcription elongation regulator 1; PDBTitle: solution structure of the ff domain 2 of human transcription2 elongation factor ca150
71	c1p84E_	Alignment	not modelled	13.0	19	PDB header: oxidoreductase Chain: E; PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
72	d3bpya1	Alignment	not modelled	12.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
73	c1e17A_	Alignment	not modelled	12.5	18	PDB header: dna binding domain Chain: A; PDB Molecule: afx; PDBTitle: solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
74	c2mbfA_	Alignment	not modelled	12.5	12	PDB header: transcription Chain: A; PDB Molecule: fork head domain containing protein; PDBTitle: solution structure of the forkhead domain of brugia malayi daf-16a
75	c2i25A_	Alignment	not modelled	12.4	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: np_888769.1
76	c1kq8A_	Alignment	not modelled	12.3	23	PDB header: transcription Chain: A; PDB Molecule: hepatocyte nuclear factor 3 forkhead homolog 1; PDBTitle: solution structure of winged helix protein hfh-1
77	d1kq8a_	Alignment	not modelled	12.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
78	c4e7pA_	Alignment	not modelled	12.3	10	PDB header: transcription regulator Chain: A; PDB Molecule: response regulator; PDBTitle: crystal structure of receiver domain of putative narl family response2 regulator spr1814 from streptococcus pneumoniae in the presence of3 the phosphoryl analog beryllofluoride
						PDB header: transport protein

79	c6b3yA_	Alignment	not modelled	12.2	6	Chain: A: PDB Molecule: denn domain-containing protein 3; PDBTitle: crystal structure of the ph-like domain from denn3
80	d1hw1a1	Alignment	not modelled	12.0	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
81	c6o58H_	Alignment	not modelled	11.7	44	PDB header: transport protein Chain: H: PDB Molecule: essential mcu regulator, mitochondrial; PDBTitle: human mcu-emre complex, dimer of channel
82	c6o58P_	Alignment	not modelled	11.7	44	PDB header: transport protein Chain: P: PDB Molecule: essential mcu regulator, mitochondrial; PDBTitle: human mcu-emre complex, dimer of channel
83	c5ocnG_	Alignment	not modelled	11.5	11	PDB header: transcription Chain: G: PDB Molecule: forkhead box protein n1; PDBTitle: crystal structure of the forkhead domain of human foxn1
84	c3co7C_	Alignment	not modelled	11.4	15	PDB header: transcription/dna Chain: C: PDB Molecule: forkhead box protein o1; PDBTitle: crystal structure of foxo1 dbd bound to dbe2 dna
85	c2kimA_	Alignment	not modelled	11.3	28	PDB header: transferase Chain: A: PDB Molecule: o6-methylguanine-dna methyltransferase; PDBTitle: 1.7-mm microcryoprobe solution nmr structure of an o6-methylguanine2 dna methyltransferase family protein from vibrio parahaemolyticus.3 northeast structural genomics consortium target vpr247.
86	c2e71A_	Alignment	not modelled	11.3	20	PDB header: transcription Chain: A: PDB Molecule: transcription elongation regulator 1; PDBTitle: solution structure of the second ff domain of human2 transcription factor ca150
87	c2fynO_	Alignment	not modelled	11.1	19	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
88	d1wdea_	Alignment	not modelled	10.9	9	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
89	c3pg8B_	Alignment	not modelled	10.9	14	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
90	d1ys7a2	Alignment	not modelled	10.8	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
91	d1tdja2	Alignment	not modelled	10.8	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: Allosteric threonine deaminase C-terminal domain
92	c2rjnA_	Alignment	not modelled	10.7	9	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
93	c3lk6A_	Alignment	not modelled	10.7	13	PDB header: hydrolase Chain: A: PDB Molecule: lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
94	c4gvgB_	Alignment	not modelled	10.7	9	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of salmonella typhimurium family 3 glycoside2 hydrolase (nagz)
95	c2vycA_	Alignment	not modelled	10.6	11	PDB header: lyase Chain: A: PDB Molecule: biodegradative arginine decarboxylase; PDBTitle: crystal structure of acid induced arginine decarboxylase2 from e. coli
96	d1a04a2	Alignment	not modelled	10.6	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
97	c5ewnA_	Alignment	not modelled	10.6	20	PDB header: viral protein Chain: A: PDB Molecule: structural protein; PDBTitle: crystal structure of the human astrovirus 1 capsid protein core domain2 at 2.6 a resolution
98	d1q42a_	Alignment	not modelled	10.6	28	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
99	c3ic7A_	Alignment	not modelled	10.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator of gntR family2 from bacteroides thetaiotaomicron