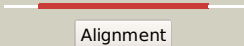

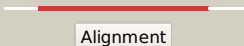

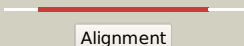







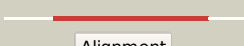






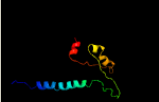


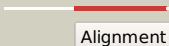
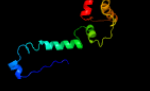



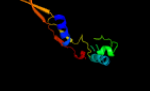
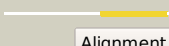
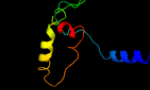
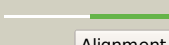

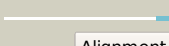
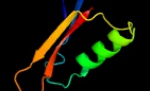
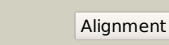



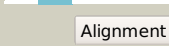

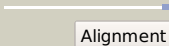
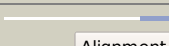
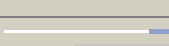
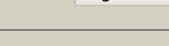
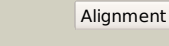
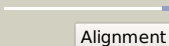
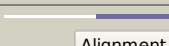



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0798c_cfp29_891475_892272
Date	Fri Jul 26 01:50:38 BST 2019
Unique Job ID	245bc07054d26848

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dktD_	 Alignment		100.0	35	PDB header: structural protein/virus like particle Chain: D: PDB Molecule: maritimacin; PDBTitle: crystal structure of thermotoga maritima encapsulin
2	c4pt2B_	 Alignment		100.0	23	PDB header: virus like particle Chain: B: PDB Molecule: encapsulin protein; PDBTitle: myxococcus xanthus encapsulin protein (enca)
3	c2e0zA_	 Alignment		100.0	21	PDB header: virus like particle Chain: A: PDB Molecule: virus-like particle; PDBTitle: crystal structure of virus-like particle from pyrococcus2 furiosus
4	c5wk1C_	 Alignment		99.3	10	PDB header: virus Chain: C: PDB Molecule: major capsid protein; PDBTitle: structure of the major capsid protein and the capsid stabilizing2 protein of the marine siphovirus tw1
5	d2ft1a1	 Alignment		99.1	14	Fold: Major capsid protein gp5 Superfamily: Major capsid protein gp5 Family: Major capsid protein gp5
6	c1if0A_	 Alignment		98.9	13	PDB header: virus Chain: A: PDB Molecule: protein (major capsid protein gp5); PDBTitle: pseudo-atomic model of bacteriophage hk97 procapsid2 (prohead ii)
7	c5tjtA_	 Alignment		98.4	12	PDB header: viral protein Chain: A: PDB Molecule: major capsid protein; PDBTitle: t5 bacteriophage major capsid protein - one pb8 hexon
8	c3jb5C_	 Alignment		98.2	10	PDB header: virus Chain: C: PDB Molecule: major capsid protein; PDBTitle: capsid structure of the propionibacterium acnes bacteriophage2 atcc_clear
9	c6b0xG_	 Alignment		98.0	8	PDB header: virus Chain: G: PDB Molecule: major head protein; PDBTitle: capsid protein and c-terminal part of scaffolding protein in the2 staphylococcus aureus phage 80alpha procapsid
10	c4bmlA_	 Alignment		94.2	20	PDB header: virus Chain: A: PDB Molecule: major capsid protein; PDBTitle: c-alpha backbone trace of major capsid protein gp39 found in marine2 virus syn5.
11	c3p8qF_	 Alignment		93.1	15	PDB header: virus Chain: F: PDB Molecule: gp5, head protein; PDBTitle: hk97 prohead i encapsidating inactive virally encoded protease

12	c5i35D_	 Alignment		92.3	11	PDB header: virus Chain: D: PDB Molecule: gene 5 protein; PDBTitle: cryo-em structure of bacteriophage sf6 at 2.9 angstrom resolution
13	c3j7wF_	 Alignment		90.2	14	PDB header: virus Chain: F: PDB Molecule: major capsid protein 10a; PDBTitle: capsid expansion mechanism of bacteriophage t7 revealed by multi-state2 atomic models derived from cryo-em reconstructions
14	c3j1aE_	 Alignment		86.8	16	PDB header: virus Chain: E: PDB Molecule: capsid protein; PDBTitle: hk97-like fold fitted into 3d reconstruction of bacteriophage cw02
15	c2xd8F_	 Alignment		70.9	20	PDB header: virus Chain: F: PDB Molecule: t7-like capsid protein; PDBTitle: capsid structure of the infectious prochlorococcus cyanophage p-ssp7
16	c3bjqA_	 Alignment		59.6	16	PDB header: viral protein Chain: A: PDB Molecule: phage-related protein; PDBTitle: crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
17	c6hwlB_	 Alignment		34.2	16	PDB header: transferase Chain: B: PDB Molecule: glucosamine kinase; PDBTitle: glucosamine kinase in complex with glucosamine, adp and inorganic2 phosphate
18	c3izqG_	 Alignment		32.6	19	PDB header: virus Chain: G: PDB Molecule: major capsid protein 10a; PDBTitle: bacteriophage t7 prohead shell em-derived atomic model
19	c5jy7I_	 Alignment		31.1	21	PDB header: isomerase/transferase Chain: I: PDB Molecule: maltokinase; PDBTitle: complex of mycobacterium smegmatis trehalose synthase with maltokinase
20	c2v7sA_	 Alignment		30.3	5	PDB header: unknown function Chain: A: PDB Molecule: probable conserved lipoprotein lppa; PDBTitle: crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
21	d1g0wa1	 Alignment	not modelled	23.6	18	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
22	c5hmqE_	 Alignment	not modelled	23.1	19	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
23	c5jy7K_	 Alignment	not modelled	22.4	19	PDB header: isomerase/transferase Chain: K: PDB Molecule: maltokinase; PDBTitle: complex of mycobacterium smegmatis trehalose synthase with maltokinase
24	c5ey0A_	 Alignment	not modelled	21.9	21	PDB header: transcription Chain: A: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: crystal structure of cody from staphylococcus aureus with gtp and ile
25	d1qh4a1	 Alignment	not modelled	21.0	18	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
26	d2b0la1	 Alignment	not modelled	19.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cody HTH domain
27	d1sp9a_	 Alignment	not modelled	19.0	13	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradriol dioxygenases
28	c1tfzA_	 Alignment	not modelled	18.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: structural basis for herbicidal inhibitor selectivity revealed

						by2 comparison of crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
29	c1sqia_	Alignment	not modelled	18.4	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: 4-hydroxyphenylpyruvic acid dioxygenase; PDBTitle: structural basis for inhibitor selectivity revealed by2 crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
30	c2r5vA_	Alignment	not modelled	17.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pcza361.1; PDBTitle: hydroxymandelate synthase crystal structure
31	d2cqqa1	Alignment	not modelled	17.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
32	d1sqda2	Alignment	not modelled	17.4	13	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
33	d2i9xa1	Alignment	not modelled	17.1	14	Fold: SpoVG-like Superfamily: SpoVG-like Family: SpoVG-like
34	c2i9zB_	Alignment	not modelled	17.1	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative septation protein spovg; PDBTitle: structural genomics, the crystal structure of full-length spovg from2 staphylococcus epidermidis atcc 12228
35	d1sqia2	Alignment	not modelled	16.7	17	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
36	c3r5eA_	Alignment	not modelled	16.5	18	PDB header: transferase Chain: A: PDB Molecule: transaldolase; PDBTitle: transaldolase from corynebacterium glutamicum
37	c5ey2A_	Alignment	not modelled	16.1	24	PDB header: transcription Chain: A: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: crystal structure of cody from bacillus cereus
38	d1vrpa1	Alignment	not modelled	15.0	18	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
39	c5abxB_	Alignment	not modelled	14.5	31	PDB header: translation Chain: B: PDB Molecule: 4e-binding protein mexkli; PDBTitle: complex of c. elegans eif4e-3 with the 4e-binding protein2 mexkli and cap analog
40	c2w7nA_	Alignment	not modelled	12.7	22	PDB header: transcription/dna Chain: A: PDB Molecule: trfb transcriptional repressor protein; PDBTitle: crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
41	d1piia2	Alignment	not modelled	12.7	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
42	c1piiA_	Alignment	not modelled	11.8	17	PDB header: bifunctional(isomerase and synthase) Chain: A: PDB Molecule: zn-(5'phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution
43	d2cfxa1	Alignment	not modelled	11.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
44	d1qm4a3	Alignment	not modelled	10.9	33	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
45	d2p02a3	Alignment	not modelled	10.9	33	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
46	d1v4ra1	Alignment	not modelled	10.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
47	d1tj1a1	Alignment	not modelled	10.4	7	Fold: N-terminal domain of bifunctional PutA protein Superfamily: N-terminal domain of bifunctional PutA protein Family: N-terminal domain of bifunctional PutA protein
48	d1vetb_	Alignment	not modelled	10.3	12	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
49	d1cjxa2	Alignment	not modelled	10.1	14	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
50	d1i4na_	Alignment	not modelled	10.1	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
51	c1cxC_	Alignment	not modelled	10.0	11	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: crystal structure of pseudomonas fluorescens hppd
52	d2cyya1	Alignment	not modelled	9.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
53	d2ia9a1	Alignment	not modelled	9.9	14	Fold: SpoVG-like Superfamily: SpoVG-like Family: SpoVG-like

54	d1lga1	Alignment	not modelled	9.6	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
55	c4a5mH_	Alignment	not modelled	9.4	12	PDB header: transcription Chain: H: PDB Molecule: uncharacterized hth-type transcriptional regulator yybr; PDBTitle: redox regulator hypr in its oxidized form
56	d1mxaa3	Alignment	not modelled	9.2	27	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
57	c5hs9A_	Alignment	not modelled	9.1	19	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator yodb; PDBTitle: crystal structure of the quinone-bound yodb from b. subtilis
58	d1wfa1	Alignment	not modelled	8.9	25	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
59	c3tqkA_	Alignment	not modelled	8.8	24	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: structure of phospho-2-dehydro-3-deoxyheptonate aldolase from2 francisella tularensis schu s4
60	d2cg4a1	Alignment	not modelled	8.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
61	c4le5A_	Alignment	not modelled	8.6	33	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: structure of an unusual s-adenosylmethionine synthetase from2 campylobacter jejuni
62	c1i0eD_	Alignment	not modelled	8.5	16	PDB header: transferase Chain: D: PDB Molecule: creatine kinase,m chain; PDBTitle: crystal structure of creatine kinase from human muscle
63	c1t47A_	Alignment	not modelled	8.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: structure of fe2-hppd bound to ntbc
64	c4wzyA_	Alignment	not modelled	8.4	21	PDB header: transferase Chain: A: PDB Molecule: maltokinase; PDBTitle: structure of mycobacterial maltokinase, the missing link in the2 essential glge-pathway (atp complex)
65	c2obvA_	Alignment	not modelled	8.2	33	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthetase isoform type-1; PDBTitle: crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
66	c4odjA_	Alignment	not modelled	8.2	33	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of a putative s-adenosylmethionine synthetase from2 cryptosporidium hominis in complex with s-adenosyl-methionine
67	c3so4C_	Alignment	not modelled	8.2	33	PDB header: transferase Chain: C: PDB Molecule: methionine-adenosyltransferase; PDBTitle: methionine-adenosyltransferase from entamoeba histolytica
68	c3rv2B_	Alignment	not modelled	8.0	27	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
69	c3imlB_	Alignment	not modelled	8.0	33	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
70	d1e4ft1	Alignment	not modelled	7.9	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
71	c1j3wB_	Alignment	not modelled	7.9	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: gliding protein-mglb; PDBTitle: structure of gliding protein-mglb from thermus thermophilus hb8
72	d1yyva1	Alignment	not modelled	7.7	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
73	c5h9uC_	Alignment	not modelled	7.6	33	PDB header: transferase Chain: C: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of a thermostable methionine adenosyltransferase
74	c1rg9D_	Alignment	not modelled	7.5	27	PDB header: transferase Chain: D: PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: s-adenosylmethionine synthetase complexed with sam and ppnp
75	c3nzpA_	Alignment	not modelled	7.5	13	PDB header: lyase Chain: A: PDB Molecule: arginine decarboxylase; PDBTitle: crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
76	c4uisA_	Alignment	not modelled	7.5	30	PDB header: hydrolase Chain: A: PDB Molecule: gamma-secretase; PDBTitle: the cryoem structure of human gamma-secretase complex
77	c4gcvD_	Alignment	not modelled	7.4	22	PDB header: transcription Chain: D: PDB Molecule: putative transcription protein; PDBTitle: structure of a putative transcription factor (pa1374)from pseudomonas2 aeruginosa
78	d1j3wa_	Alignment	not modelled	7.3	9	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
79	c2riaC_	Alignment	not modelled	7.2	17	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: golgi to er traffic protein 1;

79	c3jdg	Alignment	not modelled	7.3	47	PDBTitle: crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain PDB header: viral protein
80	c3l32B	Alignment	not modelled	7.3	9	Chain: B; PDB Molecule: phosphoprotein; PDBTitle: structure of the dimerisation domain of the rabies virus2 phosphoprotein
81	c5o9zG	Alignment	not modelled	7.2	56	PDB header: splicing Chain: G; PDB Molecule: pre-mrna-processing factor 6; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
82	d2fswa1	Alignment	not modelled	7.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
83	d2hzta1	Alignment	not modelled	6.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
84	d1t47a2	Alignment	not modelled	6.8	20	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
85	d1z7ua1	Alignment	not modelled	6.8	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
86	c2gesA	Alignment	not modelled	6.6	19	PDB header: transferase Chain: A; PDB Molecule: pantothenate kinase; PDBTitle: pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
87	c3zgiA	Alignment	not modelled	6.6	22	PDB header: oxidoreductase Chain: A; PDB Molecule: 4-hydroxyphenylpyruvic acid dioxygenase; PDBTitle: s221m v223f y359a mutant of 4-hydroxymandelate synthase2 from streptomyces coelicolor
88	d1zs4a1	Alignment	not modelled	6.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Bacteriophage CII protein
89	c3sjbC	Alignment	not modelled	6.2	17	PDB header: hydrolase/transport protein Chain: C; PDB Molecule: golgi to er traffic protein 1; PDBTitle: crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
90	d1u7ka	Alignment	not modelled	6.1	17	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
91	c2jppB	Alignment	not modelled	5.9	24	PDB header: translation/rna Chain: B; PDB Molecule: translational repressor; PDBTitle: structural basis of rsma/csra rna recognition: structure of2 rsmc bound to the shine-dalgarno sequence of hcna mrna
92	c3nzqB	Alignment	not modelled	5.8	13	PDB header: lyase Chain: B; PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
93	d1qqga2	Alignment	not modelled	5.8	19	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)
94	c2o6yF	Alignment	not modelled	5.7	16	PDB header: lyase Chain: F; PDB Molecule: putative histidine ammonia-lyase; PDBTitle: tyrosine ammonia-lyase from rhodobacter sphaeroides
95	c4rv7C	Alignment	not modelled	5.7	13	PDB header: transferase Chain: C; PDB Molecule: diadenylate cyclase; PDBTitle: characterization of an essential diadenylate cyclase
96	d1nkga3	Alignment	not modelled	5.7	50	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Rhamnogalacturonase B, RhgB, N-terminal domain
97	c3sggA	Alignment	not modelled	5.6	11	PDB header: hydrolase Chain: A; PDB Molecule: hypothetical hydrolase; PDBTitle: crystal structure of a putative hydrolase (bt_2193) from bacteroides2 thetaiotaomicron vpi-5482 at 1.25 a resolution
98	c4hsnA	Alignment	not modelled	5.5	19	PDB header: transferase Chain: A; PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: crystal structure of dah7ps from neisseria meningitidis
99	d2f2ea1	Alignment	not modelled	5.5	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like