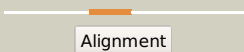

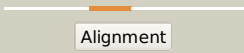

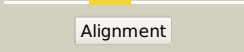

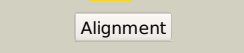



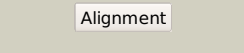

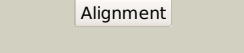
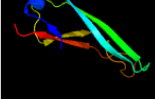

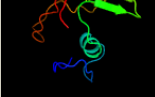
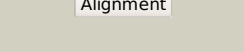
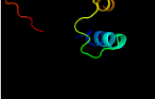
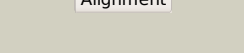

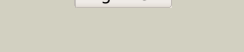
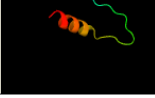











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0740 (-) _831779_832306
Date	Fri Jul 26 01:50:31 BST 2019
Unique Job ID	54b13a3758cbc882

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5jxfA_	 Alignment		83.6	18	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
2	c5jxpA_	 Alignment		83.2	21	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
3	c4y01B_	 Alignment		78.8	12	PDB header: hydrolase Chain: B: PDB Molecule: peptidase s46; PDBTitle: crystal structure of dipeptidyl peptidase 11 (dpp11) from2 porphyromonas gingivalis
4	c3wolB_	 Alignment		75.9	21	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl aminopeptidase bii; PDBTitle: crystal structure of the dap bii dipeptide complex i
5	c3ushB_	 Alignment		62.1	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q2s0r5 protein from salinibacter ruber,2 northeast structural genomics consortium target srr207
6	d1a8ra_	 Alignment		59.2	19	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
7	d1c3ga1	 Alignment		55.2	19	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
8	c4iohA_	 Alignment		50.1	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tll1086 protein; PDBTitle: crystal structure of the tll1086 protein from thermosynechococcus2 elongatus, northeast structural genomics consortium target ter258
9	c2xxzA_	 Alignment		45.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of the human jmjd3 jumonji domain
10	c2lq3A_	 Alignment		39.1	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of syc0711_d from synechococcus sp., northeast2 structural genomics consortium (nesg) target snr212
11	c1wm9D_	 Alignment		38.7	29	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase i; PDBTitle: structure of gtp cyclohydrolase i from thermus thermophilus hb8

12	dlwura1	Alignment		38.7	29	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
13	c4ktzB_	Alignment		31.9	70	PDB header: hydrolase Chain: B: PDB Molecule: ruvc endonuclease; PDBTitle: lactococcus phage 67 ruvc
14	c4uqfB_	Alignment		31.2	35	PDB header: hydrolase Chain: B: PDB Molecule: gtp cyclohydrolase 1; PDBTitle: crystal structure of listeria monocytogenes gtp cyclohydrolase i
15	dlwpia_	Alignment		31.1	32	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
16	c1is7F_	Alignment		30.9	32	PDB header: hydrolase/protein binding Chain: F: PDB Molecule: gtp cyclohydrolase i; PDBTitle: crystal structure of rat gtpchi/grp stimulatory complex
17	c2wfuB_	Alignment		23.6	50	PDB header: signaling protein Chain: B: PDB Molecule: probable insulin-like peptide 5 b chain; PDBTitle: crystal structure of dilp5 variant db
18	c6feyF_	Alignment		23.6	46	PDB header: peptide binding protein Chain: F: PDB Molecule: probable insulin-like peptide 5; PDBTitle: crystal structure of drosophila neural ectodermal development factor2 imp-l2 with drosophila dilp5 insulin
19	c2wfvB_	Alignment		23.2	50	PDB header: signaling protein Chain: B: PDB Molecule: probable insulin-like peptide 5 b chain; PDBTitle: crystal structure of dilp5 variant c4
20	d2diia1	Alignment		22.2	75	Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
21	c2diiA_	Alignment	not modelled	21.3	75	PDB header: transcription Chain: A: PDB Molecule: tfiih basal transcription factor complex p62 PDBTitle: solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
22	c6feyH_	Alignment	not modelled	20.9	46	PDB header: peptide binding protein Chain: H: PDB Molecule: probable insulin-like peptide 5; PDBTitle: crystal structure of drosophila neural ectodermal development factor2 imp-l2 with drosophila dilp5 insulin
23	c3opwA_	Alignment	not modelled	16.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: dna damage-responsive transcriptional repressor rph1; PDBTitle: crystal structure of the rph1 catalytic core
24	c3avsA_	Alignment	not modelled	16.4	56	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6a; PDBTitle: catalytic fragment of utx/kdm6a bound with n-oxyalylglycine, and2 ni(ii)
25	c4ezhA_	Alignment	not modelled	16.4	56	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: the crystal structure of kdm6b bound with h3k27me3 peptide
26	c2q8eB_	Alignment	not modelled	15.6	40	PDB header: oxidoreductase Chain: B: PDB Molecule: jmjc domain-containing histone demethylation protein 3a; PDBTitle: specificity and mechanism of jmjd2a, a trimethyllysine-specific2 histone demethylase
27	d1pmia_	Alignment	not modelled	15.4	28	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Type I phosphomannose isomerase
28	c3r67A_	Alignment	not modelled	15.0	35	PDB header: hydrolase Chain: A: PDB Molecule: putative glycosidase; PDBTitle: crystal structure of a putative glycosidase (bt_4094) from

						bacteroides2 thetaiotaomicron vpi-5482 at 2.30 a resolution
29	c4iqpA	Alignment	not modelled	15.0	36	PDB header: structural protein Chain: A: PDB Molecule: os05g0196500 protein; PDBTitle: histone h3 lysine 4 demethylating rice jmj703 apo enzyme
30	c6maiA	Alignment	not modelled	13.9	35	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5'-triphosphate nucleotidohydrolase2 from legionella pneumophila philadelphia 1
31	c4plaA	Alignment	not modelled	13.6	34	PDB header: transferase,hydrolase Chain: A: PDB Molecule: chimera protein of phosphatidylinositol 4-kinase type 2- PDBTitle: crystal structure of phosphatidyl inositol 4-kinase ii alpha in2 complex with atp
32	c2xueB	Alignment	not modelled	13.4	56	PDB header: oxidoreductase Chain: B: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of jmj3
33	c3on5B	Alignment	not modelled	13.3	38	PDB header: oxidoreductase Chain: B: PDB Molecule: bh1974 protein; PDBTitle: crystal structure of a xanthine dehydrogenase (bh1974) from bacillus2 halodurans at 2.80 a resolution
34	d1qwra	Alignment	not modelled	13.1	28	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Type I phosphomannose isomerase
35	c2qkiC	Alignment	not modelled	12.8	20	PDB header: immune system/hydrolase inhibitor Chain: C: PDB Molecule: complement c3; PDBTitle: human c3c in complex with the inhibitor compstatin
36	c3h1yA	Alignment	not modelled	12.6	28	PDB header: isomerase Chain: A: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
37	d1t62a	Alignment	not modelled	12.4	29	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical protein EF3133
38	c3s9xA	Alignment	not modelled	11.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: asch domain; PDBTitle: high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
39	c2w2iC	Alignment	not modelled	11.8	27	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate oxygenase; PDBTitle: crystal structure of the human 2-oxoglutarate oxygenase2 loc390245
40	c2lqtA	Alignment	not modelled	11.7	18	PDB header: unknown function Chain: A: PDB Molecule: coiled-coil-helix-coiled-coil-helix domain-containing PDBTitle: solution structure of chchd7
41	d1gnta	Alignment	not modelled	11.2	27	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Hybrid cluster protein (prismane protein)
42	c2os2A	Alignment	not modelled	11.2	27	PDB header: oxidoreductase Chain: A: PDB Molecule: jmj3c domain-containing histone demethylation protein 3a; PDBTitle: crystal structure of jmj2a complexed with histone h3 peptide2 trimethylated at lys36
43	c2q2gA	Alignment	not modelled	11.1	16	PDB header: chaperone Chain: A: PDB Molecule: heat shock 40 kda protein, putative (fragment); PDBTitle: crystal structure of dimerization domain of hsp40 from2 cryptosporidium parvum, cg2_1800
44	c5yknA	Alignment	not modelled	10.3	25	PDB header: gene regulation Chain: A: PDB Molecule: probable lysine-specific demethylase jmj14; PDBTitle: crystal structure of arabidopsis thaliana jmj14 catalytic domain
45	d1kafa	Alignment	not modelled	10.3	57	Fold: MotA C-terminal domain-like Superfamily: DNA-binding C-terminal domain of the transcription factor MotA Family: DNA-binding C-terminal domain of the transcription factor MotA
46	d1rnja	Alignment	not modelled	10.3	42	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
47	c2we7A	Alignment	not modelled	10.2	45	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
48	d2rh2a1	Alignment	not modelled	9.4	47	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: R67 dihydrofolate reductase
49	c5wrwA	Alignment	not modelled	9.2	23	PDB header: hydrolase Chain: A: PDB Molecule: probable inorganic pyrophosphatase; PDBTitle: crystal structure of type i inorganic pyrophosphatase from p2 falciparum
50	d1euwa	Alignment	not modelled	8.8	42	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
51	c2bruB	Alignment	not modelled	8.5	26	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
52	c4bhrA	Alignment	not modelled	8.5	18	PDB header: cell adhesion Chain: A: PDB Molecule: pilin, type iv; PDBTitle: structure of the thta1221 type iv pilin protein from2 thermus thermophilus
						PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate

53	c3tqzA	Alignment	not modelled	8.4	38	nucleotidohydrolase; PDBTitle: structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from coxiella burnetii
54	d1yqha1	Alignment	not modelled	8.2	11	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
55	c2ypdB	Alignment	not modelled	8.2	22	PDB header: oxidoreductase Chain: B: PDB Molecule: probable jmjc domain-containing histone demethylation prot PDBTitle: crystal structure of the jumonji domain of human jumonji domain2 containing 1c protein
56	c4uedB	Alignment	not modelled	7.8	28	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation factor 4e-binding protein 1; PDBTitle: complex of human eif4e with the 4e binding protein 4e-bp1
57	c6ip4A	Alignment	not modelled	7.8	28	PDB header: gene regulation Chain: A: PDB Molecule: arabidopsis jmj13; PDBTitle: crystal structure of arabidopsis thaliana jmj13 catalytic domain in2 complex with nog and an h3k27me3 peptide
58	c3tawA	Alignment	not modelled	7.8	36	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical glycoside hydrolase; PDBTitle: crystal structure of a putative glycoside hydrolase (bdj_3141) from2 parabacteroides distasonis atcc 8503 at 1.70 a resolution
59	c4onzA	Alignment	not modelled	7.6	28	PDB header: hydrolase Chain: A: PDB Molecule: putative glycoside hydrolase; PDBTitle: crystal structure of a putative glycoside hydrolase (bacova_02161)2 from bacteroides ovatus atcc 8483 at 1.85 a resolution
60	c5jyxB	Alignment	not modelled	7.4	11	PDB header: transferase Chain: B: PDB Molecule: archaeosine synthase quef-like; PDBTitle: crystal structure of the covalent thioimide intermediate of the2 archaeosine synthase quef-like
61	c2bazA	Alignment	not modelled	7.4	25	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein bsu20020; PDBTitle: structure of yoss, a putative dutpase from bacillus subtilis
62	d2iboA1	Alignment	not modelled	7.2	9	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
63	c5cehA	Alignment	not modelled	7.0	28	PDB header: oxidoreductase/inhibitor Chain: A: PDB Molecule: lysine-specific demethylase 5a; PDBTitle: structure of histone lysine demethylase kdm5a in complex with2 selective inhibitor
64	c2my3B	Alignment	not modelled	6.9	83	PDB header: splicing Chain: B: PDB Molecule: pre-mrna leakage protein 1; PDBTitle: snu17p-pml1p structure intermediate during res complex assembly
65	c6b4eC	Alignment	not modelled	6.7	67	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup42; PDBTitle: crystal structure of saccharomyces cerevisiae gle1 ctd-nup42 gbm2 complex
66	c2mxqA	Alignment	not modelled	6.6	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: paneth cell-specific alpha-defensin 1; PDBTitle: the solution structure of defa1, a highly potent antimicrobial peptide2 from the horse
67	d2z1ea2	Alignment	not modelled	6.6	38	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
68	c5a1fA	Alignment	not modelled	6.6	28	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 5b, lysine-specific PDBTitle: crystal structure of the catalytic domain of plu1 in complex with2 n-oxalylglycine.
69	c3zxkB	Alignment	not modelled	6.5	10	PDB header: hydrolase Chain: B: PDB Molecule: hiaxhd3; PDBTitle: engineering the active site of a gh43 glycoside hydrolase generates a2 biotechnologically significant enzyme that displays both endo-3 xylanase and exo-arabinofuranosidase activity
70	c5ynpA	Alignment	not modelled	6.5	27	PDB header: transferase Chain: A: PDB Molecule: nsp16 protein; PDBTitle: crystal structure of mers-cov nsp16/nsp10 complex bound to sinefungin2 and m7gpppa
71	c2lv4A	Alignment	not modelled	6.5	24	PDB header: protein binding Chain: A: PDB Molecule: putative outer membrane or exported protein; PDBTitle: zirs c-terminal domain
72	c2n1dA	Alignment	not modelled	6.4	29	PDB header: protein binding Chain: A: PDB Molecule: mrg/morf4l-binding protein; PDBTitle: solution structure of the mrg15-mrgbp complex
73	c2mkcB	Alignment	not modelled	6.4	83	PDB header: splicing Chain: B: PDB Molecule: pre-mrna leakage protein 1; PDBTitle: cooperative structure of the heterotrimeric pre-mrna retention and2 splicing complex
74	c3alxB	Alignment	not modelled	6.3	45	PDB header: viral protein/membrane protein Chain: B: PDB Molecule: hemagglutinin,linker,cdw150; PDBTitle: crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (mv-h(1482r)-slam(n102h/r108y) fusion)
75	d1vk8a	Alignment	not modelled	6.2	20	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
76	c5zwoZ	Alignment	not modelled	6.0	83	PDB header: splicing Chain: Z: PDB Molecule: pre-mrna leakage protein 1; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
77	d1gnla	Alignment	not modelled	5.9	27	Fold: Prismane protein-like Superfamily: Prismane protein-like

						Family: Hybrid cluster protein (prismane protein)
78	c1r46B_	Alignment	not modelled	5.8	63	PDB header: hydrolase Chain: B: PDB Molecule: alpha-galactosidase a; PDBTitle: structure of human alpha-galactosidase
79	c2n0pA_	Alignment	not modelled	5.7	54	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein aq_1974; PDBTitle: solution structure of aquifex aeolicus aq1974
80	d1sgva2	Alignment	not modelled	5.7	22	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
81	c3lz8A_	Alignment	not modelled	5.7	17	PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.
82	c4ar1A_	Alignment	not modelled	5.6	33	PDB header: hydrolase Chain: A: PDB Molecule: colh protein; PDBTitle: crystal structure of the peptidase domain of collagenase h from2 clostridium histolyticum at 2.01 angstrom resolution.
83	c3qc2A_	Alignment	not modelled	5.5	28	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase; PDBTitle: crystal structure of a glycosyl hydrolase (bacova_03624) from2 bacteroides ovatus at 2.30 a resolution
84	d3clsd2	Alignment	not modelled	5.5	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
85	c2e5qA_	Alignment	not modelled	5.3	58	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 19; PDBTitle: solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
86	c2yx8A_	Alignment	not modelled	5.3	50	PDB header: protein transport Chain: A: PDB Molecule: receptor activity-modifying protein 1; PDBTitle: crystal structure of the extracellular domain of human ramp1
87	c3a5vA_	Alignment	not modelled	5.2	50	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of alpha-galactosidase i from mortierella vinacea