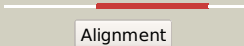

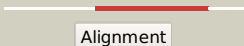

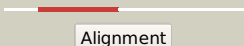







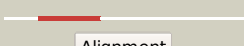








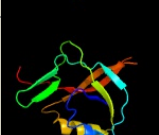




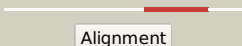

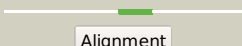

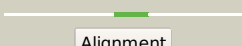

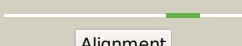

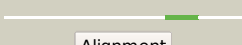





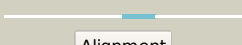
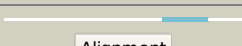
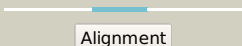
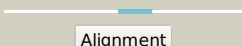


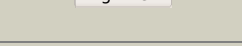


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0923c_(-)_1029517_1030581
Date	Fri Jul 26 01:50:51 BST 2019
Unique Job ID	b8716019b37501cf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a9lB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: poly-gamma-glutamate hydrolase; PDBTitle: structure of bacteriophage poly-gamma-glutamate hydrolase
2	c5onkA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: yndl; PDBTitle: native yndl
3	c2qikA_	 Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0131 protein ykqa; PDBTitle: crystal structure of ykqa from bacillus subtilis. northeast structural2 genomics target sr631
4	c2rbhA_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyl cyclotransferase; PDBTitle: gamma-glutamyl cyclotransferase
5	c2g0qA_	 Alignment		99.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: at5g39720.1 protein; PDBTitle: solution structure of at5g39720.1 from arabidopsis thaliana
6	c2jqvA_	 Alignment		99.7	20	PDB header: structural genomics Chain: A: PDB Molecule: ai2 protein-like; PDBTitle: solution structure at3g28950.1 from arabidopsis thaliana
7	d1xhsa_	 Alignment		99.7	20	Fold: Gamma-glutamyl cyclotransferase-like Superfamily: Gamma-glutamyl cyclotransferase-like Family: Gamma-glutamyl cyclotransferase-like
8	d1v30a_	 Alignment		99.3	11	Fold: Gamma-glutamyl cyclotransferase-like Superfamily: Gamma-glutamyl cyclotransferase-like Family: Gamma-glutamyl cyclotransferase-like
9	d1vkba_	 Alignment		99.3	21	Fold: Gamma-glutamyl cyclotransferase-like Superfamily: Gamma-glutamyl cyclotransferase-like Family: Gamma-glutamyl cyclotransferase-like
10	c5hwiA_	 Alignment		99.3	24	PDB header: transferase Chain: A: PDB Molecule: glutathione-specific gamma-glutamylcyclotransferase; PDBTitle: crystal structure of selenomethionine labelled gamma glutamyl2 cyclotransferase specific to glutathione from yeast
11	c3jubA_	 Alignment		99.2	24	PDB header: transferase Chain: A: PDB Molecule: ai2-like domain-containing protein 1; PDBTitle: human gamma-glutamylamine cyclotransferase

12	c5c5zA_		Alignment		96.2	12	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl-trna amidotransferase; PDBTitle: crystal structure analysis of c4763, a uropathogenic e. coli-specific2 protein
13	d2q7sa1		Alignment		94.7	14	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FGase-like
14	d2odfa1		Alignment		93.5	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FGase-like
15	c2r60A_		Alignment		55.6	27	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
16	c3bjrA_		Alignment		54.2	15	PDB header: hydrolase Chain: A: PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
17	c5d92B_		Alignment		51.7	24	PDB header: membrane protein Chain: B: PDB Molecule: af2299 protein,phosphatidylinositol synthase; PDBTitle: structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
18	c2qjwA_		Alignment		50.8	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein xcc1541; PDBTitle: crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
19	c5synB_		Alignment		46.4	11	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: acyl-protein thioesterase 2; PDBTitle: cocrystal structure of the human acyl protein thioesterase 2 with an2 isoform-selective inhibitor, ml349
20	c4o6mA_		Alignment		41.6	24	PDB header: transferase Chain: A: PDB Molecule: af2299, a cdp-alcohol phosphotransferase; PDBTitle: structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
21	c5zesA_		Alignment	not modelled	38.1	30	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:tetrahydrobiopterin glycosyltransferase; PDBTitle: udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex
22	c5jyuA_		Alignment	not modelled	34.3	18	PDB header: sigaling protein Chain: A: PDB Molecule: two-component sensor histidine kinase; PDBTitle: nmr structure of pseudo receiver domain of cika from2 thermosynechococcus elongatus
23	c4wy5A_		Alignment	not modelled	33.9	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
24	c2jlmH_		Alignment	not modelled	32.7	21	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
25	c2m2jA_		Alignment	not modelled	31.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative periplasmic protein; PDBTitle: solution nmr structure of the n-terminal domain of stm1478 from2 salmonella typhimurium lt2: target str147a of the northeast3 structural genomics consortium (nesg), and apc101565 of the midwest4 center for structural genomics (mcsq).
26	c3nohA_		Alignment	not modelled	31.5	18	PDB header: peptide binding protein Chain: A: PDB Molecule: putative peptide binding protein; PDBTitle: crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
27	c5xb6D_		Alignment	not modelled	29.6	16	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein ycyj; PDBTitle: crystal structure of ycyj from e. coli

28	d1luaa2	Alignment	not modelled	29.2	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
29	d1uxoa_	Alignment	not modelled	28.5	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
30	d1xova2	Alignment	not modelled	28.4	14	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: N-acetylmuramoyl-L-alanine amidase-like
31	c3eikB_	Alignment	not modelled	28.4	17	PDB header: transcription Chain: B; PDB Molecule: tata-box-binding protein; PDBTitle: double stranded dna binding protein
32	c5g59A_	Alignment	not modelled	27.5	8	PDB header: structural protein Chain: A; PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
33	d1xjca_	Alignment	not modelled	26.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
34	c3fakA_	Alignment	not modelled	24.8	18	PDB header: hydrolase Chain: A; PDB Molecule: esterase/lipase; PDBTitle: structural and functional analysis of a hormone-sensitive2 lipase like este5 from a metagenome library
35	c5n0lC_	Alignment	not modelled	24.6	15	PDB header: transcription Chain: C; PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: the structure of the cofactor binding gaf domain of the nutrient2 sensor cody from clostridium difficile
36	c1ngmM_	Alignment	not modelled	23.5	18	PDB header: transcription/dna Chain: M; PDB Molecule: transcription initiation factor tfiid; PDBTitle: crystal structure of a yeast brf1-tbp-dna ternary complex
37	c6d9tA_	Alignment	not modelled	22.9	21	PDB header: transferase Chain: A; PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
38	d2ejna1	Alignment	not modelled	22.6	14	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
39	c4m6iA_	Alignment	not modelled	21.3	19	PDB header: hydrolase Chain: A; PDB Molecule: peptidoglycan amidase rv3717; PDBTitle: structure of the reduced, zn-bound form of mycobacterium tuberculosis2 peptidoglycan amidase rv3717
40	c3f6sl_	Alignment	not modelled	20.4	21	PDB header: electron transport Chain: I; PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin alternate2 conformers
41	c3majA_	Alignment	not modelled	19.6	19	PDB header: dna binding protein Chain: A; PDB Molecule: dna processing chain a; PDBTitle: crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
42	d1dxha2	Alignment	not modelled	19.5	24	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
43	c1rm1A_	Alignment	not modelled	18.6	18	PDB header: transcription/dna Chain: A; PDB Molecule: tata-box binding protein; PDBTitle: structure of a yeast tfiia/tbp/tata-box dna complex
44	d1qb5d_	Alignment	not modelled	18.6	31	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
45	c1mp9B_	Alignment	not modelled	18.1	14	PDB header: dna binding protein Chain: B; PDB Molecule: tata-binding protein; PDBTitle: tbp from a mesothermophilic archaeon, sulfobolus acidocaldarius
46	d2iv2x1	Alignment	not modelled	17.9	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
47	d1lutga_	Alignment	not modelled	17.2	25	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
48	c2z8uQ_	Alignment	not modelled	17.2	23	PDB header: transcription Chain: Q; PDB Molecule: tata-box-binding protein; PDBTitle: methanococcus jannaschii tbp
49	c3m1pA_	Alignment	not modelled	16.9	17	PDB header: isomerase Chain: A; PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with alllose-6-phosphate
50	c3k7pA_	Alignment	not modelled	16.9	17	PDB header: isomerase Chain: A; PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
51	d1q6za1	Alignment	not modelled	16.8	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
52	d1hh1a_	Alignment	not modelled	16.6	22	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
53	d1v77a_	Alignment	not modelled	16.5	19	Fold: 7-stranded beta/alpha barrel Superfamily: PHP domain-like Family: RNase P subunit p30
54	c2zshA_	Alignment	not modelled	16.1	17	PDB header: hormone receptor Chain: A; PDB Molecule: probable gibberellin receptor gid111; PDBTitle: structural basis of gibberellin(ga3)-induced della2

						recognition by the gibberellin receptor
55	c3hxB	Alignment	not modelled	16.0	29	PDB header: hydrolase Chain: B: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of a sugar hydrolase (yeeb) from lactococcus lactis,2 northeast structural genomics consortium target kr108
56	d1wu7a1	Alignment	not modelled	15.9	15	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
57	c4h2dB	Alignment	not modelled	15.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
58	d2noca1	Alignment	not modelled	15.6	10	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
59	c1ycdA	Alignment	not modelled	15.1	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical 27.3 kda protein in aap1-smf2 PDBTitle: crystal structure of yeast fsh1/yrh049w, a member of the2 serine hydrolase family
60	c4b0aA	Alignment	not modelled	15.1	17	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 1, linker, PDBTitle: the high-resolution structure of ytbp-ytaf1 identifies2 conserved and competing interaction surfaces in3 transcriptional activation
61	c2ejnB	Alignment	not modelled	15.0	14	PDB header: allergen Chain: B: PDB Molecule: major allergen i polypeptide chain 1, chain 2; PDBTitle: structural characterization of the tetrameric form of the major cat2 allergen fel d 1
62	c2dfwA	Alignment	not modelled	14.6	29	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
63	c1d3uA	Alignment	not modelled	14.5	20	PDB header: gene regulation/dna Chain: A: PDB Molecule: tata-binding protein; PDBTitle: tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
64	c3gpiA	Alignment	not modelled	14.3	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of putative nad-dependent epimerase/dehydratase from2 methylobacillus flagellatus
65	c2wtmC	Alignment	not modelled	14.3	14	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
66	c6mu0A	Alignment	not modelled	14.3	15	PDB header: isomerase Chain: A: PDB Molecule: probable ribose-5-phosphate isomerase b; PDBTitle: crystal structure of ribose-5-phosphate isomerase b from mycoplasma2 genitalium with bound ribulose-5-phosphate
67	d2v4ja2	Alignment	not modelled	14.1	17	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
68	c5vtoA	Alignment	not modelled	14.1	22	PDB header: hydrolase Chain: A: PDB Molecule: blasticidin m; PDBTitle: solution structure of blsm
69	c3s5pA	Alignment	not modelled	14.0	28	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
70	c2i3dA	Alignment	not modelled	13.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu1826; PDBTitle: crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
71	d2i3da1	Alignment	not modelled	13.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
72	c4qnnC	Alignment	not modelled	13.8	12	PDB header: hydrolase Chain: C: PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom
73	c6fxsA	Alignment	not modelled	13.7	10	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase, putative; PDBTitle: structure of trypanosoma brucei type b ribose 5-phosphate isomerase
74	d1utra	Alignment	not modelled	13.6	19	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
75	c4xb6D	Alignment	not modelled	13.6	30	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
76	d1g8ka1	Alignment	not modelled	13.4	25	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
77	d1txga2	Alignment	not modelled	13.1	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
78	c2hdwB	Alignment	not modelled	13.0	21	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
79	c1pvaA	Alignment	not modelled	12.6	13	PDB header: allergen Chain: A: PDB Molecule: major allergen i polypeptide, fused chain

79	c1p0vA	Alignment	not modelled	12.0	13	2, chain 1; PDBTitle: crystal structure of fel d 1- the major cat allergen
80	d1miua4	Alignment	not modelled	12.5	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
81	d1o1xa	Alignment	not modelled	12.4	17	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
82	c2iv3B	Alignment	not modelled	12.4	24	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
83	d2vvpa1	Alignment	not modelled	12.2	17	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
84	d2dfaa1	Alignment	not modelled	12.1	21	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
85	c4em8A	Alignment	not modelled	12.0	22	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
86	d1kn6a	Alignment	not modelled	11.9	26	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Prohormone convertase 1 pro-domain
87	d2auna2	Alignment	not modelled	11.7	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
88	c3he8A	Alignment	not modelled	11.6	22	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
89	c5b3kA	Alignment	not modelled	11.5	17	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa
90	c2ydyA	Alignment	not modelled	11.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine adenosyltransferase 2 subunit beta; PDBTitle: crystal structure of human s-adenosylmethionine synthetase 2, beta2 subunit in orthorhombic crystal form
91	d1ccda	Alignment	not modelled	11.5	19	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
92	d1iioa	Alignment	not modelled	11.5	17	Fold: EF Hand-like Superfamily: Hypothetical protein MTH865 Family: Hypothetical protein MTH865
93	c6ejjA	Alignment	not modelled	11.5	18	PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
94	c4za1A	Alignment	not modelled	11.4	5	PDB header: transferase Chain: A: PDB Molecule: nosa; PDBTitle: crystal structure of nosa involved in nosiheptide biosynthesis
95	c3guxA	Alignment	not modelled	11.4	19	PDB header: hydrolase Chain: A: PDB Molecule: putative zn-dependent exopeptidase; PDBTitle: crystal structure of a putative zn-dependent exopeptidase (bvu_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
96	d1h0ha1	Alignment	not modelled	11.4	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
97	d1j1ta	Alignment	not modelled	11.3	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Alginate lyase
98	d1nn4a	Alignment	not modelled	10.9	22	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
99	d1cdwa1	Alignment	not modelled	10.8	13	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain