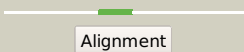
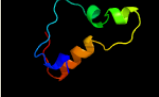
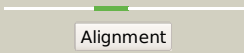

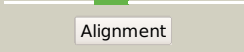
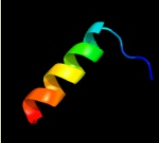
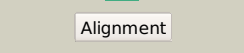
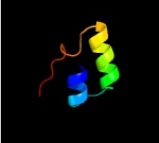

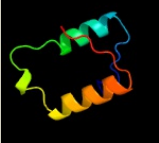
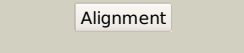

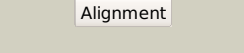



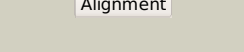

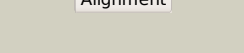

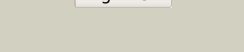












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3732_(-)_4183112_4184170
Date	Fri Aug 9 18:20:43 BST 2019
Unique Job ID	889f8b4b3e16579f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gk3a1	 Alignment		57.9	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
2	c2z0lA_	 Alignment		57.3	32	PDB header: replication Chain: A: PDB Molecule: early antigen protein d; PDBTitle: crystal structure of ebv-dna polymerase accessory protein2 bmr1
3	c3hslX_	 Alignment		56.7	26	PDB header: replication Chain: X: PDB Molecule: orf59; PDBTitle: the crystal structure of pf-8, the dna polymerase accessory subunit2 from kaposi's sarcoma-associated herpesvirus
4	c2arfA_	 Alignment		46.5	39	PDB header: hydrolase Chain: A: PDB Molecule: wilson disease atpase; PDBTitle: solution structure of the wilson atpase n-domain in the2 presence of atp
5	d1t0ba_	 Alignment		39.9	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: ThuA-like
6	c3rhtB_	 Alignment		39.1	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: (gatase1)-like protein; PDBTitle: crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
7	c4ifsA_	 Alignment		38.2	7	PDB header: transcription, replication Chain: A: PDB Molecule: fact complex subunit ssrp1; PDBTitle: crystal structure of the hssrp1 middle domain
8	c2kngA_	 Alignment		31.4	16	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2
9	d1q7ra_	 Alignment		29.7	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
10	d2dl6a1	 Alignment		28.5	27	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
11	d2nv0a1	 Alignment		27.5	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

12	d2axtj1	Alignment		27.2	21	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
13	c3a0hj_	Alignment		27.2	21	PDB header: electron transport Chain: J; PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
14	c4e5vA_	Alignment		27.1	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative thua-like protein; PDBTitle: crystal structure of a putative thua-like protein (parmer_02418) from 2 parabacteroides merdae atcc 43184 at 1.75 a resolution
15	c5lbkA_	Alignment		24.0	15	PDB header: hydrolase Chain: A; PDB Molecule: copper-transporting atpase paa2, chloroplastic; PDBTitle: crystal structure of the n-domain of hma8, a copper-transporting p-2 type atpase
16	c5vidG_	Alignment		23.3	23	PDB header: toxin Chain: G; PDB Molecule: bot.0671.2; PDBTitle: receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2
17	c5vidI_	Alignment		23.3	23	PDB header: toxin Chain: I; PDB Molecule: bot.0671.2; PDBTitle: receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2
18	d1r2aa_	Alignment		21.2	24	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
19	c3jcuJ_	Alignment		20.9	26	PDB header: membrane protein Chain: J; PDB Molecule: photosystem ii reaction center protein j; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
20	c5xnmj_	Alignment		20.3	26	PDB header: membrane protein Chain: J; PDB Molecule: photosystem ii reaction center protein j; PDBTitle: structure of unstacked c2s2m2-type psii-lhcii supercomplex from pismus2 sativum
21	c1wwuA_	Alignment	not modelled	20.0	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein flj21935; PDBTitle: solution structure of the sam_pnt domain of human protein2 flj21935
22	c2issF_	Alignment	not modelled	20.0	16	PDB header: lyase, transferase Chain: F; PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
23	c3mi6A_	Alignment	not modelled	19.5	14	PDB header: hydrolase Chain: A; PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
24	d2qmsa1	Alignment	not modelled	18.1	26	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
25	c5kzoA_	Alignment	not modelled	18.1	31	PDB header: transcription Chain: A; PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: notch1 transmembrane and associated juxtamembrane segment
26	c5hhaB_	Alignment	not modelled	17.5	11	PDB header: hydrolase Chain: B; PDB Molecule: pvdo; PDBTitle: structure of pvdo from pseudomonas aeruginosa
27	c2ckaA_	Alignment	not modelled	16.6	24	PDB header: hydrolase Chain: A; PDB Molecule: chromodomain-helicase-dna-binding protein 8; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
						Fold: GYF/BRK domain-like

28	d2ckaa1	Alignment	not modelled	16.6	24	Superfamily: BRK domain-like Family: BRK domain-like
29	d1qf6a1	Alignment	not modelled	16.2	15	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
30	c2e8mA	Alignment	not modelled	15.9	25	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of f2 epidermal growth receptor pathway substrate 8
31	c5vymB	Alignment	not modelled	15.8	13	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase bgab; PDBTitle: crystal structure of beta-galactosidase from bifidobacterium2 adolescentis
32	d2auwa1	Alignment	not modelled	15.3	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
33	c2koyA	Alignment	not modelled	14.5	28	PDB header: metal transport Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: structure of the e1064a mutant of the n-domain of wilson disease2 associated protein
34	c4jqsC	Alignment	not modelled	14.0	20	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative thua-like protein (bacuni_01602) from2 bacteroides uniformis atcc 8492 at 2.30 a resolution
35	c6eeqA	Alignment	not modelled	13.4	17	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxyphenylacetaldehyde synthase; PDBTitle: crystal structure of rhodiola rosea 4-hydroxyphenylacetaldehyde2 synthase
36	c2lowA	Alignment	not modelled	13.1	19	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip
37	c4iapB	Alignment	not modelled	13.1	33	PDB header: lipid binding protein/ hydrolase Chain: B: PDB Molecule: oxysterol-binding protein homolog 3, endolysin, oxysterol- PDBTitle: crystal structure of ph domain of osh3 from saccharomyces cerevisiae
38	c2lnvA	Alignment	not modelled	12.8	10	PDB header: transport protein Chain: A: PDB Molecule: general secretion pathway protein c; PDBTitle: solution structure of gspc-hr of typeii secretion system
39	d1f44a1	Alignment	not modelled	12.6	17	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
40	c2kmvA	Alignment	not modelled	12.4	28	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the nucleotide binding domain of the2 human menkes protein in the atp-free form
41	c4divH	Alignment	not modelled	11.6	24	PDB header: viral protein Chain: H: PDB Molecule: orf48; PDBTitle: the structure of a 1.8 mda viral genome injection device suggests2 alternative infection mechanisms
42	d1nyra1	Alignment	not modelled	11.4	14	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
43	c6a4tB	Alignment	not modelled	11.0	21	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
44	d1rh6a	Alignment	not modelled	10.8	30	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
45	c3l4eA	Alignment	not modelled	10.7	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
46	c3sozC	Alignment	not modelled	10.3	20	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: cytoplasmic protein stm1381; PDBTitle: cytoplasmic protein stm1381 from salmonella typhimurium lt2
47	c4zdtB	Alignment	not modelled	10.2	21	PDB header: hydrolase Chain: B: PDB Molecule: structure-specific endonuclease subunit slx4; PDBTitle: crystal structure of the ring finger domain of slx1 in complex with2 the c-terminal domain of slx4
48	c2zf9D	Alignment	not modelled	10.2	14	PDB header: structural protein Chain: D: PDB Molecule: scae cell-surface anchored scaffoldin protein; PDBTitle: crystal structure of a type iii cohesin module from the cellulosomal2 scae cell-surface anchoring scaffoldin of ruminococcus flavifaciens
49	c2rvfA	Alignment	not modelled	9.6	14	PDB header: signaling protein Chain: A: PDB Molecule: predicted protein; PDBTitle: solution nmr structure of monosiga brevicollis crk/crk1 homolog2 (crka1) sh2 domain
50	d1y7qa1	Alignment	not modelled	9.5	7	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: SCAN domain
51	c2n2aA	Alignment	not modelled	9.4	28	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
52	c4gf4A	Alignment	not modelled	9.1	47	PDB header: transport protein Chain: A: PDB Molecule: porin b; PDBTitle: low ph structure of pseudomonas putida oprb
53	c3qxyA	Alignment	not modelled	9.1	20	PDB header: transferase Chain: A: PDB Molecule: n-lysine methyltransferase setd6;

						PDBTitle: human setd6 in complex with rela lys310
54	d1lt7a_	Alignment	not modelled	8.7	25	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
55	d1pm6a_	Alignment	not modelled	8.4	30	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
56	c4rwwB_	Alignment	not modelled	8.2	13	PDB header: protein binding Chain: B: PDB Molecule: lmo2692 protein; PDBTitle: crystal structure of l. monocytogenes psta in complex with cyclic-di-2 amp
57	c2momB_	Alignment	not modelled	8.2	10	PDB header: membrane protein Chain: B: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
58	c2momC_	Alignment	not modelled	8.2	10	PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
59	d2d9ia1	Alignment	not modelled	8.2	14	Fold: IF3-like Superfamily: SMR domain-like Family: Smr domain
60	d2obba1	Alignment	not modelled	8.1	11	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
61	d1ou9a_	Alignment	not modelled	7.8	27	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
62	c2auwB_	Alignment	not modelled	7.7	19	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
63	d1wu2a1	Alignment	not modelled	7.6	13	Fold: beta-clip Superfamily: MoeA C-terminal domain-like Family: MoeA C-terminal domain-like
64	c4rleA_	Alignment	not modelled	7.2	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yaaq; PDBTitle: crystal structure of the c-di-amp binding pii-like protein dara
65	c5fr7B_	Alignment	not modelled	7.1	33	PDB header: signaling protein Chain: B: PDB Molecule: amyr; PDBTitle: erwinia amylovora amyr amyovoror repressor, a member of the ybjn2 protein family
66	c5z34A_	Alignment	not modelled	7.0	18	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: the structure of a chitin deacetylase from bombyx mori provide the2 first insight into insect chitin deacetylation mechanism
67	d1tlea2	Alignment	not modelled	7.0	11	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Subtilase propeptides/inhibitors
68	c2ipxA_	Alignment	not modelled	7.0	14	PDB header: transferase Chain: A: PDB Molecule: rrna 2'-o-methyltransferase fibrillarin; PDBTitle: human fibrillarlin
69	c4fnrB_	Alignment	not modelled	6.9	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha-galactosidase agaa; PDBTitle: crystal structure of gh36 alpha-galactosidase agaa from geobacillus2 stearothermophilus
70	d1kwga1	Alignment	not modelled	6.9	17	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
71	c2xn1B_	Alignment	not modelled	6.9	19	PDB header: hydrolase Chain: B: PDB Molecule: alpha-galactosidase; PDBTitle: structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
72	d1un8a4	Alignment	not modelled	6.8	21	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
73	c4wk1A_	Alignment	not modelled	6.7	17	PDB header: signaling protein Chain: A: PDB Molecule: psta; PDBTitle: crystal structure of staphylococcus aureus psta in complex with c-di-2 amp
74	c2shpA_	Alignment	not modelled	6.7	19	PDB header: tyrosine phosphatase Chain: A: PDB Molecule: shp-2; PDBTitle: tyrosine phosphatase shp-2
75	c2k4zA_	Alignment	not modelled	6.6	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dsrr; PDBTitle: solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
76	d1nrva_	Alignment	not modelled	6.5	19	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
77	c5h77B_	Alignment	not modelled	6.5	25	PDB header: signaling protein, immune system Chain: B: PDB Molecule: camp-dependent protein kinase type ii-alpha regulatory PDBTitle: crystal structure of the pka-protein a fusion protein
78	d2hwna1	Alignment	not modelled	6.5	27	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
						Fold: IF3-like

79	d1dcja_	Alignment	not modelled	6.4	10	Superfamily: SirA-like Family: SirA-like
80	d1y1oa_	Alignment	not modelled	6.4	18	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: RecU-like
81	d1y4ja1	Alignment	not modelled	6.4	11	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Sulfatase-modifying factor-like
82	c1y1oC_	Alignment	not modelled	6.4	18	PDB header: recombination Chain: C: PDB Molecule: penicillin-binding protein-related factor a; PDBTitle: x-ray crystal structure of penicillin-binding protein-2 related factor a from bacillus stearothermophilus
83	d2bu1a1	Alignment	not modelled	6.3	22	Fold: RNA bacteriophage capsid protein Superfamily: RNA bacteriophage capsid protein Family: RNA bacteriophage capsid protein
84	c3m05A_	Alignment	not modelled	6.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pepe_1480; PDBTitle: the crystal structure of a functionally unknown protein pepe_1480 from2 pediococcus pentosaceus atcc 25745
85	c2kcuA_	Alignment	not modelled	6.2	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ctr107; PDBTitle: nmr solution structure of an uncharacterized protein from chlorobium2 tepidum. northeast structural genomics target ctr107
86	c4ce4I_	Alignment	not modelled	6.0	25	PDB header: ribosome Chain: L: PDB Molecule: PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
87	c1rznB_	Alignment	not modelled	5.9	18	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein u; PDBTitle: crystal structure of penicillin-binding protein-related2 factor a from bacillus subtilis.
88	d1oi2a_	Alignment	not modelled	5.8	14	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
89	d2v0ea1	Alignment	not modelled	5.8	27	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
90	c2yfnA_	Alignment	not modelled	5.8	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase-sucrose kinase agask; PDBTitle: galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
91	c2vkcA_	Alignment	not modelled	5.8	6	PDB header: hydrolase Chain: A: PDB Molecule: nedd4-binding protein 2; PDBTitle: solution structure of the b3bp smr domain
92	d1bpoa1	Alignment	not modelled	5.8	16	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Clathrin heavy-chain linker domain
93	c2w56B_	Alignment	not modelled	5.8	17	PDB header: unknown function Chain: B: PDB Molecule: vc0508; PDBTitle: structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
94	d2essa1	Alignment	not modelled	5.7	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
95	c3icfB_	Alignment	not modelled	5.7	13	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase t; PDBTitle: structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5
96	d1evsa_	Alignment	not modelled	5.7	55	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Long-chain cytokines
97	c5svtA_	Alignment	not modelled	5.6	20	PDB header: membrane protein Chain: A: PDB Molecule: p2x purinoceptor 3; PDBTitle: anomalous cs+ signal reveals the site of na+ ion entry to the channel2 pore of the human p2x3 ion channel through the extracellular3 fenestrations
98	c6eemB_	Alignment	not modelled	5.6	12	PDB header: lyase Chain: B: PDB Molecule: tyrosine/dopa decarboxylase; PDBTitle: crystal structure of papaver somniferum tyrosine decarboxylase in2 complex with l-tyrosine
99	c2iu6B_	Alignment	not modelled	5.5	16	PDB header: transferase Chain: B: PDB Molecule: dihydroxyacetone kinase; PDBTitle: regulation of the dha operon of lactococcus lactis