

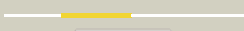
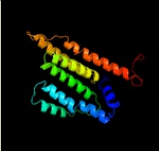
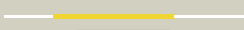



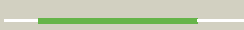


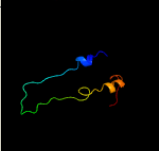




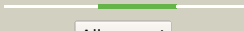


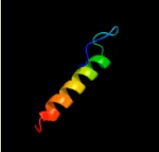




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3792 (-) _4238110_4240041
Date	Fri Aug 9 18:20:50 BST 2019
Unique Job ID	Oba6fe626153ad6e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5f15A_	 Alignment		94.0	13	PDB header: transferase Chain: A: PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
2	c6p25A_	 Alignment		73.7	13	PDB header: transferase Chain: A: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
3	c3wajA_	 Alignment		72.9	13	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
4	c4ymkA_	 Alignment		69.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase 1; PDBTitle: crystal structure of stearyl-coenzyme a desaturase 1
5	c6eznF_	 Alignment		57.7	12	PDB header: membrane protein Chain: F: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
6	c4fypA_	 Alignment		57.0	17	PDB header: plant protein Chain: A: PDB Molecule: vegetative storage protein 1; PDBTitle: crystal structure of plant vegetative storage protein
7	c1okgA_	 Alignment		53.9	13	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
8	c4dh4A_	 Alignment		50.6	23	PDB header: isomerase Chain: A: PDB Molecule: mif; PDBTitle: macrophage migration inhibitory factor toxoplasma gondii
9	c5ir6B_	 Alignment		50.4	11	PDB header: oxidoreductase Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
10	c4nsmA_	 Alignment		48.1	43	PDB header: structural protein Chain: A: PDB Molecule: collagen-like protein sclb; PDBTitle: crystal structure of the streptococcal collagen-like protein 22 globular domain from invasive m3-type group a streptococcus
11	c3utnX_	 Alignment		45.9	22	PDB header: transferase Chain: X: PDB Molecule: thiosulfate sulfurtransferase tum1; PDBTitle: crystal structure of tum1 protein from saccharomyces cerevisiae

12	c6cuqB_	Alignment		45.9	11	PDB header: cytokine Chain: B: PDB Molecule: macrophage migration inhibitory factor-like protein; PDBTitle: crystal structure of macrophage migration inhibitory factor-like2 protein (ehmif) from entamoeba histolytica
13	d1y5ic1	Alignment		42.1	24	Fold: Heme-binding four-helical bundle Superfamily: Respiratory nitrate reductase 1 gamma chain Family: Respiratory nitrate reductase 1 gamma chain
14	c2m7gA_	Alignment		38.6	24	PDB header: cell adhesion, structural protein, elect Chain: A: PDB Molecule: geopilin domain 1 protein; PDBTitle: structure of the type iva major pilin from the electrically conductive2 bacterial nanowires of geobacter sulfurreducens
15	d2ji7a3	Alignment		38.1	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
16	d1ypze2	Alignment		38.0	37	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
17	c5un4C_	Alignment		37.8	17	PDB header: hydrolase Chain: C: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of native fused 4-ot
18	c1yo8A_	Alignment		37.7	26	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-2; PDBTitle: structure of the c-terminal domain of human thrombospondin-2
19	c1ux6A_	Alignment		36.2	30	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-1; PDBTitle: structure of a thrombospondin c-terminal fragment reveals a novel2 calcium core in the type 3 repeats
20	c3zm8A_	Alignment		36.0	43	PDB header: hydrolase Chain: A: PDB Molecule: gh26 endo-beta-1,4-mannanase; PDBTitle: crystal structure of podospora anserina gh26-cbm352 beta-(1,4)-mannanase
21	c3sy6A_	Alignment	not modelled	34.4	37	PDB header: cell adhesion Chain: A: PDB Molecule: fimbrial protein bf1861; PDBTitle: crystal structure of a fimbrial protein bf1861 [bacteroides fragilis2 nctc 9343] (bf1861) from bacteroides fragilis nctc 9343 at 1.90 a3 resolution
22	d2gdqa1	Alignment	not modelled	33.8	20	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
23	c3fbyC_	Alignment	not modelled	33.7	34	PDB header: cell adhesion Chain: C: PDB Molecule: cartilage oligomeric matrix protein; PDBTitle: the crystal structure of the signature domain of cartilage oligomeric2 matrix protein.
24	d2d9ra1	Alignment	not modelled	32.9	30	Fold: Double-split beta-barrel Superfamily: AF2212/PG0164-like Family: PG0164-like
25	d1gd0a_	Alignment	not modelled	32.1	18	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
26	c4b8yA_	Alignment	not modelled	32.0	11	PDB header: transport protein/siderophore Chain: A: PDB Molecule: fhud2; PDBTitle: ferrichrome-bound fhud2
27	c4p55A_	Alignment	not modelled	31.6	29	PDB header: dna binding protein Chain: A: PDB Molecule: viral irf2-like protein; PDBTitle: crystal structure of dna binding domain of k11 from kshv
28	d1hxma2	Alignment	not modelled	30.8	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
29	c6ntwA_	Alignment	not modelled	30.7	17	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable l,d-transpeptidase yccb;

						PDBTitle: crystal structure of e. coli yccb
30	c3rceA	Alignment	not modelled	30.6	12	PDB header: transferase/peptide Chain: A: PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb
31	c3ufiA	Alignment	not modelled	30.5	33	PDB header: cell adhesion Chain: A: PDB Molecule: hypothetical protein bacova_04980; PDBTitle: crystal structure of a putative cell adhesion protein (bacova_04980)2 from bacteroides ovatus atcc 8483 at 2.18 a resolution
32	c4v3aC	Alignment	not modelled	29.8	75	PDB header: transport protein Chain: C: PDB Molecule: pleurotolysin b; PDBTitle: membrane bound pleurotolysin prepore (tmh1 lock) trapped with2 engineered disulphide cross-link
33	c6hpfA	Alignment	not modelled	29.6	60	PDB header: hydrolase Chain: A: PDB Molecule: endo-b-mannanase; PDBTitle: structure of inactive e165q mutant of fungal non-cbm carrying gh262 endo-b-mannanase from yunnania penicillata in complex with alpha-62-3 61-di-galactosyl-mannotriose
34	c6basA	Alignment	not modelled	28.3	26	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase roda; PDBTitle: crystal structure of thermus thermophilus rod shape determining2 protein roda d255a mutant (q5six3_thet8)
35	c4m1eC	Alignment	not modelled	27.7	12	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from2 planctomyces limnophilus dsm 3776, nysgrc target 029364.
36	c3kopB	Alignment	not modelled	27.7	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
37	c3tjA	Alignment	not modelled	27.3	16	PDB header: membrane protein Chain: A: PDB Molecule: nupc family protein; PDBTitle: crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
38	c3fwtA	Alignment	not modelled	27.2	26	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: crystal structure of leishmania major mif2
39	c2oq2B	Alignment	not modelled	27.2	21	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
40	c5flyB	Alignment	not modelled	27.0	13	PDB header: metal transport Chain: B: PDB Molecule: ferrichrome-binding periplasmic protein; PDBTitle: the fhud protein from s.pseudintermedius
41	c4k4kA	Alignment	not modelled	26.6	42	PDB header: cell adhesion Chain: A: PDB Molecule: putative cell adhesion protein; PDBTitle: crystal structure of a putative cell adhesion protein (bacuni_00621)2 from bacteroides uniformis atcc 8492 at 1.67 a resolution
42	c3caiA	Alignment	not modelled	26.0	18	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
43	c5l2bC	Alignment	not modelled	25.7	19	PDB header: transport protein Chain: C: PDB Molecule: nucleoside permease; PDBTitle: structure of cntnw n149s, e332a in an outward-facing state
44	d1ulza2	Alignment	not modelled	25.7	17	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
45	d1ku0a	Alignment	not modelled	25.6	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
46	c5zbhA	Alignment	not modelled	25.5	15	PDB header: signaling protein Chain: A: PDB Molecule: neuropeptide y receptor type 1,t4 lysozyme,neuropeptide y PDBTitle: the crystal structure of human neuropeptide y y1 receptor with bms-2 193885
47	c6c14A	Alignment	not modelled	25.5	19	PDB header: membrane protein, metal transport Chain: A: PDB Molecule: protocadherin-15; PDBTitle: cryoem structure of mouse pcdh15-1ec-lhfp15 complex
48	c4tvrA	Alignment	not modelled	25.4	17	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase uhrf2; PDBTitle: tandem tudor and phd domains of uhrf2
49	c5wt2A	Alignment	not modelled	24.8	11	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase iscs; PDBTitle: nifs from helicobacter pylori
50	d1n2za	Alignment	not modelled	24.1	9	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
51	c4or2A	Alignment	not modelled	24.1	17	PDB header: signaling protein Chain: A: PDB Molecule: soluble cytochrome b562, metabotropic glutamate receptor 1; PDBTitle: human class c g protein-coupled metabotropic glutamate receptor 1 in2 complex with a negative allosteric modulator
52	d1wi0a	Alignment	not modelled	24.0	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
53	c6nqiB	Alignment	not modelled	23.4	17	PDB header: splicing Chain: B: PDB Molecule: pre-mrna splicing factor prp8; PDBTitle: prp8 rh domain from c. merolae
54	c5ip0C	Alignment	not modelled	23.4	15	PDB header: structural protein Chain: C: PDB Molecule: pha granule-associated protein;

						PDBTitle: pha binding protein phap (phasin)
55	c2i34B_	Alignment	not modelled	23.2	28	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: the crystal structure of class c acid phosphatase from bacillus2 anthracis with tungstate bound
56	c4ic7B_	Alignment	not modelled	23.2	27	PDB header: transferase Chain: B: PDB Molecule: dual specificity mitogen-activated protein kinase kinase 5; PDBTitle: crystal structure of the erk5 kinase domain in complex with an mkk52 binding fragment
57	c2hihB_	Alignment	not modelled	23.1	25	PDB header: hydrolase Chain: B: PDB Molecule: lipase 46 kda form; PDBTitle: crystal structure of staphylococcus hyicus lipase
58	c5ah1A_	Alignment	not modelled	22.8	25	PDB header: hydrolase Chain: A: PDB Molecule: triacylglycerol lipase; PDBTitle: structure of esta from clostridium botulinum
59	c2bvtB_	Alignment	not modelled	22.3	44	PDB header: hydrolase Chain: B: PDB Molecule: beta-1,4-mannanase; PDBTitle: the structure of a modular endo-beta-1,4-mannanase from cellulomonas2 fimi explains the product specificity of glycoside hydrolase family3 26 mannanases.
60	c6eazA_	Alignment	not modelled	22.3	23	PDB header: metal binding protein Chain: A: PDB Molecule: calcium uptake protein 2, mitochondrial; PDBTitle: apo structure of the mitochondrial calcium uniporter protein micu2
61	c3siiA_	Alignment	not modelled	22.0	23	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: poly(adp-ribose) glycohydrolase; PDBTitle: the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
62	c4epzA_	Alignment	not modelled	22.0	25	PDB header: transcription Chain: A: PDB Molecule: transcription anti-terminator antagonist upxz; PDBTitle: crystal structure of a transcription anti-terminator antagonist upxz2 (bacuni_04315) from bacteroides uniformis atcc 8492 at 1.68 a3 resolution
63	d2abwa1	Alignment	not modelled	21.8	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
64	c3b64A_	Alignment	not modelled	21.7	30	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: macrophage migration inhibitory factor (mif) from2 /leishmania major
65	c3pntA_	Alignment	not modelled	21.7	46	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: nad+-glycohydrolase; PDBTitle: crystal structure of the streptococcus pyogenes nad+ glycohydrolase2 spn in complex with ifs, the immunity factor for spn
66	c5ah0B_	Alignment	not modelled	21.4	8	PDB header: hydrolase Chain: B: PDB Molecule: lipase; PDBTitle: structure of lipase 1 from pelosinus fermentans
67	d1ur4a_	Alignment	not modelled	21.4	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
68	c3e77A_	Alignment	not modelled	21.3	15	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: human phosphoserine aminotransferase in complex with plp
69	d1ji3a_	Alignment	not modelled	21.2	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
70	c3wdrA_	Alignment	not modelled	21.2	50	PDB header: hydrolase Chain: A: PDB Molecule: beta-mannanase; PDBTitle: crystal structure of beta-mannanase from a symbiotic protist of the2 termite reticulitermes speratus complexed with gluco-manno-3 oligosaccharide
71	c4qb7A_	Alignment	not modelled	21.1	33	PDB header: cell adhesion Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a fimbrial protein (bvu_2522) from bacteroides2 vulgatus atcc 8482 at 2.55 a resolution
72	c5j1sB_	Alignment	not modelled	21.1	17	PDB header: hydrolase Chain: B: PDB Molecule: torsin-1a-interacting protein 2; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
73	c4kmhB_	Alignment	not modelled	21.0	43	PDB header: protein binding Chain: B: PDB Molecule: suppressor of fused homolog; PDBTitle: crystal structure of suppressor of fused d20
74	d1jmxg_	Alignment	not modelled	20.6	27	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Quinohemoprotein amine dehydrogenase C chain Family: Quinohemoprotein amine dehydrogenase C chain
75	c3t2IA_	Alignment	not modelled	20.2	42	PDB header: cell adhesion Chain: A: PDB Molecule: putative cell adhesion protein; PDBTitle: crystal structure of a putative cell adhesion protein (bf1858) from2 bacteroides fragilis nctc 9343 at 2.33 a resolution
76	c4c82A_	Alignment	not modelled	20.1	13	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: ispf (plasmodium falciparum) unliganded structure
77	d2cyga1	Alignment	not modelled	20.1	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
78	c5iwvD_	Alignment	not modelled	19.9	19	PDB header: lyase Chain: D: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from bacillus subtilis complexed with cmp and mg2+

79	c5f5nA_	Alignment	not modelled	19.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: monoxygenase; PDBTitle: the structure of monoxygenase ksta11 in complex with nad and its2 substrate
80	d1w23a_	Alignment	not modelled	19.7	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
81	d1ux6a2	Alignment	not modelled	19.6	18	Fold: TSP type-3 repeat Superfamily: TSP type-3 repeat Family: TSP type-3 repeat
82	c5msmD_	Alignment	not modelled	19.6	29	PDB header: cell cycle Chain: D: PDB Molecule: sister chromatid cohesion protein dcc1; PDBTitle: structure of the dcc1-ctf8-ctf18c trimer
83	d2fug21	Alignment	not modelled	19.6	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like
84	c4f6oA_	Alignment	not modelled	19.6	25	PDB header: hydrolase Chain: A: PDB Molecule: metacaspase-1; PDBTitle: crystal structure of the yeast metacaspase yca1
85	c6fkib_	Alignment	not modelled	19.5	20	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
86	c3cbwA_	Alignment	not modelled	19.4	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ydht protein; PDBTitle: crystal structure of the ydht protein from bacillus subtilis
87	c5lqdA_	Alignment	not modelled	19.4	16	PDB header: cell adhesion Chain: A: PDB Molecule: platelet glycoprotein 4; PDBTitle: the cidra domain from mcvr1 pfemp1 bound to cd36
88	c6hf4A_	Alignment	not modelled	19.2	50	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase family 26; PDBTitle: the structure of boman26b, a gh26 beta-mannanase from bacteroides2 ovatus, complexed with g1m4
89	c3ca8B_	Alignment	not modelled	19.0	42	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydcf; PDBTitle: crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
90	c1kyqC_	Alignment	not modelled	19.0	24	PDB header: oxidoreductase, lyase Chain: C: PDB Molecule: siroheme biosynthesis protein met8; PDBTitle: met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatae involved in siroheme synthesis.
91	d1okga1	Alignment	not modelled	18.8	14	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
92	d1kyqa2	Alignment	not modelled	18.7	18	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
93	c4f7bA_	Alignment	not modelled	18.4	21	PDB header: cell adhesion Chain: A: PDB Molecule: lysosome membrane protein 2; PDBTitle: structure of the lysosomal domain of limp-2
94	c4r6yA_	Alignment	not modelled	18.4	14	PDB header: transport protein Chain: A: PDB Molecule: putative 2-aminoethylphosphonate-binding periplasmic PDBTitle: crystal structure of solute-binding protein stm0429 from salmonella2 enterica subsp. enterica serovar typhimurium str. lt2, target efi-3 510776, a closed conformation, in complex with glycerol and acetate
95	c2wqqA_	Alignment	not modelled	18.4	32	PDB header: transferase Chain: A: PDB Molecule: alpha-2,3-/2,8-sialyltransferase; PDBTitle: crystallographic analysis of monomeric cstii
96	c5v6hC_	Alignment	not modelled	18.3	33	PDB header: protein binding Chain: C: PDB Molecule: pdz domain-containing protein gjpc2; PDBTitle: crystal structure of myosin vi in complex with gh2 domain of gjpc2
97	c4z8wA_	Alignment	not modelled	18.0	23	PDB header: allergen Chain: A: PDB Molecule: major pollen allergen pla l 1; PDBTitle: crystal structure of the major plantain pollen allergen pla l 1
98	c3d8kD_	Alignment	not modelled	18.0	14	PDB header: hydrolase Chain: D: PDB Molecule: protein phosphatase 2c; PDBTitle: crystal structure of a phosphatase from a toxoplasma gondii
99	d1g9ka2	Alignment	not modelled	18.0	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain