




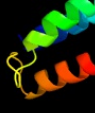





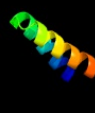





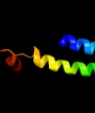



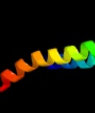


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3413c_(-)_3832326_3833225
Date	Fri Aug 9 18:20:08 BST 2019
Unique Job ID	538a8af8d9f489b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3vepC_	 Alignment		98.9	100	PDB header: membrane protein/transcription Chain: C; PDB Molecule: uncharacterized protein rv3413c/mt3522; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
2	c3vepX_	 Alignment		98.8	100	PDB header: membrane protein/transcription Chain: X; PDB Molecule: uncharacterized protein rv3413c/mt3522; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
3	c4ma1B_	 Alignment		93.2	25	PDB header: unknown function Chain: B; PDB Molecule: motility protein fimv; PDBTitle: tpr3 of fimv from p. aeruginosa (pao1)
4	c4fx5A_	 Alignment		74.0	12	PDB header: blood clotting Chain: A; PDB Molecule: von willebrand factor type a; PDBTitle: von willebrand factor type a from catenulispora acidiphila
5	c3dzaB_	 Alignment		68.5	11	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized putative membrane protein; PDBTitle: crystal structure of a putative membrane protein of unknown function2 (yfdx) from klebsiella pneumoniae subsp. at 1.65 a resolution
6	c6a09C_	 Alignment		68.0	11	PDB header: unknown function Chain: C; PDB Molecule: yfdx protein; PDBTitle: salmonella typhi yfdx in the p222 space group
7	d256ba_	 Alignment		65.4	17	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome b562
8	c4er9A_	 Alignment		63.7	11	PDB header: electron transport Chain: A; PDB Molecule: soluble cytochrome b562; PDBTitle: crystal structure of cytochrome b562 from salmonella enterica subsp.2 enterica serovar typhimurium str. 14028s
9	c4l6rA_	 Alignment		56.0	12	PDB header: membrane protein Chain: A; PDB Molecule: soluble cytochrome b562 and glucagon receptor chimera; PDBTitle: structure of the class b human glucagon g protein coupled receptor
10	c1wcrA_	 Alignment		53.5	12	PDB header: transferase Chain: A; PDB Molecule: pts system, n, n'-diacetylchitobiose-specific PDBTitle: trimeric structure of the enzyme iia from escherichia coli2 phosphotransferase system specific for n,n'-3 diacetylchitobiose
11	c3l8rA_	 Alignment		52.4	10	PDB header: transferase Chain: A; PDB Molecule: putative pts system, cellobiose-specific iia PDBTitle: the crystal structure of ptca from s. mutans

12	d2e2aa_	Alignment		51.7	17	Fold: Spectrin repeat-like Superfamily: Enzyme Ila from lactose specific PTS, Ila-lac Family: Enzyme Ila from lactose specific PTS, Ila-lac
13	c2kc7A_	Alignment		51.3	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bfr218_protein; PDBTitle: solution nmr structure of bacteroides fragilis protein2 bfr1650. northeast structural genomics consortium target3 bfr218
14	c4fm3B_	Alignment		50.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized hypothetical protein; PDBTitle: crystal structure of a duf4398 family protein (pa2901) from2 pseudomonas aeruginosa pao1 at 2.47 a resolution
15	d1vh6a_	Alignment		47.3	13	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone FlIS Family: Flagellar export chaperone FlIS
16	c1vh6A_	Alignment		47.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of a flagellar protein
17	c6iiuA_	Alignment		47.2	16	PDB header: signaling protein Chain: A: PDB Molecule: soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, PDBTitle: crystal structure of the human thromboxane a2 receptor bound to2 ramatroban
18	c3zsuA_	Alignment		43.8	13	PDB header: photosynthesis Chain: A: PDB Molecule: tl12057 protein; PDBTitle: structure of the cyanoq protein from thermosynechococcus elongatus
19	c3k1iA_	Alignment		43.2	6	PDB header: chaperone Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal strcture of flis-hp1076 complex in h. pylori
20	c5b3hD_	Alignment		42.3	19	PDB header: transcription Chain: D: PDB Molecule: protein scarecrow; PDBTitle: the crystal structure of the jackdaw/idd10 bound to the heterodimeric2 shr-scr complex
21	c5fimA_	Alignment	not modelled	38.7	16	PDB header: unknown function Chain: A: PDB Molecule: ygau; PDBTitle: the structure of kbp.k from e. coli
22	c3ls1A_	Alignment	not modelled	38.5	9	PDB header: photosynthesis Chain: A: PDB Molecule: sll1638 protein; PDBTitle: crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
23	c3k1sE_	Alignment	not modelled	38.1	17	PDB header: transferase Chain: E: PDB Molecule: pts system, cellobiose-specific iia component; PDBTitle: crystal structure of the pts cellobiose specific enzyme iia from2 bacillus anthracis
24	c4uicA_	Alignment	not modelled	38.0	17	PDB header: sugar binding protein Chain: A: PDB Molecule: surface layer protein; PDBTitle: crystal structure of the s-layer protein rsbsc(31-844)
25	d2gy9t1	Alignment	not modelled	36.0	26	Fold: Spectrin repeat-like Superfamily: Ribosomal protein S20 Family: Ribosomal protein S20
26	c2ra1A_	Alignment	not modelled	33.1	17	PDB header: sugar binding protein Chain: A: PDB Molecule: surface layer protein; PDBTitle: crystal structure of the n-terminal part of the bacterial s-layer2 protein sbsc
27	c6g7oA_	Alignment	not modelled	33.0	16	PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562; PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
28	c5xefA_	Alignment	not modelled	32.9	9	PDB header: chaperone Chain: A: PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of flagellar chaperone from bacteria

29	c4cqiA_	Alignment	not modelled	31.3	18	PDB header: structural protein Chain: A: PDB Molecule: tubulin-binding cofactor a; PDBTitle: crystal structure of recombinant tubulin-binding cofactor a2 (tbca) from leishmania major
30	c2pv7B_	Alignment	not modelled	29.4	9	PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
31	d2cpa1	Alignment	not modelled	27.9	17	Fold: SAM domain-like Superfamily: HRDC-like Family: EXOSC10 HRDC domain-like
32	d2uubt1	Alignment	not modelled	27.5	21	Fold: Spectrin repeat-like Superfamily: Ribosomal protein S20 Family: Ribosomal protein S20
33	c5o5IT_	Alignment	not modelled	26.3	15	PDB header: ribosome Chain: T: PDB Molecule: 30s ribosomal protein s20; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
34	c2rpaA_	Alignment	not modelled	25.9	9	PDB header: hydrolase Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a1; PDBTitle: the solution structure of n-terminal domain of microtubule severing2 enzyme
35	c6p2iA_	Alignment	not modelled	24.2	9	PDB header: oxidoreductase, biosynthetic protein Chain: A: PDB Molecule: glycerate dehydrogenase; PDBTitle: acyclic imino acid reductase (bsp5) in complex with nadph and d-arg
36	c5oxeA_	Alignment	not modelled	23.9	38	PDB header: virus Chain: A: PDB Molecule: major virion protein; PDBTitle: structure of major capsid protein vp1 of aeropyrum pernix bacilliform2 virus 1 apbv1
37	c6grjG_	Alignment	not modelled	23.1	7	PDB header: toxin Chain: G: PDB Molecule: ahlb; PDBTitle: structure of the ahlb pore of the tripartite alpha-pore forming toxin,2 ahl, from aeromonas hydrophila.
38	c6fkhe_	Alignment	not modelled	21.9	18	PDB header: membrane protein Chain: E: PDB Molecule: atp synthase subunit alpha, chloroplastic; PDBTitle: chloroplast f1fo conformation 2
39	c3u8pB_	Alignment	not modelled	20.5	17	PDB header: fluorescent protein, electron transport Chain: B: PDB Molecule: cytochrome b562 integral fusion with enhanced green PDBTitle: cytochrome b562 integral fusion with egfp
40	d2np3a1	Alignment	not modelled	20.4	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
41	c5b3hB_	Alignment	not modelled	20.2	18	PDB header: transcription Chain: B: PDB Molecule: protein short-root; PDBTitle: the crystal structure of the jackdaw/idd10 bound to the heterodimeric2 shr-scr complex
42	c2rt6A_	Alignment	not modelled	20.1	15	PDB header: dna binding protein Chain: A: PDB Molecule: primosomal replication protein n"; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for pric n-2 terminal domain
43	d2f1ka1	Alignment	not modelled	19.5	16	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
44	c3gw4B_	Alignment	not modelled	18.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
45	c6q45P_	Alignment	not modelled	17.8	10	PDB header: hydrolase Chain: P: PDB Molecule: atp synthase epsilon chain; PDBTitle: f1-atpase from fusobacterium nucleatum
46	c1nzeA_	Alignment	not modelled	17.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: oxygen-evolving enhancer protein 3; PDBTitle: crystal structure of psbq polypeptide of photosystem ii2 from higher plants
47	d1nzea_	Alignment	not modelled	17.7	11	Fold: Four-helical up-and-down bundle Superfamily: Oxygen-evolving enhancer protein 3, Family: Oxygen-evolving enhancer protein 3,
48	d1y7ma2	Alignment	not modelled	17.3	24	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
49	d1yt3a2	Alignment	not modelled	17.3	26	Fold: SAM domain-like Superfamily: HRDC-like Family: RNase D C-terminal domains
50	c2mkxA_	Alignment	not modelled	16.9	27	PDB header: hydrolase Chain: A: PDB Molecule: autolysin; PDBTitle: solution structure of lysm the peptidoglycan binding domain of2 autolysin atla from enterococcus faecalis
51	c2y8nC_	Alignment	not modelled	16.7	14	PDB header: lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate decarboxylase large subunit; PDBTitle: crystal structure of glycy radical enzyme
52	c5i2gB_	Alignment	not modelled	16.2	25	PDB header: lyase Chain: B: PDB Molecule: diol dehydratase; PDBTitle: 1,2-propanediol dehydration in roseburia inulinivorans; structural2 basis for substrate and enantiomer selectivity
53	c4or2A_	Alignment	not modelled	16.2	18	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 PDB header: structural protein

54	c6ch3B_	Alignment	not modelled	15.9	13	Chain: B: PDB Molecule: flagellar secretion chaperone flis,flagellin; PDBTitle: crystal structure of the cytoplasmic domain of flha and flis-flh2 complex
55	c4ntxC_	Alignment	not modelled	15.6	35	PDB header: transport protein/toxin Chain: C: PDB Molecule: basic phospholipase a2 homolog tx-beta; PDBTitle: structure of acid-sensing ion channel in complex with snake toxin and2 amiloride
56	d1orjb_	Alignment	not modelled	14.6	15	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone Flh5 Family: Flagellar export chaperone Flh5
57	d1fe5a_	Alignment	not modelled	14.3	41	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
58	d1m8ra_	Alignment	not modelled	13.9	29	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
59	c4qfjA_	Alignment	not modelled	13.6	12	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topo-78, an n-terminal 78kda fragment of2 topoisomerase v
60	c4uz2D_	Alignment	not modelled	13.3	26	PDB header: hydrolase Chain: D: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the n-terminal lysm domains from the putative2 nlpc/p60 d,l endopeptidase from t. thermophilus
61	c5wzmA_	Alignment	not modelled	13.3	24	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: group iie secretory phospholipase a2; PDBTitle: crystal structure of human secreted phospholipase a2 group iie
62	c4xa8A_	Alignment	not modelled	13.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase nad-binding; PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from xanthobacter autotrophicus py2
63	c3zpjA_	Alignment	not modelled	13.1	20	PDB header: unknown function Chain: A: PDB Molecule: ton_1535; PDBTitle: crystal structure of ton1535 from thermococcus onnurineus na1
64	c5a8jA_	Alignment	not modelled	12.7	23	PDB header: transcription Chain: A: PDB Molecule: vwa2; PDBTitle: crystal structure of the arnb paralogue vwa2 from2 sulfobolbus acidocaldarius
65	c5k2lA_	Alignment	not modelled	12.7	20	PDB header: hydrolase Chain: A: PDB Molecule: chitinase, lysozyme; PDBTitle: crystal structure of lysm domain from volvox carteri chitinase
66	d1g2xa_	Alignment	not modelled	12.6	35	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
67	c3mxzA_	Alignment	not modelled	12.6	21	PDB header: chaperone Chain: A: PDB Molecule: tubulin-specific chaperone a; PDBTitle: crystal structure of tubulin folding cofactor a from arabidopsis2 thaliana
68	d2pv7a1	Alignment	not modelled	12.5	9	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
69	c2lbgA_	Alignment	not modelled	12.4	38	PDB header: membrane protein Chain: A: PDB Molecule: major prion protein; PDBTitle: structure of the chr of the prion protein in dpc micelles
70	d2a26a1	Alignment	not modelled	12.2	16	Fold: Long alpha-hairpin Superfamily: Calcyclin-binding protein-like Family: Siah interacting protein N terminal domain-like
71	d1p7oa_	Alignment	not modelled	12.1	41	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
72	c4fnvA_	Alignment	not modelled	11.8	32	PDB header: lyase Chain: A: PDB Molecule: heparinase iii protein, heparitin sulfate lyase; PDBTitle: crystal structure of heparinase iii
73	d1g0za_	Alignment	not modelled	11.7	41	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
74	d1s6ba_	Alignment	not modelled	11.7	35	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
75	c6f5dH_	Alignment	not modelled	11.6	15	PDB header: hydrolase Chain: H: PDB Molecule: atp synthase subunit delta, mitochondrial; PDBTitle: trypanosoma brucei f1-atpase
76	c2r5sB_	Alignment	not modelled	11.4	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp0806; PDBTitle: the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
77	d1po8a_	Alignment	not modelled	11.4	35	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
78	c2momC_	Alignment	not modelled	11.3	13	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
79	c2momB_	Alignment	not modelled	11.3	13	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
80	d1poaa_	Alignment	not modelled	11.3	35	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
81	c2w6jH_	Alignment	not modelled	11.2	14	PDB header: hydrolase Chain: H: PDB Molecule: f1-atpase delta subunit; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 5.
82	c2djpA_	Alignment	not modelled	11.1	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein sb145; PDBTitle: the solution structure of the lysm domain of human2 hypothetical protein sb145
83	c5gjqR_	Alignment	not modelled	11.1	11	PDB header: hydrolase Chain: R: PDB Molecule: 26s proteasome non-atpase regulatory subunit 6; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
84	c2rq7A_	Alignment	not modelled	11.0	18	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase epsilon chain; PDBTitle: solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1
85	c2ke3A_	Alignment	not modelled	11.0	67	PDB header: hydrolase Chain: A: PDB Molecule: neuroendocrine convertase 1; PDBTitle: pc1/3 dcsq sorting domain in chaps
86	d1e0ga_	Alignment	not modelled	11.0	22	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
87	d2f4la1	Alignment	not modelled	10.9	42	Fold: CUB-like Superfamily: Acetamidase/Formamidase-like Family: Acetamidase/Formamidase-like
88	c5b7jA_	Alignment	not modelled	10.9	32	PDB header: dna binding protein/dna Chain: A: PDB Molecule: switch-activating protein 1; PDBTitle: structure model of sap1-dna complex
89	d1ijla_	Alignment	not modelled	10.9	29	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
90	c3myfB_	Alignment	not modelled	10.9	11	PDB header: transferase Chain: B: PDB Molecule: sensor protein; PDBTitle: the crystal structure of the hpt domain from the hpt sensor hybrid2 histidine kinase from shewanella to 1.80a
91	d1g4ia_	Alignment	not modelled	10.7	41	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
92	c5fayA_	Alignment	not modelled	10.7	14	PDB header: lyase Chain: A: PDB Molecule: choline trimethylamine-lyase; PDBTitle: y208f mutant of choline tma-lyase
93	c2e76D_	Alignment	not modelled	10.4	9	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
94	c2rhfA_	Alignment	not modelled	10.3	25	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase recq; PDBTitle: d. radiodurans recq hrdc domain 3
95	c4ebzA_	Alignment	not modelled	10.0	10	PDB header: transferase Chain: A: PDB Molecule: chitin elicitor receptor kinase 1; PDBTitle: crystal structure of the ectodomain of a receptor like kinase
96	d1mh2a_	Alignment	not modelled	10.0	29	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
97	c4ymrB_	Alignment	not modelled	10.0	20	PDB header: protein transport Chain: B: PDB Molecule: protein snx21; PDBTitle: crystal structure of the domain swapped pxb/tpr domain of mouse snx21
98	c2l9yA_	Alignment	not modelled	10.0	24	PDB header: sugar binding protein Chain: A: PDB Molecule: cvnh-lysm lectin; PDBTitle: solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgs_03307)
99	c2fynO_	Alignment	not modelled	9.9	11	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex