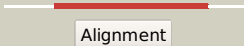
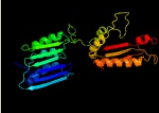










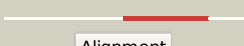






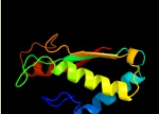


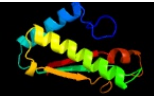







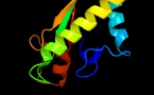


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0899_ (ompA)_1002815_1003795
Date	Fri Jul 26 01:50:49 BST 2019
Unique Job ID	5b6ca89c57077e7c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l26A_	 Alignment		100.0	100	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein rv0899/mt0922; PDBTitle: rv0899 from mycobacterium tuberculosis contains two separated domains
2	c5wtlB_	 Alignment		100.0	38	PDB header: membrane protein Chain: B: PDB Molecule: ompa family protein; PDBTitle: crystal structure of the periplasmic portion of outer membrane protein2 a (ompa) from capnocytophaga gingivalis
3	c5jirB_	 Alignment		100.0	32	PDB header: unknown function Chain: B: PDB Molecule: oop family ompa-ompf porin; PDBTitle: crystal structure of treponema pallidum protein tp0624
4	c2kgwA_	 Alignment		100.0	100	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein a; PDBTitle: solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
5	c6aeoA_	 Alignment		100.0	33	PDB header: protein transport Chain: A: PDB Molecule: maltose/maltodextrin-binding periplasmic protein,tssl; PDBTitle: tssl periplasmic domain
6	c4b5cC_	 Alignment		100.0	28	PDB header: lipid transport Chain: C: PDB Molecule: putative ompa family lipoprotein; PDBTitle: crystal structure of the peptidoglycan-associated lipoprotein from2 burkholderia pseudomallei
7	d2aizp1	 Alignment		100.0	26	Fold: Bacillus chorismate mutase-like Superfamily: OmpA-like Family: OmpA-like
8	c4zhwA_	 Alignment		100.0	38	PDB header: signaling protein Chain: A: PDB Molecule: yfib; PDBTitle: crystal structure of a bacterial signalling protein (n-terminal2 truncation)
9	c4zhvB_	 Alignment		100.0	39	PDB header: signaling protein Chain: B: PDB Molecule: yfib; PDBTitle: crystal structure of a bacterial signalling protein
10	c3khnB_	 Alignment		100.0	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: motb protein, putative; PDBTitle: crystal structure of putative motb like protein dvu_2228 from2 desulfovibrio vulgaris.
11	c6jfwA_	 Alignment		100.0	47	PDB header: membrane protein Chain: A: PDB Molecule: pa0833-pd protein; PDBTitle: crystal structure of pa0833 periplasmic domain from pseudomonas2 aeruginosa reveals an unexpected enlarged peptidoglycan binding3 pocket

12	c2k1sA	Alignment		100.0	48	PDB header: lipoprotein Chain: A: PDB Molecule: inner membrane lipoprotein yiad; PDBTitle: solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics consortium target3 er553.
13	c3s0yA	Alignment		100.0	31	PDB header: motor protein Chain: A: PDB Molecule: motility protein b; PDBTitle: the crystal structure of the periplasmic domain of motb (residues 64-2 256).
14	d2hqsc1	Alignment		100.0	30	Fold: Bacillus chorismate mutase-like Superfamily: OmpA-like Family: OmpA-like
15	c4g4xA	Alignment		100.0	31	PDB header: peptide binding protein Chain: A: PDB Molecule: peptidoglycan-associated lipoprotein; PDBTitle: crystal structure of peptidoglycan-associated lipoprotein from2 acinetobacter baumannii
16	c3td4D	Alignment		100.0	37	PDB header: membrane protein,peptide binding protein Chain: D: PDB Molecule: outer membrane protein omp38; PDBTitle: crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate
17	c5u1hB	Alignment		100.0	40	PDB header: peptide binding protein Chain: B: PDB Molecule: outer membrane porin f; PDBTitle: crystal structure of the c-terminal peptidoglycan binding domain of2 oprf (pa1777) from pseudomonas aeruginosa
18	c5m38A	Alignment		100.0	35	PDB header: sugar binding protein Chain: A: PDB Molecule: ompa family protein; PDBTitle: structure of the tagl peptidoglycan binding domain from eae6 t6ss
19	c3cyqM	Alignment		100.0	31	PDB header: membrane protein Chain: M: PDB Molecule: chemotaxis protein motb; PDBTitle: the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid
20	c4b62A	Alignment		100.0	37	PDB header: membrane protein Chain: A: PDB Molecule: tss11; PDBTitle: the structure of the cell wall anchor of the t6ss from pseudomonas2 aeruginosa
21	c1r1mA	Alignment	not modelled	100.0	38	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein class 4; PDBTitle: structure of the ompa-like domain of rmpm from neisseria2 meningitidis
22	d1r1ma	Alignment	not modelled	100.0	38	Fold: Bacillus chorismate mutase-like Superfamily: OmpA-like Family: OmpA-like
23	c3s0wB	Alignment	not modelled	100.0	31	PDB header: motor protein Chain: B: PDB Molecule: motility protein b; PDBTitle: the crystal structure of the periplasmic domain of helicobacter pylori2 motb (residues 78-256).
24	c4erhB	Alignment	not modelled	100.0	34	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein a; PDBTitle: the crystal structure of ompa domain of ompa from salmonella enterica2 subsp. enterica serovar typhimurium str. 14028s
25	c2zvYB	Alignment	not modelled	100.0	31	PDB header: membrane protein Chain: B: PDB Molecule: chemotaxis protein motb; PDBTitle: structure of the periplasmic domain of motb from salmonella2 (crystal form ii)
26	c3wpwB	Alignment	not modelled	100.0	33	PDB header: membrane protein Chain: B: PDB Molecule: pomb; PDBTitle: structure of pombc5, a periplasmic fragment of pomb from vibrio
27	c3ldtA	Alignment	not modelled	99.9	30	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein, ompa family protein; PDBTitle: crystal structure of an outer membrane protein(ompa)from2 legionella pneumophila
28	c3oonA	Alignment	not modelled	99.9	34	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein (tpn50); PDBTitle: the structure of an outer membrane protein from borrelia burgdorferi2 b31

29	c2zovA	Alignment	not modelled	99.9	32	PDB header: membrane protein Chain: A: PDB Molecule: chemotaxis protein motb; PDBTitle: structure of the periplasmic domain of motb from salmonella2 (crystal form i)
30	c2zf8A	Alignment	not modelled	99.8	27	PDB header: structural protein Chain: A: PDB Molecule: component of sodium-driven polar flagellar motor; PDBTitle: crystal structure of moty
31	c2kgsA	Alignment	not modelled	99.6	100	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein rv0899/mt0922; PDBTitle: solution structure of the amino-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
32	c6k2IA	Alignment	not modelled	62.4	11	PDB header: flavoprotein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of the siderophore-interacting protein sips from2 aeromonas hydrophila
33	c2r6hC	Alignment	not modelled	62.2	22	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:ubiquinone oxidoreductase, na translocating, f PDBTitle: crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
34	d1gvha3	Alignment	not modelled	61.1	27	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavo-hemoglobin, C-terminal domain
35	c3uuuA	Alignment	not modelled	58.7	28	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
36	c1gvhA	Alignment	not modelled	56.8	27	PDB header: oxidoreductase Chain: A: PDB Molecule: flavo-hemoprotein; PDBTitle: the x-ray structure of ferric escherichia coli2 flavo-hemoglobin reveals an unsuspected geometry of the3 distal heme pocket
37	c6qppA	Alignment	not modelled	54.5	28	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
38	c4u9uB	Alignment	not modelled	51.5	25	PDB header: oxidoreductase Chain: B: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit f; PDBTitle: crystal structure of nqr fad-binding domain from vibrio cholerae
39	c5gw8A	Alignment	not modelled	47.7	24	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
40	c3g7nA	Alignment	not modelled	45.8	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
41	d1tiaa	Alignment	not modelled	43.8	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
42	c4g1bB	Alignment	not modelled	41.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: flavo-hemoglobin; PDBTitle: x-ray structure of yeast flavo-hemoglobin in complex with econazole
43	c4eh1A	Alignment	not modelled	41.5	30	PDB header: oxidoreductase Chain: A: PDB Molecule: flavo-hemoprotein; PDBTitle: crystal structure of the flavo-hem-like-fad/nad binding domain of2 nitric oxide dioxygenase from vibrio cholerae o1 biovar el tor
44	c6gehA	Alignment	not modelled	41.2	17	PDB header: metal transport Chain: A: PDB Molecule: fad-binding 9, siderophore-interacting domain protein; PDBTitle: structure and reactivity of a siderophore-interacting protein from the2 marine bacterium shewanella reveals unanticipated functional3 versatility.
45	d1tiba	Alignment	not modelled	40.1	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
46	d1cqa3	Alignment	not modelled	39.2	20	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavo-hemoglobin, C-terminal domain
47	c6o0aA	Alignment	not modelled	36.7	26	PDB header: oxidoreductase Chain: A: PDB Molecule: flavo-hemoglobin; PDBTitle: crystal structure of flavo-hemoglobin from malassezia yamatoensis with2 bound fad and heme determined by iron sad phasing
48	c2gpiA	Alignment	not modelled	35.9	13	PDB header: fad-binding protein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
49	d1tvca2	Alignment	not modelled	34.1	11	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
50	c1cqxB	Alignment	not modelled	33.8	22	PDB header: lipid binding protein Chain: B: PDB Molecule: flavo-hemoprotein; PDBTitle: crystal structure of the flavo-hemoglobin from alcaligenes eutrophus at2 1.75 a resolution
51	c3l7pA	Alignment	not modelled	33.7	37	PDB header: transcription Chain: A: PDB Molecule: putative nitrogen regulatory protein pii; PDBTitle: crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
						PDB header: hydrolase

52	c3ngmB_	Alignment	not modelled	30.7	26	Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
53	c5xk2A_	Alignment	not modelled	30.4	19	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
54	c1tvcA_	Alignment	not modelled	30.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: methane monooxygenase component c; PDBTitle: fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
55	c4ozlA_	Alignment	not modelled	28.6	26	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen regulatory protein p-ii; PDBTitle: glnK2 from haloferax mediterranei complexed with amp
56	c3o0dF_	Alignment	not modelled	24.4	22	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
57	c5l8xA_	Alignment	not modelled	23.2	23	PDB header: transferase Chain: A: PDB Molecule: tetrahydromethanopterin s-methyltransferase subunit a; PDBTitle: x-ray structure of apo methanocaldococcus jannaschii methyltransferase2 subunit a at 1.85 angstrom
58	d1krha2	Alignment	not modelled	22.7	12	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
59	d1uzhc1	Alignment	not modelled	22.7	27	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
60	c4p6vF_	Alignment	not modelled	20.5	25	PDB header: oxidoreductase Chain: F: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit f; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
61	d1svdm1	Alignment	not modelled	20.2	19	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
62	c3ds8A_	Alignment	not modelled	20.2	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
63	d1rbli_	Alignment	not modelled	20.2	19	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
64	d1qy7a_	Alignment	not modelled	20.2	24	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
65	d1gk8i_	Alignment	not modelled	18.6	23	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
66	d1bwvs_	Alignment	not modelled	18.2	16	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
67	d1ej7s_	Alignment	not modelled	17.9	26	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
68	c3gbsA_	Alignment	not modelled	17.5	23	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
69	d1uwca_	Alignment	not modelled	17.5	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
70	d1cexa_	Alignment	not modelled	17.2	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
71	d8rucj_	Alignment	not modelled	17.1	26	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
72	d1lr1s_	Alignment	not modelled	17.1	27	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
73	c5o1uB_	Alignment	not modelled	16.8	21	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase; PDBTitle: structure of wildtype t.maritima pde (tm1595) with amp and mn2+
74	d1uzdc1	Alignment	not modelled	16.7	23	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
75	c5mz2l_	Alignment	not modelled	16.5	13	PDB header: photosynthesis Chain: I: PDB Molecule: rubisco small subunit; PDBTitle: rubisco from thalassiosira antarctica
76	d2v6ai1	Alignment	not modelled	16.1	23	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
77	c6eslB_	Alignment	not modelled	16.1	9	PDB header: hydrolase Chain: B: PDB Molecule: bacterial leucyl aminopeptidase; PDBTitle: crystal structure of the legionella pneumoppila lapa
78	d1wdds_	Alignment	not modelled	15.4	29	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit

79	c2bgjB_	Alignment	not modelled	14.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp(h) reductase; PDBTitle: x-ray structure of the ferredoxin-nadp(h) reductase from rhodobacter2 capsulatus at 2.1 angstroms
80	d1qoza_	Alignment	not modelled	14.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
81	d2v0ea1	Alignment	not modelled	14.9	25	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
82	d1g66a_	Alignment	not modelled	14.3	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
83	c3mhyC_	Alignment	not modelled	14.3	18	PDB header: signaling protein Chain: C: PDB Molecule: pii-like protein pz; PDBTitle: a new pii protein structure
84	c3pe3D_	Alignment	not modelled	14.3	18	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnae transferase and its complex with a peptide2 substrate
85	c3dd5F_	Alignment	not modelled	14.1	23	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
86	c2czqB_	Alignment	not modelled	14.1	27	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
87	c2yijA_	Alignment	not modelled	14.1	28	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1-iigamma; PDBTitle: crystal structure of phospholipase a1
88	c5x88A_	Alignment	not modelled	14.1	19	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
89	c4psdA_	Alignment	not modelled	14.0	21	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
90	d1ul3a_	Alignment	not modelled	14.0	27	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
91	c4f7dA_	Alignment	not modelled	13.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin-nadp reductase from burkholderia2 thailandensis e264
92	d2ckca1	Alignment	not modelled	13.7	23	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
93	c2ckcA_	Alignment	not modelled	13.7	23	PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 7; 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
94	c6mr1A_	Alignment	not modelled	13.6	20	PDB header: protein binding Chain: A: PDB Molecule: carbon dioxide concentrating mechanism protein; PDBTitle: rbcs-like subdomain of ccmm
95	d1bxni_	Alignment	not modelled	13.6	9	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
96	c6hbbA_	Alignment	not modelled	12.8	16	PDB header: protein binding Chain: A: PDB Molecule: carbon dioxide concentrating mechanism protein ccmm; PDBTitle: crystal structure of the small subunit-like domain 1 of ccmm from2 synechococcus elongatus (strain pcc 7942)
97	c3cqyA_	Alignment	not modelled	12.8	21	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetylmuramic acid kinase; PDBTitle: crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
98	c3iteB_	Alignment	not modelled	12.8	16	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
99	c2ybvN_	Alignment	not modelled	12.7	17	PDB header: lyase Chain: N: PDB Molecule: ribulose bisphosphate carboxylase small subunit; PDBTitle: structure of rubisco from thermosynechococcus elongatus