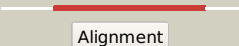



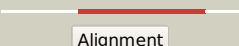





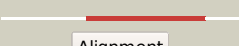










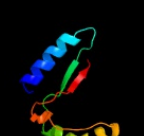

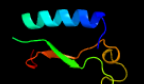


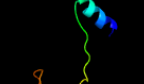
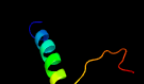
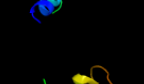

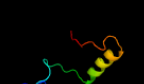


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0838_(lpqR)_934723_935493
Date	Fri Jul 26 01:50:42 BST 2019
Unique Job ID	fb34aa0205aa3f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r44a_	 Alignment		100.0	29	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanX-like
2	c4jidA_	 Alignment		99.7	22	PDB header: hydrolase Chain: A: PDB Molecule: d-alanyl-d-alanine carboxypeptidase family protein; PDBTitle: crystal structure of baldcb / vany-like I,d-carboxypeptidase zinc(ii)-2 free
3	c4ox3A_	 Alignment		99.6	23	PDB header: hydrolase Chain: A: PDB Molecule: putative carboxypeptidase yodj; PDBTitle: structure of the ldcb Id-carboxypeptidase reveals the molecular basis2 of peptidoglycan recognition
4	c4murA_	 Alignment		99.5	26	PDB header: hydrolase Chain: A: PDB Molecule: d,d-dipeptidase/d,d-carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-dipeptidase/d,d-2 pentapeptidase vanxyc d59s mutant
5	c5hnmC_	 Alignment		99.4	23	PDB header: hydrolase Chain: C: PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-pentapeptidase vany2 e175a mutant from vanb-type resistance cassette in complex with3 zn(ii)
6	c2vo9C_	 Alignment		99.4	17	PDB header: hydrolase Chain: C: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: crystal structure of the enzymatically active domain of the listeria2 monocytogenes bacteriophage 500 endolysin ply500
7	d2vo9a1	 Alignment		99.4	19	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanY-like
8	c4ox5A_	 Alignment		98.7	30	PDB header: hydrolase Chain: A: PDB Molecule: ldcb Id-carboxypeptidase; PDBTitle: structure of the ldcb Id-carboxypeptidase reveals the molecular basis2 of peptidoglycan recognition
9	c4f78A_	 Alignment		98.5	25	PDB header: hydrolase Chain: A: PDB Molecule: d,d-dipeptidase/d,d-carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-dipeptidase vanxyg
10	c2mxzA_	 Alignment		97.8	14	PDB header: hydrolase Chain: A: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: bacteriophage t5 l-alanyl-d-glutamate peptidase complex with zn2+2 (endo t5-zn2+)
11	c5opzB_	 Alignment		96.8	25	PDB header: hydrolase Chain: B: PDB Molecule: chix; PDBTitle: crystal structure of serratia marcescens l-ala d-glu endopeptidase2 chix

12	d3d1ma1	Alignment		95.1	22	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Hedgehog (development protein), N-terminal signaling domain
13	c3m1nB_	Alignment		94.3	22	PDB header: signaling protein Chain: B: PDB Molecule: sonic hedgehog protein; PDBTitle: crystal structure of human sonic hedgehog n-terminal domain
14	d2ibge1	Alignment		90.5	17	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Hedgehog (development protein), N-terminal signaling domain
15	c1lbuA_	Alignment		72.9	19	PDB header: hydrolase Chain: A: PDB Molecule: muramoyl-pentapeptide carboxypeptidase; PDBTitle: hydrolase metallo (zn) dd-peptidase
16	c1eiya_	Alignment		58.8	24	PDB header: ligase/rna Chain: A: PDB Molecule: phenylalanyl-trna synthetase; PDBTitle: the crystal structure of phenylalanyl-trna synthetase from thermus2 thermophilus complexed with cognate trnaphe
17	c4nz3A_	Alignment		56.6	23	PDB header: hydrolase Chain: A: PDB Molecule: deacetylase da1; PDBTitle: structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21
18	c3l4gl_	Alignment		53.7	25	PDB header: ligase Chain: I: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
19	d1lbua2	Alignment		51.6	19	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Muramoyl-pentapeptide carboxypeptidase
20	c2k4za_	Alignment		50.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dsrrr; PDBTitle: solution nmr structure of allochromatium vinosum dsrrr:2 northeast structural genomics consortium target op5
21	c3l4gC_	Alignment	not modelled	45.9	15	PDB header: ligase Chain: C: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
22	d1vk9a_	Alignment	not modelled	40.4	16	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Hypothetical protein TM1506
23	d1lvaa3	Alignment	not modelled	34.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
24	c6btmD_	Alignment	not modelled	25.1	17	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
25	d1r89a3	Alignment	not modelled	24.4	0	Fold: Ferredoxin-like Superfamily: PAP/Archaeal CCA-adding enzyme, C-terminal domain Family: Archaeal tRNA CCA-adding enzyme
26	c3r0pB_	Alignment	not modelled	24.0	14	PDB header: hydrolase Chain: B: PDB Molecule: l-psp putative endoribonuclease; PDBTitle: crystal structure of l-psp putative endoribonuclease from uncultured2 organism
27	c1wsuA_	Alignment	not modelled	23.1	9	PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: c-terminal domain of elongation factor selb complexed with2 secis rna
28	d2r4qa1	Alignment	not modelled	21.5	28	Fold: Phosphotyrosine protein phosphatases l-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
						PDB header: membrane protein

29	c6f0kD_	Alignment	not modelled	20.4	30	Chain: D: PDB Molecule: actcd; PDBTitle: alternative complex iii
30	d1qd9a_	Alignment	not modelled	18.4	18	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
31	d2cvla1	Alignment	not modelled	18.4	26	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
32	c2kyrA_	Alignment	not modelled	17.9	28	PDB header: transferase Chain: A: PDB Molecule: fructose-like phosphotransferase enzyme iib component 1; PDBTitle: solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
33	d2r48a1	Alignment	not modelled	17.6	39	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
34	d1nwba_	Alignment	not modelled	16.9	15	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
35	c3m4sC_	Alignment	not modelled	16.6	22	PDB header: unknown function Chain: C: PDB Molecule: putative endoribonuclease I-psp; PDBTitle: crystal structure of a putative endoribonuclease I-psp from entamoeba2 histolytica, orthorhombic form
36	c4brwB_	Alignment	not modelled	16.6	38	PDB header: hydrolase Chain: B: PDB Molecule: dna topoisomerase 2-associated protein pat1; PDBTitle: crystal structure of the yeast dhh1-pat1 complex
37	c2r5xA_	Alignment	not modelled	16.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein yugn from2 geobacillus kaustophilus hta426
38	c5dleD_	Alignment	not modelled	16.4	17	PDB header: transferase Chain: D: PDB Molecule: pts system, fructose-specific iabc component; PDBTitle: crystal structure from a domain (thr161-f265) from fructose-specific2 iabc component (pts system) from borrelia burgdorferi
39	c2plyB_	Alignment	not modelled	16.4	16	PDB header: translation/rna Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
40	c2ccaA_	Alignment	not modelled	16.4	27	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxidase/catalase t; PDBTitle: crystal structure of the catalase-peroxidase (katg) and2 s315t mutant from mycobacterium tuberculosis
41	d1onia_	Alignment	not modelled	16.3	21	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
42	d1jca_	Alignment	not modelled	16.2	22	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
43	c2apnA_	Alignment	not modelled	16.0	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hi1723; PDBTitle: hi1723 solution structure
44	c4g2nA_	Alignment	not modelled	15.7	28	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; PDBTitle: crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js666
45	c4jxdA_	Alignment	not modelled	15.5	17	PDB header: transferase Chain: A: PDB Molecule: fructose-like phosphotransferase enzyme iib component 3; PDBTitle: crystal structure of predicted fructose specific iib from escherichia2 coli
46	c2m1zA_	Alignment	not modelled	14.6	22	PDB header: transferase Chain: A: PDB Molecule: lmo0427 protein; PDBTitle: solution structure of uncharacterized protein lmo0427
47	c3pcoC_	Alignment	not modelled	14.1	21	PDB header: ligase Chain: C: PDB Molecule: phenylalanyl-trna synthetase, alpha subunit; PDBTitle: crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
48	c2rgmA_	Alignment	not modelled	13.9	28	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: rice bglu1 beta-glucosidase, a plant exoglucanase/beta-glucosidase
49	d2pwwa1	Alignment	not modelled	13.5	14	Fold: TBP-like Superfamily: YugN-like Family: YugN-like
50	c4j7oA_	Alignment	not modelled	13.4	12	PDB header: cell invasion Chain: A: PDB Molecule: putative surface cell antigen sca2; PDBTitle: structure of the n-terminal repeat domain of rickettsia sca2
51	c4fo5A_	Alignment	not modelled	12.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-like protein; PDBTitle: crystal structure of a thioredoxin-like protein (bdi_1100) from2 parabacteroides distasonis atcc 8503 at 2.02 a resolution
52	d1nq3a_	Alignment	not modelled	11.8	20	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
53	d1qaha_	Alignment	not modelled	11.3	18	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like

						Family: YjgF/L-PSP
54	c4zbdD	Alignment	not modelled	11.0	38	PDB header: structural protein Chain: D: PDB Molecule: ubiquitin-1; PDBTitle: ubn1 peptide bound to h3.3/h4/asf1
55	c5wkaC	Alignment	not modelled	10.9	14	PDB header: hydrolase Chain: C: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of a gh1 beta-glucosidase retrieved from microbial2 metagenome of poraque amazon lake
56	d1qoxa	Alignment	not modelled	10.3	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
57	c2dgaA	Alignment	not modelled	9.9	23	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of hexameric beta-glucosidase in wheat
58	c4jhoA	Alignment	not modelled	9.8	28	PDB header: hydrolase Chain: A: PDB Molecule: beta-mannosidase/beta-glucosidase; PDBTitle: structural analysis and insights into glycon specificity of the rice2 gh1 os7bglu26 beta-d-mannosidase
59	c2ekIA	Alignment	not modelled	9.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
60	c1lvaA	Alignment	not modelled	9.6	16	PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of a c-terminal fragment of moorella2 thermoacetica elongation factor selb
61	d2j78a1	Alignment	not modelled	9.5	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
62	d2nlva1	Alignment	not modelled	9.1	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase
63	c2ov2O	Alignment	not modelled	8.7	18	PDB header: protein binding/transferase Chain: O: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
64	c1b70A	Alignment	not modelled	8.6	22	PDB header: ligase Chain: A: PDB Molecule: phenylalanyl-trna synthetase; PDBTitle: phenylalanyl trna synthetase complexed with phenylalanine
65	c1fftG	Alignment	not modelled	8.5	24	PDB header: oxidoreductase Chain: G: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli
66	c3sciE	Alignment	not modelled	8.5	13	PDB header: hydrolase/viral protein Chain: E: PDB Molecule: spike glycoprotein; PDBTitle: crystal structure of spike protein receptor-binding domain from a2 predicted sars coronavirus human strain complexed with human receptor3 ace2
67	c6cxdA	Alignment	not modelled	8.5	25	PDB header: hydrolase Chain: A: PDB Molecule: peptidase b; PDBTitle: crystal structure of peptidase b from yersinia pestis co92 at 2.75 a2 resolution
68	d1prtc1	Alignment	not modelled	8.5	12	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
69	d1yuja	Alignment	not modelled	7.9	56	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
70	d2b33a1	Alignment	not modelled	7.9	25	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
71	c5jx6C	Alignment	not modelled	7.9	45	PDB header: hydrolase Chain: C: PDB Molecule: glucanase; PDBTitle: gh6 orpinomyces sp. y102 enzyme
72	c1ybaC	Alignment	not modelled	7.7	23	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
73	c5yhsB	Alignment	not modelled	7.7	16	PDB header: hydrolase Chain: B: PDB Molecule: pyruvylated beta-d-galactosidase; PDBTitle: pyruvylated beta-d-galactosidase from bacillus sp. hma207, apo form
74	c6akIC	Alignment	not modelled	7.6	35	PDB header: protein binding Chain: C: PDB Molecule: striatin-3; PDBTitle: crystal structure of striatin3 in complex with sike1 coiled-coil2 domain
75	c3cmqA	Alignment	not modelled	7.5	18	PDB header: ligase Chain: A: PDB Molecule: phenylalanyl-trna synthetase, mitochondrial; PDBTitle: crystal structure of human mitochondrial phenylalanine trna synthetase
76	c6g6bA	Alignment	not modelled	7.5	24	PDB header: de novo protein Chain: A: PDB Molecule: cc-type2-II-I17q; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-II-I17q
77	d2cwja1	Alignment	not modelled	7.4	25	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
78	c3gnoA	Alignment	not modelled	7.3	26	PDB header: hydrolase Chain: A: PDB Molecule: os03g0212800 protein; PDBTitle: crystal structure of a rice os3bglu6 beta-glucosidase
79	d2gmga1	Alignment	not modelled	7.3	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF0610-like

80	c2a7rD	Alignment	not modelled	7.3	9	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
81	c5i84H	Alignment	not modelled	7.2	6	PDB header: transport protein Chain: H: PDB Molecule: phosphate-binding protein pst5; PDBTitle: structure of the xanthomonas citri phosphate-binding protein phox
82	d2nsfa2	Alignment	not modelled	7.2	8	Fold: SCP-like Superfamily: SCP-like Family: Micthiol-dependent maleylpyruvate isomerase C-terminal domain-like
83	c2atmA	Alignment	not modelled	7.2	21	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure of the recombinant allergen ves v 2
84	c1dxyA	Alignment	not modelled	7.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyisocaproate dehydrogenase; PDBTitle: structure of d-2-hydroxyisocaproate dehydrogenase
85	c5v4dE	Alignment	not modelled	7.2	18	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: putative translational inhibitor protein; PDBTitle: crystal structure of the protein of unknown function of the conserved2 rid protein family yyfa from yersinia pestis
86	c4ftdA	Alignment	not modelled	7.1	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4623 family protein (bacegg_03550) from bacteroides eggerthii dsm 20697 at 1.91 a resolution
87	c5xgzA	Alignment	not modelled	7.0	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-glycosidase; PDBTitle: metagenomic glucose-tolerant glycosidase
88	c5gnyC	Alignment	not modelled	6.8	19	PDB header: hydrolase Chain: C: PDB Molecule: beta-glucosidase; PDBTitle: the structure of wt bgl6
89	c3bazA	Alignment	not modelled	6.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
90	c5lnkn	Alignment	not modelled	6.7	21	PDB header: oxidoreductase Chain: N: PDB Molecule: mitochondrial complex i, nd2 subunit; PDBTitle: entire ovine respiratory complex i
91	c3ptkB	Alignment	not modelled	6.5	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase os4bglu12; PDBTitle: the crystal structure of rice (oryza sativa l.) os4bglu12
92	c6g6bB	Alignment	not modelled	6.4	24	PDB header: de novo protein Chain: B: PDB Molecule: cc-type2-ll-117q; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-ll-117q
93	c4ksiA	Alignment	not modelled	6.2	20	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase 1, chloroplastic; PDBTitle: crystal structure analysis of the acidic leucine aminopeptidase of2 tomato
94	c6ih2B	Alignment	not modelled	6.2	28	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphite dehydrogenase; PDBTitle: crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
95	c3wq4A	Alignment	not modelled	6.1	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-primeverosidase; PDBTitle: crystal structure of beta-primeverosidase
96	c5yj7C	Alignment	not modelled	6.1	21	PDB header: hydrolase Chain: C: PDB Molecule: glycoside hydrolase; PDBTitle: structural insight into the beta-gh1 glucosidase bgl1 from oleaginous2 microalgae nannochloropsis
97	d1itka1	Alignment	not modelled	6.1	21	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
98	c3o2iB	Alignment	not modelled	6.1	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein from leptospirillum sp. group ii uba
99	c1txqB	Alignment	not modelled	6.0	38	PDB header: structural protein/protein binding Chain: B: PDB Molecule: microtubule-associated protein rp/eb family PDBTitle: crystal structure of the eb1 c-terminal domain complexed2 with the cap-gly domain of p150glued