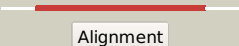



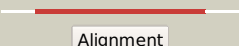





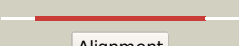













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2782c_(pepR)_3089055_3090371
Date	Wed Aug 7 12:50:44 BST 2019
Unique Job ID	a8b2d12e26a931b4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1hr9D_	 Alignment		100.0	28	PDB header: hydrolase Chain: D: PDB Molecule: mitochondrial processing peptidase beta subunit; PDBTitle: yeast mitochondrial processing peptidase beta-e73q mutant2 complexed with malate dehydrogenase signal peptide
2	c1sqpA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: ubiquinol-cytochrome-c reductase complex core protein I, PDBTitle: crystal structure analysis of bovine bc1 with myxothiazol
3	c1nu1A_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: ubiquinol-cytochrome c reductase complex core protein I, PDBTitle: crystal structure of mitochondrial cytochrome bc1 complexed with 2-2 nonyl-4-hydroxyquinoline n-oxide (nqno)
4	c1hr6C_	 Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: mitochondrial processing peptidase alpha subunit; PDBTitle: yeast mitochondrial processing peptidase
5	c3hdiA_	 Alignment		100.0	38	PDB header: hydrolase Chain: A: PDB Molecule: processing protease; PDBTitle: crystal structure of bacillus halodurans metallo peptidase
6	c5eufA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: protease; PDBTitle: the crystal structure of a protease from helicobacter pylori
7	c3eoqB_	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: putative zinc protease; PDBTitle: the crystal structure of putative zinc protease beta-2 subunit from thermus thermophilus hb8
8	c1l0lB_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase complex core protein 2; PDBTitle: structure of bovine mitochondrial cytochrome bc1 complex with a bound2 fungicide famoxadone
9	c5hxcC_	 Alignment		100.0	29	PDB header: hydrolase Chain: C: PDB Molecule: zinc-dependent peptidase; PDBTitle: structure of ttha1265
10	c3amiB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: zinc peptidase; PDBTitle: the crystal structure of the m16b metallopeptidase subunit from2 sphingomonas sp. a1
11	c3gwbA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: peptidase m16 inactive domain family protein; PDBTitle: crystal structure of peptidase m16 inactive domain from pseudomonas2 fluorescens. northeast structural genomics target plr293l

12	c3amjB_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: zinc peptidase inactive subunit; PDBTitle: the crystal structure of the heterodimer of m16b peptidase from2 sphingomonas sp. a1
13	c4nnzB_	Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: probable zinc protease; PDBTitle: subunit pa0372 of heterodimeric zinc protease pa0371-pa0372
14	c3cx5L_	Alignment		100.0	19	PDB header: oxidoreductase Chain: L: PDB Molecule: cytochrome b-c1 complex subunit 1, mitochondrial; PDBTitle: structure of complex iii with bound cytochrome c in reduced state and2 definition of a minimal core interface for electron transfer.
15	c4xeaA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: peptidase m16 domain protein; PDBTitle: crystal structure of putative m16-like peptidase from alicyclobacillus2 acidocaldarius
16	c6b05A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: putative zinc protease; PDBTitle: the crystal structure of the ferredoxin protease fusc e83a mutant in2 complex with arabidopsis ferredoxin
17	c1q2IA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: protease iii; PDBTitle: crystal structure of pitrilyisin
18	c3go9A_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: insulinase family protease; PDBTitle: predicted insulinase family protease from yersinia pestis
19	c2wk3A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: insulin degrading enzyme; PDBTitle: crystal structure of human insulin-degrading enzyme in2 complex with amyloid-beta (1-42)
20	c2jbuB_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: insulin-degrading enzyme; PDBTitle: crystal structure of human insulin degrading enzyme complexed with co-2 purified peptides.
21	c3d3yA_	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a conserved protein from enterococcus faecalis2 v583
22	c5cioA_	Alignment	not modelled	100.0	21	PDB header: metal binding protein Chain: A: PDB Molecule: pyrroloquinoline quinone biosynthesis protein pqqf; PDBTitle: crystal structure of pqqf
23	c2fgeA_	Alignment	not modelled	100.0	17	PDB header: hydrolase, plant protein Chain: A: PDB Molecule: zinc metalloprotease (insulinase family); PDBTitle: crystal structure of presequence protease prep from2 arabidopsis thaliana
24	c3s5mA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: falcilysin; PDBTitle: crystal structures of falcilysin, a m16 metalloprotease from the2 malaria parasite plasmodium falciparum
25	c3s5kA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: falcilysin; PDBTitle: crystal structures of falcilysin, a m16 metalloprotease from the2 malaria parasite plasmodium falciparum
26	c4l3tB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: presequence protease, mitochondrial; PDBTitle: crystal structure of substrate-free human presequence protease
27	c3cxhM_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: M: PDB Molecule: cytochrome b-c1 complex subunit 2, mitochondrial; PDBTitle: structure of yeast complex iii with isoform-2 cytochrome c bound and2 definition of a minimal core interface for electron transfer.
28	d1ppja1	Alignment	not modelled	100.0	34	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase

						Family: MPP-like
29	d1hr6b1	Alignment	not modelled	100.0	35	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
30	d1bccal	Alignment	not modelled	100.0	33	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
31	d1hr6a1	Alignment	not modelled	100.0	24	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
32	d1q2la4	Alignment	not modelled	100.0	24	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
33	d1ppjb1	Alignment	not modelled	100.0	21	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
34	d1bccb1	Alignment	not modelled	100.0	21	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
35	d3cx5a1	Alignment	not modelled	100.0	21	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
36	d2fgea4	Alignment	not modelled	100.0	21	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
37	d3cx5b1	Alignment	not modelled	100.0	22	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
38	d1hr6a2	Alignment	not modelled	100.0	26	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
39	d1ppjb2	Alignment	not modelled	100.0	23	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
40	d1hr6b2	Alignment	not modelled	99.9	20	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
41	d1bccal2	Alignment	not modelled	99.9	22	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
42	c3ivIA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: putative zinc protease; PDBTitle: the crystal structure of the inactive peptidase domain of a putative2 zinc protease from bordetella parapertussis to 2.2a
43	d1bccb2	Alignment	not modelled	99.9	21	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
44	d1ppja2	Alignment	not modelled	99.9	23	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
45	d1q2la1	Alignment	not modelled	99.9	12	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
46	d3cx5a2	Alignment	not modelled	99.9	18	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
47	d2fgea2	Alignment	not modelled	99.9	12	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
48	d2fgea3	Alignment	not modelled	99.6	12	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
49	d2fgea1	Alignment	not modelled	99.5	10	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
50	d1q2la2	Alignment	not modelled	99.5	10	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
51	d1q2la3	Alignment	not modelled	98.8	10	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
52	d1nsha_	Alignment	not modelled	31.9	14	Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins
53	c6cy1B_	Alignment	not modelled	28.5	10	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
54	c2rgiA_	Alignment	not modelled	24.2	11	PDB header: metal binding protein Chain: A: PDB Molecule: protein s100-a2; PDBTitle: crystal structure of ca2+-free s100a2 at 1.6 a resolution
55	d1qlsa_	Alignment	not modelled	23.5	11	Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins
						PDB header: glycosyltransferase

56	c1qapA	Alignment	not modelled	20.7	16	Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
57	c5yhvA	Alignment	not modelled	20.5	13	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
58	d1zavz1	Alignment	not modelled	20.4	29	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
59	c1zawZ	Alignment	not modelled	20.4	29	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
60	c1zavZ	Alignment	not modelled	20.4	29	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
61	d2azeb1	Alignment	not modelled	20.3	21	Fold: E2F-DP heterodimerization region Superfamily: E2F-DP heterodimerization region Family: E2F dimerization segment
62	c1zawX	Alignment	not modelled	19.8	29	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
63	c1zawY	Alignment	not modelled	19.8	29	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
64	c2y5iF	Alignment	not modelled	18.5	12	PDB header: metal-binding protein Chain: F: PDB Molecule: s100 calcium binding protein z; PDBTitle: s100z from zebrafish in complex with calcium
65	c5tuvB	Alignment	not modelled	18.5	27	PDB header: transcription Chain: B: PDB Molecule: transcription factor e2f5; PDBTitle: crystal structure of the e2f5-dp1-p107 ternary complex
66	c3tcmB	Alignment	not modelled	18.2	9	PDB header: transferase Chain: B: PDB Molecule: alanine aminotransferase 2; PDBTitle: crystal structure of alanine aminotransferase from hordeum vulgare
67	c4ix9A	Alignment	not modelled	18.2	7	PDB header: hydrolase Chain: A: PDB Molecule: v-type proton atpase subunit f; PDBTitle: crystal structure of subunit f of v-atpase from s. cerevisiae
68	c1zavU	Alignment	not modelled	17.9	28	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
69	c1zaxU	Alignment	not modelled	17.9	28	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
70	d1zavu1	Alignment	not modelled	17.9	28	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
71	c1zaxV	Alignment	not modelled	17.9	28	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
72	c1zaxW	Alignment	not modelled	17.9	28	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
73	c1zavV	Alignment	not modelled	17.9	28	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
74	c1zavW	Alignment	not modelled	17.9	28	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
75	c1zavX	Alignment	not modelled	17.7	28	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
76	c1zavY	Alignment	not modelled	17.7	28	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
77	c1zaxY	Alignment	not modelled	17.7	28	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
78	c1zaxX	Alignment	not modelled	17.7	28	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
79	d1b5pa	Alignment	not modelled	17.5	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
80	c1dd3D	Alignment	not modelled	17.3	28	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
81	c1dd3C	Alignment	not modelled	17.3	28	PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima PDB header: transferase

82	c3pajA_	Alignment	not modelled	16.3	13	Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
83	d1e8aa_	Alignment	not modelled	15.5	5	Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins
84	c3ihjA_	Alignment	not modelled	15.2	11	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
85	d1c7na_	Alignment	not modelled	15.1	6	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
86	c4drwC_	Alignment	not modelled	14.9	10	PDB header: exocytosis/protein binding Chain: C: PDB Molecule: protein s100-a10/annexin a2 chimeric protein; PDBTitle: crystal structure of the ternary complex between s100a10, an annexin a2 n-terminal peptide and an ahnak peptide
87	d1cr6a2_	Alignment	not modelled	14.6	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
88	c1zawU_	Alignment	not modelled	14.6	29	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
89	c1zawW_	Alignment	not modelled	14.6	29	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
90	c1zawV_	Alignment	not modelled	14.6	29	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
91	c3gnnA_	Alignment	not modelled	14.6	18	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 burkholderi pseudomallei
92	c5wmiA_	Alignment	not modelled	14.6	13	PDB header: transferase Chain: A: PDB Molecule: bifunctional aspartate aminotransferase and PDBTitle: arabidopsis thaliana prephenate aminotransferase mutant- t84v
93	c1yhpA_	Alignment	not modelled	14.5	15	PDB header: cell adhesion Chain: A: PDB Molecule: calcium-dependent cell adhesion molecule-1; PDBTitle: solution structure of ca2+-free ddcad-1
94	c1x1oC_	Alignment	not modelled	14.4	18	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
95	c1zaxZ_	Alignment	not modelled	14.3	29	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
96	c3ff5B_	Alignment	not modelled	14.0	21	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
97	d1dd4c_	Alignment	not modelled	13.7	28	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
98	c4f4fB_	Alignment	not modelled	13.3	18	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
99	d1d2fa_	Alignment	not modelled	13.3	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like