



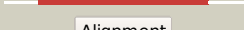

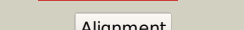







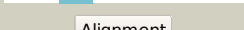

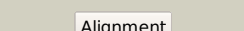

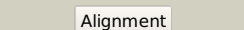














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2112c (-) _2370913_2372577
Date	Mon Aug 5 13:25:23 BST 2019
Unique Job ID	e12fcf04cc6a29e6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4b0sA_	 Alignment		100.0	63	PDB header: hydrolase Chain: A: PDB Molecule: deamidase-depupylase dop; PDBTitle: structure of the deamidase-depupylase dop of the prokaryotic2 ubiquitin-like modification pathway in complex with atp
2	c4b0tB_	 Alignment		100.0	38	PDB header: ligase Chain: B: PDB Molecule: pup--protein ligase; PDBTitle: structure of the pup ligase pafa of the prokaryotic2 ubiquitin-like modification pathway in complex with adp
3	c4bjrA_	 Alignment		100.0	36	PDB header: ligase Chain: A: PDB Molecule: pup--protein ligase, prokaryotic ubiquitin-like protein PDBTitle: crystal structure of the complex between prokaryotic2 ubiquitin-like protein pup and its ligase pafa
4	d1r8ga_	 Alignment		95.1	15	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
5	c5cywB_	 Alignment		48.4	36	PDB header: viral protein Chain: B: PDB Molecule: interferon antagonist c7; PDBTitle: crystal structure of vaccinia virus c7
6	c5cz3B_	 Alignment		46.5	36	PDB header: viral protein Chain: B: PDB Molecule: m64r; PDBTitle: crystal structure of myxoma virus m64
7	d2jg0a1	 Alignment		37.7	16	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Trehalase-like
8	c2jg0A_	 Alignment		37.7	16	PDB header: hydrolase Chain: A: PDB Molecule: periplasmic trehalase; PDBTitle: family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
9	d1tt4a_	 Alignment		30.2	17	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
10	c1tt4B_	 Alignment		29.7	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cytoplasmic protein; PDBTitle: structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium
11	c4i9gB_	 Alignment		29.2	18	PDB header: hydrolase Chain: B: PDB Molecule: glycerol 3-phosphate phosphatase; PDBTitle: crystal structure of glycerol phosphate phosphatase rv1692 from2 mycobacterium tuberculosis in complex with magnesium

12	c2kseA_	Alignment		26.6	17	PDB header: transferase Chain: A: PDB Molecule: sensor protein qsec; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor qsec, center for structures of membrane proteins (csmp)3 target 4311c
13	c5gmxA_	Alignment		26.4	27	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of a family viii carboxylesterase
14	c5e2hB_	Alignment		23.7	26	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of d-alanine carboxypeptidase ampC from2 mycobacterium smegmatis
15	c2h2wA_	Alignment		22.8	14	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
16	d2qc6a1	Alignment		20.1	21	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folylpolyglutamate synthetase, C-terminal domain
17	c2qz6A_	Alignment		20.1	29	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: first crystal structure of a psychrophile class c beta-2 lactamase
18	c5tqfB_	Alignment		19.1	27	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative beta-lactamase from bacteroides dorei2 dsm 17855
19	d1yqsa1	Alignment		17.8	31	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
20	c6njka_	Alignment		17.8	31	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from sulfitobacter sp. ee-36
21	c3ex7I_	Alignment	not modelled	17.2	17	PDB header: hydrolase/rna binding protein/rna Chain: I: PDB Molecule: protein casc3; PDBTitle: the crystal structure of eJC in its transition state
22	c5evIA_	Alignment	not modelled	16.7	30	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 chromobacterium violaceum
23	c2vvdA_	Alignment	not modelled	16.7	36	PDB header: viral protein Chain: A: PDB Molecule: spike protein p1; PDBTitle: crystal structure of the receptor binding domain of the2 spike protein p1 from bacteriophage pm2
24	d2hdsa1	Alignment	not modelled	16.5	31	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
25	c3wvxA_	Alignment	not modelled	16.5	35	PDB header: hydrolase Chain: A: PDB Molecule: s12 family peptidase; PDBTitle: crystal structure of d-stereospecific amidohydrolase from streptomyces2 sp. 82f2
26	c3vepX_	Alignment	not modelled	16.2	37	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
27	d2hwja1	Alignment	not modelled	16.2	33	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Atu1540-like
28	c2qmiH_	Alignment	not modelled	16.1	42	PDB header: hydrolase Chain: H: PDB Molecule: pbp related beta-lactamase; PDBTitle: structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssi
29	c3vepC_	Alignment	not modelled	16.1	37	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
30	c5m4aA_	Alignment	not modelled	16.0	20	PDB header: hydrolase Chain: A: PDB Molecule: neutral trehalase; PDBTitle: neutral trehalase nth1 from saccharomyces cerevisiae in complex with2 trehalose
31	c5cqqB_	Alignment	not modelled	15.5	18	PDB header: transcription/dna Chain: B: PDB Molecule: regulatory protein zeste; PDBTitle: crystal structure of the drosophila zeste dna binding domain in2 complex with dna
32	d1dy2a_	Alignment	not modelled	15.5	18	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Endostatin
33	c3tadB_	Alignment	not modelled	15.5	17	PDB header: protein binding Chain: B: PDB Molecule: liprin-alpha-2; PDBTitle: crystal structure of the liprin-alpha/liprin-beta complex
34	c6f36M_	Alignment	not modelled	15.3	31	PDB header: proton transport Chain: M: PDB Molecule: mitochondrial atp synthase subunit 6; PDBTitle: polytomella fo model
35	c3o3vB_	Alignment	not modelled	15.3	31	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of clbp peptidase domain
36	c2wzzA_	Alignment	not modelled	14.8	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03
37	d1tvfa2	Alignment	not modelled	14.4	25	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
38	d1u7ka_	Alignment	not modelled	14.3	15	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
39	d2olra2	Alignment	not modelled	13.4	11	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
40	d1rgya_	Alignment	not modelled	13.3	31	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
41	c5e2gA_	Alignment	not modelled	13.0	38	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of d-alanine carboxypeptidase ampc from burkholderia2 cenocepacia
42	c3hleA_	Alignment	not modelled	13.0	48	PDB header: transferase Chain: A: PDB Molecule: transesterase; PDBTitle: simvastatin synthase (lovD), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
43	d1u7za_	Alignment	not modelled	12.7	19	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
44	c3ws1A_	Alignment	not modelled	12.4	35	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: n288q-n321q mutant beta-lactamase derived from chromohalobacter sp.5602 (condition-1b)
45	c3ozhA_	Alignment	not modelled	11.8	33	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase/d-alanine carboxypeptidase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis
46	d1o5za1	Alignment	not modelled	11.6	33	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folylpolyglutamate synthetase, C-terminal domain
47	c4gdnB_	Alignment	not modelled	11.4	39	PDB header: hydrolase Chain: B: PDB Molecule: protein flp; PDBTitle: structure of fmta-like protein
48	c5gkvA_	Alignment	not modelled	11.3	35	PDB header: hydrolase Chain: A: PDB Molecule: esterase a; PDBTitle: crystal structure of a novel penicillin-binding protein (pbp) homolog2 from caulobacter crescentus
49	c2f7IA_	Alignment	not modelled	11.3	16	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
50	d2hmva1	Alignment	not modelled	11.2	42	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
51	d1ci9a_	Alignment	not modelled	11.2	42	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
52	c2vveB_	Alignment	not modelled	11.1	36	PDB header: viral protein Chain: B: PDB Molecule: spike protein p1; PDBTitle: crystal structure of the stem and receptor binding domain2 of the spike protein p1 from bacteriophage pm2
53	c4p6bB_	Alignment	not modelled	11.1	35	PDB header: hydrolase Chain: B: PDB Molecule: est-y29; PDBTitle: crystal structure of est-y29,a novel penicillin-binding protein/beta-2 lactamase homolog from a metagenomic library
54	c3btpB_	Alignment	not modelled	10.9	55	PDB header: dna binding protein, chaperone Chain: B: PDB Molecule: protein vire1; PDBTitle: crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
55	c2mn3A_	Alignment	not modelled	10.9	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-bvl; PDBTitle: structure of platypus 'intermediate' defensin-like peptide

						(int-dlp)
56	c5yisC	Alignment	not modelled	10.9	20	PDB header: protein binding Chain: C: PDB Molecule: ankyrin-2; PDBTitle: crystal structure of ank b lir/lc3b complex
57	c4netA	Alignment	not modelled	10.8	17	PDB header: hydrolase Chain: A: PDB Molecule: ampc; PDBTitle: crystal structure of adc-1 beta-lactamase
58	c4wa0A	Alignment	not modelled	10.7	38	PDB header: cell adhesion Chain: A: PDB Molecule: possible adhesin; PDBTitle: the structure of a possible adhesin c-terminal domain from 2 caldicellulosiruptor kronotskyensis
59	c1exdA	Alignment	not modelled	10.7	24	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: crystal structure of a tight-binding glutamine trna bound 2 to glutamine aminoacyl trna synthetase
60	d1onha	Alignment	not modelled	10.7	38	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
61	c6mtgB	Alignment	not modelled	10.6	29	PDB header: transferase Chain: B: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: a single reactive noncanonical amino acid is able to dramatically 2 stabilize protein structure
62	c3tg9A	Alignment	not modelled	10.6	35	PDB header: penicillin binding protein Chain: A: PDB Molecule: penicillin-binding protein; PDBTitle: the crystal structure of penicillin binding protein from bacillus 2 halodurans
63	d2ghra1	Alignment	not modelled	10.4	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
64	d1pixa3	Alignment	not modelled	10.4	24	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
65	d2dkya1	Alignment	not modelled	10.4	32	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
66	c3zytA	Alignment	not modelled	10.3	26	PDB header: hydrolase Chain: A: PDB Molecule: esterase a; PDBTitle: structure determination of esta from arthrobacter nitroguajacolicus 2 rue61a
67	c1zkjA	Alignment	not modelled	10.3	29	PDB header: hydrolase Chain: A: PDB Molecule: extended-spectrum beta-lactamase; PDBTitle: structural basis for the extended substrate spectrum of cmv-2 10, a plasmid-encoded class c beta-lactamase
68	c5eviC	Alignment	not modelled	9.8	26	PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase/d-alanine carboxypeptidase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from 2 pseudomonas syringae
69	c2xkyl	Alignment	not modelled	9.7	23	PDB header: metal transport Chain: I: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: single particle analysis of kir2.1nc_4 in negative stain
70	d1wo8a1	Alignment	not modelled	9.3	22	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
71	c3i7jB	Alignment	not modelled	9.3	26	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase mb2281c; PDBTitle: crystal structure of a beta-lactamase (mb2281c) from mycobacterium 2 bovis, northeast structural genomics consortium target mbr246
72	d1rzhh1	Alignment	not modelled	9.1	21	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
73	c4h3sA	Alignment	not modelled	9.0	24	PDB header: ligase Chain: A: PDB Molecule: glutamine-trna ligase; PDBTitle: the structure of glutamyl-trna synthetase from saccharomyces 2 cerevisiae
74	c4ivkA	Alignment	not modelled	9.0	48	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterases; PDBTitle: crystal structure of a family viii carboxylesterase in a complex with 2 cephalothin.
75	c5zdoA	Alignment	not modelled	8.9	29	PDB header: ligase Chain: A: PDB Molecule: glutamine-trna ligase; PDBTitle: crystal structure analysis of ttqrs in co-crystallised with atp
76	d2drwa1	Alignment	not modelled	8.9	26	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
77	c4im2A	Alignment	not modelled	8.9	28	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: serine/threonine-protein kinase tbk1; PDBTitle: structure of tank-binding kinase 1
78	c5zh8B	Alignment	not modelled	8.9	31	PDB header: hydrolase Chain: B: PDB Molecule: protein fmta; PDBTitle: crystal structure of fmta from staphylococcus aureus at 2.58 a
79	c1w8xM	Alignment	not modelled	8.7	36	PDB header: virus Chain: M: PDB Molecule: protein p30; PDBTitle: structural analysis of prd1
80	d1x4ka2	Alignment	not modelled	8.6	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
81	d1fs2b1	Alignment	not modelled	8.6	7	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like

82	c4k7cA	Alignment	not modelled	8.6	18	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase c; PDBTitle: crystal structure of pepw from lactobacillus rhamnosis hn001 (dr20)2 determined as the selenomet derivative
83	c5bnzA	Alignment	not modelled	8.6	24	PDB header: ligase Chain: A: PDB Molecule: glutamine--trna ligase; PDBTitle: crystal structure of glutamine-trna ligase /glutaminyl-trna synthetase2 (glnrs) from pseudomonas aeruginosa
84	c3kuzA	Alignment	not modelled	8.4	18	PDB header: signaling protein Chain: A: PDB Molecule: plexin-c1; PDBTitle: crystal structure of the ubiquitin like domain of plxnc1
85	c3gp8A	Alignment	not modelled	8.3	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
86	d1cpqa	Alignment	not modelled	8.3	33	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
87	c2my5A	Alignment	not modelled	8.2	20	PDB header: transport protein Chain: A: PDB Molecule: peptidyl carrier protein; PDBTitle: solution structure of kstb-pcp in kosinostatin biosynthesis
88	d1e85a	Alignment	not modelled	8.1	33	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
89	c4ye6A	Alignment	not modelled	8.0	29	PDB header: ligase Chain: A: PDB Molecule: glutamine--trna ligase; PDBTitle: the crystal structure of the intact human glnrs
90	c2w0cL	Alignment	not modelled	8.0	36	PDB header: virus Chain: L: PDB Molecule: protein 2; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
91	c3h6nA	Alignment	not modelled	8.0	26	PDB header: signaling protein Chain: A: PDB Molecule: plexin-d1; PDBTitle: crystal structure of the ubiquitin-like domain of plexin d1
92	d1nosa	Alignment	not modelled	7.8	10	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
93	c2i5nH	Alignment	not modelled	7.8	28	PDB header: photosynthesis Chain: H: PDB Molecule: reaction center protein h chain; PDBTitle: 1.96 a x-ray structure of photosynthetic reaction center from2 rhodospseudomonas viridis:crystals grown by microfluidic technique
94	d1s05a	Alignment	not modelled	7.8	50	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
95	c3c85A	Alignment	not modelled	7.7	36	PDB header: transport protein Chain: A: PDB Molecule: putative glutathione-regulated potassium-efflux system PDBTitle: crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
96	c5hw3A	Alignment	not modelled	7.7	23	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a beta lactamase from burkholderia vietnamiensis
97	c4hesA	Alignment	not modelled	7.6	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase class a-like protein; PDBTitle: structure of a beta-lactamase class a-like protein from veillonella2 parvula.
98	c4zqaA	Alignment	not modelled	7.5	22	PDB header: transcription repressor Chain: A: PDB Molecule: sin3 histone deacetylase corepressor complex component PDBTitle: crystal structure of the sds3 dimerization domain
99	c5butG	Alignment	not modelled	7.5	42	PDB header: membrane protein Chain: G: PDB Molecule: ktr system potassium uptake protein a,ktr system potassium PDBTitle: crystal structure of inactive conformation of ktrab k+ transporter