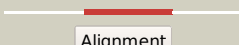



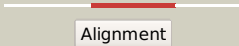


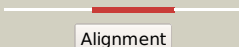



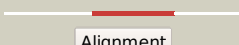



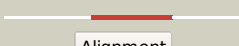







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3811 (-)_4274976_4276595
Date	Fri Aug 9 18:20:52 BST 2019
Unique Job ID	408f05c6235ff838

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4z8iA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan recognition protein 3; PDBTitle: crystal structure of branchiostoma belcheri tsingtauense peptidoglycan2 recognition protein 3
2	d1sxra_	 Alignment		100.0	31	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
3	c1s2jA_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan recognition protein sa cg11709-pa; PDBTitle: crystal structure of the drosophila pattern-recognition2 receptor pgrp-sa
4	c6ckhA_	 Alignment		100.0	24	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein; PDBTitle: manduca sexta peptidoglycan recognition protein-1
5	c5xz3D_	 Alignment		100.0	25	PDB header: immune system Chain: D: PDB Molecule: peptidoglycan-recognition protein; PDBTitle: the x-ray structure of apis mellifera pgrp-sa
6	d2cb3a1	 Alignment		100.0	28	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
7	c2rkqA_	 Alignment		100.0	28	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein-sd; PDBTitle: crystal structure of drosophila peptidoglycan recognition2 protein sd (pgrp-sd)
8	c3ep1B_	 Alignment		100.0	29	PDB header: immune system Chain: B: PDB Molecule: pgrp-hd - peptidoglycan recognition protein PDBTitle: structure of the pgrp-hd from alvinella pompejana
9	d2f2la1	 Alignment		100.0	26	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
10	d1ycka1	 Alignment		100.0	35	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
11	d2f2lx1	 Alignment		100.0	28	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like

12	c2xz4A_	Alignment		100.0	29	PDB header: immune system Chain: A; PDB Molecule: peptidoglycan-recognition protein If; PDBTitle: crystal structure of the Ifz ectodomain of the2 peptidoglycan recognition protein If
13	d1ohta_	Alignment		100.0	24	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
14	c1ohta_	Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: cg14704 protein; PDBTitle: peptidoglycan recognition protein-Ib
15	d1sk4a_	Alignment		100.0	31	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
16	c6fhgB_	Alignment		100.0	22	PDB header: antimicrobial protein Chain: B; PDB Molecule: lyst endolysin; PDBTitle: crystal structure of the ts2631 endolysin from thermus scotoductus2 phage with the unique n-terminal moiety responsible for peptidoglycan3 anchoring
17	c2xz8A_	Alignment		100.0	18	PDB header: immune system Chain: A; PDB Molecule: peptidoglycan-recognition protein If; PDBTitle: crystal structure of the Ifw ectodomain of the2 peptidoglycan recognition protein If
18	d1lbaa_	Alignment		100.0	28	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
19	d2bgxa2	Alignment		99.9	16	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
20	d1yb0a1	Alignment		99.9	14	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
21	c3hmaA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylmuramoyl-l-alanine amidase xlya; PDBTitle: amidase from bacillus subtilis
22	c4bxdB_	Alignment	not modelled	99.9	26	PDB header: hydrolase/peptide Chain: B; PDB Molecule: ampdh3; PDBTitle: crystal structure of ampdh3 from pseudomonas aeruginosa in2 complex with tetrasaccharide pentapeptide
23	d1j3ga_	Alignment	not modelled	99.8	13	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
24	c4bolA_	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: A; PDB Molecule: ampdh2; PDBTitle: crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
25	c2bh7A_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: crystal structure of a semet derivative of amid at 2.22 angstroms
26	c4olsA_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: A; PDB Molecule: endolysin; PDBTitle: the amidase-2 domain of lysgh15
27	c4ivvA_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A; PDB Molecule: autolysin; PDBTitle: catalytic amidase domain of the major autolysin lyta from2 streptococcus pneumoniae
28	c3latB_	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: B; PDB Molecule: bifunctional autolysin; PDBTitle: crystal structure of staphylococcus peptidoglycan hydrolase2 amie PDB header: hydrolase

29	c4x36A	Alignment	not modelled	97.9	19	Chain: A: PDB Molecule: autolysin; PDBTitle: crystal structure of the autolysin lyta from streptococcus pneumoniae2 tigr4
30	d3d85d3	Alignment	not modelled	75.3	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
31	c5aj3d	Alignment	not modelled	67.1	29	PDB header: ribosome Chain: D: PDB Molecule: PDBTitle: structure of the small subunit of the mammalian mitoribosome
32	c3v6oB	Alignment	not modelled	62.3	44	PDB header: immune system Chain: B: PDB Molecule: leptin receptor; PDBTitle: leptin receptor-antibody complex
33	d1f6fb2	Alignment	not modelled	62.1	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
34	d3d48r2	Alignment	not modelled	61.5	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
35	c1kf9C	Alignment	not modelled	59.2	20	PDB header: hormone/growth factor Chain: C: PDB Molecule: extracellular domain human growth hormone PDBTitle: phage display derived variant of human growth hormone2 complexed with two copies of the extracellular domain of3 its receptor
36	c1f6fB	Alignment	not modelled	58.1	31	PDB header: hormone/growth factor/hormone receptor Chain: B: PDB Molecule: prolactin receptor; PDBTitle: crystal structure of the ternary complex between ovine2 placental lactogen and the extracellular domain of the rat3 prolactin receptor
37	c4nn5C	Alignment	not modelled	55.8	20	PDB header: cytokine/cytokine receptor Chain: C: PDB Molecule: cytokine receptor-like factor 2; PDBTitle: cytokine receptor complex - crystal form 1a
38	d2gysa4	Alignment	not modelled	55.3	44	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
39	d1iarb2	Alignment	not modelled	53.0	39	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
40	c4rs1B	Alignment	not modelled	52.7	31	PDB header: cytokine receptor/cytokine Chain: B: PDB Molecule: granulocyte-macrophage colony-stimulating factor receptor PDBTitle: crystal structure of receptor-cytokine complex
41	c3bpoB	Alignment	not modelled	50.6	39	PDB header: cytokine/cytokine receptor Chain: B: PDB Molecule: interleukin-4 receptor alpha chain; PDBTitle: crystal structure of the il13-il4r-il13ra ternary complex
42	c6cgaC	Alignment	not modelled	49.4	21	PDB header: hydrolase Chain: C: PDB Molecule: ubiquitin carboxyl-terminal hydrolase calypso; PDBTitle: structure of the pr-dub complex
43	d2d9qb2	Alignment	not modelled	48.6	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
44	d1uc6a	Alignment	not modelled	48.6	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
45	d1cd9b2	Alignment	not modelled	48.1	38	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
46	c3di3B	Alignment	not modelled	48.0	31	PDB header: cytokine/cytokine receptor Chain: B: PDB Molecule: interleukin-7 receptor subunit alpha; PDBTitle: crystal structure of the complex of human interleukin-7 with2 glycosylated human interleukin-7 receptor alpha ectodomain
47	c3cxeC	Alignment	not modelled	45.2	28	PDB header: cytokine Chain: C: PDB Molecule: granulocyte-macrophage colony-stimulating factor receptor PDBTitle: structure of the gm-csf receptor complex
48	c6dg5B	Alignment	not modelled	45.1	44	PDB header: biosynthetic protein/protein binding Chain: B: PDB Molecule: interleukin-2 receptor subunit beta; PDBTitle: structure of a de novo designed interleukin-2/interleukin-15 mimetic2 complex with il-2rb and il-2rg
49	c2yh5A	Alignment	not modelled	43.2	6	PDB header: lipid binding protein Chain: A: PDB Molecule: dapx protein; PDBTitle: structure of the c-terminal domain of bamc
50	c4nn5B	Alignment	not modelled	42.5	38	PDB header: cytokine/cytokine receptor Chain: B: PDB Molecule: interleukin-7 receptor subunit alpha; PDBTitle: cytokine receptor complex - crystal form 1a
51	c3tgxA	Alignment	not modelled	40.9	33	PDB header: cytokine/cytokine receptor Chain: A: PDB Molecule: interleukin-21 receptor; PDBTitle: il-21:il21r complex
52	c4nkqB	Alignment	not modelled	40.2	28	PDB header: cytokine/cytokine receptor Chain: B: PDB Molecule: granulocyte-macrophage colony-stimulating factor receptor PDBTitle: structure of a cytokine receptor complex
53	d1erna2	Alignment	not modelled	38.9	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
54	d1a9xb1	Alignment	not modelled	37.5	39	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Carbamoyl phosphate synthetase, small subunit N-terminal domain Family: Carbamoyl phosphate synthetase, small subunit N-terminal domain PDB header: hormone/receptor

55	c3hhrC	Alignment	not modelled	37.4	33	Chain: C; PDB Molecule: human growth hormone receptor (hghbp); PDBTitle: human growth hormone and extracellular domain of its2 receptor: crystal structure of the complex
56	c5mzvC	Alignment	not modelled	37.4	28	PDB header: cytokine Chain: C; PDB Molecule: interleukin-23 receptor; PDBTitle: il-23:il-23r:nb22e11 complex
57	d2b5ic1	Alignment	not modelled	36.5	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
58	c1p9mC	Alignment	not modelled	35.1	31	PDB header: signaling protein/cytokine Chain: C; PDB Molecule: interleukin-6 receptor alpha chain; PDBTitle: crystal structure of the hexameric human il-6/il-6 alpha2 receptor/gp130 complex
59	c5j12C	Alignment	not modelled	34.9	44	PDB header: signaling protein Chain: C; PDB Molecule: cytokine receptor-like factor 2; PDBTitle: structure of human tslp:tslr in complex with mouse il-7ralpha
60	c1pgrD	Alignment	not modelled	33.3	38	PDB header: cytokine Chain: D; PDB Molecule: protein (g-csf receptor); PDBTitle: 2:2 complex of g-csf with its receptor
61	c5d28A	Alignment	not modelled	32.1	31	PDB header: viral protein Chain: A; PDB Molecule: gm-csf/il-2 inhibition factor; PDBTitle: complex of gm-csf/il-2 inhibition factor with granulocyte-macrophage2 colony-stimulating factor
62	c2b5iC	Alignment	not modelled	31.7	28	PDB header: cytokine/cytokine receptor Chain: C; PDB Molecule: cytokine receptor common gamma chain; PDBTitle: cytokine receptor complex
63	d1aixb2	Alignment	not modelled	30.8	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
64	d2gysa2	Alignment	not modelled	29.9	38	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
65	c6cl5F	Alignment	not modelled	28.9	35	PDB header: viral protein Chain: F; PDB Molecule: tail fiber protein; PDBTitle: structure of p. aeruginosa r1 pyocin fiber pales_06171 comprising c-2 terminal residues 323-701
66	d1cmxa	Alignment	not modelled	28.4	29	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin carboxyl-terminal hydrolase UCH-L
67	c2p5qA	Alignment	not modelled	27.3	33	PDB header: oxidoreductase Chain: A; PDB Molecule: glutathione peroxidase 5; PDBTitle: crystal structure of the poplar glutathione peroxidase 5 in the2 reduced form
68	c2ywiA	Alignment	not modelled	26.5	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
69	c6cl6E	Alignment	not modelled	26.2	29	PDB header: viral protein Chain: E; PDB Molecule: tail fiber protein; PDBTitle: structure of p. aeruginosa r2 pyocin fiber pa0620 comprising c-2 terminal residues 323-691
70	d1xd3a	Alignment	not modelled	25.3	24	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin carboxyl-terminal hydrolase UCH-L
71	d1p9ma3	Alignment	not modelled	25.3	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
72	c2e8pA	Alignment	not modelled	23.5	12	PDB header: signaling protein Chain: A; PDB Molecule: elf3 protein; PDBTitle: solution structure of the n-terminal sam-domain of e74-like2 factor 3
73	c5ns5A	Alignment	not modelled	23.2	12	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidase glij; PDBTitle: cys-gly dipeptidase glij in complex with cu2+ and zn2+
74	c2d9qB	Alignment	not modelled	23.1	31	PDB header: signaling protein/cytokine Chain: B; PDB Molecule: granulocyte colony-stimulating factor receptor; PDBTitle: crystal structure of the human gcsf-receptor signaling complex
75	c4jzjD	Alignment	not modelled	23.1	22	PDB header: cytokine receptor/immune system Chain: D; PDB Molecule: interleukin-3 receptor subunit alpha; PDBTitle: crystal structure of receptor-fab complex
76	d1n26a3	Alignment	not modelled	22.9	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
77	c2erjF	Alignment	not modelled	22.6	44	PDB header: immune system/cytokine Chain: F; PDB Molecule: interleukin-2 receptor beta chain; PDBTitle: crystal structure of the heterotrimeric interleukin-2 receptor in2 complex with interleukin-2
78	c1ernA	Alignment	not modelled	22.5	39	PDB header: cytokine Chain: A; PDB Molecule: protein (erythropoietin receptor); PDBTitle: native structure of the extracellular domain of2 erythropoietin (epo) receptor [ebp]
79	c1keeH	Alignment	not modelled	22.4	39	PDB header: ligase Chain: H; PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
80	d2etla1	Alignment	not modelled	22.3	16	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin carboxyl-terminal hydrolase UCH-L
81	c1u3aM	Alignment	not modelled	22.2	41	PDB header: dna binding protein/dna Chain: M; PDB Molecule: hnh homing endonuclease;

81	c1u3em_	Alignment	not modelled	22.2	41	PDBTitle: dna binding and cleavage by the hnh homing endonuclease i-hmui PDB header: viral protein/cytokine
82	c4zkcA_	Alignment	not modelled	22.1	21	Chain: A: PDB Molecule: chemokine binding protein; PDBTitle: the chemokine binding protein of orf virus complexed with ccl7
83	c3d87D_	Alignment	not modelled	21.6	28	PDB header: cytokine Chain: D: PDB Molecule: interleukin-12 subunit p40; PDBTitle: crystal structure of interleukin-23
84	d1zofa1	Alignment	not modelled	21.1	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
85	c2lrtA_	Alignment	not modelled	20.8	10	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the uncharacterized thioredoxin-like protein2 bvu_1432 from bacteroides vulgatus
86	c5ltvA_	Alignment	not modelled	20.8	27	PDB header: signaling protein Chain: A: PDB Molecule: chemotactic transducer pctc; PDBTitle: ligand binding regions of pseudomonas aeruginosa pao1 amino acid2 chemoreceptors pctc in complex with gaba
87	c2erjC_	Alignment	not modelled	20.4	33	PDB header: immune system/cytokine Chain: C: PDB Molecule: cytokine receptor common gamma chain; PDBTitle: crystal structure of the heterotrimeric interleukin-2 receptor in2 complex with interleukin-2
88	d1t23a_	Alignment	not modelled	19.9	19	Fold: Chromosomal protein MC1 Superfamily: Chromosomal protein MC1 Family: Chromosomal protein MC1
89	c1n26A_	Alignment	not modelled	19.8	31	PDB header: cytokine Chain: A: PDB Molecule: il-6 receptor alpha chain; PDBTitle: crystal structure of the extra-cellular domains of human interleukin-62 receptor alpha chain
90	c5d0qC_	Alignment	not modelled	18.1	6	PDB header: protein transport Chain: C: PDB Molecule: outer membrane protein assembly factor bamc; PDBTitle: bamacde complex, outer membrane beta-barrel assembly machinery (bam)2 complex
91	c4ig7A_	Alignment	not modelled	17.6	9	PDB header: hydrolase/signaling protein Chain: A: PDB Molecule: ubiquitin c-terminal hydrolase 37; PDBTitle: crystal structure of trichinella spiralis uch37 bound to ubiquitin2 vinyl methyl ester
92	c3wp6A_	Alignment	not modelled	17.6	21	PDB header: hydrolase Chain: A: PDB Molecule: cdbfv; PDBTitle: the complex structure of cdbfv e109a with xylotriase
93	d1m4wa_	Alignment	not modelled	17.4	24	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Xylanase/endoglucanase 11/12
94	c1l1rA_	Alignment	not modelled	17.0	26	PDB header: cytokine Chain: A: PDB Molecule: interleukin-6 receptor beta chain; PDBTitle: crystal structure of a cytokine/receptor complex
95	c4tr3A_	Alignment	not modelled	16.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: type iii iodothyronine deiodinase; PDBTitle: mouse iodothyronine deiodinase 3 catalytic core, semet-labeled active2 site mutant secys->cys
96	c3dvwB_	Alignment	not modelled	16.6	25	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione peroxidase-like protein; PDBTitle: glutathione peroxidase-type tryparedoxin peroxidase, oxidized form
97	d1cmra_	Alignment	not modelled	16.6	42	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
98	d2b5ib2	Alignment	not modelled	16.1	38	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
99	c2ov2O_	Alignment	not modelled	15.9	24	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)