

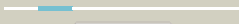






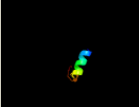



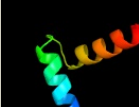



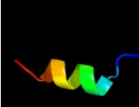






Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2862A_(RVBD2862A)_3174757_3175005
 Date Wed Aug 7 12:50:53 BST 2019
 Unique Job ID 6812a1ea2fb24039

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6qeqD_	 Alignment		69.1	17	PDB header: dna binding protein Chain: D; PDB Molecule: pcff; PDBTitle: pcff from enterococcus faecalis pcf10
2	c5yirH_	 Alignment		32.1	64	PDB header: protein binding Chain: H; PDB Molecule: ankyrin-2; PDBTitle: crystal structure of ankb lir/gabarap complex
3	c5yirG_	 Alignment		26.9	64	PDB header: protein binding Chain: G; PDB Molecule: ankyrin-2; PDBTitle: crystal structure of ankb lir/gabarap complex
4	d1ujka_	 Alignment		24.0	16	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
5	d1mija_	 Alignment		18.7	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
6	c2o7aA_	 Alignment		17.8	32	PDB header: hydrolase Chain: A; PDB Molecule: lysozyme; PDBTitle: t4 lysozyme c-terminal fragment
7	c6ajnF_	 Alignment		17.8	18	PDB header: toxin Chain: F; PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atar bound with accoa
8	c4e6tA_	 Alignment		17.0	16	PDB header: transferase Chain: A; PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: structure of lpxa from acinetobacter baumannii at 1.8a resolution2 (p212121 form)
9	c5yisC_	 Alignment		16.7	64	PDB header: protein binding Chain: C; PDB Molecule: ankyrin-2; PDBTitle: crystal structure of ankb lir/lc3b complex
10	c6gtsC_	 Alignment		16.2	18	PDB header: transcription Chain: C; PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
11	c2lmdA_	 Alignment		16.1	29	PDB header: transcription Chain: A; PDB Molecule: prospero homeobox protein 1; PDBTitle: minimal constraints solution nmr structure of prospero homeobox2 protein 1 from homo sapiens, northeast structural genomics consortium3 target hr4660b

12	d1c07a_	Alignment		15.7	7	Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain)
13	c2d46A_	Alignment		15.6	45	PDB header: metal transport Chain: A: PDB Molecule: calcium channel, voltage-dependent, beta 4 PDBTitle: solution structure of the human beta4a-a domain
14	c3eujB_	Alignment		14.1	29	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpggammas complex, symmetric dimer
15	c4r36A_	Alignment		14.0	18	PDB header: transferase Chain: A: PDB Molecule: putative acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343
16	d1p5ca_	Alignment		13.9	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
17	c5y70A_	Alignment		13.3	40	PDB header: membrane protein Chain: A: PDB Molecule: kinetoplastid membrane protein 11; PDBTitle: nmr structure of kmp11 in dpc micelle
18	c4xsiA_	Alignment		13.3	32	PDB header: transport protein Chain: A: PDB Molecule: lysozyme,calcium uniporter protein, mitochondrial; PDBTitle: crystal structure of the n-terminal domain of the human mitochondrial2 calcium uniporter fused with t4 lysozyme
19	c2kg5A_	Alignment		12.7	35	PDB header: signaling protein Chain: A: PDB Molecule: arf-gap, rho-gap domain, ank repeat and ph PDBTitle: nmr solution structure of arap3-sam
20	c2k5jB_	Alignment		12.6	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
21	d1cg5a_	Alignment	not modelled	12.1	14	Fold: Globin-like Superfamily: Globin-like Family: Globins
22	c5b2gG_	Alignment	not modelled	11.9	32	PDB header: membrane protein Chain: G: PDB Molecule: endolysin,claudin-4; PDBTitle: crystal structure of human claudin-4 in complex with c-terminal2 fragment of clostridium perfringens enterotoxin
23	d1qzma_	Alignment	not modelled	11.4	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
24	c4iapB_	Alignment	not modelled	10.9	32	PDB header: lipid binding protein/ hydrolase Chain: B: PDB Molecule: oxysterol-binding protein homolog 3,endolysin,oxysterol- PDBTitle: crystal structure of ph domain of osh3 from saccharomyces cerevisiae
25	d1juqa_	Alignment	not modelled	10.7	12	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
26	c3sn6R_	Alignment	not modelled	10.6	32	PDB header: signaling protein/hydrolase Chain: R: PDB Molecule: endolysin,beta-2 adrenergic receptor; PDBTitle: crystal structure of the beta2 adrenergic receptor-gs protein complex
27	c1x37A_	Alignment	not modelled	10.5	38	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease la 1; PDBTitle: structure of bacillus subtilis lon protease ssd domain
28	c5vbaA_	Alignment	not modelled	10.4	32	PDB header: chaperone, hydrolase Chain: A: PDB Molecule: lysozyme, esx-1 secretion-associated protein espg1 chimera; PDBTitle: structure of espg1 chaperone from the type vii (esx-1) secretion2 system determined with the assistance of n-terminal t4

						lysozyme3 fusion
29	c6qajB_	Alignment	not modelled	10.3	33	PDB header: nuclear protein Chain: B: PDB Molecule: endolysin,transcription intermediary factor 1-beta; PDBTitle: structure of the tripartite motif of kap1/trim28
30	c5v88A_	Alignment	not modelled	10.0	32	PDB header: ligase / protein binding Chain: A: PDB Molecule: lysozyme,dcn1-like protein 1; PDBTitle: structure of dcn1 bound to nacm-cov
31	c6a9eA_	Alignment	not modelled	10.0	32	PDB header: lipid transport Chain: A: PDB Molecule: endolysin,autophagy-related protein 2; PDBTitle: crystal structure of the n-terminal domain of atg2
32	c3eukJ_	Alignment	not modelled	9.7	29	PDB header: cell cycle Chain: J: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpgammas complex, asymmetric dimer
33	d1fs2b1	Alignment	not modelled	9.6	25	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
34	d1lpya_	Alignment	not modelled	9.3	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
35	c5yqrA_	Alignment	not modelled	9.0	32	PDB header: transport protein Chain: A: PDB Molecule: endolysin/membrane-anchored lipid-binding protein lam6 PDBTitle: crystal structure of the ph-like domain of lam6
36	c2qnlA_	Alignment	not modelled	9.0	31	PDB header: signaling protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dna damage-inducible protein2 (chu_0679) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
37	d1ucva_	Alignment	not modelled	8.7	13	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
38	c5zrzB_	Alignment	not modelled	8.5	24	PDB header: protein binding Chain: B: PDB Molecule: sterile alpha motif domain-containing protein 5; PDBTitle: crystal structure of epha5/samd5 complex
39	c3omyB_	Alignment	not modelled	8.5	42	PDB header: dna binding protein Chain: B: PDB Molecule: protein tram; PDBTitle: crystal structure of the ped208 tram n-terminal domain
40	c6fxfA_	Alignment	not modelled	8.4	29	PDB header: signaling protein Chain: A: PDB Molecule: sam and sh3 domain-containing protein 3; PDBTitle: crystal structure of the sam domain of murine sly1
41	c3wknG_	Alignment	not modelled	8.2	50	PDB header: immune system Chain: G: PDB Molecule: affinger p17; PDBTitle: crystal structure of the artificial protein affinger p17 (af.p17)2 complexed with fc fragment of human igg
42	c1yybA_	Alignment	not modelled	8.2	57	PDB header: apoptosis Chain: A: PDB Molecule: programmed cell death protein 5; PDBTitle: solution structure of 1-26 fragment of human programmed2 cell death 5 protein
43	c2qb0D_	Alignment	not modelled	8.2	32	PDB header: hydrolase regulator Chain: D: PDB Molecule: telsam domain - lysozyme chimera; PDBTitle: structure of the 2tel crystallization module fused to t4 lysozyme with2 an ala-gly-pro linker.
44	c4arjB_	Alignment	not modelled	8.1	32	PDB header: hydrolase Chain: B: PDB Molecule: pesticin, lysozyme; PDBTitle: crystal structure of a pesticin (translocation and receptor binding2 domain) from y. pestis and t4-lysozyme chimera
45	c2ctoA_	Alignment	not modelled	8.0	70	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: novel protein; PDBTitle: solution structure of the hmg box like domain from human2 hypothetical protein flj14904
46	d176la_	Alignment	not modelled	8.0	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
47	c2n6yA_	Alignment	not modelled	7.9	24	PDB header: ligase Chain: A: PDB Molecule: hmwp2 nonribosomal peptide synthetase; PDBTitle: solution structure of holo arcp from yersiniabactin synthetase
48	d2h80a1	Alignment	not modelled	7.8	60	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
49	d1o7ka_	Alignment	not modelled	7.8	38	Fold: PX domain Superfamily: PX domain Family: PX domain
50	c2zetD_	Alignment	not modelled	7.8	34	PDB header: signaling protein Chain: D: PDB Molecule: melanophilin; PDBTitle: crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
51	c2ba3A_	Alignment	not modelled	7.6	31	PDB header: dna binding protein Chain: A: PDB Molecule: nika; PDBTitle: nmr structure of nika n-terminal fragment
52	d1rg6a_	Alignment	not modelled	7.5	27	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
53	d1k28a3	Alignment	not modelled	7.1	26	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
54	c3fxeA_	Alignment	not modelled	7.0	40	PDB header: unknown function Chain: A: PDB Molecule: protein icmq; PDBTitle: crystal structure of interacting domains of icmr and icmq (seleno-2 derivative) Fold: DNA/RNA-binding 3-helical bundle

55	d2foka2	Alignment	not modelled	6.9	40	Superfamily: "Winged helix" DNA-binding domain Family: Restriction endonuclease FokI, N-terminal (recognition) domain
56	c5vx3H	Alignment	not modelled	6.7	75	PDB header: apoptosis Chain: H: PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
57	c5vx3F	Alignment	not modelled	6.7	75	PDB header: apoptosis Chain: F: PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
58	c5vx3D	Alignment	not modelled	6.7	75	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
59	d1heka	Alignment	not modelled	6.6	78	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: EIAV matrix antigen
60	c2kwuA	Alignment	not modelled	6.6	27	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
61	c5vx0B	Alignment	not modelled	6.5	75	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak in complex with bim-h3glg
62	c5vx2D	Alignment	not modelled	6.5	75	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim-h3pc-rt
63	c5vvyB	Alignment	not modelled	6.5	75	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-h3pc-rt
64	c5vx3B	Alignment	not modelled	6.5	75	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
65	c5vx0D	Alignment	not modelled	6.5	75	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak in complex with bim-h3glg
66	d1dp3a	Alignment	not modelled	6.4	50	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: DNA-binding domain (fragment?) of the TraM protein
67	c5vx2B	Alignment	not modelled	6.4	75	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim-h3pc-rt
68	d1fs1b1	Alignment	not modelled	6.4	24	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
69	c4exmB	Alignment	not modelled	6.3	32	PDB header: toxin, hydrolase Chain: B: PDB Molecule: pesticin, lysozyme chimera; PDBTitle: the crystal structure of an engineered phage lysin containing the2 binding domain of pesticin and the killing domain of t4-lysozyme
70	d1oxja1	Alignment	not modelled	6.3	21	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
71	c4ydeB	Alignment	not modelled	6.3	19	PDB header: transferase Chain: B: PDB Molecule: protein farnesyltransferase/geranylgeranyltransferase type- PDBTitle: crystal structure of candida albicans protein farnesyltransferase2 binary complex with the isoprenoid farnesyldiphosphate
72	c5zrzA	Alignment	not modelled	6.1	18	PDB header: protein binding Chain: A: PDB Molecule: ephrin type-a receptor 5; PDBTitle: crystal structure of epha5/samd5 complex
73	d2dkya1	Alignment	not modelled	6.1	50	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
74	d1coka	Alignment	not modelled	6.1	27	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
75	c6a73B	Alignment	not modelled	6.1	32	PDB header: signaling protein Chain: B: PDB Molecule: cop9 signalosome complex subunit 2, endolysin; PDBTitle: complex structure of csn2 with ip6
76	c2o4wA	Alignment	not modelled	6.0	32	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: t4 lysozyme circular permutant
77	d1nexa1	Alignment	not modelled	6.0	23	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
78	c4dwnB	Alignment	not modelled	5.8	55	PDB header: apoptosis Chain: B: PDB Molecule: bcl10-interacting card protein; PDBTitle: crystal structure of human bincard card
79	c5kw2A	Alignment	not modelled	5.8	32	PDB header: fatty acid binding protein/hydrolase Chain: A: PDB Molecule: free fatty acid receptor 1, lysozyme, free fatty acid PDBTitle: the extra-helical binding site of gpr40 and the structural basis for2 allosteric agonism and incretin stimulation
80	c3gr1A	Alignment	not modelled	5.7	21	PDB header: membrane protein Chain: A: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3s inner membrane protein prgh from2 s.typhimurium (fragment 170-392)
81	c2p11A	Alignment	not modelled	5.7	20	PDB header: motor protein, protein transport Chain: A: PDB Molecule: unconventional myosin-vi;

81	c2111A	Alignment	not modelled	5.7	39	PDBTitle: solution structure of human myosin vi isoform3 (998-1071)
82	c2lmrA	Alignment	not modelled	5.6	47	PDB header: signaling protein Chain: A; PDB Molecule: ankyrin repeat and sam domain-containing protein 1a; PDBTitle: solution structure of the first sam domain of odin
83	c6gvwF	Alignment	not modelled	5.5	26	PDB header: signaling protein Chain: F; PDB Molecule: brca1-a complex subunit abraxas 1; PDBTitle: crystal structure of the brca1-a complex
84	c4gitA	Alignment	not modelled	5.5	29	PDB header: hydrolase Chain: A; PDB Molecule: lon protease; PDBTitle: crystal structure of alpha sub-domain of lon protease from2 brevibacillus thermoruber
85	c2qkqA	Alignment	not modelled	5.5	33	PDB header: transferase Chain: A; PDB Molecule: ephrin type-b receptor 4; PDBTitle: structure of the sam domain of human ephrin type-b receptor2 4
86	d1iufa1	Alignment	not modelled	5.5	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
87	d1mlda2	Alignment	not modelled	5.4	13	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
88	d157la	Alignment	not modelled	5.4	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
89	c2k6rA	Alignment	not modelled	5.4	46	PDB header: de novo protein Chain: A; PDB Molecule: full sequence design 1 synthetic superstable; PDBTitle: protein folding on a highly rugged landscape: experimental observation2 of glassy dynamics and structural frustration
90	c5vwwD	Alignment	not modelled	5.3	60	PDB header: apoptosis Chain: D; PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-rt - tetragonal
91	d1t8fa	Alignment	not modelled	5.2	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
92	c5ndzA	Alignment	not modelled	5.2	32	PDB header: membrane protein Chain: A; PDB Molecule: lysozyme,proteinase-activated receptor 2,soluble cytochrome PDBTitle: crystal structure of a thermostabilised human protease-activated2 receptor-2 (par2) in complex with az3451 at 3.6 angstrom resolution
93	c3njcA	Alignment	not modelled	5.1	40	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: yslb protein; PDBTitle: crystal structure of the yslb protein from bacillus subtilis.2 northeast structural genomics consortium target sr460.
94	d1b4ua	Alignment	not modelled	5.1	20	Fold: LigA subunit of an aromatic-ring-opening dioxygenase LigAB Superfamily: LigA subunit of an aromatic-ring-opening dioxygenase LigAB Family: LigA subunit of an aromatic-ring-opening dioxygenase LigAB
95	d2ctza1	Alignment	not modelled	5.1	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
96	d2ovra1	Alignment	not modelled	5.0	25	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
97	c1fsdA	Alignment	not modelled	5.0	46	PDB header: novel sequence Chain: A; PDB Molecule: full sequence design 1 of beta beta alpha motif; PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures