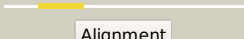
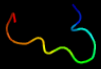
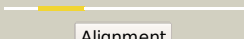

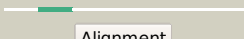


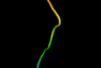
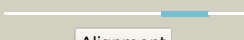






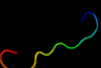



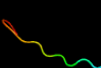




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3770A (-) _4216059_4216241
Date	Fri Aug 9 18:20:47 BST 2019
Unique Job ID	b141b6fb7afea6a7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xkua_	 Alignment		72.7	62	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
2	c1xkuA_	 Alignment		72.7	62	PDB header: structural protein Chain: A: PDB Molecule: decorin; PDBTitle: crystal structure of the dimeric protein core of decorin, the2 archetypal small leucine-rich repeat proteoglycan
3	c3j32B_	 Alignment		45.6	67	PDB header: oxygen transport Chain: B: PDB Molecule: hemocyanin isoform 1; PDBTitle: an asymmetric unit map from electron cryo-microscopy of haliotis2 diversicolor molluscan hemocyanin isoform 1 (hdh1)
4	c4wala_	 Alignment		43.2	50	PDB header: protein binding/rna Chain: A: PDB Molecule: branchpoint-bridging protein; PDBTitle: crystal structure of selenomethionine msl5 protein in complex with rna2 at 2.2 a
5	d2bl5a1	 Alignment		35.7	43	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
6	c4jvhA_	 Alignment		35.2	41	PDB header: rna binding protein Chain: A: PDB Molecule: protein quaking; PDBTitle: structure of the star domain of quaking protein in complex with rna
7	c4bstB_	 Alignment		31.8	57	PDB header: signaling protein Chain: B: PDB Molecule: leucine-rich repeat-containing g-protein coupled receptor PDBTitle: structure of the ectodomain of lgr5 in complex with r-spondin-12 (fu1fu2) in p6122 crystal form
8	d1k1ga_	 Alignment		31.5	36	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
9	d2phna1	 Alignment		29.4	26	Fold: CofE-like Superfamily: CofE-like Family: CofE-like
10	c5el3D_	 Alignment		28.2	21	PDB header: rna binding protein Chain: D: PDB Molecule: kh domain-containing, rna-binding, signal transduction- PDBTitle: structure of the kh domain of t-star
11	d1myka_	 Alignment		26.9	36	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors

12	c4pbwB_	Alignment		26.4	36	PDB header: signaling protein Chain: B: PDB Molecule: nt-3 growth factor receptor; PDBTitle: crystal structure of chicken receptor protein tyrosine phosphatase2 sigma in complex with trkc
13	d1baza_	Alignment		26.1	36	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
14	c4u71A_	Alignment		24.7	36	PDB header: signaling protein Chain: A: PDB Molecule: leucine-rich repeats and immunoglobulin-like domains PDBTitle: Irig1 extracellular domain: structure and function analysis
15	c5eltB_	Alignment		23.6	21	PDB header: rna binding protein Chain: B: PDB Molecule: kh domain-containing, rna-binding, signal transduction- PDBTitle: structure of the qua1-kh domain of t-star in complex with uauu rna
16	d1bdta_	Alignment		23.2	36	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
17	c4jvvA_	Alignment		20.7	50	PDB header: rna binding protein Chain: A: PDB Molecule: female germline-specific tumor suppressor gld-1; PDBTitle: structure of the star (signal transduction and activation of rna)2 domain of gld-1 bound to rna
18	c4qxeA_	Alignment		20.5	50	PDB header: membrane protein Chain: A: PDB Molecule: leucine-rich repeat-containing g-protein coupled receptor PDBTitle: crystal structure of lgr4 fused with hagfish vlr
19	c4qdhA_	Alignment		20.1	36	PDB header: immune system Chain: A: PDB Molecule: variable lymphocyte receptor b, toll-like receptor 9 PDBTitle: crystal structure of the c-terminal domain of mouse tlr9
20	c4kt1A_	Alignment		19.9	50	PDB header: hormone receptor/cell adhesion Chain: A: PDB Molecule: leucine-rich repeat-containing g-protein coupled receptor PDBTitle: complex of r-spondin 1 with lgr4 extracellular domain
21	c4y61B_	Alignment	not modelled	19.6	22	PDB header: hydrolase/signaling protein Chain: B: PDB Molecule: slit and ntrk-like protein 2; PDBTitle: crystal structure of the complex between slitrk2 lrr1 and ptp delta2 ig1-fn1
22	d1w8aa_	Alignment	not modelled	19.0	45	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
23	c5jy5A_	Alignment	not modelled	18.6	50	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 1 from cryptococcus neoformans at 1.82 angstroms resolution
24	c2ft3B_	Alignment	not modelled	18.6	55	PDB header: structural protein, signaling protein Chain: B: PDB Molecule: biglycan; PDBTitle: crystal structure of the biglycan dimer core protein
25	c2dj0A_	Alignment	not modelled	18.2	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: thioredoxin-related transmembrane protein 2; PDBTitle: the solution structure of the thioredoxin domain of human2 thioredoxin-related transmembrane protein 2
26	c3hypB_	Alignment	not modelled	17.9	44	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of bacteroides fragilis trxp_s105g mutant
27	c5a5cD_	Alignment	not modelled	16.2	36	PDB header: signaling protein Chain: D: PDB Molecule: lrrtm; PDBTitle: structure of an engineered neuronal lrrtm2 adhesion molecule
28	c3zzxB_	Alignment	not modelled	15.9	50	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystallographic structure of thioredoxin from litopenaeus vannamei

29	c2v70D_	Alignment	not modelled	15.8	45	PDB header: structural protein Chain: D: PDB Molecule: slit homolog 2 protein n-product; PDBTitle: third lrr domain of human slit2
30	c2l6dA_	Alignment	not modelled	15.7	38	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution structure of desulfthioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
31	c5e37A_	Alignment	not modelled	15.7	44	PDB header: oxidoreductase Chain: A: PDB Molecule: ef-hand domain-containing thioredoxin; PDBTitle: redox protein from chlamydomonas reinhardtii
32	c2mcsA_	Alignment	not modelled	15.3	63	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution nmr structure of a putative thioredoxin (ech_0218) in the2 reduced state from ehrlichia chaffeensis, the etiological agent3 responsible for human monocytic ehrlichiosis. seattle structural4 genomics center for infectious disease target ehcha.00546.a
33	d1ozna_	Alignment	not modelled	14.9	57	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
34	d2fc6a1	Alignment	not modelled	14.6	63	Fold: CCCH zinc finger Superfamily: CCCH zinc finger Family: CCCH zinc finger
35	c4bsrB_	Alignment	not modelled	14.3	57	PDB header: signaling protein Chain: B: PDB Molecule: leucine-rich repeat-containing g-protein coupled receptor PDBTitle: structure of the ectodomain of lgr5 in complex with r-spondin-12 (fu1fu2) in p22121 crystal form
36	c4p8sA_	Alignment	not modelled	14.1	46	PDB header: membrane protein Chain: A: PDB Molecule: reticulon-4 receptor-like 2; PDBTitle: crystal structure of nogo-receptor-2
37	c4v2eA_	Alignment	not modelled	13.7	36	PDB header: signaling protein Chain: A: PDB Molecule: fibronectin leucine rich transmembrane protein 3; PDBTitle: flrt3 lrr domain
38	c2fc6A_	Alignment	not modelled	13.7	63	PDB header: transcription Chain: A: PDB Molecule: target of egr1, member 1; PDBTitle: solution structure of the zf-ccch domain of target of egr1,2 member 1 (nuclear)
39	c2v1vA_	Alignment	not modelled	13.5	50	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h isoform 2.;; PDBTitle: crystal structure of barley thioredoxin h isoform 2 in partially2 radiation-reduced state
40	c6bkvB_	Alignment	not modelled	13.4	63	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from helicobacter pylori (strain g27)
41	c4xsqA_	Alignment	not modelled	13.1	42	PDB header: immune system Chain: A: PDB Molecule: variable lymphocyte receptor-like protein bf66946; PDBTitle: structure of a variable lymphocyte receptor-like protein bf66946 from2 branchiostoma floridae
42	c2vm2C_	Alignment	not modelled	13.0	50	PDB header: oxidoreductase Chain: C: PDB Molecule: thioredoxin h isoform 1.;; PDBTitle: crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant
43	c2f51B_	Alignment	not modelled	13.0	63	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: structure of trichomonas vaginalis thioredoxin
44	c2oe0B_	Alignment	not modelled	12.5	50	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin-3; PDBTitle: crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
45	d1xfla_	Alignment	not modelled	12.5	50	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
46	d1mylb_	Alignment	not modelled	12.4	33	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
47	c5o0oB_	Alignment	not modelled	12.3	50	PDB header: signaling protein Chain: B: PDB Molecule: reticulon-4 receptor; PDBTitle: deglycosylated nogo receptor with native disulfide structure 5
48	c5hccD_	Alignment	not modelled	12.2	47	PDB header: immune system Chain: D: PDB Molecule: dermacentor andersoni raci3; PDBTitle: ternary complex of human complement c5 with ornithodoros moubata omci2 and dermacentor andersoni raci3.
49	c6gn9A_	Alignment	not modelled	11.5	63	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a thioredoxin from clostridium acetobutylicum at2 1.75 a resolution
50	d1bazb_	Alignment	not modelled	11.0	38	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
51	c2yqrA_	Alignment	not modelled	10.9	55	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0907 protein; PDBTitle: solution structure of the kh domain in kiaa0907 protein
52	c2o6sA_	Alignment	not modelled	10.9	45	PDB header: immune system Chain: A: PDB Molecule: variable lymphocyte receptor b; PDBTitle: structural diversity of the hagfish variable lymphocyte2 receptors b59
53	c2pptA_	Alignment	not modelled	10.8	63	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
						PDB header: unknown function

54	c5i65A_	Alignment	not modelled	10.8	26	Chain: A: PDB Molecule: nonstructural proteins ort1a; PDBTitle: porcine reproductive and respiratory syndrome virus nonstructural2 protein 7 alpha (nsp7 alpha)
55	c4ui9U_	Alignment	not modelled	10.7	67	PDB header: cell cycle Chain: U: PDB Molecule: peptide; PDBTitle: atomic structure of the human anaphase-promoting complex
56	d1z5ye1	Alignment	not modelled	10.5	38	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
57	c4cw9A_	Alignment	not modelled	10.4	38	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: entamoeba histolytica thioredoxin c34s mutant
58	c3wgdD_	Alignment	not modelled	10.4	63	PDB header: isomerase Chain: D: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: crystal structure of erp46 trx1
59	d1gh2a_	Alignment	not modelled	10.4	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
60	d1i5ga_	Alignment	not modelled	10.2	50	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
61	c2z66A_	Alignment	not modelled	9.8	36	PDB header: immune system Chain: A: PDB Molecule: variable lymphocyte receptor b, toll-like receptor 4; PDBTitle: crystal structure of the vt3 hybrid of human tlr4 and hagfish virb.61
62	d1kyza1	Alignment	not modelled	9.8	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Plant O-methyltransferase, N-terminal domain
63	c2dizA_	Alignment	not modelled	9.6	44	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin domain-containing protein 5; PDBTitle: the solution structure of the third thioredoxin domain of2 human thioredoxin domain-containing protein 5
64	c1e9kA_	Alignment	not modelled	9.5	83	PDB header: hydrolase Chain: A: PDB Molecule: camp-specific 3',5'-cyclic phosphodiesterase 4d; PDBTitle: the structure of the rack1 interaction sites located within the unique2 n-terminal region of the camp-specific phosphodiesterase, pde4d5.
65	c2he3A_	Alignment	not modelled	9.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 2; PDBTitle: crystal structure of the selenocysteine to cysteine mutant of human2 glutathione peroxidase 2 (gpx2)
66	c2l8kA_	Alignment	not modelled	9.4	34	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 7; PDBTitle: nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
67	c4qxfB_	Alignment	not modelled	9.2	50	PDB header: membrane protein Chain: B: PDB Molecule: leucine-rich repeat-containing g-protein coupled receptor PDBTitle: crystal structure of human lgr4 and rspo1
68	c3p2aB_	Alignment	not modelled	9.0	63	PDB header: oxidoreductase Chain: B: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis
69	d1myla_	Alignment	not modelled	9.0	33	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
70	c4cnmA_	Alignment	not modelled	8.9	57	PDB header: cell adhesion Chain: A: PDB Molecule: trophoblast glycoprotein; PDBTitle: crystal structure of human 5t4 (wnt-activated inhibitory2 factor 1, trophoblast glycoprotein)
71	d1b28a_	Alignment	not modelled	8.8	33	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
72	c5mx0B_	Alignment	not modelled	8.3	57	PDB header: structural protein Chain: B: PDB Molecule: fibromodulin; PDBTitle: crystal structure of human fibromodulin
73	d1nhoa_	Alignment	not modelled	8.2	43	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
74	c3me8B_	Alignment	not modelled	7.8	19	PDB header: electron transport Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of putative electron transfer protein aq_2194 from2 aquifex aeolicus vf5
75	c4v2dA_	Alignment	not modelled	7.7	36	PDB header: signaling protein Chain: A: PDB Molecule: fibronectin leucine rich transmembrane protein 2; PDBTitle: flrt2 lrr domain
76	d1knga_	Alignment	not modelled	7.6	36	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
77	c1w89E_	Alignment	not modelled	7.5	50	PDB header: electron transport Chain: E: PDB Molecule: thioredoxin; PDBTitle: structure of the reduced form of human thioredoxin 2
78	c4i8bA_	Alignment	not modelled	7.5	44	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from schistosoma japonicum
79	c3p2aA_	Alignment	not modelled	7.5	63	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis
						PDB header: immune system Chain: A: PDB Molecule: variable lvmhocvte receptor a diversity

80	c3m18A_	Alignment	not modelled	7.2	17	region; PDBTitle: crystal structure of variable lymphocyte receptor vlra.r2.1 in complex2 with hen egg lysozyme
81	c4mnnA_	Alignment	not modelled	7.2	50	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin related protein; PDBTitle: the crystal structure of sso1120 from sulfolobus solfataricus
82	d1xwdc1	Alignment	not modelled	7.2	36	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
83	c2wfhB_	Alignment	not modelled	7.1	36	PDB header: splicing Chain: B: PDB Molecule: slit homolog 2 protein c-product; PDBTitle: the human slit 2 dimerization domain d4
84	c5y30A_	Alignment	not modelled	7.0	45	PDB header: cell adhesion Chain: A: PDB Molecule: leucine-rich glioma-inactivated protein 1; PDBTitle: crystal structure of Ig1 lrr domain
85	c2yoiA_	Alignment	not modelled	6.9	50	PDB header: oxidoreductase Chain: A: PDB Molecule: leca thioredoxin; PDBTitle: crystal structure of ancestral thioredoxin relative to last eukaryotes2 common ancestor (leca) from the precambrian period
86	c3g3aA_	Alignment	not modelled	6.9	45	PDB header: hydrolase/immune system Chain: A: PDB Molecule: variable lymphocyte receptor vlrb.2d; PDBTitle: structure of a lamprey variable lymphocyte receptor in2 complex with a protein antigen
87	c4bedA_	Alignment	not modelled	6.9	56	PDB header: oxygen transport Chain: A: PDB Molecule: hemocyanin klh1; PDBTitle: keyhole limpet hemocyanin (klh): 9a cryoem structure and molecular2 model of the klh1 didecamer reveal the interfaces and intricate3 topology of the 160 functional units
88	c5lhzE_	Alignment	not modelled	6.8	75	PDB header: structural protein Chain: E: PDB Molecule: scl-interrupting locus protein; PDBTitle: pb3 domain of human plk4 in complex with coiled-coil domain of stil
89	c4yypB_	Alignment	not modelled	6.8	75	PDB header: transferase Chain: B: PDB Molecule: scl-interrupting locus protein; PDBTitle: crystal structure of human plk4-pb3 in complex with stil-cc
90	c2vafA_	Alignment	not modelled	6.8	13	PDB header: metal binding protein Chain: A: PDB Molecule: calsequestrin-2; PDBTitle: crystal structure of human cardiac calsequestrin
91	c2jmoA_	Alignment	not modelled	6.7	60	PDB header: ligase Chain: A: PDB Molecule: parkin; PDBTitle: ibr domain of human parkin
92	c3rfeB_	Alignment	not modelled	6.6	63	PDB header: cell adhesion Chain: B: PDB Molecule: platelet glycoprotein ib beta chain; PDBTitle: crystal structure of glycoprotein gpib ectodomain
93	c5lhzF_	Alignment	not modelled	6.5	75	PDB header: structural protein Chain: F: PDB Molecule: scl-interrupting locus protein; PDBTitle: pb3 domain of human plk4 in complex with coiled-coil domain of stil
94	c5lhzD_	Alignment	not modelled	6.5	75	PDB header: structural protein Chain: D: PDB Molecule: scl-interrupting locus protein; PDBTitle: pb3 domain of human plk4 in complex with coiled-coil domain of stil
95	c1j08A_	Alignment	not modelled	6.5	22	PDB header: isomerase Chain: A: PDB Molecule: glutaredoxin-like protein; PDBTitle: crystal structure of glutaredoxin-like protein from2 pyrococcus horikoshii
96	c5lhwA_	Alignment	not modelled	6.5	75	PDB header: structural protein Chain: A: PDB Molecule: scl-interrupting locus protein; PDBTitle: central coiled-coil domain of human stil
97	c2yzuA_	Alignment	not modelled	6.5	50	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
98	c3ia1A_	Alignment	not modelled	6.4	26	PDB header: oxidoreductase Chain: A: PDB Molecule: thio-disulfide isomerase/thioredoxin; PDBTitle: crystal structure of thio-disulfide isomerase from thermus2 thermophilus
99	c5z8yE_	Alignment	not modelled	6.2	36	PDB header: cell adhesion Chain: E: PDB Molecule: leucine-rich repeat transmembrane neuronal protein 2; PDBTitle: crystal structure of human lrrtm2 in complex with neurexin 1beta