
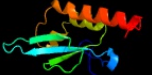

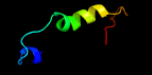






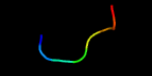


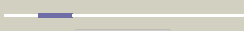
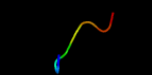

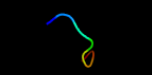













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2840c_(-)_3147969_3148268
Date	Wed Aug 7 12:50:50 BST 2019
Unique Job ID	64cc21fa1a5b7fed

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1g2ra_	 Alignment		100.0	21	Fold: YlxR-like Superfamily: YlxR-like Family: YlxR-like
2	d1rutx1	 Alignment		14.2	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
3	c2lc0A_	 Alignment		13.1	16	PDB header: protein binding Chain: A; PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: rv0020c_ nter structure
4	c2hfgR_	 Alignment		11.5	63	PDB header: immune system Chain: R; PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of hbr3 bound to cb3s-fab
5	d1kxpd3	 Alignment		11.2	7	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
6	d1osxa_	 Alignment		11.2	63	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: BAFF receptor-like
7	c1osxA_	 Alignment		11.2	63	PDB header: immune system Chain: A; PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: solution structure of the extracellular domain of blys2 receptor 3 (br3)
8	c1oqeR_	 Alignment		11.0	63	PDB header: immune system Chain: R; PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
9	c1oqeK_	 Alignment		11.0	63	PDB header: immune system Chain: K; PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
10	c1oqeP_	 Alignment		11.0	63	PDB header: immune system Chain: P; PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
11	d1oqek_	 Alignment		11.0	63	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: BAFF receptor-like

12	c1oqeM_	Alignment		11.0	63	PDB header: immune system Chain: M: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
13	c1oqeO_	Alignment		11.0	63	PDB header: immune system Chain: Q: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
14	c1oqeL_	Alignment		11.0	63	PDB header: immune system Chain: L: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
15	c1p0tw_	Alignment		10.8	63	PDB header: protein binding Chain: W: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
16	c1p0t5_	Alignment		10.8	63	PDB header: protein binding Chain: 5: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
17	c1p0tv_	Alignment		10.8	63	PDB header: protein binding Chain: V: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
18	c1p0tK_	Alignment		10.8	63	PDB header: protein binding Chain: K: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
19	c1p0tn_	Alignment		10.8	63	PDB header: protein binding Chain: N: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
20	c1p0t1_	Alignment		10.8	63	PDB header: protein binding Chain: 1: PDB Molecule: PDB Fragment: residues 1-63; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
21	c1p0t0_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: 0: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
22	c1p0th_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: H: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
23	c1p0tG_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: G: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
24	c1p0tQ_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: Q: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
25	c1p0tY_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: Y: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
26	c1p0tf_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: F: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
27	c1p0tc_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
28	c1p0tj_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: J: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
						PDB header: protein binding

55	c1p0t8_	Alignment	not modelled	10.8	63	Chain: 8: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
56	c1p0to_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: O: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
57	c1p0tD_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: D: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
58	c1p0ts_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: S: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
59	c1p0ti_	Alignment	not modelled	10.8	63	PDB header: protein binding Chain: I: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
60	d1oqen_	Alignment	not modelled	10.8	63	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: BAFF receptor-like
61	c1oqeN_	Alignment	not modelled	10.8	63	PDB header: immune system Chain: N: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
62	c4adoA_	Alignment	not modelled	10.8	21	PDB header: antibiotic resistance Chain: A: PDB Molecule: far1; PDBTitle: fusidic acid resistance protein fusb
63	c4xizM_	Alignment	not modelled	10.7	22	PDB header: lipid transport/oxidoreductase Chain: M: PDB Molecule: mitochondrial distribution and morphology protein 35; PDBTitle: structure of a phospholipid trafficking complex with substrate
64	d1k82a3	Alignment	not modelled	10.6	8	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
65	c1oqeO_	Alignment	not modelled	10.5	63	PDB header: immune system Chain: O: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
66	c1p0tW_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: W: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
67	c1p0tp_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: P: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
68	c1p0tV_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: V: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
69	c1p0ti_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: L: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
70	c1p0tC_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
71	c1p0tX_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: X: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
72	c1p0tU_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: U: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
73	c1p0tk_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: K: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
74	c1p0tN_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: N: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
75	c1p0t3_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: 3: PDB Molecule: PDB Fragment: residues 1-63; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
76	c1p0tA_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
77	c1p0t9_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: 9: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
78	c1p0tB_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
79	c1p0tx_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: X: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
80	c1p0tj_	Alignment	not modelled	10.3	63	PDB header: protein binding Chain: J: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
						Fold: Ferredoxin-like

81	d1mg7a2	Alignment	not modelled	10.3	57	Superfamily: GHMP Kinase, C-terminal domain Family: Early switch protein XOL-1
82	c2yb5F	Alignment	not modelled	10.2	12	PDB header: translation Chain: F; PDB Molecule: putative fusidic acid resistance protein; PDBTitle: structure of the fusidic acid resistance protein fusc
83	d2ieca1	Alignment	not modelled	9.8	17	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
84	d1r2za3	Alignment	not modelled	9.5	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
85	d1tdza3	Alignment	not modelled	9.5	36	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
86	d1ee8a3	Alignment	not modelled	8.6	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
87	c4atul	Alignment	not modelled	8.3	13	PDB header: hydrolase Chain: I; PDB Molecule: neuronal migration protein doublecortin; PDBTitle: human doublecortin n-dc repeat plus linker, and tubulin (2xrp) docked2 into an 8a cryo-em map of doublecortin-stabilised microtubules3 reconstructed in absence of kinesin
88	d1mjda	Alignment	not modelled	8.2	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
89	c3wknG	Alignment	not modelled	8.2	67	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
90	d1l1ta3	Alignment	not modelled	8.1	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
91	c1mg7B	Alignment	not modelled	8.1	57	PDB header: gene regulation Chain: B; PDB Molecule: early switch protein xol-1 2.2k splice form; PDBTitle: crystal structure of xol-1
92	d1djqa3	Alignment	not modelled	7.8	50	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
93	c6q8iK	Alignment	not modelled	7.6	63	PDB header: splicing Chain: K; PDB Molecule: protein red; PDBTitle: nterminal domain of human smu1 in complex with human redmid
94	d1k3xa3	Alignment	not modelled	7.6	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
95	d2f1da2	Alignment	not modelled	7.3	64	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
96	c6q8iL	Alignment	not modelled	7.0	63	PDB header: splicing Chain: L; PDB Molecule: protein red; PDBTitle: nterminal domain of human smu1 in complex with human redmid
97	c2cqyA	Alignment	not modelled	7.0	14	PDB header: ligase Chain: A; PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit
98	c2du9A	Alignment	not modelled	7.0	18	PDB header: transcription Chain: A; PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
99	c6g5iy	Alignment	not modelled	6.9	23	PDB header: ribosome Chain: Y; PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r