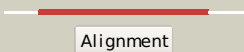

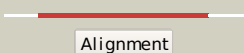

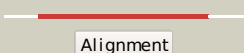
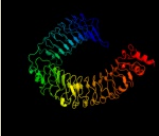
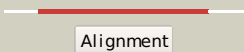
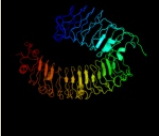
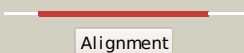

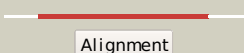

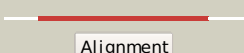

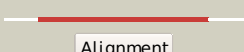

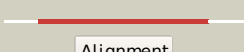
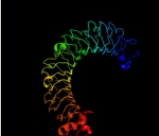
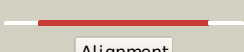

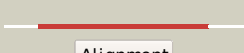




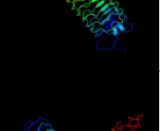
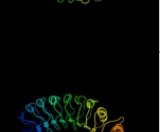



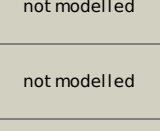


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fxiA_	 Alignment		100.0	21	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 4; PDBTitle: crystal structure of the human tlr4-human md-2-e.coli lps ra complex
2	c2a0zA_	 Alignment		100.0	22	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: the molecular structure of toll-like receptor 3 ligand binding domain
3	c2z64A_	 Alignment		100.0	23	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 4; PDBTitle: crystal structure of mouse tlr4 and mouse md-2 complex
4	c3j0aB_	 Alignment		100.0	24	PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 5; PDBTitle: homology model of human toll-like receptor 5 fitted into an electron2 microscopy single particle reconstruction
5	c2z63A_	 Alignment		100.0	20	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 4, variable lymphocyte receptor b; PDBTitle: crystal structure of the tv8 hybrid of human tlr4 and hagfish vlrb.61
6	c1ziwA_	 Alignment		100.0	22	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: human toll-like receptor 3 extracellular domain structure
7	c2z81A_	 Alignment		100.0	20	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 2, variable lymphocyte receptor b; PDBTitle: crystal structure of the tlr1-tlr2 heterodimer induced by binding of a2 tri-acylated lipopeptide
8	c3a79A_	 Alignment		100.0	21	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 2, variable lymphocyte receptor b; PDBTitle: crystal structure of tlr2-tlr6-pam2csk4 complex
9	c2id5D_	 Alignment		100.0	32	PDB header: ligand binding protein,membrane protein Chain: D: PDB Molecule: leucine rich repeat neuronal 6a; PDBTitle: crystal structure of the lingo-1 ectodomain
10	c3rgxA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: protein brassinosteroid insensitive 1; PDBTitle: structural insight into brassinosteroid perception by bri1
11	c3a79B_	 Alignment		100.0	20	PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 6, variable lymphocyte receptor b; PDBTitle: crystal structure of tlr2-tlr6-pam2csk4 complex

12	c2z7xB_	Alignment		100.0	18	PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 1, variable lymphocyte receptor b; PDBTitle: crystal structure of the tlr1-tlr2 heterodimer induced by binding of a2 tri-acylated lipopeptide
13	d1ozna_	Alignment		100.0	37	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
14	c3rg1l_	Alignment		100.0	16	PDB header: immune system Chain: I: PDB Molecule: cd180 molecule; PDBTitle: crystal structure of the rp105/md-1 complex
15	c3ojaB_	Alignment		100.0	25	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
16	c2z66A_	Alignment		100.0	31	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 vlrb.61
17	c2z80A_	Alignment		100.0	22	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 2, variable lymphocyte receptor b; PDBTitle: crystal structure of the tlr1-tlr2 heterodimer induced by binding of a2 tri-acylated lipopeptide
18	c2o6gA_	Alignment		100.0	59	PDB header: immune system Chain: A: PDB Molecule: variable lymphocyte receptor a; PDBTitle: structural diversity of the hagfish variable lymphocyte2 receptors a29
19	c2omwA_	Alignment		100.0	13	PDB header: cell invasion/cell adhesion Chain: A: PDB Molecule: internalin-a; PDBTitle: crystal structure of inla s192n y369s/mec1 complex
20	d2omza2	Alignment		100.0	19	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Internalin LRR domain
21	c2v9sC_	Alignment	not modelled	100.0	39	PDB header: structural protein Chain: C: PDB Molecule: slit homolog 2 protein n-product; PDBTitle: second lrr domain of human slit2
22	c2v70D_	Alignment	not modelled	100.0	31	PDB header: structural protein Chain: D: PDB Molecule: slit homolog 2 protein n-product; PDBTitle: third lrr domain of human slit2
23	c2ft3B_	Alignment	not modelled	100.0	21	PDB header: structural protein, signaling protein Chain: B: PDB Molecule: biglycan; PDBTitle: crystal structure of the biglycan dimer core protein
24	d1xkua_	Alignment	not modelled	100.0	29	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
25	c1xkuA_	Alignment	not modelled	100.0	29	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
26	c2z62A_	Alignment	not modelled	100.0	28	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 4, variable lymphocyte receptor b; PDBTitle: crystal structure of the tv3 hybrid of human tlr4 and hagfish vlrb.61
27	d1p9ag_	Alignment	not modelled	100.0	60	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
28	c3o6nA_	Alignment	not modelled	100.0	27	PDB header: protein binding Chain: A: PDB Molecule: apl1; PDBTitle: crystal structure of apl1 leucine-rich repeat domain
						PDB header: hydrolase Chain: G: PDB Molecule: platelet glycoprotein ib alpha chain

29	c1ookG_	Alignment	not modelled	100.0	45	precursor; PDBTitle: crystal structure of the complex of platelet receptor gpib-alpha and2 human alpha-thrombin
30	c2xotA_	Alignment	not modelled	100.0	30	PDB header: cell adhesion Chain: A: PDB Molecule: amphoterin-induced protein 1; PDBTitle: crystal structure of neuronal leucine rich repeat protein amigo-1
31	d1ogqa_	Alignment	not modelled	100.0	22	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Polygalacturonase inhibiting protein PGIP
32	c3e6jA_	Alignment	not modelled	100.0	36	PDB header: immune system Chain: A: PDB Molecule: variable lymphocyte receptor diversity region; PDBTitle: crystal structure of variable lymphocyte receptor (v1r) rbc36 in2 complex with h-trisaccharide
33	c3bz5A_	Alignment	not modelled	100.0	13	PDB header: cell adhesion Chain: A: PDB Molecule: internalin-j; PDBTitle: functional domain of inlj from listeria monocytogenes2 includes a cysteine ladder
34	c2r9uC_	Alignment	not modelled	100.0	29	PDB header: immune system Chain: C: PDB Molecule: variable lymphocyte receptor; PDBTitle: crystal structure of lamprey variable lymphocyte receptor 29132 ectodomain
35	c2o6rA_	Alignment	not modelled	100.0	36	PDB header: immune system Chain: A: PDB Molecule: variable lymphocyte receptor b; PDBTitle: structural diversity of the hagfish variable lymphocyte2 receptors b61
36	c2ifgB_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: structure of the extracellular segment of human trka in complex with2 nerve growth factor
37	c3ojaA_	Alignment	not modelled	99.9	23	PDB header: protein binding Chain: A: PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of Irim1/apl1c complex
38	c2o6sA_	Alignment	not modelled	99.9	39	PDB header: immune system Chain: A: PDB Molecule: variable lymphocyte receptor b; PDBTitle: structural diversity of the hagfish variable lymphocyte2 receptors b59
39	d1w8aa_	Alignment	not modelled	99.9	34	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
40	c3g3aA_	Alignment	not modelled	99.9	34	PDB header: hydrolase/immune system Chain: A: PDB Molecule: variable lymphocyte receptor v1rb.2d; PDBTitle: structure of a lamprey variable lymphocyte receptor in2 complex with a protein antigen
41	c2wfhB_	Alignment	not modelled	99.9	33	PDB header: splicing Chain: B: PDB Molecule: slit homolog 2 protein c-product; PDBTitle: the human Slit 2 dimerization domain d4
42	d1z7xw1	Alignment	not modelled	99.9	17	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: RNI-like Family: 28-residue LRR
43	c3g06A_	Alignment	not modelled	99.9	48	PDB header: ligase Chain: A: PDB Molecule: ssph2 (leucine-rich repeat protein); PDBTitle: the salmonella virulence effector ssph2 functions as a2 novel e3 ligase
44	d2bnha_	Alignment	not modelled	99.9	16	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: RNI-like Family: 28-residue LRR
45	c1g9uA_	Alignment	not modelled	99.9	23	PDB header: toxin Chain: A: PDB Molecule: outer protein yopm; PDBTitle: crystal structure of yopm-leucine rich effector protein from yersinia2 pestis
46	d1jl5a_	Alignment	not modelled	99.9	23	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Leucine rich effector protein YopM
47	c3o53A_	Alignment	not modelled	99.9	16	PDB header: protein binding Chain: A: PDB Molecule: protein Irim1; PDBTitle: crystal structure of Irim1 leucine-rich repeat domain
48	d2ifga3	Alignment	not modelled	99.9	19	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
49	d1xwdc1	Alignment	not modelled	99.9	30	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like
50	c3m18A_	Alignment	not modelled	99.9	34	PDB header: immune system Chain: A: PDB Molecule: variable lymphocyte receptor a diversity region; PDBTitle: crystal structure of variable lymphocyte receptor v1ra.r2.1 in complex2 with hen egg lysozyme
51	c1wwlA_	Alignment	not modelled	99.8	38	PDB header: immune system Chain: A: PDB Molecule: monocyte differentiation antigen cd14; PDBTitle: crystal structure of cd14
52	c1ltxA_	Alignment	not modelled	99.8	26	PDB header: transferase/protein binding Chain: A: PDB Molecule: rab geranylgeranyltransferase alpha subunit; PDBTitle: structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
53	c1m9sA_	Alignment	not modelled	99.8	22	PDB header: signaling protein Chain: A: PDB Molecule: internalin b; PDBTitle: crystal structure of internalin b (inlb), a listeria2 monocytogenes virulence protein containing sh3-like3 domains.
						PDB header: protein binding

54	c2y5qA	Alignment	not modelled	99.8	24	Chain: A: PDB Molecule: internalin b; PDBTitle: listeria monocytogenes inlb (internalin b) residues 36-392
55	c2uzuA	Alignment	not modelled	99.8	17	PDB header: signaling protein/receptor Chain: A: PDB Molecule: internalin b; PDBTitle: structure of the human receptor tyrosine kinase met in2 complex with the listeria monocytogenes invasion protein3 inlb: low resolution, crystal form ii
56	c1h6uA	Alignment	not modelled	99.7	20	PDB header: cell adhesion Chain: A: PDB Molecule: internalin h; PDBTitle: internalin h: crystal structure of fused n-terminal2 domains.
57	c3rfeB	Alignment	not modelled	99.7	33	PDB header: cell adhesion Chain: B: PDB Molecule: platelet glycoprotein ib beta chain; PDBTitle: crystal structure of glycoprotein gpib ectodomain
58	c3cvrA	Alignment	not modelled	99.7	30	PDB header: ligase Chain: A: PDB Molecule: invasion plasmid antigen; PDBTitle: crystal structure of the full length ipah3
59	c3g04C	Alignment	not modelled	99.7	34	PDB header: immune system Chain: C: PDB Molecule: thyrotropin receptor; PDBTitle: crystal structure of the tsh receptor in complex with a thyroid-2 stimulating autoantibody
60	c2je0E	Alignment	not modelled	99.7	24	PDB header: nuclear protein Chain: E: PDB Molecule: acidic leucine-rich nuclear phosphoprotein 32 family PDBTitle: crystal structure of pp32
61	d2astb2	Alignment	not modelled	99.6	19	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: RNI-like Family: Cyclin A/CDK2-associated p19, Skp2
62	d2ca6a1	Alignment	not modelled	99.6	14	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: RNI-like Family: Rna1p (RanGAP1), N-terminal domain
63	c1k5dL	Alignment	not modelled	99.5	15	PDB header: signaling protein/signaling activator Chain: L: PDB Molecule: ran gtpase activating protein 1; PDBTitle: crystal structure of ran-gppnhp-ranbp1-rangap complex
64	d1dcea3	Alignment	not modelled	99.5	31	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Rab geranylgeranyltransferase alpha-subunit, C-terminal domain
65	d2omxa2	Alignment	not modelled	99.4	18	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Internalin LRR domain
66	c1otnA	Alignment	not modelled	99.4	14	PDB header: cell adhesion Chain: A: PDB Molecule: internalin b; PDBTitle: calcium-binding mutant of the internalin b lrr domain
67	d1a9na	Alignment	not modelled	99.4	19	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: U2A'-like
68	c1xeuA	Alignment	not modelled	99.4	14	PDB header: cell invasion Chain: A: PDB Molecule: internalin c; PDBTitle: crystal structure of internalin c from listeria2 monocytogenes
69	d1h6ua2	Alignment	not modelled	99.3	43	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Internalin LRR domain
70	d1h6ta2	Alignment	not modelled	99.3	55	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Internalin LRR domain
71	c3gozA	Alignment	not modelled	99.3	37	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: leucine-rich repeat-containing protein; PDBTitle: crystal structure of the leucine-rich repeat-containing2 protein legl7 from legionella pneumophila. northeast3 structural genomics consortium target lgr148
72	c2ra8A	Alignment	not modelled	99.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein q64v53_bacfr; PDBTitle: crystal structure of the q64v53_bacfr protein from bacteroides2 fragilis. northeast structural genomics consortium target bfr43
73	c3sb4B	Alignment	not modelled	99.0	15	PDB header: protein binding Chain: B: PDB Molecule: hypothetical leucine rich repeat protein; PDBTitle: crystal structure of a hypothetical leucine rich repeat protein2 (bt_1240) from bacteroides thetaiotaomicron vpi-5482 at 1.99 a3 resolution
74	d1m9la	Alignment	not modelled	99.0	23	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: Outer arm dynein light chain 1 Family: Outer arm dynein light chain 1
75	c2p1nE	Alignment	not modelled	98.9	14	PDB header: signaling protein Chain: E: PDB Molecule: transport inhibitor response 1 protein; PDBTitle: mechanism of auxin perception by the tir1 ubiquitin ligase
76	d1fs2a2	Alignment	not modelled	98.7	15	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: RNI-like Family: Cyclin A/CDK2-associated p19, Skp2
77	d1koha1	Alignment	not modelled	98.7	26	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: mRNA export factor tap
78	c1kooD	Alignment	not modelled	98.6	27	PDB header: rna binding protein Chain: D: PDB Molecule: tip associating protein; PDBTitle: the crystal structure and mutational analysis of a novel2 rna-binding domain found in the human tap nuclear mrna3 export

					factor
79	c3oglD_	Alignment	not modelled	98.6	13 PDB header: protein binding Chain: D: PDB Molecule: coronatine-insensitive protein 1; PDBTitle: structure of coil-ask1 in complex with ja-isoleucine and the jaz12 degnon
80	c3ogmB_	Alignment	not modelled	98.6	12 PDB header: protein binding Chain: B: PDB Molecule: coronatine-insensitive protein 1; PDBTitle: structure of coil-ask1 in complex with coronatine and the jaz1 degnon
81	c3e2jA_	Alignment	not modelled	98.5	18 PDB header: electron transport Chain: A: PDB Molecule: atp synthase subunit s, mitochondrial; PDBTitle: crystal structure of bovine coupling factor b
82	c1fqvK_	Alignment	not modelled	97.9	15 PDB header: ligase Chain: K: PDB Molecule: skp2; PDBTitle: insights into scf ubiquitin ligases from the structure of2 the skp1-skp2 complex
83	d1pgva_	Alignment	not modelled	97.5	16 Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: RNI-like Family: 28-residue LRR
84	c1pgvA_	Alignment	not modelled	97.5	16 PDB header: protein binding Chain: A: PDB Molecule: tropomodulin tmd-1; PDBTitle: structural genomics of caenorhabditis elegans: tropomodulin2 c-terminal domain
85	d1io0a_	Alignment	not modelled	97.2	16 Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: RNI-like Family: 28-residue LRR
86	c3ghgD_	Alignment	not modelled	24.4	33 PDB header: blood clotting Chain: D: PDB Molecule: fibrinogen alpha chain; PDBTitle: crystal structure of human fibrinogen
87	c1m1jA_	Alignment	not modelled	17.8	25 PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha subunit; PDBTitle: crystal structure of native chicken fibrinogen with two different2 bound ligands
88	c2a45j_	Alignment	not modelled	15.4	33 PDB header: hydrolase/hydrolase inhibitor Chain: J: PDB Molecule: fibrinogen alpha chain; PDBTitle: crystal structure of the complex between thrombin and the central "e"2 region of fibrin