

Description Undefined

Date Fri Jul 8 15:33:22 BST 2022

Unique Job ID bda63ef864e4a957

Detailed template information

info	rmation					
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5d3iA_	Alignment		100.0	67	PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 2; PDBTitle: crystal structure of the ssl3-tlr2 complex PDB Entry: PDBe RCSB PDBj
2	<u>c2z81A</u> _	Alignment		100.0	63	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 PDB Entry: PDBe RCSB PDBj
3	<u>c3a79A_</u>	Alignment		100.0	62	PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 2, variable lymphocyte receptor b; PDBTitle: crystal structure of tlr2-tlr6-pam2csk4 complex PDB Entry: PDBe RCSB PDBj
4	<u>c2z80A</u> _	Alignment		100.0	75	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 PDB Entry: PDBe RCSB PDBj
5	<u>c3j0aA_</u>	Alignment		100.0	21	PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 5; PDBTitle: homology model of human toll-like receptor 5 fitted into an electron2 microscopy single particle reconstruction PDB Entry: PDBe RCSB PDBj
6	c7cynB_	Alignment		100.0	25	PDB header:immune system Chain: B: PDB Molecule:toll-like receptor 7; PDBTitle: cryo-em structure of human tlr7 in complex with unc93b1 PDB Entry: PDBe RCSB PDBj
7	<u>c3w3jB</u> _	Alignment		100.0	26	PDB header:immune system Chain: B: PDB Molecule:toll-like receptor 8; PDBTitle: crystal structure of human tlr8 in complex with cl097 PDB Entry: PDBe RCSB PDBj
8	c5gmgA_	Alignment		100.0	25	PDB header:immune system/rna Chain: A: PDB Molecule:toll-like receptor 7; PDBTitle: crystal structure of monkey tlr7 in complex with loxoribine and polyu PDB Entry: PDBe RCSB PDBj
9	d1fyxa_	Alignment		100.0	93	Fold: Flavodoxin-like Superfamily: Toll/Interleukin receptor TIR domain Family: Toll/Interleukin receptor TIR domain PDB entry: PDBe RCSB PDBj
10	<u>c7c76A</u> _	Alignment		100.0	23	PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 3; PDBTitle: cryo-em structure of human tlr3 in complex with unc93b1 PDB Entry: PDBe RCSB PDBj
11	<u>c2a0zA_</u>	Alignment		100.0	23	PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 3; PDBTitle: the molecular structure of toll-like receptor 3 ligand binding domain PDB Entry: PDBe RCSB PDBj

12	<u>c4g8aB_</u>	Alignment		100.0	PDB header:immune system Chain: B: PDB Molecule:toll-like receptor 4; PDBTitle: crystal structure of human tlr4 polymorphic variant d299g and t399i in2 complex with md-2 and lps PDB Entry: PDBe RCSB PDBj
13	c3wpbA_	Alignment		100.0	PDB header:dna binding protein Chain: A: PDB Molecule:toll-like receptor 9; PDBTitle: crystal structure of horse tlr9 (unliganded form) PDB Entry: PDBe RCSB PDBj
14	c7drcC_	Alignment		100.0	PDB header:plant protein Chain: C: PDB Molecule:membrane-localized Irr receptor-like protein; PDBTitle: cryo-em structure of plant receptor like protein rxeg1 in complex with2 xyloglucanase xeg1 and bak1 PDB Entry: PDBe RCSB PDBi
15	c4lsxB_	Alignment		100.0	PDB header:steroid binding protein/protein binding Chain: B: PDB Molecule:protein brassinosteroid insensitive 1; PDBTitle: plant steroid receptor ectodomain bound to brassinolide and serk1 co-2 receptor ectodomain PDB Entry: PDBe RCSB PDBj
16	c3fxiA_	Alignment		100.0	PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 4; 22 PDBTitle: crystal structure of the human tlr4-human md-2-e.coli lps ra complex PDB Entry: PDBe RCSB PDBj
17	c6s6qB_	Alignment		100.0	PDB header:signaling protein Chain: B: PDB Molecule:Irr receptor-like serine/threonine-protein kinase gso1; 24 PDBTitle: crystal structure of the Irr ectodomain of the plant membrane receptor2 kinase gassho1/schengen3 from arabidopsis thaliana in complex with3 casparian strip integrity factor 2. PDB Entry: PDBe RCSB PDBj
18	c1ziwA_	Alignment		100.0	PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 3; PDBTitle: human toll-like receptor 3 extracellular domain structure PDB Entry: PDBe RCSB PDBj
19	c4z0cA_	Alignment		100.0	PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 13; PDBTitle: crystal structure of tlr13-ssrna13 complex PDB Entry: PDBe RCSB PDBj
20	c5gr8A_	Alignment		100.0	PDB header:transferase Chain: A: PDB Molecule:leucine-rich repeat receptor-like protein kinase pepr1; PDBTitle: crystal structure of pepr1-atpep1 PDB Entry: PDBe RCSB PDBj
21	c6wmlC_	Alignment	not modelled	100.0	PDB header:immune system Chain: C: PDB Molecule:toll-like receptor 8; 23 PDBTitle: human tlr8 bound to the potent agonist, gs-9688 (selgantolimod) PDB Entry: PDBe RCSB PDBj
22	<u>c3j0aB_</u>	Alignment	not modelled	100.0	PDB header:immune system Chain: B: PDB Molecule:toll-like receptor 5; 20 PDBTitle: homology model of human toll-like receptor 5 fitted into an electron2 microscopy single particle reconstruction PDB Entry: PDBe RCSB PDBj
23	c5z8yE_	Alignment	not modelled	100.0	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 PDB Entry: PDBe RCSB PDBi
24	c4mn8A_	Alignment	not modelled	100.0	PDB header:transferase/transferase receptor Chain: A: PDB Molecule:Irr receptor-like serine/threonine-protein kinase fls2; PDBTitle: crystal structure of flg22 in complex with the fls2 and bak12 ectodomains PDB Entry: PDBe RCSB PDBj
25	c3rgxA_	Alignment	not modelled	100.0	PDB header:transferase Chain: A: PDB Molecule:protein brassinosteroid insensitive 1; PDBTitle: structural insight into brassinosteroid perception by bril PDB Entry: PDBe RCSB PDBj
26	c3rg1B_	Alignment	not modelled	100.0	PDB header:immune system Chain: B: PDB Molecule:cd180 molecule; PDBTitle: crystal structure of the rp105/md-1 complex PDB Entry: PDBe RCSB PDBj
27	<u>c3a79B</u> _	Alignment	not modelled	100.0	PDB header:immune system Chain: B: PDB Molecule:toll-like receptor 6, variable lymphocyte receptor b; PDBTitle: crystal structure of tlr2-tlr6-pam2csk4 complex

						DDD Fatour DDD a DCCD DDD:
						PDB Entry: PDBe RCSB PDBj PDB header:immune system
						Chain: A: PDB Molecule:toll-like receptor 4, variable lymphocyte
28	<u>c2z63A_</u>	Alignment	not modelled	100.0	20	receptor b; PDBTitle: crystal structure of the tv8 hybrid of human tlr4 and
						hagfish vlrb.61
		<u> </u>	_			PDB Entry: PDBe RCSB PDBj PDB header:hormone
29	c4z62A_	Alignment	not modelled	100.0	21	Chain: A: PDB Molecule:phytosulfokine receptor 1;
23	CTZOZA_	Alignment	not modelied	100.0	21	PDBTitle: the plant peptide hormone free receptor PDB Entry: PDBe RCSB PDBi
						PDB header:transferase
20	c/mna/	Allerman	not modelled	100.0	21	Chain: A: PDB Molecule: Irr receptor-like serine/threonine-protein
30	<u>c4mnaA_</u>	Alignment	not modelled	100.0	21	kinase fls2; PDBTitle: crystal structure of the free fls2 ectodomains
						PDB Entry: PDBe RCSB PDBj
						PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 4;
31	<u>c2z64A_</u>	Alignment	not modelled	100.0	19	PDBTitle: crystal structure of mouse tlr4 and mouse md-2 complex
						PDB Entry: PDBe RCSB PDBj PDB header:transferase
						Chain: B: PDB Molecule:probable lrr receptor-like serine/threonine-
32	c5hyxB_	Alignment	not modelled	100.0	21	protein kinase PDBTitle: plant peptide hormone receptor rgfr1 in complex with
						rgf1
						PDB Entry: PDBe RCSB PDBj
						PDB header:immune system Chain: B: PDB Molecule:toll-like receptor 1, variable lymphocyte
33	c2z7xB_	Alignment	not modelled	100.0	20	receptor b;
		Aligiliticit				PDBTitle: crystal structure of the tlr1-tlr2 heterodimer induced by binding of a2 tri-acylated lipopeptide
						PDB Entry: PDBe RCSB PDB
			_			PDB header:transferase Chain: A: PDB Molecule:serine/threonine-protein kinase bri1-like 1;
34	c4j0mA_	Alignment	not modelled	100.0	21	PDBTitle: crystal structure of brl1 (lrr) in complex with brassinolide
						PDB Entry: PDBe RCSB PDBi
						PDB header:immune system Chain: I: PDB Molecule:leucine-rich repeat-containing protein 32;
35	c6gffl_	Alignment	not modelled	100.0	20	PDBTitle: structure of garp (Irrc32) in complex with latent tgf-beta1
						and mhg-82 fab PDB Entry: PDBe RCSB PDBi
			_			PDB header:signaling protein
36	c5iyxA_	Alignment	not modelled	100.0	21	Chain: A: PDB Molecule:receptor-like protein kinase 5; PDBTitle: crystal structure of the arabidopsis receptor kinase haesa
30	<u>CSIYAA_</u>	Aligninent	not modelica	100.0		in complex2 with the peptide hormone ida and the co-receptor serk1
						PDB Entry: PDBe RCSB PDBj PDB header:hydrolase
						Chain: B: PDB Molecule:rab family protein;
37	c6hluB_	Alignment	not modelled	100.0	25	PDBTitle: crystal structure of the Irr-roc-cor domain of the
						chlorobium tepidum2 roco protein PDB Entry: PDBe RCSB PDBi
						PDB header:signaling protein
20	41 5			1000		Chain: B: PDB Molecule:leucine-rich repeat-containing g-protein coupled receptor
38	c4bsrB_	Alignment	not modelled	100.0	22	PDBTitle: structure of the ectodomain of lgr5 in complex with r-
						spondin-12 (fu1fu2) in p22121 crystal form PDB Entry: PDBe RCSB PDBi
						PDB header:hormone receptor/cell adhesion
39	c4kt1A_	Alignment	not modelled	100.0	22	Chain: A: PDB Molecule:leucine-rich repeat-containing g-protein coupled receptor
	<u>CTRCL/T</u>	Aligilitietic	nocmodened	100.0		PDBTitle: complex of r-spondin 1 with lgr4 extracellular domain
						PDB Entry: PDBe RCSB PDBi PDB header:signaling protein
						Chain: D: PDB Molecule:Irrtm;
40	<u>c5a5cD_</u>	Alignment	not modelled	100.0	30	PDBTitle: structure of an engineered neuronal lrrtm2 adhesion molecule
						PDB Entry: PDBe RCSB PDBj
						PDB header:plant protein Chain: C: PDB Molecule:membrane-localized lrr receptor-like
41	<u>c7w3vC_</u>	Alianmont	not modelled	100.0	19	protein;
71	<u></u>	Alignment	nocmodelled	100.0	19	PDBTitle: plant receptor like protein rxeg1 in complex with xyloglucanase xeg1
						PDB Entry: PDBe RCSB PDBj
						PDB header:membrane protein
42	c4qxeA_	Alignment	not modelled	100.0	22	Chain: A: PDB Molecule:leucine-rich repeat-containing g-protein coupled receptor
		g				PDBTitle: crystal structure of lgr4 fused with hagfish vlr
						PDB Entry: PDBe RCSB PDBj PDB header:signaling protein
						Chain: B: PDB Molecule:leucine-rich repeat receptor-like protein
43	<u>c5gijB_</u>	Alignment	not modelled	100.0	20	kinase tdr; PDBTitle: crystal structure of tdr-tdif complex
						PDB Entry: PDBe RCSB PDBi
						PDB header:immune system
44	c4qdhA_	Alignment	not modelled	100.0	24	Chain: A: PDB Molecule:variable lymphocyte receptor b, toll-like receptor 9
		5				PDBTitle: crystal structure of the c-terminal domain of mouse tlr9
						PDB Entry: PDBe RCSB PDBj PDB header:signaling protein
						Chain: A: PDB Molecule:leucine-rich repeats and immunoglobulin-
45	<u>c4u7lA_</u>	Alignment	not modelled	100.0	21	like domains PDBTitle: Irig1 extracellular domain: structure and function analysis
						PDB Entry: PDBe RCSB PDBj
			-			PDB header:unknown function Chain: A: PDB Molecule:lic12759;
46	<u>c4u09A_</u>	Alignment	not modelled	100.0	24	PDBTitle: structure of leptospira interrogans lrr protein lic12759
						PDB Entry: PDBe RCSB PDBj
						PDB header:immune system/cytokine Chain: A: PDB Molecule:protein toll;
47	<u>c4lxrA_</u>	Alignment	not modelled	100.0	18	PDBTitle: structure of the toll - spatzle complex, a molecular hub in
						drosophila2 development and innate immunity PDB Entry: PDBe RCSB PDBi
						PDB header:signaling protein

48	c4bstB_	Alignment	not modelled	100.0	21	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
49	<u>c4z64A_</u>	Alignment	not modelled	100.0	19	PDB Entry: PDBe RCSB PDBj PDB header:hormone Chain: A: PDB Molecule:phytosulfokine receptor 1; PDBTitle: the plant peptide hormone receptor complex in arabidopsis PDB Entry: PDBe RCSB PDBj
50	c4qxfB_	Alignment	not modelled	100.0	31	PDB header:membrane protein Chain: B: PDB Molecule:leucine-rich repeat-containing g-protein coupled receptor PDBTitle: crystal structure of human lgr4 and rspo1 PDB Entry: PDBe RCSB PDBj
51	<u>c4u08A</u> _	Alignment	not modelled	100.0	23	PDB header:unknown function Chain: A: PDB Molecule:lic11098; PDBTitle: structure of leptospira interrogans lrr protein lic11098 PDB Entry: PDBe RCSB PDBj
52	<u>c3v47B</u> _	Alignment	not modelled	100.0	21	PDB header:immune system Chain: B: PDB Molecule:toll-like receptor 5b and variable lymphocyte receptor b.61 PDBTitle: crystal structure of the n-terminal fragment of zebrafish tlr5 in2 complex with salmonella flagellin PDB Entry: PDBe RCSB PDBi
53	c2id5D_	Alignment	not modelled	100.0	24	PDB header:ligand binding protein,membrane protein Chain: D: PDB Molecule:leucine rich repeat neuronal 6a; PDBTitle: crystal structure of the lingo-1 ectodomain PDB Entry: PDBe RCSB PDBj
54	c5lfnC_	Alignment	not modelled	100.0	28	PDB header:cell adhesion Chain: C: PDB Molecule:chondroadherin; PDBTitle: crystal structure of human chondroadherin PDB Entry: PDBe RCSB PDBi
55	c4v2eA_	Alignment	not modelled	100.0	28	PDB header:signaling protein Chain: A: PDB Molecule:fibronectin leucine rich transmembrane protein 3; PDBTitle: flrt3 lrr domain PDB Entry: PDBe RCSB PDBi
56	<u>c4ecnA</u>	Alignment	not modelled	100.0	17	PDB header:unknown function Chain: A: PDB Molecule:leucine-rich repeat protein; PDBTitle: crystal structure of a leucine-rich repeat protein (bt_0210) from2 bacteroides thetaiotaomicron vpi-5482 at 2.80 a resolution PDB Entry: PDBe RCSB PDBi
57	<u>c3v44A_</u>	Alignment	not modelled	100.0	22	PDB header:immune system Chain: A: PDB Molecule:toll-like receptor 5b and variable lymphocyte receptor b.61 PDBTitle: crystal structure of the n-terminal fragment of zebrafish tlr5 PDB Februs PDBS PCSR PDB:
58	<u>c7jluA_</u>	Alignment	not modelled	100.0	19	PDB Entry: PDBe RCSB PDBj PDB header:immune system Chain: A: PDB Molecule:disease resistance protein roq1; PDBTitle: structure of the activated roq1 resistosome directly recognizing the2 pathogen effector xopq PDB Entry: PDBe RCSB PDBj
59	c5xjxB_	Alignment	not modelled	100.0	17	PDB header:transferase/membrane protein Chain: B: PDB Molecule:Irr receptor-like serine/threonine-protein kinase erl1; PDBTitle: pre-formed plant receptor erl1-tmm complex PDB Entry: PDBe RCSB PDBj
60	<u>c7li4A_</u>	Alignment	not modelled	100.0	20	PDB header:transferase, hydrolase Chain: A: PDB Molecule:leucine-rich repeat serine/threonine- protein kinase 2; PDBTitle: structure of lrrk2 after symmetry expansion PDB Entry: PDBe RCSB PDBi
61	<u>c2z66A_</u>	Alignment	not modelled	100.0	28	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 PDB Entry: PDBe RCSB PDBi
62	c4ow2D_	Alignment	not modelled	100.0	20	PDB header:toxin Chain: D: PDB Molecule:yop effector yopm; PDBTitle: yopm from yersinia enterocolitica wa-314 PDB Entry: PDBe RCSB PDBi
63	c4ecoA_	Alignment	not modelled	100.0	16	PDB header:unknown function Chain: A: PDB Molecule:uncharacterized protein; PDBTitle: crystal structure of a leucine-rich repeat protein (bacegg_03329) from2 bacteroides eggerthii dsm 20697 at 2.70 a resolution PDB Entry: PDBe RCSB PDBi
64	c5xjxC_	Alignment	not modelled	99.9	24	PDB header:transferase/membrane protein Chain: C: PDB Molecule:protein too many mouths; PDBTitle: pre-formed plant receptor erl1-tmm complex PDB Entry: PDBe RCSB PDBi
65	<u>c4v2dA</u>	Alignment	not modelled	100.0	25	PDB header:signaling protein Chain: A: PDB Molecule:fibronectin leucine rich transmembrane protein 2; PDBTitle: flrt2 lrr domain PDB Entry: PDBe RCSB PDBi
66	c3ojaB_	Alignment	not modelled	100.0	23	PDB header::protein binding Chain: B: PDB Molecule:anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex PDB Entry: PDBE RCSB PDBI
67	<u>c3rg1l_</u>	Alignment	not modelled	100.0	20	PDB header:immune system Chain: I: PDB Molecule:cd180 molecule; PDBTitle: crystal structure of the rp105/md-1 complex PDB Entry: PDBe RCSB PDBj
68	c7tvgD_	Alignment	not modelled	100.0	17	PDB header:signaling protein Chain: D: PDB Molecule:leucine-rich repeat protein shoc-2; PDBTitle: crystal structure of shoc2 to a resolution of 2.4 angstrom PDB Entry: PDBe RCSB PDBj
		_	_			Fold: Flavodoxin-like

69	d1fyva_	Alignment	not modelled	100.0	48	Superfamily: Toll/Interleukin receptor TIR domain Family: Toll/Interleukin receptor TIR domain PDB entry: PDBe RCSB PDBj
70	c4r6gA_	Alignment	not modelled	100.0	18	PDB header:de novo protein Chain: A: PDB Molecule:leucine rich repeats dlrr_k; PDBTitle: crystal structure of computational designed leucine rich repeats2 dlrr_k in space group p22121 PDB Entry: PDBe RCSB PDBj
71	<u>c2z62A_</u>	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 PDB Entry: PDBe RCSB PDBi
72	c4hq1A_	Alignment	not modelled	100.0	18	PDB header:transferase Chain: A: PDB Molecule:probable receptor protein kinase tmk1; PDBTitle: crystal structure of an Irr protein with two solenoids PDB Entry: PDBe RCSB PDBj
73	<u>c6g9oA_</u>	Alignment	not modelled	100.0	20	PDB header:membrane protein Chain: A: PDB Molecule:volume-regulated anion channel subunit Irrc8a; PDBTitle: structure of full-length homomeric mlrrc8a volume- regulated anion2 channel at 4.25 a resolution PDB Entry: PDBe RCSB PDBj
74	c7sd1A_	Alignment	not modelled	100.0	16	PDB header:signaling protein Chain: A: PDB Molecule:leucine-rich repeat protein shoc-2; PDBTitle: crystal structure of shoc2 PDB Entry: PDBe RCSB PDBj
75	c6nysB_	Alignment	not modelled	98.4	17	PDB header:unknown function Chain: B: PDB Molecule:crov588; PDBTitle: the crystal structure of crov588 a novel circular Irr protein2 structure PDB Entry: PDBe RCSB PDBj
76	<u>c3o6nA_</u>	Alignment	not modelled	100.0	20	PDB header:protein binding Chain: A: PDB Molecule:apl1; PDBTitle: crystal structure of apl1 leucine-rich repeat domain PDB Entry: PDBe RCSB PDBi
77	<u>c2j67B_</u>	Alignment	not modelled	100.0	53	PDB header:receptor Chain: B: PDB Molecule:toll like receptor 10; PDBTitle: the tir domain of human toll-like receptor 10 (tlr10) PDB Entry: PDBe RCSB PDBj
78	c7crcB_	Alignment	not modelled	99.9	16	PDB header:plant protein Chain: B: PDB Molecule:nad+ hydrolase (nadase); PDBTitle: cryo-em structure of plant nlr rpp1 tetramer in complex with atr1 PDB Entry: PDBe RCSB PDBj
79	c4glpA_	Alignment	not modelled	99.9	24	PDB header:immune system Chain: A: PDB Molecule:monocyte differentiation antigen cd14; PDBTitle: the crystal structure of soluble human cd14 reveals a bent solenoid2 with a hydrophobic amino-terminal pocket. PDB Entry: PDBe RCSB PDBj
80	<u>c6m04B</u> _	Alignment	not modelled	100.0	18	PDB header:membrane protein Chain: B: PDB Molecule:volume-regulated anion channel subunit Irrc8d; PDBTitle: structure of the human homo-hexameric Irrc8d channel at 4.36 angstroms PDB Entry: PDBe RCSB PDBi
81	<u>c5o0oB_</u>	Alignment	not modelled	99.9	22	PDB header:signaling protein Chain: B: PDB Molecule:reticulon-4 receptor; PDBTitle: deglycosylated nogo receptor with native disulfide structure 5 PDB Entry: PDBe RCSB PDBj
82	c7pzcH_	Alignment	not modelled	99.8	18	PDB header:immune system Chain: H: PDB Molecule:nacht, Irr and pyd domains-containing protein 3; PDBTitle: cryo-em structure of the nlrp3 decamer bound to the inhibitor crid3 PDB Entry: PDBe RCSB PDBj
83	c2omwA_	Alignment	not modelled	100.0	15	PDB header:cell invasion/cell adhesion Chain: A: PDB Molecule:internalin-a; PDBTitle: crystal structure of inla s192n y369s/mec1 complex PDB Entry: PDBe RCSB PDBj
84	d1ozna_	Alignment	not modelled	100.0	23	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like PDB entry: PDB eRCSB PDBj
85	c7brcA_	Alignment	not modelled	100.0	16	PDB header:transferase Chain: A: PDB Molecule:receptor-like kinase tmk3; PDBTitle: crystal structure of the tmk3 lrr domain PDB Entry: PDBe RCSB PDBj PDB header:blood clotting
86	<u>c6ejxD</u> _	Alignment	not modelled	99.9	27	Chain: D: PDB Molecule:platelet glycoprotein ib alpha chain; PDBTitle: the metal ion-dependent adhesion site (midas) of the alphambeta22 integrin mac-1 i-domain promiscuously and competitively binds3 multiple ligands in the regulation of leukocyte function PDB Entry: PDBe RCSB PDBi
87	c3bz5A_	Alignment	not modelled	99.9	16	PDB header:cell adhesion Chain: A: PDB Molecule:internalin-j; PDBTitle: functional domain of inlj from listeria monocytogenes includes a2 cysteine ladder PDB Entry: PDBe RCSB PDBj
88	c4bv4R_	Alignment	not modelled	100.0	15	PDB header:immune system Chain: R: PDB Molecule:protein toll, variable lymphocyte receptor b chimera; PDBTitle: structure and allostery in toll-spatzle recognition PDB Entry: PDBe RCSB PDBj
89	d2omza2	Alignment	not modelled	100.0	17	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Internalin LRR domain PDB entry: PDBe RCSB PDBj
						PDB header:immune system Chain: P: PDB Molecule:nlr family card domain-containing protein

90	c4kxfP_	Alignment	not modelled	99.7	18	4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition
						mechanism PDB Entry: PDBe RCSB PDBj
91	<u>c5il7B</u> _	Alignment	not modelled	100.0	15	PDB header:signaling protein Chain: B: PDB Molecule:rab family protein; PDBTitle: leucine rich repeat domain of the chlorobium tepidum roco protein PDB Entry: PDBe RCSB PDBi
92	d1p9ag_	Alignment	not modelled	99.9	26	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like PDB entry: PDBe RCSB PDBj
93	c1ookG_	Alignment	not modelled	99.9	27	PDB header:hydrolase Chain: G: PDB Molecule:platelet glycoprotein ib alpha chain precursor; PDBTitle: crystal structure of the complex of platelet receptor gpib- alpha and2 human alpha-thrombin DDB Extra DDB ACCO DDB
94	c2p1nE_	Alignment	not modelled	99.8	14	PDB Entry: PDBe RCSB PDBj PDB header:signaling protein Chain: E: PDB Molecule:transport inhibitor response 1 protein; PDBTitle: mechanism of auxin perception by the tir1 ubiqutin ligase PDB Entry: PDBe RCSB PDBj
95	c5mx0B_	Alignment	not modelled	99.9	20	PDB header:structural protein Chain: B: PDB Molecule:fibromodulin; PDBTitle: crystal structure of human fibromodulin PDB Entry: PDBe RCSB PDBi
96	c4perA_	Alignment	not modelled	99.8	15	PDB header:hydrolase/hydrolase inhibitor Chain: A: PDB Molecule:ribonuclease inhibitor; PDBTitle: structure of gallus gallus ribonuclease inhibitor complexed with2 gallus gallus ribonuclease i PDB Entry: PDBe RCSB PDBj
97	<u>c2o6qA</u> _	Alignment	not modelled	99.9	27	PDB header:immune system Chain: A: PDB Molecule:variable lymphocyte receptor a; PDBTitle: structural diversity of the hagfish variable lymphocyte2 receptors a29 PDB Entry: PDBe RCSB PDBj
98	c3oglD_	Alignment	not modelled	99.7	14	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 degron PDB Entry: PDBe RCSB PDBj
99	c3ogmB_	Alignment	not modelled	99.7	14	PDB header:protein binding Chain: B: PDB Molecule:coronatine-insensitive protein 1; PDBTitle: structure of coil-askl in complex with coronatine and the jazl degron PDB Entry: PDBe RCSB PDBj
100	d2bnha_	Alignment	not modelled	99.7	16	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: RNI-like Family: 28-residue LRR PDB entry: PDBe RCSB PDBj
101	c1xkuA_	Alignment	not modelled	99.9	19	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 PDB Entry: PDBe RCSB PDBj
102	d1xkua_	Alignment	not modelled	99.9	19	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Ngr ectodomain-like PDB entry: PDBe RCSB PDBj
103	<u>c1g9uA_</u>	Alignment	not modelled	99.8	17	PDB header:toxin Chain: A: PDB Molecule:outer protein yopm; PDBTitle: crystal structure of yopm-leucine rich effector protein from yersinia2 pestis PDB Entry: PDBe RCSB PDBj
104	<u>d1jl5a_</u>	Alignment	not modelled	99.8	17	Fold: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) Superfamily: L domain-like Family: Leucine rich effector protein YopM PDB entry: PDBe RCSB PDBi
105	c4p8sA_	Alignment	not modelled	99.9	24	PDB header:membrane protein Chain: A: PDB Molecule:reticulon-4 receptor-like 2; PDBTitle: crystal structure of nogo-receptor-2 PDB Entry: PDBe RCSB PDBj
106	<u>c4k17B</u> _	Alignment	not modelled	99.8	15	PDB header:lipid binding protein Chain: B: PDB Molecule:leucine-rich repeat-containing protein 16a; PDBTitle: crystal structure of mouse carmil residues 1-668 PDB Entry: PDBe RCSB PDBj
107	<u>c3ojaA_</u>	Alignment	not modelled	99.9	23	PDB header:protein binding Chain: A: PDB Molecule:leucine-rich immune molecule 1; PDBTitle: crystal structure of lrim1/apl1c complex PDB Entry: PDBe RCSB PDBj
108	<u>c4cp6A_</u>	Alignment	not modelled	99.2	15	PDB header:choline binding protein Chain: A: PDB Molecule:choline binding protein pcpa; PDBTitle: the crystal structure of pneumococcal vaccine antigen pcpa PDB Entry: PDBe RCSB PDBj
109	c6npyA_	Alignment	not modelled	99.7	18	PDB header:immune system Chain: A: PDB Molecule:nacht, Irr and pyd domains-containing protein 3; PDBTitle: cryo-em structure of nlrp3 bound to nek7 PDB Entry: PDBe RCSB PDBj
110	c7wbuA_	Alignment	not modelled	99.7	14	PDB header:immune system Chain: A: PDB Molecule:nacht, Irr and pyd domains-containing protein 9; PDBTitle: cryo-em structure of bovine nlrp9 PDB Entry: PDBe RCSB PDBj
111	<u>c3g06A</u> _	Alignment	not modelled	99.9	21	PDB header:ligase Chain: A: PDB Molecule:ssph2 (leucine-rich repeat protein); PDBTitle: the salmonella virulence effector ssph2 functions as a2 novel e3 ligase PDB Entry: PDBe RCSB PDBj
		_	-			PDB header:de novo protein Chain: A: PDB Molecule:leucine rich repeat protein;

112	c4r5cA_	Alignment	not modelled	99.8	18	PDBTitle: crystal structure of computational designed leucine rich repeats2 dlrr_e in space group of p212121 PDB Entry: PDBe RCSB PDBi
113	c4fmzA_	Alignment	not modelled	99.9	16	PDB header:cell adhesion, cell invasion Chain: A: PDB Molecule:internalin; PDBTitle: crystal structure of an internalin (inlf) from listeria monocytogenes2 str. 4b f2365 at 1.91 a resolution PDB Entry: PDBe RCSB PDBj
114	<u>c6w78A</u> _	Alignment	not modelled	99.8	19	PDB header:antifreeze protein Chain: A: PDB Molecule:antifreeze polypeptide; PDBTitle: crystal structure of a plant ice-binding protein PDB Entry: PDBe RCSB PDBj
115	<u>c3m18A</u> _	Alignment	not modelled	99.9	24	PDB header:immune system Chain: A: PDB Molecule:variable lymphocyte receptor a diversity region; PDBTitle: crystal structure of variable lymphocyte receptor vlra.r2.1 in complex2 with hen egg lysozyme PDB Entry: PDBe RCSB PDBj
116	<u>c4q62A_</u>	Alignment	not modelled	99.9	15	PDB header:unknown function Chain: A: PDB Molecule:leucine-rich repeat-and coiled coil- containing protein; PDBTitle: crystal structure of leucine-rich repeat- and coiled coil- containing2 protein from legionella pneumophila PDB Entry: PDBe RCSB PDBj
117	c6mkyB_	Alignment	not modelled	99.8	20	PDB header:signaling protein Chain: B: PDB Molecule:protein phosphatase 1 regulatory subunit 7; PDBTitle: human sds22 PDB Entry: PDBe RCSB PDBj
118	c5yq5C_	Alignment	not modelled	99.9	17	PDB header:protein fibril Chain: C: PDB Molecule:osteomodulin; PDBTitle: crystal structure of human osteomodulin PDB Entry: PDBe RCSB PDBj
119	<u>c4kxfF</u>	Alignment	not modelled	99.7	14	PDB header:immune system Chain: F: PDB Molecule:nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism PDB Entry: PDBe RCSB PDBj
120	c4pufA_	Alignment	not modelled	100.0	20	PDB header:ligase/oxidoreductase Chain: A: PDB Molecule:e3 ubiquitin-protein ligase slrp; PDBTitle: complex between the salmonella t3ss effector slrp and its human target2 thioredoxin-1 PDB Entry: PDBe RCSB PDBj