Phyre2

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Description	Q9ERV7
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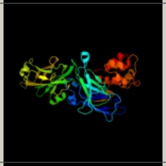
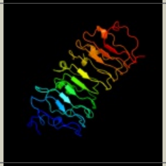
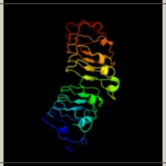
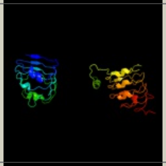
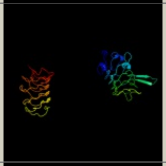
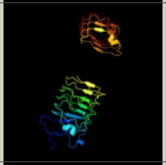
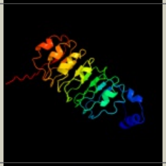
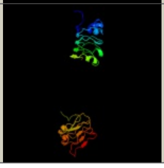
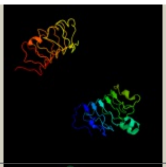
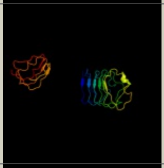
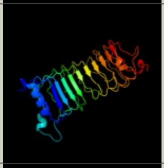
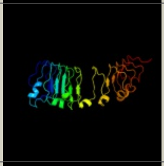
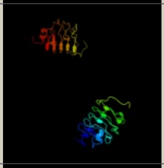
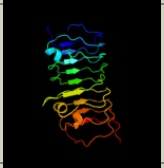
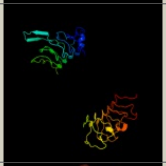
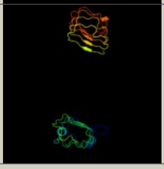
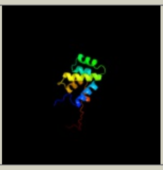
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4d8oA_	Alignment		100.0	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-2; **PDBTitle:** crystal structure of the ankyrin-b zu5-zu5-upa-dd tandem
2	c3ud2C_	Alignment		100.0	25	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**ankyrin-1; **PDBTitle:** crystal structure of selenomethionine zu5a-zu5b protein domains of2 human erythrocyte ankyrin
3	c3g5bA_	Alignment		100.0	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**netrin receptor unc5b; **PDBTitle:** the structure of unc5b cytoplasmic domain
4	c4ecnA_	Alignment		100.0	16	**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
5	c4ecoA_	Alignment		100.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein (bacegg_03329) from2 bacteroides eggerthii dsm 20697 at 2.70 a resolution
6	c3rgxA_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein brassinosteroid insensitive 1; **PDBTitle:** structural insight into brassinosteroid perception by bri1
7	c1ziwA_	Alignment		100.0	31	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 3; **PDBTitle:** human toll-like receptor 3 extracellular domain structure
8	c3ojaA_	Alignment		99.9	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
9	c3ojaB_	Alignment		99.9	26	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
10	c1m9sA_	Alignment		99.9	25	**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.
11	c4hq1A_	Alignment		99.9	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable receptor protein kinase tmk1; **PDBTitle:** crystal structure of an lrr protein with two solenoids

12	c2z64A_	Alignment		99.9	31	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 4; **PDBTitle:** crystal structure of mouse tlr4 and mouse md-2 complex
13	c4g8aB_	Alignment		99.9	36	**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
14	c3a79B_	Alignment		99.9	45	**PDB header:**immune system **Chain:** B: **PDB Molecule:**toll-like receptor 6, variable lymphocyte receptor b; **PDBTitle:** crystal structure of tlr2-tlr6-pam2csk4 complex
15	c1wwlA_	Alignment		99.9	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**monocyte differentiation antigen cd14; **PDBTitle:** crystal structure of cd14
16	c3g06A_	Alignment		99.9	35	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ssph2 (leucine-rich repeat protein); **PDBTitle:** the salmonella virulence effector ssph2 functions as a2 novel e3 ligase
17	c4kt1A_	Alignment		99.9	38	**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
18	c3cvrA_	Alignment		99.9	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**invasion plasmid antigen; **PDBTitle:** crystal structure of the full length ipah3
19	c3a79A_	Alignment		99.9	31	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 2, variable lymphocyte receptor b; **PDBTitle:** crystal structure of tlr2-tlr6-pam2csk4 complex
20	c4bstB_	Alignment		99.9	47	**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
21	c2of5K_	Alignment	not modelled	99.9	86	**PDB header:**apoptosis **Chain:** K: **PDB Molecule:**leucine-rich repeat and death domain-containing **PDBTitle:** oligomeric death domain complex
22	c2z7xB_	Alignment	not modelled	99.9	43	**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
23	c2z81A_	Alignment	not modelled	99.9	31	**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
24	c2a0zA_	Alignment	not modelled	99.9	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 3; **PDBTitle:** the molecular structure of toll-like receptor 3 ligand binding domain
25	c3f59A_	Alignment	not modelled	99.9	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** crystal structure of zu5-ank, the spectrin binding region of human2 erythroid ankyrin
26	c3j0aA_	Alignment	not modelled	99.9	27	**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
27	c4glpA_	Alignment	not modelled	99.9	27	**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 header:signaling protein **Chain:** B: **PDB Molecule:**leucine-rich repeat-containing g-protein

28	c4bsrB_	Alignment	not modelled	99.9	41	coupled receptor **PDBTitle:** structure of the ectodomain of lgr5 in complex with r-spondin-12 (fu1fu2) in p22121 crystal form
29	c2id5D_	Alignment	not modelled	99.9	29	**PDB header:**ligand binding protein,membrane protein **Chain:** D: **PDB Molecule:**leucine rich repeat neuronal 6a; **PDBTitle:** crystal structure of the lingo-1 ectodomain
30	d2omza2	Alignment	not modelled	99.9	22	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
31	c3rg1B_	Alignment	not modelled	99.9	22	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cd180 molecule; **PDBTitle:** crystal structure of the rp105/md-1 complex
32	c3w3jB_	Alignment	not modelled	99.9	27	**PDB header:**immune system **Chain:** B: **PDB Molecule:**toll-like receptor 8; **PDBTitle:** crystal structure of human tlr8 in complex with cl097
33	c2xotA_	Alignment	not modelled	99.9	32	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**amphoterin-induced protein 1; **PDBTitle:** crystal structure of neuronal leucine rich repeat protein amigo-1
34	c3v47B_	Alignment	not modelled	99.9	24	**PDB header:**immune system **Chain:** B: **PDB Molecule:**toll-like receptor 5b and variable lymphocyte receptor b.61 **PDBTitle:** crystal structure of the n-tetminal fragment of zebrafish tlr5 in2 complex with salmonella flagellin
35	c2yqfA_	Alignment		99.9	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** solution structure of the death domain of ankyrin-1
36	c3fxiA_	Alignment	not modelled	99.9	24	**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
37	c3j0aB_	Alignment	not modelled	99.9	26	**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
38	c2ft3B_	Alignment	not modelled	99.9	29	**PDB header:**structural protein, signaling protein **Chain:** B: **PDB Molecule:**biglycan; **PDBTitle:** crystal structure of the biglycan dimer core protein
39	c2omwA_	Alignment	not modelled	99.8	26	**PDB header:**cell invasion/cell adhesion **Chain:** A: **PDB Molecule:**internalin-a; **PDBTitle:** crystal structure of inla s192n y369s/mec1 complex
40	c3v44A_	Alignment	not modelled	99.8	23	**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
41	c3rg1I_	Alignment	not modelled	99.8	31	**PDB header:**immune system **Chain:** I: **PDB Molecule:**cd180 molecule; **PDBTitle:** crystal structure of the rp105/md-1 complex
42	d1xkua_	Alignment	not modelled	99.8	27	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
43	c1xkuA_	Alignment	not modelled	99.8	27	**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
44	c2z63A_	Alignment	not modelled	99.8	23	**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
45	c1ltxA_	Alignment	not modelled	99.8	35	**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
46	c4fcgA_	Alignment	not modelled	99.8	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of the leucine-rich repeat domain of the type iii effector2 xcv3220 (xopl)
47	c1wxpA_	Alignment	not modelled	99.8	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tho complex subunit 1; **PDBTitle:** solution structure of the death domain of nuclear matrix2 protein p84
48	c4b8cD_	Alignment	not modelled	99.8	28	**PDB header:**hydrolase/cell cycle **Chain:** D: **PDB Molecule:**glucose-repressible alcohol dehydrogenase transcriptional **PDBTitle:** nuclease module of the yeast ccr4-not complex
49	c4arnD_	Alignment	not modelled	99.8	23	**PDB header:**immune system **Chain:** D: **PDB Molecule:**toll receptor, variable lymphocyte receptor b.61 chimera; **PDBTitle:** crystal structure of the n-terminal domain of drosophila toll2 receptor
50	c1ookG_	Alignment	not modelled	99.8	33	**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
51	d1ddfa_	Alignment	not modelled	99.8	17	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
						PDB header:immune system

52	c4k5uD_	Alignment	not modelled	99.8	27	**Chain:** D: **PDB Molecule:**variable lymphocyte receptor; **PDBTitle:** recognition of the bg-h antigen by a lamprey variable lymphocyte2 receptor
53	d1ogqa_	Alignment	not modelled	99.8	30	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Polygalacturonase inhibiting protein PGIP
54	d1p9ag_	Alignment	not modelled	99.8	34	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
55	d1fada_	Alignment	not modelled	99.8	24	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
56	c3o6nA_	Alignment	not modelled	99.8	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**apl1; **PDBTitle:** crystal structure of apl1 leucine-rich repeat domain
57	c3e6jA_	Alignment	not modelled	99.8	29	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor diversity region; **PDBTitle:** crystal structure of variable lymphocyte receptor (vlr) rbc36 in2 complex with h-trisaccharide
58	c3oq9C_	Alignment	not modelled	99.8	17	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6; **PDBTitle:** structure of the fas/fadd death domain assembly
59	c2o6sA_	Alignment	not modelled	99.8	28	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor b; **PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors b59
60	c2o6qA_	Alignment	not modelled	99.8	34	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor a; **PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors a29
61	c1ichA_	Alignment	not modelled	99.8	22	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor-1; **PDBTitle:** solution structure of the tumor necrosis factor receptor-12 death domain
62	d1icha_	Alignment	not modelled	99.8	22	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
63	c2gf5A_	Alignment	not modelled	99.8	24	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fadd protein; **PDBTitle:** structure of intact fadd (mort1)
64	c3bz5A_	Alignment	not modelled	99.8	26	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**internalin-j; **PDBTitle:** functional domain of inlj from listeria monocytogenes2 includes a cysteine ladder
65	c2of5A_	Alignment	not modelled	99.8	21	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain-containing protein cradd; **PDBTitle:** oligomeric death domain complex
66	c4fmzA_	Alignment	not modelled	99.8	36	**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
67	c1g9uA_	Alignment	not modelled	99.8	40	**PDB header:**toxin **Chain:** A: **PDB Molecule:**outer protein yopm; **PDBTitle:** crystal structure of yopm-leucine rich effector protein from yersinia2 pestis
68	d2gf5a1	Alignment	not modelled	99.8	25	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
69	d1jl5a_	Alignment	not modelled	99.8	40	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Leucine rich effector protein YopM
70	c2z80A_	Alignment	not modelled	99.8	32	**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
71	c4b8cL_	Alignment	not modelled	99.8	29	**PDB header:**hydrolase/cell cycle **Chain:** L: **PDB Molecule:**glucose-repressible alcohol dehydrogenase transcriptional **PDBTitle:** nuclease module of the yeast ccr4-not complex
72	c3o53A_	Alignment	not modelled	99.8	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein lrim1; **PDBTitle:** crystal structure of lrim1 leucine-rich repeat domain
73	c3rfsA_	Alignment	not modelled	99.7	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**internalin b, repeat modules, variable lymphocyte receptor **PDBTitle:** design of a binding scaffold based on variable lymphocyte receptors of2 jawless vertebrates by module engineering
74	c3m18A_	Alignment	not modelled	99.7	27	**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
75	d2omxa2	Alignment	not modelled	99.7	26	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
76	d2astb2	Alignment	not modelled	99.7	19	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**Cyclin A/CDK2-associated p19, Skp2
77	c1h6uA_	Alignment	not modelled	99.7	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**internalin h; **PDBTitle:** internalin h: crystal structure of fused n-terminal2 domains.

78	c4ay9Z_	Alignment	not modelled	99.7	28	**PDB header:**hormone/receptor **Chain:** Z: **PDB Molecule:**follicle-stimulating hormone receptor; **PDBTitle:** structure of follicle-stimulating hormone in complex with2 the entire ectodomain of its receptor
79	c2ra8A_	Alignment	not modelled	99.7	15	**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
80	c2o6rA_	Alignment	not modelled	99.7	27	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor b; **PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors b61
81	c2v9sC_	Alignment	not modelled	99.7	24	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**slit homolog 2 protein n-product; **PDBTitle:** second lrr domain of human slit2
82	c2v70D_	Alignment	not modelled	99.7	28	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**slit homolog 2 protein n-product; **PDBTitle:** third lrr domain of human slit2
83	c2z62A_	Alignment	not modelled	99.7	29	**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
84	d1ozna_	Alignment	not modelled	99.7	27	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
85	c2je0E_	Alignment	not modelled	99.6	26	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**acidic leucine-rich nuclear phosphoprotein 32 family **PDBTitle:** crystal structure of pp32
86	c4ezgB_	Alignment	not modelled	99.6	20	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a leucine rich hypothetical protein2 (lmof2365_1307) from listeria monocytogenes str. li 2 at 1.50 a3 resolution
87	d2bnha_	Alignment	not modelled	99.6	25	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
88	c2wfhB_	Alignment	not modelled	99.6	33	**PDB header:**splicing **Chain:** B: **PDB Molecule:**slit homolog 2 protein c-product; **PDBTitle:** the human slit 2 dimerization domain d4
89	c2ib1A_	Alignment	not modelled	99.6	20	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain containing membrane protein nradd; **PDBTitle:** solution structure of p45 death domain
90	c2r9uC_	Alignment	not modelled	99.6	26	**PDB header:**immune system **Chain:** C: **PDB Molecule:**variable lymphocyte receptor; **PDBTitle:** crystal structure of lamprey variable lymphocyte receptor 29132 ectodomain
91	d1dcea3	Alignment	not modelled	99.6	35	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Rab geranylgeranyltransferase alpha-subunit, C-terminal domain
92	d1h6ta2	Alignment	not modelled	99.6	24	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
93	c2z66A_	Alignment	not modelled	99.6	24	**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
94	d1w8aa_	Alignment	not modelled	99.6	26	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
95	c1otnA_	Alignment	not modelled	99.6	24	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**internalin b; **PDBTitle:** calcium-binding mutant of the internalin b lrr domain
96	d1z7xw1	Alignment	not modelled	99.6	47	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
97	c2y5qA_	Alignment	not modelled	99.6	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**internalin b; **PDBTitle:** listeria monocytogenes inlb (internalin b) residues 36-392
98	c1xeuA_	Alignment	not modelled	99.6	29	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**internalin c; **PDBTitle:** crystal structure of internalin c from listeria2 monocytogenes
99	c3g3aA_	Alignment	not modelled	99.5	24	**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
100	d1h6ua2	Alignment	not modelled	99.5	23	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
101	d2ifga3	Alignment	not modelled	99.5	24	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
102	c3g04C_	Alignment	not modelled	99.5	19	**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
103	d1a9na_	Alignment	not modelled	99.5	22	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like

						Family:U2A'-like
104	c2uzyA_	Alignment	not modelled	99.5	21	**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
105	d1xwdc1	Alignment	not modelled	99.5	22	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
106	d2ca6a1	Alignment	not modelled	99.4	24	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**Rna1p (RanGAP1), N-terminal domain
107	c1k5dL_	Alignment	not modelled	99.4	19	**PDB header:**signaling protein/signaling activator **Chain:** L: **PDB Molecule:**ran gtpase activating protein 1; **PDBTitle:** crystal structure of ran-gppnhp-ranbp1-rangap complex
108	d1m9la_	Alignment	not modelled	99.4	22	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**Outer arm dynein light chain 1 **Family:**Outer arm dynein light chain 1
109	d1ngra_	Alignment	not modelled	99.4	27	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
110	c2ifgB_	Alignment	not modelled	99.4	23	**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
111	c2kxrA_	Alignment	not modelled	99.3	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** zo1 zu5 domain mc/aa mutation
112	c2kxsA_	Alignment	not modelled	99.3	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tight junction protein zo-1, linker, peptide of myocardium- **PDBTitle:** zo1 zu5 domain in complex with grinl1a peptide
113	c3un9A_	Alignment	not modelled	99.3	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**nlr family member x1; **PDBTitle:** crystal structure of an immune receptor
114	c3mopC_	Alignment	not modelled	99.3	28	**PDB header:**signaling protein, immune system **Chain:** C: **PDB Molecule:**myeloid differentiation primary response protein myd88; **PDBTitle:** the ternary death domain complex of myd88, irak4, and irak2
115	c2p1nE_	Alignment	not modelled	99.3	15	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**transport inhibitor response 1 protein; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
116	d1fs2a2	Alignment	not modelled	99.2	21	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**Cyclin A/CDK2-associated p19, Skp2
117	c3gozA_	Alignment	not modelled	99.2	19	**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
118	c3oglD_	Alignment	not modelled	99.1	18	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**coronatine-insensitive protein 1; **PDBTitle:** structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron
119	c3ogmB_	Alignment	not modelled	99.1	18	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronatine-insensitive protein 1; **PDBTitle:** structure of coi1-ask1 in complex with coronatine and the jaz1 degron
120	d1d2za_	Alignment	not modelled	99.1	13	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD