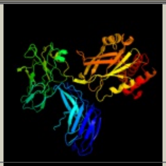
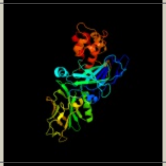
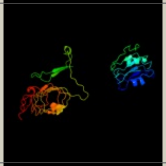
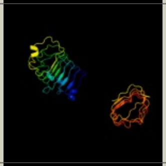
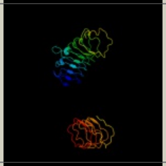
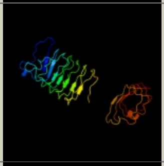
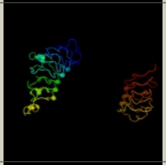
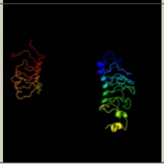
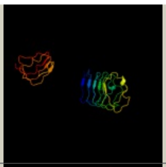
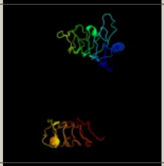
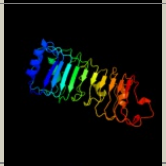
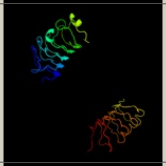
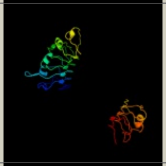
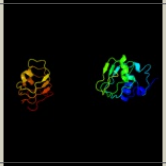
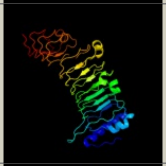
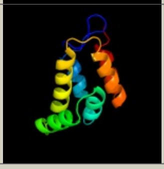
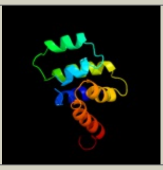
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q9HB75
Date	Wed May 9 17:48:56 BST 2012
Unique Job ID	7e48d0e511d74c90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4d8oA_	Alignment		100.0	27	**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	26	**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	15	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**netrin receptor unc5b; **PDBTitle:** the structure of unc5b cytoplasmic domain
4	c3rgxA_	Alignment		100.0	54	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein brassinosteroid insensitive 1; **PDBTitle:** structural insight into brassinosteroid perception by bri1
5	c1ziwA_	Alignment		100.0	27	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 3; **PDBTitle:** human toll-like receptor 3 extracellular domain structure
6	c2a0zA_	Alignment		99.9	27	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 3; **PDBTitle:** the molecular structure of toll-like receptor 3 ligand binding domain
7	c3ojaA_	Alignment		99.9	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
8	c3ojaB_	Alignment		99.9	25	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
9	c2z64A_	Alignment		99.9	25	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 4; **PDBTitle:** crystal structure of mouse tlr4 and mouse md-2 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	c3fxiA_	Alignment		99.9	29	**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

12	c3a79B_	Alignment		99.9	53	**PDB header:**immune system **Chain:** B: **PDB Molecule:**toll-like receptor 6, variable lymphocyte receptor b; **PDBTitle:** crystal structure of tlr2-tlr6-pam2csk4 complex
13	c3a79A_	Alignment		99.9	30	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 2, variable lymphocyte receptor b; **PDBTitle:** crystal structure of tlr2-tlr6-pam2csk4 complex
14	c1wwlA_	Alignment		99.9	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**monocyte differentiation antigen cd14; **PDBTitle:** crystal structure of cd14
15	c2z63A_	Alignment		99.9	33	**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
16	c2z7xB_	Alignment		99.9	32	**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
17	d2omza2	Alignment		99.9	25	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR 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	c3g06A_	Alignment		99.9	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ssph2 (leucine-rich repeat protein); **PDBTitle:** the salmonella virulence effector ssph2 functions as a2 novel e3 ligase
20	c2of5K_	Alignment		99.9	99	**PDB header:**apoptosis **Chain:** K: **PDB Molecule:**leucine-rich repeat and death domain-containing **PDBTitle:** oligomeric death domain complex
21	c2id5D_	Alignment	not modelled	99.9	25	**PDB header:**ligand binding protein,membrane protein **Chain:** D: **PDB Molecule:**leucine rich repeat neuronal 6a; **PDBTitle:** crystal structure of the lingo-1 ectodomain
22	c2xotA_	Alignment	not modelled	99.9	33	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**amphoterin-induced protein 1; **PDBTitle:** crystal structure of neuronal leucine rich repeat protein amigo-1
23	c3f59A_	Alignment	not modelled	99.9	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** crystal structure of zu5-ank, the spectrin binding region of human2 erythroid ankyrin
24	c2z81A_	Alignment	not modelled	99.9	28	**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
25	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
26	c2ft3B_	Alignment	not modelled	99.9	34	**PDB header:**structural protein, signaling protein **Chain:** B: **PDB Molecule:**biglycan; **PDBTitle:** crystal structure of the biglycan dimer core protein
27	c2omwA_	Alignment	not modelled	99.9	28	**PDB header:**cell invasion/cell adhesion **Chain:** A: **PDB Molecule:**internalin-a; **PDBTitle:** crystal structure of inla s192n y369s/mec1 complex
28	c3rg1I_	Alignment	not modelled	99.8	30	**PDB header:**immune system **Chain:** I: **PDB Molecule:**cd180 molecule; **PDBTitle:** crystal structure of the rp105/md-1 complex

29	c3v47B_	Alignment	not modelled	99.8	33	**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
30	d1xkua_	Alignment	not modelled	99.8	31	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
31	c1xkuA_	Alignment	not modelled	99.8	31	**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
32	c1ltxA_	Alignment	not modelled	99.8	23	**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
33	c3v44A_	Alignment	not modelled	99.8	28	**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
34	d1ogqa_	Alignment	not modelled	99.8	26	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Polygalacturonase inhibiting protein PGIP
35	c3o6nA_	Alignment	not modelled	99.8	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**apl1; **PDBTitle:** crystal structure of apl1 leucine-rich repeat domain
36	c2yqfA_	Alignment	not modelled	99.8	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** solution structure of the death domain of ankyrin-1
37	c3e6jA_	Alignment	not modelled	99.8	31	**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
38	c2o6sA_	Alignment	not modelled	99.8	29	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor b; **PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors b59
39	c3bz5A_	Alignment	not modelled	99.8	29	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**internalin-j; **PDBTitle:** functional domain of inlj from listeria monocytogenes2 includes a cysteine ladder
40	d1p9ag_	Alignment	not modelled	99.8	33	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
41	c1g9uA_	Alignment	not modelled	99.8	35	**PDB header:**toxin **Chain:** A: **PDB Molecule:**outer protein yopm; **PDBTitle:** crystal structure of yopm-leucine rich effector protein from yersinia2 pestis
42	d1jl5a_	Alignment	not modelled	99.8	35	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Leucine rich effector protein YopM
43	c1ookG_	Alignment	not modelled	99.8	34	**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
44	d1ddfa_	Alignment		99.7	17	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
45	d1fada_	Alignment	not modelled	99.7	25	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
46	c1wxpA_	Alignment	not modelled	99.7	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
47	c2o6qA_	Alignment	not modelled	99.7	27	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor a; **PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors a29
48	d1icha_	Alignment	not modelled	99.7	25	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
49	c1ichA_	Alignment	not modelled	99.7	25	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor-1; **PDBTitle:** solution structure of the tumor necrosis factor receptor-12 death domain
50	c3oq9C_	Alignment	not modelled	99.7	16	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6; **PDBTitle:** structure of the fas/fadd death domain assembly
51	c2gf5A_	Alignment	not modelled	99.7	25	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fadd protein; **PDBTitle:** structure of intact fadd (mort1)
52	c2z80A_	Alignment	not modelled	99.7	30	**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
53	d2gf5a1	Alignment	not modelled	99.7	26	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
54	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
55	c3o53A_	Alignment	not modelled	99.7	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein lrim1; **PDBTitle:** crystal structure of lrim1 leucine-rich repeat domain
56	c2of5A_	Alignment	not modelled	99.7	20	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain-containing protein cradd; **PDBTitle:** oligomeric death domain complex
57	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
58	d2omxa2	Alignment	not modelled	99.7	25	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
59	d2astb2	Alignment	not modelled	99.7	20	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**Cyclin A/CDK2-associated p19, Skp2
60	c1h6uA_	Alignment	not modelled	99.7	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**internalin h; **PDBTitle:** internalin h: crystal structure of fused n-terminal2 domains.
61	d2bnha_	Alignment	not modelled	99.6	32	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
62	c2o6rA_	Alignment	not modelled	99.6	32	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor b; **PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors b61
63	c2v70D_	Alignment	not modelled	99.6	28	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**slit homolog 2 protein n-product; **PDBTitle:** third lrr domain of human slit2
64	d1ozna_	Alignment	not modelled	99.6	27	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
65	c2v9sC_	Alignment	not modelled	99.6	25	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**slit homolog 2 protein n-product; **PDBTitle:** second lrr domain of human slit2
66	c2ra8A_	Alignment	not modelled	99.6	14	**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
67	c2je0E_	Alignment	not modelled	99.6	27	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**acidic leucine-rich nuclear phosphoprotein 32 family **PDBTitle:** crystal structure of pp32
68	d1z7xw1	Alignment	not modelled	99.6	43	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
69	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
70	c2z62A_	Alignment	not modelled	99.6	24	**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
71	d1dcea3	Alignment	not modelled	99.6	37	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Rab geranylgeranyltransferase alpha-subunit, C-terminal domain
72	c2z66A_	Alignment	not modelled	99.6	27	**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
73	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
74	c1xeuA_	Alignment	not modelled	99.6	28	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**internalin c; **PDBTitle:** crystal structure of internalin c from listeria2 monocytogenes
75	c2r9uC_	Alignment	not modelled	99.5	25	**PDB header:**immune system **Chain:** C: **PDB Molecule:**variable lymphocyte receptor; **PDBTitle:** crystal structure of lamprey variable lymphocyte receptor 29132 ectodomain
76	d1w8aa_	Alignment	not modelled	99.5	25	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
						Fold: Leucine-rich repeat, LRR (right-handed beta-alpha

77	d1h6ta2	Alignment	not modelled	99.5	26	superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
78	c2uzyA_	Alignment	not modelled	99.5	25	**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
79	d1h6ua2	Alignment	not modelled	99.5	24	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
80	d2ifga3	Alignment	not modelled	99.5	23	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
81	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
82	c1otnA_	Alignment	not modelled	99.5	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**internalin b; **PDBTitle:** calcium-binding mutant of the internalin b lrr domain
83	c3g04C_	Alignment	not modelled	99.5	16	**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
84	c2ib1A_	Alignment	not modelled	99.5	23	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain containing membrane protein nradd; **PDBTitle:** solution structure of p45 death domain
85	c1k5dL_	Alignment	not modelled	99.4	21	**PDB header:**signaling protein/signaling activator **Chain:** L: **PDB Molecule:**ran gtpase activating protein 1; **PDBTitle:** crystal structure of ran-gppnhp-ranbp1-rangap complex
86	d1a9na_	Alignment	not modelled	99.4	22	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**U2A'-like
87	d1xwdc1	Alignment	not modelled	99.4	21	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
88	d2ca6a1	Alignment	not modelled	99.4	21	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**Rna1p (RanGAP1), N-terminal domain
89	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
90	d1m9la_	Alignment	not modelled	99.4	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
91	d1fs2a2	Alignment	not modelled	99.3	23	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**Cyclin A/CDK2-associated p19, Skp2
92	d1ngra_	Alignment	not modelled	99.3	26	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
93	c2p1nE_	Alignment	not modelled	99.3	16	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**transport inhibitor response 1 protein; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
94	c3un9A_	Alignment	not modelled	99.2	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**nlr family member x1; **PDBTitle:** crystal structure of an immune receptor
95	c2kxsA_	Alignment	not modelled	99.2	23	**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
96	c3gozA_	Alignment	not modelled	99.2	22	**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
97	c2kxrA_	Alignment	not modelled	99.2	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** zo1 zu5 domain mc/aa mutation
98	c3mopC_	Alignment	not modelled	99.1	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
99	c3oglD_	Alignment	not modelled	99.0	16	**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
100	c3ogmB_	Alignment	not modelled	99.0	16	**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
101	d1d2za_	Alignment	not modelled	98.7	13	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
						PDB header:protein binding **Chain:** B: **PDB Molecule:**hypothetical leucine rich repeat protein;

102	c3sb4B_	Alignment	not modelled	98.6	14	**PDBTitle:** crystal structure of a hypothetical leucine rich repeat protein2 (bt_1240) from bacteroides thetaiotaomicron vpi-5482 at 1.99 a3 resolution
103	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
104	d1wmga_	Alignment	not modelled	98.2	21	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
105	d1koha1	Alignment	not modelled	98.1	26	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**mRNA export factor tap
106	d1io0a_	Alignment	not modelled	98.1	18	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
107	c1fqvK_	Alignment	not modelled	98.0	22	**PDB header:**ligase **Chain:** K: **PDB Molecule:**skp2; **PDBTitle:** insights into scf ubiquitin ligases from the structure of2 the skp1-skp2 complex
108	c1pgvA_	Alignment	not modelled	98.0	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tropomodulin tmd-1; **PDBTitle:** structural genomics of caenorhabditis elegans: tropomodulin2 c-terminal domain
109	d1pgva_	Alignment	not modelled	98.0	19	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
110	c2d96A_	Alignment	not modelled	97.9	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear factor nf-kappa-b p100 subunit; **PDBTitle:** solution structure of the death domain of nuclear factor nf-2 kappa-b p100
111	c2dbfA_	Alignment	not modelled	97.7	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nuclear factor nf-kappa-b p105 subunit; **PDBTitle:** solution structure of the death domain in human nuclear2 factor nf-kappa-b p105 subunit
112	c3rfeB_	Alignment	not modelled	97.3	28	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**platelet glycoprotein ib beta chain; **PDBTitle:** crystal structure of glycoprotein gpib ectodomain
113	c3e2jA_	Alignment	not modelled	97.3	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**atp synthase subunit s, mitochondrial; **PDBTitle:** crystal structure of bovine coupling factor b
114	d1wh4a_	Alignment	not modelled	96.7	20	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
115	c1rh1A_	Alignment	not modelled	95.1	10	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**colicin b; **PDBTitle:** crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution
116	c3cl3A_	Alignment	not modelled	93.7	16	**PDB header:**viral protein/signaling protein **Chain:** A: **PDB Molecule:**orf k13; **PDBTitle:** crystal structure of a vflip-ikkgamma complex: insights2 into viral activation of the ikk signalosome
117	c3mopM_	Alignment	not modelled	93.7	23	**PDB header:**signaling protein, immune system **Chain:** M: **PDB Molecule:**interleukin-1 receptor-associated kinase-like 2; **PDBTitle:** the ternary death domain complex of myd88, irak4, and irak2
118	d1cy5a_	Alignment	not modelled	93.6	12	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
119	d3ygsp_	Alignment	not modelled	91.3	17	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
120	c2bbrA_	Alignment	not modelled	91.2	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**viral casp8 and fadd-like apoptosis regulator; **PDBTitle:** crystal structure of mc159 reveals molecular mechanism of2 disc assembly and vflip inhibition