Phyre^2

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Description	P76321
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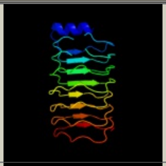
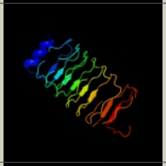
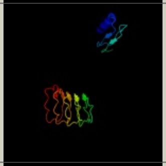
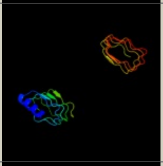
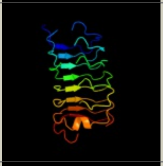
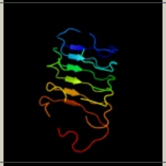
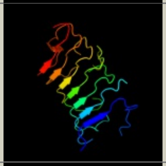
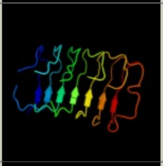
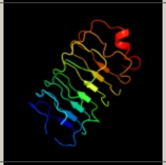
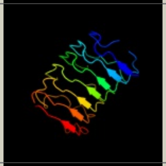
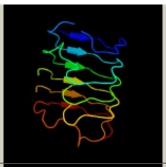
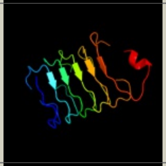
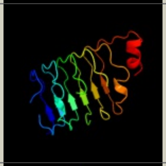
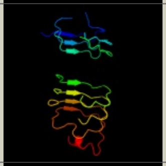
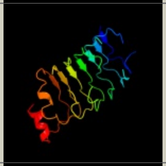
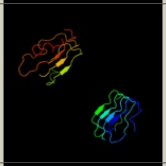
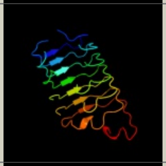
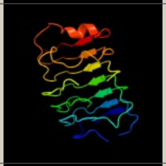
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g06A_	Alignment		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
2	c3cvrA_	Alignment		99.9	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**invasion plasmid antigen; **PDBTitle:** crystal structure of the full length ipah3
3	d1jl5a_	Alignment		99.9	57	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Leucine rich effector protein YopM
4	c1g9uA_	Alignment		99.9	34	**PDB header:**toxin **Chain:** A: **PDB Molecule:**outer protein yopm; **PDBTitle:** crystal structure of yopm-leucine rich effector protein from yersinia2 pestis
5	c1m9sA_	Alignment		99.8	19	**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.
6	c3a79B_	Alignment		99.7	17	**PDB header:**immune system **Chain:** B: **PDB Molecule:**toll-like receptor 6, variable lymphocyte receptor b; **PDBTitle:** crystal structure of tlr2-tlr6-pam2csk4 complex
7	c1wwlA_	Alignment		99.7	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**monocyte differentiation antigen cd14; **PDBTitle:** crystal structure of cd14
8	c2a0zA_	Alignment		99.7	18	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 3; **PDBTitle:** the molecular structure of toll-like receptor 3 ligand binding domain
9	c1ziwA_	Alignment		99.7	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 3; **PDBTitle:** human toll-like receptor 3 extracellular domain structure
10	c2z64A_	Alignment		99.7	14	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 4; **PDBTitle:** crystal structure of mouse tlr4 and mouse md-2 complex
11	c3j0aB_	Alignment		99.6	10	**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

12	c3fxiA_	Alignment		99.6	13	**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
13	c2z7xB_	Alignment		99.6	12	**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
14	c2o6rA_	Alignment		99.6	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor b; **PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors b61
15	c1ookG_	Alignment		99.6	21	**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
16	c3e6jA_	Alignment		99.6	18	**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
17	c2ft3B_	Alignment		99.6	19	**PDB header:**structural protein, signaling protein **Chain:** B: **PDB Molecule:**biglycan; **PDBTitle:** crystal structure of the biglycan dimer core protein
18	c2o6sA_	Alignment		99.6	14	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor b; **PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors b59
19	c2z63A_	Alignment		99.6	14	**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
20	c3ojaA_	Alignment		99.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
21	d1p9ag_	Alignment	not modelled	99.6	20	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
22	c2xotA_	Alignment	not modelled	99.5	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**amphoterin-induced protein 1; **PDBTitle:** crystal structure of neuronal leucine rich repeat protein amigo-1
23	c3a79A_	Alignment	not modelled	99.5	16	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 2, variable lymphocyte receptor b; **PDBTitle:** crystal structure of tlr2-tlr6-pam2csk4 complex
24	c2z81A_	Alignment	not modelled	99.5	16	**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	c2r9uC_	Alignment	not modelled	99.5	15	**PDB header:**immune system **Chain:** C: **PDB Molecule:**variable lymphocyte receptor; **PDBTitle:** crystal structure of lamprey variable lymphocyte receptor 29132 ectodomain
26	c1ltxA_	Alignment	not modelled	99.5	17	**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
27	d1xkua_	Alignment	not modelled	99.5	22	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
28	c1xkuA_	Alignment	not modelled	99.5	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**decorin;

28	c1xkuA_	Alignment	not modelled	99.5	22	**PDBTitle:** crystal structure of the dimeric protein core of decorin, the2 archetypal small leucine-rich repeat proteoglycan
29	c2wfhB_	Alignment	not modelled	99.5	22	**PDB header:**splicing **Chain:** B: **PDB Molecule:**slit homolog 2 protein c-product; **PDBTitle:** the human slit 2 dimerization domain d4
30	d2omza2	Alignment	not modelled	99.4	50	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
31	c2v70D_	Alignment	not modelled	99.4	14	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**slit homolog 2 protein n-product; **PDBTitle:** third lrr domain of human slit2
32	c3rgxA_	Alignment	not modelled	99.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein brassinosteroid insensitive 1; **PDBTitle:** structural insight into brassinosteroid perception by bri1
33	c2v9sC_	Alignment	not modelled	99.4	18	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**slit homolog 2 protein n-product; **PDBTitle:** second lrr domain of human slit2
34	c2o6qA_	Alignment	not modelled	99.4	18	**PDB header:**immune system **Chain:** A: **PDB Molecule:**variable lymphocyte receptor a; **PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors a29
35	d1w8aa_	Alignment	not modelled	99.4	19	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
36	c3g3aA_	Alignment	not modelled	99.3	21	**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
37	c2id5D_	Alignment	not modelled	99.3	17	**PDB header:**ligand binding protein,membrane protein **Chain:** D: **PDB Molecule:**leucine rich repeat neuronal 6a; **PDBTitle:** crystal structure of the lingo-1 ectodomain
38	c3rg1I_	Alignment	not modelled	99.3	19	**PDB header:**immune system **Chain:** I: **PDB Molecule:**cd180 molecule; **PDBTitle:** crystal structure of the rp105/md-1 complex
39	c2z80A_	Alignment	not modelled	99.3	23	**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
40	d1dcea3	Alignment	not modelled	99.2	18	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Rab geranylgeranyltransferase alpha-subunit, C-terminal domain
41	c3m18A_	Alignment	not modelled	99.2	19	**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
42	d1ozna_	Alignment	not modelled	99.2	14	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
43	c3ojaB_	Alignment	not modelled	99.2	8	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
44	c2z62A_	Alignment	not modelled	99.2	21	**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
45	c2je0E_	Alignment	not modelled	99.1	17	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**acidic leucine-rich nuclear phosphoprotein 32 family **PDBTitle:** crystal structure of pp32
46	c3bz5A_	Alignment	not modelled	99.0	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**internalin-j; **PDBTitle:** functional domain of inlj from listeria monocytogenes2 includes a cysteine ladder
47	d2omxa2	Alignment	not modelled	99.0	20	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
48	c1xeuA_	Alignment	not modelled	99.0	14	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**internalin c; **PDBTitle:** crystal structure of internalin c from listeria2 monocytogenes
49	c1h6uA_	Alignment	not modelled	99.0	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**internalin h; **PDBTitle:** internalin h: crystal structure of fused n-terminal2 domains.
50	c3g04C_	Alignment	not modelled	99.0	21	**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
51	c3o6nA_	Alignment	not modelled	99.0	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**apl1; **PDBTitle:** crystal structure of apl1 leucine-rich repeat domain
52	d1ogqa_	Alignment	not modelled	98.9	26	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Polygalacturonase inhibiting protein PGIP
53	c2y5qA_	Alignment	not modelled	98.9	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**internalin b; **PDBTitle:** listeria monocytogenes inlb (internalin b) residues 36-

						392
54	c1otnA_	Alignment	not modelled	98.9	26	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**internalin b; **PDBTitle:** calcium-binding mutant of the internalin b lrr domain
55	d1xwdc1	Alignment	not modelled	98.9	32	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
56	d1a9na_	Alignment	not modelled	98.8	16	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**U2A'-like
57	d1h6ta2	Alignment	not modelled	98.8	22	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
58	d1h6ua2	Alignment	not modelled	98.8	23	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Internalin LRR domain
59	c2ifgB_	Alignment	not modelled	98.8	14	**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
60	c3o53A_	Alignment	not modelled	98.8	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein lrim1; **PDBTitle:** crystal structure of lrim1 leucine-rich repeat domain
61	c2uzyA_	Alignment	not modelled	98.8	19	**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
62	d2ifga3	Alignment	not modelled	98.8	12	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**Ngr ectodomain-like
63	c2z66A_	Alignment	not modelled	98.7	16	**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
64	c2omwA_	Alignment	not modelled	98.5	16	**PDB header:**cell invasion/cell adhesion **Chain:** A: **PDB Molecule:**internalin-a; **PDBTitle:** crystal structure of inla s192n y369s/mec1 complex
65	c1kooD_	Alignment	not modelled	98.1	9	**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
66	c3gozA_	Alignment	not modelled	98.0	32	**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
67	d1m9la_	Alignment	not modelled	97.9	18	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**Outer arm dynein light chain 1 **Family:**Outer arm dynein light chain 1
68	d1z7xw1	Alignment	not modelled	97.8	16	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
69	c2ra8A_	Alignment	not modelled	97.7	13	**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
70	d1koha1	Alignment	not modelled	97.6	9	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**mRNA export factor tap
71	d2bnha_	Alignment	not modelled	97.3	7	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
72	d2ca6a1	Alignment	not modelled	97.0	7	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**Rna1p (RanGAP1), N-terminal domain
73	c3rfeB_	Alignment	not modelled	96.9	12	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**platelet glycoprotein ib beta chain; **PDBTitle:** crystal structure of glycoprotein gpib ectodomain
74	c1k5dL_	Alignment	not modelled	96.8	8	**PDB header:**signaling protein/signaling activator **Chain:** L: **PDB Molecule:**ran gtpase activating protein 1; **PDBTitle:** crystal structure of ran-gppnhp-ranbp1-rangap complex
75	d2astb2	Alignment	not modelled	95.0	6	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**Cyclin A/CDK2-associated p19, Skp2
76	c3oglD_	Alignment	not modelled	93.2	10	**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
77	c3ogmB_	Alignment	not modelled	93.0	10	**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
						PDB header:electron transport

78	c3e2jA_	Alignment	not modelled	92.7	8	**Chain:** A: **PDB Molecule:**atp synthase subunit s, mitochondrial; **PDBTitle:** crystal structure of bovine coupling factor b
79	c2p1nE_	Alignment	not modelled	91.8	10	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**transport inhibitor response 1 protein; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
80	d1fs2a2	Alignment	not modelled	89.9	9	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**Cyclin A/CDK2-associated p19, Skp2
81	c1pgvA_	Alignment	not modelled	82.8	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tropomodulin tmd-1; **PDBTitle:** structural genomics of caenorhabditis elegans: tropomodulin2 c-terminal domain
82	d1pgva_	Alignment	not modelled	82.8	9	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
83	d1io0a_	Alignment	not modelled	75.1	8	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**RNI-like **Family:**28-residue LRR
84	c1fqvK_	Alignment	not modelled	15.3	9	**PDB header:**ligase **Chain:** K: **PDB Molecule:**skp2; **PDBTitle:** insights into scf ubiquitin ligases from the structure of2 the skp1-skp2 complex