
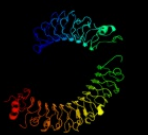































| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c3fxiA_</a> |  Alignment   |    | 100.0      | 21     | <b>PDB header:</b> immune system<br><b>Chain: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

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| 12 | <a href="#">c2z7xB_</a> | Alignment |     | 100.0 | 18 | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> toll-like receptor 1, variable lymphocyte receptor b;<br><b>PDBTitle:</b> crystal structure of the tlr1-tlr2 heterodimer induced by binding of a2 tri-acylated lipopeptide |
| 13 | <a href="#">d1ozna_</a> | Alignment |    | 100.0 | 37 | <b>Fold:</b> Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br><b>Superfamily:</b> L domain-like<br><b>Family:</b> Ngr ectodomain-like  |
| 14 | <a href="#">c3rg1l_</a> | Alignment |    | 100.0 | 16 | <b>PDB header:</b> immune system<br><b>Chain:</b> I: <b>PDB Molecule:</b> cd180 molecule;<br><b>PDBTitle:</b> crystal structure of the rp105/md-1 complex  |
| 15 | <a href="#">c3ojaB_</a> | Alignment |    | 100.0 | 25 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein<br><b>PDBTitle:</b> crystal structure of Irim1/apl1c complex   |
| 16 | <a href="#">c2z66A_</a> | Alignment |    | 100.0 | 31 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> variable lymphocyte receptor b, toll-like receptor 4;<br><b>PDBTitle:</b> crystal structure of the vt3 hybrid of human tlr4 and hagfish vlrb.61                            |
| 17 | <a href="#">c2z80A_</a> | Alignment |    | 100.0 | 22 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> toll-like receptor 2, variable lymphocyte receptor b;<br><b>PDBTitle:</b> crystal structure of the tlr1-tlr2 heterodimer induced by binding of a2 tri-acylated lipopeptide |
| 18 | <a href="#">c2o6gA_</a> | Alignment |   | 100.0 | 59 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> variable lymphocyte receptor a;<br><b>PDBTitle:</b> structural diversity of the hagfish variable lymphocyte2 receptors a29   |
| 19 | <a href="#">c2omwA_</a> | Alignment |  | 100.0 | 13 | <b>PDB header:</b> cell invasion/cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> internalin-a;<br><b>PDBTitle:</b> crystal structure of inla s192n y369s/mec1 complex   |
| 20 | <a href="#">d2omza2</a> | Alignment |  | 100.0 | 19 | <b>Fold:</b> Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br><b>Superfamily:</b> L domain-like<br><b>Family:</b> Internalin LRR domain  |
| 21 | <a href="#">c2v9sC_</a> | Alignment | not modelled  | 100.0 | 39 | <b>PDB header:</b> structural protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> slit homolog 2 protein n-product;<br><b>PDBTitle:</b> second lrr domain of human slit2  |
| 22 | <a href="#">c2v70D_</a> | Alignment | not modelled  | 100.0 | 31 | <b>PDB header:</b> structural protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> slit homolog 2 protein n-product;<br><b>PDBTitle:</b> third lrr domain of human slit2   |
| 23 | <a href="#">c2ft3B_</a> | Alignment | not modelled  | 100.0 | 21 | <b>PDB header:</b> structural protein, signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> biglycan;<br><b>PDBTitle:</b> crystal structure of the biglycan dimer core protein   |
| 24 | <a href="#">d1xkua_</a> | Alignment | not modelled  | 100.0 | 29 | <b>Fold:</b> Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br><b>Superfamily:</b> L domain-like<br><b>Family:</b> Ngr ectodomain-like  |
| 25 | <a href="#">c1xkuA_</a> | Alignment | not modelled  | 100.0 | 29 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> decorin;<br><b>PDBTitle:</b> crystal structure of the dimeric protein core of decorin, the2 archetypal small leucine-rich repeat proteoglycan                         |
| 26 | <a href="#">c2z62A_</a> | Alignment | not modelled  | 100.0 | 28 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> toll-like receptor 4, variable lymphocyte receptor b;<br><b>PDBTitle:</b> crystal structure of the tv3 hybrid of human tlr4 and hagfish vlrb.61                            |
| 27 | <a href="#">d1p9ag_</a> | Alignment | not modelled  | 100.0 | 60 | <b>Fold:</b> Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br><b>Superfamily:</b> L domain-like<br><b>Family:</b> Ngr ectodomain-like  |
| 28 | <a href="#">c3o6nA_</a> | Alignment | not modelled  | 100.0 | 27 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> apl1;<br><b>PDBTitle:</b> crystal structure of apl1 leucine-rich repeat domain   |
|    |                         |           |   |       |    | <b>PDB header:</b> hydrolase<br><b>Chain:</b> G: <b>PDB Molecule:</b> platelet glycoprotein ib alpha chain   |

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

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

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