# Phyre2

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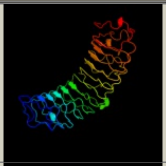
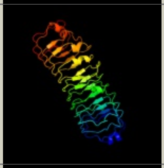
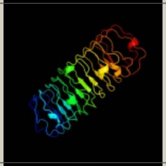
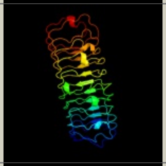
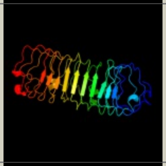
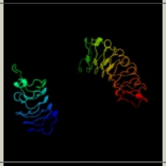
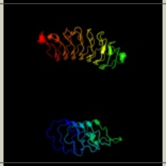
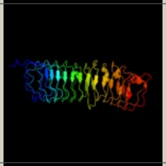
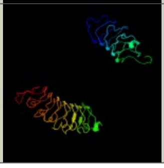
| Email | l.a.kelley@imperial.ac.uk |
| Description | P76123 |
| Date | Thu Jan 5 12:19:16 GMT 2012 |
| Unique Job ID | 9bcdf97e57716955 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2ft3B_ | Alignment |  | 100.0 | 13 | **PDB header:**structural protein, signaling protein<br>**Chain:** B: **PDB Molecule:**biglycan;<br>**PDBTitle:** crystal structure of the biglycan dimer core protein |
| 2 | c3ojaB_ | Alignment |  | 100.0 | 15 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein<br>**PDBTitle:** crystal structure of lrim1/apl1c complex |
| 3 | d2omza2 | Alignment |  | 100.0 | 14 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Internalin LRR domain |
| 4 | c1xkuA_ | Alignment |  | 100.0 | 15 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**decorin;<br>**PDBTitle:** crystal structure of the dimeric protein core of decorin, the2 archetypal small leucine-rich repeat proteoglycan |
| 5 | d1xkua_ | Alignment |  | 100.0 | 15 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Ngr ectodomain-like |
| 6 | c2id5D_ | Alignment |  | 100.0 | 13 | **PDB header:**ligand binding protein,membrane protein<br>**Chain:** D: **PDB Molecule:**leucine rich repeat neuronal 6a;<br>**PDBTitle:** crystal structure of the lingo-1 ectodomain |
| 7 | c2z63A_ | Alignment |  | 100.0 | 14 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll-like receptor 4, variable lymphocyte receptor b;<br>**PDBTitle:** crystal structure of the tv8 hybrid of human tlr4 and hagfish vlrb.61 |
| 8 | c2omwA_ | Alignment |  | 100.0 | 15 | **PDB header:**cell invasion/cell adhesion<br>**Chain:** A: **PDB Molecule:**internalin-a;<br>**PDBTitle:** crystal structure of inla s192n y369s/mec1 complex |
| 9 | c2z64A_ | Alignment |  | 100.0 | 16 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll-like receptor 4;<br>**PDBTitle:** crystal structure of mouse tlr4 and mouse md-2 complex |
| 10 | c3o6nA_ | Alignment |  | 100.0 | 15 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**apl1;<br>**PDBTitle:** crystal structure of apl1 leucine-rich repeat domain |
| 11 | c3fxiA_ | Alignment |  | 99.9 | 15 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll-like receptor 4;<br>**PDBTitle:** crystal structure of the human tlr4-human md-2-e.coli lps ra complex |

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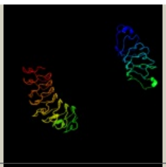
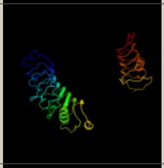
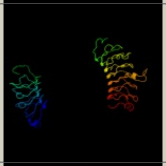
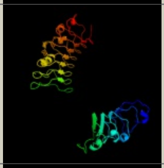
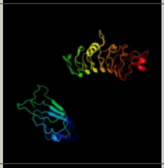
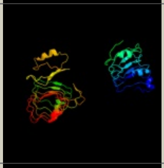
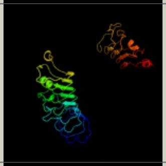
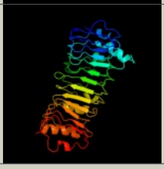
| 12 | c1ziwA_ | Alignment |  | 99.9 | 17 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll-like receptor 3;<br>**PDBTitle:** human toll-like receptor 3 extracellular domain structure |
| 13 | c3rg1l_ | Alignment |  | 99.9 | 11 | **PDB header:**immune system<br>**Chain:** l: **PDB Molecule:**cd180 molecule;<br>**PDBTitle:** crystal structure of the rp105/md-1 complex |
| 14 | c3a79A_ | Alignment |  | 99.9 | 16 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll-like receptor 2, variable lymphocyte receptor b;<br>**PDBTitle:** crystal structure of tlr2-tlr6-pam2csk4 complex |
| 15 | c2a0zA_ | Alignment |  | 99.9 | 18 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll-like receptor 3;<br>**PDBTitle:** the molecular structure of toll-like receptor 3 ligand binding domain |
| 16 | c2z7xB_ | Alignment |  | 99.9 | 18 | **PDB header:**immune system<br>**Chain:** B: **PDB Molecule:**toll-like receptor 1, variable lymphocyte receptor b;<br>**PDBTitle:** crystal structure of the tlr1-tlr2 heterodimer induced by binding of a2 tri-acylated lipopeptide |
| 17 | c3a79B_ | Alignment |  | 99.9 | 15 | **PDB header:**immune system<br>**Chain:** B: **PDB Molecule:**toll-like receptor 6, variable lymphocyte receptor b;<br>**PDBTitle:** crystal structure of tlr2-tlr6-pam2csk4 complex |
| 18 | c3rgxA_ | Alignment |  | 99.9 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein brassinosteroid insensitive 1;<br>**PDBTitle:** structural insight into brassinosteroid perception by bri1 |
| 19 | c2z81A_ | Alignment |  | 99.9 | 16 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll-like receptor 2, variable lymphocyte receptor b;<br>**PDBTitle:** crystal structure of the tlr1-tlr2 heterodimer induced by binding of a2 tri-acylated lipopeptide |
| 20 | c2z80A_ | Alignment |  | 99.9 | 15 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll-like receptor 2, variable lymphocyte receptor b;<br>**PDBTitle:** crystal structure of the tlr1-tlr2 heterodimer induced by binding of a2 tri-acylated lipopeptide |
| 21 | c1g9uA_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**outer protein yopm;<br>**PDBTitle:** crystal structure of yopm-leucine rich effector protein from yersinia2 pestis |
| 22 | d1jl5a_ | Alignment | not modelled | 99.9 | 13 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Leucine rich effector protein YopM |
| 23 | c3bz5A_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**internalin-j;<br>**PDBTitle:** functional domain of inlj from listeria monocytogenes2 includes a cysteine ladder |
| 24 | c3j0aB_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**immune system<br>**Chain:** B: **PDB Molecule:**toll-like receptor 5;<br>**PDBTitle:** homology model of human toll-like receptor 5 fitted into an electron2 microscopy single particle reconstruction |
| 25 | d1ogqa_ | Alignment | not modelled | 99.9 | 13 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Polygalacturonase inhibiting protein PGIP |
| 26 | d1p9ag_ | Alignment | not modelled | 99.9 | 19 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Ngr ectodomain-like |
| 27 | c2z62A_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll-like receptor 4, variable lymphocyte receptor b;<br>**PDBTitle:** crystal structure of the tv3 hybrid of human tlr4 and hagfish vlrb.61 |
| 28 | c2o6qA_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**variable lymphocyte receptor a;<br>**PDBTitle:** structural diversity of the hagfish variable lymphocyte2 |

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| | | | | | | receptors a29 |
| 29 | c3m18A_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**variable lymphocyte receptor a diversity region;<br>**PDBTitle:** crystal structure of variable lymphocyte receptor vlra.r2.1 in complex2 with hen egg lysozyme |
| 30 | c3o53A_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**protein lrim1;<br>**PDBTitle:** crystal structure of lrim1 leucine-rich repeat domain |
| 31 | d1xwdc1 | Alignment | not modelled | 99.8 | 11 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Ngr ectodomain-like |
| 32 | c1ookG_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**hydrolase<br>**Chain:** G: **PDB Molecule:**platelet glycoprotein ib alpha chain precursor;<br>**PDBTitle:** crystal structure of the complex of platelet receptor gpib-alpha and2 human alpha-thrombin |
| 33 | c3ojaA_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1;<br>**PDBTitle:** crystal structure of lrim1/apl1c complex |
| 34 | c3g04C_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**immune system<br>**Chain:** C: **PDB Molecule:**thyrotropin receptor;<br>**PDBTitle:** crystal structure of the tsh receptor in complex with a thyroid-2 stimulating autoantibody |
| 35 | d2bnha_ | Alignment | not modelled | 99.8 | 10 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**RNI-like<br>**Family:**28-residue LRR |
| 36 | c1m9sA_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**internalin b;<br>**PDBTitle:** crystal structure of internalin b (inlb), a listeria2 monocytogenes virulence protein containing sh3-like3 domains. |
| 37 | d1ozna_ | Alignment | not modelled | 99.8 | 12 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Ngr ectodomain-like |
| 38 | c3e6jA_ | Alignment | not modelled | 99.8 | 23 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**variable lymphocyte receptor diversity region;<br>**PDBTitle:** crystal structure of variable lymphocyte receptor (vlr) rbc36 in2 complex with h-trisaccharide |
| 39 | c1h6uA_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**internalin h;<br>**PDBTitle:** internalin h: crystal structure of fused n-terminal2 domains. |
| 40 | c3g06A_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**ssph2 (leucine-rich repeat protein);<br>**PDBTitle:** the salmonella virulence effector ssph2 functions as a2 novel e3 ligase |
| 41 | c1ltxA_ | Alignment | not modelled | 99.8 | 27 | **PDB header:**transferase/protein binding<br>**Chain:** A: **PDB Molecule:**rab geranylgeranyltransferase alpha subunit;<br>**PDBTitle:** structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid |
| 42 | c2y5qA_ | Alignment | not modelled | 99.8 | 23 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**internalin b;<br>**PDBTitle:** listeria monocytogenes inlb (internalin b) residues 36-392 |
| 43 | c2o6sA_ | Alignment | not modelled | 99.8 | 21 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**variable lymphocyte receptor b;<br>**PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors b59 |
| 44 | d1z7xw1 | Alignment | not modelled | 99.8 | 7 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**RNI-like<br>**Family:**28-residue LRR |
| 45 | d1h6ua2 | Alignment | not modelled | 99.8 | 18 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Internalin LRR domain |
| 46 | c1otnA_ | Alignment | not modelled | 99.7 | 10 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**internalin b;<br>**PDBTitle:** calcium-binding mutant of the internalin b lrr domain |
| 47 | c3cvrA_ | Alignment | not modelled | 99.7 | 24 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**invasion plasmid antigen;<br>**PDBTitle:** crystal structure of the full length ipah3 |
| 48 | c2z66A_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**variable lymphocyte receptor b, toll-like receptor 4;<br>**PDBTitle:** crystal structure of the vt3 hybrid of human tlr4 and hagfish vlrb.61 |
| 49 | c2xotA_ | Alignment | not modelled | 99.7 | 20 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**amphoterin-induced protein 1;<br>**PDBTitle:** crystal structure of neuronal leucine rich repeat protein amigo-1 |
| 50 | c2uzyA_ | Alignment | not modelled | 99.7 | 18 | **PDB header:**signaling protein/receptor<br>**Chain:** A: **PDB Molecule:**internalin b;<br>**PDBTitle:** structure of the human receptor tyrosine kinase met in2 complex with the listeria monocytogenes invasion protein3 inlb: low resolution, crystal form ii |
| 51 | d2ca6a1 | Alignment | not modelled | 99.7 | 10 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**RNI-like<br>**Family:**Rna1p (RanGAP1), N-terminal domain |
| 52 | c1k5dL_ | Alignment | not modelled | 99.7 | 9 | **PDB header:**signaling protein/signaling activator<br>**Chain:** L: **PDB Molecule:**ran gtpase activating protein 1;<br>**PDBTitle:** crystal structure of ran-gppnhp-ranbp1-rangap complex |
| | | | | | | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha |

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| 53 | d1h6ta2 | Alignment | not modelled | 99.7 | 21 | superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Internalin LRR domain |
| 54 | c1xeuA_ | Alignment | not modelled | 99.7 | 23 | **PDB header:**cell invasion<br>**Chain:** A: **PDB Molecule:**internalin c;<br>**PDBTitle:** crystal structure of internalin c from listeria2 monocytogenes |
| 55 | d2omxa2 | Alignment | not modelled | 99.6 | 22 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Internalin LRR domain |
| 56 | c3gozA_ | Alignment | not modelled | 99.6 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**leucine-rich repeat-containing protein;<br>**PDBTitle:** crystal structure of the leucine-rich repeat-containing2 protein legl7 from legionella pneumophila. northeast3 structural genomics consortium target lgr148 |
| 57 | c2r9uC_ | Alignment | not modelled | 99.6 | 22 | **PDB header:**immune system<br>**Chain:** C: **PDB Molecule:**variable lymphocyte receptor;<br>**PDBTitle:** crystal structure of lamprey variable lymphocyte receptor 29132 ectodomain |
| 58 | c1wwlA_ | Alignment | not modelled | 99.6 | 18 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**monocyte differentiation antigen cd14;<br>**PDBTitle:** crystal structure of cd14 |
| 59 | c2v9sC_ | Alignment | not modelled | 99.5 | 16 | **PDB header:**structural protein<br>**Chain:** C: **PDB Molecule:**slit homolog 2 protein n-product;<br>**PDBTitle:** second lrr domain of human slit2 |
| 60 | c2o6rA_ | Alignment | not modelled | 99.5 | 37 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**variable lymphocyte receptor b;<br>**PDBTitle:** structural diversity of the hagfish variable lymphocyte2 receptors b61 |
| 61 | c2v70D_ | Alignment | not modelled | 99.5 | 17 | **PDB header:**structural protein<br>**Chain:** D: **PDB Molecule:**slit homolog 2 protein n-product;<br>**PDBTitle:** third lrr domain of human slit2 |
| 62 | c2wfhB_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**splicing<br>**Chain:** B: **PDB Molecule:**slit homolog 2 protein c-product;<br>**PDBTitle:** the human slit 2 dimerization domain d4 |
| 63 | d1w8aa_ | Alignment | not modelled | 99.5 | 21 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Ngr ectodomain-like |
| 64 | c2ifgB_ | Alignment | not modelled | 99.4 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**high affinity nerve growth factor receptor;<br>**PDBTitle:** structure of the extracellular segment of human trka in complex with2 nerve growth factor |
| 65 | d2astb2 | Alignment | not modelled | 99.4 | 16 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**RNI-like<br>**Family:**Cyclin A/CDK2-associated p19, Skp2 |
| 66 | c3g3aA_ | Alignment | not modelled | 99.4 | 22 | **PDB header:**hydrolase/immune system<br>**Chain:** A: **PDB Molecule:**variable lymphocyte receptor vlrb.2d;<br>**PDBTitle:** structure of a lamprey variable lymphocyte receptor in2 complex with a protein antigen |
| 67 | d1dcea3 | Alignment | not modelled | 99.4 | 42 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Rab geranylgeranyltransferase alpha-subunit, C-terminal domain |
| 68 | c2je0E_ | Alignment | not modelled | 99.3 | 21 | **PDB header:**nuclear protein<br>**Chain:** E: **PDB Molecule:**acidic leucine-rich nuclear phosphoprotein 32 family<br>**PDBTitle:** crystal structure of pp32 |
| 69 | d1fs2a2 | Alignment | not modelled | 99.2 | 20 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**RNI-like<br>**Family:**Cyclin A/CDK2-associated p19, Skp2 |
| 70 | c2ra8A_ | Alignment | not modelled | 99.0 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein q64v53_bacfr;<br>**PDBTitle:** crystal structure of the q64v53_bacfr protein from bacteroides2 fragilis. northeast structural genomics consortium target bfr43 |
| 71 | c3sb4B_ | Alignment | not modelled | 99.0 | 12 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**hypothetical leucine rich repeat protein;<br>**PDBTitle:** crystal structure of a hypothetical leucine rich repeat protein2 (bt_1240) from bacteroides thetaiotaomicron vpi-5482 at 1.99 a3 resolution |
| 72 | d1a9na_ | Alignment | not modelled | 99.0 | 16 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**U2A'-like |
| 73 | d2ifga3 | Alignment | not modelled | 99.0 | 18 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**Ngr ectodomain-like |
| 74 | d1m9la_ | Alignment | not modelled | 98.5 | 19 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**Outer arm dynein light chain 1<br>**Family:**Outer arm dynein light chain 1 |
| 75 | c3rfeB_ | Alignment | not modelled | 98.3 | 16 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**platelet glycoprotein ib beta chain;<br>**PDBTitle:** crystal structure of glycoprotein gpib ectodomain |
| 76 | c3oglD_ | Alignment | not modelled | 98.2 | 9 | **PDB header:**protein binding<br>**Chain:** D: **PDB Molecule:**coronatine-insensitive protein 1;<br>**PDBTitle:** structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron |
| 77 | c3ogmB_ | Alignment | not modelled | 98.2 | 9 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**coronatine-insensitive protein 1;<br>**PDBTitle:** structure of coi1-ask1 in complex with coronatine and the jaz1 degron |

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| 78 | c1kooD_ | Alignment | not modelled | 98.2 | 20 | **PDB header:**rna binding protein<br>**Chain:** D: **PDB Molecule:**tip associating protein;<br>**PDBTitle:** the crystal structure and mutational analysis of a novel2 rna-binding domain found in the human tap nuclear mrna3 export factor |
| 79 | c2p1nE_ | Alignment | not modelled | 98.0 | 8 | **PDB header:**signaling protein<br>**Chain:** E: **PDB Molecule:**transport inhibitor response 1 protein;<br>**PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase |
| 80 | d1koha1 | Alignment | not modelled | 97.9 | 20 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**L domain-like<br>**Family:**mRNA export factor tap |
| 81 | c1fqvK_ | Alignment | not modelled | 97.3 | 15 | **PDB header:**ligase<br>**Chain:** K: **PDB Molecule:**skp2;<br>**PDBTitle:** insights into scf ubiquitin ligases from the structure of2 the skp1-skp2 complex |
| 82 | c3e2jA_ | Alignment | not modelled | 97.3 | 14 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**atp synthase subunit s, mitochondrial;<br>**PDBTitle:** crystal structure of bovine coupling factor b |
| 83 | d1io0a_ | Alignment | not modelled | 95.7 | 18 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**RNI-like<br>**Family:**28-residue LRR |
| 84 | d1pgva_ | Alignment | not modelled | 95.5 | 12 | **Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)<br>**Superfamily:**RNI-like<br>**Family:**28-residue LRR |