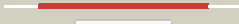

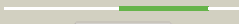
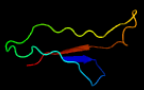

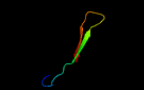



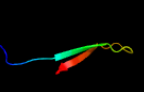







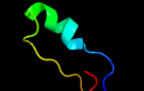






Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1606_(hisl)_1805660_1806007
 Date Fri Aug 2 13:30:19 BST 2019
 Unique Job ID 51541a436d9eec24

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d1zpsa1 |  Alignment |  | 100.0 | 53 | Fold: Hisl-like Superfamily: Hisl-like Family: Hisl-like |
| 2 | d1m4ka2 |  Alignment |  | 59.4 | 11 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains |
| 3 | d1ulva4 |  Alignment |  | 58.9 | 19 | Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like |
| 4 | d1nkra2 |  Alignment |  | 55.6 | 12 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains |
| 5 | d1lf6a2 |  Alignment |  | 50.9 | 8 | Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like |
| 6 | c5lp4A |  Alignment |  | 37.8 | 18 | PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 2 (pbp2); PDBTitle: penicillin-binding protein (pbp2) from helicobacter pylori |
| 7 | c4avrA |  Alignment |  | 31.1 | 24 | PDB header: unknown function Chain: A: PDB Molecule: pa4485; PDBTitle: crystal structure of the hypothetical protein pa4485 from2 pseudomonas aeruginosa |
| 8 | d1j3ea |  Alignment |  | 30.8 | 16 | Fold: Replication modulator SeqA, C-terminal DNA-binding domain Superfamily: Replication modulator SeqA, C-terminal DNA-binding domain Family: Replication modulator SeqA, C-terminal DNA-binding domain |
| 9 | c4mnrA |  Alignment |  | 29.5 | 33 | PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of d,d-transpeptidase domain of peptidoglycan2 glycosyltransferase from eggerthella lenta |
| 10 | c1qmfa |  Alignment |  | 28.8 | 17 | PDB header: cell cycle Chain: A: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex |
| 11 | d1pyya4 |  Alignment |  | 28.6 | 18 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c4ovdA_ | Alignment | | 25.6 | 14 | PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a putative peptidoglycan glycosyltransferase from2 atopobium parvulum dsm 20469 |
| 13 | d2afja1 | Alignment | | 24.3 | 16 | Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: SPRY domain |
| 14 | c3equB_ | Alignment | | 22.4 | 23 | PDB header: biosynthetic protein Chain: B; PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae |
| 15 | c4eskA_ | Alignment | | 21.8 | 20 | PDB header: immune system Chain: A; PDB Molecule: leukocyte-associated immunoglobulin-like receptor 1; PDBTitle: crystal structure of a strand-swapped dimer of mouse leukocyte-2 associated immunoglobulin-like receptor 1 (nysgrc-006047)ig-like3 domain |
| 16 | d2fnja1 | Alignment | | 19.7 | 18 | Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: SPRY domain |
| 17 | d1k25a4 | Alignment | | 19.7 | 24 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 18 | c6bsrA_ | Alignment | | 19.3 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: pbp4 protein; PDBTitle: crystal structure of penicillin-binding protein 4 (pbp4) from2 enterococcus faecalis in the benzylpenicillin bound form. |
| 19 | c4jbfB_ | Alignment | | 18.8 | 23 | PDB header: transferase Chain: B; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of peptidoglycan glycosyltransferase from atopobium2 parvulum dsm 20469. |
| 20 | c5crfA_ | Alignment | | 16.9 | 24 | PDB header: penicillin-binding protein Chain: A; PDB Molecule: penicillin-binding protein 1a; PDBTitle: structure of the penicillin-binding protein pon1 from mycobacterium2 tuberculosis |
| 21 | c5uy7A_ | Alignment | not modelled | 16.9 | 31 | PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a peptidoglycan glycosyltransferase from2 burkholderia ambifaria |
| 22 | c1mwuA_ | Alignment | not modelled | 16.9 | 17 | PDB header: biosynthetic protein Chain: A; PDB Molecule: penicillin-binding protein 2a; PDBTitle: structure of methicillin acyl-penicillin binding protein 2a from2 methicillin resistant staphylococcus aureus strain 27r at 2.60 a3 resolution. |
| 23 | d2od6a1 | Alignment | not modelled | 16.9 | 40 | Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Marine metagenome family DABB1 |
| 24 | d1m4ka1 | Alignment | not modelled | 15.8 | 18 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains |
| 25 | c6g9fA_ | Alignment | not modelled | 15.5 | 29 | PDB header: hydrolase/antibiotic Chain: A; PDB Molecule: peptidoglycan d,d-transpeptidase mrda; PDBTitle: structural basis for the inhibition of e. coli pbp2 |
| 26 | d1nkra1 | Alignment | not modelled | 13.8 | 9 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains |
| 27 | c5dvyA_ | Alignment | not modelled | 13.4 | 23 | PDB header: penicillin-binding protein Chain: A; PDB Molecule: penicillin binding protein 2 prime; PDBTitle: 2.95 angstrom crystal structure of the dimeric form of penicillin2 binding protein 2 prime from enterococcus faecium |
| 28 | d2ahme1 | Alignment | not modelled | 13.0 | 25 | Fold: Coronavirus NSP8-like Superfamily: Coronavirus NSP8-like Family: Coronavirus NSP8-like |
| | | | | | | PDB header: transferase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c3lo7A_ | Alignment | not modelled | 12.3 | 25 | Chain: A; PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis |
| 30 | d2dl2a1 | Alignment | not modelled | 12.2 | 18 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains |
| 31 | c3ue3A_ | Alignment | not modelled | 12.0 | 25 | PDB header: transferase Chain: A; PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3 |
| 32 | c3loeA_ | Alignment | not modelled | 11.7 | 29 | PDB header: antimicrobial protein Chain: A; PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (f28a mutant) |
| 33 | d2cqaa1 | Alignment | not modelled | 11.5 | 11 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain |
| 34 | c2olvA_ | Alignment | not modelled | 11.4 | 18 | PDB header: transferase Chain: A; PDB Molecule: penicillin-binding protein 2; PDBTitle: structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex |
| 35 | c3gnyA_ | Alignment | not modelled | 11.4 | 29 | PDB header: antimicrobial protein Chain: A; PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1) |
| 36 | d1aixb1 | Alignment | not modelled | 11.2 | 27 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III |
| 37 | d1ex4a1 | Alignment | not modelled | 10.7 | 42 | Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase |
| 38 | d2f09a1 | Alignment | not modelled | 10.4 | 14 | Fold: Streptavidin-like Superfamily: YdhA-like Family: YdhA-like |
| 39 | c1ug9A_ | Alignment | not modelled | 10.3 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: glucodextranase; PDBTitle: crystal structure of glucodextranase from arthrobacter globiformis i42 |
| 40 | c5gmkj_ | Alignment | not modelled | 10.2 | 71 | PDB header: rna binding protein/rna Chain: J; PDB Molecule: pre-mrna-splicing factor cwc21; PDBTitle: cryo-em structure of the catalytic step i spliceosome (c complex) at2 3.4 angstrom resolution |
| 41 | c3hj2B_ | Alignment | not modelled | 10.1 | 29 | PDB header: antimicrobial protein Chain: B; PDB Molecule: human neutrophil peptide 1; PDBTitle: crystal structure of covalent dimer of hnp1 |
| 42 | c2ahmG_ | Alignment | not modelled | 9.9 | 25 | PDB header: viral protein, replication Chain: G; PDB Molecule: replicase polyprotein 1ab, heavy chain; PDBTitle: crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer |
| 43 | c5u47A_ | Alignment | not modelled | 9.7 | 17 | PDB header: lipid-binding protein Chain: A; PDB Molecule: penicillin binding protein 2x; PDBTitle: 1.95 angstrom resolution crystal structure of penicillin binding2 protein 2x from streptococcus thermophilus |
| 44 | c3ub0D_ | Alignment | not modelled | 9.7 | 23 | PDB header: replication Chain: D; PDB Molecule: non-structural protein 6, nsp6,; PDBTitle: crystal structure of the nonstructural protein 7 and 8 complex of2 feline coronavirus |
| 45 | d1pjua2 | Alignment | not modelled | 9.6 | 28 | Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors |
| 46 | c2jtdA_ | Alignment | not modelled | 9.4 | 5 | PDB header: cell adhesion Chain: A; PDB Molecule: myomesin-1; PDBTitle: skelemin immunoglobulin c2 like domain 4 |
| 47 | c5ewoA_ | Alignment | not modelled | 9.3 | 22 | PDB header: viral protein Chain: A; PDB Molecule: structural protein; PDBTitle: crystal structure of the human astrovirus 1 capsid protein spike2 domain at 0.95-a resolution |
| 48 | c6ni0A_ | Alignment | not modelled | 9.2 | 21 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from burkholderia2 thailandensis |
| 49 | c3pbna_ | Alignment | not modelled | 9.0 | 17 | PDB header: hydrolase/antibiotic Chain: A; PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of apo pbp3 from pseudomonas aeruginosa |
| 50 | d1ugna2 | Alignment | not modelled | 8.7 | 9 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains |
| 51 | c3dwcC_ | Alignment | not modelled | 8.6 | 18 | PDB header: transferase Chain: C; PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer |
| 52 | c4bjpA_ | Alignment | not modelled | 8.6 | 21 | PDB header: transferase Chain: A; PDB Molecule: penicillin binding protein transpeptidase domain protein; PDBTitle: crystal structure of e. coli penicillin binding protein 3 |
| 53 | d2jnw1 | Alignment | not modelled | 8.6 | 45 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: XPF/Rad1/Mus81 nuclease |
| 54 | c3lo7B_ | Alignment | not modelled | 8.4 | 25 | PDB header: transferase Chain: B; PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis |
| 55 | d1vqqa3 | Alignment | not modelled | 8.4 | 13 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |

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|----|--------------------------|-----------|--------------|-----|----|---|
| 56 | d1rp5a4 | Alignment | not modelled | 8.2 | 24 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 57 | d2a1ia1 | Alignment | not modelled | 8.2 | 45 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: XPF/Rad1/Mus81 nuclease |
| 58 | d2c5wb1 | Alignment | not modelled | 8.2 | 18 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 59 | c5iznH_ | Alignment | not modelled | 8.2 | 19 | PDB header: ribosomal protein Chain: H: PDB Molecule: 50s ribosomal protein l25; PDBTitle: the crystal structure of 50s ribosomal protein l25 from vibrio2 vulnificus cmcp6 |
| 60 | d1wjka_ | Alignment | not modelled | 8.1 | 22 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 61 | d2z3qa1 | Alignment | not modelled | 8.0 | 27 | Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines |
| 62 | c3zg8B_ | Alignment | not modelled | 7.7 | 29 | PDB header: penicillin-binding protein Chain: B: PDB Molecule: penicillin-binding protein 4; PDBTitle: crystal structure of penicillin binding protein 4 from2 listeria monocytogenes in the ampicillin bound form |
| 63 | d1y0ga_ | Alignment | not modelled | 7.7 | 18 | Fold: Streptavidin-like Superfamily: Ycel-like Family: Ycel-like |
| 64 | c4ye5A_ | Alignment | not modelled | 7.6 | 53 | PDB header: penicillin binding protein Chain: A: PDB Molecule: peptidoglycan synthetase penicillin-binding protein 3; PDBTitle: the crystal structure of a peptidoglycan synthetase from2 bifidobacterium adolescentis atcc 15703 |
| 65 | d1v0aa1 | Alignment | not modelled | 7.3 | 8 | Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: CBM11 |
| 66 | d2olua2 | Alignment | not modelled | 7.3 | 12 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 67 | d1lucta2 | Alignment | not modelled | 7.2 | 18 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains |
| 68 | d3b5ha2 | Alignment | not modelled | 7.1 | 26 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains |
| 69 | d1k38a_ | Alignment | not modelled | 7.1 | 30 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 70 | c3vslB_ | Alignment | not modelled | 7.1 | 41 | PDB header: penicillin-binding protein Chain: B: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 (pbp3) from2 methicilin-resistant staphylococcus aureus in the cefotaxime bound3 form. |
| 71 | c1ux6A_ | Alignment | not modelled | 7.0 | 29 | PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-1; PDBTitle: structure of a thrombospondin c-terminal fragment reveals a novel2 calcium core in the type 3 repeats |
| 72 | c4ht4A_ | Alignment | not modelled | 7.0 | 22 | PDB header: hydrolase/dna Chain: A: PDB Molecule: nicking enzyme; PDBTitle: molecular basis of vancomycin resistance transfer in staphylococcus2 aureus |
| 73 | d1ux6a1 | Alignment | not modelled | 6.7 | 29 | Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Thrombospondin C-terminal domain |
| 74 | c3sk7B_ | Alignment | not modelled | 6.6 | 10 | PDB header: replication inhibitor Chain: B: PDB Molecule: protein seqa; PDBTitle: crystal structure of v. cholerae seqa |
| 75 | c3hpeB_ | Alignment | not modelled | 6.6 | 17 | PDB header: transport protein Chain: B: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: crystal structure of ycei (hp1286) from helicobacter pylori |
| 76 | d1tocr1 | Alignment | not modelled | 6.6 | 32 | Fold: BPTI-like Superfamily: BPTI-like Family: Soft tick anticoagulant proteins |
| 77 | c3ukwC_ | Alignment | not modelled | 6.5 | 43 | PDB header: protein transport/inhibitor Chain: C: PDB Molecule: bimax1 peptide; PDBTitle: mouse importin alpha: bimax1 peptide complex |
| 78 | c5kouB_ | Alignment | not modelled | 6.5 | 11 | PDB header: viral protein Chain: B: PDB Molecule: capsid polyprotein vp25; PDBTitle: crystal structure of the human astrovirus 2 capsid protein spike2 domain at 1.87-a resolution |
| 79 | d2dlxa1 | Alignment | not modelled | 6.4 | 6 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: UAS domain |
| 80 | c5lj3R_ | Alignment | not modelled | 6.4 | 71 | PDB header: splicing Chain: R: PDB Molecule: pre-mrna-splicing factor cwc21; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching |
| 81 | d1jlxal | Alignment | not modelled | 6.3 | 16 | Fold: beta-Trefoil Superfamily: Agglutinin Family: Agglutinin |
| 82 | c3oc2A_ | Alignment | not modelled | 6.2 | 15 | PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 3; |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 82 | c3uc2A | Alignment | not modelled | 6.3 | 13 | PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa PDB header: cell adhesion |
| 83 | c1yo8A | Alignment | not modelled | 6.3 | 29 | Chain: A; PDB Molecule: thrombospondin-2; PDBTitle: structure of the c-terminal domain of human thrombospondin-2 |
| 84 | c2wadB | Alignment | not modelled | 6.2 | 35 | PDB header: peptide binding protein Chain: B; PDB Molecule: penicillin-binding protein 2b; PDBTitle: penicillin-binding protein 2b (pbp-2b) from streptococcus2 pneumoniae (strain 5204) |
| 85 | c1jlxB | Alignment | not modelled | 6.1 | 11 | PDB header: lectin Chain: B; PDB Molecule: agglutinin; PDBTitle: agglutinin in complex with t-disaccharide |
| 86 | c5ounA | Alignment | not modelled | 5.9 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: rvvb-like protein 2; PDBTitle: nmr solution structure of the external dii domain of rvb2 from2 saccharomyces cerevisiae |
| 87 | c3fmtF | Alignment | not modelled | 5.9 | 13 | PDB header: replication inhibitor/dna Chain: F; PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna |
| 88 | d1ihwa | Alignment | not modelled | 5.9 | 42 | Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase |
| 89 | c3fbyC | Alignment | not modelled | 5.8 | 21 | PDB header: cell adhesion Chain: C; PDB Molecule: cartilage oligomeric matrix protein; PDBTitle: the crystal structure of the signature domain of cartilage oligomeric2 matrix protein. |
| 90 | d2dypd2 | Alignment | not modelled | 5.8 | 18 | Fold: immunoglobulin-like beta-sandwich Superfamily: immunoglobulin Family: l set domains |
| 91 | c2mt7A | Alignment | not modelled | 5.7 | 40 | PDB header: toxin Chain: A; PDB Molecule: hs1a; PDBTitle: solution structure of spider-venom peptide hs1a |
| 92 | c6bk8K | Alignment | not modelled | 5.5 | 71 | PDB header: rna binding protein Chain: K; PDB Molecule: pre-mrna-splicing factor cwc21; PDBTitle: s. cerevisiae spliceosomal post-catalytic p complex |
| 93 | c1pmdA | Alignment | not modelled | 5.4 | 20 | PDB header: peptidoglycan synthesis Chain: A; PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x) |
| 94 | c2z56B | Alignment | not modelled | 5.3 | 36 | PDB header: hydrolase Chain: B; PDB Molecule: tk-subtilisin; PDBTitle: crystal structure of g56s-propeptide:s324a-subtilisin complex |
| 95 | c2bcxB | Alignment | not modelled | 5.3 | 33 | PDB header: calcium binding protein Chain: B; PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of calmodulin in complex with a ryanodine receptor2 peptide |
| 96 | d1dfup | Alignment | not modelled | 5.3 | 6 | Fold: Ribosomal protein L25-like Superfamily: Ribosomal protein L25-like Family: Ribosomal protein L25-like |
| 97 | c5ov3B | Alignment | not modelled | 5.2 | 14 | PDB header: structural protein Chain: B; PDB Molecule: retinoblastoma-binding protein 5; PDBTitle: structure of the rbbp5 beta-propeller domain |
| 98 | c4fqjA | Alignment | not modelled | 5.2 | 33 | PDB header: viral protein/immune system Chain: A; PDB Molecule: hemagglutinin; PDBTitle: influenza b/florida/4/2006 hemagglutinin fab cr8071 complex |
| 99 | c6bduA | Alignment | not modelled | 5.1 | 44 | PDB header: dna binding protein Chain: A; PDB Molecule: dna repair protein ppra; PDBTitle: crystal structure of ppra from deinococcus radiodurans |