



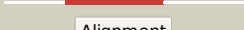

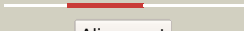







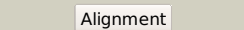

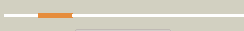



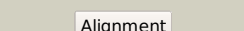

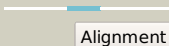
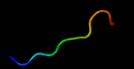
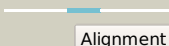

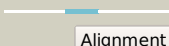
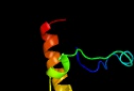
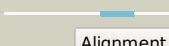
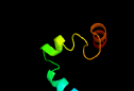
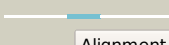

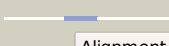

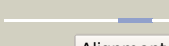

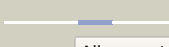



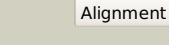
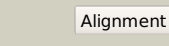
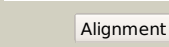
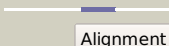


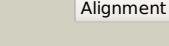
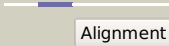


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3795_(embB)_4246692_4249988 |
| Date | Fri Aug 9 18:20:50 BST 2019 |
| Unique Job ID | ad895cb3fa035f93 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c3ptyA_ |  Alignment |  | 100.0 | 51 | PDB header: transferase Chain: A; PDB Molecule: arabinosyltransferase c; PDBTitle: crystal structure of the c-terminal extracellular domain of2 mycobacterium tuberculosis embc |
| 2 | c3bywB_ |  Alignment |  | 100.0 | 30 | PDB header: transferase Chain: B; PDB Molecule: putative arabinofuranosyltransferase; PDBTitle: crystal structure of the c-terminal extracellular domain of2 arabinofuranosyltransferase from corynebacterium diphtheriae |
| 3 | c5f15A_ |  Alignment |  | 99.3 | 13 | PDB header: transferase Chain: A; PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate |
| 4 | c3rceA_ |  Alignment |  | 98.4 | 11 | PDB header: transferase/peptide Chain: A; PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb |
| 5 | c3wajA_ |  Alignment |  | 96.6 | 15 | PDB header: transferase Chain: A; PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate |
| 6 | c6p2rB_ |  Alignment |  | 92.3 | 13 | PDB header: transferase Chain: B; PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor |
| 7 | c6p25A_ |  Alignment |  | 88.2 | 12 | PDB header: transferase Chain: A; PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor |
| 8 | c6eznF_ |  Alignment |  | 83.3 | 11 | PDB header: membrane protein Chain: F; PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex |
| 9 | c6btmD_ |  Alignment |  | 82.3 | 22 | PDB header: membrane protein Chain: D; PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type) |
| 10 | c6f0kD_ |  Alignment |  | 66.8 | 15 | PDB header: membrane protein Chain: D; PDB Molecule: actd; PDBTitle: alternative complex iii |
| 11 | c2lopA_ |  Alignment |  | 44.6 | 12 | PDB header: membrane protein Chain: A; PDB Molecule: transmembrane protein 14a; PDBTitle: backbone structure of human membrane protein tmem14a |

| | | | | | | |
|----|-------------------------|---|---|------|----|--|
| 12 | c4rrfD |  Alignment |  | 38.2 | 45 | PDB header: ligase Chain: D: PDB Molecule: threonine--trna ligase; PDBTitle: editing domain of threonyl-trna synthetase from methanococcus2 jannaschii with l-ser3aa |
| 13 | c2hl2A |  Alignment |  | 36.4 | 45 | PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate |
| 14 | c4rlrA |  Alignment |  | 32.9 | 26 | PDB header: electron transport Chain: A: PDB Molecule: cytochrome c, 1 heme-binding site; PDBTitle: structure of monoheme cytochrome pchh from geobacter sulfurreducens |
| 15 | c5zr1F |  Alignment |  | 32.7 | 17 | PDB header: dna binding protein/dna Chain: F: PDB Molecule: origin recognition complex subunit 6; PDBTitle: saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element |
| 16 | c4rrcA |  Alignment |  | 30.6 | 45 | PDB header: ligase Chain: A: PDB Molecule: probable threonine--trna ligase 2; PDBTitle: n-terminal editing domain of threonyl-trna synthetase from aeropyrum2 pernix with l-thr3aa (snapshot 3) |
| 17 | c5x5iC |  Alignment |  | 28.8 | 17 | PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator rcda; PDBTitle: the x-ray crystal structure of a tetr family transcription regulator2 rcda involved in the regulation of biofilm formation in escherichia3 coli |
| 18 | c3jd8A |  Alignment |  | 28.0 | 25 | PDB header: membrane protein Chain: A: PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom |
| 19 | d1gmnbl |  Alignment |  | 22.5 | 50 | Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Hairpin loop containing domain |
| 20 | d1iyjb3 |  Alignment |  | 21.3 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB |
| 21 | c5j7dG |  Alignment | not modelled | 21.2 | 9 | PDB header: de novo protein Chain: G: PDB Molecule: designed thioredoxin df106; PDBTitle: computationally designed thioredoxin df106 |
| 22 | c1rwuA |  Alignment | not modelled | 20.3 | 33 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli |
| 23 | d1rwua |  Alignment | not modelled | 20.3 | 33 | Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like |
| 24 | c2losA |  Alignment | not modelled | 18.1 | 12 | PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 14c; PDBTitle: backbone structure of human membrane protein tmem14c |
| 25 | c5v2dA |  Alignment | not modelled | 18.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: dioxygenase; PDBTitle: crystal structure of pseudomonas brassicacearum lignostilbene2 dioxygenase |
| 26 | c1hymB |  Alignment | not modelled | 17.8 | 32 | PDB header: hydrolase (serine proteinase) Chain: B: PDB Molecule: hydrolyzed cucurbita maxima trypsin inhibitor v; PDBTitle: hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr structure) |
| 27 | c4gicB |  Alignment | not modelled | 17.7 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus |
| 28 | c6fhtB |  Alignment | not modelled | 17.7 | 22 | PDB header: lyase Chain: B: PDB Molecule: bacteriophytochrome,adenylate cyclase; PDBTitle: crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form |

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|----|--------------------------|-----------|--------------|------|----|--|
| 29 | c6dmoA_ | Alignment | not modelled | 16.8 | 22 | PDB header: protein binding Chain: A: PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l |
| 30 | c5ovyA_ | Alignment | not modelled | 16.7 | 18 | PDB header: dna binding protein Chain: A: PDB Molecule: putative transcriptional regulator, tetr family; PDBTitle: crystal structure of mab 4384 tetr |
| 31 | c1emzA_ | Alignment | not modelled | 16.2 | 33 | PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein e1; PDBTitle: solution structure of fragment (350-370) of the2 transmembrane domain of hepatitis c envelope glycoprotein3 e1 |
| 32 | c2mc7A_ | Alignment | not modelled | 15.7 | 25 | PDB header: membrane protein Chain: A: PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgr |
| 33 | c5j54A_ | Alignment | not modelled | 15.5 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: carotenoid oxygenase; PDBTitle: the structure and mechanism of nov1, a resveratrol-cleaving2 dioxygenase |
| 34 | c2m20B_ | Alignment | not modelled | 14.6 | 26 | PDB header: signaling protein Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure. |
| 35 | c5u90A_ | Alignment | not modelled | 14.4 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: carotenoid oxygenase 1; PDBTitle: crystal structure of co-cao1 in complex with resveratrol |
| 36 | d1rc2a_ | Alignment | not modelled | 14.3 | 13 | Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like |
| 37 | c6ithA_ | Alignment | not modelled | 14.1 | 35 | PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles |
| 38 | c2y0nE_ | Alignment | not modelled | 13.5 | 60 | PDB header: transcription Chain: E: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3 |
| 39 | c2pptA_ | Alignment | not modelled | 13.5 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2 |
| 40 | c3zqiB_ | Alignment | not modelled | 13.3 | 14 | PDB header: transcription Chain: B: PDB Molecule: tetracycline repressor protein class b from transposon PDBTitle: structure of tetracycline repressor in complex with inducer peptide-2 tip2 |
| 41 | c1t0jA_ | Alignment | not modelled | 13.1 | 7 | PDB header: signaling protein Chain: A: PDB Molecule: voltage-gated calcium channel subunit beta2a; PDBTitle: crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit |
| 42 | c4z9cA_ | Alignment | not modelled | 12.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: pertussis toxin-like subunit arta; PDBTitle: ecpltab oxidized |
| 43 | c2y0nG_ | Alignment | not modelled | 12.9 | 75 | PDB header: transcription Chain: G: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3 |
| 44 | c2y0nH_ | Alignment | not modelled | 12.9 | 75 | PDB header: transcription Chain: H: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3 |
| 45 | c4s21B_ | Alignment | not modelled | 12.4 | 19 | PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome (light-regulated signal transduction PDBTitle: crystal structure of the photosensory core module of2 bacteriophytochrome rpa3015 from r. palustris |
| 46 | c1bdsA_ | Alignment | not modelled | 12.3 | 45 | PDB header: anti-hypertensive, anti-viral protein Chain: A: PDB Molecule: bds-i; PDBTitle: determination of the three-dimensional solution structure of the2 antihypertensive and antiviral protein bds-i from the sea anemone3 anemonia sulcata. a study using nuclear magnetic resonance and hybrid4 distance geometry-dynamical simulated annealing |
| 47 | d1bdsa_ | Alignment | not modelled | 12.3 | 45 | Fold: Defensin-like Superfamily: Defensin-like Family: Defensin |
| 48 | c4huqS_ | Alignment | not modelled | 12.0 | 22 | PDB header: hydrolase Chain: S: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a transporter |
| 49 | c4ruvA_ | Alignment | not modelled | 11.3 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325 |
| 50 | d1miau3 | Alignment | not modelled | 11.0 | 29 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB |
| 51 | c2zopA_ | Alignment | not modelled | 11.0 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein tthb164; PDBTitle: x-ray crystal structure of a crispr-associated cmr5 family2 protein from thermus thermophilus hb8 |
| 52 | c3fsnA_ | Alignment | not modelled | 11.0 | 36 | PDB header: isomerase Chain: A: PDB Molecule: retinal pigment epithelium-specific 65 kda protein; PDBTitle: crystal structure of rpe65 at 2.14 angstrom resolution |
| 53 | d1losna_ | Alignment | not modelled | 11.0 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases |

| | | | | | | Family:Nucleotide and nucleoside kinases |
|----|-------------------------|-----------|--------------|------|----|---|
| 54 | c2lonA | Alignment | not modelled | 10.6 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein higd1b |
| 55 | c1miuA | Alignment | not modelled | 10.5 | 23 | PDB header: gene regulation/antitumor protein Chain: A: PDB Molecule: breast cancer type 2 susceptibility protein; PDBTitle: structure of a brca2-dss1 complex |
| 56 | d2joqa1 | Alignment | not modelled | 10.5 | 22 | Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: HP0495-like |
| 57 | c1w8jD | Alignment | not modelled | 10.2 | 28 | PDB header: motor protein Chain: D: PDB Molecule: myosin va; PDBTitle: crystal structure of myosin v motor domain -2 nucleotide-free |
| 58 | d1fpoa1 | Alignment | not modelled | 10.2 | 42 | Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain |
| 59 | c5wcoC | Alignment | not modelled | 10.2 | 50 | PDB header: viral protein Chain: C: PDB Molecule: ns2; PDBTitle: matrix protein (m1) of infectious salmon anaemia virus |
| 60 | c6d6vE | Alignment | not modelled | 10.2 | 33 | PDB header: replication Chain: E: PDB Molecule: telomerase holoenzyme teb2 subunit; PDBTitle: cryoem structure of tetrahymena telomerase with telomeric dna at 4.82 angstrom resolution |
| 61 | c1iyjB | Alignment | not modelled | 10.1 | 19 | PDB header: gene regulation/antitumor protein Chain: B: PDB Molecule: breast cancer susceptibility; PDBTitle: structure of a brca2-dss1 complex |
| 62 | c4wkkA | Alignment | not modelled | 10.0 | 19 | PDB header: signaling protein Chain: A: PDB Molecule: bacteriophytochrome protein; PDBTitle: the photosensory module (pas-gaf-phy) of the bacterial phytochrome2 agp1 (atbphp1) in the pr form, chromophore modelled with an exocyclic3 double bond at pyrrole ring a. |
| 63 | c5i0hA | Alignment | not modelled | 10.0 | 17 | PDB header: motor protein Chain: A: PDB Molecule: unconventional myosin-x; PDBTitle: crystal structure of myosin x motor domain in pre-powerstroke state |
| 64 | c6ir8A | Alignment | not modelled | 9.9 | 22 | PDB header: transcription/dna Chain: A: PDB Molecule: oswrky45; PDBTitle: rice wrky/dna complex |
| 65 | d1w96a1 | Alignment | not modelled | 9.7 | 12 | Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like |
| 66 | c4gkfA | Alignment | not modelled | 9.7 | 18 | PDB header: unknown function Chain: A: PDB Molecule: crispr system cmr subunit cmr5; PDBTitle: crystal structure and characterization of cmr5 protein from pyrococcus2 furiosus |
| 67 | c4zg4E | Alignment | not modelled | 9.5 | 29 | PDB header: motor protein Chain: E: PDB Molecule: premyosin-vc; PDBTitle: myosin vc pre-powerstroke |
| 68 | c4rfuB | Alignment | not modelled | 9.5 | 27 | PDB header: viral protein Chain: B: PDB Molecule: coat protein; PDBTitle: crystal structure of truncated p-domain from grouper nervous necrosis2 virus capsid protein at 1.2a |
| 69 | c2biwC | Alignment | not modelled | 9.5 | 37 | PDB header: oxidoreductase Chain: C: PDB Molecule: apocarotenoid-cleaving oxygenase; PDBTitle: crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme |
| 70 | d1y0ja1 | Alignment | not modelled | 9.4 | 23 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1 |
| 71 | c2q24A | Alignment | not modelled | 9.4 | 19 | PDB header: transcription Chain: A: PDB Molecule: putative tetr family transcriptional regulator; PDBTitle: crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor |
| 72 | c2k58B | Alignment | not modelled | 9.3 | 18 | PDB header: transport protein Chain: B: PDB Molecule: neuronal acetylcholine receptor subunit beta-2; PDBTitle: nmr structures of the first transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit |
| 73 | c2n2aA | Alignment | not modelled | 9.3 | 15 | PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: spatial structure of her2/erbb2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains |
| 74 | c3etoB | Alignment | not modelled | 9.2 | 20 | PDB header: signaling protein Chain: B: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: 2 angstrom xray structure of the notch1 negative regulatory region2 (nrr) |
| 75 | c2i9hA | Alignment | not modelled | 9.1 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin i; PDBTitle: nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1) |
| 76 | c5dynA | Alignment | not modelled | 9.1 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: putative peptidase; PDBTitle: b. fragilis cysteine protease |
| 77 | c2lx0A | Alignment | not modelled | 9.0 | 31 | PDB header: membrane protein Chain: A: PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles |
| 78 | c6m9tA | Alignment | not modelled | 9.0 | 40 | PDB header: membrane protein Chain: A: PDB Molecule: prostaglandin e2 receptor ep3 subtype, endolysin chimera; PDBTitle: crystal structure of ep3 receptor bound to misoprostol-fa |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 79 | c1ldaA | Alignment | not modelled | 8.9 | 17 | PDB header: transport protein Chain: A: PDB Molecule: glycerol uptake facilitator protein; PDBTitle: crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol |
| 80 | d1fx8a | Alignment | not modelled | 8.9 | 17 | Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like |
| 81 | c3npeA | Alignment | not modelled | 8.9 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: 9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; PDBTitle: structure of vp14 in complex with oxygen |
| 82 | c6ojrA | Alignment | not modelled | 8.9 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: lignostilbene-alpha,beta-dioxygenase isozyme i; PDBTitle: crystal structure of sphingomonas paucimobilis tmy1009 apo-lsda |
| 83 | c3emlA | Alignment | not modelled | 8.9 | 20 | PDB header: membrane protein, receptor Chain: A: PDB Molecule: human adenosine a2a receptor/t4 lysozyme chimera; PDBTitle: the 2.6 a crystal structure of a human a2a adenosine receptor bound to2 zm241385. |
| 84 | c3x27C | Alignment | not modelled | 8.8 | 13 | PDB header: lyase Chain: C: PDB Molecule: cucumopine synthase; PDBTitle: structure of mccb in complex with tryptophan |
| 85 | c4ip8B | Alignment | not modelled | 8.7 | 47 | PDB header: protein binding Chain: B: PDB Molecule: serum amyloid a-1 protein; PDBTitle: structure of human serum amyloid a1 |
| 86 | d1oedc | Alignment | not modelled | 8.7 | 18 | Fold: Neurotransmitter-gated ion-channel transmembrane pore Superfamily: Neurotransmitter-gated ion-channel transmembrane pore Family: Neurotransmitter-gated ion-channel transmembrane pore |
| 87 | c1fgeA | Alignment | not modelled | 8.7 | 57 | PDB header: blood coagulation inhibitor Chain: A: PDB Molecule: thrombomodulin; PDBTitle: epidermal growth factor (egf) subdomain of human2 thrombomodulin (nmr, 14 structures) |
| 88 | d1p6xa | Alignment | not modelled | 8.4 | 45 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 89 | d2oeba1 | Alignment | not modelled | 8.4 | 17 | Fold: ATPD N-terminal domain-like Superfamily: AF1862-like Family: Cas Cmr5-like |
| 90 | c3ctwB | Alignment | not modelled | 8.4 | 30 | PDB header: protein binding Chain: B: PDB Molecule: rcda; PDBTitle: crystal structure of rcda from caulobacter crescentus cb15 |
| 91 | c4xesA | Alignment | not modelled | 8.3 | 9 | PDB header: signaling protein, hydrolase Chain: A: PDB Molecule: neurotensin receptor type 1, endolysin chimera; PDBTitle: structure of active-like neurotensin receptor |
| 92 | c2mn9A | Alignment | not modelled | 8.3 | 35 | PDB header: antimicrobial protein Chain: A: PDB Molecule: maculatin g15; PDBTitle: peptoid analogue of maculatin g15 - peptoid trans-nleu at position 13 |
| 93 | c2mn8A | Alignment | not modelled | 8.3 | 35 | PDB header: antimicrobial protein Chain: A: PDB Molecule: maculatin g15; PDBTitle: nmr structure of a peptoid analogue of maculatin g15 containing cis-2 nleu at position 13 |
| 94 | c2b5fD | Alignment | not modelled | 8.3 | 12 | PDB header: transport protein,membrane protein Chain: D: PDB Molecule: aquaporin; PDBTitle: crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution |
| 95 | c6e59A | Alignment | not modelled | 8.3 | 30 | PDB header: signaling protein Chain: A: PDB Molecule: substance-p receptor, glga glycogen synthase, substance-p PDBTitle: crystal structure of the human nk1 tachykinin receptor |
| 96 | c6cfwE | Alignment | not modelled | 8.2 | 8 | PDB header: membrane protein Chain: E: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase |
| 97 | c6iiuA | Alignment | not modelled | 8.2 | 30 | PDB header: signaling protein Chain: A: PDB Molecule: soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, PDBTitle: crystal structure of the human thromboxane a2 receptor bound to2 ramatroban |
| 98 | d1gpqa | Alignment | not modelled | 8.2 | 11 | Fold: Inhibitor of vertebrate lysozyme, lvy Superfamily: Inhibitor of vertebrate lysozyme, lvy Family: Inhibitor of vertebrate lysozyme, lvy |
| 99 | c2kcyA | Alignment | not modelled | 8.1 | 25 | PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8e; PDBTitle: solution structure of ribosomal protein s8e from2 methanothermobacter thermautotrophicus,3 northeaststructural genomics consortium (nseg) target tr71d |