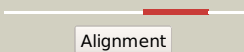

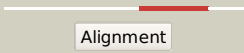



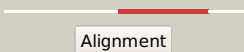

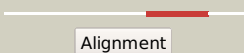









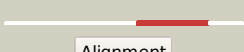





Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3786c_(-)_4232552_4233775 |
| Date | Fri Aug 9 18:20:49 BST 2019 |
| Unique Job ID | e2bd96cfbd56284a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3sluB_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315 |
| 2 | c2gu1A_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae |
| 3 | c2hsiB_ |  Alignment |  | 100.0 | 26 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium |
| 4 | c4rnzA_ |  Alignment |  | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd3 from the hexagonal crystal |
| 5 | d1qwya_ |  Alignment |  | 100.0 | 26 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM |
| 6 | c4lxcA_ |  Alignment |  | 100.0 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: lysostaphin; PDBTitle: the antimicrobial peptidase lysostaphin from staphylococcus simulans |
| 7 | c3nyvA_ |  Alignment |  | 100.0 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: putative glycyl-glycine endopeptidase lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution |
| 8 | c5j1mD_ |  Alignment |  | 100.0 | 25 | PDB header: hydrolase Chain: D: PDB Molecule: tox-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer ii |
| 9 | c4bh5B_ |  Alignment |  | 100.0 | 21 | PDB header: cell cycle Chain: B: PDB Molecule: murein hydrolase activator envc; PDBTitle: lytm domain of envc, an activator of cell wall amidases in2 escherichia coli |
| 10 | c5kvpA_ |  Alignment |  | 100.0 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: zoocin a endopeptidase; PDBTitle: solution structure of the catalytic domain of zoocin a |
| 11 | c5kqbA_ |  Alignment |  | 100.0 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: peptidase m23; PDBTitle: identification and structural characterization of lytu |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | c5j1A_ | Alignment | | 100.0 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer i |
| 13 | c2b44A_ | Alignment | | 100.0 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form |
| 14 | c4qpB_ | Alignment | | 100.0 | 28 | PDB header: hydrolase Chain: B: PDB Molecule: lysostaphin; PDBTitle: catalytic domain of the antimicrobial peptidase lysostaphin from2 staphylococcus simulans crystallized in the absence of phosphate |
| 15 | c3tufB_ | Alignment | | 100.0 | 22 | PDB header: signaling protein Chain: B: PDB Molecule: stage ii sporulation protein q; PDBTitle: structure of the spoiiiq-spoiiiah pore forming complex. |
| 16 | c3uz0D_ | Alignment | | 100.0 | 21 | PDB header: transport protein Chain: D: PDB Molecule: stage ii sporulation protein q; PDBTitle: crystal structure of spoiiiah and spoiiq complex |
| 17 | c5qt1A_ | Alignment | | 100.0 | 25 | PDB header: choline-binding protein Chain: A: PDB Molecule: choline binding protein a; PDBTitle: crystal structure of cbpa from l. salivarius ren |
| 18 | c3it5B_ | Alignment | | 99.9 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa |
| 19 | c5b0hB_ | Alignment | | 99.9 | 19 | PDB header: metal binding protein Chain: B: PDB Molecule: leukocyte cell-derived chemotaxin-2; PDBTitle: crystal structure of human leukocyte cell-derived chemotaxin 2 |
| 20 | c5tz8C_ | Alignment | | 99.9 | 19 | PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars |
| 21 | c3flYC_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus |
| 22 | c3ckvA_ | Alignment | not modelled | 99.9 | 26 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein |
| 23 | c3csqC_ | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail |
| 24 | c5mm1A_ | Alignment | not modelled | 99.9 | 18 | PDB header: membrane protein Chain: A: PDB Molecule: dolichol monophosphate mannose synthase; PDBTitle: dolichyl phosphate mannose synthase in complex with gdp and dolichyl2 phosphate mannose |
| 25 | d1omza_ | Alignment | not modelled | 99.9 | 13 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin |
| 26 | c5ekeB_ | Alignment | not modelled | 99.9 | 13 | PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase slI0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant) |
| 27 | c2z86D_ | Alignment | not modelled | 99.9 | 23 | PDB header: transferase Chain: D: PDB Molecule: chondroitin synthase; PDBTitle: crystal structure of chondroitin polymerase from escherichia coli2 strain k4 (k4cp) complexed with udp-glcua and udp |
| 28 | d1xhba2 | Alignment | not modelled | 99.9 | 15 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal |

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|----|-------------------------|-----------|--------------|------|---|
| | | | | | domain |
| 29 | c6h4mA_ | Alignment | not modelled | 99.9 | 15 PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop |
| 30 | c1omxB_ | Alignment | not modelled | 99.8 | 13 PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2) |
| 31 | c2ffuA_ | Alignment | not modelled | 99.8 | 15 PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2 |
| 32 | c1xhbA_ | Alignment | not modelled | 99.8 | 17 PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1 |
| 33 | c2d7iA_ | Alignment | not modelled | 99.8 | 18 PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+ |
| 34 | c6iwqE_ | Alignment | not modelled | 99.8 | 19 PDB header: transferase Chain: E: PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+ |
| 35 | d1qq8a_ | Alignment | not modelled | 99.8 | 13 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA |
| 36 | c6e4rB_ | Alignment | not modelled | 99.8 | 14 PDB header: transferase Chain: B: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b |
| 37 | c5nqaA_ | Alignment | not modelled | 99.8 | 14 PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3 |
| 38 | c4fixA_ | Alignment | not modelled | 99.8 | 17 PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2 |
| 39 | c5heaA_ | Alignment | not modelled | 99.8 | 20 PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer |
| 40 | c3bcvA_ | Alignment | not modelled | 99.7 | 15 PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis |
| 41 | c5z8bB_ | Alignment | not modelled | 99.7 | 16 PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form |
| 42 | c4hg6A_ | Alignment | not modelled | 99.6 | 17 PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate |
| 43 | c3zf8A_ | Alignment | not modelled | 99.6 | 12 PDB header: transferase Chain: A: PDB Molecule: mannan polymerase complexes subunit mnn9; PDBTitle: crystal structure of saccharomyces cerevisiae mnn9 in2 complex with gdp and mn. |
| 44 | c2qgiA_ | Alignment | not modelled | 99.5 | 10 PDB header: transferase Chain: A: PDB Molecule: atp synthase subunits region of 6; PDBTitle: the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus |
| 45 | c5ggfC_ | Alignment | not modelled | 99.4 | 18 PDB header: transferase, sugar binding protein Chain: C: PDB Molecule: protein o-linked-mannose beta-1,2-n- PDBTitle: crystal structure of human protein o-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii |
| 46 | c6p61D_ | Alignment | not modelled | 99.4 | 19 PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197) |
| 47 | d2bo4a1 | Alignment | not modelled | 98.9 | 11 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like |
| 48 | c6fxyA_ | Alignment | not modelled | 98.2 | 13 PDB header: transferase Chain: A: PDB Molecule: procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; PDBTitle: crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long-wavelength3 s-sad |
| 49 | d1fo8a_ | Alignment | not modelled | 97.7 | 16 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I |
| 50 | c4irqB_ | Alignment | not modelled | 97.3 | 14 PDB header: transferase Chain: B: PDB Molecule: beta-1,4-galactosyltransferase 7; PDBTitle: crystal structure of catalytic domain of human beta1,2 4galactosyltransferase 7 in closed conformation in complex with3 manganese and udp |
| 51 | c5vcmA_ | Alignment | not modelled | 97.0 | 18 PDB header: transferase Chain: A: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n- PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate |

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|----|-------------------------|-----------|--------------|------|----|--|
| 52 | c2px7A_ | Alignment | not modelled | 96.5 | 13 | cytidyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8 |
| 53 | d2gpra_ | Alignment | not modelled | 96.3 | 19 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 54 | d2f3ga_ | Alignment | not modelled | 96.2 | 18 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 55 | d1glaf_ | Alignment | not modelled | 96.2 | 18 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 56 | d1gpra_ | Alignment | not modelled | 96.0 | 16 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 57 | d1pzta_ | Alignment | not modelled | 95.9 | 21 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1) |
| 58 | c2lmcB_ | Alignment | not modelled | 95.9 | 24 | PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex |
| 59 | d1vpaa_ | Alignment | not modelled | 95.7 | 9 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase |
| 60 | c2wvma_ | Alignment | not modelled | 95.7 | 19 | PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii) |
| 61 | c3okrC_ | Alignment | not modelled | 95.6 | 18 | PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) |
| 62 | d1vh3a_ | Alignment | not modelled | 95.5 | 7 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase |
| 63 | c2wawA_ | Alignment | not modelled | 95.3 | 12 | PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1 |
| 64 | d1ci3m2 | Alignment | not modelled | 95.2 | 31 | Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain |
| 65 | c5ddtA_ | Alignment | not modelled | 95.0 | 11 | PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i |
| 66 | d1vgwa_ | Alignment | not modelled | 94.8 | 13 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase |
| 67 | c2zu8A_ | Alignment | not modelled | 94.8 | 12 | PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii |
| 68 | c1w57A_ | Alignment | not modelled | 94.7 | 14 | PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn |
| 69 | d1i52a_ | Alignment | not modelled | 94.4 | 15 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase |
| 70 | d1e2wa2 | Alignment | not modelled | 94.1 | 19 | Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain |
| 71 | c2aukA_ | Alignment | not modelled | 93.7 | 13 | PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert |
| 72 | c4kt7A_ | Alignment | not modelled | 93.4 | 16 | PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548 |
| 73 | c6oewB_ | Alignment | not modelled | 93.3 | 14 | PDB header: transferase Chain: B: PDB Molecule: cytidyltransferase; PDBTitle: structure of a cytidyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197) |
| 74 | c4ys8B_ | Alignment | not modelled | 93.2 | 17 | PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) from burkholderia thailandensis |
| 75 | c1e2vB_ | Alignment | not modelled | 92.9 | 21 | PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii |
| 76 | c4iqzD_ | Alignment | not modelled | 92.8 | 27 | PDB header: unknown function Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: the crystal structure of a large insert in rna polymerase (rpoC)2 subunit from e. coli PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 77 | c3oamD_ | Alignment | not modelled | 92.6 | 10 | cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae |
| 78 | c4cgkA_ | Alignment | not modelled | 92.3 | 9 | PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus2 pneumoniae |
| 79 | c1ctmA_ | Alignment | not modelled | 92.3 | 19 | PDB header: electron transport(cytochrome) Chain: A: PDB Molecule: cytochrome f; PDBTitle: crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation |
| 80 | d1w77a1 | Alignment | not modelled | 92.3 | 13 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase |
| 81 | d1brwa3 | Alignment | not modelled | 91.1 | 27 | Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain |
| 82 | c1q90A_ | Alignment | not modelled | 90.9 | 20 | PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastoquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii |
| 83 | c3d5nB_ | Alignment | not modelled | 90.4 | 11 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from sulfolobus2 solfataricus. nesg target ssr125. |
| 84 | d1dcza_ | Alignment | not modelled | 90.2 | 22 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 85 | c2vshB_ | Alignment | not modelled | 90.1 | 13 | PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae |
| 86 | c2jxmB_ | Alignment | not modelled | 89.7 | 29 | PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex |
| 87 | c2kccA_ | Alignment | not modelled | 89.4 | 11 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2 |
| 88 | c2ejgD_ | Alignment | not modelled | 89.1 | 22 | PDB header: ligase Chain: D: PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3 |
| 89 | d2tpta3 | Alignment | not modelled | 88.4 | 25 | Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain |
| 90 | c3okrA_ | Alignment | not modelled | 87.7 | 17 | PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) |
| 91 | c1tu2B_ | Alignment | not modelled | 87.0 | 33 | PDB header: electron transport Chain: B: PDB Molecule: apocytochrome f; PDBTitle: the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures |
| 92 | c6ifdD_ | Alignment | not modelled | 86.6 | 10 | PDB header: sugar binding protein Chain: D: PDB Molecule: cmp-n-acetylneuraminate synthetase; PDBTitle: crystal structure of cmp-n-acetylneuraminate synthetase from vibrio2 cholerae in complex with cdp and mg2+. |
| 93 | d1uoua3 | Alignment | not modelled | 86.1 | 20 | Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain |
| 94 | c4xwiA_ | Alignment | not modelled | 85.0 | 10 | PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa |
| 95 | c5c22A_ | Alignment | not modelled | 84.8 | 17 | PDB header: protein transport Chain: A: PDB Molecule: chromosomal hemolysin d; PDBTitle: crystal structure of zn-bound hlyd from e. coli |
| 96 | c3tw6B_ | Alignment | not modelled | 84.7 | 19 | PDB header: ligase/activator Chain: B: PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a |
| 97 | c4y7uA_ | Alignment | not modelled | 84.4 | 15 | PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru |
| 98 | c5xu0B_ | Alignment | not modelled | 84.4 | 26 | PDB header: transport protein Chain: B: PDB Molecule: membrane-fusion protein; PDBTitle: structure of the membrane fusion protein spr0693 from streptococcus2 pneumoniae r6 |
| 99 | c3polA_ | Alignment | not modelled | 84.4 | 13 | PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii. |
| 100 | d1tu2b2 | Alignment | not modelled | 83.7 | 31 | Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain |
| | | | | | | PDB header: transferase Chain: B: PDB Molecule: putative 2-c-methyl-d-erythritol 4- |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 101 | c3f1cB_ | Alignment | not modelled | 83.4 | 11 | phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from listeria monocytogenes |
| 102 | c2j0fC_ | Alignment | not modelled | 83.2 | 20 | PDB header: transferase Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design |
| 103 | c1otpA_ | Alignment | not modelled | 83.1 | 25 | PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase |
| 104 | c4p6vA_ | Alignment | not modelled | 82.9 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae |
| 105 | c4mybA_ | Alignment | not modelled | 82.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidyltransferase (ispd) |
| 106 | c2b8gA_ | Alignment | not modelled | 82.4 | 15 | PDB header: biosynthetic protein Chain: A: PDB Molecule: biotin/lipoyl attachment protein; PDBTitle: solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure) |
| 107 | c3h5qA_ | Alignment | not modelled | 81.8 | 28 | PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus |
| 108 | c2aujD_ | Alignment | not modelled | 80.7 | 29 | PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert |
| 109 | c4jisB_ | Alignment | not modelled | 80.3 | 11 | PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidyltransferase (tari)2 from bacillus subtilis |
| 110 | c5xhwA_ | Alignment | not modelled | 80.3 | 11 | PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis |
| 111 | c4l8jA_ | Alignment | not modelled | 79.8 | 22 | PDB header: transport protein Chain: A: PDB Molecule: putative efflux transporter; PDBTitle: crystal structure of a putative efflux transporter (bacegg_01895) from2 bacteroides eggerthii dsm 20697 at 2.06 a resolution |
| 112 | c3bg3A_ | Alignment | not modelled | 79.7 | 28 | PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus) |
| 113 | c1t5eB_ | Alignment | not modelled | 79.6 | 26 | PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa |
| 114 | c4tkoB_ | Alignment | not modelled | 79.5 | 26 | PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra |
| 115 | d1fxoa_ | Alignment | not modelled | 79.2 | 10 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase |
| 116 | d1bdoa_ | Alignment | not modelled | 78.8 | 16 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 117 | c2k33A_ | Alignment | not modelled | 78.4 | 22 | PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation |
| 118 | d1qwja_ | Alignment | not modelled | 78.2 | 14 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase |
| 119 | d1o78a_ | Alignment | not modelled | 77.9 | 17 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 120 | c3lnnB_ | Alignment | not modelled | 77.8 | 35 | PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans |