
















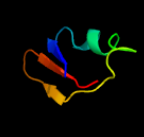

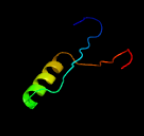


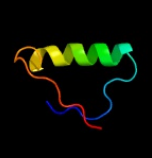

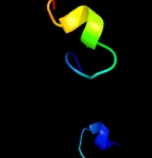
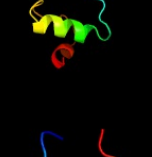
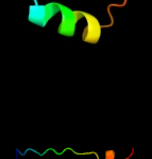
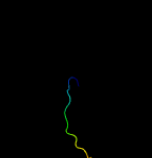
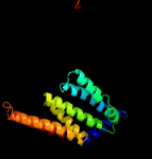
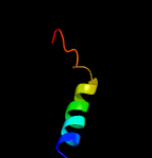
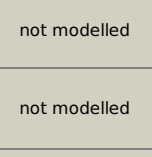


Phyre2

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|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0226c (-) _269834_271564 |
| Date | Tue Jul 23 14:50:28 BST 2019 |
| Unique Job ID | b625655bc2a756b5 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | c3wajA_ |  Alignment |  | 99.1 | 10 | 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 |
| 2 | c3rceA_ |  Alignment |  | 98.6 | 11 | PDB header: transferase/peptide Chain: A: PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb |
| 3 | c6eznF_ |  Alignment |  | 98.4 | 12 | PDB header: membrane protein Chain: F: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex |
| 4 | c5f15A_ |  Alignment |  | 97.6 | 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 |
| 5 | c3vu0B_ |  Alignment |  | 33.6 | 12 | PDB header: transferase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-s2, af_0040, o30195_arcfu) from3 archaeoglobus fulgidus |
| 6 | c3vgpA_ |  Alignment |  | 25.3 | 14 | PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase, putative; PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (af_0329) from archaeoglobus fulgidus |
| 7 | c2l9uA_ |  Alignment |  | 25.3 | 42 | PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain |
| 8 | c3waiA_ |  Alignment |  | 21.9 | 10 | PDB header: transferase, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, transmembrane PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion |
| 9 | c4dl0I_ |  Alignment |  | 21.1 | 28 | PDB header: hydrolase Chain: I: PDB Molecule: v-type proton atpase subunit c; PDBTitle: crystal structure of the heterotrimeric egthead peripheral stalk2 complex of the yeast vacuolar atpase |
| 10 | d1qkia1 |  Alignment |  | 19.9 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 11 | c6p25A_ |  Alignment |  | 18.7 | 5 | 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 |

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|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | d1h9aa1 | Alignment |  | 18.1 | 26 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 13 | c5vylA | Alignment |  | 17.9 | 37 | PDB header: viral protein Chain: A: PDB Molecule: inner tegument protein; PDBTitle: crystal structure of n-terminal half of herpes simplex virus type 12 ul37 protein |
| 14 | c4k70B | Alignment |  | 17.1 | 25 | PDB header: viral protein Chain: B: PDB Molecule: ul37; PDBTitle: crystal structure of n-terminal half of pseudorabiesvirus ul37 protein |
| 15 | d1a77a2 | Alignment |  | 13.1 | 19 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 16 | c3gxA | Alignment |  | 12.0 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase (duf442); PDBTitle: crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution |
| 17 | c4j2IC | Alignment |  | 12.0 | 40 | PDB header: transcription regulator Chain: C: PDB Molecule: protein capicua homolog; PDBTitle: crystal structure of axh domain complexed with capicua |
| 18 | c4j2ID | Alignment |  | 12.0 | 40 | PDB header: transcription regulator Chain: D: PDB Molecule: protein capicua homolog; PDBTitle: crystal structure of axh domain complexed with capicua |
| 19 | c6p2rB | Alignment |  | 11.7 | 7 | 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 |
| 20 | c5kzoA | Alignment |  | 11.6 | 17 | PDB header: transcription Chain: A: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: notch1 transmembrane and associated juxtamembrane segment |
| 21 | d1u7la | Alignment | not modelled | 11.5 | 28 | Fold: Vacuolar ATP synthase subunit C Superfamily: Vacuolar ATP synthase subunit C Family: Vacuolar ATP synthase subunit C |
| 22 | d2i5nm1 | Alignment | not modelled | 11.2 | 18 | Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| 23 | c2b5dX | Alignment | not modelled | 10.5 | 21 | PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima |
| 24 | c2f46A | Alignment | not modelled | 10.2 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution |
| 25 | d1rxwa2 | Alignment | not modelled | 10.1 | 13 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 26 | d1eysl | Alignment | not modelled | 9.7 | 11 | Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| 27 | d1vkia | Alignment | not modelled | 9.7 | 6 | Fold: YbaK/ProRS associated domain Superfamily: YbaK/ProRS associated domain Family: YbaK/ProRS associated domain |
| 28 | d1eysm | Alignment | not modelled | 9.6 | 13 | Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| | | | | | | Fold: Bacterial photosystem II reaction centre, L and M subunits |

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|----|-------------------------|-----------|--------------|-----|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | d2axtd1 | Alignment | not modelled | 9.4 | 14 | Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| 30 | c2m7yA | Alignment | not modelled | 9.4 | 29 | PDB header: viral protein Chain: A: PDB Molecule: leader peptide; PDBTitle: the mengovirus leader protein |
| 31 | d2j8cm1 | Alignment | not modelled | 9.3 | 15 | Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| 32 | d2i5nl1 | Alignment | not modelled | 9.3 | 13 | Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| 33 | d1u6ka1 | Alignment | not modelled | 9.2 | 22 | Fold: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Superfamily: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Family: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) |
| 34 | c4witB | Alignment | not modelled | 9.2 | 20 | PDB header: lipid transport Chain: B: PDB Molecule: predicted protein; PDBTitle: tmem16 lipid scramblase in crystal form 2 |
| 35 | c1k1yA | Alignment | not modelled | 9.1 | 26 | PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose |
| 36 | d2b5dx2 | Alignment | not modelled | 9.0 | 21 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like |
| 37 | c3n92A | Alignment | not modelled | 8.9 | 25 | PDB header: transferase Chain: A: PDB Molecule: alpha-amylase, gh57 family; PDBTitle: crystal structure of tk1436, a gh57 branching enzyme from 2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex 3 with glucose |
| 38 | d2pp6a1 | Alignment | not modelled | 8.8 | 22 | Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like |
| 39 | d2j8cl1 | Alignment | not modelled | 8.8 | 10 | Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| 40 | d1l9bm | Alignment | not modelled | 8.8 | 14 | Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| 41 | c2lowA | Alignment | not modelled | 8.7 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip |
| 42 | d2axta1 | Alignment | not modelled | 8.6 | 13 | Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| 43 | c5yq7M | Alignment | not modelled | 8.2 | 14 | PDB header: photosynthesis Chain: M: PDB Molecule: precursor for m subunits of photosynthetic reaction center; PDBTitle: cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii |
| 44 | c5yq7L | Alignment | not modelled | 8.1 | 6 | PDB header: photosynthesis Chain: L: PDB Molecule: precursor for l subunits of photosynthetic reaction center; PDBTitle: cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii |
| 45 | c2bhbB | Alignment | not modelled | 8.0 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose 6-phosphate dehydrogenase (deletion2 variant) complexed with glucose-6-phosphate |
| 46 | c2n1pA | Alignment | not modelled | 8.0 | 38 | PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein |
| 47 | c6q90J | Alignment | not modelled | 7.9 | 50 | PDB header: splicing Chain: J: PDB Molecule: u1 small nuclear ribonucleoprotein component snu71; PDBTitle: prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2) |
| 48 | d1m1ha2 | Alignment | not modelled | 7.8 | 6 | Fold: Ferredoxin-like Superfamily: N-utilization substance G protein NusG, N-terminal domain Family: N-utilization substance G protein NusG, N-terminal domain |
| 49 | d1tu7a2 | Alignment | not modelled | 7.7 | 5 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain |
| 50 | c1qkiE | Alignment | not modelled | 7.4 | 24 | PDB header: oxidoreductase Chain: E: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose 6-phosphate dehydrogenase (variant2 canton r459l) complexed with structural nadp+ |
| 51 | d1ufaa2 | Alignment | not modelled | 7.3 | 21 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like |
| 52 | c1a77A | Alignment | not modelled | 7.3 | 19 | PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii |
| 53 | d2cvda2 | Alignment | not modelled | 7.2 | 12 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like |

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|----|-------------------------|-----------|--------------|-----|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | | | | | | Family: Glutathione S-transferase (GST), N-terminal domain |
| 54 | d1k1xa3 | Alignment | not modelled | 7.2 | 26 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: 4-alpha-glucanotransferase, N-terminal domain |
| 55 | c1ufaA | Alignment | not modelled | 7.2 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tt1467 protein; PDBTitle: crystal structure of tt1467 from thermus thermophilus hb8 |
| 56 | c1h9aA | Alignment | not modelled | 6.8 | 26 | PDB header: oxidoreductase (choh(d) - nad(p)) Chain: A: PDB Molecule: glucose 6-phosphate 1-dehydrogenase; PDBTitle: complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from I. mesenteroides with coenzyme nadp |
| 57 | c5n6mA | Alignment | not modelled | 6.8 | 16 | PDB header: membrane protein Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: structure of the membrane integral lipoprotein n-acyltransferase Int2 from p. aeruginosa |
| 58 | d1m6ja | Alignment | not modelled | 6.6 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) |
| 59 | c3qeaZ | Alignment | not modelled | 6.4 | 16 | PDB header: hydrolase/dna Chain: Z: PDB Molecule: exonuclease 1; PDBTitle: crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii) |
| 60 | c4y8fA | Alignment | not modelled | 6.4 | 20 | PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from clostridium2 perfringens |
| 61 | c1b43A | Alignment | not modelled | 6.3 | 19 | PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus |
| 62 | c3s6dA | Alignment | not modelled | 6.2 | 20 | PDB header: isomerase Chain: A: PDB Molecule: putative triosephosphate isomerase; PDBTitle: crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis |
| 63 | c4y9aB | Alignment | not modelled | 6.2 | 20 | PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from streptomyces2 coelicolor |
| 64 | d2j07a2 | Alignment | not modelled | 6.2 | 21 | Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain |
| 65 | d1b43a2 | Alignment | not modelled | 6.1 | 19 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 66 | c5nc8B | Alignment | not modelled | 6.1 | 18 | PDB header: transport protein Chain: B: PDB Molecule: potassium efflux system protein; PDBTitle: shewanella denitrificans kef ctd in amp bound form |
| 67 | c4mknA | Alignment | not modelled | 6.1 | 24 | PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of chloroplastic triosephosphate isomerase from2 chlamydomonas reinhardtii at 1.1 a of resolution |
| 68 | c4lqvA | Alignment | not modelled | 6.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray crystal structure of glucose-6-phosphate 1-dehydrogenase from2 mycobacterium avium |
| 69 | d2bea1 | Alignment | not modelled | 5.9 | 4 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 70 | d1ul1x2 | Alignment | not modelled | 5.9 | 21 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 71 | c3op6B | Alignment | not modelled | 5.8 | 14 | PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an oligo-nucleotide binding protein (lpg1207)2 from legionella pneumophila subsp. pneumophila str. philadelphia 1 at3 2.00 a resolution |
| 72 | c5zg5B | Alignment | not modelled | 5.8 | 24 | PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase sadsubaaa mutant from2 opisthorchis viverrini |
| 73 | c2jgqB | Alignment | not modelled | 5.8 | 12 | PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori |
| 74 | c5ujwD | Alignment | not modelled | 5.8 | 18 | PDB header: isomerase Chain: D: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from francisella2 tularensis subsp. tularensis schu s4 |
| 75 | c2mkvA | Alignment | not modelled | 5.8 | 13 | PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles |
| 76 | c2ct6A | Alignment | not modelled | 5.8 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sh3 domain-binding glutamic acid-rich-like PDBTitle: solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2 |
| 77 | c3orvA | Alignment | not modelled | 5.8 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus |
| 78 | c2l9uB | Alignment | not modelled | 5.8 | 24 | PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erb3-3; PDBTitle: spatial structure of dimeric erb3 transmembrane domain |
| | | | | | | PDB header: virus |

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|----|-------------------------|-----------|--------------|-----|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 79 | c5wsnD_ | Alignment | not modelled | 5.7 | 16 | Chain: D: PDB Molecule: m protein; PDBTitle: structure of japanese encephalitis virus |
| 80 | c3krsB_ | Alignment | not modelled | 5.7 | 18 | PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution |
| 81 | c3th6B_ | Alignment | not modelled | 5.6 | 18 | PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus. |
| 82 | c4e9iB_ | Alignment | not modelled | 5.6 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi |
| 83 | d1o5xa_ | Alignment | not modelled | 5.6 | 0 | Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) |
| 84 | c3j2pD_ | Alignment | not modelled | 5.5 | 16 | PDB header: viral protein Chain: D: PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer |
| 85 | c4nvtD_ | Alignment | not modelled | 5.5 | 24 | PDB header: isomerase Chain: D: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from brucella2 melitensis |
| 86 | c4y90B_ | Alignment | not modelled | 5.5 | 29 | PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from deinococcus2 radiodurans |
| 87 | c5ibxB_ | Alignment | not modelled | 5.5 | 24 | PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: 1.65 angstrom crystal structure of triosephosphate isomerase (tim)2 from streptococcus pneumoniae |
| 88 | d2ozua1 | Alignment | not modelled | 5.4 | 20 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 89 | d1b9ba_ | Alignment | not modelled | 5.4 | 29 | Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) |
| 90 | d2ctda2 | Alignment | not modelled | 5.3 | 50 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 91 | c3m9yB_ | Alignment | not modelled | 5.3 | 35 | PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution |
| 92 | c5uprA_ | Alignment | not modelled | 5.3 | 18 | PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: x-ray structure of a putative triosephosphate isomerase from2 toxoplasma gondii me49 |
| 93 | d1sw3a_ | Alignment | not modelled | 5.3 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) |
| 94 | c1yyaA_ | Alignment | not modelled | 5.3 | 18 | PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8 |
| 95 | c5ireD_ | Alignment | not modelled | 5.3 | 22 | PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus |
| 96 | c1p58F_ | Alignment | not modelled | 5.2 | 13 | PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction |
| 97 | c1p58E_ | Alignment | not modelled | 5.2 | 13 | PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction |
| 98 | d1aw1a_ | Alignment | not modelled | 5.2 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) |
| 99 | d1vpqa_ | Alignment | not modelled | 5.2 | 14 | Fold: TIM beta/alpha-barrel Superfamily: TM1631-like Family: TM1631-like |