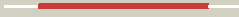























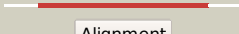

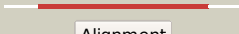
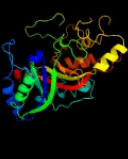






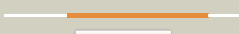


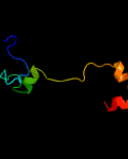
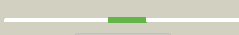
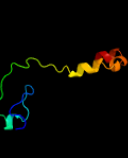
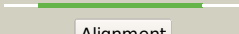
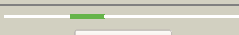







Phyre2

| | |
|------------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0799c (-)_892269_893276 |
| Date | Fri Jul 26 01:50:38 BST 2019 |
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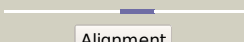
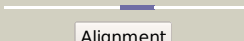

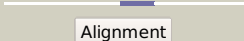
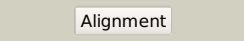
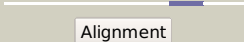
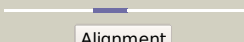

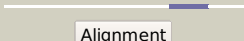


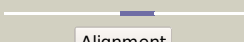
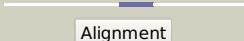







Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | d2iiza1 |  Alignment |  | 100.0 | 35 | Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Dyp-type peroxidase-like |
| 2 | c3qnsA |  Alignment |  | 100.0 | 59 | PDB header: oxidoreductase Chain: A: PDB Molecule: dyp peroxidase; PDBTitle: dypb from rhodococcus jostii rha1, crystal form 2 |
| 3 | c4gu7C |  Alignment |  | 100.0 | 60 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative uncharacterized protein sco7193; PDBTitle: crystal structure of dyp-type peroxidase (sco7193) from streptomyces2 coelicolor |
| 4 | d2gvka1 |  Alignment |  | 100.0 | 46 | Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Dyp-type peroxidase-like |
| 5 | c5gt2A |  Alignment |  | 100.0 | 36 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable deferrochelate/oxidoreductase yfex; PDBTitle: crystal structure and biochemical features of dye-decolorizing2 peroxidase yfex from escherichia coli o157 |
| 6 | c5de0D |  Alignment |  | 100.0 | 38 | PDB header: oxidoreductase Chain: D: PDB Molecule: deferrochelate; PDBTitle: dye-decolorizing protein from v. cholerae |
| 7 | c4gs1A |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: dyp-type peroxidase; PDBTitle: crystal structure of dyp-type peroxidase from thermobifida2 cellulolytica |
| 8 | c4gt2A |  Alignment |  | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein sco3963; PDBTitle: crystal structure of dyp-type peroxidase (sco3963) from streptomyces2 coelicolor |
| 9 | c6qzoG |  Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: G: PDB Molecule: peroxidase; PDBTitle: crystal structure of dyp-type peroxidase from cellulomonas bogoriensis |
| 10 | c5jxuA |  Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: dyp-type peroxidase family; PDBTitle: structural basis for the catalytic activity of thermomonospora curvata2 heme-containing dyp-type peroxidase. |
| 11 | c4grcA |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative membrane protein; PDBTitle: crystal structure of dyp-type peroxidase (sco2276) from streptomyces2 coelicolor |

| | | | | | | |
|----|-------------------------|---|---|-------|----|--|
| 12 | c2wx6B_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: peroxidase ycdb; PDBTitle: x-ray crystallographic structure of e. coli apo-efeb |
| 13 | c4au9A_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: dyp-type peroxidase i; PDBTitle: crystal structure of a fungal dyp-type peroxidase from2 auricularia auricula-judae |
| 14 | d2d3qa1 |  Alignment |  | 100.0 | 23 | Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Dyp-type peroxidase-like |
| 15 | c5c2iC_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: alr1585 protein; PDBTitle: crystal structure of anabaena sp. dyp-type peroxidase (anapx) |
| 16 | c4g2cB_ |  Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: dyp2; PDBTitle: dyp2 from amycolatopsis sp. atcc 39116 |
| 17 | c6fskA_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: dyp-type peroxidase; PDBTitle: f194y mutant of the dye-decolorizing peroxidase (dyp) from pleurotus2 ostreatus |
| 18 | c3nn4C_ |  Alignment |  | 83.5 | 16 | PDB header: oxidoreductase Chain: C: PDB Molecule: chlorite dismutase; PDBTitle: structure of chlorite dismutase from candidatus nitrospira defluviu2 r173k mutant |
| 19 | c4pfbA_ |  Alignment |  | 58.5 | 16 | PDB header: transport protein Chain: A: PDB Molecule: c4-dicarboxylate-binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 fusobacterium nucleatum (fn1258, target efi-510120) with bound sn-3 glycerol-3-phosphate |
| 20 | c4petA_ |  Alignment |  | 56.9 | 9 | PDB header: solute-binding protein Chain: A: PDB Molecule: extracellular solute-binding protein, family 7; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 colwellia psychrerythraea (cps_0129, target efi-510097) with bound3 calcium and pyruvate |
| 21 | c5a13J_ |  Alignment | not modelled | 55.1 | 15 | PDB header: oxidoreductase Chain: J: PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of chlorite dismutase from2 magnetospirillum sp. in complex with thiocyanate |
| 22 | c3dtzB_ |  Alignment | not modelled | 54.8 | 15 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative chlorite dismutase ta0507; PDBTitle: crystal structure of putative chlorite dismutase ta0507 |
| 23 | c5im2A_ |  Alignment | not modelled | 52.3 | 17 | PDB header: transport protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of a trap solute binding protein from rhodofera2 ferrireducens t118 (rfer_2570, target efi-510210) in complex with3 copurified benzoate |
| 24 | c4mcoC_ |  Alignment | not modelled | 50.7 | 19 | PDB header: transport protein Chain: C: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodofera2 ferrireducens (rfer_1840), target efi-510211, with bound3 malonate |
| 25 | c1u2zC_ |  Alignment | not modelled | 50.1 | 12 | PDB header: transferase Chain: C: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-79 PDBTitle: crystal structure of histone k79 methyltransferase dot1p2 from yeast |
| 26 | c4pbhA_ |  Alignment | not modelled | 48.7 | 15 | PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit, putative; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 ruegeria pomeroyi dss-3 (spo1773, target efi-510260) with bound3 benzoic acid |
| | |  Alignment | | | | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 27 | c4n6kA_ | Alignment | not modelled | 47.3 | 14 | subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Desulfovibrio salexigens</i> DSM 2638, target efi-510113 (desal_0342), 3 complex with diglycerolphosphate |
| 28 | c3u65B_ | Alignment | not modelled | 47.3 | 11 | PDB header: transport protein Chain: B: PDB Molecule: tp33 protein; PDBTitle: the crystal structure of tat-p(t) (tp0957) |
| 29 | c4o8mA_ | Alignment | not modelled | 47.3 | 21 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Actinobacillus succinogenes</i> 130z, target efi-510004, with bound l-3 galactonate |
| 30 | c2vxhF_ | Alignment | not modelled | 46.3 | 20 | PDB header: oxidoreductase Chain: F: PDB Molecule: chlorite dismutase; PDBTitle: the crystal structure of chlorite dismutase: a detox enzyme 2 producing molecular oxygen |
| 31 | c4mncA_ | Alignment | not modelled | 46.3 | 17 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Polaromonas</i> sp. js666 (bpro_4736), target efi-510156, with bound 3 benzoyl formate, space group p21 |
| 32 | c2hpgB_ | Alignment | not modelled | 45.0 | 13 | PDB header: ligand binding protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding PDBTitle: the crystal structure of a thermophilic trap periplasmic 2 binding protein |
| 33 | c4n6dA_ | Alignment | not modelled | 44.0 | 19 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Desulfovibrio salexigens</i> DSM 2638 (desal_3247), target efi-510112, 3 phased with i3c, open complex, c-terminus of symmetry mate bound in 4 ligand binding site |
| 34 | c4pf6A_ | Alignment | not modelled | 43.6 | 31 | PDB header: transport protein Chain: A: PDB Molecule: c4-dicarboxylate-binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Roseobacter denitrificans</i> (rd1_0742, target efi-510239) with bound 3-3 deoxy-d-manno-oct-2-ulosonic acid (kdo) |
| 35 | c4wwsE_ | Alignment | not modelled | 43.6 | 18 | PDB header: oxidoreductase Chain: E: PDB Molecule: putative heme-dependent peroxidase lmo2113; PDBTitle: structure of chlorite dismutase-like protein from <i>Listeria monocytogenes</i> |
| 36 | c4xeqC_ | Alignment | not modelled | 43.0 | 16 | PDB header: transport protein Chain: C: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Desulfovibrio vulgaris</i> (deval_0042, target efi-510114) bound to 3 copurified (r)-pantoic acid |
| 37 | c4p56C_ | Alignment | not modelled | 42.2 | 22 | PDB header: solute-binding protein Chain: C: PDB Molecule: putative extracellular solute-binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Bordetella bronchiseptica</i> , target efi-510038 (bb2442), with bound 3 (r)-mandelate and (s)-mandelate |
| 38 | c4pbqC_ | Alignment | not modelled | 40.9 | 11 | PDB header: solute-binding protein Chain: C: PDB Molecule: putative trap periplasmic solute binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Haemophilus influenzae</i> Rdw (hicg_00826, target efi-510123) with 3 bound l-gulonate |
| 39 | d1t0tv_ | Alignment | not modelled | 40.8 | 24 | Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like |
| 40 | d1u2za_ | Alignment | not modelled | 37.9 | 12 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Catalytic, N-terminal domain of histone methyltransferase Dot11 |
| 41 | c4mnpA_ | Alignment | not modelled | 37.4 | 21 | PDB header: sugar binding protein Chain: A: PDB Molecule: n-acetylneuraminic acid-binding protein; PDBTitle: structure of the sialic acid binding protein from <i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> ATCC 25586 |
| 42 | c2pfyA_ | Alignment | not modelled | 37.3 | 14 | PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp7, a <i>Bordetella pertussis</i> 2 extracytoplasmic solute receptor binding pyroglutamic acid |
| 43 | c4nguA_ | Alignment | not modelled | 37.1 | 15 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Desulfovibrio alaskensis</i> g20 (dde_1548), target efi-510103, with 3 bound d-ala-d-ala |
| 44 | c4n4uA_ | Alignment | not modelled | 37.0 | 17 | PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter periplasmic solute-binding PDBTitle: crystal structure of abc transporter solute binding protein bb07192 from <i>Bordetella bronchiseptica</i> rb50, target efi-510049 |
| 45 | c4pe3A_ | Alignment | not modelled | 35.6 | 10 | PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Rhodobacter sphaeroides</i> (rsph17029_3620, target efi-510199), apo open 3 structure |
| 46 | c5i7iB_ | Alignment | not modelled | 34.9 | 26 | PDB header: transport protein Chain: B: PDB Molecule: trap solute binding protein; PDBTitle: crystal structure of a marine metagenome trap solute binding protein 2 specific for aromatic acid ligands (sorcerer ii global ocean sampling 3 expedition, unidentified microbe, locus tag gos_1523157) in complex 4 with co-crystallized 3-hydroxybenzoate |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 47 | c4y66C_ | Alignment | not modelled | 30.9 | 12 | PDB header: cell cycle Chain: C: PDB Molecule: mnd1; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex |
| 48 | c4ovrA_ | Alignment | not modelled | 29.3 | 18 | PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 xanthobacter autotrophicus py2, target efi-510329, with bound beta-d-3 galacturonate |
| 49 | c4pfiA_ | Alignment | not modelled | 28.3 | 15 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 marinobacter aquaeolei vt8 (maqu_2829, target efi-510133), apo open3 structure |
| 50 | c4nhbB_ | Alignment | not modelled | 27.4 | 15 | PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio desulfuricans (ddes_1525), target efi-510107, with3 bound sn-glycerol-3-phosphate |
| 51 | d1s6na_ | Alignment | not modelled | 27.4 | 34 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain |
| 52 | d1vjja1 | Alignment | not modelled | 25.7 | 23 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain |
| 53 | d1g0da1 | Alignment | not modelled | 24.5 | 41 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain |
| 54 | c2h0pA_ | Alignment | not modelled | 22.6 | 17 | PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: nmr structure of the dengue-4 virus envelope protein domain2 iii |
| 55 | d1ok8a1 | Alignment | not modelled | 21.3 | 20 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain |
| 56 | d1ex0a1 | Alignment | not modelled | 21.2 | 27 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain |
| 57 | d2q3za1 | Alignment | not modelled | 21.1 | 32 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain |
| 58 | c3egpA_ | Alignment | not modelled | 20.0 | 26 | PDB header: viral protein Chain: A: PDB Molecule: envelope protein; PDBTitle: crystal structure analysis of dengue-1 envelope protein2 domain iii |
| 59 | d1pjwa_ | Alignment | not modelled | 19.1 | 26 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain |
| 60 | d2cg4a2 | Alignment | not modelled | 18.7 | 8 | Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain |
| 61 | d2piea1 | Alignment | not modelled | 18.4 | 23 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 62 | c1uzgA_ | Alignment | not modelled | 17.7 | 17 | PDB header: viral protein Chain: A: PDB Molecule: major envelope protein e; PDBTitle: crystal structure of the dengue type 3 virus envelope2 protein |
| 63 | d1vdha_ | Alignment | not modelled | 17.5 | 18 | Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like |
| 64 | d1z66a1 | Alignment | not modelled | 16.1 | 21 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain |
| 65 | c4yicA_ | Alignment | not modelled | 16.1 | 21 | PDB header: transport protein Chain: A: PDB Molecule: trap transporter solute binding protein; PDBTitle: crystal structure of a trap transporter solute binding protein2 (ipr025997) from bordetella bronchiseptica rb50 (bb0280, target efi-3 500035) with bound picolinic acid |
| 66 | d1svba1 | Alignment | not modelled | 15.8 | 21 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain |
| 67 | c2jqmA_ | Alignment | not modelled | 14.8 | 25 | PDB header: transferase Chain: A: PDB Molecule: envelope protein e; PDBTitle: yellow fever envelope protein domain iii nmr structure2 (s288-k398) |
| 68 | c4napD_ | Alignment | not modelled | 14.8 | 26 | PDB header: transport protein Chain: D: PDB Molecule: extracellular solute-binding protein, family 7; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio alaskensis g20 (dde_0634), target efi-510102, with3 bound d-tryptophan |
| 69 | c4p1eA_ | Alignment | not modelled | 14.7 | 16 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 escherichia fergusonii (efer_1530), target efi-510119, apo open3 structure, phased with iodide |
| 70 | c4xfeA_ | Alignment | not modelled | 14.3 | 26 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter subunit dctp; PDBTitle: crystal structure of a trap periplasmic solute binding |

| | | | | | | |
|----|-------------------------|---|--------------|------|----|--|
| | |  | | | | protein from2 pseudomonas putida f1 (pput_1203), target efi-500184, with bound d-3 glucuronate |
| 71 | c5fn1A_ | Alignment | not modelled | 13.6 | 19 | PDB header: virus Chain: A: PDB Molecule: coat protein; PDBTitle: electron cryo-microscopy of filamentous flexible virus pepmv (pepino2 mosaic virus) |
| 72 | c4p8bA_ |  | not modelled | 13.3 | 32 | PDB header: transport protein Chain: A: PDB Molecule: trap-type transporter, periplasmic component; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 ralstonia eutropha h16 (h16_a1328), target efi-510189, with bound3 (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-acetolactate) |
| 73 | c4n8gC_ |  | not modelled | 12.9 | 11 | PDB header: transport protein Chain: C: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 chromohalobacter salexigens dsm 3043 (csal_0660), target efi-501075,3 with bound d-alanine-d-alanine |
| 74 | c4pf8A_ |  | not modelled | 12.9 | 21 | PDB header: transport protein Chain: A: PDB Molecule: trap-t family transporter, dctp (periplasmic binding) PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 sulfitebacter sp. nas-14.1 (target efi-510299) with bound beta-d-3 galacturonate |
| 75 | c4o94B_ |  | not modelled | 12.8 | 26 | PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodopseudomonas palustris haa2 (rpb_3329), target efi-510223, with3 bound succinate |
| 76 | c2qdrA_ |  | not modelled | 12.7 | 13 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dioxygenase (npun_f5605) from nostoc2 punctiforme pcc 73102 at 2.60 a resolution |
| 77 | d1o6ea_ |  | not modelled | 12.4 | 8 | Fold: Herpes virus serine proteinase, assemblin Superfamily: Herpes virus serine proteinase, assemblin Family: Herpes virus serine proteinase, assemblin |
| 78 | c4doxA_ |  | not modelled | 12.3 | 26 | PDB header: viral protein Chain: A: PDB Molecule: coat protein; PDBTitle: crystal structure of papaya mosaic virus capsid protein |
| 79 | c2vpnB_ |  | not modelled | 12.2 | 26 | PDB header: transport Chain: B: PDB Molecule: periplasmic substrate binding protein; PDBTitle: high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata |
| 80 | d1soua_ |  | not modelled | 11.9 | 16 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: Methenyltetrahydrofolate synthetase |
| 81 | c4n91A_ |  | not modelled | 11.7 | 11 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 anaerococcus prevotii dsm 20548 (apre_1383), target efi-510023, with3 bound alpha/beta d-glucuronate |
| 82 | c4x8rB_ |  | not modelled | 11.6 | 21 | PDB header: solute-binding protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_2138, target efi-510205) with3 bound glucuronate |
| 83 | c2zzxD_ |  | not modelled | 11.6 | 32 | PDB header: transport protein Chain: D: PDB Molecule: abc transporter, solute-binding protein; PDBTitle: crystal structure of a periplasmic substrate binding protein in2 complex with lactate |
| 84 | c3gyyC_ |  | not modelled | 11.4 | 22 | PDB header: transport protein Chain: C: PDB Molecule: periplasmic substrate binding protein; PDBTitle: the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state |
| 85 | c2hzkB_ |  | not modelled | 11.1 | 21 | PDB header: ligand binding, transport protein Chain: B: PDB Molecule: trap-t family sorbitol/mannitol transporter, periplasmic PDBTitle: crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form |
| 86 | c4pddA_ |  | not modelled | 10.7 | 11 | PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 polaromonas sp js666 (bpro_0088, target efi-510167) bound to d-3 erythronate |
| 87 | c3fxbB_ |  | not modelled | 10.6 | 21 | PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha |
| 88 | c4nn3A_ |  | not modelled | 10.6 | 25 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens (desal_2161), target efi-510109, with bound3 orotic acid |
| 89 | c3uajA_ |  | not modelled | 10.5 | 21 | PDB header: viral protein/immune system Chain: A: PDB Molecule: envelope protein; PDBTitle: crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2 |
| 90 | c3b0vD_ |  | not modelled | 10.3 | 10 | PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna |
| | |  | | | | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp |

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|----|-------------------------|-----------|--------------|------|----|---|
| 91 | c4p1A_ | Alignment | not modelled | 10.3 | 32 | subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 chromohalobacter salexigens dsm 3043 (csal_2479), target efi-510085,3 with bound d-glucuronate, spg i213 |
| 92 | c4ln5A_ | Alignment | not modelled | 10.2 | 32 | PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 burkholderia ambifaria (bamb_6123), target efi-510059, with bound3 glycerol and chloride ion |
| 93 | c1urzC_ | Alignment | not modelled | 10.1 | 21 | PDB header: virus/viral protein Chain: C: PDB Molecule: envelope protein; PDBTitle: low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus |
| 94 | c4mx6A_ | Alignment | not modelled | 10.1 | 26 | PDB header: transport protein Chain: A: PDB Molecule: trap-type c4-dicarboxylate:h+ symport system substrate- PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 shewanella oneidensis (so_3134), target efi-510275, with bound3 succinate |
| 95 | c3c6dB_ | Alignment | not modelled | 9.8 | 23 | PDB header: virus Chain: B: PDB Molecule: polyprotein; PDBTitle: the pseudo-atomic structure of dengue immature virus |
| 96 | c3uzeC_ | Alignment | not modelled | 9.7 | 22 | PDB header: immune system Chain: C: PDB Molecule: envelope protein; PDBTitle: crystal structure of the dengue virus serotype 3 envelope protein2 domain iii in complex with the variable domains of mab 4e11 |
| 97 | c6epkA_ | Alignment | not modelled | 9.5 | 25 | PDB header: viral protein Chain: A: PDB Molecule: envelope protein e; PDBTitle: crystal structure of the precursor membrane protein-envelope protein2 heterodimer from the yellow fever virus |
| 98 | c4ovqA_ | Alignment | not modelled | 9.4 | 16 | PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate abc transporter, substrate-binding PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 roseobacter denitrificans, target efi-510230, with bound beta-d-3 glucuronate |
| 99 | c4ng7A_ | Alignment | not modelled | 9.4 | 21 | PDB header: transport protein Chain: A: PDB Molecule: trap periplasmic solute binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 citrobacter koseri (cko_04899), target efi-510094, apo, open3 structure |