

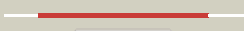








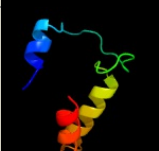

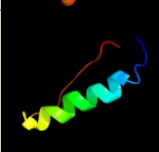





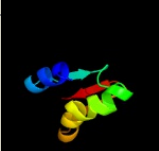




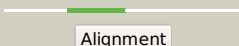



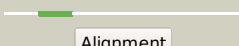

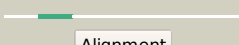

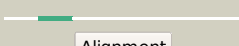

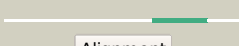
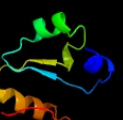




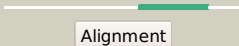
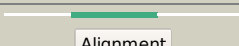


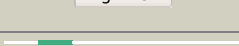
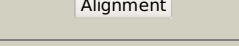
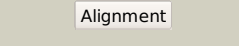
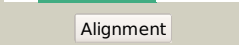
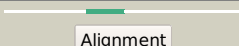


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1594_(nadA)_1794763_1795812 |
| Date | Fri Aug 2 13:30:18 BST 2019 |
| Unique Job ID | 375bb001322147d0 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4p3xA_ |  Alignment |  | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: quinolinate synthase a; PDBTitle: structure of the fe4s4 quinolinate synthase nada from thermotoga2 maritima |
| 2 | c2qs0A_ |  Alignment |  | 100.0 | 42 | PDB header: biosynthetic protein Chain: A: PDB Molecule: quinolinate synthetase a; PDBTitle: quinolinate synthase from pyrococcus furiosus |
| 3 | d1wzua1 |  Alignment |  | 100.0 | 43 | Fold: NadA-like Superfamily: NadA-like Family: NadA-like |
| 4 | c6mgdA_ |  Alignment |  | 84.4 | 14 | PDB header: transferase Chain: A: PDB Molecule: capsular polysaccharide export system protein kpssc; PDBTitle: thermosulfurimonas dismutans kpssc, beta kdo 2,4 transferase |
| 5 | c5ldrA_ |  Alignment |  | 71.5 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: beta-d-galactosidase; PDBTitle: crystal structure of a cold-adapted dimeric beta-d-galactosidase from2 paracoccus sp. 32d strain in complex with galactose |
| 6 | c6j7aB_ |  Alignment |  | 66.8 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: heme oxygenase 1,nadph--cytochrome p450 reductase; PDBTitle: fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa) |
| 7 | d1xhja_ |  Alignment |  | 62.4 | 24 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like |
| 8 | c1zq1B_ |  Alignment |  | 59.6 | 27 | PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi |
| 9 | d1j97a_ |  Alignment |  | 58.2 | 18 | Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase |
| 10 | c3p04B_ |  Alignment |  | 56.6 | 17 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8 |
| 11 | c6b61B_ |  Alignment |  | 54.5 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 2, sugar binding domain protein; PDBTitle: the crystal structure of glycosyl hydrolase family 2 (gh2) member from2 bacteroides cellulosilyticus dsm 14838 |

| | | | | | | |
|----|-------------------------|---|---|------|----|--|
| 12 | c5t9gD_ |  Alignment |  | 54.1 | 24 | PDB header: hydrolase Chain: D: PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of bugh2cwt in complex with galactoisofagomine |
| 13 | d1hrua_ |  Alignment |  | 53.9 | 14 | Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like |
| 14 | c3zihB_ |  Alignment |  | 52.8 | 19 | PDB header: cell cycle Chain: B: PDB Molecule: cell division protein sepf; PDBTitle: bacillus subtilis sepf, c-terminal domain |
| 15 | c6dxuB_ |  Alignment |  | 51.9 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 2, tim barrel domain protein; PDBTitle: crystal structure of parabacteroides merdae beta-glucuronidase (gus) |
| 16 | c3fn9B_ |  Alignment |  | 49.6 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis |
| 17 | c6d8kD_ |  Alignment |  | 49.5 | 20 | PDB header: hydrolase Chain: D: PDB Molecule: glycosyl hydrolase family 2, sugar binding domain protein; PDBTitle: bacteroides multiple species beta-glucuronidase |
| 18 | c5nkzC_ |  Alignment |  | 48.7 | 16 | PDB header: transferase Chain: C: PDB Molecule: peroxin 22; PDBTitle: crystal structure of h. polymorpha ubiquitin conjugating enzyme pex4p2 in complex with soluble domain of pex22p |
| 19 | c3cmgA_ |  Alignment |  | 48.6 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis |
| 20 | c3p04A_ |  Alignment |  | 48.6 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8 |
| 21 | d1pswa_ |  Alignment | not modelled | 47.5 | 16 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II |
| 22 | c2e55D_ |  Alignment | not modelled | 47.0 | 20 | PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus |
| 23 | d1veha_ |  Alignment | not modelled | 44.6 | 11 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like |
| 24 | c5un8B_ |  Alignment | not modelled | 43.8 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: protein o-glcnacase; PDBTitle: crystal structure of human o-glcnacase in complex with glycopeptide2 p53 |
| 25 | c4ypjB_ |  Alignment | not modelled | 42.9 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: beta galactosidase; PDBTitle: x-ray structure of the mutant of glycoside hydrolase |
| 26 | c6mvgB_ |  Alignment | not modelled | 42.7 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: beta-glucuronidase; PDBTitle: crystal structure of fmn-binding beta-glucuronidase from ruminococcus2 gnavus |
| 27 | c2q5cA_ |  Alignment | not modelled | 42.5 | 13 | PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum |
| 28 | c3hbmA_ |  Alignment | not modelled | 42.2 | 9 | PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni |
| 29 | c2p07A_ |  Alignment | not modelled | 42.2 | 22 | PDB header: ligase Chain: A: PDB Molecule: uroporphyrinogen iii cosynthase (hemd); |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c3p2a | Alignment | not modelled | 42.2 | 22 | PDBTitle: crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695 PDB header: hydrolase |
| 30 | c4cucA | Alignment | not modelled | 41.0 | 12 | Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: unravelling the multiple functions of the architecturally intricate2 streptococcus pneumoniae beta-galactosidase, bgaa. |
| 31 | c5uj6A | Alignment | not modelled | 41.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolases family 2, sugar binding domain protein; PDBTitle: crystal structure of bacteroides uniformis beta-glucuronidase |
| 32 | c3uuuA | Alignment | not modelled | 40.5 | 7 | PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa |
| 33 | c4lkuB | Alignment | not modelled | 40.0 | 24 | PDB header: transport protein Chain: B: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 34 | c4lkuA | Alignment | not modelled | 40.0 | 24 | PDB header: transport protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 35 | c5d95A | Alignment | not modelled | 39.8 | 13 | PDB header: transferase Chain: A: PDB Molecule: aminotransferase class-iii; PDBTitle: structure of thermostable omega-transaminase |
| 36 | c6a4cA | Alignment | not modelled | 39.3 | 25 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein mxan_0049; PDBTitle: solution structure of mxan_0049 |
| 37 | c6mgbA | Alignment | not modelled | 39.1 | 29 | PDB header: transferase Chain: A: PDB Molecule: capsular polysaccharide export system protein kpsc; PDBTitle: thermosulfurimonas dismutans kpsc, beta kdo 2,4 transferase |
| 38 | c6d1pB | Alignment | not modelled | 36.9 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolases family 2, sugar binding domain protein; PDBTitle: apo structure of bacteroides uniformis beta-glucuronidase 3 |
| 39 | c6ed1B | Alignment | not modelled | 36.8 | 24 | PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 2, sugar binding domain protein; PDBTitle: bacteroides dorei beta-glucuronidase |
| 40 | d2pjuA1 | Alignment | not modelled | 36.5 | 17 | Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like |
| 41 | c6mvfA | Alignment | not modelled | 35.5 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase/beta-glucuronidase; PDBTitle: crystal structure of fmn-binding beta-glucuronidase from2 facaelibacterium prausnitzii I2-6 |
| 42 | c4ra6A | Alignment | not modelled | 35.3 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of linker less pyrococcus furiosus l-asparaginase |
| 43 | c3pg6D | Alignment | not modelled | 35.1 | 32 | PDB header: ligase Chain: D: PDB Molecule: e3 ubiquitin-protein ligase dtx3l; PDBTitle: the carboxyl terminal domain of human deltex 3-like |
| 44 | c3tovB | Alignment | not modelled | 34.1 | 11 | PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase family 9; PDBTitle: the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008 |
| 45 | c6dxuA | Alignment | not modelled | 33.9 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase family 2, tim barrel domain protein; PDBTitle: crystal structure of parabacteroides merdae beta-glucuronidase (gus) |
| 46 | c5j21C | Alignment | not modelled | 32.8 | 19 | PDB header: hydrolase Chain: C: PDB Molecule: bifunctional oligoribonuclease and pap phosphatase nrna; PDBTitle: structure of bacillus nanornase a (wt) |
| 47 | c1jz6C | Alignment | not modelled | 31.5 | 19 | PDB header: hydrolase Chain: C: PDB Molecule: beta-galactosidase; PDBTitle: e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole |
| 48 | d1z7da1 | Alignment | not modelled | 31.3 | 10 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like |
| 49 | c3gm8A | Alignment | not modelled | 31.1 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 2, candidate beta-glycosidase; PDBTitle: crystal structure of a beta-glycosidase from bacteroides vulgatus |
| 50 | d1wova1 | Alignment | not modelled | 30.7 | 23 | Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: Eukaryotic type heme oxygenase |
| 51 | c5kqwD | Alignment | not modelled | 30.7 | 9 | PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: directed evolution of transaminases by ancestral reconstruction. using2 old proteins for new chemistries |
| 52 | c5dmyA | Alignment | not modelled | 29.3 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: beta-galactosidase - construct 33-930 |
| 53 | c2y1hA | Alignment | not modelled | 27.4 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn3; PDBTitle: crystal structure of the human tatdn-domain protein 3 (tatdn3) |

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|----|-------------------------|-----------|--------------|------|----|--|
| 54 | c2ekcA | Alignment | not modelled | 26.8 | 20 | PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5 |
| 55 | c4lkuD | Alignment | not modelled | 26.7 | 24 | PDB header: transport protein Chain: D: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 56 | c5gw8A | Alignment | not modelled | 26.5 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa |
| 57 | c4lkuC | Alignment | not modelled | 26.5 | 24 | PDB header: transport protein Chain: C: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 58 | c5g2pA | Alignment | not modelled | 25.6 | 20 | PDB header: transferase Chain: A: PDB Molecule: transaminase; PDBTitle: the crystal structure of a s-selective transaminase from2 arthrobacter sp. |
| 59 | c6oviA | Alignment | not modelled | 25.6 | 20 | PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate |
| 60 | c2d6fA | Alignment | not modelled | 25.6 | 30 | PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln) |
| 61 | c2xsbA | Alignment | not modelled | 25.3 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: ogoga pugnac complex |
| 62 | c6j9mF | Alignment | not modelled | 25.0 | 50 | PDB header: hydrolase/hydrolase inhibitor Chain: F: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: nmebh+acriic2 |
| 63 | c5t98B | Alignment | not modelled | 24.9 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of bugh2awt |
| 64 | c6iz9B | Alignment | not modelled | 24.7 | 19 | PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: crystal structure of the apo form of a beta-transaminase from2 mesorhizobium sp. strain luk |
| 65 | c3nm3D | Alignment | not modelled | 24.7 | 24 | PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes |
| 66 | c3mv14 | Alignment | not modelled | 23.9 | 19 | PDB header: hydrolase Chain: 4: PDB Molecule: beta-galactosidase; PDBTitle: e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium |
| 67 | c6j9mA | Alignment | not modelled | 23.9 | 50 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: nmebh+acriic2 |
| 68 | c2cjdA | Alignment | not modelled | 23.8 | 16 | PDB header: transferase Chain: A: PDB Molecule: l-lysine-epsilon aminotransferase; PDBTitle: lysine aminotransferase from m. tuberculosis in external aldimine form |
| 69 | d1agxa | Alignment | not modelled | 23.6 | 27 | Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase |
| 70 | c2gzxB | Alignment | not modelled | 23.5 | 15 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative tatd related dnase; PDBTitle: crystal structure of the tatd deoxyribonuclease mw0446 from2 staphylococcus aureus. northeast structural genomics consortium3 target zr237. |
| 71 | d1zq1a2 | Alignment | not modelled | 23.2 | 24 | Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase |
| 72 | c5ey5A | Alignment | not modelled | 23.2 | 20 | PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats |
| 73 | d1jcua | Alignment | not modelled | 23.1 | 17 | Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like |
| 74 | c2r8zC | Alignment | not modelled | 23.1 | 9 | PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion |
| 75 | c5wmiA | Alignment | not modelled | 22.2 | 18 | PDB header: transferase Chain: A: PDB Molecule: bifunctional aspartate aminotransferase and PDBTitle: arabidopsis thaliana prephenate aminotransferase mutant- t84v |
| 76 | c3m1pA | Alignment | not modelled | 22.1 | 11 | PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate |
| 77 | c3k7pA | Alignment | not modelled | 22.1 | 11 | PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi. |
| 78 | d1xi3a | Alignment | not modelled | 21.7 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | Family: Thiamin phosphate synthase |
| 79 | c3sggA | Alignment | not modelled | 21.5 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: hypothetical hydrolase; PDBTitle: crystal structure of a putative hydrolase (bt_2193) from bacteroides2 thetaiotaomicron vpi-5482 at 1.25 a resolution |
| 80 | c1nijA | Alignment | not modelled | 21.5 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein |
| 81 | c3iz6A | Alignment | not modelled | 21.5 | 12 | PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 82 | c5diyB | Alignment | not modelled | 20.8 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: hyaluronidase; PDBTitle: thermobaculum terrenum o-glcnac hydrolase mutant - d120n |
| 83 | c3bgaB | Alignment | not modelled | 20.2 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482 |
| 84 | c4lkuE | Alignment | not modelled | 19.9 | 25 | PDB header: transport protein Chain: E: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 85 | c4rajA | Alignment | not modelled | 19.9 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of heme oxygenase 2 from chlamydomonas reinhardtii2 without heme. |
| 86 | c3ssoE | Alignment | not modelled | 19.8 | 16 | PDB header: transferase Chain: E: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2 |
| 87 | d1jr2a | Alignment | not modelled | 19.7 | 13 | Fold: HemD-like Superfamily: HemD-like Family: HemD-like |
| 88 | c1jr2A | Alignment | not modelled | 19.7 | 13 | PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase |
| 89 | c5xxuM | Alignment | not modelled | 18.9 | 15 | PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein es12; PDBTitle: small subunit of toxoplasma gondii ribosome |
| 90 | c2zsmA | Alignment | not modelled | 18.8 | 23 | PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form |
| 91 | d1ojra | Alignment | not modelled | 18.8 | 7 | Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase |
| 92 | c6etzA | Alignment | not modelled | 18.8 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: cold-adapted beta-d-galactosidase from arthrobacter sp. 32cb |
| 93 | d1pj3a1 | Alignment | not modelled | 18.1 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain |
| 94 | c3g7nA | Alignment | not modelled | 18.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3 |
| 95 | d1k7ja | Alignment | not modelled | 17.9 | 9 | Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like |
| 96 | c3m1yA | Alignment | not modelled | 17.8 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori |
| 97 | c5cgaC | Alignment | not modelled | 17.4 | 22 | PDB header: transferase Chain: C: PDB Molecule: hydroxyethylthiazole kinase; PDBTitle: structure of hydroxyethylthiazole kinase thim from staphylococcus2 aureus in complex with substrate analog 2-(1,3,5-trimethyl-1h-3 pyrazole-4-yl)ethanol |
| 98 | c3l7mC | Alignment | not modelled | 17.3 | 6 | PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a |
| 99 | c1yq2C | Alignment | not modelled | 16.9 | 21 | PDB header: hydrolase Chain: C: PDB Molecule: beta-galactosidase; PDBTitle: beta-galactosidase from arthrobacter sp. c2-2 (isoenzyme c2-2 2-1) |