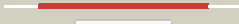



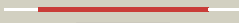




























Phyre2

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|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2222c_glnA2_2492410_2493750 |
| Date | Mon Aug 5 13:25:35 BST 2019 |
| Unique Job ID | ca14e6832b091edf |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c1fpyE_ |  Alignment |  | 100.0 | 38 | PDB header: ligase Chain: E; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin |
| 2 | c1htoB_ |  Alignment |  | 100.0 | 31 | PDB header: ligase Chain: B; PDB Molecule: glutamine synthetase; PDBTitle: crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis |
| 3 | c3ng0A_ |  Alignment |  | 100.0 | 34 | PDB header: ligase Chain: A; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803 |
| 4 | c5zlpH_ |  Alignment |  | 100.0 | 32 | PDB header: ligase Chain: H; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from helicobacter pylori |
| 5 | c3qajL_ |  Alignment |  | 100.0 | 45 | PDB header: ligase Chain: L; PDB Molecule: glutamine synthetase; PDBTitle: x-ray crystal structure of glutamine synthetase from bacillus subtilis2 cocrystallized with atp |
| 6 | c4s17E_ |  Alignment |  | 100.0 | 32 | PDB header: ligase Chain: E; PDB Molecule: glutamine synthetase; PDBTitle: the crystal structure of glutamine synthetase from bifidobacterium2 adolescentis atcc 15703 |
| 7 | c4hpaA_ |  Alignment |  | 100.0 | 27 | PDB header: ligase Chain: A; PDB Molecule: probable glutamine synthetase; PDBTitle: crystal structure of novel glutamine synthase homolog |
| 8 | c2j9iL_ |  Alignment |  | 100.0 | 26 | PDB header: ligase Chain: L; PDB Molecule: glutamate-ammonia ligase domain-containing protein 1; PDBTitle: lengsin is a survivor of an ancient family of class i glutamine2 synthetases in eukaryotes that has undergone evolutionary re-3 engineering for a tissue-specific role in the vertebrate eye lens. |
| 9 | c5dm3A_ |  Alignment |  | 100.0 | 31 | PDB header: ligase Chain: A; PDB Molecule: l-glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from chromohalobacter2 salexigens dsm 3043(csa1_0679, target efi-550015) with bound adp |
| 10 | d1f52a2 |  Alignment |  | 100.0 | 38 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain |
| 11 | d2bvca2 |  Alignment |  | 100.0 | 33 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | c2qc8J_ | Alignment |  | 100.0 | 21 | PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate |
| 13 | c4baxH_ | Alignment |  | 100.0 | 22 | PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from streptomyces2 coelicolor |
| 14 | c2d3aj_ | Alignment |  | 100.0 | 21 | PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate |
| 15 | c3fkyD_ | Alignment |  | 100.0 | 22 | PDB header: ligase Chain: D: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae |
| 16 | c4is4G_ | Alignment |  | 100.0 | 22 | PDB header: ligase Chain: G: PDB Molecule: glutamine synthetase; PDBTitle: the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer |
| 17 | c3o6xC_ | Alignment |  | 100.0 | 19 | PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis |
| 18 | d1f52a1 | Alignment |  | 99.9 | 40 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain |
| 19 | d2bvca1 | Alignment |  | 99.9 | 27 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain |
| 20 | c1tt4B_ | Alignment |  | 98.9 | 21 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cytoplasmic protein; PDBTitle: structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium |
| 21 | d1tt4a_ | Alignment | not modelled | 98.9 | 21 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2) |
| 22 | d1r8ga_ | Alignment | not modelled | 98.7 | 19 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2) |
| 23 | c2gwcE_ | Alignment | not modelled | 98.2 | 18 | PDB header: ligase Chain: E: PDB Molecule: glutamate cysteine ligase; PDBTitle: crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue |
| 24 | d1ur4a_ | Alignment | not modelled | 70.1 | 13 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases |
| 25 | d1u8sa2 | Alignment | not modelled | 40.3 | 9 | Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor |
| 26 | c5op0B_ | Alignment | not modelled | 40.3 | 9 | PDB header: transferase Chain: B: PDB Molecule: dna polymerase ligd, polymerase domain; PDBTitle: structure of prim-polc from mycobacterium smegmatis |
| 27 | c1u8sB_ | Alignment | not modelled | 33.3 | 10 | PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional repressor PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor |
| 28 | c3it5B_ | Alignment | not modelled | 32.2 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa |
| | | | | | | PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c2dr1A | Alignment | not modelled | 31.5 | 14 | aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3 |
| 30 | c1gvhA | Alignment | not modelled | 26.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavoheomprotein; PDBTitle: the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket |
| 31 | c3g12A | Alignment | not modelled | 25.9 | 11 | PDB header: lyase Chain: A: PDB Molecule: putative lactoylglutathione lyase; PDBTitle: crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus |
| 32 | d1sxc1 | Alignment | not modelled | 23.5 | 14 | Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain |
| 33 | d2bs2a3 | Alignment | not modelled | 22.1 | 20 | Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain |
| 34 | d1gvha3 | Alignment | not modelled | 22.1 | 25 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavoheomoglobin, C-terminal domain |
| 35 | c3lzcA | Alignment | not modelled | 21.0 | 16 | PDB header: biosynthetic protein Chain: A: PDB Molecule: dph2; PDBTitle: crystal structure of dph2 from pyrococcus horikoshii |
| 36 | d2c0ra1 | Alignment | not modelled | 20.9 | 15 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like |
| 37 | c2btwA | Alignment | not modelled | 20.5 | 17 | PDB header: transferase Chain: A: PDB Molecule: alr0975 protein; PDBTitle: crystal structure of alr0975 |
| 38 | d1neka3 | Alignment | not modelled | 19.1 | 12 | Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain |
| 39 | d1u8sa1 | Alignment | not modelled | 18.4 | 7 | Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor |
| 40 | d1ppva | Alignment | not modelled | 18.1 | 7 | Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like |
| 41 | c3p2oA | Alignment | not modelled | 18.0 | 21 | PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni |
| 42 | c4uirB | Alignment | not modelled | 17.4 | 10 | PDB header: lyase Chain: B: PDB Molecule: oleate hydratase; PDBTitle: structure of oleate hydratase from elizabethkingia2 meningoseptica |
| 43 | d1iqpa1 | Alignment | not modelled | 17.1 | 24 | Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain |
| 44 | d2bu3a1 | Alignment | not modelled | 16.4 | 17 | Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Phytochelatin synthase |
| 45 | c3p2oB | Alignment | not modelled | 16.1 | 21 | PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni |
| 46 | d1zpa1 | Alignment | not modelled | 16.1 | 3 | Fold: Ferredoxin-like Superfamily: ACT-like Family: SPO238-like |
| 47 | c5iwyD | Alignment | not modelled | 15.8 | 19 | PDB header: lyase Chain: D: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from bacillus subtilis complexed with cmp and mg2+ |
| 48 | c4bt7A | Alignment | not modelled | 15.7 | 17 | PDB header: lyase Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: acetolactate decarboxylase with a bound phosphate ion |
| 49 | c4biyD | Alignment | not modelled | 15.4 | 10 | PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2) |
| 50 | c2igoG | Alignment | not modelled | 15.0 | 21 | PDB header: oxidoreductase Chain: G: PDB Molecule: pyranose oxidase; PDBTitle: crystal structure of pyranose 2-oxidase h167a mutant with 2-fluoro-2-2 deoxy-d-glucose |
| 51 | d1chua3 | Alignment | not modelled | 14.6 | 19 | Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain |
| 52 | c4owtB | Alignment | not modelled | 14.2 | 18 | PDB header: dna binding protein Chain: B: PDB Molecule: soxx complex subunit b1; PDBTitle: structural basis of soxx1 complex assembly |
| 53 | d1ysia2 | Alignment | not modelled | 13.6 | 18 | Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | Family: Bacterial exopeptidase dimerisation domain |
| 54 | c2nyiB_ | Alignment | not modelled | 13.5 | 16 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria |
| 55 | c2gu1A_ | Alignment | not modelled | 13.5 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae |
| 56 | c3tnfF_ | Alignment | not modelled | 13.3 | 36 | PDB header: translation, toxin Chain: F: PDB Molecule: antitoxin vapb; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex |
| 57 | c5yhkB_ | Alignment | not modelled | 13.1 | 17 | PDB header: metal binding protein Chain: B: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterbacter2 aerogenes |
| 58 | c3pzqA_ | Alignment | not modelled | 13.0 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family PDBTitle: structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol |
| 59 | d1a4ia2 | Alignment | not modelled | 12.8 | 22 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase |
| 60 | c2jy5A_ | Alignment | not modelled | 12.8 | 32 | PDB header: signaling protein Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr structure of ubiquilin 1 uba domain |
| 61 | c3pg8B_ | Alignment | not modelled | 12.6 | 25 | PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima |
| 62 | d1z2la2 | Alignment | not modelled | 12.6 | 19 | Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain |
| 63 | c5z70B_ | Alignment | not modelled | 12.4 | 5 | PDB header: hydrolase Chain: B: PDB Molecule: oleate hydratase; PDBTitle: crystal strcure of oleate hydratase from stenotrophomonas sp. kctc2 12332 |
| 64 | c3d3aA_ | Alignment | not modelled | 12.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron |
| 65 | d1xv2a_ | Alignment | not modelled | 11.9 | 28 | Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: Alpha-acetolactate decarboxylase-like |
| 66 | c6ithA_ | Alignment | not modelled | 11.5 | 31 | PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles |
| 67 | c3uz0D_ | Alignment | not modelled | 11.3 | 25 | PDB header: transport protein Chain: D: PDB Molecule: stage ii sporulation protein q; PDBTitle: crystal structure of spoiiiah and spoiiq complex |
| 68 | c3kziE_ | Alignment | not modelled | 11.1 | 30 | PDB header: electron transport Chain: E: PDB Molecule: cytochrome b559 subunit alpha; PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii |
| 69 | c4e8cA_ | Alignment | not modelled | 11.1 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 35; PDBTitle: crystal structure of streptococcal beta-galactosidase in complex with2 galactose |
| 70 | c2pebB_ | Alignment | not modelled | 11.1 | 25 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative dioxygenase; PDBTitle: crystal structure of a putative dioxygenase (npun_f1925) from nostoc2 punctiforme pcc 73102 at 1.46 a resolution |
| 71 | d1sxd1 | Alignment | not modelled | 11.1 | 20 | Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain |
| 72 | d1prtc1 | Alignment | not modelled | 11.1 | 32 | Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits |
| 73 | c5knwA_ | Alignment | not modelled | 10.9 | 18 | PDB header: rna binding protein Chain: A: PDB Molecule: la-related protein 7; PDBTitle: solution nmr structure of human larp7 xrrm2 |
| 74 | c4madA_ | Alignment | not modelled | 10.9 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of beta-galactosidase c (bgac) from bacillus2 circulans atcc 31382 |
| 75 | c3ln7A_ | Alignment | not modelled | 10.8 | 12 | PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida |
| 76 | c4zonB_ | Alignment | not modelled | 10.6 | 21 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: verruculogen synthase; PDBTitle: structure of ftmox1 with fumitremorgen b complex |
| 77 | c3qm2A_ | Alignment | not modelled | 10.5 | 10 | PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium |
| 78 | c5yhoA_ | Alignment | not modelled | 10.3 | 17 | PDB header: metal binding protein Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | enterobacter2 cloacae |
| 79 | c2hsiB_ | Alignment | not modelled | 10.3 | 19 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from 2 pseudomonas aeruginosa, new york structural genomics3 consortium |
| 80 | c3jcue_ | Alignment | not modelled | 10.2 | 30 | PDB header: membrane protein Chain: E: PDB Molecule: cytochrome b559 subunit alpha; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution |
| 81 | d2axte1 | Alignment | not modelled | 9.9 | 30 | Fold: Single transmembrane helix Superfamily: Cytochrome b559 subunits Family: Cytochrome b559 subunits |
| 82 | c5xneA_ | Alignment | not modelled | 9.8 | 22 | PDB header: lyase Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: x-ray crystal structure of alpha-acetolactate decarboxylase from 2 bacillus subtilis strain 168 |
| 83 | d1eeja2 | Alignment | not modelled | 9.8 | 16 | Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like |
| 84 | d1sxb1 | Alignment | not modelled | 9.8 | 25 | Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain |
| 85 | c3ln6A_ | Alignment | not modelled | 9.7 | 15 | PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from 2 streptococcus agalactiae |
| 86 | c1vp7D_ | Alignment | not modelled | 9.6 | 38 | PDB header: hydrolase Chain: D: PDB Molecule: exodeoxyribonuclease vii small subunit; PDBTitle: crystal structure of exodeoxyribonuclease vii small subunit2 (np_881400.1) from bordetella pertussis at 2.40 a resolution |
| 87 | c6gcsF_ | Alignment | not modelled | 9.6 | 16 | PDB header: oxidoreductase Chain: F: PDB Molecule: nufm subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica |
| 88 | c3tufB_ | Alignment | not modelled | 9.5 | 19 | PDB header: signaling protein Chain: B: PDB Molecule: stage ii sporulation protein q; PDBTitle: structure of the spoiii-spoiiiah pore forming complex. |
| 89 | d1prt1 | Alignment | not modelled | 9.3 | 29 | Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits |
| 90 | c1nvpD_ | Alignment | not modelled | 9.2 | 26 | PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia gamma chain; PDBTitle: human tfiia/tbp/dna complex |
| 91 | c5kqbA_ | Alignment | not modelled | 9.1 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: peptidase m23; PDBTitle: identification and structural characterization of lytu |
| 92 | d1tz9a_ | Alignment | not modelled | 9.1 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like |
| 93 | c1a8pA_ | Alignment | not modelled | 9.1 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadph\;ferredoxin oxidoreductase; PDBTitle: ferredoxin reductase from azotobacter vinelandii |
| 94 | d1t3ba2 | Alignment | not modelled | 8.9 | 14 | Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like |
| 95 | c3re3B_ | Alignment | not modelled | 8.8 | 15 | PDB header: lyase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis |
| 96 | c3s5pA_ | Alignment | not modelled | 8.7 | 13 | PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia |
| 97 | c1cqxB_ | Alignment | not modelled | 8.4 | 37 | PDB header: lipid binding protein Chain: B: PDB Molecule: flavohemoprotein; PDBTitle: crystal structure of the flavohemoglobin from alcaligenes eutrophus at 2 1.75 a resolution |
| 98 | c4g1bB_ | Alignment | not modelled | 8.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: flavohemoglobin; PDBTitle: x-ray structure of yeast flavohemoglobin in complex with econazole |
| 99 | c3htnA_ | Alignment | not modelled | 7.9 | 13 | PDB header: metal binding protein Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: crystal structure of a putative dna binding protein (bt_1116) from 2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution |