

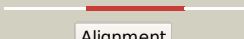

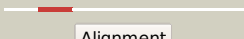



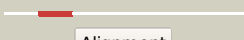














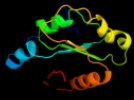


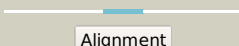

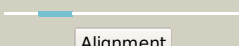
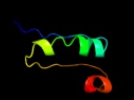
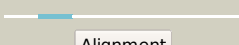

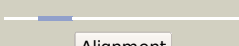
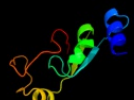
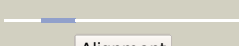
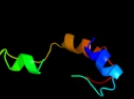



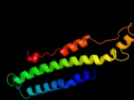
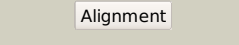



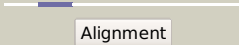
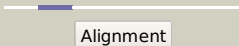




Phyre2

| | |
|---------------|------------------------------|
| Email | l.a.kelley@imperial.ac.uk |
| Description | A2A6C4 |
| Date | Wed Jul 10 14:09:18 BST 2013 |
| Unique Job ID | 3942da38da4d6729 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c3icuA_ |  Alignment |  | 99.4 | 16 | PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase rnf128; PDBTitle: protease-associated domain of the e3 ligase grail |
| 2 | c4hydA_ |  Alignment |  | 98.6 | 20 | PDB header: membrane protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a presenilin family intramembrane aspartate protease in2 c2221 space group |
| 3 | d1de4c2 |  Alignment |  | 98.1 | 24 | Fold: The "swivelling" beta/beta/alpha domain Superfamily: PA domain Family: PA domain |
| 4 | d3bi1a2 |  Alignment |  | 98.0 | 26 | Fold: The "swivelling" beta/beta/alpha domain Superfamily: PA domain Family: PA domain |
| 5 | c2ootA_ |  Alignment |  | 97.8 | 26 | PDB header: hydrolase Chain: A; PDB Molecule: glutamate carboxypeptidase 2; PDBTitle: a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii |
| 6 | c1xf1A_ |  Alignment |  | 97.7 | 25 | PDB header: hydrolase Chain: A; PDB Molecule: c5a peptidase; PDBTitle: structure of c5a peptidase- a key virulence factor from2 streptococcus |
| 7 | c3rbuA_ |  Alignment |  | 97.7 | 26 | PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: glutamate carboxypeptidase 2; PDBTitle: n-terminally avitev-tagged human glutamate carboxypeptidase ii in2 complex with 2-pmpa |
| 8 | c1cx8F_ |  Alignment |  | 97.6 | 21 | PDB header: metal transport Chain: F; PDB Molecule: transferrin receptor protein; PDBTitle: crytal structure of the ectodomain of human transferrin receptor |
| 9 | c2kr6A_ |  Alignment |  | 97.3 | 33 | PDB header: hydrolase Chain: A; PDB Molecule: presenilin-1; PDBTitle: solution structure of presenilin-1 ctf subunit |
| 10 | c2ek8A_ |  Alignment |  | 97.3 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1 |
| 11 | c3iibA_ |  Alignment |  | 96.2 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: peptidase m28; PDBTitle: crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution |

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|----|-------------------------|---|---|------|----|--|
| 12 | c4kngF_ |  Alignment |  | 95.4 | 20 | PDB header: signaling protein, membrane protein Chain: F: PDB Molecule: e3 ubiquitin-protein ligase rnf43; PDBTitle: crystal structure of human lgr5-rspo1-rnf43 |
| 13 | c3vtaB_ |  Alignment |  | 73.8 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: cucumisin; PDBTitle: crystal structure of cucumisin, a subtilisin-like endoprotease from2 cucumis melo l |
| 14 | c2rh1A_ |  Alignment |  | 36.2 | 15 | PDB header: membrane protein / hydrolase Chain: A: PDB Molecule: beta-2-adrenergic receptor/t4-lysozyme chimera; PDBTitle: high resolution crystal structure of human b2-adrenergic g protein-2 coupled receptor. |
| 15 | c2l69A_ |  Alignment |  | 33.7 | 18 | PDB header: de novo protein Chain: A: PDB Molecule: rossmann 2x3 fold protein; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28 |
| 16 | c3i74B_ |  Alignment |  | 33.2 | 7 | PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: subtilisin-like protease; PDBTitle: crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor |
| 17 | c2hj0A_ |  Alignment |  | 24.3 | 17 | PDB header: lyase Chain: A: PDB Molecule: putative citrate lyase, alfa subunit; PDBTitle: crystal structure of the putative alfa subunit of citrate lyase in2 complex with citrate from streptococcus mutans, northeast structural3 genomics target smr12 (casp target). |
| 18 | c3femB_ |  Alignment |  | 20.8 | 24 | PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae |
| 19 | d1rk4a2 |  Alignment |  | 20.4 | 33 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain |
| 20 | c4jkvA_ |  Alignment |  | 20.3 | 12 | PDB header: membrane protein Chain: A: PDB Molecule: soluble cytochrome b562, smoothed homolog; PDBTitle: structure of the human smoothed 7tm receptor in complex with an2 antitumor agent |
| 21 | c3rgbG_ |  Alignment | not modelled | 19.1 | 21 | PDB header: oxidoreductase Chain: G: PDB Molecule: methane monooxygenase subunit c2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath) |
| 22 | c4adsF_ |  Alignment | not modelled | 18.5 | 22 | PDB header: transferase/transferase Chain: F: PDB Molecule: pyridoxine biosynthetic enzyme pdx1 homologue, putative; PDBTitle: crystal structure of plasmodial plp synthase complex |
| 23 | c3uonA_ |  Alignment | not modelled | 16.1 | 17 | PDB header: signaling protein/antagonist Chain: A: PDB Molecule: human m2 muscarinic acetylcholine, receptor t4 lysozyme PDBTitle: structure of the human m2 muscarinic acetylcholine receptor bound to2 an antagonist |
| 24 | c1jy4A_ |  Alignment | not modelled | 15.9 | 57 | PDB header: de novo protein Chain: A: PDB Molecule: b4dimer; PDBTitle: b4dimer: a de novo designed eight-stranded beta-sheet2 assembled using a disulfide bond |
| 25 | c3rrlC_ |  Alignment | not modelled | 15.6 | 13 | PDB header: transferase Chain: C: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; PDBTitle: complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695 |
| 26 | c2k2jA_ |  Alignment | not modelled | 15.4 | 17 | PDB header: hydrolase, signaling protein Chain: A: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate PDBTitle: nmr solution structure of the split ph domain from2 phospholipase c gamma 2 |
| 27 | d1twda_ |  Alignment | not modelled | 15.2 | 20 | Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like |
| 28 | c3iwpK_ |  Alignment | not modelled | 14.4 | 20 | PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein |

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|----|--------------------------|-----------|--------------|------|----|--|
| | | | | | | cutc |
| 29 | c1tla_ | Alignment | not modelled | 13.8 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase, brain; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution. |
| 30 | c1xr4B_ | Alignment | not modelled | 13.5 | 11 | PDB header: hydrolase/transferase Chain: B: PDB Molecule: putative citrate lyase alpha chain/citrate-acp transferase; PDBTitle: x-ray crystal structure of putative citrate lyase alpha chain/citrate-2 acp transferase [salmonella typhimurium] |
| 31 | c3frk_ | Alignment | not modelled | 13.4 | 20 | PDB header: oxidoreductase Chain: K: PDB Molecule: pmoc; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m |
| 32 | c2nv2U_ | Alignment | not modelled | 13.3 | 22 | PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis |
| 33 | c2kzkA_ | Alignment | not modelled | 12.6 | 40 | PDB header: protein transport Chain: A: PDB Molecule: uncharacterized protein yol083w; PDBTitle: solution structure of alpha-mannosidase binding domain of atg34 |
| 34 | d1n7za_ | Alignment | not modelled | 12.5 | 35 | Fold: Baseplate structural protein gp8 Superfamily: Baseplate structural protein gp8 Family: Baseplate structural protein gp8 |
| 35 | c4grvA_ | Alignment | not modelled | 11.8 | 17 | PDB header: signaling protein/agonist Chain: A: PDB Molecule: neurotensin receptor type 1, lysozyme chimera; PDBTitle: the crystal structure of the neurotensin receptor nts1 in complex with2 neurotensin (8-13) |
| 36 | c2ovsB_ | Alignment | not modelled | 11.5 | 21 | PDB header: gene regulation, ligand binding protein Chain: B: PDB Molecule: l0044; PDBTitle: crystal structure of a type three secretion system protein |
| 37 | c4firB_ | Alignment | not modelled | 11.4 | 22 | PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxal biosynthesis lyase pdxs from pyrococcus |
| 38 | c3lerA_ | Alignment | not modelled | 11.4 | 35 | PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168 |
| 39 | c2kzbA_ | Alignment | not modelled | 11.2 | 40 | PDB header: protein transport Chain: A: PDB Molecule: autophagy-related protein 19; PDBTitle: solution structure of alpha-mannosidase binding domain of atg19 |
| 40 | c1zgwA_ | Alignment | not modelled | 11.1 | 44 | PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna |
| 41 | c2zbtB_ | Alignment | not modelled | 11.0 | 26 | PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8 |
| 42 | d1tla2_ | Alignment | not modelled | 10.8 | 32 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like |
| 43 | c2v9dB_ | Alignment | not modelled | 10.8 | 28 | PDB header: lyase Chain: B: PDB Molecule: yage; PDBTitle: crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12 |
| 44 | c2yv5A_ | Alignment | not modelled | 10.7 | 5 | PDB header: hydrolase Chain: A: PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus |
| 45 | d1xxa1_ | Alignment | not modelled | 10.4 | 35 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 46 | d2a6na1_ | Alignment | not modelled | 10.1 | 28 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 47 | c3daqB_ | Alignment | not modelled | 10.0 | 18 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus |
| 48 | d1poia_ | Alignment | not modelled | 10.0 | 14 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 49 | d1ja1a2_ | Alignment | not modelled | 9.9 | 33 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like |
| 50 | c3fluD_ | Alignment | not modelled | 9.6 | 33 | PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis |
| 51 | c2r8wB_ | Alignment | not modelled | 9.5 | 35 | PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58 |
| 52 | d2dk8a1_ | Alignment | not modelled | 9.4 | 34 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RPO3F domain-like |
| 53 | c1bkbA_ | Alignment | not modelled | 9.4 | 8 | PDB header: translation Chain: A: PDB Molecule: translation initiation factor 5a; PDBTitle: initiation factor 5a from archebacterium pyrobaculum2 aerophilum |
| 54 | d1ohfa_ | Alignment | not modelled | 9.4 | 35 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tetrahiridae-like VP |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 55 | c2nuxB | Alignment | not modelled | 9.0 | 11 | PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfobobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution |
| 56 | d1ooya2 | Alignment | not modelled | 8.9 | 17 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 57 | c1qp6B | Alignment | not modelled | 8.8 | 28 | PDB header: de novo protein Chain: B: PDB Molecule: protein (alpha2d); PDBTitle: solution structure of alpha2d |
| 58 | c2rfgB | Alignment | not modelled | 8.7 | 35 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution |
| 59 | c3vw7A | Alignment | not modelled | 8.7 | 9 | PDB header: signaling protein/antagonist Chain: A: PDB Molecule: protease-activated receptor 1, lysozyme; PDBTitle: crystal structure of human protease-activated receptor 1 (par1) bound2 with antagonist vorapaxar at 2.2 angstrom |
| 60 | c3hr4C | Alignment | not modelled | 8.7 | 22 | PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex |
| 61 | d1o5ka | Alignment | not modelled | 8.7 | 33 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 62 | c3n2xB | Alignment | not modelled | 8.6 | 26 | PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate |
| 63 | c3dm5A | Alignment | not modelled | 8.5 | 63 | PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus. |
| 64 | c3lciA | Alignment | not modelled | 8.4 | 17 | PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w |
| 65 | c3s5oA | Alignment | not modelled | 8.4 | 17 | PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; PDBTitle: crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate |
| 66 | c2j37W | Alignment | not modelled | 8.4 | 63 | PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein PDBTitle: model of mammalian srp bound to 80s rncs |
| 67 | c4g7xA | Alignment | not modelled | 8.3 | 36 | PDB header: protein binding/protein binding Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a complex between the ctxphi piii n-terminal2 domain and the vibrio cholerae tola c-terminal domain |
| 68 | d2ahua2 | Alignment | not modelled | 8.3 | 11 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 69 | c3bi8A | Alignment | not modelled | 8.3 | 33 | PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum |
| 70 | c3si9B | Alignment | not modelled | 8.3 | 26 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae |
| 71 | c3cprB | Alignment | not modelled | 8.2 | 41 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution |
| 72 | c4h2dB | Alignment | not modelled | 8.2 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1 |
| 73 | c3f59A | Alignment | not modelled | 8.2 | 24 | PDB header: structural protein Chain: A: PDB Molecule: ankyrin-1; PDBTitle: crystal structure of zu5-ank, the spectrin binding region of human2 erythroid ankyrin |
| 74 | c3d0cB | Alignment | not modelled | 8.2 | 33 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution |
| 75 | c3na8A | Alignment | not modelled | 8.2 | 18 | PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa |
| 76 | d1hnra | Alignment | not modelled | 8.1 | 86 | Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins |
| 77 | c1qzwC | Alignment | not modelled | 8.1 | 75 | PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication |
| 78 | c4g7wB | Alignment | not modelled | 8.0 | 36 | PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of the minor coat protein2 piii from ctxphi |
| 79 | c3e96B | Alignment | not modelled | 8.0 | 29 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii |
| | | | | | | PDB header: lyase |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 80 | c3noeA | Alignment | not modelled | 8.0 | 33 | Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa |
| 81 | d1p42a1 | Alignment | not modelled | 7.9 | 17 | Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC |
| 82 | c3pueA | Alignment | not modelled | 7.8 | 33 | PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution |
| 83 | c2hmcA | Alignment | not modelled | 7.8 | 41 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens |
| 84 | c2yzzB | Alignment | not modelled | 7.8 | 24 | PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii |
| 85 | c3epmB | Alignment | not modelled | 7.8 | 29 | PDB header: biosynthetic protein Chain: B: PDB Molecule: thiamine biosynthesis protein thic; PDBTitle: crystal structure of caulobacter crescentus thic |
| 86 | c3fkkA | Alignment | not modelled | 7.8 | 29 | PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase |
| 87 | c2r94B | Alignment | not modelled | 7.7 | 24 | PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax |
| 88 | d1b1ca | Alignment | not modelled | 7.6 | 33 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like |
| 89 | c1j9zB | Alignment | not modelled | 7.6 | 33 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g |
| 90 | c3b4uB | Alignment | not modelled | 7.6 | 22 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58 |
| 91 | d1eyfa | Alignment | not modelled | 7.5 | 44 | Fold: Ada DNA repair protein, N-terminal domain (N-Ada 10) Superfamily: Ada DNA repair protein, N-terminal domain (N-Ada 10) Family: Ada DNA repair protein, N-terminal domain (N-Ada 10) |
| 92 | d1jb0L | Alignment | not modelled | 7.5 | 35 | Fold: Photosystem I reaction center subunit XI, PsaL Superfamily: Photosystem I reaction center subunit XI, PsaL Family: Photosystem I reaction center subunit XI, PsaL |
| 93 | c3cz6A | Alignment | not modelled | 7.5 | 18 | PDB header: protein binding Chain: A: PDB Molecule: dna-binding protein rap1; PDBTitle: crystal structure of the rap1 c-terminus |
| 94 | c3ixzB | Alignment | not modelled | 7.3 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride |
| 95 | d1k6da | Alignment | not modelled | 7.3 | 19 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like |
| 96 | d2nsfa2 | Alignment | not modelled | 7.3 | 21 | Fold: SCP-like Superfamily: SCP-like Family: Micthiol-dependent maleylpyruvate isomerase C-terminal domain-like |
| 97 | d1xe7a | Alignment | not modelled | 7.2 | 38 | Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YML079-like |
| 98 | c4dppB | Alignment | not modelled | 7.2 | 11 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase 2, chloroplastic; PDBTitle: the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana |
| 99 | d1w3ia | Alignment | not modelled | 7.2 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |