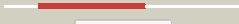
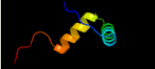

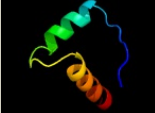

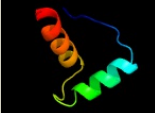

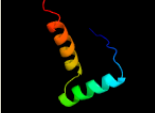






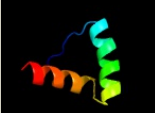






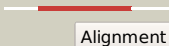

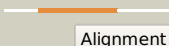

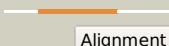



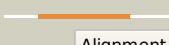
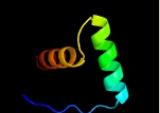
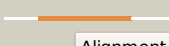

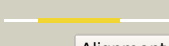

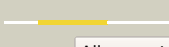

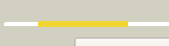
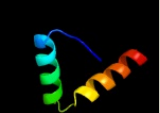
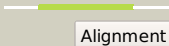
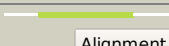
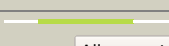
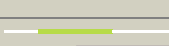
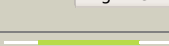
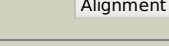
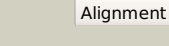
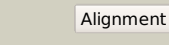
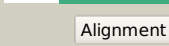


Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1241_(-)_1384284_1384544 |
| Date | Wed Jul 31 22:05:33 BST 2019 |
| Unique Job ID | 0e18ef713a503a8e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c5x3tA_ |  Alignment |  | 95.9 | 24 | PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapb26; PDBTitle: vapbc from mycobacterium tuberculosis |
| 2 | c2bj3D_ |  Alignment |  | 95.1 | 10 | PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo |
| 3 | c1q5vB_ |  Alignment |  | 94.3 | 38 | PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr |
| 4 | c2k5jB_ |  Alignment |  | 94.2 | 18 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1 |
| 5 | d2bsqe1 |  Alignment |  | 94.2 | 9 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like |
| 6 | d2bj7a1 |  Alignment |  | 94.2 | 10 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 7 | c2h1oH_ |  Alignment |  | 93.8 | 9 | PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment |
| 8 | d1p94a_ |  Alignment |  | 93.6 | 19 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 9 | c2ca9B_ |  Alignment |  | 93.6 | 13 | PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation |
| 10 | c6a7vU_ |  Alignment |  | 92.9 | 25 | PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex |
| 11 | d2hzaa1 |  Alignment |  | 92.1 | 38 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |

| | | | | | | |
|----|-------------------------|---|---|------|----|--|
| 12 | d2hzab1 |  Alignment |  | 91.2 | 38 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 13 | c4aaiB |  Alignment |  | 86.6 | 30 | PDB header: viral protein Chain: B: PDB Molecule: orf e73; PDBTitle: thermostable protein from hyperthermophilic virus ssv-rh |
| 14 | c4a1qB |  Alignment |  | 86.6 | 30 | PDB header: viral protein Chain: B: PDB Molecule: orf e73; PDBTitle: solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park |
| 15 | c6g1nB |  Alignment |  | 83.5 | 16 | PDB header: antitoxin Chain: B: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb |
| 16 | c3kk4B |  Alignment |  | 81.4 | 15 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i |
| 17 | c4p7dA |  Alignment |  | 80.1 | 15 | PDB header: toxin Chain: A: PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure |
| 18 | c5yrzC |  Alignment |  | 79.2 | 19 | PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae |
| 19 | c2an7A |  Alignment |  | 77.1 | 17 | PDB header: dna binding protein Chain: A: PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard |
| 20 | c2k29A |  Alignment |  | 73.3 | 14 | PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb |
| 21 | d1mnta |  Alignment | not modelled | 64.4 | 15 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors |
| 22 | c1ea4K |  Alignment | not modelled | 64.1 | 23 | PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex |
| 23 | d2cpga |  Alignment | not modelled | 64.1 | 23 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 24 | c4hv0B |  Alignment | not modelled | 63.6 | 19 | PDB header: transcription, viral protein Chain: B: PDB Molecule: avtr; PDBTitle: structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus |
| 25 | c6iyaD |  Alignment | not modelled | 61.0 | 24 | PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso |
| 26 | d1xrx1 |  Alignment | not modelled | 50.4 | 25 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like |
| 27 | c1xrxD |  Alignment | not modelled | 50.4 | 25 | PDB header: replication inhibitor Chain: D: PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein |
| 28 | c1rrbA |  Alignment | not modelled | 48.8 | 22 | PDB header: transferase Chain: A: PDB Molecule: raf proto-oncogene serine/threonine-protein PDBTitle: the ras-binding domain of raf-1 from rat, nmr, 1 structure |
| 29 | c3fntF |  Alignment | not modelled | 48.4 | 20 | PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | PDBTitle: crystal structure of seqa bound to dna |
| 30 | c4fxeB_ | Alignment | not modelled | 42.5 | 15 | PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex |
| 31 | c2rbfB_ | Alignment | not modelled | 41.4 | 21 | PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2) |
| 32 | c3kxeD_ | Alignment | not modelled | 41.2 | 27 | PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex |
| 33 | c3h87D_ | Alignment | not modelled | 39.3 | 17 | PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis |
| 34 | c2kelB_ | Alignment | not modelled | 34.2 | 16 | PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1 |
| 35 | d1gtma2 | Alignment | not modelled | 29.5 | 23 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases |
| 36 | c4pg8B_ | Alignment | not modelled | 29.1 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of s. aureus homoserine dehydrogenase at pH8.5 |
| 37 | d1hwxa2 | Alignment | not modelled | 28.1 | 18 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases |
| 38 | c1u9pA_ | Alignment | not modelled | 27.9 | 15 | PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc |
| 39 | d1bvua2 | Alignment | not modelled | 27.7 | 23 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases |
| 40 | c5k12F_ | Alignment | not modelled | 26.7 | 18 | PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate dehydrogenase 1, mitochondrial; PDBTitle: cryo-em structure of glutamate dehydrogenase at 1.8 a resolution |
| 41 | d1euza2 | Alignment | not modelled | 25.7 | 23 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases |
| 42 | c2mdvB_ | Alignment | not modelled | 25.4 | 29 | PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38 |
| 43 | d1bgva2 | Alignment | not modelled | 25.2 | 23 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases |
| 44 | d1q9ja2 | Alignment | not modelled | 24.8 | 16 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase) |
| 45 | c6bwqB_ | Alignment | not modelled | 22.4 | 16 | PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp |
| 46 | d1b26a2 | Alignment | not modelled | 22.2 | 23 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases |
| 47 | d1c1yb_ | Alignment | not modelled | 21.9 | 22 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD |
| 48 | d1v9la2 | Alignment | not modelled | 21.0 | 32 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases |
| 49 | d1vhb_ | Alignment | not modelled | 20.6 | 17 | Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain |
| 50 | c5xviA_ | Alignment | not modelled | 20.1 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of aspergillus niger apo- glutamate dehydrogenase |
| 51 | c3aogA_ | Alignment | not modelled | 19.4 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form) |
| 52 | d1l1fa2 | Alignment | not modelled | 19.3 | 18 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases |
| 53 | c3mtjA_ | Alignment | not modelled | 19.3 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a |
| 54 | c6noyB_ | Alignment | not modelled | 18.4 | 25 | PDB header: structural protein Chain: B: PDB Molecule: maintenance of carboxysome positioning b protein, mcsb; PDBTitle: structure of cyanothecce mcdb |
| 55 | c3sboA_ | Alignment | not modelled | 18.2 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-specific glutamate dehydrogenase; |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: structure of e.coli gdh from native source |
| 56 | c6dzsD_ | Alignment | not modelled | 17.9 | 11 | PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp |
| 57 | c3k8zD_ | Alignment | not modelled | 17.8 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudb1 a decrypted secondary glutamate2 dehydrogenase from b. subtilis |
| 58 | c3do5A_ | Alignment | not modelled | 17.6 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution |
| 59 | d1v71a1 | Alignment | not modelled | 17.3 | 10 | Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes |
| 60 | c3ingA_ | Alignment | not modelled | 17.2 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution |
| 61 | c6gtsC_ | Alignment | not modelled | 17.2 | 18 | PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna |
| 62 | c4q2uM_ | Alignment | not modelled | 16.8 | 12 | PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex |
| 63 | c2bmaA_ | Alignment | not modelled | 15.7 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase (nadp+); PDBTitle: the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs |
| 64 | c5yxiA_ | Alignment | not modelled | 15.7 | 26 | PDB header: de novo protein Chain: A: PDB Molecule: drafx6; PDBTitle: designed protein drafx6 |
| 65 | c5ijzH_ | Alignment | not modelled | 15.7 | 23 | PDB header: oxidoreductase Chain: H: PDB Molecule: nadp-specific glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase(gdh) from corynebacterium2 glutamicum |
| 66 | d1ebfa2 | Alignment | not modelled | 15.4 | 17 | Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like |
| 67 | c4xgiA_ | Alignment | not modelled | 15.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase from burkholderia2 thailandensis |
| 68 | c1v9lA_ | Alignment | not modelled | 14.8 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad |
| 69 | d1b3ta_ | Alignment | not modelled | 14.7 | 17 | Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain |
| 70 | c3r3jC_ | Alignment | not modelled | 14.5 | 23 | PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: kinetic and structural characterization of plasmodium falciparum2 glutamate dehydrogenase 2 |
| 71 | c3c8mA_ | Alignment | not modelled | 14.2 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium |
| 72 | c3i12A_ | Alignment | not modelled | 13.5 | 9 | PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2 |
| 73 | c3aoeC_ | Alignment | not modelled | 13.4 | 32 | PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form) |
| 74 | c1hrdA_ | Alignment | not modelled | 12.9 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: glutamate dehydrogenase |
| 75 | c1bvuf_ | Alignment | not modelled | 12.6 | 23 | PDB header: oxidoreductase Chain: F: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: glutamate dehydrogenase from thermococcus litoralis |
| 76 | c2tmgD_ | Alignment | not modelled | 12.3 | 23 | PDB header: oxidoreductase Chain: D: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e |
| 77 | c6ajnF_ | Alignment | not modelled | 12.2 | 23 | PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atatr bound with accoa |
| 78 | c2yfqA_ | Alignment | not modelled | 11.8 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus |
| 79 | d1rfma_ | Alignment | not modelled | 11.1 | 7 | Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like |
| 80 | d1vrpa1 | Alignment | not modelled | 11.1 | 15 | Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain |
| | | | | | | PDB header: oxidoreductase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 81 | c1nr1A_ | Alignment | not modelled | 10.8 | 18 | Chain: A: PDB Molecule: glutamate dehydrogenase 1; PDBTitle: crystal structure of the r463a mutant of human glutamate dehydrogenase |
| 82 | c5cegC_ | Alignment | not modelled | 10.7 | 11 | PDB header: toxin Chain: C: PDB Molecule: addiction module antidote protein, copg/arc/metj family; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum |
| 83 | c3i71B_ | Alignment | not modelled | 10.0 | 34 | PDB header: unknown function Chain: B: PDB Molecule: ethanolamine utilization protein eutk; PDBTitle: ethanolamine utilization microcompartment shell subunit, eutk c-2 terminal domain |
| 84 | d1y9ba1 | Alignment | not modelled | 9.9 | 18 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like |
| 85 | d1i0ea1 | Alignment | not modelled | 9.5 | 12 | Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain |
| 86 | d1u6ra1 | Alignment | not modelled | 9.4 | 15 | Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain |
| 87 | d1crka1 | Alignment | not modelled | 8.9 | 9 | Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain |
| 88 | c1x93B_ | Alignment | not modelled | 8.9 | 19 | PDB header: transcription Chain: B: PDB Molecule: hypothetical protein hp0222; PDBTitle: nmr structure of helicobacter pylori hp0222 |
| 89 | d1x93a1 | Alignment | not modelled | 8.9 | 19 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 90 | c2ejwB_ | Alignment | not modelled | 8.7 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8 |
| 91 | c4xb1B_ | Alignment | not modelled | 8.3 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: 319aa long hypothetical homoserine dehydrogenase; PDBTitle: hyperthermophilic archaeal homoserine dehydrogenase in complex with2 nadph |
| 92 | c1ebuA_ | Alignment | not modelled | 7.7 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase complex with nad analogue and l-2 homoserine |
| 93 | d1qh4a1 | Alignment | not modelled | 7.2 | 15 | Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain |
| 94 | c3qoqC_ | Alignment | not modelled | 7.0 | 14 | PDB header: transcription/dna Chain: C: PDB Molecule: alginate and motility regulator z; PDBTitle: crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site |
| 95 | d1g0wa1 | Alignment | not modelled | 6.8 | 9 | Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain |
| 96 | c1yx5A_ | Alignment | not modelled | 6.6 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: 26s proteasome non-atpase regulatory subunit 4; PDBTitle: solution structure of s5a uim-1/ubiquitin complex |
| 97 | c1h2iG_ | Alignment | not modelled | 6.4 | 35 | PDB header: dna binding protein Chain: G: PDB Molecule: dna repair protein rad52 homolog; PDBTitle: human rad52 protein, n-terminal domain |
| 98 | d1rhta2 | Alignment | not modelled | 6.3 | 15 | Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain |
| 99 | c3c19A_ | Alignment | not modelled | 6.2 | 12 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19 |