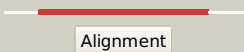

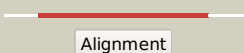

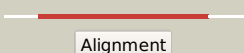

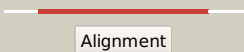

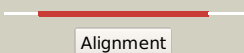

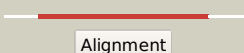
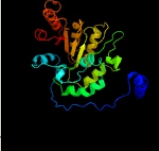

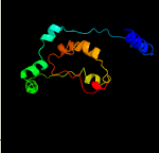
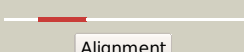
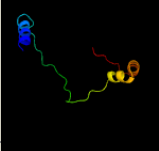



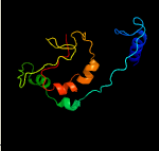
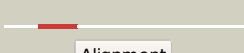
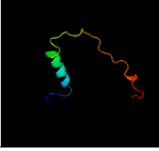

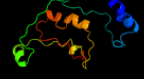

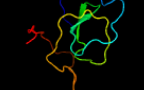

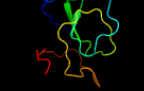
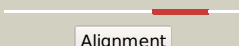

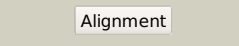



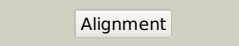
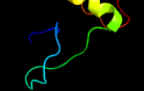
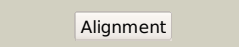


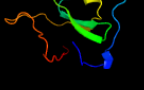

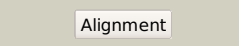
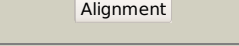
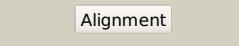
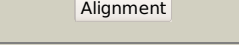
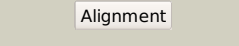
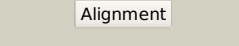
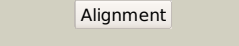


Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0263c_(-)_314864_315766 |
| Date | Tue Jul 23 14:50:32 BST 2019 |
| Unique Job ID | ef11e2204f17dac6 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | c3mmlE_ |  Alignment |  | 100.0 | 79 | PDB header: hydrolase Chain: E; PDB Molecule: allophanate hydrolase subunit 2; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436 |
| 2 | c5dudA_ |  Alignment |  | 100.0 | 34 | PDB header: unknown function Chain: A; PDB Molecule: ybgk; PDBTitle: crystal structure of e. coli ybgk |
| 3 | c3oepA_ |  Alignment |  | 100.0 | 31 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative uncharacterized protein ttha0988; PDBTitle: crystal structure of ttha0988 in space group p43212 |
| 4 | c3va7A_ |  Alignment |  | 100.0 | 28 | PDB header: ligase Chain: A; PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase |
| 5 | c5i8iD_ |  Alignment |  | 100.0 | 28 | PDB header: hydrolase Chain: D; PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase |
| 6 | c5vz0D_ |  Alignment |  | 99.3 | 10 | PDB header: ligase Chain: D; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp |
| 7 | c3bg5B_ |  Alignment |  | 99.1 | 12 | PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase |
| 8 | c4qskB_ |  Alignment |  | 98.9 | 7 | PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp |
| 9 | c4hnbB_ |  Alignment |  | 98.5 | 9 | PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase |
| 10 | c3hblA_ |  Alignment |  | 98.3 | 13 | PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant |
| 11 | c3tw6B_ |  Alignment |  | 97.9 | 11 | PDB header: ligase/activator Chain: B; PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a |

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|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | c2qf7A_ |  Alignment |  | 96.3 | 14 | PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli |
| 13 | c2phcB_ |  Alignment |  | 95.0 | 18 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii |
| 14 | d2phcb1 |  Alignment |  | 93.9 | 18 | Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like |
| 15 | c2zp2B_ |  Alignment |  | 93.9 | 17 | PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis |
| 16 | c5dudB_ |  Alignment |  | 90.7 | 23 | PDB header: unknown function Chain: B: PDB Molecule: ybgj; PDBTitle: crystal structure of e. coli ybgjk |
| 17 | d1x7fa1 |  Alignment |  | 90.4 | 15 | Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Outer surface protein, C-terminal domain |
| 18 | c2p0oA_ |  Alignment |  | 88.5 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf871; PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function |
| 19 | c3elsA_ |  Alignment |  | 88.3 | 17 | PDB header: splicing Chain: A: PDB Molecule: pre-mrna leakage protein 1; PDBTitle: crystal structure of yeast pm11p, residues 51-204 |
| 20 | c3mmlD_ |  Alignment |  | 87.9 | 24 | PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436 |
| 21 | c2jkdB_ |  Alignment | not modelled | 87.7 | 12 | PDB header: gene regulation Chain: B: PDB Molecule: pre-mrna leakage protein 1; PDBTitle: structure of the yeast pm11 splicing factor and its2 integration into the res complex |
| 22 | c1x7fa_ |  Alignment | not modelled | 87.2 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein |
| 23 | d2piea1 |  Alignment | not modelled | 87.0 | 12 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 24 | c1gxcA_ |  Alignment | not modelled | 86.1 | 21 | PDB header: phosphoprotein-binding domain Chain: A: PDB Molecule: serine/threonine-protein kinase chk2; PDBTitle: fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide |
| 25 | d1gxca_ |  Alignment | not modelled | 86.1 | 21 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 26 | d1uhta_ |  Alignment | not modelled | 82.0 | 22 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 27 | c4jonA_ |  Alignment | not modelled | 81.6 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: centrosomal protein of 170 kda; PDBTitle: crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom) |
| 28 | c3poaA_ |  Alignment | not modelled | 79.7 | 30 | PDB header: peptide binding protein Chain: A: PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: structural and functional analysis of phosphothreonine-dependent fha2 domain interactions |

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|----|-------------------------|-----------|--------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | c4h87A | Alignment | not modelled | 77.6 | 17 | PDB header: peptide binding protein Chain: A: PDB Molecule: kanadaplin; PDBTitle: crystal structure of a fha domain of kanadaplin (slc4a1ap) from homo2 sapiens at 1.55 a resolution |
| 30 | c3vpyA | Alignment | not modelled | 77.3 | 11 | PDB header: protein binding Chain: A: PDB Molecule: fha domain-containing protein ddl; PDBTitle: crystal structure of arabidopsis ddl fha domain |
| 31 | c5yyxA | Alignment | not modelled | 74.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: meiosis-specific serine/threonine-protein kinase mek1; PDBTitle: crystal structure of the mek1 fha domain |
| 32 | c2n84A | Alignment | not modelled | 74.7 | 17 | PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the fha domain of tbpar42 |
| 33 | c3ounA | Alignment | not modelled | 73.5 | 30 | PDB header: protein binding/transferase Chain: A: PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: crystal structure of the fhaa domain complexed with the2 intracellular domain of rv3910 |
| 34 | c5z58X | Alignment | not modelled | 72.0 | 8 | PDB header: splicing Chain: X: PDB Molecule: smad nuclear-interacting protein 1; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom. |
| 35 | c5djoB | Alignment | not modelled | 71.3 | 19 | PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein; PDBTitle: crystal structure of the cc1-fha tandem of kinesin-3 kif13a |
| 36 | c2jpeA | Alignment | not modelled | 71.0 | 6 | PDB header: transcription Chain: A: PDB Molecule: nuclear inhibitor of protein phosphatase 1; PDBTitle: fha domain of nipp1 |
| 37 | d1yjma1 | Alignment | not modelled | 70.8 | 18 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 38 | c3fm8A | Alignment | not modelled | 68.8 | 20 | PDB header: transport protein/hydrolase activator Chain: A: PDB Molecule: kinesin-like protein kif13b; PDBTitle: crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target) |
| 39 | d2brfa1 | Alignment | not modelled | 68.5 | 13 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 40 | c3kt9A | Alignment | not modelled | 67.3 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: aprataxin; PDBTitle: aprataxin fha domain |
| 41 | c5fwhA | Alignment | not modelled | 66.5 | 24 | PDB header: structural protein Chain: A: PDB Molecule: essc; PDBTitle: n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus |
| 42 | c5t2sA | Alignment | not modelled | 65.5 | 20 | PDB header: cell cycle Chain: A: PDB Molecule: ddk kinase regulatory subunit dbf4,serine/threonine-protein PDBTitle: structure of the fha1 domain of rad53 bound simultaneously to the brct2 domain of dbf4 and a phosphopeptide. |
| 43 | c4eqxA | Alignment | not modelled | 61.9 | 24 | PDB header: transport protein Chain: A: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a cc1-fha tandem |
| 44 | c6cahA | Alignment | not modelled | 61.5 | 23 | PDB header: protein binding Chain: A: PDB Molecule: abc transporter atp-binding/permease protein rv1747; PDBTitle: nmr-based structure of the fha-2 domain from mycobacterium2 tuberculosis abc transporter rv1747 |
| 45 | d2ff4a3 | Alignment | not modelled | 61.2 | 16 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 46 | d1g3ga | Alignment | not modelled | 58.9 | 20 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 47 | d1ujxa | Alignment | not modelled | 55.4 | 17 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 48 | c1yj5C | Alignment | not modelled | 54.1 | 11 | PDB header: transferase Chain: C: PDB Molecule: 5' polynucleotide kinase-3' phosphatase fha domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme |
| 49 | c3kf6B | Alignment | not modelled | 53.3 | 27 | PDB header: structural protein Chain: B: PDB Molecule: protein ten1; PDBTitle: crystal structure of s. pombe stn1-ten1 complex |
| 50 | d2g1la1 | Alignment | not modelled | 53.0 | 23 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 51 | c5z81A | Alignment | not modelled | 52.5 | 23 | PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 15; PDBTitle: trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution |
| 52 | d1dmza | Alignment | not modelled | 49.1 | 17 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 53 | c2kkIA | Alignment | not modelled | 49.0 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mb1858; PDBTitle: solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155). |
| 54 | c3hx1B | Alignment | not modelled | 48.8 | 27 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: slr1951 protein; PDBTitle: crystal structure of the slr1951 protein from |

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|----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | | | | | | synechocystis sp.2 northeast structural genomics consortium target sgr167a |
| 55 | c1zeqX_ | Alignment | not modelled | 48.7 | 20 | PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli |
| 56 | d2affa1 | Alignment | not modelled | 46.6 | 14 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 57 | c6ar2B_ | Alignment | not modelled | 46.0 | 17 | PDB header: membrane protein Chain: B: PDB Molecule: sarcolemmal membrane-associated protein; PDBTitle: structure of human slmap fha domain in complex with pmst2 |
| 58 | c2kfuA_ | Alignment | not modelled | 45.3 | 16 | PDB header: protein binding Chain: A: PDB Molecule: rv1827 pthr 22; PDBTitle: pknb-phosphorylated rv1827 |
| 59 | c2eh0A_ | Alignment | not modelled | 45.3 | 24 | PDB header: transport protein Chain: A: PDB Molecule: kinesin-like protein kif1b; PDBTitle: solution structure of the fha domain from human kinesin-2 like protein kif1b |
| 60 | c1dm9A_ | Alignment | not modelled | 45.1 | 15 | PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd |
| 61 | d1dm9a_ | Alignment | not modelled | 45.1 | 15 | Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kd |
| 62 | c2k6pA_ | Alignment | not modelled | 43.3 | 26 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423 |
| 63 | c1r21A_ | Alignment | not modelled | 42.8 | 14 | PDB header: cell cycle Chain: A: PDB Molecule: antigen ki-67; PDBTitle: solution structure of human ki67 fha domain |
| 64 | c2i55A_ | Alignment | not modelled | 41.3 | 13 | PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans |
| 65 | d1wlna1 | Alignment | not modelled | 40.7 | 18 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 66 | d1w96c1 | Alignment | not modelled | 39.4 | 15 | Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like |
| 67 | d1lgpa_ | Alignment | not modelled | 39.4 | 24 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |
| 68 | c3uotB_ | Alignment | not modelled | 37.8 | 17 | PDB header: cell cycle Chain: B: PDB Molecule: mediator of dna damage checkpoint protein 1; PDBTitle: crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus |
| 69 | c4ejqB_ | Alignment | not modelled | 36.2 | 26 | PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a c-cc1-fha |
| 70 | c5a8iA_ | Alignment | not modelled | 34.9 | 13 | PDB header: transcription Chain: A: PDB Molecule: arna; PDBTitle: crystal structure of the fha domain of arna from sulfobolus2 acidocaldarius |
| 71 | c3gmgB_ | Alignment | not modelled | 34.7 | 19 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rv1825/mt1873; PDBTitle: crystal structure of an uncharacterized conserved protein from2 mycobacterium tuberculosis |
| 72 | d2cu3a1 | Alignment | not modelled | 34.4 | 20 | Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS |
| 73 | c2g1eA_ | Alignment | not modelled | 34.4 | 27 | PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895 |
| 74 | d1zud21 | Alignment | not modelled | 32.2 | 33 | Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS |
| 75 | d1sida_ | Alignment | not modelled | 28.9 | 22 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group I dsDNA viruses Family: Papovaviridae-like VP |
| 76 | c5cu1A_ | Alignment | not modelled | 27.4 | 18 | PDB header: lyase Chain: A: PDB Molecule: dmsp lyase; PDBTitle: crystal structure of dmsp lyase dddq from ruegeria pomeroyi dss-3 |
| 77 | c2jq1A_ | Alignment | not modelled | 26.7 | 14 | PDB header: cell cycle Chain: A: PDB Molecule: dna damage response protein kinase dun1; PDBTitle: nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1 |
| 78 | c3di4A_ | Alignment | not modelled | 26.4 | 15 | PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf1989; PDBTitle: crystal structure of a duf1989 family protein (spo0365) from2 silicibacter pomeroyi dss-3 at 1.60 a resolution |
| 79 | d1g6ga_ | Alignment | not modelled | 26.3 | 17 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |

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|----|-------------------------|-----------|--------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 80 | d1tkea1 | Alignment | not modelled | 25.5 | 23 | Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain |
| 81 | c3cwiA | Alignment | not modelled | 25.0 | 20 | PDB header: biosynthetic protein Chain: A: PDB Molecule: thiamine-biosynthesis protein this; PDBTitle: crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137 |
| 82 | c3po0A | Alignment | not modelled | 24.8 | 19 | PDB header: protein binding Chain: A: PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii |
| 83 | c4n6eB | Alignment | not modelled | 24.6 | 24 | PDB header: lyase/biosynthetic protein Chain: B: PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex |
| 84 | c2q1dX | Alignment | not modelled | 24.5 | 21 | PDB header: lyase Chain: X: PDB Molecule: 2-keto-3-deoxy-d-arabinonate dehydratase; PDBTitle: 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate |
| 85 | c3rlgA | Alignment | not modelled | 23.4 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase d lisictox-alpha1a; PDBTitle: crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant |
| 86 | c3hvvB | Alignment | not modelled | 23.2 | 27 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a |
| 87 | c5mpoA | Alignment | not modelled | 23.1 | 19 | PDB header: transferase Chain: A: PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex |
| 88 | c3zn5D | Alignment | not modelled | 23.1 | 24 | PDB header: viral protein Chain: D: PDB Molecule: vp16; PDBTitle: vp16, a capsid protein of bacteriophage p23-77 (vp16-virus-derived) |
| 89 | c2kmmA | Alignment | not modelled | 23.1 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: guanosine-3',5'-bis(diphosphate) 3'- PDBTitle: solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481) |
| 90 | d1v10a2 | Alignment | not modelled | 23.0 | 15 | Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins |
| 91 | d1kf6b2 | Alignment | not modelled | 22.2 | 11 | Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins |
| 92 | c2kl0A | Alignment | not modelled | 21.7 | 30 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325 |
| 93 | c4a0eB | Alignment | not modelled | 20.4 | 17 | PDB header: transport protein Chain: B: PDB Molecule: type iii secretion protein; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of yersinia2 pestis yscd |
| 94 | d1snoa | Alignment | not modelled | 20.3 | 16 | Fold: OB-fold Superfamily: Staphylococcal nuclease Family: Staphylococcal nuclease |
| 95 | c4ml1D | Alignment | not modelled | 19.8 | 28 | PDB header: isomerase Chain: D: PDB Molecule: dsbp; PDBTitle: disulfide isomerase (dsbp) from multidrug resistance inca/c2 transferable plasmid in oxidized state (p212121 space group) |
| 96 | d1nyra2 | Alignment | not modelled | 19.7 | 18 | Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain |
| 97 | c6iyxB | Alignment | not modelled | 19.5 | 46 | PDB header: hydrolase Chain: B: PDB Molecule: 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase; PDBTitle: fumarylacetoacetate hydrolase (eafah) from psychrophilic2 exiguobacterium antarcticum |
| 98 | c4mbyB | Alignment | not modelled | 19.3 | 26 | PDB header: viral protein Chain: B: PDB Molecule: major capsid protein vp1; PDBTitle: structure of b-lymphotropic polyomavirus vp1 in complex with 3'-2 sialyllactose |
| 99 | d1mzka | Alignment | not modelled | 18.6 | 15 | Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain |