

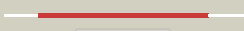























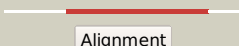

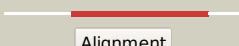

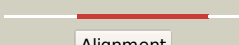

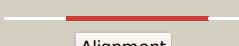






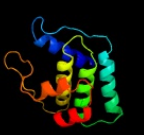
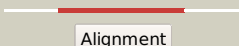
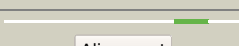
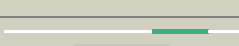
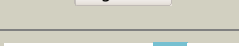
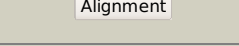
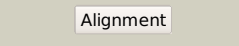
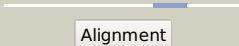
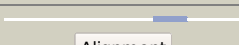



Phyre2

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|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
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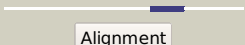


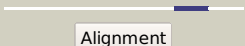
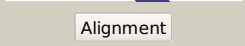
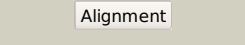

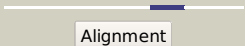

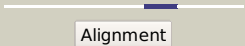
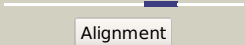
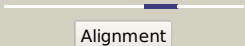

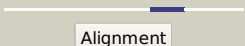
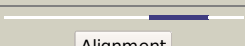
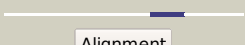



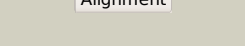
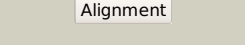

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | c3eqxB_ |  Alignment |  | 100.0 | 16 | PDB header: dna binding protein Chain: B: PDB Molecule: fic domain containing transcriptional regulator; PDBTitle: crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution |
| 2 | c4rglA_ |  Alignment |  | 100.0 | 20 | PDB header: dna binding protein Chain: A: PDB Molecule: filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution |
| 3 | c3cucB_ |  Alignment |  | 100.0 | 13 | PDB header: signaling protein Chain: B: PDB Molecule: protein of unknown function with a fic domain; PDBTitle: crystal structure of a fic domain containing signaling protein2 (bt_2513) from bacteroides thetaiotaomicron vpi-5482 at 2.71 a3 resolution |
| 4 | c4u0zH_ |  Alignment |  | 100.0 | 15 | PDB header: transferase Chain: H: PDB Molecule: adenosine monophosphate-protein transferase ficd; PDBTitle: eukaryotic fic domain containing protein with bound apcpp |
| 5 | c5jj6A_ |  Alignment |  | 100.0 | 16 | PDB header: transferase Chain: A: PDB Molecule: adenosine monophosphate-protein transferase ficd homolog; PDBTitle: fic-1 (aa134 - 508) from c. elegans |
| 6 | c4x2eA_ |  Alignment |  | 100.0 | 12 | PDB header: transferase Chain: A: PDB Molecule: fic family protein putative filamentation induced by camp PDBTitle: clostridium difficile wild type fic protein |
| 7 | c3n3vA_ |  Alignment |  | 99.9 | 10 | PDB header: transferase Chain: A: PDB Molecule: adenosine monophosphate-protein transferase ibpa; PDBTitle: crystal structure of ibpafic2-h3717a in complex with adenyllylated2 cdc42 |
| 8 | c5jffC_ |  Alignment |  | 99.9 | 15 | PDB header: transferase Chain: C: PDB Molecule: probable adenosine monophosphate-protein transferase fic; PDBTitle: e. coli ecfict mutant g55r in complex with ecfica |
| 9 | c4lu4A_ |  Alignment |  | 99.9 | 13 | PDB header: transferase Chain: A: PDB Molecule: putative cell filamentation protein; PDBTitle: crystal structure of the n-terminal fic domain of a putative cell2 filamentation protein (virb-translocated bep effector protein) from3 bartonella quintana |
| 10 | c3shgA_ |  Alignment |  | 99.8 | 13 | PDB header: transferase/protein binding Chain: A: PDB Molecule: vbht; PDBTitle: vbht fic protein from bartonella schoenbuchensis in complex with vbha2 antitoxin |
| 11 | c2f6sA_ |  Alignment |  | 99.8 | 12 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cell filamentation protein, putative; PDBTitle: structure of cell filamentation protein (fic) from helicobacter pylori |

| | | | | | | |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | c5nwfB |  Alignment |  | 99.8 | 12 | PDB header: toxin Chain: B: PDB Molecule: fic family protein; PDBTitle: enterococcus faecalis fic protein (h111a). |
| 13 | d2f6sa1 |  Alignment |  | 99.8 | 12 | Fold: Fic-like Superfamily: Fic-like Family: Fic-like |
| 14 | c4xi8B |  Alignment |  | 99.8 | 11 | PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the fic domain of bep5 protein (virb-translocated2 bartonella effector protein) from bartonella clarridgeiae |
| 15 | c4py3B |  Alignment |  | 99.8 | 11 | PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the n-terminal fic domain of bep8 protein (virb-2 translocated bartonella effector protein) from bartonella sp. 1-1c |
| 16 | d2g03a1 |  Alignment |  | 99.8 | 13 | Fold: Fic-like Superfamily: Fic-like Family: Fic-like |
| 17 | c4m16A |  Alignment |  | 99.7 | 9 | PDB header: cell adhesion Chain: A: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the n-terminal fic domain of bartonella effector2 protein (bep); substrate of virb t4ss (virb-translocated bep effector3 protein) from bartonella sp. ar 15-3 |
| 18 | c4npsA |  Alignment |  | 99.7 | 12 | PDB header: cell adhesion Chain: A: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of bep1 protein (virb-translocated bartonella2 effector protein) from bartonella clarridgeiae |
| 19 | c2vzaD |  Alignment |  | 99.4 | 14 | PDB header: cell adhesion Chain: D: PDB Molecule: cell filamentation protein; PDBTitle: type iv secretion system effector protein bepa |
| 20 | c3dd7A |  Alignment |  | 98.8 | 17 | PDB header: ribosome inhibitor Chain: A: PDB Molecule: death on curing protein; PDBTitle: structure of doch66y in complex with the c-terminal domain of phd |
| 21 | c3letB |  Alignment | not modelled | 98.3 | 10 | PDB header: transferase Chain: B: PDB Molecule: adenosine monophosphate-protein transferase vops; PDBTitle: crystal structure of fic domain containing ampylator, vops |
| 22 | d1v54h |  Alignment | not modelled | 50.0 | 11 | Fold: Cytochrome c oxidase subunit h Superfamily: Cytochrome c oxidase subunit h Family: Cytochrome c oxidase subunit h |
| 23 | c6h1nA |  Alignment | not modelled | 40.9 | 16 | PDB header: apoptosis Chain: A: PDB Molecule: bcl2-like 10 (apoptosis facilitator); PDBTitle: crystal structure of a zebra-fish pro-survival protein nrz- apo |
| 24 | d1yl7a1 |  Alignment | not modelled | 34.2 | 37 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 25 | d1u8fo1 |  Alignment | not modelled | 28.5 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 26 | d1j0xo1 |  Alignment | not modelled | 28.0 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 27 | d1dja1 |  Alignment | not modelled | 25.6 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 28 | d1ggaa1 |  Alignment | not modelled | 24.5 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| | |  Alignment | | | | Fold: NAD(P)-binding Rossmann-fold domains |

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|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | d3gpdg1 | Alignment | not modelled | 24.1 | 21 | Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 30 | d1s2xa | Alignment | not modelled | 23.6 | 27 | Fold: STAT-like Superfamily: Cag-Z Family: Cag-Z |
| 31 | c1s2xA | Alignment | not modelled | 23.6 | 27 | PDB header: unknown function Chain: A: PDB Molecule: cag-z; PDBTitle: crystal structure of cag-z from helicobacter pylori |
| 32 | d1k3ta1 | Alignment | not modelled | 23.0 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 33 | c3ijpA | Alignment | not modelled | 22.7 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution |
| 34 | d2b4ro1 | Alignment | not modelled | 22.3 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 35 | d1s0pa | Alignment | not modelled | 20.4 | 12 | Fold: N-terminal domain of adenylylcyase associated protein, CAP Superfamily: N-terminal domain of adenylylcyase associated protein, CAP Family: N-terminal domain of adenylylcyase associated protein, CAP |
| 36 | d1hdgo1 | Alignment | not modelled | 20.3 | 25 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 37 | d1gado1 | Alignment | not modelled | 19.7 | 29 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 38 | c1yl7F | Alignment | not modelled | 19.3 | 37 | PDB header: oxidoreductase Chain: F: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c) |
| 39 | d1obfo1 | Alignment | not modelled | 19.0 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 40 | c4aezC | Alignment | not modelled | 18.4 | 10 | PDB header: cell cycle Chain: C: PDB Molecule: mitotic spindle checkpoint component mad3; PDBTitle: crystal structure of mitotic checkpoint complex |
| 41 | c3idwA | Alignment | not modelled | 18.0 | 13 | PDB header: endocytosis Chain: A: PDB Molecule: actin cytoskeleton-regulatory complex protein sla1; PDBTitle: crystal structure of sla1 homology domain 2 |
| 42 | c5lcwS | Alignment | not modelled | 17.1 | 12 | PDB header: cell cycle Chain: S: PDB Molecule: mitotic checkpoint serine/threonine-protein kinase bub1 PDBTitle: cryo-em structure of the anaphase-promoting complex/cyclosome, in2 complex with the mitotic checkpoint complex (apc/c-mcc) at 4.23 angstrom resolution |
| 43 | c1d5rA | Alignment | not modelled | 16.9 | 9 | PDB header: hydrolase Chain: A: PDB Molecule: phosphoinositide phosphatase pten; PDBTitle: crystal structure of the pten tumor suppressor |
| 44 | d1vc2a1 | Alignment | not modelled | 15.8 | 26 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 45 | c2p58C | Alignment | not modelled | 15.7 | 22 | PDB header: transport protein/chaperone Chain: C: PDB Molecule: putative type iii secretion protein yscg; PDBTitle: structure of the yersinia pestis type iii secretion system needle2 protein yscf in complex with its chaperones ysce/yscg |
| 46 | d1rm4a1 | Alignment | not modelled | 15.5 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 47 | c5kt0A | Alignment | not modelled | 15.2 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis. |
| 48 | c5eesA | Alignment | not modelled | 14.8 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dapb in complex with nadp+ from corynebacterium2 glutamicum |
| 49 | c5wolA | Alignment | not modelled | 14.8 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase dapb from coxiella2 burnetii |
| 50 | d1vm6a3 | Alignment | not modelled | 14.6 | 8 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 51 | d3cmco1 | Alignment | not modelled | 14.6 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 52 | c6dzpg | Alignment | not modelled | 13.9 | 29 | PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: cryo-em structure of mycobacterium smegmatis c(minus) 50s ribosomal2 subunit |
| 53 | d1dcca1 | Alignment | not modelled | 13.6 | 25 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains |

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|----|-------------------------|-----------|--------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 53 | d1ussy1 | Alignment | not modelled | 13.8 | 23 | Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 54 | d3etja2 | Alignment | not modelled | 12.7 | 22 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like |
| 55 | d2pkqo1 | Alignment | not modelled | 12.6 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 56 | c5ugjC_ | Alignment | not modelled | 12.5 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis |
| 57 | c1i32D_ | Alignment | not modelled | 12.4 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors |
| 58 | d1i32a1 | Alignment | not modelled | 12.2 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 59 | d1uzxa_ | Alignment | not modelled | 12.1 | 10 | Fold: UBC-like Superfamily: UBC-like Family: UEV domain |
| 60 | c2j034_ | Alignment | not modelled | 12.0 | 22 | PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii. |
| 61 | d2j0141 | Alignment | not modelled | 12.0 | 22 | Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p |
| 62 | c3hq4R_ | Alignment | not modelled | 11.5 | 26 | PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase 1; PDBTitle: crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution |
| 63 | c3bhwA_ | Alignment | not modelled | 11.3 | 9 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from magnetospirillum2 magneticum |
| 64 | d1vs6z1 | Alignment | not modelled | 11.1 | 20 | Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p |
| 65 | c5ld5C_ | Alignment | not modelled | 11.1 | 21 | PDB header: oxidoreductase Chain: C: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of a bacterial dehydrogenase at 2.19 angstroms2 resolution |
| 66 | d1bf4a_ | Alignment | not modelled | 10.4 | 20 | Fold: SH3-like barrel Superfamily: Chromo domain-like Family: "Histone-like" proteins from archaea |
| 67 | c2ksdA_ | Alignment | not modelled | 10.3 | 11 | PDB header: transferase Chain: A: PDB Molecule: aerobic respiration control sensor protein arcb; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor arcb, center for structures of membrane proteins (csm)3 target 4310c |
| 68 | c6hu9j_ | Alignment | not modelled | 10.3 | 16 | PDB header: oxidoreductase/electron transport Chain: J: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae |
| 69 | d2g82a1 | Alignment | not modelled | 9.9 | 25 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 70 | c1hdgO_ | Alignment | not modelled | 9.7 | 25 | PDB header: oxidoreductase (aldehy(d)-nad(a)) dehydrogenase; Chain: O: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: the crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase2 from the hyperthermophilic bacterium thermotoga maritima at 2.53 angstroms resolution |
| 71 | c2yyvB_ | Alignment | not modelled | 9.7 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase |
| 72 | c2ep7B_ | Alignment | not modelled | 9.5 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structural study of project id aq_1065 from aquifex aeolicus vf5 |
| 73 | c6g21B_ | Alignment | not modelled | 9.4 | 7 | PDB header: hydrolase Chain: B: PDB Molecule: probable feruloyl esterase b-2; PDBTitle: crystal structure of an esterase from aspergillus oryzae |
| 74 | c6fqbe_ | Alignment | not modelled | 9.4 | 12 | PDB header: ligase Chain: E: PDB Molecule: cobyrinic acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6 |
| 75 | c1drwA_ | Alignment | not modelled | 9.4 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex |
| 76 | d2j01d1 | Alignment | not modelled | 9.0 | 30 | Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2 |

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|----|-------------------------|-------------------------------------------------------------------------------------|--------------|-----|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 77 | c5ur0B_ |  | not modelled | 9.0 | 29 | PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystallographic structure of glyceraldehyde-3-phosphate dehydrogenase2 from naegleria gruberi |
| 78 | c3pk1A_ |  | not modelled | 9.0 | 13 | PDB header: apoptosis/apoptosis regulator Chain: A: PDB Molecule: induced myeloid leukemia cell differentiation protein mcl- PDBTitle: crystal structure of mcl-1 in complex with the baxbh3 domain |
| 79 | c4p40A_ |  | not modelled | 8.8 | 9 | PDB header: transport protein Chain: A: PDB Molecule: copn; PDBTitle: chlamydia pneumoniae copn |
| 80 | c3wmtA_ |  | not modelled | 8.8 | 7 | PDB header: hydrolase Chain: A: PDB Molecule: probable feruloyl esterase b-1; PDBTitle: crystal structure of feruloyl esterase b from aspergillus oryzae |
| 81 | c3nfqA_ |  | not modelled | 8.7 | 15 | PDB header: transcription Chain: A: PDB Molecule: transcription factor iws1; PDBTitle: crystal structure of the conserved central domain of yeast spn1/iws1 |
| 82 | d1adta1 |  | not modelled | 8.7 | 5 | Fold: Domain of early E2A DNA-binding protein, ADDBP Superfamily: Domain of early E2A DNA-binding protein, ADDBP Family: Domain of early E2A DNA-binding protein, ADDBP |
| 83 | c4qx6A_ |  | not modelled | 8.6 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 streptococcus agalactiae nem316 at 2.46 angstrom resolution |
| 84 | c3lhIA_ |  | not modelled | 8.5 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: putative agmatinase; PDBTitle: crystal structure of a putative agmatinase from clostridium difficile |
| 85 | c3cieC_ |  | not modelled | 8.4 | 29 | PDB header: oxidoreductase Chain: C: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum |
| 86 | d1v54g_ |  | not modelled | 8.4 | 17 | Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIa Family: Mitochondrial cytochrome c oxidase subunit VIa |
| 87 | c3wg7T_ |  | not modelled | 8.4 | 17 | PDB header: oxidoreductase Chain: T: PDB Molecule: cytochrome c oxidase subunit 6a2, mitochondrial; PDBTitle: a 1.9 angstrom radiation damage free x-ray structure of large (420kda)2 protein by femtosecond crystallography |
| 88 | c5z62G_ |  | not modelled | 8.3 | 33 | PDB header: electron transport Chain: G: PDB Molecule: cytochrome c oxidase subunit 6a1, mitochondrial; PDBTitle: structure of human cytochrome c oxidase |
| 89 | c3zd0A_ |  | not modelled | 8.3 | 18 | PDB header: transport protein Chain: A: PDB Molecule: p7 protein; PDBTitle: the solution structure of monomeric hepatitis c virus p72 yields potent inhibitors of virion release |
| 90 | c2gd1P_ |  | not modelled | 8.1 | 29 | PDB header: oxidoreductase(aldehyde(d)-nad(a)) Chain: P: PDB Molecule: apo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: coenzyme-induced conformational changes in glyceraldehyde-3-2 phosphate dehydrogenase from bacillus stearothermophilus |
| 91 | d1sw8a_ |  | not modelled | 8.0 | 20 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 92 | c5iyfB_ |  | not modelled | 8.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structures of streptococcus agalactiae gbs gapdh in different2 enzymatic states |
| 93 | c3b20R_ |  | not modelled | 8.0 | 20 | PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase (nadp+); PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase2 complexed with nadfrom synechococcus elongatus" |
| 94 | c4l8nA_ |  | not modelled | 7.9 | 38 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pdz domain protein; PDBTitle: crystal structure of a pdz domain protein (bdi_1242) from2 parabacteroides distasonis atcc 8503 at 2.50 a resolution |
| 95 | c3h9eO_ |  | not modelled | 7.9 | 28 | PDB header: oxidoreductase Chain: O: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase, testis-specific; PDBTitle: crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate |
| 96 | c2vfwB_ |  | not modelled | 7.9 | 22 | PDB header: transferase Chain: B: PDB Molecule: short-chain z-isoprenyl diphosphate synthetase; PDBTitle: rv1086 native |
| 97 | c2b664_ |  | not modelled | 7.7 | 29 | PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400 |
| 98 | c2b4rQ_ |  | not modelled | 7.7 | 21 | PDB header: oxidoreductase Chain: Q: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom |

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|----|-------------------------|-----------|--------------|-----|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 99 | c4r7rA_ | Alignment | not modelled | 7.6 | 45 | <p>resolution reveals intriguing3 extra electron density in the active site</p> <p>PDB header:lipid binding protein</p> <p>Chain: A: PDB Molecule:putative lipoprotein;</p> <p>PDBTitle: crystal structure of putative lipoprotein from clostridium perfringens</p> |
|----|-------------------------|-----------|--------------|-----|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|