






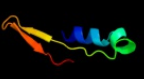


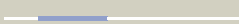







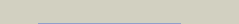



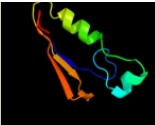

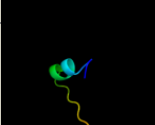
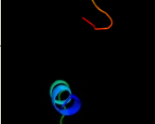







| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | d2hh8a1 |  Alignment |  | 100.0 | 100 | Fold: YdfO-like Superfamily: YdfO-like Family: YdfO-like |
| 2 | d3elga1 |  Alignment |  | 88.3 | 8 | Fold: BLIP-like Superfamily: BT0923-like Family: BT0923-like |
| 3 | d3duea1 |  Alignment |  | 79.7 | 6 | Fold: BLIP-like Superfamily: BT0923-like Family: BT0923-like |
| 4 | c2w3nA |  Alignment |  | 25.1 | 24 | PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase 2; PDBTitle: structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans |
| 5 | c2qlxA |  Alignment |  | 23.9 | 15 | PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose |
| 6 | c2qlwA |  Alignment |  | 23.9 | 15 | PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum |
| 7 | c1irjG |  Alignment |  | 23.2 | 15 | PDB header: metal binding protein Chain: G: PDB Molecule: migration inhibitory factor-related protein 14; PDBTitle: crystal structure of the mrp14 complexed with chaps |
| 8 | c3l23A |  Alignment |  | 21.7 | 11 | PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution |
| 9 | c3fm2A |  Alignment |  | 21.3 | 11 | PDB header: heme-binding protein Chain: A: PDB Molecule: uncharacterized protein, distantly related to a heme PDBTitle: crystal structure of a putative heme-binding protein (ava_4353) from2 anabaena variabilis atcc 29413 at 1.80 a resolution |
| 10 | d1avsa |  Alignment |  | 21.1 | 16 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 11 | c3ot2A |  Alignment |  | 20.7 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution |

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|----|--------------------------|-----------|---|------|----|--|
| 12 | c3ot2B_ | Alignment |  | 20.7 | 17 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution |
| 13 | d1urra_ | Alignment |  | 20.5 | 21 | Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like |
| 14 | c2ph7B_ | Alignment |  | 19.4 | 33 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein af_2093; PDBTitle: crystal structure of af2093 from archaeoglobus fulgidus |
| 15 | d1lapsa_ | Alignment |  | 17.3 | 10 | Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like |
| 16 | c3obeB_ | Alignment |  | 17.0 | 11 | PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution |
| 17 | d1xk4a1 | Alignment |  | 16.2 | 16 | Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |
| 18 | d1j3ea_ | Alignment |  | 15.5 | 24 | Fold: Replication modulator SeqA, C-terminal DNA-binding domain Superfamily: Replication modulator SeqA, C-terminal DNA-binding domain Family: Replication modulator SeqA, C-terminal DNA-binding domain |
| 19 | c2hklB_ | Alignment |  | 14.4 | 10 | PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant |
| 20 | d2acva_ | Alignment |  | 14.0 | 14 | Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like |
| 21 | d1x8da1 | Alignment | not modelled | 14.0 | 21 | Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: YiiL-like |
| 22 | c2bjeA_ | Alignment | not modelled | 13.5 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: acylphosphatase; PDBTitle: acylphosphatase from sulfobolus solfataricus. monoclinic p212 space group |
| 23 | c2k7ba_ | Alignment | not modelled | 13.3 | 6 | PDB header: metal binding protein Chain: A: PDB Molecule: calcium-binding protein 1; PDBTitle: nmr structure of mg2+-bound cabp1 n-domain |
| 24 | d1w2ia_ | Alignment | not modelled | 12.9 | 21 | Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like |
| 25 | d1k8ua_ | Alignment | not modelled | 12.7 | 27 | Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |
| 26 | c1f8aB_ | Alignment | not modelled | 12.4 | 12 | PDB header: isomerase Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase nima- PDBTitle: structural basis for the phosphoserine-proline recognition2 by group iv ww domains |
| 27 | d1i6pa_ | Alignment | not modelled | 12.3 | 14 | Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab |
| 28 | d4icba_ | Alignment | not modelled | 12.2 | 18 | Fold: EF Hand-like Superfamily: EF-hand Family: Calbindin D9K |
| 29 | d1j55a_ | Alignment | not modelled | 12.0 | 12 | Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |

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|----|-------------------------|-----------|--------------|------|----|---|
| 30 | d1ekja_ | Alignment | not modelled | 12.0 | 14 | Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab |
| 31 | d1ulra_ | Alignment | not modelled | 11.4 | 16 | Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like |
| 32 | c2a4iA_ | Alignment | not modelled | 11.4 | 14 | PDB header: structural protein Chain: A: PDB Molecule: centrin 2; PDBTitle: solution structure of the c-terminal domain (t94-y172) of2 the human centrin 2 in complex with a 17 residues peptide3 (p1-xpc) from xeroderma pigmentosum group c protein |
| 33 | d1m39a_ | Alignment | not modelled | 11.4 | 15 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 34 | d1dj0a_ | Alignment | not modelled | 11.4 | 12 | Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase TruA |
| 35 | d2gaxa1 | Alignment | not modelled | 11.3 | 17 | Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II |
| 36 | c2ggmA_ | Alignment | not modelled | 11.1 | 14 | PDB header: cell cycle Chain: A: PDB Molecule: centrin-2; PDBTitle: human centrin 2 xeroderma pigmentosum group c protein2 complex |
| 37 | c2kaxA_ | Alignment | not modelled | 11.1 | 23 | PDB header: metal binding protein Chain: A: PDB Molecule: protein s100-a5; PDBTitle: solution structure and dynamics of s100a5 in the apo and2 ca2+ -bound states |
| 38 | d1e8aa_ | Alignment | not modelled | 11.0 | 19 | Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |
| 39 | c2k7wB_ | Alignment | not modelled | 10.8 | 35 | PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bax activation is initiated at a novel interaction site |
| 40 | d1pvaa_ | Alignment | not modelled | 10.6 | 13 | Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin |
| 41 | d1c7va_ | Alignment | not modelled | 10.2 | 9 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 42 | c3br8A_ | Alignment | not modelled | 10.1 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: crystal structure of acylphosphatase from bacillus subtilis |
| 43 | d2g0wa1 | Alignment | not modelled | 10.1 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Ioll-like |
| 44 | d2o5ha1 | Alignment | not modelled | 10.1 | 17 | Fold: NMB0513-like Superfamily: NMB0513-like Family: NMB0513-like |
| 45 | c3p6lA_ | Alignment | not modelled | 9.9 | 4 | PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution |
| 46 | c2rgiA_ | Alignment | not modelled | 9.9 | 23 | PDB header: metal binding protein Chain: A: PDB Molecule: protein s100-a2; PDBTitle: crystal structure of ca2+-free s100a2 at 1.6 a resolution |
| 47 | c2rqsA_ | Alignment | not modelled | 9.9 | 16 | PDB header: isomerase Chain: A: PDB Molecule: parvulin-like peptidyl-prolyl isomerase; PDBTitle: 3d structure of pin from the psychrophilic archeon cenarchaeum2 symbiosum (cspin) |
| 48 | c2i18A_ | Alignment | not modelled | 9.9 | 7 | PDB header: metal binding protein Chain: A: PDB Molecule: calcium-binding protein; PDBTitle: the refined structure of c-terminal domain of an ef-hand2 calcium binding protein from entamoeba histolytica |
| 49 | c2kz2A_ | Alignment | not modelled | 9.7 | 7 | PDB header: metal binding protein Chain: A: PDB Molecule: calmodulin; PDBTitle: calmodulin, c-terminal domain, f92e mutant |
| 50 | c1ponB_ | Alignment | not modelled | 9.5 | 30 | PDB header: calcium-binding protein Chain: B: PDB Molecule: troponin c; PDBTitle: site iii-site iv troponin c heterodimer, nmr |
| 51 | d1xk4c1 | Alignment | not modelled | 9.5 | 15 | Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |
| 52 | d1j6ya_ | Alignment | not modelled | 9.3 | 12 | Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase |
| 53 | c2b1uA_ | Alignment | not modelled | 9.3 | 11 | PDB header: metal binding protein Chain: A: PDB Molecule: calmodulin-like protein 5; PDBTitle: solution structure of calmodulin-like skin protein c2 terminal domain |
| 54 | d1oqpa_ | Alignment | not modelled | 9.1 | 19 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 55 | d5pala_ | Alignment | not modelled | 9.0 | 25 | Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin |
| 56 | c2ciuA_ | Alignment | not modelled | 9.0 | 16 | PDB header: protein transport Chain: A: PDB Molecule: import inner membrane translocase subunit tim21 |

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|----|-------------------------|-----------|--------------|-----|--|
| | | | | | PDBTitle: structure of the ims domain of the mitochondrial import2 protein tim21 from s. cerevisiae |
| 57 | d2p5zx2 | Alignment | not modelled | 8.9 | 16 Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like |
| 58 | d1m45a_ | Alignment | not modelled | 8.7 | 13 Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 59 | d1a4pa_ | Alignment | not modelled | 8.7 | 13 Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |
| 60 | d1cb1a_ | Alignment | not modelled | 8.5 | 19 Fold: EF Hand-like Superfamily: EF-hand Family: Calbindin D9K |
| 61 | d1zmba1 | Alignment | not modelled | 8.4 | 18 Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Putative acetylxylnan esterase-like |
| 62 | d2pq3a1 | Alignment | not modelled | 8.3 | 13 Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 63 | c2l0vB_ | Alignment | not modelled | 8.2 | 15 PDB header: metal binding protein Chain: B: PDB Molecule: protein s100-a16; PDBTitle: solution structure of calcium(ii) bound s100a16 |
| 64 | c3ucoB_ | Alignment | not modelled | 8.2 | 19 PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: coccomyxa beta-carbonic anhydrase in complex with iodide |
| 65 | d1ksoa_ | Alignment | not modelled | 8.2 | 31 Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |
| 66 | c3cnyA_ | Alignment | not modelled | 8.2 | 13 PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution |
| 67 | d1g33a_ | Alignment | not modelled | 8.2 | 14 Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin |
| 68 | d1qlka_ | Alignment | not modelled | 7.9 | 25 Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |
| 69 | d1wrka1 | Alignment | not modelled | 7.8 | 10 Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 70 | d1qx2a_ | Alignment | not modelled | 7.8 | 16 Fold: EF Hand-like Superfamily: EF-hand Family: Calbindin D9K |
| 71 | c3h4sE_ | Alignment | not modelled | 7.7 | 6 PDB header: motor protein/calcium binding protein Chain: E: PDB Molecule: kcbp interacting ca2+-binding protein; PDBTitle: structure of the complex of a mitotic kinesin with its2 calcium binding regulator |
| 72 | c2p5zX_ | Alignment | not modelled | 7.7 | 16 PDB header: structural genomics, unknown function Chain: X: PDB Molecule: type vi secretion system component; PDBTitle: the e. coli c3393 protein is a component of the type vi secretion2 system and exhibits structural similarity to t4 bacteriophage tail3 proteins gp27 and gp5 |
| 73 | d1yuta1 | Alignment | not modelled | 7.6 | 16 Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |
| 74 | c3fs7D_ | Alignment | not modelled | 7.6 | 11 PDB header: metal binding protein Chain: D: PDB Molecule: parvalbumin, thymic; PDBTitle: crystal structure of gallus gallus beta-parvalbumin (avian2 thymic hormone) |
| 75 | c3lmzA_ | Alignment | not modelled | 7.5 | 13 PDB header: isomerase Chain: A: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution |
| 76 | d1ggza_ | Alignment | not modelled | 7.5 | 10 Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 77 | c2ktgA_ | Alignment | not modelled | 7.5 | 10 PDB header: ca-binding protein Chain: A: PDB Molecule: calmodulin, putative; PDBTitle: calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein |
| 78 | d3d37a1 | Alignment | not modelled | 7.5 | 17 Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like |
| 79 | c1vs3B_ | Alignment | not modelled | 7.4 | 11 PDB header: isomerase Chain: B: PDB Molecule: trna pseudouridine synthase a; PDBTitle: crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8 |
| 80 | d1zaca_ | Alignment | not modelled | 7.4 | 16 Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 81 | c3ec8A_ | Alignment | not modelled | 7.3 | 4 PDB header: cell adhesion Chain: A: PDB Molecule: putative uncharacterized protein flj10324; PDBTitle: the crystal structure of the ra domain of flj10324 (radiI) |
| | | | | | Fold: beta-Grasp (ubiquitin-like) |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 82 | dlwxaa1 | Alignment | not modelled | 7.2 | 5 | Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD |
| 83 | dlsw8a_ | Alignment | not modelled | 7.2 | 13 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 84 | c1bomB_ | Alignment | not modelled | 7.1 | 17 | PDB header: insulin-like brain-secretory peptide Chain: B: PDB Molecule: bombyxin-ii,bombyxin a-6; PDBTitle: three-dimensional structure of bombyxin-ii, an insulin-2 related brain-secretory peptide of the silkmoth bombyx3 mori: comparison with insulin and relaxin |
| 85 | c3ngfA_ | Alignment | not modelled | 7.1 | 22 | PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family 2; PDBTitle: crystal structure of ap endonuclease, family 2 from brucella2 melitensis |
| 86 | c2dk6A_ | Alignment | not modelled | 7.1 | 21 | PDB header: signaling protein Chain: A: PDB Molecule: parp11 protein; PDBTitle: solution structure of wwe domain in poly (adp-ribose)2 polymerase family, member 11 (parp 11) |
| 87 | c1ozsA_ | Alignment | not modelled | 7.0 | 13 | PDB header: structural protein Chain: A: PDB Molecule: troponin c, slow skeletal and cardiac muscles; PDBTitle: c-domain of human cardiac troponin c in complex with the2 inhibitory region of human cardiac troponin i |
| 88 | c2kdha_ | Alignment | not modelled | 7.0 | 15 | PDB header: structural protein Chain: A: PDB Molecule: troponin c, slow skeletal and cardiac muscles; PDBTitle: the solution structure of human cardiac troponin c in2 complex with the green tea polyphenol; (-)-3 epigallocatechin-3-gallate |
| 89 | d2obha1 | Alignment | not modelled | 7.0 | 15 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 90 | c2pmyB_ | Alignment | not modelled | 6.8 | 21 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ras and ef-hand domain-containing protein; PDBTitle: ef-hand domain of human rasef |
| 91 | c2gv1A_ | Alignment | not modelled | 6.8 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: nmr solution structure of the acylphosphatase from2 eschaerichia coli |
| 92 | c2z4hB_ | Alignment | not modelled | 6.7 | 8 | PDB header: signaling protein activator Chain: B: PDB Molecule: copper homeostasis protein cutf; PDBTitle: crystal structure of the cpx pathway activator nlpe from2 escherichia coli |
| 93 | c2a8cE_ | Alignment | not modelled | 6.7 | 11 | PDB header: lyase Chain: E: PDB Molecule: carbonic anhydrase 2; PDBTitle: haemophilus influenzae beta-carbonic anhydrase |
| 94 | c1jc2A_ | Alignment | not modelled | 6.7 | 19 | PDB header: structural protein Chain: A: PDB Molecule: troponin c, skeletal muscle; PDBTitle: complex of the c-domain of troponin c with residues 1-40 of2 troponin i |
| 95 | d1jc2a_ | Alignment | not modelled | 6.7 | 19 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 96 | c1q88B_ | Alignment | not modelled | 6.6 | 9 | PDB header: dna binding protein Chain: B: PDB Molecule: 39 kda initiator binding protein; PDBTitle: crystal structure of the c-domain of the t.vaginalis inr2 binding protein, ibp39 (monoclinic form) |
| 97 | d3c1va1 | Alignment | not modelled | 6.4 | 43 | Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins |
| 98 | c2vtgA_ | Alignment | not modelled | 6.4 | 7 | PDB header: metal-binding protein Chain: A: PDB Molecule: ionized calcium-binding adapter molecule 2; PDBTitle: crystal structure of human iba2, trigonal crystal form |
| 99 | d1cmga_ | Alignment | not modelled | 6.4 | 3 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |