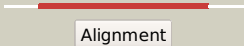

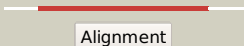

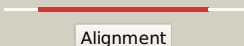







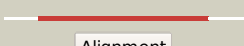




















Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2213_(pepB)_2478346_2479893 |
| Date | Mon Aug 5 13:25:34 BST 2019 |
| Unique Job ID | 6dff93443d9dff6 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3h8gC_ |  |  | 100.0 | 38 | PDB header: hydrolase Chain: C: PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida |
| 2 | c4ksiA_ |  |  | 100.0 | 31 | PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase 1, chloroplastic; PDBTitle: crystal structure analysis of the acidic leucine aminopeptidase of2 tomato |
| 3 | c6omeA_ |  |  | 100.0 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of a probable cytosol aminopeptidase (leucine2 aminopeptidase, lap) from chlamydia trachomatis d/uw-3/cx |
| 4 | c1gytG_ |  |  | 100.0 | 34 | PDB header: hydrolase Chain: G: PDB Molecule: cytosol aminopeptidase; PDBTitle: e. coli aminopeptidase a (pepa) |
| 5 | c3kzwD_ |  |  | 100.0 | 29 | PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col |
| 6 | c3jruB_ |  |  | 100.0 | 32 | PDB header: hydrolase Chain: B: PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331 |
| 7 | c1lanA_ |  |  | 100.0 | 32 | PDB header: hydrolase (alpha-aminoacylpeptide) Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: leucine aminopeptidase complex with l-leucinal |
| 8 | c4zi6D_ |  |  | 100.0 | 31 | PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of leucine aminopeptidase from helicobacter pylori |
| 9 | c5lhkA_ |  |  | 100.0 | 40 | PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase 2, chloroplastic; PDBTitle: bottromycin maturation enzyme botp in complex with mn |
| 10 | c3kr5E_ |  |  | 100.0 | 28 | PDB header: hydrolase Chain: E: PDB Molecule: m17 leucyl aminopeptidase; PDBTitle: structure of a protease 4 |
| 11 | c3ij3A_ |  |  | 100.0 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | c3peiA | Alignment |  | 100.0 | 31 | PDB header: hydrolase Chain: A; PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis |
| 13 | c5ntgA | Alignment |  | 100.0 | 30 | PDB header: hydrolase Chain: A; PDB Molecule: aminopeptidase; PDBTitle: structure of leucyl aminopeptidase from trypanosoma cruzi in complex2 with citrate |
| 14 | c2hc9A | Alignment |  | 100.0 | 25 | PDB header: hydrolase Chain: A; PDB Molecule: leucine aminopeptidase 1; PDBTitle: structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1) |
| 15 | c4efdF | Alignment |  | 100.0 | 29 | PDB header: hydrolase Chain: F; PDB Molecule: aminopeptidase; PDBTitle: crystal structure of an m17 aminopeptidase from trypanosoma brucei,2 tb427tmp.02.4440 |
| 16 | c5nthA | Alignment |  | 100.0 | 29 | PDB header: hydrolase Chain: A; PDB Molecule: putative aminopeptidase; PDBTitle: structure of leucyl aminopeptidase from leishmania major in complex2 with actinonin |
| 17 | d1lama1 | Alignment |  | 100.0 | 39 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain |
| 18 | d1gyta2 | Alignment |  | 100.0 | 42 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain |
| 19 | c6cxda | Alignment |  | 100.0 | 31 | PDB header: hydrolase Chain: A; PDB Molecule: peptidase b; PDBTitle: crystal structure of peptidase b from yersinia pestis co92 at 2.75 a2 resolution |
| 20 | d1gyta1 | Alignment |  | 99.9 | 18 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Leucine aminopeptidase (Aminopeptidase A), N-terminal domain |
| 21 | d1lama2 | Alignment | not modelled | 99.8 | 18 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Leucine aminopeptidase (Aminopeptidase A), N-terminal domain |
| 22 | c3rzaA | Alignment | not modelled | 96.4 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: tripeptidase; PDBTitle: crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution |
| 23 | d1vhea2 | Alignment | not modelled | 96.4 | 14 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 24 | d1xfoa2 | Alignment | not modelled | 96.0 | 15 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 25 | d2grea2 | Alignment | not modelled | 95.0 | 14 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 26 | d1yloa2 | Alignment | not modelled | 94.9 | 17 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 27 | c3ct9B | Alignment | not modelled | 94.4 | 12 | PDB header: hydrolase Chain: B; PDB Molecule: acetylornithine deacetylase; PDBTitle: crystal structure of a putative zinc peptidase (np_812461.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.31 a resolution |
| 28 | d1cg2a1 | Alignment | not modelled | 93.1 | 16 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| | | | | | | PDB header: hydrolase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c4ewtC | Alignment | not modelled | 92.9 | 19 | Chain: C: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: the crystal structure of a putative aminohydrolase from methicillin2 resistant staphylococcus aureus |
| 30 | c4h2kA | Alignment | not modelled | 92.8 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of succinyl-diaminopimelate2 desuccinylase from haemophilus influenzae |
| 31 | d1vgya1 | Alignment | not modelled | 92.6 | 11 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 32 | c3t6mA | Alignment | not modelled | 91.2 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of dape protein from 2 v.cholerea in the zn bound form |
| 33 | d2fvga2 | Alignment | not modelled | 90.3 | 13 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 34 | d1fnoa4 | Alignment | not modelled | 89.8 | 16 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 35 | c3gb0A | Alignment | not modelled | 88.8 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: peptidase t; PDBTitle: crystal structure of aminopeptidase pept (np_980509.1) from bacillus2 cereus atcc 10987 at 2.04 a resolution |
| 36 | c1ysiB | Alignment | not modelled | 87.2 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: protein yxep; PDBTitle: crystal structure of bacillus subtilis yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family |
| 37 | c1q7IA | Alignment | not modelled | 85.1 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human aminoacylase-2 i |
| 38 | d1vhoo2 | Alignment | not modelled | 83.8 | 13 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 39 | c1vhoA | Alignment | not modelled | 83.6 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of a putative peptidase/endoglucanase |
| 40 | c3pfoB | Alignment | not modelled | 83.0 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: crystal structure of a putative acetylornithine deacetylase (rpa2325)2 from rhodospseudomonas palustris cga009 at 1.90 a resolution |
| 41 | c5ds0F | Alignment | not modelled | 82.9 | 20 | PDB header: hydrolase Chain: F: PDB Molecule: peptidase m42; PDBTitle: crystal structure of tet aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon scgc ab-539-e09 |
| 42 | c2q43A | Alignment | not modelled | 82.3 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: iaa-amino acid hydrolase ilr1-like 2; PDBTitle: ensemble refinement of the protein crystal structure of iaa-aminoacid2 hydrolase from arabidopsis thaliana gene at5g56660 |
| 43 | d1z2la1 | Alignment | not modelled | 81.1 | 19 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 44 | c2greC | Alignment | not modelled | 79.8 | 15 | PDB header: hydrolase Chain: C: PDB Molecule: deblocking aminopeptidase; PDBTitle: crystal structure of deblocking aminopeptidase from bacillus cereus |
| 45 | c1vheA | Alignment | not modelled | 78.8 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aminopeptidase/glucanase homolog; PDBTitle: crystal structure of a aminopeptidase/glucanase homolog |
| 46 | d1xmba1 | Alignment | not modelled | 78.3 | 19 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 47 | c3pfeA | Alignment | not modelled | 78.0 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of a m20a metallo peptidase (dape, lpg0809) from 2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 1.503 a resolution |
| 48 | c4wwwvA | Alignment | not modelled | 77.1 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase from family m42; PDBTitle: aminopeptidase apdkam598 from the archaeon desulfurococcus2 kamchatkensis |
| 49 | d2hgaa1 | Alignment | not modelled | 75.2 | 16 | Fold: PDZ domain-like Superfamily: PDZ domain-like Family: MTH1368 C-terminal domain-like |
| 50 | c2fvga | Alignment | not modelled | 73.3 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution |
| 51 | c4mmoB | Alignment | not modelled | 72.4 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: sso-cp2 metallo-carboxypeptidase; PDBTitle: the crystal structure of a m20 family metallo-carboxypeptidase sso-cp22 from sulfolobus solfataricus |
| 52 | c5k8nE | Alignment | not modelled | 68.7 | 15 | PDB header: hydrolase Chain: E: PDB Molecule: 5-nitroanthranilic acid aminohydrolase; PDBTitle: 5naa-bound 5-nitroanthranilate aminohydrolase |
| 53 | c4q7aD | Alignment | not modelled | 68.0 | 17 | PDB header: hydrolase Chain: D: PDB Molecule: n-acetyl-ornithine/n-acetyl-lysine deacetylase; PDBTitle: crystal structure of n-acetyl-ornithine/n-acetyl-lysine deacetylase2 from sphaerobacter thermophilus |
| 54 | c3tx8A | Alignment | not modelled | 66.8 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of a succinyl-diaminopimelate desuccinylase (arge)2 from corynebacterium glutamicum atcc |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | 13032 at 2.97 a resolution |
| 55 | c1vgvB_ | Alignment | not modelled | 64.1 | 12 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of succinyl diaminopimelate desuccinylase |
| 56 | c4fuuA_ | Alignment | not modelled | 63.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a leucine aminopeptidase precursor (bt_2548) from2 bacteroides thetaiotaomicron vpi-5482 at 1.30 a resolution |
| 57 | c5hj1A_ | Alignment | not modelled | 61.9 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: pullulanase c protein; PDBTitle: crystal structure of pdz domain of pullulanase c protein of type ii2 secretion system from klebsiella pneumoniae in complex with fatty3 acid |
| 58 | c3isxA_ | Alignment | not modelled | 60.2 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1050) from thermotoga maritima2 at 1.40 a resolution |
| 59 | c4ri0A_ | Alignment | not modelled | 59.7 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: serine protease htra3; PDBTitle: serine protease htra3, mutationally inactivated |
| 60 | c3tc8A_ | Alignment | not modelled | 59.6 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a zn-dependent exopeptidase (bdi_3547) from2 parabacteroides distazonis atcc 8503 at 1.06 a resolution |
| 61 | c2pokB_ | Alignment | not modelled | 58.8 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae |
| 62 | d1sota1 | Alignment | not modelled | 58.6 | 14 | Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtraA-like serine proteases |
| 63 | c3mruB_ | Alignment | not modelled | 56.1 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: aminoacyl-histidine dipeptidase; PDBTitle: crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus |
| 64 | c2qyvB_ | Alignment | not modelled | 55.8 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: xaa-his dipeptidase; PDBTitle: crystal structure of putative xaa-his dipeptidase (yp_718209.1) from2 haemophilus somnus 129pt at 2.11 a resolution |
| 65 | c3i18A_ | Alignment | not modelled | 55.5 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2051 protein; PDBTitle: crystal structure of the pdz domain of the sdrc-like protein (lmo2051)2 from listeria monocytogenes, northeast structural genomics consortium3 target lmr166b |
| 66 | c3ramC_ | Alignment | not modelled | 53.1 | 12 | PDB header: hydrolase Chain: C: PDB Molecule: hmra protein; PDBTitle: crystal structure of hmra |
| 67 | c2p3wB_ | Alignment | not modelled | 53.0 | 27 | PDB header: protein binding Chain: B: PDB Molecule: probable serine protease htra3; PDBTitle: crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv) |
| 68 | d1ky9a1 | Alignment | not modelled | 51.8 | 22 | Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtraA-like serine proteases |
| 69 | c4flnB_ | Alignment | not modelled | 50.8 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 2, chloroplastic; PDBTitle: crystal structure of plant protease deg2 |
| 70 | d1ky9b2 | Alignment | not modelled | 50.7 | 24 | Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtraA-like serine proteases |
| 71 | d2z9ia1 | Alignment | not modelled | 50.7 | 20 | Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtraA-like serine proteases |
| 72 | c2kl1A_ | Alignment | not modelled | 49.7 | 23 | PDB header: protein binding Chain: A: PDB Molecule: ybl1 protein; PDBTitle: solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c |
| 73 | c1yloA_ | Alignment | not modelled | 49.5 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein sf2450; PDBTitle: crystal structure of protein of unknown function (possible2 aminopeptidase) s2589 from shigella flexneri 2a str. 2457t |
| 74 | c5y09B_ | Alignment | not modelled | 49.1 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9 at 295 k |
| 75 | c3khzA_ | Alignment | not modelled | 48.9 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: putative dipeptidase sacol1801; PDBTitle: crystal structure of r350a mutant of staphylococcus aureus2 metallopeptidase (sapep/dape) in the apo-form |
| 76 | c5y2dA_ | Alignment | not modelled | 48.3 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra |
| 77 | c2joaA_ | Alignment | not modelled | 45.7 | 16 | PDB header: protein binding Chain: A: PDB Molecule: serine protease htra1; PDBTitle: htra1 bound to an optimized peptide: nmr assignment of pdz2 domain and ligand resonances |
| 78 | d1ysja1 | Alignment | not modelled | 45.0 | 18 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 79 | c2kjpA_ | Alignment | not modelled | 44.8 | 28 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ybl1; PDBTitle: solution structure of protein ybl1 (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 |

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|-----|-------------------------|-----------|--------------|------|---|
| | | | | | sr713a |
| 80 | c3x3eA_ | Alignment | not modelled | 44.5 | 13 PDB header: hydrolase Chain: A: PDB Molecule: n-acetyl-lysine deacetylase; PDBTitle: crystal structure of lysk from thermophilus complex with2 lysine |
| 81 | d1lcyA1 | Alignment | not modelled | 44.2 | 29 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtraA-like serine proteases |
| 82 | c5xdyA_ | Alignment | not modelled | 44.1 | 17 PDB header: hydrolase Chain: A: PDB Molecule: heat shock protein htra; PDBTitle: crystal structure of htra1 from mycobacterium tuberculosis |
| 83 | c2zplA_ | Alignment | not modelled | 43.1 | 28 PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain a |
| 84 | d1ed7a_ | Alignment | not modelled | 41.0 | 40 Fold: WW domain-like Superfamily: Carbohydrate binding domain Family: Carbohydrate binding domain |
| 85 | d1mfga_ | Alignment | not modelled | 40.8 | 23 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain |
| 86 | c2r3yC_ | Alignment | not modelled | 40.1 | 17 PDB header: hydrolase/hydrolase activator Chain: C: PDB Molecule: protease degs; PDBTitle: crystal structure of the degs protease in complex with the2 ywf activating peptide |
| 87 | d1vixa1 | Alignment | not modelled | 38.9 | 12 Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 88 | d2i4sa1 | Alignment | not modelled | 38.5 | 20 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: EpsC C-terminal domain-like |
| 89 | c2dkrA_ | Alignment | not modelled | 38.5 | 25 PDB header: protein transport Chain: A: PDB Molecule: lin-7 homolog b; PDBTitle: solution structure of the pdz domain from human lin-72 homolog b |
| 90 | d2i6va1 | Alignment | not modelled | 38.5 | 20 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: EpsC C-terminal domain-like |
| 91 | c6qh2A_ | Alignment | not modelled | 38.5 | 23 PDB header: signaling protein Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: solution nmr ensemble for a chimeric kh-s1 domain construct of2 exosomal polynucleotide phosphorylase at 298k compiled using the3 comand method |
| 92 | c1ky9A_ | Alignment | not modelled | 37.6 | 26 PDB header: hydrolase Chain: A: PDB Molecule: protease do; PDBTitle: crystal structure of degp (htra) |
| 93 | c3pv4A_ | Alignment | not modelled | 37.6 | 27 PDB header: hydrolase Chain: A: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (delta-pdz2 variant) |
| 94 | c2i97A_ | Alignment | not modelled | 37.0 | 20 PDB header: protein binding Chain: A: PDB Molecule: putative serine protease; PDBTitle: solution structure of htra pdz domain from streptococcus pneumoniae |
| 95 | c3bpuA_ | Alignment | not modelled | 36.9 | 14 PDB header: transferase Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz domain- PDBTitle: crystal structure of the 3rd pdz domain of human membrane associated2 guanylate kinase, c677s and c709s double mutant |
| 96 | c3fj1A_ | Alignment | not modelled | 35.5 | 21 PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution |
| 97 | c1lcyA_ | Alignment | not modelled | 35.5 | 30 PDB header: hydrolase Chain: A: PDB Molecule: htra2 serine protease; PDBTitle: crystal structure of the mitochondrial serine protease htra2 |
| 98 | c2n7pA_ | Alignment | not modelled | 34.1 | 44 PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of pdz domain |
| 99 | c4o06A_ | Alignment | not modelled | 33.8 | 21 PDB header: chaperone Chain: A: PDB Molecule: probable 26s proteasome regulatory subunit p27; PDBTitle: 1.15a resolution structure of the proteasome assembly chaperone nas22 pdz domain |
| 100 | d2h3la1 | Alignment | not modelled | 32.3 | 23 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain |
| 101 | d1o2da_ | Alignment | not modelled | 32.2 | 31 Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase |
| 102 | c5iitC_ | Alignment | not modelled | 31.6 | 7 PDB header: inositol phosphate binding protein Chain: C: PDB Molecule: vacuolar transporter chaperone 4,core histone macro-h2a.1; PDBTitle: structure of spx domain of the yeast inorganic polyphosphate polymerase2 vtc4 crystallized by carrier-driven crystallization in fusion with3 the macro domain of human histone macroh2a1.1 |
| 103 | d1fc6a3 | Alignment | not modelled | 31.3 | 33 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Tail specific protease PDZ domain |
| 104 | c3l4fD_ | Alignment | not modelled | 30.8 | 25 PDB header: signaling protein/protein binding Chain: D: PDB Molecule: sh3 and multiple ankyrin repeat domains protein 1; |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: crystal structure of betapix coiled-coil domain and shank pdz complex |
| 105 | d1sroa_ | Alignment | not modelled | 30.3 | 36 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 106 | c3d5bD_ | Alignment | not modelled | 30.2 | 22 | PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l2; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400. |
| 107 | c5b0mB_ | Alignment | not modelled | 30.0 | 42 | PDB header: transferase, dna binding protein Chain: B: PDB Molecule: moen5,dna-binding protein 7d; PDBTitle: structure of moen5-ss07d fusion protein in complex with beta-dodecyl2 maltoside |
| 108 | c5jykB_ | Alignment | not modelled | 29.7 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: deg9 crystal under 289k |
| 109 | c3ixzA_ | Alignment | not modelled | 29.6 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride |
| 110 | c2zpmA_ | Alignment | not modelled | 29.3 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain b |
| 111 | c4ifdl_ | Alignment | not modelled | 29.2 | 25 | PDB header: hydrolase/rna Chain: I: PDB Molecule: exosome complex component csl4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna |
| 112 | c2hc8A_ | Alignment | not modelled | 29.2 | 17 | PDB header: transport protein Chain: A: PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain |
| 113 | c4jj0B_ | Alignment | not modelled | 29.0 | 40 | PDB header: electron transport Chain: B: PDB Molecule: mamp; PDBTitle: crystal structure of mamp |
| 114 | c2cauA_ | Alignment | not modelled | 29.0 | 23 | PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean |
| 115 | c4ifdH_ | Alignment | not modelled | 28.8 | 28 | PDB header: hydrolase/rna Chain: H: PDB Molecule: exosome complex component rrp4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna |
| 116 | c5b6lA_ | Alignment | not modelled | 28.8 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: putative serine protease hhoa; PDBTitle: structure of deg protease hhoa from synechocystis sp. pcc 6803 |
| 117 | d2asba1 | Alignment | not modelled | 27.8 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 118 | c3j3wC_ | Alignment | not modelled | 27.7 | 22 | PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein l2; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a) |
| 119 | d1gmua1 | Alignment | not modelled | 27.5 | 40 | Fold: Urease metallochaperone UreE, N-terminal domain Superfamily: Urease metallochaperone UreE, N-terminal domain Family: Urease metallochaperone UreE, N-terminal domain |
| 120 | d1zr5a1 | Alignment | not modelled | 27.5 | 6 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain |