Phyre2

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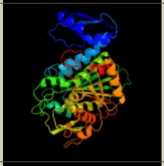
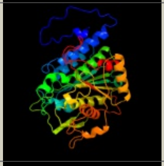
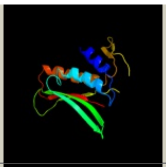
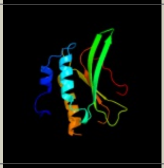
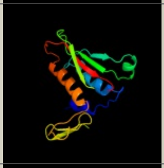
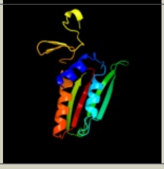
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kzwD_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
2	c3h8gC_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
3	c3jruB_	Alignment		100.0	33	**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
4	c1lanA_	Alignment		100.0	33	**PDB header:**hydrolase (alpha-aminoacylpeptide) **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** leucine aminopeptidase complex with l-leucinal
5	c1gytG_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** e. coli aminopeptidase a (pepa)
6	c3ij3A_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
7	c3kr5E_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**m17 leucyl aminopeptidase; **PDBTitle:** structure of a protease 4
8	d1gyta2	Alignment		100.0	38	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
9	d1lama1	Alignment		100.0	36	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
10	c2hc9A_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase 1; **PDBTitle:** structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
11	c3peiA_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from francisella2 tularensis

12	d1vhea2	Alignment		96.0	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
13	d2grea2	Alignment		92.0	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
14	d1yloa2	Alignment		91.5	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
15	c3rzaA_	Alignment		90.2	10	**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
16	d1vhoa2	Alignment		83.9	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
17	c3ct9B_	Alignment		83.6	11	**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
18	d2fvga2	Alignment		81.9	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
19	c3gb0A_	Alignment		78.6	9	**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
20	c3t6mA_	Alignment		78.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of the catalytic domain of dape protein from2 v.cholerea in the zn bound form
21	d1vgya1	Alignment	not modelled	76.4	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
22	d2hgaa1	Alignment	not modelled	73.8	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**MTH1368 C-terminal domain-like
23	d1xmba1	Alignment	not modelled	71.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
24	d1cg2a1	Alignment	not modelled	64.3	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
25	c3pfoB_	Alignment	not modelled	63.1	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative acetylornithine deacetylase (rpa2325)2 from rhodopseudomonas palustris cga009 at 1.90 a resolution
26	c1ysjB_	Alignment	not modelled	61.9	13	**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
27	c2q43A_	Alignment	not modelled	60.5	14	**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
28	d1sota1	Alignment	not modelled	58.4	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases

29	c3i18A_	Alignment	not modelled	56.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2051 protein; **PDBTitle:** crystal structure of the pdz domain of the sdrc-like protein2 (lmo2051) from listeria monocytogenes, northeast structural3 genomics consortium target lmr166b
30	c1vhoA_	Alignment	not modelled	54.6	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of a putative peptidase/endoglucanase
31	d1z2la1	Alignment	not modelled	53.6	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
32	c2p3wB_	Alignment	not modelled	52.4	30	**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)
33	c2qyvB_	Alignment	not modelled	51.2	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
34	c3pfeA_	Alignment	not modelled	48.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of a m20a metallo peptidase (dape, lpg0809) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 1.503 a resolution
35	d2z9ia1	Alignment	not modelled	48.1	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
36	d1ky9a1	Alignment	not modelled	47.4	33	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
37	c2kl1A_	Alignment	not modelled	46.6	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ylbl protein; **PDBTitle:** solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
38	c2greC_	Alignment	not modelled	45.2	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deblocking aminopeptidase; **PDBTitle:** crystal structure of deblocking aminopeptidase from bacillus cereus
39	d1mfga_	Alignment	not modelled	43.9	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
40	d1ky9b2	Alignment	not modelled	43.9	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
41	c3io1B_	Alignment	not modelled	42.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminobenzoyl-glutamate utilization protein; **PDBTitle:** crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
42	c2joaA_	Alignment	not modelled	42.4	20	**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
43	d1xfoa2	Alignment	not modelled	41.7	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
44	d1lcya1	Alignment	not modelled	41.6	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
45	c2zplA_	Alignment	not modelled	41.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain a
46	d1ysja1	Alignment	not modelled	41.4	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
47	c2kjpA_	Alignment	not modelled	40.3	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ylbl; **PDBTitle:** solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
48	d2h3la1	Alignment	not modelled	39.4	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
49	c3pv4A_	Alignment	not modelled	38.3	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (delta-pdz2 variant)
50	c1vgyB_	Alignment	not modelled	35.7	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of succinyl diaminopimelate desuccinylase
51	c3tc8A_	Alignment	not modelled	34.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** crystal structure of a hypothetical zn-dependent exopeptidase2 (bdi_3547) from parabacteroides distasonis atcc 8503 at 1.06 a3 resolution
52	c1ky9A_	Alignment	not modelled	34.2	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease do; **PDBTitle:** crystal structure of degp (htra)
53	c2r3yC_	Alignment	not modelled	34.0	22	**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

54	c1lcyA_	Alignment	not modelled	33.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**htra2 serine protease; **PDBTitle:** crystal structure of the mitochondrial serine protease htra2
55	d2i4sa1	Alignment	not modelled	32.9	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
56	d2i6va1	Alignment	not modelled	32.8	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
57	d1fc6a3	Alignment	not modelled	31.8	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
58	c3bpuA_	Alignment	not modelled	31.8	32	**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
59	c3mruB_	Alignment	not modelled	31.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacyl-histidine dipeptidase; **PDBTitle:** crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
60	c1vheA_	Alignment	not modelled	29.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**aminopeptidase/glucanase homolog; **PDBTitle:** crystal structure of a aminopeptidase/glucanase homolog
61	c2hc8A_	Alignment	not modelled	29.4	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
62	c1q7lA_	Alignment	not modelled	28.0	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
63	d1ed7a_	Alignment	not modelled	28.0	30	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
64	c2lbfA_	Alignment	not modelled	26.9	28	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p1; **PDBTitle:** solution structure of the dimerization domain of human ribosomal2 protein p1/p2 heterodimer
65	c3l4fD_	Alignment	not modelled	26.2	20	**PDB header:**signaling protein/protein binding **Chain:** D: **PDB Molecule:**sh3 and multiple ankyrin repeat domains protein **PDBTitle:** crystal structure of betapix coiled-coil domain and shank2 pdz complex
66	c2cauA_	Alignment	not modelled	25.0	23	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
67	c2zxeA_	Alignment	not modelled	24.5	19	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**na, k-atpase alpha subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
68	c3pv5B_	Alignment	not modelled	24.2	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (n189g/p190g variant)
69	c3ixzA_	Alignment	not modelled	23.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
70	d1sroa_	Alignment	not modelled	22.8	32	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
71	c2zpmA_	Alignment	not modelled	22.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
72	c2fvgA_	Alignment	not modelled	22.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
73	c3stjC_	Alignment	not modelled	22.5	37	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
74	c1cg2D_	Alignment	not modelled	22.2	14	**PDB header:**metallocarboxypeptidase **Chain:** D: **PDB Molecule:**carboxypeptidase g2; **PDBTitle:** carboxypeptidase g2
75	c3gdsA_	Alignment	not modelled	21.6	20	**PDB header:**hydrolase/hydrolase activator **Chain:** A: **PDB Molecule:**protease degs; **PDBTitle:** crystal structure of degs h198p/d320a mutant modified by dfp in2 complex with dnrdgnvyyf peptide
76	d1l1ca_	Alignment	not modelled	21.1	29	**Fold:**GroES-like **Superfamily:**SacY-like RNA-binding domain **Family:**BglG-like antiterminator proteins
77	c3isxA_	Alignment	not modelled	21.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1050) from thermotoga2 maritima at 1.40 a resolution
78	c3shuB_	Alignment	not modelled	20.9	13	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3
79	c2d90A_	Alignment	not modelled	20.0	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pdz domain containing protein 1; **PDBTitle:** solution structure of the third pdz domain of pdz

						domain2 containing protein 1
80	c3khzA_	Alignment	not modelled	19.8	13	**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
81	c2pokB_	Alignment	not modelled	19.1	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
82	c2eguA_	Alignment	not modelled	18.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
83	c2z9iB_	Alignment	not modelled	18.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable serine protease pepd; **PDBTitle:** crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
84	d1uepa_	Alignment	not modelled	18.6	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
85	d2nn6i1	Alignment	not modelled	18.5	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
86	d2fi9a1	Alignment	not modelled	18.4	47	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
87	d1qvpa_	Alignment	not modelled	17.8	39	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
88	c3k50A_	Alignment	not modelled	17.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative s41 protease; **PDBTitle:** crystal structure of putative s41 protease (yp_211611.1) from2 bacteroides fragilis nctc 9343 at 2.00 a resolution
89	d2v4jc1	Alignment	not modelled	17.5	43	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
90	c3qo6B_	Alignment	not modelled	17.5	71	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**protease do-like 1, chloroplastic; **PDBTitle:** crystal structure analysis of the plant protease deg1
91	c2es4D_	Alignment	not modelled	17.3	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**lipase chaperone; **PDBTitle:** crystal structure of the burkholderia glumae lipase-2 specific foldase in complex with its cognate lipase
92	d2es4d1	Alignment	not modelled	17.3	21	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Lipase chaperone-like **Family:**Lipase chaperone LifO-like
93	d1gmua1	Alignment	not modelled	17.1	28	**Fold:**Urease metallochaperone UreE, N-terminal domain **Superfamily:**Urease metallochaperone UreE, N-terminal domain **Family:**Urease metallochaperone UreE, N-terminal domain
94	d2ba0a1	Alignment	not modelled	17.0	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
95	c1lfwA_	Alignment	not modelled	16.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pepv; **PDBTitle:** crystal structure of pepv
96	d2plta_	Alignment	not modelled	16.6	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
97	c2edvA_	Alignment	not modelled	16.4	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ferm and pdz domain-containing protein 1; **PDBTitle:** solution structure of the pdz domain from human ferm and2 pdz domain containing 1
98	c2q3gA_	Alignment	not modelled	16.3	19	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**pdz and lim domain protein 7; **PDBTitle:** structure of the pdz domain of human pdlim7 bound to a c-2 terminal extension from human beta-tropomyosin
99	c2eqsA_	Alignment	not modelled	16.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dhx8; **PDBTitle:** solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8