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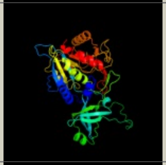
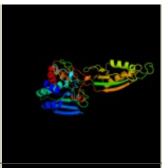
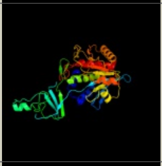
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vheA_	Alignment		100.0	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**aminopeptidase/glucanase homolog; **PDBTitle:** crystal structure of a aminopeptidase/glucanase homolog
2	c1yloA_	Alignment		100.0	31	**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
3	c3kl9F_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**glutamyl aminopeptidase; **PDBTitle:** crystal structure of pepa from streptococcus pneumoniae
4	c1y0yA_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**frv operon protein frvx; **PDBTitle:** crystal structure of tetrahedral aminopeptidase from p. horikoshii in2 complex with amastatin
5	c2pe3A_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**354aa long hypothetical operon protein frv; **PDBTitle:** crystal structure of frv operon protein frvx (ph1821)from pyrococcus2 horikoshii ot3
6	c3isxA_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1050) from thermotoga2 maritima at 1.40 a resolution
7	c3gb0A_	Alignment		100.0	13	**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
8	c3rzaA_	Alignment		100.0	13	**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
9	c2cf4A_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein ph0519; **PDBTitle:** pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
10	c3pfoB_	Alignment		100.0	11	**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
11	c1cg2D_	Alignment		100.0	15	**PDB header:**metallocarboxypeptidase **Chain:** D: **PDB Molecule:**carboxypeptidase g2; **PDBTitle:** carboxypeptidase g2

12	c1vgyB_	Alignment		100.0	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of succinyl diaminopimelate desuccinylase
13	c1vhoA_	Alignment		100.0	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of a putative peptidase/endoglucanase
14	c1vixA_	Alignment		100.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of a putative peptidase t
15	c3tx8A_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of a succinyl-diaminopimelate desuccinylase (arge)2 from corynebacterium glutamicum atcc 13032 at 2.97 a resolution
16	c3ifeA_	Alignment		100.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** 1.55 angstrom resolution crystal structure of peptidase t (pept-1)2 from bacillus anthracis str. 'ames ancestor'.
17	c2qyvB_	Alignment		100.0	12	**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
18	c2pokB_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae
19	c3ic1A_	Alignment		100.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
20	c2rb7A_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of co-catalytic metallopeptidase (yp_387682.1) from2 desulfovibrio desulfuricans g20 at 1.60 a resolution
21	c3mruB_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacyl-histidine dipeptidase; **PDBTitle:** crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
22	c2imoA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoate amidohydrolase; **PDBTitle:** crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
23	c3n5fB_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-carbamoyl-l-amino acid hydrolase; **PDBTitle:** crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
24	c2fvgA_	Alignment	not modelled	100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
25	c1ysjB_	Alignment	not modelled	100.0	10	**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
26	c3dljB_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-ala-his dipeptidase; **PDBTitle:** crystal structure of human carnosine dipeptidase 1
27	c2v8gD_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-alanine synthase; **PDBTitle:** crystal structure of beta-alanine synthase from2 saccharomyces kluyveri in complex with the product beta-3 alanine
28	c2greC_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deblocking aminopeptidase; **PDBTitle:** crystal structure of deblocking aminopeptidase from bacillus cereus

29	c3ramC_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hmra protein; **PDBTitle:** crystal structure of hmra
30	c2zogA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic non-specific dipeptidase; **PDBTitle:** crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
31	c3pfeA_	Alignment	not modelled	100.0	10	**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
32	c3ct9B_	Alignment	not modelled	100.0	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
33	c2f7vA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aectylcitrulline deacetylase; **PDBTitle:** structure of acetylcitrulline deacetylase complexed with2 one co
34	c2q43A_	Alignment	not modelled	100.0	11	**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
35	c3cpxC_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**aminopeptidase, m42 family; **PDBTitle:** crystal structure of putative m42 glutamyl aminopeptidase2 (yp_676701.1) from cytophaga hutchinsonii atcc 33406 at 2.39 a3 resolution
36	c1lfwA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pepv; **PDBTitle:** crystal structure of pepv
37	d1vixa1	Alignment	not modelled	100.0	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
38	d1xfoa2	Alignment	not modelled	100.0	32	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
39	d1yloa2	Alignment	not modelled	100.0	34	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
40	d1fnoa4	Alignment	not modelled	100.0	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
41	d1vhea2	Alignment	not modelled	100.0	26	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
42	d1vhoa2	Alignment	not modelled	100.0	30	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
43	d1z2la1	Alignment	not modelled	100.0	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
44	c3khzA_	Alignment	not modelled	100.0	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
45	d2fvga2	Alignment	not modelled	100.0	30	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
46	c3l6sA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartyl aminopeptidase; **PDBTitle:** crystal structure of human aspartyl aminopeptidase (dnpep),2 in complex with aspartic acid hydroxamate
47	c3io1B_	Alignment	not modelled	99.9	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminobenzoyl-glutamate utilization protein; **PDBTitle:** crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
48	c3t6mA_	Alignment	not modelled	99.9	18	**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
49	d1lfwa1	Alignment	not modelled	99.9	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
50	c2glfB_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** crystal structure of aminipeptidase (m18 family) from thermotoga2 maritima
51	d2grea2	Alignment	not modelled	99.9	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
52	d1cg2a1	Alignment	not modelled	99.9	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
53	c2ijzF_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**probable m18-family aminopeptidase 2; **PDBTitle:** crystal structure of aminopeptidase
54	d1r3na1	Alignment	not modelled	99.9	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases

						Family: Bacterial dinuclear zinc exopeptidases
55	c1y7eA_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
56	d1y0ya2	Alignment	not modelled	99.8	32	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
57	d1xmba1	Alignment	not modelled	99.8	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
58	c1q7lA_	Alignment	not modelled	99.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
59	d1ysja1	Alignment	not modelled	99.8	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
60	c2gljR_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:** **PDBTitle:** crystal structure of aminopeptidase i from clostridium2 acetobutylicum
61	d1vgya1	Alignment	not modelled	99.7	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
62	d1y7ea2	Alignment	not modelled	99.6	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
63	d1tkja1	Alignment	not modelled	99.5	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
64	d1rtqa_	Alignment	not modelled	99.4	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
65	c3tc8A_	Alignment	not modelled	99.4	19	**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
66	c1q7lB_	Alignment	not modelled	99.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
67	c3guxA_	Alignment	not modelled	99.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zn-dependent exopeptidase; **PDBTitle:** crystal structure of a putative zn-dependent exopeptidase (bvu_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
68	c3pb6X_	Alignment	not modelled	99.0	23	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glutaminyl-peptide cyclotransferase-like protein; **PDBTitle:** crystal structure of the catalytic domain of human golgi-resident2 glutaminyl cyclase at ph 6.5
69	d2afwa1	Alignment	not modelled	98.9	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Glutaminyl-peptide cyclotransferase-like
70	c2ek8A_	Alignment	not modelled	98.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** aminopeptidase from aneurinibacillus sp. strain am-1
71	c3iibA_	Alignment	not modelled	98.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m28; **PDBTitle:** crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution
72	d3bi1a3	Alignment	not modelled	98.5	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
73	c2ootA_	Alignment	not modelled	98.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
74	d1cg2a2	Alignment	not modelled	97.9	7	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
75	d1vgya2	Alignment	not modelled	97.9	8	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
76	c1cx8F_	Alignment	not modelled	97.8	20	**PDB header:**metal transport **Chain:** F: **PDB Molecule:**transferrin receptor protein; **PDBTitle:** crytal structure of the ectodomain of human transferrin receptor
77	d1z2la2	Alignment	not modelled	97.8	13	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
78	d1de4c3	Alignment	not modelled	97.8	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
79	d1r3na2	Alignment	not modelled	97.5	7	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
80	d1vhea1	Alignment	not modelled	96.1	34	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain

						Family: Aminopeptidase/glucanase lid domain
81	d1lfwa2	Alignment	not modelled	95.0	10	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
82	d1ysja2	Alignment	not modelled	94.9	4	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
83	c3k9tA_	Alignment	not modelled	93.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase (np_348812.1) from clostridium2 acetobutylicum at 2.37 a resolution
84	d2grea1	Alignment	not modelled	91.5	26	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
85	d1y0ya1	Alignment	not modelled	81.4	35	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
86	d1xmba2	Alignment	not modelled	79.4	12	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
87	d1yloa1	Alignment	not modelled	74.1	30	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
88	d1vhoa1	Alignment	not modelled	66.2	31	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
89	d2fvga1	Alignment	not modelled	64.5	32	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
90	c3hlyA_	Alignment	not modelled	49.7	8	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
91	c3fniA_	Alignment	not modelled	47.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
92	c3qnmA_	Alignment	not modelled	43.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** haloalkane dehalogenase family member from bacteroides2 thetaiotaomicron of unknown function
93	d1vmea1	Alignment	not modelled	41.6	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
94	d1e5da1	Alignment	not modelled	39.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
95	c3ij3A_	Alignment	not modelled	39.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
96	d1ycga1	Alignment	not modelled	38.6	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
97	c3na6A_	Alignment	not modelled	38.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase; **PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
98	c1sz1A_	Alignment	not modelled	38.0	15	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna nucleotidyltransferase; **PDBTitle:** mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
99	d2fz5a1	Alignment	not modelled	37.0	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
100	c2k9mA_	Alignment	not modelled	36.3	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
101	c3kzwD_	Alignment	not modelled	35.8	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
102	c2k9lA_	Alignment	not modelled	35.5	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
103	d1r89a2	Alignment	not modelled	35.2	24	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Archaeal tRNA CCA-adding enzyme catalytic domain
104	c2hnbA_	Alignment	not modelled	34.6	9	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
105	c3f6sI_	Alignment	not modelled	34.0	15	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
106	d1lama1	Alignment	not modelled	31.4	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain

107	c2ho4A_	Alignment	not modelled	30.8	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase domain **PDBTitle:** crystal structure of protein from mouse mm.236127
108	c1bvyF_	Alignment	not modelled	29.5	7	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
109	d1bvyf_	Alignment	not modelled	29.5	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
110	d1f4pa_	Alignment	not modelled	29.2	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
111	d1ykga1	Alignment	not modelled	28.4	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
112	d5nula_	Alignment	not modelled	28.3	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
113	c3fd0B_	Alignment	not modelled	28.0	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative cystathionine beta-lyase involved in aluminum **PDBTitle:** crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
114	d1b1ca_	Alignment	not modelled	27.9	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
115	c3pdwA_	Alignment	not modelled	26.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized hydrolase yutf; **PDBTitle:** crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
116	d2o2xa1	Alignment	not modelled	26.1	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
117	c1lanA_	Alignment	not modelled	25.9	15	**PDB header:**hydrolase (alpha-aminoacylpeptide) **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** leucine aminopeptidase complex with l-leucinal
118	d1x42a1	Alignment	not modelled	25.2	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
119	c3peiA_	Alignment	not modelled	25.2	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from francisella2 tularensis
120	c2pkeA_	Alignment	not modelled	23.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid delahogenase-like family hydrolase; **PDBTitle:** crystal structure of haloacid delahogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution