Phyre^2

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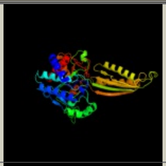
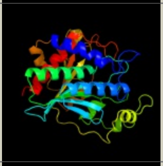
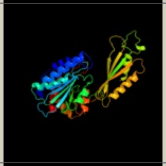
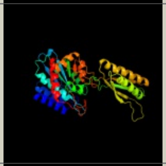
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2imoA_	Alignment		100.0	95	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoate amidohydrolase; **PDBTitle:** crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
2	c3n5fB_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-carbamoyl-l-amino acid hydrolase; **PDBTitle:** crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
3	c2v8gD_	Alignment		100.0	27	**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
4	d1z2la1	Alignment		100.0	100	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
5	c3ramC_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hmra protein; **PDBTitle:** crystal structure of hmra
6	c3gb0A_	Alignment		100.0	20	**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
7	c3pfoB_	Alignment		100.0	16	**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
8	c2zogA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic non-specific dipeptidase; **PDBTitle:** crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
9	c1cg2D_	Alignment		100.0	18	**PDB header:**metallocarboxypeptidase **Chain:** D: **PDB Molecule:**carboxypeptidase g2; **PDBTitle:** carboxypeptidase g2
10	c3ifeA_	Alignment		100.0	17	**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'.
11	c1vixA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of a putative peptidase t

12	c2pokB_	Alignment		100.0	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
13	c3dljB_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-ala-his dipeptidase; **PDBTitle:** crystal structure of human carnosine dipeptidase 1
14	c1vgyB_	Alignment		100.0	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of succinyl diaminopimelate desuccinylase
15	c3rzaA_	Alignment		100.0	20	**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	c2rb7A_	Alignment		100.0	15	**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
17	c2qyvB_	Alignment		100.0	18	**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	c3mruB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacyl-histidine dipeptidase; **PDBTitle:** crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
19	c1ysjB_	Alignment		100.0	14	**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
20	d1r3na1	Alignment		100.0	31	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
21	c3ic1A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
22	c3pfeA_	Alignment	not modelled	100.0	15	**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
23	c1lfwA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pepv; **PDBTitle:** crystal structure of pepv
24	c3tx8A_	Alignment	not modelled	100.0	15	**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
25	c3io1B_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminobenzoyl-glutamate utilization protein; **PDBTitle:** crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
26	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
27	c3ct9B_	Alignment	not modelled	100.0	18	**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
						PDB header:hydrolase

28	c2q43A_	Alignment	not modelled	100.0	18	**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
29	c3khzA_	Alignment	not modelled	100.0	16	**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
30	c1vheA_	Alignment	not modelled	100.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**aminopeptidase/glucanase homolog; **PDBTitle:** crystal structure of a aminopeptidase/glucanase homolog
31	c3kl9F_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**glutamyl aminopeptidase; **PDBTitle:** crystal structure of pepa from streptococcus pneumoniae
32	c1yloA_	Alignment	not modelled	100.0	15	**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
33	c2cf4A_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein ph0519; **PDBTitle:** pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
34	c1y0yA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**frv operon protein frvx; **PDBTitle:** crystal structure of tetrahedral aminopeptidase from p. horikoshii in2 complex with amastatin
35	d1vixa1	Alignment	not modelled	100.0	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
36	c1vhoA_	Alignment	not modelled	100.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of a putative peptidase/endoglucanase
37	c3isxA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1050) from thermotoga2 maritima at 1.40 a resolution
38	c2pe3A_	Alignment	not modelled	100.0	19	**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
39	d1fnoa4	Alignment	not modelled	100.0	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
40	c2fvgA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
41	d1lfwa1	Alignment	not modelled	100.0	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
42	c3cpxC_	Alignment	not modelled	99.9	13	**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
43	d1xfoa2	Alignment	not modelled	99.9	25	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
44	d1vhoa2	Alignment	not modelled	99.9	25	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
45	d1vhea2	Alignment	not modelled	99.9	27	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
46	d1yloa2	Alignment	not modelled	99.9	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
47	c3t6mA_	Alignment	not modelled	99.9	20	**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
48	d1cg2a1	Alignment	not modelled	99.9	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
49	c2greC_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deblocking aminopeptidase; **PDBTitle:** crystal structure of deblocking aminopeptidase from bacillus cereus
50	d2fvga2	Alignment	not modelled	99.9	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
51	d1xmba1	Alignment	not modelled	99.9	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
52	d1ysja1	Alignment	not modelled	99.8	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
53	c1q7lA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i

54	d1vgya1	Alignment	not modelled	99.8	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
55	d2grea2	Alignment	not modelled	99.8	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
56	d1z2la2	Alignment	not modelled	99.8	100	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
57	d1tkja1	Alignment	not modelled	99.7	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
58	d1r3na2	Alignment	not modelled	99.6	26	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
59	d1cg2a2	Alignment	not modelled	99.6	15	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
60	d1rtqa_	Alignment	not modelled	99.5	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
61	d1vgya2	Alignment	not modelled	99.5	14	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
62	c2glfB_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** crystal structure of aminipeptidase (m18 family) from thermotoga2 maritima
63	d1ysja2	Alignment	not modelled	99.4	13	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
64	c1q7lB_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
65	c3tc8A_	Alignment	not modelled	99.4	17	**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	c2ijzF_	Alignment	not modelled	99.3	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**probable m18-family aminopeptidase 2; **PDBTitle:** crystal structure of aminopeptidase
67	c3l6sA_	Alignment	not modelled	99.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartyl aminopeptidase; **PDBTitle:** crystal structure of human aspartyl aminopeptidase (dnpep),2 in complex with aspartic acid hydroxamate
68	c3pb6X_	Alignment	not modelled	99.2	22	**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	99.2	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Glutaminyl-peptide cyclotransferase-like
70	c3guxA_	Alignment	not modelled	99.1	14	**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
71	d1y0ya2	Alignment	not modelled	99.1	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
72	d3bi1a3	Alignment	not modelled	99.0	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
73	d1xmba2	Alignment	not modelled	98.9	21	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
74	d1de4c3	Alignment	not modelled	98.6	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
75	d1lfwa2	Alignment	not modelled	98.6	13	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
76	c1y7eA_	Alignment	not modelled	98.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
77	c3iibA_	Alignment	not modelled	98.4	29	**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
78	c2ek8A_	Alignment	not modelled	98.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** aminopeptidase from aneurinibacillus sp. strain am-1
79	d1y7ea2	Alignment	not modelled	98.3	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
						PDB header:hydrolase

80	c2gljR_	Alignment	not modelled	98.2	22	**Chain:** R: **PDB Molecule:** **PDBTitle:** crystal structure of aminopeptidase i from clostridium2 acetobutylicum
81	c2ootA_	Alignment	not modelled	98.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
82	c3rbuA_	Alignment	not modelled	98.0	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** n-terminally avitev-tagged human glutamate carboxypeptidase ii in2 complex with 2-pmpa
83	c1cx8F_	Alignment	not modelled	97.9	14	**PDB header:**metal transport **Chain:** F: **PDB Molecule:**transferrin receptor protein; **PDBTitle:** crytal structure of the ectodomain of human transferrin receptor
84	d1fnoa3	Alignment	not modelled	97.2	11	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
85	c3k9tA_	Alignment	not modelled	88.1	16	**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
86	c2k9lA_	Alignment	not modelled	26.1	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
87	c3h16A_	Alignment	not modelled	24.3	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tir protein; **PDBTitle:** crystal structure of a bacteria tir domain, pdtir from2 paracoccus denitrificans
88	d2io8a1	Alignment	not modelled	19.7	26	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Glutathionylspermidine synthase substrate-binding domain-like
89	c2jvfA_	Alignment	not modelled	19.4	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
90	c1qysA_	Alignment	not modelled	19.4	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
91	d1t1ea2	Alignment	not modelled	19.2	17	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
92	c3qbuD_	Alignment	not modelled	16.6	9	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of putative peptidoglyacn deactelyase (hp0310) from2 helicobacter pylori
93	d1gxha_	Alignment	not modelled	16.5	16	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
94	d1ayia_	Alignment	not modelled	15.1	14	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
95	d1jhfa1	Alignment	not modelled	15.0	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
96	c3fdfA_	Alignment	not modelled	14.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fr253; **PDBTitle:** crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
97	c3o2qB_	Alignment	not modelled	13.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
98	c3o2sB_	Alignment	not modelled	13.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72 complex
99	d2cu6a1	Alignment	not modelled	12.5	5	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like