Phyre2

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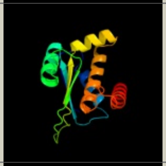
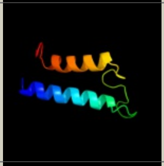
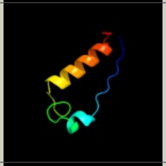
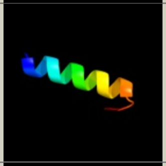
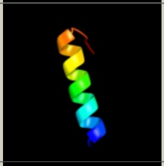
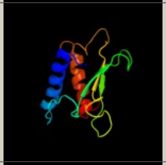
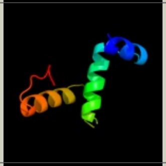
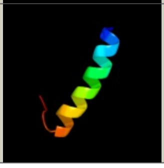
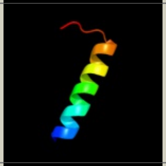
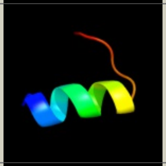
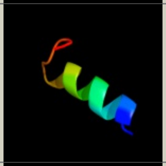
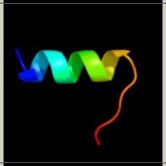
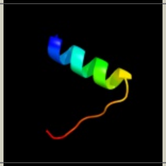
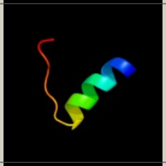
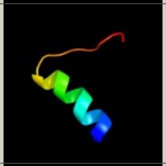
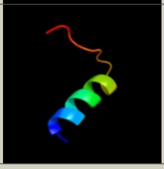
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xm5a_	Alignment		100.0	100	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
2	c1xaxA_	Alignment		100.0	69	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
3	d1oz9a_	Alignment		100.0	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
4	d1tvia_	Alignment		100.0	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
5	d1xfia_	Alignment		65.4	12	**Fold:**AF1104-like **Superfamily:**AF1104-like **Family:**AF1104-like
6	d1lmla_	Alignment		65.0	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
7	c2xhqA_	Alignment		59.4	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
8	c2x7mA_	Alignment		55.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
9	d1k7ia2	Alignment		50.3	11	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
10	c1u9pA_	Alignment		49.2	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
11	c1qysA_	Alignment		45.2	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold

12	d1wgna_	Alignment		44.5	15	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
13	c2jvfA_	Alignment		44.4	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
14	d1asta_	Alignment		41.1	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin
15	c3edhA_	Alignment		41.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bone morphogenetic protein 1; **PDBTitle:** crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dmso
16	c3lqbA_	Alignment		40.5	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
17	d1hv5a_	Alignment		40.4	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
18	d1y93a1	Alignment		40.3	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
19	d1fbla2	Alignment		38.8	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
20	d2ovxa1	Alignment		38.2	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
21	d1cgla_	Alignment	not modelled	36.8	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
22	d1hova_	Alignment	not modelled	36.2	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
23	d1hfca_	Alignment	not modelled	36.1	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
24	d1xuca1	Alignment	not modelled	34.9	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
25	d1q3aa_	Alignment	not modelled	34.8	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
26	c2jsdA_	Alignment	not modelled	34.1	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
27	d1rm8a_	Alignment	not modelled	32.5	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
28	d1i76a_	Alignment	not modelled	31.1	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
29	d1qiba_	Alignment	not modelled	30.6	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain

						Family: Matrix metalloproteases, catalytic domain
30	c3lq0A_	Alignment	not modelled	28.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proastacin; **PDBTitle:** zymogen structure of crayfish astacin metallopeptidase
31	c3lmcA_	Alignment	not modelled	28.3	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase, zinc-dependent; **PDBTitle:** crystal structure of zinc-dependent peptidase from methanocorpusculum2 labreanum (strain z), northeast structural genomics consortium target3 mur16
32	c2xs4A_	Alignment	not modelled	27.2	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
33	d1mmqa_	Alignment	not modelled	25.9	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
34	c1slmA_	Alignment	not modelled	25.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
35	c3qyyB_	Alignment	not modelled	24.6	12	**PDB header:**signaling protein/inhibitor **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
36	d1cxva_	Alignment	not modelled	24.4	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
37	c3i5bA_	Alignment	not modelled	21.5	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wspr from2 pseudomonas aeruginosa
38	d1hy7a_	Alignment	not modelled	20.9	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
39	d1eaka2	Alignment	not modelled	18.8	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
40	c3hvaA_	Alignment	not modelled	18.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
41	c2a97B_	Alignment	not modelled	17.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**botulinum neurotoxin type f; **PDBTitle:** crystal structure of catalytic domain of clostridium2 botulinum neurotoxin serotype f
42	d1w25a3	Alignment	not modelled	15.6	17	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
43	c1jmtB_	Alignment	not modelled	13.2	31	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**splicing factor u2af 65 kda subunit; **PDBTitle:** x-ray structure of a core u2af65/u2af35 heterodimer
44	c3i5cA_	Alignment	not modelled	11.2	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fusion of general control protein gcn4 and wspr response **PDBTitle:** crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
45	c1om8A_	Alignment	not modelled	10.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serralysin; **PDBTitle:** crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallyzed with 10 mm edta
46	c1dowB_	Alignment	not modelled	10.1	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**beta-catenin; **PDBTitle:** crystal structure of a chimera of beta-catenin and alpha-2 catenin
47	c3ba0A_	Alignment	not modelled	10.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
48	c3bkdC_	Alignment	not modelled	9.7	50	**PDB header:**viral protein, membrane protein **Chain:** C: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
49	c3bkdH_	Alignment	not modelled	9.7	50	**PDB header:**viral protein, membrane protein **Chain:** H: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
50	c3bkdB_	Alignment	not modelled	9.7	50	**PDB header:**viral protein, membrane protein **Chain:** B: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
51	c3bkdA_	Alignment	not modelled	9.7	50	**PDB header:**viral protein, membrane protein **Chain:** A: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
52	c3bkdG_	Alignment	not modelled	9.7	50	**PDB header:**viral protein, membrane protein **Chain:** G: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
53	c3bkdD_	Alignment	not modelled	9.7	50	**PDB header:**viral protein, membrane protein **Chain:** D: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane

						domain of m22 protein
54	c3bkdE_	Alignment	not modelled	9.7	50	**PDB header:**viral protein, membrane protein **Chain:** E: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
55	c3bkdF_	Alignment	not modelled	9.7	50	**PDB header:**viral protein, membrane protein **Chain:** F: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
56	d1sata2	Alignment	not modelled	9.7	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
57	d3e11a1	Alignment	not modelled	9.6	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
58	d1gtda_	Alignment	not modelled	9.1	30	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
59	d1bqqm_	Alignment	not modelled	8.8	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
60	c2rjqA_	Alignment	not modelled	8.7	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
61	c3iclA_	Alignment	not modelled	8.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**eal/ggdef domain protein; **PDBTitle:** x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
62	c2erpA_	Alignment	not modelled	8.5	38	**PDB header:**toxin **Chain:** A: **PDB Molecule:**vascular apoptosis-inducing protein 1; **PDBTitle:** crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
63	d1kufa_	Alignment	not modelled	8.4	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
64	c3ignA_	Alignment	not modelled	8.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase; **PDBTitle:** crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
65	c2gjhA_	Alignment	not modelled	7.7	35	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
66	c3gr1A_	Alignment	not modelled	7.6	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
67	c2cltB_	Alignment	not modelled	7.5	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
68	c2zw2B_	Alignment	not modelled	7.5	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
69	d1atla_	Alignment	not modelled	7.5	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
70	c2dgbA_	Alignment	not modelled	7.4	42	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
71	d1k1fa_	Alignment	not modelled	7.4	16	**Fold:**Bcr-Abl oncoprotein oligomerization domain **Superfamily:**Bcr-Abl oncoprotein oligomerization domain **Family:**Bcr-Abl oncoprotein oligomerization domain
72	c3pjwA_	Alignment	not modelled	7.3	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
73	c3b8zB_	Alignment	not modelled	7.0	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
74	c2dw1B_	Alignment	not modelled	6.8	30	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
75	c3e5aB_	Alignment	not modelled	6.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**targeting protein for xklp2; **PDBTitle:** crystal structure of aurora a in complex with vx-680 and tpx2
76	d1r55a_	Alignment	not modelled	6.7	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
77	d1t4aa_	Alignment	not modelled	6.7	31	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
78	c3c0tB_	Alignment	not modelled	6.4	67	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mediator of rna polymerase ii transcription **PDBTitle:** structure of the schizosaccharomyces pombe mediator2 subcomplex med8c/18

79	c1p9iA_	Alignment	not modelled	6.4	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cortexillin i/gcn4 hybrid peptide; **PDBTitle:** coiled-coil x-ray structure at 1.17 a resolution
80	d2b7ea1	Alignment	not modelled	6.2	42	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
81	c3ipfA_	Alignment	not modelled	6.2	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q251q8_deshy protein from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr8c.
82	c2awyB_	Alignment	not modelled	6.1	13	**PDB header:**oxygen storage/transport **Chain:** B: **PDB Molecule:**hemerythrin-like domain protein dcrh; **PDBTitle:** met-dcrh-hr
83	d2a6aa2	Alignment	not modelled	6.1	29	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
84	d1qf6a4	Alignment	not modelled	6.0	19	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
85	c3o7kA_	Alignment	not modelled	6.0	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline2 decarboxylase from klebsiella pneumoniae
86	c3b6nA_	Alignment	not modelled	5.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax
87	c2ppwA_	Alignment	not modelled	5.8	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
88	c3f6nA_	Alignment	not modelled	5.8	29	**PDB header:**viral protein, dna-binding protein **Chain:** A: **PDB Molecule:**virion-associated protein; **PDBTitle:** crystal structure of the virion-associated protein p3 from2 caulimovirus
89	d1kapp2	Alignment	not modelled	5.6	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
90	d2g8la1	Alignment	not modelled	5.6	13	**Fold:**AF1104-like **Superfamily:**AF1104-like **Family:**AF1104-like
91	c2kadA_	Alignment	not modelled	5.6	40	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
92	c2kadB_	Alignment	not modelled	5.6	40	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
93	c2kadD_	Alignment	not modelled	5.6	40	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
94	c2kadC_	Alignment	not modelled	5.6	40	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
95	c2v4bB_	Alignment	not modelled	5.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
96	c3dl1A_	Alignment	not modelled	5.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent hydrolase; **PDBTitle:** crystal structure of a putative metal-dependent hydrolase2 (yp_001336084.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.20 a resolution
97	c1fdfA_	Alignment	not modelled	5.5	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rhodopsin; **PDBTitle:** helix 7 bovine rhodopsin
98	d1qmya_	Alignment	not modelled	5.4	38	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**FMDV leader protease
99	c3k4tB_	Alignment	not modelled	5.4	29	**PDB header:**viral protein, dna-binding protein **Chain:** B: **PDB Molecule:**virion-associated protein; **PDBTitle:** crystal structure of the virion-associated protein p3 from2 caulimovirus