

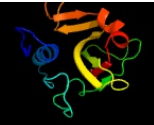








Table S2: Three-dimensional alignment results of LysPEF1-1 with similar protein templates.





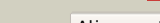



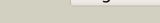










Phyre2




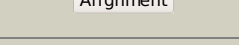

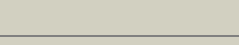


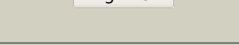

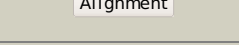
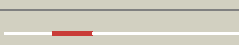
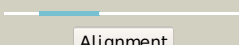

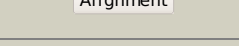



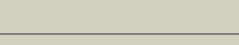

Email	wangchen950518@gmail.com
Description	LysPEF-1_290_aa_
Date	Wed Aug 21 04:14:06 BST 2024
Unique Job ID	69ab052c5c7c03e2























Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c8h1iA_</a>	Alignment		99.6	23	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> crystal structure of plygrcs, a bacteriophage endolysin in complex2 with cold shock protein c <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
2	<a href="#">c5udmA_</a>	Alignment		99.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phage-associated cell wall hydrolase; <b>PDBTitle:</b> phage-associated cell wall hydrolase plypy from streptococcus2 pyogenes, space group p6522 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
3	<a href="#">c8tw1A_</a>	Alignment		100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endolysin lys2972; <b>PDBTitle:</b> crystal structure of lys2972, a phage endolysin targeting2 streptococcus thermophilus <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
4	<a href="#">c2mk5A_</a>	Alignment		99.4	46	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> solution structure of a protein domain <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
5	<a href="#">c4f0wA_</a>	Alignment		93.8	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of type effector tse1 c30a mutant from pseudomonas2 aeruginosa <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
6	<a href="#">c4lxcA_</a>	Alignment		98.1	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysostaphin; <b>PDBTitle:</b> the antimicrobial peptidase lysostaphin from staphylococcus simulans <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
7	<a href="#">c2xivA_</a>	Alignment		99.8	29	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical invasion protein; <b>PDBTitle:</b> structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
8	<a href="#">c8ev5A_</a>	Alignment		99.7	28	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> clan ca, family c40, nlpc/p60 superfamily cysteine <b>PDBTitle:</b> nlpc b3 covalently bound with e64 inhibitor fragment <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
9	<a href="#">c2k1gA_</a>	Alignment		99.7	26	<b>PDB header:</b> lipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein spr; <b>PDBTitle:</b> solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
10	<a href="#">c1r77A_</a>	Alignment		99.2	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell wall targeting domain of glycyglycine endopeptidase <b>PDBTitle:</b> crystal structure of the cell wall targeting domain of peptidylglycan2 hydrolase ale-1 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
11	<a href="#">c7cflB_</a>	Alignment		99.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative cell wall hydrolase phosphatase-associated <b>PDBTitle:</b> x-ray structure of autolysin acd24020 catalytic domain from2 clostridium difficile <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>

12	<a href="#">c3npfB</a>	Alignment		99.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dipeptidyl-peptidase vi; <b>PDBTitle:</b> crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
13	<a href="#">c8wt3A</a>	Alignment		99.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan dl-endopeptidase cwlo; <b>PDBTitle:</b> crystal structure of peptidoglycan dl-endopeptidase cwlo <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
14	<a href="#">d2evra2</a>	Alignment		99.9	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> NlpC/P60 <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
15	<a href="#">c8i2eD</a>	Alignment		99.7	24	<b>PDB header:</b> antimicrobial protein/inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> probable peptidoglycan endopeptidase lyte; <b>PDBTitle:</b> crystal structure of bacillus subtilis lyte in complex with isea <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
16	<a href="#">c8er5B</a>	Alignment		99.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nlp/p60 domain-containing protein; <b>PDBTitle:</b> crystal structure of nlp/p60 domain from clostridium innocuum2 nlp/p60 domain-containing protein ci_01448. <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
17	<a href="#">c7aqhH</a>	Alignment		98.9	29	<b>PDB header:</b> viral protein <b>Chain:</b> H: <b>PDB Molecule:</b> orf007; <b>PDBTitle:</b> cell wall binding domain of the staphylococcal phage 2638a endolysin <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
18	<a href="#">c6b8cA</a>	Alignment		99.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60; <b>PDBTitle:</b> crystal structure of nlp/p60 domain of peptidoglycan hydrolase saga <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
19	<a href="#">c3pbiA</a>	Alignment		99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> invasion protein; <b>PDBTitle:</b> structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
20	<a href="#">c3h41A</a>	Alignment		99.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60 family protein; <b>PDBTitle:</b> crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
21	<a href="#">c4hpeA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell wall hydrolase tn916-like,ctn1-orf17; <b>PDBTitle:</b> crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
22	<a href="#">c8jiaE</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> probable endopeptidase mt2245; <b>PDBTitle:</b> cryo-em structure of mycobacterium tuberculosis atp bound ftse(e165q)2 x/ripic complex in peptidisc <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
23	<a href="#">c7bk8A</a>	Alignment	not modelled	98.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> magc; <b>PDBTitle:</b> x-ray crystal structure of pseudomonas aeruginosa magc <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
24	<a href="#">c2fg0B</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cog0791: cell wall-associated hydrolases (invasion- <b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
25	<a href="#">c4olkB</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> the chap domain of lysgh15 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
26	<a href="#">c4f4mA</a>	Alignment	not modelled	93.2	30	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> papain peptidoglycan amidase effector tse1; <b>PDBTitle:</b> structure of the type vi peptidoglycan amidase effector tse1 (c30a)2 from pseudomonas aeruginosa <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a> <b>PDB header:</b> hydrolase

27	<a href="#">c6istC</a>	 Alignment	not modelled	98.1	27	<b>Chain:</b> C: <b>PDB Molecule:</b> lysin; <b>PDBTitle:</b> crystal structure of a wild type endolysin lysime-ef1 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
28	<a href="#">c8aucB</a>	 Alignment	not modelled	99.9	20	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell wall-associated hydrolases (invasion-associated) <b>PDBTitle:</b> structure of peptidoglycan hydrolase cg1735 from corynebacterium2 glutamicum, trigonal crystal form <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
29	<a href="#">c8audB</a>	 Alignment	not modelled	99.9	20	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell wall-associated hydrolases (invasion-associated) <b>PDBTitle:</b> structure of peptidoglycan hydrolase cg1735 from corynebacterium2 glutamicum, orthorhombic crystal form <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
30	<a href="#">c6biqA</a>	 Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> clan ca, family c40, nlpc/p60 superfamily cysteine <b>PDBTitle:</b> structure of nlpc2 from trichomonas vaginalis <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
31	<a href="#">c4xcmB</a>	 Alignment	not modelled	99.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cell wall-binding endopeptidase-related protein; <b>PDBTitle:</b> crystal structure of the putative nlpc/p60 d,l endopeptidase from t.2 thermophilus <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
32	<a href="#">c5d74B</a>	 Alignment	not modelled	98.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phage lysin; <b>PDBTitle:</b> the crystal structure of ly7917 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
33	<a href="#">c4fdyA</a>	 Alignment	not modelled	99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> similar to lipoprotein, nlp/p60 family; <b>PDBTitle:</b> crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
34	<a href="#">c4hfkC</a>	 Alignment	not modelled	38.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi effector-immunity complex tae4-tai42 from enterobacter cloacae <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
35	<a href="#">c4hffA</a>	 Alignment	not modelled	58.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi effector-immunity complex tae4-tai42 from salmonella typhimurium <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
36	<a href="#">c4hzbA</a>	 Alignment	not modelled	98.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
37	<a href="#">c3i86A</a>	 Alignment	not modelled	99.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
38	<a href="#">c2jtcA</a>	 Alignment	not modelled	25.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> streptopain; <b>PDBTitle:</b> 3d structure and backbone dynamics of spe b <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
39	<a href="#">c3m1uB</a>	 Alignment	not modelled	98.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative gamma-d-glutamyl-l-diamino acid endopeptidase; <b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dnu_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
40	<a href="#">c4emeB</a>	 Alignment	not modelled	45.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> m18 aspartyl aminopeptidase; <b>PDBTitle:</b> x-ray crystal structure and specificity of the plasmodium falciparum2 malaria aminopeptidase <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
41	<a href="#">c6sqxA</a>	 Alignment	not modelled	98.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide-binding protein; <b>PDBTitle:</b> insights into a novel nlpc/p60 endopeptidase from photobacterium2 damsela subsp. piscicida <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
42	<a href="#">c3bb7A</a>	 Alignment	not modelled	21.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interpain a; <b>PDBTitle:</b> structure of prevotella intermedia ppointerpain a fragment 39-3592 (mutant c154a) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
43	<a href="#">c2lieA</a>	 Alignment	not modelled	30.5	21	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ccl2 lectin; <b>PDBTitle:</b> nmr structure of the lectin ccl2 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
44	<a href="#">c3gt2A</a>	 Alignment	not modelled	99.7	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
45	<a href="#">c4xaaA</a>	 Alignment	not modelled	53.8	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxygenase; <b>PDBTitle:</b> crystal structure of avio1 from streptomyces viridochromogenes tue57 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
46	<a href="#">c4h4jA</a>	Alignment	not modelled	74.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a n-acetylmuramoyl-l-alanine amidase2 (bacuni_02947) from bacteroides uniformis atcc 8492 at 1.15 a3 resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
						<b>PDB header:</b> hydrolase

47	<a href="#">c5t1qB</a>	 Alignment	not modelled	93.8	20	<b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase domain-containing <b>PDBTitle:</b> 2.15 angstrom crystal structure of n-acetylmuramoyl-l-alanine amidase2 from staphylococcus aureus. <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
48	<a href="#">c8b2sA</a>	 Alignment	not modelled	93.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gh24 family muramidase; <b>PDBTitle:</b> gh24 family muramidase from trichophaea saccata with an sh3-like cell2 wall binding domain <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
49	<a href="#">c2p1gA</a>	 Alignment	not modelled	98.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative xylanase; <b>PDBTitle:</b> crystal structure of a putative xylanase from bacteroides fragilis <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
50	<a href="#">d1b12a</a>	 Alignment	not modelled	38.4	35	<b>Fold:</b> LexA/Signal peptidase <b>Superfamily:</b> LexA/Signal peptidase <b>Family:</b> Type 1 signal peptidase <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
51	<a href="#">c4cgkA</a>	 Alignment	not modelled	88.5	20	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> secreted 45 kda protein; <b>PDBTitle:</b> crystal structure of the essential protein pcsb from streptococcus2 pneumoniae <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
52	<a href="#">c2lrjA</a>	 Alignment	not modelled	96.4	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> staphyloxanthin biosynthesis protein, putative; <b>PDBTitle:</b> nmr solution structure of staphyloxanthin biosynthesis protein <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
53	<a href="#">c4lt5A</a>	 Alignment	not modelled	39.8	24	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> naegleria tet-like dioxygenase; <b>PDBTitle:</b> structure of a naegleria tet-like dioxygenase in complex with 5-2 methylcytosine dna <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
54	<a href="#">c4wviA</a>	 Alignment	not modelled	60.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,signal peptidase ib; <b>PDBTitle:</b> crystal structure of the type-i signal peptidase from staphylococcus2 aureus (spsb) in complex with a substrate peptide (pep2). <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
55	<a href="#">c7p2qA</a>	 Alignment	not modelled	75.8	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal peptidase complex catalytic subunit sec11c; <b>PDBTitle:</b> human signal peptidase complex paralog c (spc-c) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
56	<a href="#">c2k3aA</a>	 Alignment	not modelled	95.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chap domain protein; <b>PDBTitle:</b> nmr solution structure of staphylococcus saprophyticus chap (cysteine,2 histidine-dependent amidohydrolases/peptidases) domain protein.3 northeast structural genomics consortium target syr11 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
57	<a href="#">d1zcea1</a>	 Alignment	not modelled	84.5	21	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Atu2648/PH1033-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
58	<a href="#">d2gbsa1</a>	 Alignment	not modelled	79.8	21	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Atu2648/PH1033-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
59	<a href="#">c3kw0D</a>	 Alignment	not modelled	96.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cysteine peptidase; <b>PDBTitle:</b> crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
60	<a href="#">c8ej5A</a>	 Alignment	not modelled	32.5	12	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> gp10, tail tip lysin (spike); <b>PDBTitle:</b> tail tip structure of staphylococcus phage andhra <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
61	<a href="#">c3kopB</a>	 Alignment	not modelled	50.8	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
62	<a href="#">d2im9a1</a>	 Alignment	not modelled	36.9	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Lpg0564-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
63	<a href="#">c2im9A</a>	 Alignment	not modelled	36.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
64	<a href="#">d2io8a2</a>	 Alignment	not modelled	94.5	22	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> CHAP domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
65	<a href="#">c2ioaA</a>	 Alignment	not modelled	87.1	22	<b>PDB header:</b> ligase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional glutathionylspermidine synthetase/amidase; <b>PDBTitle:</b> e. coli bifunctional glutathionylspermidine synthetase/amidase2 incomplex with mg2+ and adp and phosphinate inhibitor <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
66	<a href="#">c5m0tA</a>	 Alignment	not modelled	42.7	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent non-heme iron oxygenase eash; <b>PDBTitle:</b> alpha-ketoglutarate-dependent non-heme iron oxygenase eash <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
						<b>PDB header:</b> oxidoreductase

67	<a href="#">c5daqA</a>	 Alignment	not modelled	26.7	28	<b>Chain:</b> A: <b>PDB Molecule:</b> phytanoyl-coa dioxygenase family protein (afu_orthologue <b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase asqj in complex with2 4-methoxycyclopeptin <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
68	<a href="#">d2a1xa1</a>	 Alignment	not modelled	44.2	32	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavamate synthase-like <b>Family:</b> PhyH-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
69	<a href="#">c5ncjB</a>	 Alignment	not modelled	37.2	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> leucine hydroxylase; <b>PDBTitle:</b> grie in complex with manganese, succinate and (2s,4r)-5-hydroxyleucine <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
70	<a href="#">c3eopB</a>	 Alignment	not modelled	77.0	17	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> thymocyte nuclear protein 1; <b>PDBTitle:</b> crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
71	<a href="#">c2rdsA</a>	 Alignment	not modelled	47.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- <b>PDBTitle:</b> crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
72	<a href="#">c4n31A</a>	 Alignment	not modelled	22.0	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> sipa; <b>PDBTitle:</b> structure and activity of streptococcus pyogenes sipa: a signal2 peptidase homologue essential for pilus polymerisation <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
73	<a href="#">c8b2gB</a>	 Alignment	not modelled	48.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sh3b domain-containing protein; <b>PDBTitle:</b> sh3-like domain from penicillium virgatum muramidase <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
74	<a href="#">d2g2xa1</a>	 Alignment	not modelled	73.5	22	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Atu2648/PH1033-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
75	<a href="#">d2evea1</a>	 Alignment	not modelled	69.8	22	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Atu2648/PH1033-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
76	<a href="#">c4pa5A</a>	 Alignment	not modelled	50.5	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> tgl - a bacterial spore coat transglutaminase - cystamine complex <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
77	<a href="#">c6yexB</a>	 Alignment	not modelled	37.2	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hnh endonuclease; <b>PDBTitle:</b> vcam4i restriction endonuclease in the absence of dna <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
78	<a href="#">c4eyzB</a>	 Alignment	not modelled	91.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cellulosome-related protein module from ruminococcus <b>PDBTitle:</b> crystal structure of an uncommon cellulosome-related protein module2 from ruminococcus flavefaciens that resembles papain-like cysteine3 peptidases <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
79	<a href="#">c4mhuB</a>	 Alignment	not modelled	35.8	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ectoine hydroxylase; <b>PDBTitle:</b> crystal structure of ectd from s. alaskensis with bound fe <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
80	<a href="#">c7dt0C</a>	 Alignment	not modelled	31.2	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> phytanoyl-coa dioxygenase; <b>PDBTitle:</b> proline hydroxylase h11-n101i mutant <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
81	<a href="#">c2lktA</a>	 Alignment	not modelled	97.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> retinoic acid receptor responder protein 3; <b>PDBTitle:</b> solution structure of n-terminal domain of human tig3 in 2 m urea <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
82	<a href="#">c5yboA</a>	 Alignment	not modelled	35.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prha; <b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase prha in complex with2 preaustinoid a1 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
83	<a href="#">d1ftra1</a>	 Alignment	not modelled	26.8	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
84	<a href="#">d2ba0a2</a>	 Alignment	not modelled	21.3	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Ribosomal L27 protein-like <b>Family:</b> ECR1 N-terminal domain-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
85	<a href="#">d2if6a1</a>	 Alignment	not modelled	97.2	11	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> YiiX-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
86	<a href="#">c2kyaA</a>	 Alignment	not modelled	97.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> group xvi phospholipase a2; <b>PDBTitle:</b> solution structure of the h-rev107 n-terminal domain <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
87	<a href="#">c7ddeV</a>	 Alignment	not modelled	42.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> V: <b>PDB Molecule:</b> aspartyl aminopeptidase 1,zz-type zinc finger-containing <b>PDBTitle:</b> cryo-em structure of the ape4 and nbr1 complex <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
		 Alignment				<b>PDB header:</b> hydrolase



88	<a href="#">c3varA_</a>	Alignment	not modelled	37.6	16	<b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl aminopeptidase; <b>PDBTitle:</b> crystal structure of dnpep, znzn form <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
89	<a href="#">d2nn6h3</a>	Alignment	not modelled	29.0	67	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I) <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
90	<a href="#">c2opwA_</a>	Alignment	not modelled	50.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phyhd1 protein; <b>PDBTitle:</b> crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
91	<a href="#">c5zm4B_</a>	Alignment	not modelled	39.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dioxygenase anda; <b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase anda with2 preandiloid c <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
92	<a href="#">c5epaE_</a>	Alignment	not modelled	34.9	24	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> snok; <b>PDBTitle:</b> crystal structure of non-heme alpha ketoglutarate dependent2 carbocyclase snok from nogalamycin biosynthesis <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
93	<a href="#">d2ar1a1</a>	Alignment	not modelled	67.7	26	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Atu2648/PH1033-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
94	<a href="#">dligga_</a>	Alignment	not modelled	46.7	46	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> Transcriptional repressor protein KorB <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
95	<a href="#">dligub_</a>	Alignment	not modelled	46.0	46	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> Transcriptional repressor protein KorB <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
96	<a href="#">d2fcta1</a>	Alignment	not modelled	37.8	23	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminate synthase-like <b>Family:</b> PhyH-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
97	<a href="#">c6winA_</a>	Alignment	not modelled	21.8	18	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> type 6 secretion amidase effector 2; <b>PDBTitle:</b> type 6 secretion amidase effector 2 (tae2) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
98	<a href="#">c3nnlB_</a>	Alignment	not modelled	56.4	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> cura; <b>PDBTitle:</b> halogenase domain from cura module (crystal form iii) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
99	<a href="#">d1knwa1</a>	Alignment	not modelled	39.8	13	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Eukaryotic ODC-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
100	<a href="#">c6dchA_</a>	Alignment	not modelled	28.1	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> scoe protein; <b>PDBTitle:</b> structure of isonitrile biosynthesis enzyme scoe <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
101	<a href="#">d1twia1</a>	Alignment	not modelled	25.5	21	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Eukaryotic ODC-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
102	<a href="#">d1m5sa1</a>	Alignment	not modelled	22.3	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
103	<a href="#">c7vbqB_</a>	Alignment	not modelled	28.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase tlxi; <b>PDBTitle:</b> heterodimer structure of fe(ii)/(alpha)ketoglutarate-dependent2 dioxygenase tlxij <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
104	<a href="#">d2jfga2</a>	Alignment	not modelled	21.3	31	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
105	<a href="#">c3l6sa_</a>	Alignment	not modelled	38.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl aminopeptidase; <b>PDBTitle:</b> crystal structure of human aspartyl aminopeptidase (dnpep), in complex2 with aspartic acid hydroxamate <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
106	<a href="#">c4j5iH_</a>	Alignment	not modelled	22.7	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent taurine dioxygenase; <b>PDBTitle:</b> crystal structure of an alpha-ketoglutarate-dependent taurine2 dioxygenase from mycobacterium smegmatis <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
107	<a href="#">c2e58D_</a>	Alignment	not modelled	20.6	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> mnm22; <b>PDBTitle:</b> crystal structure of mnm2 from aquifex aeolicus <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
108	<a href="#">c7c9jA_</a>	Alignment	not modelled	58.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> transglutaminase from geobacillus stearothermophilus (without c-2 terminal extension) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
109	<a href="#">c7qtfa_</a>	Alignment	not modelled	27.1	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> plao1; <b>PDBTitle:</b> crystal structure of the fe(ii)/alpha-ketoglutarate dependent2 dioxygenase plao1 in complex with sodium succinate <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
110	<a href="#">d2zoda2</a>	Alignment	not modelled	26.8	24	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like

						<b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a> <b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Eukaryotic ODC-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
111	<a href="#">dlnjib1</a>	Alignment	not modelled	24.0	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavamate synthase-like <b>Family:</b> TauD/TfdA-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
112	<a href="#">dloiha_</a>	Alignment	not modelled	21.4	31	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Calcium ATPase, transduction domain A <b>Family:</b> Calcium ATPase, transduction domain A <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
113	<a href="#">d1wpga1</a>	Alignment	not modelled	25.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent taurine dioxygenase; <b>PDBTitle:</b> crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
114	<a href="#">c3rljB_</a>	Alignment	not modelled	24.7	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arginine beta-hydroxylase; <b>PDBTitle:</b> crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
115	<a href="#">c4ne0A_</a>	Alignment	not modelled	21.4	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-arginine beta-hydroxylase; <b>PDBTitle:</b> crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
116	<a href="#">c4ne0B_</a>	Alignment	not modelled	20.7	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> taud/tfda family dioxygenase; <b>PDBTitle:</b> crystal structure of p.isnb complexed with tyrosine isonitrile <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
117	<a href="#">c7tclX_</a>	Alignment	not modelled	20.5	33	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> trypanothione synthetase; <b>PDBTitle:</b> trypanothione synthetase <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
118	<a href="#">c2vpmB_</a>	Alignment	not modelled	87.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> taurine dioxygenase; <b>PDBTitle:</b> crystal structure of taurine dioxygenase from burkholderia ambifaria <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
119	<a href="#">c5vn6B_</a>	Alignment	not modelled	22.8	25	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavamate synthase-like <b>Family:</b> Clavamate synthase <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
120	<a href="#">dlds1a_</a>	Alignment	not modelled	22.1	25	