

Table S3: Three-dimensional alignment results of LysPEF1-2 with similar protein templates.

Phyre2

Email

wangchen950518@gmail.com

Description

LysPEF1-2

Date

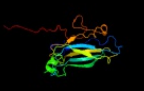








Wed Aug 21 05:45:36 BST 2024

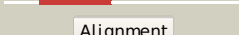

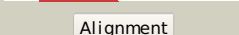
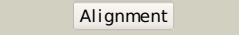
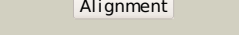

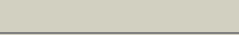

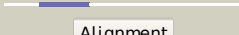

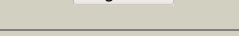


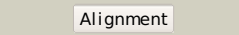

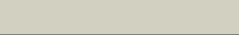
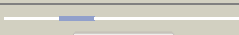
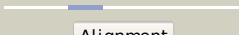




Unique Job ID

f26785b1c5a04027

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4bxdB_	Alignment		100.0	28	PDB header: hydrolase/peptide Chain: B: PDB Molecule: ampdh3; PDBT itle: crystal structure of ampdh3 from pseudomonas aeruginosa in complex2 with tetrasaccharide pentapeptide PDB Entry: PDBe RCSB PDBj
2	c4bolA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: ampdh2; PDBT itle: crystal structure of ampdh2 from pseudomonas aeruginosa in complex2 with pentapeptide PDB Entry: PDBe RCSB PDBj
3	c4olsA_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: endolysin; PDBT itle: the amidase-2 domain of lysgh15 PDB Entry: PDBe RCSB PDBj
4	c8c4dA_	Alignment		100.0	23	PDB header: antimicrobial protein Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBT itle: n-acetylmuramoyl-l-alanine amidase from enterococcus faecium prophage2 genome PDB Entry: PDBe RCSB PDBj
5	c3hmaA_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase xlya; PDBT itle: amidase from bacillus subtilis PDB Entry: PDBe RCSB PDBj
6	c2bh7A_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBT itle: crystal structure of a semet derivative of amid at 2.22 angstroms PDB Entry: PDBe RCSB PDBj
7	d2bgxa2	Alignment		100.0	26	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
8	c6sscA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBT itle: n-acetylmuramoyl-l-alanine amidase lysc from clostridium intestinale2 urnw PDB Entry: PDBe RCSB PDBj
9	c3latB_	Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: bifunctional autolysin; PDBT itle: crystal structure of staphylococcus peptidoglycan hydrolase amie PDB Entry: PDBe RCSB PDBj
10	c1ohtA_	Alignment		99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: cg14704 protein; PDBT itle: peptidoglycan recognition protein-lb PDB Entry: PDBe RCSB PDBj
11	d1ohta_	Alignment		99.9	20	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj

12	c4yu5A	Alignment		62.6	18	PDB header: hydrolase Chain: A: PDB Molecule: immune inhibitor a, metalloprotease; PDBTitle: crystal structure of selenomethionine variant of bacillus anthracis2 immune inhibitor a2 peptidase zymogen PDB Entry: PDBe RCSB PDBj
13	d1lbaa	Alignment		100.0	19	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
14	d1j3ga	Alignment		100.0	18	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
15	d1yb0a1	Alignment		100.0	18	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
16	c6fhgB	Alignment		99.9	18	PDB header: antimicrobial protein Chain: B: PDB Molecule: lyst endolysin; PDBTitle: crystal structure of the ts2631 endolysin from thermus scotoductus2 phage with the unique n-terminal moiety responsible for peptidoglycan3 anchoring PDB Entry: PDBe RCSB PDBj
17	d2cb3a1	Alignment		100.0	18	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
18	c4z8iA	Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan recognition protein 3; PDBTitle: crystal structure of branchiostoma belcheri tsingtauense peptidoglycan2 recognition protein 3 PDB Entry: PDBe RCSB PDBj
19	c2rkqA	Alignment		100.0	18	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein-sd; PDBTitle: crystal structure of drosophila peptidoglycan recognition protein sd2 (pgrp-sd) PDB Entry: PDBe RCSB PDBj
20	c7f5iA	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: x-ray structure of clostridium perfringens-specific amidase endolysin PDB Entry: PDBe RCSB PDBj
21	d1ycka1	Alignment	not modelled	100.0	17	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
22	c5xz3D	Alignment	not modelled	99.9	17	PDB header: immune system Chain: D: PDB Molecule: peptidoglycan-recognition protein; PDBTitle: the x-ray structure of apis mellifera pgrp-sa PDB Entry: PDBe RCSB PDBj
23	d2f2lx1	Alignment	not modelled	99.9	18	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
24	d1sk4a	Alignment	not modelled	99.9	17	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
25	c2xz4A	Alignment	not modelled	100.0	17	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein If; PDBTitle: crystal structure of the Ifz ectodomain of the peptidoglycan2 recognition protein If PDB Entry: PDBe RCSB PDBj
26	c3ep1B	Alignment	not modelled	99.9	15	PDB header: immune system Chain: B: PDB Molecule: pgrp-hd - peptidoglycan recognition protein homologue; PDBTitle: structure of the pgrp-hd from alvinella pompejana PDB Entry: PDBe RCSB PDBj
27	d1sxra	Alignment	not modelled	99.9	13	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
28	c6ckhA	Alignment	not modelled	99.9	14	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein; PDBTitle: manduca sexta peptidoglycan recognition protein-1 PDB Entry: PDBe RCSB PDBj

29	c1s2jA_	 Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan recognition protein sa cg11709-pa; PDBTitle: crystal structure of the drosophila pattern-recognition receptor pgrp-2 sa PDB Entry: PDBe RCSB PDBj
30	c2os2A_	 Alignment	not modelled	26.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: jmjC domain-containing histone demethylation protein 3a; PDBTitle: crystal structure of jmjD2a complexed with histone h3 peptide2 trimethylated at lys36 PDB Entry: PDBe RCSB PDBj
31	c4ivvA_	 Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: autolysin; PDBTitle: catalytic amidase domain of the major autolysin lyta from2 streptococcus pneumoniae PDB Entry: PDBe RCSB PDBj
32	c4x36A_	 Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: A: PDB Molecule: autolysin; PDBTitle: crystal structure of the autolysin lyta from streptococcus pneumoniae2 tigr4 PDB Entry: PDBe RCSB PDBj
33	c5iklD_	 Alignment	not modelled	18.3	21	PDB header: ligase Chain: D: PDB Molecule: geranyl-coa carboxylase, beta-subunit; PDBTitle: crystal structure of p. aeruginosa geranyl-coa carboxylase (gcc), beta2 subunit PDB Entry: PDBe RCSB PDBj
34	c7eebJ_	 Alignment	not modelled	47.9	14	PDB header: protein transport Chain: J: PDB Molecule: transmembrane protein 249; PDBTitle: structure of the catspermasome PDB Entry: PDBe RCSB PDBj
35	c6cuqB_	 Alignment	not modelled	15.8	21	PDB header: cytokine Chain: B: PDB Molecule: macrophage migration inhibitory factor-like protein; PDBTitle: crystal structure of macrophage migration inhibitory factor-like2 protein (ehmif) from entamoeba histolytica PDB Entry: PDBe RCSB PDBj
36	c4atbB_	 Alignment	not modelled	14.4	22	PDB header: immune system Chain: B: PDB Molecule: interleukin enhancer-binding factor 3; PDBTitle: crystal structure of the nf90-nf45 dimerisation domain complex with2 ctp PDB Entry: PDBe RCSB PDBj
37	d1vk3a2	 Alignment	not modelled	28.7	19	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like PDB entry: PDBe RCSB PDBj
38	d2dsta1	 Alignment	not modelled	16.7	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: TTHA1544-like PDB entry: PDBe RCSB PDBj
39	c6u2mC_	 Alignment	not modelled	28.2	12	PDB header: hydrolase Chain: C: PDB Molecule: halocamp v2; PDBTitle: crystal structure of a halotag-based calcium indicator, halocamp v2,2 bound to jf635 PDB Entry: PDBe RCSB PDBj
40	d2f2la1	 Alignment	not modelled	99.9	8	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like PDB entry: PDBe RCSB PDBj
41	d1sxea_	 Alignment	not modelled	13.9	21	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain PDB entry: PDBe RCSB PDBj
42	c2xz8A_	 Alignment	not modelled	99.1	10	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein If; PDBTitle: crystal structure of the Ifw ectodomain of the peptidoglycan2 recognition protein If PDB Entry: PDBe RCSB PDBj
43	c2os5C_	 Alignment	not modelled	22.3	17	PDB header: cytokine Chain: C: PDB Molecule: acemif; PDBTitle: macrophage migration inhibitory factor from ancylostoma ceylanicum PDB Entry: PDBe RCSB PDBj
44	d1e0ga_	 Alignment	not modelled	19.0	34	Fold: LysM domain Superfamily: LysM domain Family: LysM domain PDB entry: PDBe RCSB PDBj
45	d1dpta_	 Alignment	not modelled	24.5	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related PDB entry: PDBe RCSB PDBj
46	c3b64A_	 Alignment	not modelled	47.9	22	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like protein; PDBTitle: macrophage migration inhibitory factor (mif) from /leishmania major PDB Entry: PDBe RCSB PDBj
47	d1hfoa_	 Alignment	not modelled	33.6	22	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related PDB entry: PDBe RCSB PDBj
48	c8ap3A_	 Alignment	not modelled	24.5	22	PDB header: cytokine Chain: A: PDB Molecule: mif homologue; PDBTitle: structure of a. thaliana mif/d-dt-like protein-2 (mdl2) PDB Entry: PDBe RCSB PDBj
49	c7cigB_	 Alignment	not modelled	25.5	28	PDB header: lyase Chain: B: PDB Molecule: l-methionine decarboxylase; PDBTitle: crystal structure of l-methionine decarboxylase q64a mutant from2 streptomyces sp.590 in complexed with l-methionine methyl ester3 (geminal diamine form). PDB Entry: PDBe RCSB PDBj
		 Alignment				PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-

50	c3fwtA_	Alignment	not modelled	51.9	30	like protein; PDBTitle: crystal structure of leishmania major mif2 PDB Entry: PDBe RCSB PDBj
51	c2wpvG_	Alignment	not modelled	32.5	15	PDB header: protein binding Chain: G: PDB Molecule: upf0363 protein yor164c; PDBTitle: crystal structure of s. cerevisiae get4-get5 complex PDB Entry: PDBe RCSB PDBj
52	c2gwoC_	Alignment	not modelled	14.5	14	PDB header: hydrolase Chain: C: PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmdp PDB Entry: PDBe RCSB PDBj
53	d3b5ea1	Alignment	not modelled	20.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 PDB entry: PDBe RCSB PDBj
54	d1lpbb2	Alignment	not modelled	50.9	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain PDB entry: PDBe RCSB PDBj
55	d1bu8a2	Alignment	not modelled	50.8	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain PDB entry: PDBe RCSB PDBj
56	d1etha2	Alignment	not modelled	49.1	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain PDB entry: PDBe RCSB PDBj
57	c6e7kB_	Alignment	not modelled	47.9	26	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gp1hbp1 complex that mediates2 plasma triglyceride hydrolysis PDB Entry: PDBe RCSB PDBj
58	c2pvsB_	Alignment	not modelled	47.5	26	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 2 mutant n336q PDB Entry: PDBe RCSB PDBj
59	c3d0kA_	Alignment	not modelled	17.6	25	PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis PDB Entry: PDBe RCSB PDBj
60	c8dtlD_	Alignment	not modelled	13.5	35	PDB header: signaling protein Chain: D: PDB Molecule: insulin mimetic peptide s597; PDBTitle: cryo-em structure of insulin receptor (ir) bound with s597 peptide PDB Entry: PDBe RCSB PDBj
61	c8dtlC_	Alignment	not modelled	13.5	35	PDB header: signaling protein Chain: C: PDB Molecule: insulin mimetic peptide s597; PDBTitle: cryo-em structure of insulin receptor (ir) bound with s597 peptide PDB Entry: PDBe RCSB PDBj
62	c8h92A_	Alignment	not modelled	14.1	14	PDB header: plant protein Chain: A: PDB Molecule: triphosphate tunnel metalloenzyme 3-like; PDBTitle: ziziphus jujuba adenyl cyclase PDB Entry: PDBe RCSB PDBj
63	c1djyB_	Alignment	not modelled	15.7	13	PDB header: lipid degradation Chain: B: PDB Molecule: phosphoinositide-specific phospholipase c, isozyme delta1; PDBTitle: phosphoinositide-specific phospholipase c-delta1 from rat complexed2 with inositol-2,4,5-trisphosphate PDB Entry: PDBe RCSB PDBj
64	c6i28A_	Alignment	not modelled	29.0	14	PDB header: viral protein Chain: A: PDB Molecule: orf98 ptp-2; PDBTitle: crystal structure of cydia pomonella ptp-2 phosphatase PDB Entry: PDBe RCSB PDBj
65	c6lkvF_	Alignment	not modelled	72.8	10	PDB header: cytokine Chain: F: PDB Molecule: macrophage migration inhibitory factor; PDBTitle: structural and functional insights into macrophage migration2 inhibitory factor from oncomelania hupensis, the intermediate host of3 schistosoma japonicum PDB Entry: PDBe RCSB PDBj
66	c7c7lB_	Alignment	not modelled	19.2	19	PDB header: rna binding protein/rna/dna Chain: B: PDB Molecule: crispr-associated protein cas14a.1; PDBTitle: cryo-em structure of the cas12f1-sgrna-target dna complex PDB Entry: PDBe RCSB PDBj
67	c4p7nA_	Alignment	not modelled	13.8	19	PDB header: hydrolase Chain: A: PDB Molecule: poly-beta-1,6-n-acetyl-d-glucosamine n-deacetylase; PDBTitle: structure of escherichia coli pgab c-terminal domain in complex with2 glucosamine PDB Entry: PDBe RCSB PDBj
68	c6culG_	Alignment	not modelled	36.2	25	PDB header: transferase Chain: G: PDB Molecule: pyoverdine synthetase f; PDBTitle: pvdf of pyoverdin biosynthesis is a structurally unique n10-2 formyltetrahydrofolate-dependent formyltransferase PDB Entry: PDBe RCSB PDBj
69	c4as2D_	Alignment	not modelled	13.7	30	PDB header: hydrolase Chain: D: PDB Molecule: phosphorylcholine phosphatase; PDBTitle: pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form PDB Entry: PDBe RCSB PDBj
70	d1gd0a_	Alignment	not modelled	45.7	23	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related PDB entry: PDBe RCSB PDBj
71	d2gdga1	Alignment	not modelled	41.7	23	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related PDB entry: PDBe RCSB PDBj

72	dlfima_	Alignment	not modelled	38.0	23	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related PDB entry: PDBe RCSB PDBj
73	c8sl7A_	Alignment	not modelled	68.4	18	PDB header: lyase Chain: A: PDB Molecule: tryptophanase; PDBTitle: butyricococcus sp. bioml-a1 tryptophanase complex with (3s) alg-05 PDB Entry: PDBe RCSB PDBj
74	c2pplA_	Alignment	not modelled	52.0	22	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1 PDB Entry: PDBe RCSB PDBj
75	c1hplB_	Alignment	not modelled	51.8	22	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution PDB Entry: PDBe RCSB PDBj
76	d1hpla2	Alignment	not modelled	50.2	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain PDB entry: PDBe RCSB PDBj
77	c1gplA_	Alignment	not modelled	49.5	22	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase PDB Entry: PDBe RCSB PDBj
78	d1gpla2	Alignment	not modelled	39.1	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain PDB entry: PDBe RCSB PDBj
79	d2hfda1	Alignment	not modelled	14.8	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: HyaE-like PDB entry: PDBe RCSB PDBj
80	c3gacD_	Alignment	not modelled	17.8	14	PDB header: cytokine Chain: D: PDB Molecule: macrophage migration inhibitory factor-like protein; PDBTitle: structure of mif with hpp PDB Entry: PDBe RCSB PDBj
81	c4qnnC_	Alignment	not modelled	47.9	19	PDB header: hydrolase Chain: C: PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom PDB Entry: PDBe RCSB PDBj
82	c3b79A_	Alignment	not modelled	38.4	11	PDB header: nucleotide binding protein Chain: A: PDB Molecule: toxin secretion atp-binding protein; PDBTitle: crystal structure of the n-terminal peptidase c39 like2 domain of the toxin secretion atp-binding protein from3 vibrio parahaemolyticus PDB Entry: PDBe RCSB PDBj
83	c6jppA_	Alignment	not modelled	35.0	11	PDB header: signaling protein Chain: A: PDB Molecule: engulfment and cell motility protein 1; PDBTitle: solution structure of elmo1 rbd PDB Entry: PDBe RCSB PDBj
84	c2p4dA_	Alignment	not modelled	13.6	10	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase; PDBTitle: structure-assisted discovery of variola major h1 phosphatase2 inhibitors PDB Entry: PDBe RCSB PDBj
85	c5xyiM_	Alignment	not modelled	13.9	29	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein l7ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome PDB Entry: PDBe RCSB PDBj
86	c5xjvA_	Alignment	not modelled	13.9	11	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 13 isoform a; PDBTitle: two intermediate states of conformation switch in dual specificity2 phosphatase 13a PDB Entry: PDBe RCSB PDBj
87	c8dq6A_	Alignment	not modelled	38.6	11	PDB header: cytokine Chain: A: PDB Molecule: mif/d-dt-like protein-1; PDBTitle: structure of a. thaliana mif/d-dt-like protein-1 (mdl1) PDB Entry: PDBe RCSB PDBj
88	c1rp1A_	Alignment	not modelled	48.0	15	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1 PDB Entry: PDBe RCSB PDBj
89	d1rp1a2	Alignment	not modelled	47.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain PDB entry: PDBe RCSB PDBj
90	c2rpsA_	Alignment	not modelled	15.6	57	PDB header: immune system Chain: A: PDB Molecule: chemokine; PDBTitle: solution structure of a novel insect chemokine isolated from2 integument PDB Entry: PDBe RCSB PDBj
91	c8vj2C_	Alignment	not modelled	48.4	18	PDB header: cytokine Chain: C: PDB Molecule: macrophage migration inhibitory factor-1; PDBTitle: crystal structure of macrophage migration inhibitory factor-1 (mif1)2 from onchocerca volvulus PDB Entry: PDBe RCSB PDBj
92	c2zycA_	Alignment	not modelled	14.1	18	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan hydrolase flgj; PDBTitle: crystal structure of peptidoglycan hydrolase from sphingomonas sp. a1 PDB Entry: PDBe RCSB PDBj
93	c2y96A_	Alignment	not modelled	13.6	9	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27 PDB Entry: PDBe RCSB PDBj
						PDB header: immune system

94	c3t5sA_	Alignment	not modelled	54.6	14	Chain: A: PDB Molecule: macrophage migration inhibitory factor; from giardia2 lamblia PDBTitle: structure of macrophage migration inhibitory factor PDB Entry: PDBe RCSB PDBj
95	c8ur2E_	Alignment	not modelled	45.0	11	PDB header: cytokine Chain: E: PDB Molecule: macrophage migration inhibitory factor; PDBTitle: crystal structure of macrophage migration inhibitory factor (mif) from2 trichomonas vaginalis (i41 form) PDB Entry: PDBe RCSB PDBj
96	c8dqaA_	Alignment	not modelled	26.8	10	PDB header: cytokine Chain: A: PDB Molecule: Is1-like protein; PDBTitle: structure of a. thaliana mif/d-dt-like protein-3 (mdl3) PDB Entry: PDBe RCSB PDBj
97	c3zuaA_	Alignment	not modelled	14.3	6	PDB header: hydrolase Chain: A: PDB Molecule: alpha-hemolysin translocation atp-binding protein hlyb; PDBTitle: a c39-like domain PDB Entry: PDBe RCSB PDBj
98	c3og9A_	Alignment	not modelled	14.3	6	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid PDB Entry: PDBe RCSB PDBj
99	c2q0xA_	Alignment	not modelled	27.7	4	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function PDB Entry: PDBe RCSB PDBj