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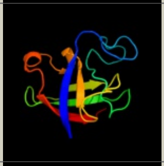
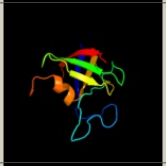
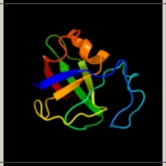
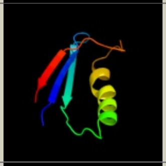
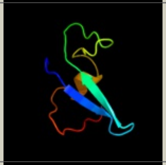
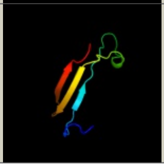
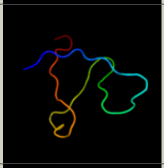
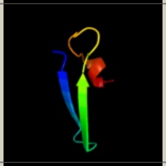
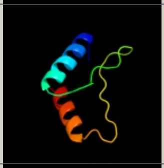
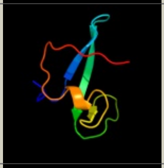
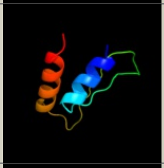
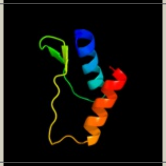
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1x60A_	 Alignment		99.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine **PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
2	d1utaa_	 Alignment		99.5	24	**Fold:**Ferredoxin-like **Superfamily:**Sporulation related repeat **Family:**Sporulation related repeat
3	c3d30A_	 Alignment		98.8	19	**PDB header:**peptidoglycan-binding protein **Chain:** A: **PDB Molecule:**expansin like protein; **PDBTitle:** structure of an expansin like protein from bacillus subtilis at 1.9a2 resolution
4	d1n10a2	 Alignment		97.7	15	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**Pollen allergen PHL P 1 N-terminal domain
5	c1n10A_	 Alignment		97.2	15	**PDB header:**allergen **Chain:** A: **PDB Molecule:**pollen allergen phl p 1; **PDBTitle:** crystal structure of phl p 1, a major timothy grass pollen allergen
6	c2hczX_	 Alignment		96.2	15	**PDB header:**allergen **Chain:** X: **PDB Molecule:**beta-expansin 1a; **PDBTitle:** crystal structure of expb1 (zea m 1), a beta-expansin and group-12 pollen allergen from maize
7	d1bw3a_	 Alignment		86.3	22	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**Barwin
8	d1wc2a1	 Alignment		85.9	11	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**Eng V-like
9	d1grja2	 Alignment		74.5	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
10	c3bmbB_	 Alignment		73.0	14	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
11	d1w2za3	 Alignment		70.7	20	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region

12	c1grjA_	Alignment		60.1	16	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
13	d1vqoq1	Alignment		45.0	20	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
14	d2f23a2	Alignment		38.9	11	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
15	c3fuyC_	Alignment		37.8	33	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative integron gene cassette protein; **PDBTitle:** structure from the mobile metagenome of cole harbour salt2 marsh: integron cassette protein hfx_cass1
16	d2c0ra1	Alignment		37.8	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
17	c2pn0D_	Alignment		37.4	7	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
18	c3caiA_	Alignment		37.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible aminotransferase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein
19	d1bs0a_	Alignment		36.7	24	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
20	d1w6ga3	Alignment		35.1	15	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
21	d1m32a_	Alignment	not modelled	33.8	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
22	c2p4vA_	Alignment	not modelled	32.3	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
23	d2etna2	Alignment	not modelled	31.2	13	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
24	c3efyB_	Alignment	not modelled	26.4	25	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cif (cell cycle inhibiting factor); **PDBTitle:** structure of the cyclomodulin cif from pathogenic2 escherichia coli
25	c2yrrA_	Alignment	not modelled	24.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class v; **PDBTitle:** hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
26	d1v72a1	Alignment	not modelled	24.6	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
27	c3gqjA_	Alignment	not modelled	22.4	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cell inhibiting factor (cif); **PDBTitle:** crystal structure of cell inhibiting factor (cif) from photorhabdus2 luminescens
28	c3m3gA_	Alignment	not modelled	22.3	20	**PDB header:**polysaccharide-binding protein **Chain:** A: **PDB Molecule:**epl1 protein; **PDBTitle:** crystal structure of sm1, an elicitor of plant defence responses from2 trichoderma virens.
						PDB header:transcription

29	c2etnA_	Alignment	not modelled	22.2	13	**Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
30	c3eitB_	Alignment	not modelled	21.9	32	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative atp/gtp binding protein; **PDBTitle:** the 2.6 angstrom crystal structure of chbp, the cif homologue from2 burkholderia pseudomallei
31	d1qz9a_	Alignment	not modelled	21.7	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
32	c2fyfB_	Alignment	not modelled	20.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
33	d1m6sa_	Alignment	not modelled	20.7	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
34	d2jioa1	Alignment	not modelled	20.6	11	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
35	d1t3ia_	Alignment	not modelled	20.6	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
36	d2f8ja1	Alignment	not modelled	20.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
37	d1g8ka1	Alignment	not modelled	19.8	11	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
38	c2huuA_	Alignment	not modelled	19.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
39	d1ogya1	Alignment	not modelled	18.9	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
40	c3iz6Y_	Alignment	not modelled	18.2	23	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**40s ribosomal protein s28 (s28e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
41	d1vq3a_	Alignment	not modelled	18.0	15	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
42	c3hqtB_	Alignment	not modelled	17.7	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
43	c3f9tB_	Alignment	not modelled	16.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-tyrosine decarboxylase mfna; **PDBTitle:** crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
44	d1j5ya2	Alignment	not modelled	16.6	11	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
45	c2yx5A_	Alignment	not modelled	16.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
46	c2zw2B_	Alignment	not modelled	15.3	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
47	c3hyjD_	Alignment	not modelled	15.1	4	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**protein duf199/whia; **PDBTitle:** crystal structure of the n-terminal laglidadg domain of duf199/whia
48	c3eh7A_	Alignment	not modelled	14.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
49	d1bjna_	Alignment	not modelled	13.5	8	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
50	d1iuga_	Alignment	not modelled	13.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
51	d1eg5a_	Alignment	not modelled	12.5	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
52	c2eefA_	Alignment	not modelled	12.2	24	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**protein phosphatase 1, regulatory (inhibitor) **PDBTitle:** solution structure of the cbm_21 domain from human protein2 phosphatase 1, regulatory (inhibitor) subunit 3b
53	d1elua_	Alignment	not modelled	12.1	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
54	c3seeA_	Alignment	not modelled	11.9	13	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**hypothetical sugar binding protein; **PDBTitle:** crystal structure of a hypothetical sugar binding protein

						(bt_4411)2 from bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
55	d1oj4a2	Alignment	not modelled	11.4	14	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
56	c3f0hA_	Alignment	not modelled	11.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
57	d1h0ca_	Alignment	not modelled	11.3	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
58	c3qm2A_	Alignment	not modelled	11.2	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
59	c2yujA_	Alignment	not modelled	11.2	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like; **PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
60	c3mazA_	Alignment	not modelled	11.0	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal-transducing adaptor protein 1; **PDBTitle:** crystal structure of the human brdg1/stap-1 sh2 domain in complex with2 the ntal ptyr136 peptide
61	d1uh6a_	Alignment	not modelled	11.0	60	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
62	d1uasa1	Alignment	not modelled	10.9	23	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
63	c3p04B_	Alignment	not modelled	10.8	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
64	d1y0ya2	Alignment	not modelled	10.4	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
65	c2l9vA_	Alignment	not modelled	10.3	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**pre-mrna-processing factor 40 homolog a; **PDBTitle:** nmr structure of the ff domain l24a mutant's folding transition state
66	d1sddb2	Alignment	not modelled	10.0	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
67	c3iz5U_	Alignment	not modelled	9.9	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
68	d1vpra1	Alignment	not modelled	9.9	50	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Dinoflagellate luciferase repeat
69	c2hzpA_	Alignment	not modelled	9.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase
70	d2gova1	Alignment	not modelled	9.6	20	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**SOUL heme-binding protein
71	c3p04A_	Alignment	not modelled	9.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
72	c3bpqD_	Alignment	not modelled	9.4	23	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin rele3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
73	c3e77A_	Alignment	not modelled	9.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** human phosphoserine aminotransferase in complex with plp
74	c2ivwA_	Alignment	not modelled	9.4	24	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**pilp pilot protein; **PDBTitle:** the solution structure of a domain from the neisseria2 meningitidis pilp pilot protein.
75	d1vjoa_	Alignment	not modelled	9.3	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
76	d2iv2x1	Alignment	not modelled	8.9	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
77	d2exda1	Alignment	not modelled	8.8	12	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
78	c2dr1A_	Alignment	not modelled	8.8	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase; **PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
79	c3h14A_	Alignment	not modelled	8.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
						PDB header:transferase

80	c3cq6E_	Alignment	not modelled	8.7	21	**Chain:** E: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
81	c2w8wA_	Alignment	not modelled	8.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
82	c2xx7B_	Alignment	not modelled	8.6	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate receptor 2; **PDBTitle:** crystal structure of 1-(4-(1-pyrrolidinylcarbonyl)phenyl)-3-2 (trifluoromethyl)-4,5,6,7-tetrahydro-1h-indazole in complex with3 the ligand binding domain of the rat glua2 receptor and glutamate4 at 2.2a resolution.
83	c3ffrA_	Alignment	not modelled	8.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase serc; **PDBTitle:** crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
84	d1s50a1	Alignment	not modelled	8.5	28	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
85	c3a2bA_	Alignment	not modelled	8.4	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
86	c4a1aP_	Alignment	not modelled	8.4	27	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l21; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
87	d1xjva2	Alignment	not modelled	8.3	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
88	d1qpga_	Alignment	not modelled	8.3	17	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
89	c3bdlA_	Alignment	not modelled	8.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**staphylococcal nuclease domain-containing **PDBTitle:** crystal structure of a truncated human tudor-sn
90	c1zc1A_	Alignment	not modelled	8.0	14	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
91	c1wwtA_	Alignment	not modelled	7.9	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase
92	c2ordA_	Alignment	not modelled	7.8	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
93	c2el8A_	Alignment	not modelled	7.8	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal-transducing adaptor protein 2; **PDBTitle:** solution structure of the human stap2 sh2 domain
94	d1gtda_	Alignment	not modelled	7.8	11	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
95	c2v3tA_	Alignment	not modelled	7.7	19	**PDB header:**receptor **Chain:** A: **PDB Molecule:**glutamate receptor delta-2 subunit synonym **PDBTitle:** structure of the ligand-binding core of the ionotropic2 glutamate receptor-like glurdelta2 in the apo form
96	c1d2fB_	Alignment	not modelled	7.7	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**maly protein; **PDBTitle:** x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression
97	d2h9fa1	Alignment	not modelled	7.5	22	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PA0793-like
98	c3dxvA_	Alignment	not modelled	7.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alpha-amino-epsilon-caprolactam racemase; **PDBTitle:** the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
99	d2gkea2	Alignment	not modelled	7.5	28	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase