Phyre^2

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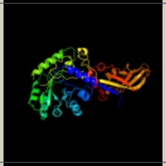
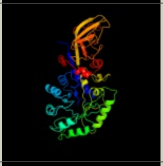
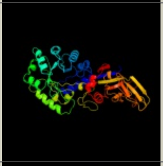
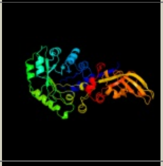
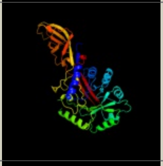
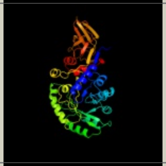
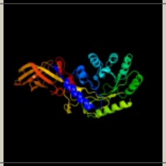
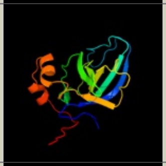
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rjgC_	Alignment		100.0	97	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of biosynthetic alaine racemase from escherichia2 coli
2	c1niuA_	Alignment		100.0	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** alanine racemase with bound inhibitor derived from l-2 cycloserine
3	c3mubB_	Alignment		100.0	31	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** the crystal structure of alanine racemase from streptococcus2 pneumoniae
4	c2odoC_	Alignment		100.0	46	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of pseudomonas fluorescens alanine racemase
5	c3kw3B_	Alignment		100.0	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
6	c3e6eC_	Alignment		100.0	33	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
7	c3oo2A_	Alignment		100.0	34	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
8	c1vftA_	Alignment		100.0	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
9	c3hurA_	Alignment		100.0	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from oenococcus oeni
10	c3co8B_	Alignment		100.0	27	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from oenococcus oeni
11	c3oo2B_	Alignment		100.0	33	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col

12	c2vd9A_	Alignment		100.0	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** the crystal structure of alanine racemase from bacillus2 anthracis (ba0252) with bound l-ala-p
13	c2dy3B_	Alignment		100.0	33	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from corynebacterium glutamicum
14	c1xfcB_	Alignment		100.0	36	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** the 1.9 a crystal structure of alanine racemase from mycobacterium2 tuberculosis contains a conserved entryway into the active site
15	d1rcqa2	Alignment		100.0	45	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
16	d1bd0a2	Alignment		100.0	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
17	d1vfsa2	Alignment		100.0	35	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
18	d1rcqa1	Alignment		100.0	45	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
19	d1vfsa1	Alignment		100.0	38	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
20	d1bd0a1	Alignment		100.0	31	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
21	c3anuA_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-serine dehydratase; **PDBTitle:** crystal structure of d-serine dehydratase from chicken kidney
22	c3gwqB_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-serine deaminase; **PDBTitle:** crystal structure of a putative d-serine deaminase (bxe_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
23	c1njjC_	Alignment	not modelled	100.0	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
24	c2j66A_	Alignment	not modelled	100.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**btrk; **PDBTitle:** structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
25	c2p3eA_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of aq1208 from aquifex aeolicus
26	c3llxA_	Alignment	not modelled	100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**predicted amino acid aldolase or racemase; **PDBTitle:** crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution
27	c2qghA_	Alignment	not modelled	100.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
28	c3r79B_	Alignment	not modelled	100.0	16	**PDB header:**structure genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharactertized protein from

						agrobacterium2 tumefaciens
29	c1w8gA_	Alignment	not modelled	100.0	12	**PDB header:**plp-binding protein **Chain:** A: **PDB Molecule:**hypothetical upf0001 protein yggs; **PDBTitle:** crystal structure of e. coli k-12 yggs
30	c3n2bD_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
31	c1tufA_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
32	d1ct5a_	Alignment	not modelled	100.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**"Hypothetical" protein ybl036c
33	c2nvaH_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** H: **PDB Molecule:**arginine decarboxylase, a207r protein; **PDBTitle:** the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
34	c3cpgA_	Alignment	not modelled	100.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an unknown protein from bifidobacterium2 adolescentis
35	c2pljA_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lysine/ornithine decarboxylase; **PDBTitle:** crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
36	c2yxxA_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure analysis of diaminopimelate decarboxylate (lysa)
37	c2o0tB_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation
38	c1knwA_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase
39	c2on3A_	Alignment	not modelled	99.9	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
40	c3btnA_	Alignment	not modelled	99.9	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**antizyme inhibitor 1; **PDBTitle:** crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
41	d1f3ta2	Alignment	not modelled	99.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
42	c3n29A_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carboxynorspermidine decarboxylase; **PDBTitle:** crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
43	c1d7kB_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**human ornithine decarboxylase; **PDBTitle:** crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
44	d7odca2	Alignment	not modelled	99.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
45	d1hkva2	Alignment	not modelled	99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
46	c3mt1B_	Alignment	not modelled	99.8	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative carboxynorspermidine decarboxylase protein; **PDBTitle:** crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
47	d1d7ka2	Alignment	not modelled	99.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
48	d1twia2	Alignment	not modelled	99.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
49	d1knwa2	Alignment	not modelled	99.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
50	c3nzpA_	Alignment	not modelled	99.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**arginine decarboxylase; **PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
51	c3nzqB_	Alignment	not modelled	99.6	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
52	c3n2oA_	Alignment	not modelled	99.5	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
53	d1y0ya1	Alignment	not modelled	69.7	27	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain

54	d2grea1	Alignment	not modelled	66.5	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
55	d1knwa1	Alignment	not modelled	58.7	25	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
56	d1twia1	Alignment	not modelled	54.9	17	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
57	c3c2qA_	Alignment	not modelled	49.1	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2
58	d2toda1	Alignment	not modelled	32.4	13	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
59	d1yloa1	Alignment	not modelled	25.1	27	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
60	d1njjb1	Alignment	not modelled	22.2	13	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
61	d1hkva1	Alignment	not modelled	17.7	24	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
62	d1vhea1	Alignment	not modelled	17.3	17	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
63	d1f3ta1	Alignment	not modelled	17.0	16	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
64	c2l55A_	Alignment	not modelled	17.0	31	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three **PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
65	c2l8kA_	Alignment	not modelled	16.9	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 7; **PDBTitle:** nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
66	d1vqoe2	Alignment	not modelled	16.4	19	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
67	c1uheA_	Alignment	not modelled	16.2	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase alpha chain; **PDBTitle:** crystal structure of aspartate decarboxylase, isoaspargine complex
68	d2fvga1	Alignment	not modelled	15.9	24	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
69	c1zeqX_	Alignment	not modelled	15.7	19	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
70	d2cbia2	Alignment	not modelled	15.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
71	d1vcta2	Alignment	not modelled	12.7	17	**Fold:**TrkA C-terminal domain-like **Superfamily:**TrkA C-terminal domain-like **Family:**TrkA C-terminal domain-like
72	d1x6oa1	Alignment	not modelled	12.6	32	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
73	d2g46a1	Alignment	not modelled	12.3	24	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Viral histone H3 Lysine 27 Methyltransferase
74	d2q07a1	Alignment	not modelled	10.3	10	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
75	c3b8iF_	Alignment	not modelled	10.1	15	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
76	d1vhoa1	Alignment	not modelled	9.4	29	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
77	d1h3ia2	Alignment	not modelled	9.3	29	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
78	c3rnvA_	Alignment	not modelled	8.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helper component proteinase; **PDBTitle:** structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase
79	d1g94a2	Alignment	not modelled	8.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
80	d1i7aa_	Alignment	not modelled	8.8	7	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Enabled/VASP homology 1 domain (EVH1 domain)

81	d1bkba1	Alignment	not modelled	8.6	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
82	c2bknA_	Alignment	not modelled	8.5	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein ph0236; **PDBTitle:** structure analysis of unknown function protein
83	c1pkvB_	Alignment	not modelled	8.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin
84	c1pkvA_	Alignment	not modelled	8.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin
85	d2eifa1	Alignment	not modelled	8.2	26	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
86	d1khia1	Alignment	not modelled	8.0	16	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
87	d1iz6a1	Alignment	not modelled	7.6	16	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
88	c3zvrA_	Alignment	not modelled	7.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of dynamin
89	c2zp2B_	Alignment	not modelled	7.5	28	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
90	d1j98a_	Alignment	not modelled	6.8	21	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
91	c3kgkA_	Alignment	not modelled	6.8	7	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**arsenical resistance operon trans-acting repressor arsd; **PDBTitle:** crystal structure of arsd
92	d2f69a2	Alignment	not modelled	6.7	30	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
93	c2vl6C_	Alignment	not modelled	6.7	38	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
94	c3mmlD_	Alignment	not modelled	6.6	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
95	c2fyuE_	Alignment	not modelled	6.6	7	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
96	c1s1hQ_	Alignment	not modelled	6.5	26	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**40s ribosomal protein s11; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
97	d2fy8a2	Alignment	not modelled	6.5	24	**Fold:**TrkA C-terminal domain-like **Superfamily:**TrkA C-terminal domain-like **Family:**TrkA C-terminal domain-like
98	d1oioa_	Alignment	not modelled	6.4	21	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**F17c-type adhesin
99	d1o75a1	Alignment	not modelled	6.4	43	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Tp47 lipoprotein, middle and C-terminal domains **Family:**Tp47 lipoprotein, middle and C-terminal domains