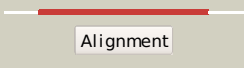

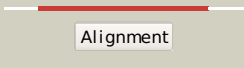

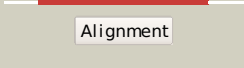

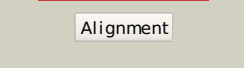

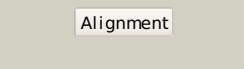

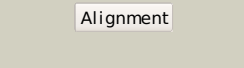

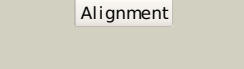

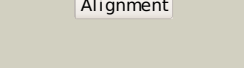

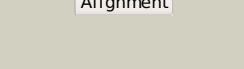

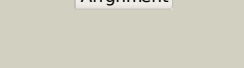

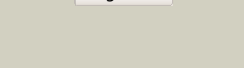

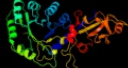







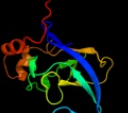


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P29012
Date	Thu Jan 5 11:45:32 GMT 2012
Unique Job ID	eae5b804c4c7b68

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1niuA_</a>			100.0	33	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> alanine racemase with bound inhibitor derived from l-2 cycloserine
2	<a href="#">c3mubB_</a>			100.0	35	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> the crystal structure of alanine racemase from streptococcus2 pneumoniae
3	<a href="#">c2odoC_</a>			100.0	48	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of pseudomonas fluorescens alanine racemase
4	<a href="#">c3kw3B_</a>			100.0	25	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
5	<a href="#">c3e6eC_</a>			100.0	35	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
6	<a href="#">c3oo2A_</a>			100.0	32	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> alanine racemase 1; <b>PDBTitle:</b> 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
7	<a href="#">c2rjgC_</a>			100.0	42	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of biosynthetic alaine racemase from escherichia2 coli
8	<a href="#">c1vftA_</a>			100.0	33	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
9	<a href="#">c3hurA_</a>			100.0	29	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from oenococcus oeni
10	<a href="#">c2vd9A_</a>			100.0	30	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> the crystal structure of alanine racemase from bacillus2 anthracis (ba0252) with bound l-ala-p
11	<a href="#">c3oo2B_</a>			100.0	30	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> alanine racemase 1; <b>PDBTitle:</b> 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col

12	<a href="#">c3co8B_</a>	Alignment		100.0	28	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from oenococcus oeni
13	<a href="#">c2dy3B_</a>	Alignment		100.0	31	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from corynebacterium glutamicum
14	<a href="#">c1xfcB_</a>	Alignment		100.0	32	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> the 1.9 a crystal structure of alanine racemase from mycobacterium tuberculosis contains a conserved entryway into the active site
15	<a href="#">d1rcqa2</a>	Alignment		100.0	44	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
16	<a href="#">d1bd0a2</a>	Alignment		100.0	30	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
17	<a href="#">d1rcqa1</a>	Alignment		100.0	53	<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> Alanine racemase
18	<a href="#">d1vfsa1</a>	Alignment		100.0	37	<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> Alanine racemase
19	<a href="#">d1vfsa2</a>	Alignment		100.0	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
20	<a href="#">d1bd0a1</a>	Alignment		100.0	40	<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> Alanine racemase
21	<a href="#">c1njjC_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
22	<a href="#">c3anuA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> d-serine dehydratase; <b>PDBTitle:</b> crystal structure of d-serine dehydratase from chicken kidney
23	<a href="#">c2p3eA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of aq1208 from aquifex aeolicus
24	<a href="#">c2j66A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> btrk; <b>PDBTitle:</b> structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
25	<a href="#">c2qghA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
26	<a href="#">c3gwqB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> d-serine deaminase; <b>PDBTitle:</b> crystal structure of a putative d-serine deaminase (bx_e_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
27	<a href="#">c3llxA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted amino acid aldolase or racemase; <b>PDBTitle:</b> crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution
28	<a href="#">c3r79B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from

						agrobacterium2 tumefaciens
29	<a href="#">c2nvaH_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> arginine decarboxylase, a207r protein; <b>PDBTitle:</b> the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
30	<a href="#">c1tufA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
31	<a href="#">c1w8gA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> plp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0001 protein yggs; <b>PDBTitle:</b> crystal structure of e. coli k-12 yggs
32	<a href="#">c3n2bD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
33	<a href="#">c3cpgA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an unknown protein from bifidobacterium2 adolescentis
34	<a href="#">c2pljA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine/ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
35	<a href="#">d1ct5a_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> "Hypothetical" protein ybl036c
36	<a href="#">c2yxxA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure analysis of diaminopimelate decarboxylate (lysa)
37	<a href="#">c2o0tB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation
38	<a href="#">c1knwA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase
39	<a href="#">c2on3A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminoxy-3 1-aminopropane
40	<a href="#">c3btuA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> antizyme inhibitor 1; <b>PDBTitle:</b> crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
41	<a href="#">c3n29A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxynorspermidine decarboxylase; <b>PDBTitle:</b> crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
42	<a href="#">c1d7kB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> human ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
43	<a href="#">d1f3ta2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
44	<a href="#">d7odca2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
45	<a href="#">d1hkva2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
46	<a href="#">c3mt1B_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative carboxynorspermidine decarboxylase protein; <b>PDBTitle:</b> crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
47	<a href="#">d1d7ka2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
48	<a href="#">d1twia2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
49	<a href="#">d1knwa2</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
50	<a href="#">c3nzqB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> biosynthetic arginine decarboxylase; <b>PDBTitle:</b> crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
51	<a href="#">c3nzpA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine decarboxylase; <b>PDBTitle:</b> crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
52	<a href="#">c3n2oA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> biosynthetic arginine decarboxylase; <b>PDBTitle:</b> x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
53	<a href="#">d1knwa1</a>	Alignment	not modelled	89.3	23	<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

54	<a href="#">d2toda1</a>	Alignment	not modelled	84.6	14	<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
55	<a href="#">d1twia1</a>	Alignment	not modelled	76.7	9	<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
56	<a href="#">d1hkva1</a>	Alignment	not modelled	74.8	23	<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
57	<a href="#">d1njbb1</a>	Alignment	not modelled	69.3	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
58	<a href="#">d1f3ta1</a>	Alignment	not modelled	63.6	15	<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
59	<a href="#">d7odca1</a>	Alignment	not modelled	55.7	17	<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
60	<a href="#">c2c3zA</a>	Alignment	not modelled	43.3	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from <i>Sulfolobus solfataricus</i>
61	<a href="#">c3c2qA</a>	Alignment	not modelled	41.2	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of conserved putative Ior/sdh protein2 from <i>Methanococcus maripaludis</i> s2
62	<a href="#">d1d7ka1</a>	Alignment	not modelled	36.3	16	<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
63	<a href="#">d1twda</a>	Alignment	not modelled	35.5	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> CutC-like <b>Family:</b> CutC-like
64	<a href="#">c3noyA</a>	Alignment	not modelled	30.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> crystal structure of ispg (gcpe)
65	<a href="#">d1y0ya1</a>	Alignment	not modelled	27.3	19	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Aminopeptidase/glucanase lid domain <b>Family:</b> Aminopeptidase/glucanase lid domain
66	<a href="#">d2q07a1</a>	Alignment	not modelled	26.8	4	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
67	<a href="#">d2grea1</a>	Alignment	not modelled	19.0	17	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Aminopeptidase/glucanase lid domain <b>Family:</b> Aminopeptidase/glucanase lid domain
68	<a href="#">c2l8kA</a>	Alignment	not modelled	17.9	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 7; <b>PDBTitle:</b> nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
69	<a href="#">c3iwpK</a>	Alignment	not modelled	17.1	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> K: <b>PDB Molecule:</b> copper homeostasis protein cutc homolog; <b>PDBTitle:</b> crystal structure of human copper homeostasis protein cutc
70	<a href="#">d2g46a1</a>	Alignment	not modelled	16.7	28	<b>Fold:</b> beta-clip <b>Superfamily:</b> SET domain <b>Family:</b> Viral histone H3 Lysine 27 Methyltransferase
71	<a href="#">d2ot2a1</a>	Alignment	not modelled	16.0	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
72	<a href="#">d1x6oa1</a>	Alignment	not modelled	14.7	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
73	<a href="#">cli18B</a>	Alignment	not modelled	12.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin synthase alpha chain; <b>PDBTitle:</b> solution structure of the n-terminal domain of riboflavin synthase2 from <i>E. coli</i>
74	<a href="#">c1hzeB</a>	Alignment	not modelled	12.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin synthase alpha chain; <b>PDBTitle:</b> solution structure of the n-terminal domain of riboflavin synthase2 from <i>E. coli</i>
75	<a href="#">c2bdqA</a>	Alignment	not modelled	11.7	8	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper homeostasis protein cutc; <b>PDBTitle:</b> crystal structure of the putative copper homeostasis2 protein cutc from <i>Streptococcus agalactiae</i> , northeast3 structural genomics target sar15.
76	<a href="#">d1bkba1</a>	Alignment	not modelled	10.1	26	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
77	<a href="#">d1i8da1</a>	Alignment	not modelled	9.9	20	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Riboflavin synthase
78	<a href="#">c2zp2B</a>	Alignment	not modelled	9.7	23	<b>PDB header:</b> transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> kinase a inhibitor; <b>PDBTitle:</b> c-terminal domain of kipi from <i>Bacillus subtilis</i>
79	<a href="#">c1o75A</a>	Alignment	not modelled	9.5	30	<b>PDB header:</b> lipoprotein null antigen <b>Chain:</b> A: <b>PDB Molecule:</b> 47 kda membrane antigen; <b>PDBTitle:</b> tp47, the 47-kilodalton lipoprotein of <i>Treponema pallidum</i>
80	<a href="#">c1vcaA</a>	Alignment	not modelled	9.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ybek;

80	<a href="#">c1y0cA</a>	Alignment	not modelled	9.4	13	<b>PDBTitle:</b> crystal structure of a the e. coli pyrimidine nucleoside hydrolase2 ybek with bound ribose
81	<a href="#">d2eifa1</a>	Alignment	not modelled	9.3	32	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
82	<a href="#">c3zvrA</a>	Alignment	not modelled	9.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dynamnin-1; <b>PDBTitle:</b> crystal structure of dynamnin
83	<a href="#">d1jdqa</a>	Alignment	not modelled	9.2	22	<b>Fold:</b> IF3-like <b>Superfamily:</b> SirA-like <b>Family:</b> SirA-like
84	<a href="#">d1iz6a1</a>	Alignment	not modelled	9.2	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
85	<a href="#">c3cpfB</a>	Alignment	not modelled	9.1	17	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5a-1; <b>PDBTitle:</b> crystal structure of human eukaryotic translation initiation factor2 eif5a
86	<a href="#">dli7aa</a>	Alignment	not modelled	9.0	9	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
87	<a href="#">d1o75a1</a>	Alignment	not modelled	8.9	43	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Tp47 lipoprotein, middle and C-terminal domains <b>Family:</b> Tp47 lipoprotein, middle and C-terminal domains
88	<a href="#">d1vcta2</a>	Alignment	not modelled	8.5	11	<b>Fold:</b> TrkA C-terminal domain-like <b>Superfamily:</b> TrkA C-terminal domain-like <b>Family:</b> TrkA C-terminal domain-like
89	<a href="#">d1khia1</a>	Alignment	not modelled	8.4	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
90	<a href="#">c3dxiB</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative aldolase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
91	<a href="#">c2p0oA</a>	Alignment	not modelled	8.2	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf871; <b>PDBTitle:</b> crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
92	<a href="#">d1h3ia2</a>	Alignment	not modelled	7.9	30	<b>Fold:</b> beta-clip <b>Superfamily:</b> SET domain <b>Family:</b> Histone lysine methyltransferases
93	<a href="#">d1ul1a1</a>	Alignment	not modelled	7.5	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
94	<a href="#">d1kzla2</a>	Alignment	not modelled	7.4	11	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Riboflavin synthase
95	<a href="#">c3pg8B</a>	Alignment	not modelled	7.0	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phospho-2-dehydro-3-deoxyheptonate aldolase; <b>PDBTitle:</b> truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
96	<a href="#">d2f69a2</a>	Alignment	not modelled	6.8	30	<b>Fold:</b> beta-clip <b>Superfamily:</b> SET domain <b>Family:</b> Histone lysine methyltransferases
97	<a href="#">d2fy8a2</a>	Alignment	not modelled	6.8	18	<b>Fold:</b> TrkA C-terminal domain-like <b>Superfamily:</b> TrkA C-terminal domain-like <b>Family:</b> TrkA C-terminal domain-like
98	<a href="#">c2xzno</a>	Alignment	not modelled	6.6	21	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> ribosomal protein s17 containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
99	<a href="#">c1s1hO</a>	Alignment	not modelled	6.5	21	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 40s ribosomal protein s11; <b>PDBTitle:</b> 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.