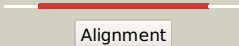



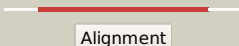

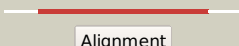

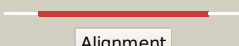

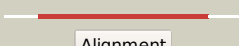

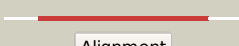











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1538c_ (ansA)_1741218_1742198
Date	Fri Aug 2 13:30:12 BST 2019
Unique Job ID	bb1f346f507c44cb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2d6fA_</a>	 Alignment		100.0	24	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit d; <b>PDBTitle:</b> crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
2	<a href="#">c1zq1B_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit d; <b>PDBTitle:</b> structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
3	<a href="#">d1zq1a2</a>	 Alignment		100.0	25	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
4	<a href="#">d2d6fa2</a>	 Alignment		100.0	24	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
5	<a href="#">d1nnsa_</a>	 Alignment		100.0	30	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
6	<a href="#">d1agxa_</a>	 Alignment		100.0	26	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
7	<a href="#">c2wltA_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> the crystal structure of helicobacter pylori l-asparaginase at 1.4 a2 resolution
8	<a href="#">d1wsaa_</a>	 Alignment		100.0	30	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
9	<a href="#">d4pgaa_</a>	 Alignment		100.0	28	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
10	<a href="#">c4q0mA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus l-asparaginase
11	<a href="#">d1o7ja_</a>	 Alignment		100.0	30	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase

12	<a href="#">c4r8kC_</a>	Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the guinea pig l-asparaginase 1 catalytic domain
13	<a href="#">c1wnfA_</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of ph0066 from pyrococcus horikoshii
14	<a href="#">d2ocda1</a>	Alignment		100.0	24	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
15	<a href="#">c3nxkE_</a>	Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> cytoplasmic l-asparaginase; <b>PDBTitle:</b> crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
16	<a href="#">c2p2dA_</a>	Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase i; <b>PDBTitle:</b> crystal structure and allosteric regulation of the cytoplasmic2 escherichia coli l-asparaginase i
17	<a href="#">c5ot0A_</a>	Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> the thermostable l-asparaginase from thermococcus kodakarensis
18	<a href="#">c4ra6A_</a>	Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of linker less pyrococcus furiosus l-asparaginase
19	<a href="#">c6cv6L_</a>	Alignment		94.5	21	<b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> 3-dehydroquinatase; <b>PDBTitle:</b> crystal structure of 3-dehydroquinatase dehydratase, type ii, from2 burkholderia phymatum stm815
20	<a href="#">c3kipU_</a>	Alignment		93.7	22	<b>PDB header:</b> lyase <b>Chain:</b> U: <b>PDB Molecule:</b> 3-dehydroquinase, type ii; <b>PDBTitle:</b> crystal structure of type-ii 3-dehydroquinase from c. albicans
21	<a href="#">d1uqra_</a>	Alignment	not modelled	92.0	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquinatase dehydratase <b>Family:</b> Type II 3-dehydroquinatase dehydratase
22	<a href="#">c3s81A_</a>	Alignment	not modelled	90.6	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aspartate racemase; <b>PDBTitle:</b> crystal structure of putative aspartate racemase from salmonella2 typhimurium
23	<a href="#">d1gqoa_</a>	Alignment	not modelled	87.8	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquinatase dehydratase <b>Family:</b> Type II 3-dehydroquinatase dehydratase
24	<a href="#">c2ad5B_</a>	Alignment	not modelled	85.6	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
25	<a href="#">c5lg5F_</a>	Alignment	not modelled	85.1	20	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> allantoin racemase; <b>PDBTitle:</b> crystal structure of allantoin racemase from pseudomonas fluorescens2 allr
26	<a href="#">c3qvjB_</a>	Alignment	not modelled	84.2	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydantoin racemase; <b>PDBTitle:</b> allantoin racemase from klebsiella pneumoniae
27	<a href="#">c4yajA_</a>	Alignment	not modelled	81.9	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
28	<a href="#">c5u03C_</a>	Alignment	not modelled	80.1	20	<b>PDB header:</b> ligase, protein fibril <b>Chain:</b> C: <b>PDB Molecule:</b> ctp synthase 1; <b>PDBTitle:</b> cryo-em structure of the human ctp synthase filament

29	<a href="#">c4zdiE_</a>	Alignment	not modelled	78.7	19	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
30	<a href="#">c3nvaB_</a>	Alignment	not modelled	77.9	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> dimeric form of ctp synthase from sulfolobus solfataricus
31	<a href="#">c3oa0B_</a>	Alignment	not modelled	77.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide biosynthesis protein wbbp; <b>PDBTitle:</b> crystal structure of the wlba (wbbp) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcna
32	<a href="#">c4p5pA_</a>	Alignment	not modelled	77.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> x-ray structure of francisella tularensis rapid encystment protein 242 kda (rep24), gene product of ftn_0841
33	<a href="#">c1uz5A_</a>	Alignment	not modelled	76.3	18	<b>PDB header:</b> molybdopterin biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> 402aa long hypothetical molybdopterin <b>PDBTitle:</b> the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii
34	<a href="#">d1pfka_</a>	Alignment	not modelled	75.4	20	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
35	<a href="#">d1uz5a3</a>	Alignment	not modelled	74.2	19	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
36	<a href="#">c2nqgA_</a>	Alignment	not modelled	74.2	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein moea; <b>PDBTitle:</b> moea r137q
37	<a href="#">c2zskA_</a>	Alignment	not modelled	73.6	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 226aa long hypothetical aspartate racemase; <b>PDBTitle:</b> crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
38	<a href="#">d2ftsa3</a>	Alignment	not modelled	69.7	13	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
39	<a href="#">d2c4va1</a>	Alignment	not modelled	69.6	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquinatase dehydratase <b>Family:</b> Type II 3-dehydroquinatase dehydratase
40	<a href="#">c4rhcH_</a>	Alignment	not modelled	68.7	16	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase; <b>PDBTitle:</b> crystal structure of 3-dehydroquinatase dehydratase from acinetobacter2 baumannii at 2.68 a resolution
41	<a href="#">c2h2wA_</a>	Alignment	not modelled	68.5	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-succinyltransferase; <b>PDBTitle:</b> crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
42	<a href="#">c2dx7B_</a>	Alignment	not modelled	66.4	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate racemase; <b>PDBTitle:</b> crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
43	<a href="#">c4wpgA_</a>	Alignment	not modelled	66.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ddtp-4-dehydrorhamnose reductase; <b>PDBTitle:</b> group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmlD)
44	<a href="#">d2nqra3</a>	Alignment	not modelled	63.9	23	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
45	<a href="#">c5l3rC_</a>	Alignment	not modelled	63.1	17	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein, chloroplastic; <b>PDBTitle:</b> structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
46	<a href="#">c5elmB_</a>	Alignment	not modelled	60.3	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> asp/glu_racemase family protein; <b>PDBTitle:</b> crystal structure of l-aspartate/glutamate specific racemase in2 complex with l-glutamate
47	<a href="#">c5xzdF_</a>	Alignment	not modelled	60.2	11	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> structure of acryloyl-coa hydratase acuh from roseovarius nubinhbens2 ism
48	<a href="#">c2uygF_</a>	Alignment	not modelled	60.1	18	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase; <b>PDBTitle:</b> crystallographic structure of the typeii 3-dehydroquinase from thermus2 thermophilus
49	<a href="#">c6mtgB_</a>	Alignment	not modelled	59.4	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine o-succinyltransferase; <b>PDBTitle:</b> a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
50	<a href="#">c5wxzA_</a>	Alignment	not modelled	57.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mcyf; <b>PDBTitle:</b> crystal structure of microcystis aeruginosa pcc 7806 aspartate2 racemase in complex with d-aspartate
51	<a href="#">d1ls1a2</a>	Alignment	not modelled	57.3	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
52	<a href="#">c3e96B_</a>	Alignment	not modelled	56.9	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
53	<a href="#">c5g2rA_</a>	Alignment	not modelled	56.5	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein cnx1; <b>PDBTitle:</b> crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
						<b>Fold:</b> Tubulin nucleotide-binding domain-like

54	<a href="#">d1tuba1</a>	Alignment	not modelled	53.3	13	<b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
55	<a href="#">c3lwzC</a>	Alignment	not modelled	53.2	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase; <b>PDBTitle:</b> 1.65 angstrom resolution crystal structure of type ii 3-dehydroquinatase2 dehydratase (arog) from yersinia pestis
56	<a href="#">c3s29C</a>	Alignment	not modelled	52.8	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sucrose synthase 1; <b>PDBTitle:</b> the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
57	<a href="#">d2csua3</a>	Alignment	not modelled	51.4	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
58	<a href="#">c1powA</a>	Alignment	not modelled	51.0	13	<b>PDB header:</b> oxidoreductase(oxygen as acceptor) <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
59	<a href="#">c4l8lA</a>	Alignment	not modelled	49.7	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase 1; <b>PDBTitle:</b> crystal structure of the type ii dehydroquinase from pseudomonas2 aeruginosa
60	<a href="#">c3oc7A</a>	Alignment	not modelled	49.3	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase from mycobacterium avium
61	<a href="#">d1uuva</a>	Alignment	not modelled	48.6	23	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
62	<a href="#">c2dwuA</a>	Alignment	not modelled	47.2	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
63	<a href="#">c4lk5B</a>	Alignment	not modelled	46.6	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from mycobacterium avium2 subsp. paratuberculosis k-10
64	<a href="#">c2jfoB</a>	Alignment	not modelled	46.4	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
65	<a href="#">c3u7rB</a>	Alignment	not modelled	45.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-dependent fmn reductase; <b>PDBTitle:</b> ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
66	<a href="#">d2f48a1</a>	Alignment	not modelled	45.0	15	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
67	<a href="#">d1wu2a3</a>	Alignment	not modelled	44.7	21	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
68	<a href="#">c5kt0A</a>	Alignment	not modelled	44.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
69	<a href="#">d1s2da</a>	Alignment	not modelled	44.1	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N-(deoxy)ribosyltransferase-like <b>Family:</b> N-deoxyribosyltransferase
70	<a href="#">c2eq5D</a>	Alignment	not modelled	43.6	26	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 228aa long hypothetical hydantoin racemase; <b>PDBTitle:</b> crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
71	<a href="#">d1ljja</a>	Alignment	not modelled	42.6	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
72	<a href="#">d1b74a1</a>	Alignment	not modelled	41.9	13	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/glutamate racemase <b>Family:</b> Aspartate/glutamate racemase
73	<a href="#">d1u9ca</a>	Alignment	not modelled	41.7	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/PfpI
74	<a href="#">c3h02F</a>	Alignment	not modelled	41.4	19	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> naphthoate synthase; <b>PDBTitle:</b> 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
75	<a href="#">c3c5yD</a>	Alignment	not modelled	41.3	16	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> ribose/galactose isomerase; <b>PDBTitle:</b> crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
76	<a href="#">c3mc3A</a>	Alignment	not modelled	40.6	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dsre/dsrf-like family protein; <b>PDBTitle:</b> crystal structure of dsre/dsrf-like family protein (np_342589.1) from2 sulfobolus solfataricus at 1.49 a resolution
77	<a href="#">c4wzzA</a>	Alignment	not modelled	40.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar abc transporter, substrate-binding protein; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
78	<a href="#">c3b9qA</a>	Alignment	not modelled	38.3	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpftsyl from arabidopsis thaliana
79	<a href="#">c5in6A</a>	Alignment	not modelled	37.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polysaccharide deacetylase;

79	<a href="#">c3jpaA</a>	Alignment	not modelled	37.8	18	<b>PDBTitle:</b> bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
80	<a href="#">d1rjma</a>	Alignment	not modelled	37.3	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
81	<a href="#">c3hfrA</a>	Alignment	not modelled	36.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from listeria monocytogenes
82	<a href="#">c2qs0A</a>	Alignment	not modelled	36.5	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinate synthetase a; <b>PDBTitle:</b> quinolinate synthase from pyrococcus furiosus
83	<a href="#">d1fuia2</a>	Alignment	not modelled	36.0	13	<b>Fold:</b> FucI/AraA N-terminal and middle domains <b>Superfamily:</b> FucI/AraA N-terminal and middle domains <b>Family:</b> L-fucose isomerase, N-terminal and second domains
84	<a href="#">c2hmcA</a>	Alignment	not modelled	35.8	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
85	<a href="#">d1xi8a3</a>	Alignment	not modelled	35.5	23	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
86	<a href="#">d1mkza</a>	Alignment	not modelled	35.2	19	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
87	<a href="#">c4m1bA</a>	Alignment	not modelled	34.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> polysaccharide deacetylase; <b>PDBTitle:</b> structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis
88	<a href="#">c3uhfB</a>	Alignment	not modelled	34.2	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni
89	<a href="#">c2is8A</a>	Alignment	not modelled	33.9	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis enzyme, moab; <b>PDBTitle:</b> crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
90	<a href="#">d1c2ya</a>	Alignment	not modelled	33.6	17	<b>Fold:</b> Lumazine synthase <b>Superfamily:</b> Lumazine synthase <b>Family:</b> Lumazine synthase
91	<a href="#">d2g2ca1</a>	Alignment	not modelled	33.5	23	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
92	<a href="#">c4ak9A</a>	Alignment	not modelled	33.3	12	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cpftsyt; <b>PDBTitle:</b> structure of chloroplast ftsy from physcomitrella patens
93	<a href="#">c3bq9A</a>	Alignment	not modelled	32.8	44	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted rossmann fold nucleotide-binding domain- <b>PDBTitle:</b> crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
94	<a href="#">c3qreA</a>	Alignment	not modelled	32.7	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, echa12_1; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase echa12_1 from2 mycobacterium marinum
95	<a href="#">c2jfqA</a>	Alignment	not modelled	32.5	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus glutamate racemase in2 complex with d- glutamate
96	<a href="#">c3p85A</a>	Alignment	not modelled	32.5	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure enoyl-coa hydratase from mycobacterium avium
97	<a href="#">c2jfnA</a>	Alignment	not modelled	32.2	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
98	<a href="#">d2nu7b1</a>	Alignment	not modelled	31.7	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
99	<a href="#">d1nqua</a>	Alignment	not modelled	31.5	24	<b>Fold:</b> Lumazine synthase <b>Superfamily:</b> Lumazine synthase <b>Family:</b> Lumazine synthase
100	<a href="#">d2f7wa1</a>	Alignment	not modelled	31.5	19	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
101	<a href="#">c1zxxA</a>	Alignment	not modelled	31.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructokinase; <b>PDBTitle:</b> the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
102	<a href="#">d1vmaa2</a>	Alignment	not modelled	31.3	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
103	<a href="#">c2jfbB</a>	Alignment	not modelled	31.2	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
104	<a href="#">c4mi2C</a>	Alignment	not modelled	31.2	22	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
						<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp/udp-n,n'-diacetyl/bacillosamine 2-

105	<a href="#">c5xvsA_</a>	Alignment	not modelled	30.5	25	epimerase <b>PDBTitle:</b> crystal structure of udp-glcnac 2-epimerase neuc complexed with udp
106	<a href="#">d1wzua1</a>	Alignment	not modelled	30.4	25	<b>Fold:</b> NadA-like <b>Superfamily:</b> NadA-like <b>Family:</b> NadA-like
107	<a href="#">c2og2A_</a>	Alignment	not modelled	29.3	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
108	<a href="#">c2qjhH_</a>	Alignment	not modelled	29.3	15	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400; <b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
109	<a href="#">c4jenB_</a>	Alignment	not modelled	29.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cmp n-glycosidase; <b>PDBTitle:</b> structure of clostridium botulinum cmp n-glycosidase, bcmb
110	<a href="#">c2iexA_</a>	Alignment	not modelled	28.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxynapthoic acid synthetase; <b>PDBTitle:</b> crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
111	<a href="#">c2gzmB_</a>	Alignment	not modelled	28.6	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of the glutamate racemase from bacillus anthracis
112	<a href="#">c2j7pA_</a>	Alignment	not modelled	28.3	14	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
113	<a href="#">c6dspB_</a>	Alignment	not modelled	28.3	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> autoinducer 2-binding protein lsrb; <b>PDBTitle:</b> lsrb from clostridium saccharobutylicum in complex with ai-2
114	<a href="#">c4r1oF_</a>	Alignment	not modelled	28.3	16	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> l-arabinose isomerase; <b>PDBTitle:</b> crystal structure of thermophilic geobacillus kaustophilus l-arabinose2 isomerase
115	<a href="#">d1h05a_</a>	Alignment	not modelled	28.2	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquinatase <b>Family:</b> Type II 3-dehydroquinatase
116	<a href="#">d1fs2b1</a>	Alignment	not modelled	28.0	5	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
117	<a href="#">c5w16D_</a>	Alignment	not modelled	27.8	16	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from thermus thermophilus in2 complex with d-glutamate
118	<a href="#">c4zu2A_</a>	Alignment	not modelled	27.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative isohexenylglutaconyl-coa hydratase; <b>PDBTitle:</b> pseudomonas aeruginosa atue
119	<a href="#">c3fduF_</a>	Alignment	not modelled	27.5	22	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii
120	<a href="#">c2ohoA_</a>	Alignment	not modelled	27.2	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> structural basis for glutamate racemase inhibitor