



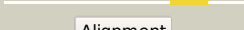
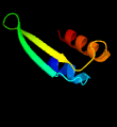

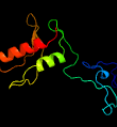



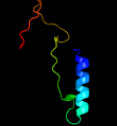
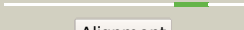
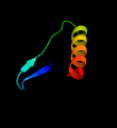
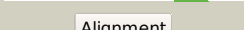






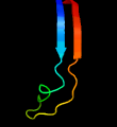


# Phyre2

Email	mdejesus@rockefeller.edu
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Date	Fri Jul 26 01:50:16 BST 2019
Unique Job ID	2dc844bf751e40d5


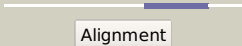

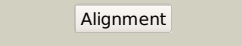
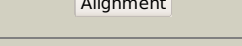
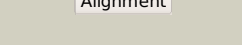

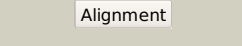
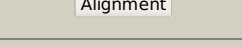





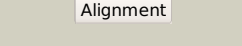
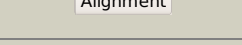
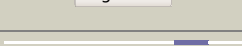



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1y7pB_</a>	 Alignment		84.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein af1403; <b>PDBTitle:</b> 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
2	<a href="#">c3o1lB_</a>	 Alignment		74.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
3	<a href="#">d2qmw2</a>	 Alignment		72.0	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phenylalanine metabolism regulatory domain
4	<a href="#">c6avhA_</a>	 Alignment		65.8	16	<b>PDB header:</b> ligase, plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> gh3.15 acyl acid amido synthetase; <b>PDBTitle:</b> gh3.15 acyl acid amido synthetase
5	<a href="#">d1xoda1</a>	 Alignment		59.7	28	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
6	<a href="#">c2im5C_</a>	 Alignment		58.4	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of nicotinate phosphoribosyltransferase from2 porphyromonas gingivalis
7	<a href="#">d1ddwa_</a>	 Alignment		54.9	14	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
8	<a href="#">c5l0lB_</a>	 Alignment		50.8	29	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein lpg0439
9	<a href="#">c2m3aA_</a>	 Alignment		48.9	35	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein knl-2; <b>PDBTitle:</b> nmr solution structure of a myb-like dna binding domain of knl-2 from2 c. elegans
10	<a href="#">c2mdaB_</a>	 Alignment		43.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine 3-monooxygenase; <b>PDBTitle:</b> the solution structure of the regulatory domain of tyrosine2 hydroxylase
11	<a href="#">c5xlmB_</a>	 Alignment		42.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pkn1; <b>PDBTitle:</b> monomer form of m.tuberculosis pkn1 sensor domain

12	<a href="#">c4j38A_</a>	Alignment		41.5	26	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> outer surface protein e; <b>PDBTitle:</b> structure of borrelia burgdorferi outer surface protein e in complex2 with factor h domains 19-20
13	<a href="#">dli7aa_</a>	Alignment		40.4	17	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
14	<a href="#">d1evha_</a>	Alignment		39.5	19	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
15	<a href="#">c3n0vD_</a>	Alignment		39.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
16	<a href="#">c2lvfB_</a>	Alignment		33.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ethylbenzene dehydrogenase beta-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum
17	<a href="#">c4yubB_</a>	Alignment		31.8	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of human nicotinic acid phosphoribosyltransferase
18	<a href="#">c6cxdA_</a>	Alignment		31.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase b; <b>PDBTitle:</b> crystal structure of peptidase b from yersinia pestis co92 at 2.75 a2 resolution
19	<a href="#">c4hl7A_</a>	Alignment		30.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of nicotinate phosphoribosyltransferase (target2 nysgr-026035) from vibrio cholerae
20	<a href="#">c3do6B_</a>	Alignment		28.5	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> formate--tetrahydrofolate ligase; <b>PDBTitle:</b> crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution
21	<a href="#">d1h70a_</a>	Alignment	not modelled	28.1	7	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Dimethylarginine dimethylaminohydrolase DDAH
22	<a href="#">c1ybeA_</a>	Alignment	not modelled	27.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a nicotinate phosphoribosyltransferase
23	<a href="#">c1zhvA_</a>	Alignment	not modelled	27.1	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu0741; <b>PDBTitle:</b> x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
24	<a href="#">c4bjuB_</a>	Alignment	not modelled	26.8	50	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylglucosamine-phosphate mutase; <b>PDBTitle:</b> genetic and structural validation of aspergillus fumigatus2 n-acetylphosphoglucosamine mutase as an antifungal target
25	<a href="#">c5td7A_</a>	Alignment	not modelled	26.7	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zgc:55652; <b>PDBTitle:</b> crystal structure of histone deacetylase 10
26	<a href="#">c4maiA_</a>	Alignment	not modelled	26.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aa11 lytic polysaccharide monooxygenase; <b>PDBTitle:</b> structure of aspergillus oryzae aa11 lytic polysaccharide2 monooxygenase with cu(i)
27	<a href="#">d1pdoa_</a>	Alignment	not modelled	25.9	16	<b>Fold:</b> PTS system fructose IIA component-like <b>Superfamily:</b> PTS system fructose IIA component-like <b>Family:</b> EIIA-man component-like
28	<a href="#">c3obiC_</a>	Alignment	not modelled	25.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase

						(np_949368)2 from rhodospseudomonas palustris cga009 at 1.95 a resolution
29	<a href="#">d1y7pa1</a>	Alignment	not modelled	25.4	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> AF1403 C-terminal domain-like
30	<a href="#">d1zy9a2</a>	Alignment	not modelled	24.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> YicI catalytic domain-like
31	<a href="#">c3iprC_</a>	Alignment	not modelled	24.2	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pts system, iia component; <b>PDBTitle:</b> crystal structure of the enterococcus faecalis gluconate2 specific eIIa phosphotransferase system component
32	<a href="#">d1xmka1</a>	Alignment	not modelled	22.4	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
33	<a href="#">c1bplA_</a>	Alignment	not modelled	22.3	19	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-glucon-4-gluconohydrolase; <b>PDBTitle:</b> glycosyltransferase
34	<a href="#">d1iuga_</a>	Alignment	not modelled	22.2	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
35	<a href="#">d1pbga_</a>	Alignment	not modelled	22.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
36	<a href="#">d1d7ka2</a>	Alignment	not modelled	21.7	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
37	<a href="#">c2jp2A_</a>	Alignment	not modelled	21.6	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sprouty-related, evh1 domain-containing protein <b>PDBTitle:</b> solution structure and resonance assignment of the n-2 terminal evh1 domain from the human spred2 protein3 (sprouty-related protein with evh1 domain isoform 2)
38	<a href="#">d1qz9a_</a>	Alignment	not modelled	21.6	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
39	<a href="#">d1ru8a_</a>	Alignment	not modelled	21.2	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
40	<a href="#">d1qc6a_</a>	Alignment	not modelled	21.2	11	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
41	<a href="#">d1nh8a2</a>	Alignment	not modelled	21.2	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> ATP phosphoribosyltransferase (ATP-PRase, HisG), regulatory C-terminal domain
42	<a href="#">c1yirA_</a>	Alignment	not modelled	20.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase 2; <b>PDBTitle:</b> crystal structure of a nicotinate phosphoribosyltransferase
43	<a href="#">c6czaB_</a>	Alignment	not modelled	20.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4fe-4s ferredoxin, iron-sulfur binding domain protein; <b>PDBTitle:</b> the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3 bound to phosphate
44	<a href="#">d1yksa2</a>	Alignment	not modelled	19.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
45	<a href="#">c4e4jl_</a>	Alignment	not modelled	19.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> arginine deiminase; <b>PDBTitle:</b> crystal structure of arginine deiminase from mycoplasma penetrans
46	<a href="#">d1m6sa_</a>	Alignment	not modelled	18.9	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
47	<a href="#">c3louB_</a>	Alignment	not modelled	18.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
48	<a href="#">d1xw8a_</a>	Alignment	not modelled	17.8	20	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
49	<a href="#">c3w7bB_</a>	Alignment	not modelled	17.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
50	<a href="#">c5mlkB_</a>	Alignment	not modelled	17.4	32	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
51	<a href="#">d1o7fa1</a>	Alignment	not modelled	17.3	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
52	<a href="#">d1szna2</a>	Alignment	not modelled	16.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
53	<a href="#">d1a1va2</a>	Alignment	not modelled	16.8	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
						<b>Fold:</b> TIM beta/alpha-barrel

54	<a href="#">d1uaa2</a>	Alignment	not modelled	16.4	28	<b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
55	<a href="#">c4yddF</a>	Alignment	not modelled	16.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dmsO reductase family type ii enzyme, iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of the perchlorate reductase pcrb from azospira2 suillum ps
56	<a href="#">c4qg5D</a>	Alignment	not modelled	15.5	26	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative phosphoglucomutase; <b>PDBTitle:</b> crystal structure of phosphoglucomutase from leishmania major at 3.52 angstrom resolution
57	<a href="#">c4ewvB</a>	Alignment	not modelled	15.0	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-substituted benzoates-glutamate ligase gh3.12; <b>PDBTitle:</b> crystal structure of gh3.12 in complex with ampcpp
58	<a href="#">d1knwa2</a>	Alignment	not modelled	14.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
59	<a href="#">c3a5vA</a>	Alignment	not modelled	14.3	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of alpha-galactosidase i from mortierella vinacea
60	<a href="#">d1vlpa2</a>	Alignment	not modelled	14.2	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase C-terminal domain
61	<a href="#">d1ybea1</a>	Alignment	not modelled	14.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase C-terminal domain
62	<a href="#">d1m32a</a>	Alignment	not modelled	14.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
63	<a href="#">d1zo0a1</a>	Alignment	not modelled	14.0	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> Ornithine decarboxylase antizyme-like
64	<a href="#">c3rmuD</a>	Alignment	not modelled	13.7	9	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> methylmalonyl-coa epimerase, mitochondrial; <b>PDBTitle:</b> crystal structure of human methylmalonyl-coa epimerase, mcee
65	<a href="#">d1kfia1</a>	Alignment	not modelled	13.4	15	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
66	<a href="#">c2ci6A</a>	Alignment	not modelled	13.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ng, ng-dimethylarginine dimethylaminohydrolase 1; <b>PDBTitle:</b> crystal structure of dimethylarginine2 dimethylaminohydrolase i bound with zinc low ph
67	<a href="#">c3a11A</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> crystal structure of rhodococcus sp. n-771 amidase complexed2 with benzamide
68	<a href="#">c5jouA</a>	Alignment	not modelled	13.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-xylosidase bogh31a; <b>PDBTitle:</b> bacteroides ovatus xyloglucan pul gh31
69	<a href="#">c4jrbA</a>	Alignment	not modelled	13.2	30	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion
70	<a href="#">c2pfuA</a>	Alignment	not modelled	13.1	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> biopolymer transport exbd protein; <b>PDBTitle:</b> nmr structure determination of the periplasmic domain of exbd from2 e.coli
71	<a href="#">c3lrmB</a>	Alignment	not modelled	12.8	34	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-galactosidase 1; <b>PDBTitle:</b> structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
72	<a href="#">c5ns6C</a>	Alignment	not modelled	12.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of beta-glucosidase bglm-g1 from marine metagenome
73	<a href="#">d1p88a</a>	Alignment	not modelled	12.7	21	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
74	<a href="#">c2rgmA</a>	Alignment	not modelled	12.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> rice bglu1 beta-glucosidase, a plant exoglucanase/beta-glucosidase
75	<a href="#">c3e9kA</a>	Alignment	not modelled	12.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
76	<a href="#">c6eacC</a>	Alignment	not modelled	12.3	35	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> selo; <b>PDBTitle:</b> pseudomonas syringae selo
77	<a href="#">c3nx3A</a>	Alignment	not modelled	12.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
78	<a href="#">c1njc</a>	Alignment	not modelled	12.1	13	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> crystal structure determination of t. brucei ornithine decarboxylase2 bound to d-ornithine and to g418
79	<a href="#">c5xgzA</a>	Alignment	not modelled	12.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glycosidase; <b>PDBTitle:</b> metagenomic glucose-tolerant glycosidase

80	<a href="#">c2pljA_</a>	 Alignment	not modelled	12.0	14	<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
81	<a href="#">c1c4gB_</a>	 Alignment	not modelled	11.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (alpha-d-glucose 1-phosphate phosphoglucomutase); <b>PDBTitle:</b> phosphoglucomutase vanadate based transition state analog complex
82	<a href="#">d2dfaa1</a>	 Alignment	not modelled	11.9	16	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
83	<a href="#">d8ohma2</a>	 Alignment	not modelled	11.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
84	<a href="#">c2hzpA_</a>	 Alignment	not modelled	11.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase
85	<a href="#">c1ti2F_</a>	 Alignment	not modelled	11.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> pyrogallol hydroxytransferase small subunit; <b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici
86	<a href="#">c6fmgC_</a>	 Alignment	not modelled	11.6	24	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pts system mannose-specific transporter subunit iiaB; <b>PDBTitle:</b> structure of the mannose transporter iia domain from streptococcus2 pneumoniae
87	<a href="#">c4nziA_</a>	 Alignment	not modelled	11.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alpha-galactosidase; <b>PDBTitle:</b> crystal structure of a putative alpha-galactosidase (bf1418) from2 bacteroides fragilis nctc 9343 at 1.57 a resolution
88	<a href="#">d1hx0a2</a>	 Alignment	not modelled	11.3	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
89	<a href="#">d1a9xa4</a>	 Alignment	not modelled	11.1	16	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
90	<a href="#">c2ro0A_</a>	 Alignment	not modelled	11.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone acetyltransferase esa1; <b>PDBTitle:</b> solution structure of the knotted tudor domain of the yeast2 histone acetyltransferase, esa1
91	<a href="#">d1r46a2</a>	 Alignment	not modelled	10.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
92	<a href="#">c3mjdA_</a>	 Alignment	not modelled	10.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
93	<a href="#">c6oswA_</a>	 Alignment	not modelled	10.8	24	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> forkhead box m1; <b>PDBTitle:</b> an order-to-disorder structural switch activates the foxm12 transcription factor
94	<a href="#">d3beda1</a>	 Alignment	not modelled	10.7	15	<b>Fold:</b> PTS system fructose IIA component-like <b>Superfamily:</b> PTS system fructose IIA component-like <b>Family:</b> EIIA-man component-like
95	<a href="#">d1yira1</a>	 Alignment	not modelled	10.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase C-terminal domain
96	<a href="#">c5gjmB_</a>	 Alignment	not modelled	10.7	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> lysine/ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of lysine decarboxylase from selenomonas ruminantium2 in c2 space group
97	<a href="#">c4fymA_</a>	 Alignment	not modelled	10.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum orotate2 phosphoribosyltransferase
98	<a href="#">d1jaea2</a>	 Alignment	not modelled	10.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
99	<a href="#">c1u8sB_</a>	 Alignment	not modelled	10.5	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> glycine cleavage system transcriptional <b>PDBTitle:</b> crystal structure of putative glycine cleavage system2 transcriptional repressor