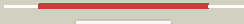



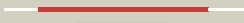



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0066c_(icd2)_72271_74508
Date	Tue Jul 23 14:50:10 BST 2019
Unique Job ID	5a69306f21973173

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1itwa_</a>	 Alignment		100.0	61	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Monomeric isocitrate dehydrogenase
2	<a href="#">c6g3uA_</a>	 Alignment		100.0	68	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> structure of pseudomonas aeruginosa isocitrate dehydrogenase, idh
3	<a href="#">c2b0tA_</a>	 Alignment		100.0	58	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp isocitrate dehydrogenase; <b>PDBTitle:</b> structure of monomeric nadp isocitrate dehydrogenase
4	<a href="#">d1lwda_</a>	 Alignment		99.3	15	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
5	<a href="#">c1zorB_</a>	 Alignment		99.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
6	<a href="#">c3us8A_</a>	 Alignment		98.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase [nadp]; <b>PDBTitle:</b> crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021
7	<a href="#">c3blxL_</a>	 Alignment		97.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit 2; <b>PDBTitle:</b> yeast isocitrate dehydrogenase (apo form)
8	<a href="#">d1wpwa_</a>	 Alignment		97.8	16	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
9	<a href="#">c3blxM_</a>	 Alignment		97.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit 1; <b>PDBTitle:</b> yeast isocitrate dehydrogenase (apo form)
10	<a href="#">d1t0la_</a>	 Alignment		97.6	25	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
11	<a href="#">c5grhB_</a>	 Alignment		97.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit gamma, <b>PDBTitle:</b> crystal structure of the alpha gamma heterodimer of human idh3 in2 complex with mg(2+)

12	<a href="#">c5hn6A_</a>	Alignment		97.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoisocitrate dehydrogenase; <b>PDBTitle:</b> crystal structure of beta-decarboxylating dehydrogenase (tk0280) from2 thermococcus kodakarensis complexed with mn and 3-isopropylmalate
13	<a href="#">c2uxqB_</a>	Alignment		97.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate dehydrogenase native; <b>PDBTitle:</b> isocitrate dehydrogenase from the psychrophilic bacterium2 desulfotalea psychrophila: biochemical properties and3 crystal structure analysis
14	<a href="#">c5grhA_</a>	Alignment		97.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit alpha, <b>PDBTitle:</b> crystal structure of the alpha gamma heterodimer of human idh3 in2 complex with mg(2+)
15	<a href="#">c2e0cA_</a>	Alignment		97.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 409aa long hypothetical nadp-dependent isocitrate <b>PDBTitle:</b> crystal structure of isocitrate dehydrogenase from sulfolobus tokodaii2 strain7 at 2.0 a resolution
16	<a href="#">c2qfyE_</a>	Alignment		97.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> isocitrate dehydrogenase [nadp]; <b>PDBTitle:</b> crystal structure of saccharomyces cerevesiae mitochondrial nadp(+)-2 dependent isocitrate dehydrogenase in complex with a-ketoglutarate
17	<a href="#">c3fmX_</a>	Alignment		96.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> tartrate dehydrogenase/decarboxylase; <b>PDBTitle:</b> crystal structure of tartrate dehydrogenase from pseudomonas putida2 complexed with nadh
18	<a href="#">d1g2ua_</a>	Alignment		96.7	20	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
19	<a href="#">d1w0da_</a>	Alignment		96.6	18	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
20	<a href="#">c2d1cB_</a>	Alignment		96.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> crystal structure of tt0538 protein from thermus thermophilus hb8
21	<a href="#">d1xaca_</a>	Alignment	not modelled	96.1	23	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
22	<a href="#">d1pb1a_</a>	Alignment	not modelled	96.0	13	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
23	<a href="#">c1x0lB_</a>	Alignment	not modelled	95.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoisocitrate dehydrogenase; <b>PDBTitle:</b> crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
24	<a href="#">c3ty3A_</a>	Alignment	not modelled	95.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable homoisocitrate dehydrogenase; <b>PDBTitle:</b> crystal structure of homoisocitrate dehydrogenase from2 schizosaccharomyces pombe bound to glycyl-glycyl-glycine
25	<a href="#">c4aoyD_</a>	Alignment	not modelled	95.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> isocitrate dehydrogenase [nadp]; <b>PDBTitle:</b> open ctidh. the complex structures of isocitrate dehydrogenase from2 clostridium thermocellum and desulfotalea psychrophila, support a new3 active site locking mechanism
26	<a href="#">c2d4vD_</a>	Alignment	not modelled	95.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
27	<a href="#">d1v53a1</a>	Alignment	not modelled	94.9	19	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
28	<a href="#">c3vl3A_</a>	Alignment	not modelled	94.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase; <b>PDBTitle:</b> 3-isopropylmalate dehydrogenase from shewanella oneidensis mr-1 at 3402 mpa <b>PDB header:</b> oxidoreductase

29	<a href="#">c1tyoA_</a>	Alignment	not modelled	94.5	18	<b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> isocitrate dehydrogenase from the hyperthermophile aeropyrum pernix in2 complex with etheno-nadp
30	<a href="#">d1hqsa_</a>	Alignment	not modelled	94.4	17	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
31	<a href="#">d1a05a_</a>	Alignment	not modelled	94.1	19	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
32	<a href="#">c4iwHA_</a>	Alignment	not modelled	94.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase; <b>PDBTitle:</b> crystal structure of a 3-isopropylmalate dehydrogenase from2 burkholderia pseudomallei
33	<a href="#">c2iv0A_</a>	Alignment	not modelled	92.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> thermal stability of isocitrate dehydrogenase from2 archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
34	<a href="#">d1vlca_</a>	Alignment	not modelled	91.2	18	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
35	<a href="#">d1cnza_</a>	Alignment	not modelled	87.1	17	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
36	<a href="#">d1cm7a_</a>	Alignment	not modelled	85.1	19	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
37	<a href="#">c3u1hA_</a>	Alignment	not modelled	84.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase; <b>PDBTitle:</b> crystal structure of ipmdh from the last common ancestor of bacillus
38	<a href="#">c3uduG_</a>	Alignment	not modelled	83.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase; <b>PDBTitle:</b> crystal structure of putative 3-isopropylmalate dehydrogenase from2 campylobacter jejuni
39	<a href="#">d3ovwa_</a>	Alignment	not modelled	83.1	25	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
40	<a href="#">c3r8wC_</a>	Alignment	not modelled	81.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase 2, chloroplastic; <b>PDBTitle:</b> structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
41	<a href="#">d1oija_</a>	Alignment	not modelled	79.5	18	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
42	<a href="#">d1cooa_</a>	Alignment	not modelled	74.2	20	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> C-terminal domain of RNA polymerase alpha subunit <b>Family:</b> C-terminal domain of RNA polymerase alpha subunit
43	<a href="#">c3w7aD_</a>	Alignment	not modelled	70.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> crystal structure of azoreductase azrc fin complex with sulfone-2 modified azo dye acid red 88
44	<a href="#">c4c90B_</a>	Alignment	not modelled	65.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucuronidase gh115; <b>PDBTitle:</b> evidence that gh115 alpha-glucuronidase activity is2 dependent on conformational flexibility
45	<a href="#">c3iydA_</a>	Alignment	not modelled	55.9	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit alpha; <b>PDBTitle:</b> three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
46	<a href="#">c3igsB_</a>	Alignment	not modelled	49.7	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase 2; <b>PDBTitle:</b> structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
47	<a href="#">d1ee6a_</a>	Alignment	not modelled	49.2	30	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Pectin lyase-like <b>Family:</b> Pectate lyase-like
48	<a href="#">c4u49B_</a>	Alignment	not modelled	48.0	27	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pectate lyase; <b>PDBTitle:</b> crystal structure of pectate lyase pel3 from pectobacterium2 carotovorum with two monomers in the a.u
49	<a href="#">c4xnnA_</a>	Alignment	not modelled	46.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiohydrolase chbi; <b>PDBTitle:</b> crystal structure of a gh7 family cellobiohydrolase from daphnia pulex
50	<a href="#">c3b90A_</a>	Alignment	not modelled	44.6	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-pectate lyase; <b>PDBTitle:</b> crystal structure of the catalytic domain of pectate lyase peli from2 erwinia chrysanthemi
51	<a href="#">d1sxd1</a>	Alignment	not modelled	44.1	9	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
52	<a href="#">c5h6iC_</a>	Alignment	not modelled	43.2	26	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> protein b; <b>PDBTitle:</b> crystal structure of gbs camp factor
53	<a href="#">c3t9gB_</a>	Alignment	not modelled	42.5	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pectate lyase; <b>PDBTitle:</b> the crystal structure of family 3 pectate lyase from2 caldicellulosiruptor bescii
54	<a href="#">c3r07C_</a>	Alignment	not modelled	42.1	7	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative lipoate-protein ligase a subunit 2; <b>PDBTitle:</b> structural analysis of an archaeal lipoylation system. a bi-

						partite2 lipoate protein ligase and its e2 lipoyl domain from thermoplasma3 acidophilum
55	<a href="#">c3b4nB_</a>	Alignment	not modelled	42.1	27	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-pectate lyase; <b>PDBTitle:</b> crystal structure analysis of pectate lyase peli from2 erwinia chrysanthemi
56	<a href="#">d1doqa_</a>	Alignment	not modelled	41.2	21	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> C-terminal domain of RNA polymerase alpha subunit <b>Family:</b> C-terminal domain of RNA polymerase alpha subunit
57	<a href="#">c4nz3A_</a>	Alignment	not modelled	40.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deacetylase da1; <b>PDBTitle:</b> structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21
58	<a href="#">c4csiB_</a>	Alignment	not modelled	38.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> crystal structure of the thermostable cellobiohydrolase2 cel7a from the fungus humicola grisea var. thermoidea.
59	<a href="#">d1lb2b_</a>	Alignment	not modelled	37.9	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> C-terminal domain of RNA polymerase alpha subunit <b>Family:</b> C-terminal domain of RNA polymerase alpha subunit
60	<a href="#">c4zmbA_</a>	Alignment	not modelled	36.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a five-domain gh115 alpha-glucuronidase from the2 marine bacterium saccharophagus degradans 2-40t
61	<a href="#">c1npyA_</a>	Alignment	not modelled	35.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical shikimate 5-dehydrogenase-like protein hi0607; <b>PDBTitle:</b> structure of shikimate 5-dehydrogenase-like protein hi0607
62	<a href="#">c3tsjA_</a>	Alignment	not modelled	34.3	14	<b>PDB header:</b> allergen, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pollen allergen phl p 4; <b>PDBTitle:</b> crystal structure of class iii chitinase from pomegranate provides the2 insight into its metal storage capacity
63	<a href="#">c5y2gA_</a>	Alignment	not modelled	33.7	22	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,protein b; <b>PDBTitle:</b> structure of mbp tagged gbs camp
64	<a href="#">c4toqC_</a>	Alignment	not modelled	32.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> class iii chitinase; <b>PDBTitle:</b> crystal structure of class iii chitinase from pomegranate provides the2 insight into its metal storage capacity
65	<a href="#">c6cg8A_</a>	Alignment	not modelled	32.2	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> upf0335 protein b7z12_12435; <b>PDBTitle:</b> structure of c. crescentus gapr-dna
66	<a href="#">c5kc1H_</a>	Alignment	not modelled	31.8	60	<b>PDB header:</b> endocytosis <b>Chain:</b> H: <b>PDB Molecule:</b> autophagy-related protein 38; <b>PDBTitle:</b> structure of the c-terminal dimerization domain of atg38
67	<a href="#">c1dvpA_</a>	Alignment	not modelled	30.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine <b>PDBTitle:</b> crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
68	<a href="#">c2gsjA_</a>	Alignment	not modelled	30.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ppl-2; <b>PDBTitle:</b> cdna cloning and 1.75a crystal structure determination of ppl2, a2 novel chimerolectin from parkia platycephala seeds exhibiting3 endochitinolytic activity
69	<a href="#">c6dxdD_</a>	Alignment	not modelled	30.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> the crystal structure of an fmn-dependent nadh-azoreductase from2 klebsiella pneumoniae
70	<a href="#">c3q58A_</a>	Alignment	not modelled	30.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
71	<a href="#">c4hapB_</a>	Alignment	not modelled	29.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gh7 family protein; <b>PDBTitle:</b> crystal structure of a gh7 family cellobiohydrolase from limnoria2 quadripunctata in complex with cellobiose
72	<a href="#">d1ebfa2</a>	Alignment	not modelled	29.3	29	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Homoserine dehydrogenase-like
73	<a href="#">d2v3ia1</a>	Alignment	not modelled	29.0	15	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
74	<a href="#">d2obba1</a>	Alignment	not modelled	28.8	29	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
75	<a href="#">c2maxA_</a>	Alignment	not modelled	28.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit alpha; <b>PDBTitle:</b> nmr structure of the rna polymerase alpha subunit c-terminal domain2 from helicobacter pylori
76	<a href="#">c2q62A_</a>	Alignment	not modelled	28.5	18	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> arsh; <b>PDBTitle:</b> crystal structure of arsh from sinorhizobium meliloti
77	<a href="#">c5f5tB_</a>	Alignment	not modelled	28.4	28	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the prp38-mfap1 complex of chaetomium2 thermophilum
78	<a href="#">c2yg1A_</a>	Alignment	not modelled	27.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose 1,4-beta-cellobiosidase; <b>PDBTitle:</b> apo structure of cellobiohydrolase 1 (cel7a) from heterobasidion2 annosum

79	<a href="#">c3bvkC</a>	Alignment	not modelled	27.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> structural basis for the iron uptake mechanism of helicobacter pylori2 ferritin
80	<a href="#">c4a54A</a>	Alignment	not modelled	27.2	19	<b>PDB header:</b> rna binding protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> edc3; <b>PDBTitle:</b> structural basis of the dcp1:dcp2 mrna decapping complex activation2 by edc3 and scd6
81	<a href="#">c4davA</a>	Alignment	not modelled	26.9	25	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> sugar fermentation stimulation protein homolog; <b>PDBTitle:</b> the structure of pyrococcus furiosus sfsa in complex with dna
82	<a href="#">d1uika2</a>	Alignment	not modelled	26.9	9	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
83	<a href="#">c1yunB</a>	Alignment	not modelled	26.4	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable nicotinate-nucleotide <b>PDBTitle:</b> crystal structure of nicotinic acid mononucleotide2 adenyllyltransferase from pseudomonas aeruginosa
84	<a href="#">d1fwxa2</a>	Alignment	not modelled	26.2	15	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> Nitrous oxide reductase, N-terminal domain <b>Family:</b> Nitrous oxide reductase, N-terminal domain
85	<a href="#">c4rpiA</a>	Alignment	not modelled	25.8	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide adenyllyltransferase; <b>PDBTitle:</b> crystal structure of nicotinate mononucleotide adenyllyltransferase2 from mycobacterium tuberculosis
86	<a href="#">c2hpaA</a>	Alignment	not modelled	24.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
87	<a href="#">d2olra2</a>	Alignment	not modelled	24.3	12	<b>Fold:</b> PEP carboxykinase N-terminal domain <b>Superfamily:</b> PEP carboxykinase N-terminal domain <b>Family:</b> PEP carboxykinase N-terminal domain
88	<a href="#">c2y9zB</a>	Alignment	not modelled	24.2	43	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> iswi one complex protein 3; <b>PDBTitle:</b> chromatin remodeling factor isw1a(del_atpase) in dna complex
89	<a href="#">c3zyqA</a>	Alignment	not modelled	23.9	7	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine kinase <b>PDBTitle:</b> crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
90	<a href="#">c2fzvC</a>	Alignment	not modelled	23.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative arsenical resistance protein; <b>PDBTitle:</b> crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
91	<a href="#">d1fxza2</a>	Alignment	not modelled	23.5	11	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
92	<a href="#">c3w8wA</a>	Alignment	not modelled	23.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fad-dependent oxygenase encm; <b>PDBTitle:</b> the crystal structure of encm
93	<a href="#">c2xuca</a>	Alignment	not modelled	22.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase; <b>PDBTitle:</b> natural product-guided discovery of a fungal chitinase inhibitor
94	<a href="#">d1qopa</a>	Alignment	not modelled	22.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
95	<a href="#">c3p0rA</a>	Alignment	not modelled	22.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> azoreductase; <b>PDBTitle:</b> crystal structure of azoreductase from bacillus anthracis str. sterne
96	<a href="#">c5zbaA</a>	Alignment	not modelled	22.0	45	<b>PDB header:</b> transferase/structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna damage response protein rtt109, putative; <b>PDBTitle:</b> crystal structure of rtt109-asf1-h3-h4-coa complex
97	<a href="#">c3c8mA</a>	Alignment	not modelled	22.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
98	<a href="#">d1juqa</a>	Alignment	not modelled	21.8	21	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ENTH/VHS domain <b>Family:</b> VHS domain
99	<a href="#">c4b16A</a>	Alignment	not modelled	21.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase like lectin; <b>PDBTitle:</b> crystal structure of tamarind chitinase like lectin (tcll) complexed2 with n-acetyl glucosamine (glcnac)
100	<a href="#">d1zsa6a1</a>	Alignment	not modelled	21.1	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleoside diphosphate kinase, NDK <b>Family:</b> Nucleoside diphosphate kinase, NDK
101	<a href="#">c3fseB</a>	Alignment	not modelled	21.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> two-domain protein containing dj-1/thij/pfpi-like and <b>PDBTitle:</b> crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
102	<a href="#">c1vw48</a>	Alignment	not modelled	21.0	64	<b>PDB header:</b> ribosome <b>Chain:</b> 8: <b>PDB Molecule:</b> 54s ribosomal protein l13, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
103	<a href="#">d1krqa</a>	Alignment	not modelled	20.5	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin

104	<a href="#">d1gpia_</a>	Alignment	not modelled	20.4	15	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
105	<a href="#">c6cfxD_</a>	Alignment	not modelled	20.4	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> upf0335 protein ase63_04290; <b>PDBTitle:</b> bosea sp gapr solved in the presence of dna
106	<a href="#">c3daoB_</a>	Alignment	not modelled	20.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphate; <b>PDBTitle:</b> crystal structure of a putative phosphate (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution