






















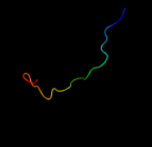
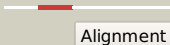
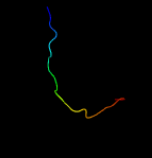
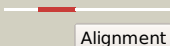
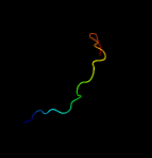




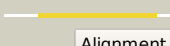

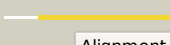

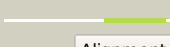
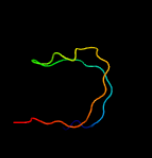

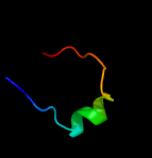
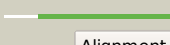

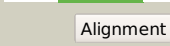

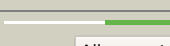


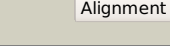


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3601c\_panD\_4044041\_4044460  
 Date Fri Aug 9 18:20:28 BST 2019  
 Unique Job ID 22f880168f08bd33

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1pt1B_</a>	 Alignment		100.0	49	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
2	<a href="#">c2c45F_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> F; <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> native precursor of pyruvoyl dependent aspartate decarboxylase
3	<a href="#">d1ppya_</a>	 Alignment		100.0	50	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Pyruvoyl dependent aspartate decarboxylase, ADC
4	<a href="#">c3ougA_</a>	 Alignment		100.0	43	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
5	<a href="#">c1vc3B_</a>	 Alignment		100.0	62	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> l-aspartate-alpha-decarboxylase heavy chain; <b>PDBTitle:</b> crystal structure of l-aspartate-alpha-decarboxylase
6	<a href="#">c1uheA_</a>	 Alignment		100.0	44	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> aspartate 1-decarboxylase alpha chain; <b>PDBTitle:</b> crystal structure of aspartate decarboxylase, isoasparagine complex
7	<a href="#">c3plxB_</a>	 Alignment		100.0	39	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
8	<a href="#">c1pyuD_</a>	 Alignment		100.0	45	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> aspartate 1-decarboxylase alfa chain; <b>PDBTitle:</b> processed aspartate decarboxylase mutant with ser25 mutated to cys
9	<a href="#">c1vc3A_</a>	 Alignment		98.3	72	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> l-aspartate-alpha-decarboxylase light chain; <b>PDBTitle:</b> crystal structure of l-aspartate-alpha-decarboxylase
10	<a href="#">c1uheB_</a>	 Alignment		98.0	63	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> aspartate 1-decarboxylase beta chain; <b>PDBTitle:</b> crystal structure of aspartate decarboxylase, isoasparagine complex
11	<a href="#">c1uhdB_</a>	 Alignment		98.0	63	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> aspartate 1-decarboxylase beta chain; <b>PDBTitle:</b> crystal structure of aspartate decarboxylase, pyruvoyl group bound2 form

12	<a href="#">c2eeoA</a>	 Alignment		97.9	68	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> crystal structure of t.th. hb8 l-aspartate-alpha-decarboxylase2 complexed with fumarate
13	<a href="#">c4d7zA</a>	 Alignment		97.4	68	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> aspartate 1-decarboxylase beta chain; <b>PDBTitle:</b> e. coli l-aspartate-alpha-decarboxylase mutant n72q to a resolution of 2.19 angstroms
14	<a href="#">c3plxA</a>	 Alignment		97.2	67	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> the crystal structure of aspartate alpha-decarboxylase from 2 campylobacter jejuni subsp. jejuni nctc 11168
15	<a href="#">c2pjhB</a>	 Alignment		96.4	17	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structural model of the p97 n domain- npl4 ubd complex
16	<a href="#">c1cz5A</a>	 Alignment		92.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
17	<a href="#">d1cz5a1</a>	 Alignment		77.6	19	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
18	<a href="#">c6opcF</a>	 Alignment		72.0	22	<b>PDB header:</b> motor protein <b>Chain:</b> F; <b>PDB Molecule:</b> cell division control protein 48; <b>PDBTitle:</b> cdc48 hexamer in a complex with substrate and shp1(ubx domain)
19	<a href="#">c3krtC</a>	 Alignment		61.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> crotonyl coa reductase; <b>PDBTitle:</b> crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
20	<a href="#">c2glwA</a>	 Alignment		58.6	33	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> 92aa long hypothetical protein; <b>PDBTitle:</b> the solution structure of phs018 from pyrococcus horikoshii
21	<a href="#">c5ifwB</a>	 Alignment	not modelled	55.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
22	<a href="#">d1ylea1</a>	 Alignment	not modelled	53.8	26	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> AstA-like
23	<a href="#">d1qw1a1</a>	 Alignment	not modelled	53.5	26	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
24	<a href="#">c4a10A</a>	 Alignment	not modelled	53.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> octenoyl-coa reductase/carboxylase; <b>PDBTitle:</b> apo-structure of 2-octenoyl-coa carboxylase reductase cinf from 2 streptomyces sp.
25	<a href="#">c4qi2B</a>	 Alignment	not modelled	52.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> crotonyl-coa carboxylase/reductase; <b>PDBTitle:</b> crotonyl-coa carboxylase/reductase
26	<a href="#">c1tufA</a>	 Alignment	not modelled	50.7	16	<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
27	<a href="#">c2ejvA</a>	 Alignment	not modelled	50.5	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> l-threonine 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of threonine 3-dehydrogenase complexed with nad+
28	<a href="#">c3qqmD</a>	 Alignment	not modelled	49.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> mlr3007 protein; <b>PDBTitle:</b> crystal structure of a putative amino-acid aminotransferase2 (np_104211.1) from mesorhizobium loti at 2.30 a

					resolution
29	<a href="#">c4ejmA</a>	Alignment	not modelled	48.8	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc-binding dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative zinc-binding dehydrogenase (target2 psi-012003) from sinorhizobium meliloti 1021 bound to nadp
30	<a href="#">d1wrua1</a>	Alignment	not modelled	47.8	23 <b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
31	<a href="#">c6p3hB</a>	Alignment	not modelled	46.3	40 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> (4e)-oxalomesaconate delta-isomerase; <b>PDBTitle:</b> crystal structure of ligu(k66m) bound to substrate
32	<a href="#">c2eihA</a>	Alignment	not modelled	46.0	29 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of nad-dependent alcohol dehydrogenase
33	<a href="#">c4gkvC</a>	Alignment	not modelled	45.4	26 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> alcohol dehydrogenase, propanol-preferring; <b>PDBTitle:</b> structure of escherichia coli adhP (ethanol-inducible dehydrogenase)2 with bound nad
34	<a href="#">c1h2bA</a>	Alignment	not modelled	45.3	26 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of the alcohol dehydrogenase from the2 hyperthermophilic archaeon aeropyrum pernix at 1.65a resolution
35	<a href="#">c1kevB</a>	Alignment	not modelled	43.9	26 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> structure of nadp-dependent alcohol dehydrogenase
36	<a href="#">c2ouiB</a>	Alignment	not modelled	42.8	26 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica
37	<a href="#">c4eezB</a>	Alignment	not modelled	41.6	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase 1; <b>PDBTitle:</b> crystal structure of lactococcus lactis alcohol dehydrogenase variant2 re1
38	<a href="#">c2vwrA</a>	Alignment	not modelled	41.0	27 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ligand of numb protein x 2; <b>PDBTitle:</b> crystal structure of the second pdz domain of numb-binding protein 2
39	<a href="#">c6dkhC</a>	Alignment	not modelled	39.4	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> l-idonate 5-dehydrogenase (nad(p)(+)); <b>PDBTitle:</b> the crystal structure of l-idonate 5-dehydrogenase from escherichia2 coli str. k-12 substr. mg1655
40	<a href="#">c2xaaC</a>	Alignment	not modelled	39.0	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> secondary alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase adh-'a' from rhodococcus ruber dsm2 44541 at ph 8.5 in complex with nad and butane-1,4-diol
41	<a href="#">c4k6nA</a>	Alignment	not modelled	38.6	23 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aminodeoxychorismate lyase; <b>PDBTitle:</b> crystal structure of yeast 4-amino-4-deoxychorismate lyase
42	<a href="#">d3cdda1</a>	Alignment	not modelled	38.3	21 <b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
43	<a href="#">c1e3jA</a>	Alignment	not modelled	38.1	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp(h)-dependent ketose reductase; <b>PDBTitle:</b> ketose reductase (sorbitol dehydrogenase) from silverleaf2 whitefly
44	<a href="#">c2dfvB</a>	Alignment	not modelled	38.0	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable l-threonine 3-dehydrogenase; <b>PDBTitle:</b> hyperthermophilic threonine dehydrogenase from pyrococcus horikoshii
45	<a href="#">d3d37a2</a>	Alignment	not modelled	37.5	16 <b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
46	<a href="#">c4z6kD</a>	Alignment	not modelled	37.4	34 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase from the antarctic psychrophile moraxella sp.2 tae 123
47	<a href="#">c2yxxA</a>	Alignment	not modelled	37.3	16 <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)
48	<a href="#">c1r37B</a>	Alignment	not modelled	36.9	23 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase from sulfolobus solfataricus2 complexed with nad(h) and 2-ethoxyethanol
49	<a href="#">c1piwA</a>	Alignment	not modelled	36.6	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical zinc-type alcohol dehydrogenase- <b>PDBTitle:</b> apo and holo structures of an nadp(h)-dependent cinnamyl2 alcohol dehydrogenase from saccharomyces cerevisiae
50	<a href="#">c3ukoA</a>	Alignment	not modelled	36.6	29 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase class-3; <b>PDBTitle:</b> crystal structure of s-nitrosoglutathione reductase from arabidopsis2 thaliana, complex with nadh
51	<a href="#">c5ylnB</a>	Alignment	not modelled	36.4	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing; <b>PDBTitle:</b> zinc dependent alcohol dehydrogenase 2 from streptococcus pneumonia -2 apo form
52	<a href="#">c1lluD</a>	Alignment	not modelled	36.3	32 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> the ternary complex of pseudomonas aeruginosa alcohol2 dehydrogenase with its coenzyme and weak substrate
53	<a href="#">c1p0fA</a>	Alignment	not modelled	32.9	41 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of the binary complex: nadp(h)-dependent vertebrate2 alcohol dehydrogenase (adh8) with the cofactor nadp

54	<a href="#">c5x7nA</a>	Alignment	not modelled	32.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of meso-diaminopimelate decarboxylase (dapdc) from2 corynebacterium glutamicum
55	<a href="#">d1uufa1</a>	Alignment	not modelled	32.4	29	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
56	<a href="#">c1pl6A</a>	Alignment	not modelled	32.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sorbitol dehydrogenase; <b>PDBTitle:</b> human sdh/nadh/inhibitor complex
57	<a href="#">d1uija1</a>	Alignment	not modelled	32.3	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
58	<a href="#">c5h81A</a>	Alignment	not modelled	32.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> heteroyohimbine synthase thas2; <b>PDBTitle:</b> heteroyohimbine synthase thas2 from catharanthus roseus - complex with2 nadp+
59	<a href="#">c2xpfB</a>	Alignment	not modelled	32.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-amino-4-deoxychorismate lyase; <b>PDBTitle:</b> crystal structure of putative aminodeoxychorismate lyase2 from pseudomonas aeruginosa
60	<a href="#">c2o0tB</a>	Alignment	not modelled	30.7	20	<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
61	<a href="#">d2csja1</a>	Alignment	not modelled	30.6	31	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
62	<a href="#">c1kolA</a>	Alignment	not modelled	29.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of formaldehyde dehydrogenase
63	<a href="#">c4a2cB</a>	Alignment	not modelled	29.5	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> galactitol-1-phosphate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of galactitol-1-phosphate dehydrogenase from2 escherichia coli
64	<a href="#">c6otvA</a>	Alignment	not modelled	29.3	32	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative isomerase ybhh; <b>PDBTitle:</b> crystal structure of putative isomerase ec2056
65	<a href="#">c5vm2A</a>	Alignment	not modelled	29.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of eck1772, an oxidoreductase/dehydrogenase of2 unknown specificity involved in membrane biogenesis from escherichia3 coli
66	<a href="#">d1nxza1</a>	Alignment	not modelled	28.9	24	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Yggj N-terminal domain-like
67	<a href="#">c3g7kD</a>	Alignment	not modelled	28.6	36	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-methylitaconate isomerase; <b>PDBTitle:</b> crystal structure of methylitaconate-delta-isomerase
68	<a href="#">c1yqxB</a>	Alignment	not modelled	28.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sinapyl alcohol dehydrogenase; <b>PDBTitle:</b> sinapyl alcohol dehydrogenase at 2.5 angstrom resolution
69	<a href="#">c5kiaA</a>	Alignment	not modelled	28.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of l-threonine 3-dehydrogenase from burkholderia2 thailandensis
70	<a href="#">c4jbiB</a>	Alignment	not modelled	28.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase (zinc); <b>PDBTitle:</b> 2.35a resolution structure of nadph bound thermostable alcohol2 dehydrogenase from pyrobaculum aerophilum
71	<a href="#">d1uika1</a>	Alignment	not modelled	27.4	10	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
72	<a href="#">c4oaqA</a>	Alignment	not modelled	27.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> r-specific carbonyl reductase; <b>PDBTitle:</b> crystal structure of the r-specific carbonyl reductase from candida2 parapsilosis atcc 7330
73	<a href="#">d1pl8a1</a>	Alignment	not modelled	27.2	23	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
74	<a href="#">c2hcyD</a>	Alignment	not modelled	26.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase 1; <b>PDBTitle:</b> yeast alcohol dehydrogenase I, saccharomyces cerevisiae fermentative2 enzyme
75	<a href="#">c4j6fB</a>	Alignment	not modelled	26.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021, nysgrc-target 012230
76	<a href="#">c4rqUA</a>	Alignment	not modelled	26.4	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase crystal structure in complex with nad
77	<a href="#">d1iyea</a>	Alignment	not modelled	26.4	15	<b>Fold:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes <b>Superfamily:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes <b>Family:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes
78	<a href="#">c6c49A</a>	Alignment	not modelled	25.8	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of alcohol dehydrogenase from acinetobacter2 baumannii
79	<a href="#">c1uufA</a>	Alignment	not modelled	25.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc-type alcohol dehydrogenase-like protein <b>PDBTitle:</b> crystal structure of a zinc-type alcohol dehydrogenase-

						like2 protein yahk
80	<a href="#">d1ee6a_</a>	Alignment	not modelled	25.7	33	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Pectin lyase-like <b>Family:</b> Pectate lyase-like
81	<a href="#">d1uepa_</a>	Alignment	not modelled	25.7	21	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
82	<a href="#">c4ilkB_</a>	Alignment	not modelled	25.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> starvation sensing protein rspb; <b>PDBTitle:</b> crystal structure of short chain alcohol dehydrogenase (rspb) from e.2 coli cft073 (efi target efi-506413) complexed with cofactor nadh
83	<a href="#">c3cswB_</a>	Alignment	not modelled	25.1	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative branched-chain-amino-acid aminotransferase; <b>PDBTitle:</b> crystal structure of a putative branched-chain amino acid2 aminotransferase (tm0831) from thermotoga maritima at 2.15 a3 resolution
84	<a href="#">c1cdoB_</a>	Alignment	not modelled	25.0	22	<b>PDB header:</b> oxidoreductase (ch-oh(d)-nad(a)) <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase (e.c.1.1.1.1) (ee isozyme) complexed with2 nicotinamide adenine dinucleotide (nad), and zinc
85	<a href="#">c5fi5A_</a>	Alignment	not modelled	24.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydroalstonine synthase; <b>PDBTitle:</b> heteroyohimbine synthase thas1 from catharanthus roseus - apo form
86	<a href="#">d1ejia_</a>	Alignment	not modelled	24.2	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
87	<a href="#">c3ggeA_</a>	Alignment	not modelled	24.1	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> pdz domain-containing protein gipc2; <b>PDBTitle:</b> crystal structure of the pdz domain of pdz domain-containing protein2 gipc2
88	<a href="#">c2dphA_</a>	Alignment	not modelled	24.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dismutase; <b>PDBTitle:</b> crystal structure of formaldehyde dismutase
89	<a href="#">c2vvpA_</a>	Alignment	not modelled	24.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose dehydrogenase; <b>PDBTitle:</b> haloferax mediterranei glucose dehydrogenase in complex with nadph and2 zn.
90	<a href="#">c2phlC_</a>	Alignment	not modelled	23.8	15	<b>PDB header:</b> plant seed storage protein(vicilin) <b>Chain:</b> C: <b>PDB Molecule:</b> phaseolin; <b>PDBTitle:</b> the structure of phaseolin at 2.2 angstroms resolution: implications2 for a common vicilin(/slash)legumin structure and the genetic3 engineering of seed storage proteins
91	<a href="#">c4o6zC_</a>	Alignment	not modelled	23.8	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase with covalently2 bound plp schiff-base from plasmodium falciparum
92	<a href="#">c6ey6G_</a>	Alignment	not modelled	23.7	9	<b>PDB header:</b> protein transport <b>Chain:</b> G: <b>PDB Molecule:</b> t9ss component cytoplasmic membrane protein porm; <b>PDBTitle:</b> c-terminal part (residues 315-516) of porm with the llama nanobody2 nb130
93	<a href="#">c5cadA_</a>	Alignment	not modelled	23.6	18	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> sm80.1 vicilin; <b>PDBTitle:</b> crystal structure of the vicilin from solanum melongena revealed2 existence of different anionic ligands in structurally similar3 pockets
94	<a href="#">d1uija2</a>	Alignment	not modelled	23.5	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
95	<a href="#">d1dgwa_</a>	Alignment	not modelled	23.5	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
96	<a href="#">c3m6iA_</a>	Alignment	not modelled	23.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinitol 4-dehydrogenase; <b>PDBTitle:</b> l-arabinitol 4-dehydrogenase
97	<a href="#">c3uogB_</a>	Alignment	not modelled	23.5	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021
98	<a href="#">c3hu2C_</a>	Alignment	not modelled	23.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs
99	<a href="#">c1rjwA_</a>	Alignment	not modelled	23.3	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of nad(+)-dependent alcohol dehydrogenase2 from bacillus stearothermophilus strain lld-r
100	<a href="#">c6bb9A_</a>	Alignment	not modelled	23.2	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-amino-4-deoxychorismate lyase; <b>PDBTitle:</b> the crystal structure of 4-amino-4-deoxychorismate lyase from2 salmonella typhimurium lt2
101	<a href="#">c2p3eA_</a>	Alignment	not modelled	23.0	14	<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
102	<a href="#">d1kola1</a>	Alignment	not modelled	22.8	25	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
103	<a href="#">c3bk7A_</a>	Alignment	not modelled	22.7	25	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abc1/rnaase-l inhibitor protein from2 pyrococcus abyssi
104	<a href="#">d1kwaa_</a>	Alignment	not modelled	22.7	28	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain



105	<a href="#">c4qglA_</a>	Alignment	not modelled	22.7	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acireductone dioxygenase; <b>PDBTitle:</b> acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
106	<a href="#">c3qwbC_</a>	Alignment	not modelled	22.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> probable quinone oxidoreductase; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae zeta-crystallin-like2 quinone oxidoreductase zta1 complexed with nadph
107	<a href="#">c5ce8B_</a>	Alignment	not modelled	22.2	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> branched-chain amino acid aminotransferase; <b>PDBTitle:</b> crystal structure of branched-chain aminotransferase from thermophilic2 archaea thermoproteus uzoniensis
108	<a href="#">c1f8fA_</a>	Alignment	not modelled	22.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> benzyl alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of benzyl alcohol dehydrogenase from acinetobacter2 calcoaceticus
109	<a href="#">c2cf5A_</a>	Alignment	not modelled	22.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cinnamyl alcohol dehydrogenase; <b>PDBTitle:</b> crystal structures of the arabidopsis cinnamyl alcohol2 dehydrogenases, atcad5
110	<a href="#">c6gkrC_</a>	Alignment	not modelled	22.0	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> branched-chain-amino-acid aminotransferase; <b>PDBTitle:</b> crystal structure of branched-chain amino acid aminotransferase from2 thermobaculum terrenum in plp-form (holo-form)
111	<a href="#">c2qg1A_</a>	Alignment	not modelled	21.8	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> multiple pdz domain protein; <b>PDBTitle:</b> crystal structure of the 11th pdz domain of mpdz (mupp1)
112	<a href="#">c6bxgA_</a>	Alignment	not modelled	21.6	40	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> tail-specific protease; <b>PDBTitle:</b> 1.45 angstrom resolution crystal structure of pdz domain of carboxy-2 terminal protease from vibrio cholerae in complex with peptide.
113	<a href="#">c4f0qA_</a>	Alignment	not modelled	21.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> restriction endonuclease; <b>PDBTitle:</b> mspji restriction endonuclease - p21 form
114	<a href="#">c4f0qC_</a>	Alignment	not modelled	21.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> restriction endonuclease; <b>PDBTitle:</b> mspji restriction endonuclease - p21 form
115	<a href="#">d2f4pa1</a>	Alignment	not modelled	21.1	30	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> TM1287-like
116	<a href="#">c3cosD_</a>	Alignment	not modelled	21.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase 4; <b>PDBTitle:</b> crystal structure of human class ii alcohol dehydrogenase (adh4) in2 complex with nad and zn
117	<a href="#">d1f3ta1</a>	Alignment	not modelled	21.0	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
118	<a href="#">c5bwaA_</a>	Alignment	not modelled	20.8	23	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of odc-plp-az1 ternary complex
119	<a href="#">d1mfga_</a>	Alignment	not modelled	20.8	37	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
120	<a href="#">d1a8pa1</a>	Alignment	not modelled	20.6	17	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like