





























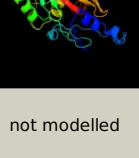


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0482_(murB)_570542_571651
Date	Tue Jul 23 14:50:56 BST 2019
Unique Job ID	57787f80d072d317

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5jzxB_</a>	 Alignment		100.0	97	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylenolpyruvoylglucosamine reductase; <b>PDBTitle:</b> crystal structure of udp-n-acetylenolpyruvoylglucosamine reductase2 (murb) from mycobacterium tuberculosis
2	<a href="#">c3i99A_</a>	 Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylenolpyruvoylglucosamine reductase; <b>PDBTitle:</b> the crystal structure of the udp-n-acetylenolpyruvoylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
3	<a href="#">c1mbbA_</a>	 Alignment		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uridine diphospho-n-acetylenolpyruvoylglucosamine <b>PDBTitle:</b> oxidoreductase
4	<a href="#">c4jayC_</a>	 Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylenolpyruvoylglucosamine reductase; <b>PDBTitle:</b> crystal structure of p. aeruginosa murB in complex with nadp+
5	<a href="#">c1hskA_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylenolpyruvoylglucosamine reductase; <b>PDBTitle:</b> crystal structure of s. aureus murB
6	<a href="#">c4pytA_</a>	 Alignment		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylenolpyruvoylglucosamine reductase; <b>PDBTitle:</b> crystal structure of a murB family ep-udp-n-acetylglucosamine2 reductase
7	<a href="#">c2gquA_</a>	 Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylenolpyruvoylglucosamine reductase; <b>PDBTitle:</b> crystal structure of udp-n-acetylenolpyruvoylglucosamine2 reductase (murb) from thermus caldophilus
8	<a href="#">d1luxy2</a>	 Alignment		100.0	39	<b>Fold:</b> Uridine diphospho-N-Acetylenolpyruvoylglucosamine reductase, MurB, C-terminal domain <b>Superfamily:</b> Uridine diphospho-N-Acetylenolpyruvoylglucosamine reductase, MurB, C-terminal domain <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvoylglucosamine reductase, MurB, C-terminal domain
9	<a href="#">d1luxy1</a>	 Alignment		100.0	27	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvoylglucosamine reductase (MurB), N-terminal domain
10	<a href="#">d1hskA1</a>	 Alignment		100.0	32	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvoylglucosamine reductase (MurB), N-terminal domain
11	<a href="#">d1hskA2</a>	 Alignment		100.0	37	<b>Fold:</b> Uridine diphospho-N-Acetylenolpyruvoylglucosamine reductase, MurB, C-terminal domain <b>Superfamily:</b> Uridine diphospho-N-Acetylenolpyruvoylglucosamine reductase, MurB, C-terminal domain <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvoylglucosamine reductase, MurB, C-terminal domain

12	<a href="#">c4ml8C_</a>	Alignment		99.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> cytokinin oxidase 2; <b>PDBTitle:</b> structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
13	<a href="#">c4oa1B_</a>	Alignment		99.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytokinin dehydrogenase 4; <b>PDBTitle:</b> crystal structure of maize cytokinin oxidase/dehydrogenase 4 (zmcko4)2 in complex with phenylurea inhibitor cppu in alternative spacegroup
14	<a href="#">c3fwaA_</a>	Alignment		99.5	15	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> reticuline oxidase; <b>PDBTitle:</b> structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
15	<a href="#">d1wvfa2</a>	Alignment		99.5	17	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> FAD-linked oxidases, N-terminal domain
16	<a href="#">c4ud8B_</a>	Alignment		99.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fad-binding and bbe domain-containing protein; <b>PDBTitle:</b> atbbe15
17	<a href="#">c3vteA_</a>	Alignment		99.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydrocannabinolic acid synthase; <b>PDBTitle:</b> crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
18	<a href="#">c5d79B_</a>	Alignment		99.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> berberine bridge enzyme-like protein; <b>PDBTitle:</b> structure of bbe-like #28 from arabidopsis thaliana
19	<a href="#">c3w8wA_</a>	Alignment		99.5	21	<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
20	<a href="#">c1zr6A_</a>	Alignment		99.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucooligosaccharide oxidase; <b>PDBTitle:</b> the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
21	<a href="#">c6eo5A_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ppbbe-like 1 d396n; <b>PDBTitle:</b> physcomitrella patens bbe-like 1 variant d396n
22	<a href="#">c2bvfa_</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> oxidase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-hydroxy-d-nicotine oxidase; <b>PDBTitle:</b> crystal structure of 6-hydroxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
23	<a href="#">c3d2hA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> berberine bridge-forming enzyme; <b>PDBTitle:</b> structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
24	<a href="#">c4bc9C_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> alkyldihydroxyacetonephosphate synthase, peroxisomal; <b>PDBTitle:</b> mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl
25	<a href="#">c3tsja_</a>	Alignment	not modelled	99.4	16	<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 phl p 4, a grass pollen allergen with glucose2 dehydrogenase activity
26	<a href="#">c6f73B_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> mtvao615; <b>PDBTitle:</b> crystal structure of vao-type flavoprotein mtvao615 at ph 5.0 from2 myceliophthora thermophila c1
27	<a href="#">c1i19B_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> crystal structure of cholesterol oxidase from b.sterolicum
28	<a href="#">c3pm9A_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution

29	<a href="#">c5l6fA_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad linked oxidase-like protein; <b>PDBTitle:</b> xylooligosaccharide oxidase from myceliophthora thermophila c1 in2 complex with xylobiose
30	<a href="#">c3bw7A_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytokinin dehydrogenase 1; <b>PDBTitle:</b> maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
31	<a href="#">c1wveB_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-cresol dehydrogenase [hydroxylating] <b>PDBTitle:</b> p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
32	<a href="#">c2uuvC_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> alkyldihydroxyacetonephosphate synthase; <b>PDBTitle:</b> alkyldihydroxyacetonephosphate synthase in p1
33	<a href="#">c4fdoA_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase dpre1; <b>PDBTitle:</b> mycobacterium tuberculosis dpre1 in complex with ct319
34	<a href="#">c6c80B_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cytokinin oxidase luckx1.1; <b>PDBTitle:</b> crystal structure of a flax cytokinin oxidase
35	<a href="#">c5i1wD_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> crmK; <b>PDBTitle:</b> crystal structure of crmK, a flavoenzyme involved in the shunt product2 recycling mechanism in caerulomycin biosynthesis
36	<a href="#">c2wdwB_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative hexose oxidase; <b>PDBTitle:</b> the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
37	<a href="#">d2i0ka2</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> FAD-linked oxidases, N-terminal domain
38	<a href="#">c3js8A_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> solvent-stable cholesterol oxidase
39	<a href="#">d1w1oa2</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> FAD-linked oxidases, N-terminal domain
40	<a href="#">c2exrA_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytokinin dehydrogenase 7; <b>PDBTitle:</b> x-ray structure of cytokinin oxidase/dehydrogenase (ckx) from2 arabidopsis thaliana at5g21482
41	<a href="#">c5fxpA_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol oxidase; <b>PDBTitle:</b> crystal structure of eugenol oxidase in complex with2 vanillin
42	<a href="#">c1ahuB_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> flavoenzyme <b>Chain:</b> B: <b>PDB Molecule:</b> vanillyl-alcohol oxidase; <b>PDBTitle:</b> structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
43	<a href="#">d1e8ga2</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> FAD-linked oxidases, N-terminal domain
44	<a href="#">c6f74B_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol oxidase; <b>PDBTitle:</b> crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1
45	<a href="#">c3popD_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> gilr oxidase; <b>PDBTitle:</b> the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
46	<a href="#">c3rjaA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate oxidase; <b>PDBTitle:</b> crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue
47	<a href="#">c2y3rC_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tamI; <b>PDBTitle:</b> structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 tamI in p21 space group
48	<a href="#">c2vfvA_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xylitol oxidase; <b>PDBTitle:</b> alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
49	<a href="#">c2ipiD_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> aclacinomycin oxidoreductase (aknox); <b>PDBTitle:</b> crystal structure of aclacinomycin oxidoreductase
50	<a href="#">c1f0xA_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme.
51	<a href="#">d1f0xa2</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> FAD-linked oxidases, N-terminal domain
52	<a href="#">d1ffvc2</a>	Alignment	not modelled	98.4	23	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CO dehydrogenase flavoprotein N-terminal domain-like
53	<a href="#">d3b9jb2</a>	Alignment	not modelled	98.3	14	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CO dehydrogenase flavoprotein N-terminal domain-like
54	<a href="#">d1v97a6</a>	Alignment	not modelled	98.2	15	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CO dehydrogenase flavoprotein N-terminal domain-like
						<b>Fold:</b> FAD-binding/transporter-associated domain-like

55	<a href="#">d1n62c2</a>	Alignment	not modelled	98.2	19	<b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CO dehydrogenase flavoprotein N-terminal domain-like
56	<a href="#">c1t3qF_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> quinoline 2-oxidoreductase medium subunit; <b>PDBTitle:</b> crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
57	<a href="#">c1ffuF_</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cutm, flavoprotein of carbon monoxide <b>PDBTitle:</b> carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
58	<a href="#">c1n62C_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carbon monoxide dehydrogenase medium chain; <b>PDBTitle:</b> crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
59	<a href="#">c2yvsA_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycolate oxidase subunit glce; <b>PDBTitle:</b> crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
60	<a href="#">c4zohB_</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase fad-binding subunit; <b>PDBTitle:</b> crystal structure of glyceraldehyde oxidoreductase
61	<a href="#">c3etrM_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> xanthine dehydrogenase/oxidase; <b>PDBTitle:</b> crystal structure of xanthine oxidase in complex with lumazine
62	<a href="#">c3hrdC_</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinate dehydrogenase fad-subunit; <b>PDBTitle:</b> crystal structure of nicotinate dehydrogenase
63	<a href="#">c5g5hB_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative xanthine dehydrogenase yags fad-binding subunit; <b>PDBTitle:</b> escherichia coli periplasmic aldehyde oxidase r440h mutant
64	<a href="#">c3b9jl_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> xanthine oxidase; <b>PDBTitle:</b> structure of xanthine oxidase with 2-hydroxy-6-methylpurine
65	<a href="#">d1t3qc2</a>	Alignment	not modelled	97.5	21	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CO dehydrogenase flavoprotein N-terminal domain-like
66	<a href="#">c5y6qB_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde oxidase medium subunit; <b>PDBTitle:</b> crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
67	<a href="#">c1wygA_</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xanthine dehydrogenase/oxidase; <b>PDBTitle:</b> crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
68	<a href="#">c1rm6E_</a>	Alignment	not modelled	97.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxybenzoyl-coa reductase beta subunit; <b>PDBTitle:</b> structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
69	<a href="#">c2w3rG_</a>	Alignment	not modelled	96.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> xanthine dehydrogenase; <b>PDBTitle:</b> crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
70	<a href="#">d1rm6b2</a>	Alignment	not modelled	96.8	21	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CO dehydrogenase flavoprotein N-terminal domain-like
71	<a href="#">d1jroa4</a>	Alignment	not modelled	96.4	15	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CO dehydrogenase flavoprotein N-terminal domain-like
72	<a href="#">c4uhxA_</a>	Alignment	not modelled	95.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde oxidase; <b>PDBTitle:</b> human aldehyde oxidase in complex with phthalazine and thioridazine
73	<a href="#">c3zyvA_</a>	Alignment	not modelled	91.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aox3; <b>PDBTitle:</b> crystal structure of the mouse liver aldehyde oxidase 3 (maox3)
74	<a href="#">c4ql6A_</a>	Alignment	not modelled	39.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxy-terminal processing protease; <b>PDBTitle:</b> structure of c. trachomatis ct441
75	<a href="#">d2pgca1</a>	Alignment	not modelled	37.1	32	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Marine metagenome family DABB3
76	<a href="#">c3mt1B_</a>	Alignment	not modelled	31.1	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative carboxynorspermidine decarboxylase protein; <b>PDBTitle:</b> crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
77	<a href="#">c2r47C_</a>	Alignment	not modelled	30.1	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein mth_862; <b>PDBTitle:</b> crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
78	<a href="#">c3eebB_</a>	Alignment	not modelled	28.0	21	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> rtx toxin rtxa; <b>PDBTitle:</b> structure of the v. cholerae rtx cysteine protease domain
79	<a href="#">c3uz0A_</a>	Alignment	not modelled	27.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein ah; <b>PDBTitle:</b> crystal structure of spoIIAh and spoIIQ complex
						<b>PDB header:</b> signaling protein

80	<a href="#">c3tufA_</a>	Alignment	not modelled	25.9	13	<b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein ah; <b>PDBTitle:</b> structure of the spoIIQ-spoIIiAh pore forming complex.
81	<a href="#">c3fzyA_</a>	Alignment	not modelled	24.1	18	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> rtx toxin rtxa; <b>PDBTitle:</b> crystal structure of pre-cleavage form of cysteine protease domain2 from vibrio cholerae rtxa toxin
82	<a href="#">c2yxxA_</a>	Alignment	not modelled	24.0	37	<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)
83	<a href="#">c3n29A_</a>	Alignment	not modelled	23.2	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxynorspermidine decarboxylase; <b>PDBTitle:</b> crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
84	<a href="#">c3dfeA_</a>	Alignment	not modelled	18.7	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative pii-like signaling protein; <b>PDBTitle:</b> crystal structure of a putative pii-like signaling protein2 (yp_323533.1) from anabaena variabilis atcc 29413 at 2.35 a3 resolution
85	<a href="#">d1vrma1</a>	Alignment	not modelled	18.4	21	<b>Fold:</b> T-fold <b>Superfamily:</b> ApbE-like <b>Family:</b> ApbE-like
86	<a href="#">d1pbaa_</a>	Alignment	not modelled	17.2	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
87	<a href="#">c6n2fB_</a>	Alignment	not modelled	17.1	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelate decarboxylase 2, chloroplastic; <b>PDBTitle:</b> meso-diaminopimelate decarboxylase from arabidopsis thaliana (isoform2 2)
88	<a href="#">d1rlka_</a>	Alignment	not modelled	16.4	10	<b>Fold:</b> Peptidyl-tRNA hydrolase II <b>Superfamily:</b> Peptidyl-tRNA hydrolase II <b>Family:</b> Peptidyl-tRNA hydrolase II
89	<a href="#">c3iwfA_</a>	Alignment	not modelled	15.3	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
90	<a href="#">c3ih1A_</a>	Alignment	not modelled	15.3	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
91	<a href="#">d1hkva1</a>	Alignment	not modelled	14.9	26	<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
92	<a href="#">c2gq8A_</a>	Alignment	not modelled	14.7	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, fmn-binding; <b>PDBTitle:</b> structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
93	<a href="#">c2j66A_</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> btrk; <b>PDBTitle:</b> structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
94	<a href="#">c2grvC_</a>	Alignment	not modelled	14.4	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> lpqw; <b>PDBTitle:</b> crystal structure of lpqw
95	<a href="#">c1xtyD_</a>	Alignment	not modelled	13.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus peptidyl-trna hydrolase
96	<a href="#">d1goua_</a>	Alignment	not modelled	13.7	25	<b>Fold:</b> Microbial ribonucleases <b>Superfamily:</b> Microbial ribonucleases <b>Family:</b> Bacterial ribonucleases
97	<a href="#">c3jb9M_</a>	Alignment	not modelled	13.6	34	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> M: <b>PDB Molecule:</b> pre-mrna-processing protein 45; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
98	<a href="#">c3gquA_</a>	Alignment	not modelled	12.9	52	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nop5p protein; <b>PDBTitle:</b> pyrococcus horikoshii nop5 rna binding domain
99	<a href="#">c2l1nA_</a>	Alignment	not modelled	12.8	43	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of the protein yp_399305.1