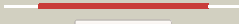



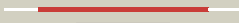




























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1726_(-)_1951859_1953244
Date	Fri Aug 2 13:30:33 BST 2019
Unique Job ID	74c19a30b34ef0e0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3w8wA_</a>	 Alignment		100.0	41	<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
2	<a href="#">c2bvfa_</a>	 Alignment		100.0	29	<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)
3	<a href="#">c6eo5A_</a>	 Alignment		100.0	21	<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
4	<a href="#">c5l6fa_</a>	 Alignment		100.0	20	<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
5	<a href="#">c3t5ja_</a>	 Alignment		100.0	23	<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
6	<a href="#">c3rjaA_</a>	 Alignment		100.0	20	<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
7	<a href="#">c3vteA_</a>	 Alignment		100.0	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
8	<a href="#">c4ud8B_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> fad-binding and bbe domain-containing protein; <b>PDBTitle:</b> atbbe15
9	<a href="#">c1zr6A_</a>	 Alignment		100.0	22	<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
10	<a href="#">c5d79B_</a>	 Alignment		100.0	22	<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
11	<a href="#">c3d2ha_</a>	 Alignment		100.0	21	<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

12	<a href="#">c2ipiD_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> aclacinomycin oxidoreductase (aknox); <b>PDBTitle:</b> crystal structure of aclacinomycin oxidoreductase
13	<a href="#">c3fwaA_</a>	Alignment		100.0	21	<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
14	<a href="#">c2wdwB_</a>	Alignment		100.0	24	<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
15	<a href="#">c5j1wD_</a>	Alignment		100.0	23	<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
16	<a href="#">c4bc9C_</a>	Alignment		100.0	13	<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
17	<a href="#">c3popD_</a>	Alignment		100.0	24	<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
18	<a href="#">c3bw7A_</a>	Alignment		100.0	15	<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
19	<a href="#">c4oa1B_</a>	Alignment		100.0	19	<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
20	<a href="#">c2y3rC_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tam1; <b>PDBTitle:</b> structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 tam1 in p21 space group
21	<a href="#">c4ml8C_</a>	Alignment	not modelled	100.0	17	<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)
22	<a href="#">c6f73B_</a>	Alignment	not modelled	100.0	19	<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
23	<a href="#">c3pm9A_</a>	Alignment	not modelled	100.0	15	<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
24	<a href="#">c6f74B_</a>	Alignment	not modelled	100.0	17	<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
25	<a href="#">c6c80B_</a>	Alignment	not modelled	100.0	18	<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
26	<a href="#">c1wveB_</a>	Alignment	not modelled	100.0	15	<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
27	<a href="#">c2exrA_</a>	Alignment	not modelled	100.0	17	<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
28	<a href="#">c5fxpA_</a>	Alignment	not modelled	100.0	13	<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

29	<a href="#">c1ahuB</a>	Alignment	not modelled	100.0	15	<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
30	<a href="#">c4fdoA</a>	Alignment	not modelled	100.0	17	<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
31	<a href="#">c2vfvA</a>	Alignment	not modelled	100.0	17	<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
32	<a href="#">c1i19B</a>	Alignment	not modelled	100.0	11	<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
33	<a href="#">c2uuvC</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> alkyldihydroxyacetonephosphate synthase; <b>PDBTitle:</b> alkyldihydroxyacetonephosphate synthase in p1
34	<a href="#">c3js8A</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> solvent-stable cholesterol oxidase
35	<a href="#">c1f0xA</a>	Alignment	not modelled	100.0	15	<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.
36	<a href="#">d1w1oa2</a>	Alignment	not modelled	100.0	23	<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
37	<a href="#">d1e8ga2</a>	Alignment	not modelled	100.0	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
38	<a href="#">d1wvfa2</a>	Alignment	not modelled	100.0	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
39	<a href="#">d2i0ka2</a>	Alignment	not modelled	100.0	12	<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="#">d1f0xa2</a>	Alignment	not modelled	100.0	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
41	<a href="#">d1luxya1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
42	<a href="#">d1hskA1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
43	<a href="#">c4pytA</a>	Alignment	not modelled	100.0	17	<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
44	<a href="#">c1hskA</a>	Alignment	not modelled	99.9	17	<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
45	<a href="#">c4jayC</a>	Alignment	not modelled	99.9	18	<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+
46	<a href="#">c1mbbA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uridine diphospho-n-acetylenolpyruvoylglucosamine <b>PDBTitle:</b> oxidoreductase
47	<a href="#">c2yvsA</a>	Alignment	not modelled	99.9	15	<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
48	<a href="#">c3i99A</a>	Alignment	not modelled	99.9	14	<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
49	<a href="#">c5jzxB</a>	Alignment	not modelled	99.9	24	<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
50	<a href="#">c2gquA</a>	Alignment	not modelled	99.8	19	<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
51	<a href="#">d1e8ga1</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
52	<a href="#">d1wvfa1</a>	Alignment	not modelled	99.1	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
53	<a href="#">d1w1oa1</a>	Alignment	not modelled	98.8	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Cytokinin dehydrogenase 1

54	<a href="#">d1f0xa1</a>	Alignment	not modelled	98.0	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> D-lactate dehydrogenase
55	<a href="#">d2i0ka1</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Cholesterol oxidase
56	<a href="#">c1n62C_</a>	Alignment	not modelled	97.0	18	<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
57	<a href="#">c1ffuF_</a>	Alignment	not modelled	97.0	13	<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="#">d1ffvc2</a>	Alignment	not modelled	96.9	13	<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
59	<a href="#">c1t3qF_</a>	Alignment	not modelled	96.9	17	<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
60	<a href="#">c3etrM_</a>	Alignment	not modelled	96.8	6	<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
61	<a href="#">c3b9jj_</a>	Alignment	not modelled	96.8	6	<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
62	<a href="#">c3hrdC_</a>	Alignment	not modelled	96.8	12	<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="#">d1n62c2</a>	Alignment	not modelled	96.7	19	<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
64	<a href="#">d1v97a6</a>	Alignment	not modelled	96.7	5	<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
65	<a href="#">c5g5hB_</a>	Alignment	not modelled	96.5	12	<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
66	<a href="#">d3b9jb2</a>	Alignment	not modelled	96.4	6	<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
67	<a href="#">c4zohB_</a>	Alignment	not modelled	96.3	7	<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
68	<a href="#">d1t3qc2</a>	Alignment	not modelled	96.2	13	<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
69	<a href="#">c5y6qB_</a>	Alignment	not modelled	96.0	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
70	<a href="#">c1rm6E_</a>	Alignment	not modelled	95.8	21	<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
71	<a href="#">d1jroa4</a>	Alignment	not modelled	95.7	20	<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="#">d1rm6b2</a>	Alignment	not modelled	95.2	20	<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
73	<a href="#">c1wygA_</a>	Alignment	not modelled	95.1	5	<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)
74	<a href="#">c2w3rG_</a>	Alignment	not modelled	94.4	17	<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
75	<a href="#">c4uhxA_</a>	Alignment	not modelled	94.0	12	<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
76	<a href="#">c3zyvA_</a>	Alignment	not modelled	90.3	7	<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)
77	<a href="#">c2vkhH_</a>	Alignment	not modelled	87.9	19	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> fatty acid synthase subunit beta; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
78	<a href="#">c2uval_</a>	Alignment	not modelled	85.2	17	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> fatty acid synthase beta subunits; <b>PDBTitle:</b> crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4

						crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
79	<a href="#">c5vbgA</a>	Alignment	not modelled	72.8	7	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein activator lpoa; <b>PDBTitle:</b> crystal structure of full-length lpoa, monoclinic form 1, from2 haemophilus influenzae
80	<a href="#">d1jaka1</a>	Alignment	not modelled	68.6	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
81	<a href="#">c6je8A</a>	Alignment	not modelled	68.6	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> crystal structure of a beta-n-acetylhexosaminidase
82	<a href="#">c5oarB</a>	Alignment	not modelled	68.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-hexosaminidase; <b>PDBTitle:</b> crystal structure of native beta-n-acetylhexosaminidase isolated from2 aspergillus oryzae
83	<a href="#">c4h04B</a>	Alignment	not modelled	67.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lacto-n-biosidase; <b>PDBTitle:</b> lacto-n-biosidase from bifidobacterium bifidum
84	<a href="#">d1yhta1</a>	Alignment	not modelled	67.2	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
85	<a href="#">c2yl8A</a>	Alignment	not modelled	65.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
86	<a href="#">d1qbaa3</a>	Alignment	not modelled	64.8	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
87	<a href="#">c3nsnA</a>	Alignment	not modelled	64.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosaminidase; <b>PDBTitle:</b> crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
88	<a href="#">d2qjxa1</a>	Alignment	not modelled	64.8	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
89	<a href="#">d1nowa1</a>	Alignment	not modelled	64.8	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
90	<a href="#">c2ylaA</a>	Alignment	not modelled	63.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
91	<a href="#">c1m04A</a>	Alignment	not modelled	63.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnc)
92	<a href="#">c1nouA</a>	Alignment	not modelled	63.7	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-hexosaminidase beta chain; <b>PDBTitle:</b> native human lysosomal beta-hexosaminidase isoform b
93	<a href="#">c3gh7A</a>	Alignment	not modelled	63.4	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-hexosaminidase; <b>PDBTitle:</b> crystal structure of beta-hexosaminidase from paenibacillus sp. ts122 in complex with galnac
94	<a href="#">c3rcnA</a>	Alignment	not modelled	63.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aureus
95	<a href="#">c2qjxE</a>	Alignment	not modelled	61.7	29	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> beta-hexosaminidase alpha chain; <b>PDBTitle:</b> crystallographic structure of human beta-hexosaminidase a
96	<a href="#">c6ezrA</a>	Alignment	not modelled	61.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylglucosaminidase nag2; <b>PDBTitle:</b> crystal structure of gh20 exo beta-n-acetylglucosaminidase from vibrio2 harveyi
97	<a href="#">c3lmyA</a>	Alignment	not modelled	59.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-hexosaminidase subunit beta; <b>PDBTitle:</b> the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
98	<a href="#">c4pysB</a>	Alignment	not modelled	58.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> the crystal structure of beta-n-acetylhexosaminidase from bacteroides2 fragilis nctc 9343
99	<a href="#">c3rpmA</a>	Alignment	not modelled	58.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetyl-hexosaminidase; <b>PDBTitle:</b> crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
100	<a href="#">c1qbaA</a>	Alignment	not modelled	56.8	10	<b>PDB header:</b> glycosyl hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitobiase; <b>PDBTitle:</b> bacterial chitobiase, glycosyl hydrolase family 20
101	<a href="#">c4fukB</a>	Alignment	not modelled	56.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> aminopeptidase from trypanosoma brucei
102	<a href="#">c1qupA</a>	Alignment	not modelled	53.4	6	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase 1 copper chaperone; <b>PDBTitle:</b> crystal structure of the copper chaperone for superoxide dismutase
103	<a href="#">c2gvsA</a>	Alignment	not modelled	52.3	29	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemosensory protein csp-sg4; <b>PDBTitle:</b> nmr solution structure of cspsg4
104	<a href="#">c2epoB</a>	Alignment	not modelled	50.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetyl-beta-d-glucosaminidase; <b>PDBTitle:</b> n-acetyl-b-d-glucosaminidase (gcna) from streptococcus



						gordonii
105	<a href="#">d1ik6a1</a>	Alignment	not modelled	50.5	7	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
106	<a href="#">d1umdb1</a>	Alignment	not modelled	48.5	11	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
107	<a href="#">d1n8va_</a>	Alignment	not modelled	47.5	24	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Chemosensory protein Csp2 <b>Family:</b> Chemosensory protein Csp2
108	<a href="#">c1jk9D_</a>	Alignment	not modelled	47.4	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> copper chaperone for superoxide dismutase; <b>PDBTitle:</b> heterodimer between h48f-ysod1 and yccs
109	<a href="#">d1kx9b_</a>	Alignment	not modelled	47.1	24	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Chemosensory protein Csp2 <b>Family:</b> Chemosensory protein Csp2
110	<a href="#">c4wbxC_</a>	Alignment	not modelled	44.2	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-keto acid:ferredoxin oxidoreductase subunit alpha; <b>PDBTitle:</b> conserved hypothetical protein pf1771 from pyrococcus furiosus solved2 by sulfur sad using swiss light source data
111	<a href="#">c6nhlB_</a>	Alignment	not modelled	43.5	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 7-carboxy-7-deazaguanine synthase; <b>PDBTitle:</b> crystal structure of quee from escherichia coli
112	<a href="#">d1poib_</a>	Alignment	not modelled	43.4	19	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase beta subunit-like
113	<a href="#">d1w85b1</a>	Alignment	not modelled	41.9	11	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
114	<a href="#">d2r8oa1</a>	Alignment	not modelled	41.1	11	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
115	<a href="#">d1qupa2</a>	Alignment	not modelled	40.6	6	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
116	<a href="#">d1itza2</a>	Alignment	not modelled	40.2	7	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
117	<a href="#">c3eafA_</a>	Alignment	not modelled	40.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate binding protein; <b>PDBTitle:</b> crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
118	<a href="#">c3komB_</a>	Alignment	not modelled	39.4	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of apo transketolase from francisella tularensis
119	<a href="#">c2yswB_</a>	Alignment	not modelled	39.2	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinatase; <b>PDBTitle:</b> crystal structure of the 3-dehydroquinatase dehydratase from aquifex2 aeolicus vf5
120	<a href="#">c2crlA_</a>	Alignment	not modelled	39.0	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> copper chaperone for superoxide dismutase; <b>PDBTitle:</b> the apo form of hma domain of copper chaperone for2 superoxide dismutase