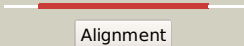

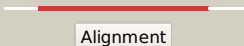

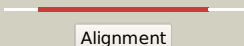







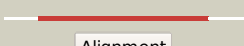











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2280_(-)_2551570_2552949
Date	Mon Aug 5 13:25:42 BST 2019
Unique Job ID	f3c6657065ac470f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3pm9A_</a>	 Alignment		100.0	29	<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
2	<a href="#">c4bc9C_</a>	 Alignment		100.0	19	<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
3	<a href="#">c1wveB_</a>	 Alignment		100.0	18	<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
4	<a href="#">c5fxpA_</a>	 Alignment		100.0	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
5	<a href="#">c3bw7A_</a>	 Alignment		100.0	16	<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
6	<a href="#">c1ahuB_</a>	 Alignment		100.0	19	<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
7	<a href="#">c4oalB_</a>	 Alignment		100.0	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
8	<a href="#">c4ml8C_</a>	 Alignment		100.0	16	<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)
9	<a href="#">c2uuuC_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> alkyldihydroxyacetonephosphate synthase; <b>PDBTitle:</b> alkyldihydroxyacetonephosphate synthase in p1
10	<a href="#">c1f0xA_</a>	 Alignment		100.0	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.
11	<a href="#">c2exrA_</a>	 Alignment		100.0	19	<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

12	<a href="#">c6c80B_</a>	Alignment		100.0	17	<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
13	<a href="#">c3vteA_</a>	Alignment		100.0	15	<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
14	<a href="#">c6f74B_</a>	Alignment		100.0	14	<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
15	<a href="#">c3w8wA_</a>	Alignment		100.0	17	<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
16	<a href="#">c2bvfa_</a>	Alignment		100.0	19	<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)
17	<a href="#">c4ud8B_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fad-binding and bbe domain-containing protein; <b>PDBTitle:</b> atbbe15
18	<a href="#">c3tsja_</a>	Alignment		100.0	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
19	<a href="#">c3rjaA_</a>	Alignment		100.0	13	<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
20	<a href="#">c6eo5A_</a>	Alignment		100.0	14	<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
21	<a href="#">c5l6fA_</a>	Alignment	not modelled	100.0	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
22	<a href="#">c6f73B_</a>	Alignment	not modelled	100.0	15	<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="#">c1zr6A_</a>	Alignment	not modelled	100.0	18	<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
24	<a href="#">c4fdoA_</a>	Alignment	not modelled	100.0	15	<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
25	<a href="#">c2vfvA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xylylitol oxidase; <b>PDBTitle:</b> alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
26	<a href="#">c3fwaA_</a>	Alignment	not modelled	100.0	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
27	<a href="#">c3d2ha_</a>	Alignment	not modelled	100.0	16	<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
28	<a href="#">c3popD_</a>	Alignment	not modelled	100.0	14	<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 gilyvocarcin biosynthesis

29	<a href="#">c5d79B_</a>	Alignment	not modelled	100.0	15	<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
30	<a href="#">c5i1wD_</a>	Alignment	not modelled	100.0	13	<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
31	<a href="#">c2ipiD_</a>	Alignment	not modelled	100.0	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
32	<a href="#">c2y3rC_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> taml; <b>PDBTitle:</b> structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 taml in p21 space group
33	<a href="#">c2wdwB_</a>	Alignment	not modelled	100.0	14	<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
34	<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
35	<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
36	<a href="#">d1wvfa2</a>	Alignment	not modelled	100.0	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
37	<a href="#">d1e8ga2</a>	Alignment	not modelled	100.0	24	<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="#">d1w1oa2</a>	Alignment	not modelled	100.0	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
39	<a href="#">d1f0xa2</a>	Alignment	not modelled	100.0	22	<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="#">d2i0ka2</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="#">d1hska1</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> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
42	<a href="#">d1uxya1</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
43	<a href="#">c4pytA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylenolpyruvylglucosamine reductase; <b>PDBTitle:</b> crystal structure of a murb family ep-udp-n-acetylglucosamine2 reductase
44	<a href="#">c1hska_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylenolpyruvylglucosamine reductase; <b>PDBTitle:</b> crystal structure of s. aureus murb
45	<a href="#">c4jayC_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylenolpyruvylglucosamine reductase; <b>PDBTitle:</b> crystal structure of p. aeruginosa murb in complex with nadp+
46	<a href="#">c2yvsA_</a>	Alignment	not modelled	99.9	33	<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
47	<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-acetylenolpyruvylglucosamine <b>PDBTitle:</b> oxidoreductase
48	<a href="#">c3i99A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylenolpyruvylglucosamine reductase; <b>PDBTitle:</b> the crystal structure of the udp-n-acetylenolpyruvylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
49	<a href="#">c5jzxB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylenolpyruvylglucosamine reductase; <b>PDBTitle:</b> crystal structure of udp-n-acetylenolpyruvylglucosamine reductase2 (murb) from mycobacterium tuberculosis
50	<a href="#">d1e8ga1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
51	<a href="#">d1wvfa1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
52	<a href="#">d1f0xa1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> D-lactate dehydrogenase
53	<a href="#">c2gqaA_</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylenolpyruvylglucosamine reductase; <b>PDBTitle:</b> crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus <b>Fold:</b> Ferredoxin-like

54	<a href="#">d1w1oa1</a>	Alignment	not modelled	99.3	16	<b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Cytokinin dehydrogenase 1
55	<a href="#">d1ffvc2</a>	Alignment	not modelled	97.4	17	<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
56	<a href="#">c5y6qB</a>	Alignment	not modelled	97.3	19	<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
57	<a href="#">c1ffuF</a>	Alignment	not modelled	97.2	17	<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="#">d1v97a6</a>	Alignment	not modelled	97.1	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="#">c1n62C</a>	Alignment	not modelled	97.1	16	<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
60	<a href="#">d3b9jb2</a>	Alignment	not modelled	97.1	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
61	<a href="#">c1t3qF</a>	Alignment	not modelled	97.0	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
62	<a href="#">c3etrM</a>	Alignment	not modelled	96.9	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
63	<a href="#">c3b9jl</a>	Alignment	not modelled	96.9	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
64	<a href="#">c3hrdC</a>	Alignment	not modelled	96.9	16	<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
65	<a href="#">d1t3qc2</a>	Alignment	not modelled	96.7	17	<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="#">d1n62c2</a>	Alignment	not modelled	96.6	16	<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	96.5	10	<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="#">c1rm6E</a>	Alignment	not modelled	96.4	17	<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="#">c5g5hB</a>	Alignment	not modelled	96.3	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
70	<a href="#">d1jroa4</a>	Alignment	not modelled	96.2	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="#">c2w3rG</a>	Alignment	not modelled	95.8	19	<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
72	<a href="#">d2i0ka1</a>	Alignment	not modelled	95.7	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Cholesterol oxidase
73	<a href="#">d1rm6b2</a>	Alignment	not modelled	95.4	17	<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
74	<a href="#">c1wygA</a>	Alignment	not modelled	95.2	17	<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)
75	<a href="#">c3zyvA</a>	Alignment	not modelled	91.7	20	<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)
76	<a href="#">c4uhxA</a>	Alignment	not modelled	90.4	22	<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
77	<a href="#">c2bp7F</a>	Alignment	not modelled	76.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase beta subunit; <b>PDBTitle:</b> new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
78	<a href="#">c1jk9D</a>	Alignment	not modelled	66.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> copper chaperone for superoxide dismutase; <b>PDBTitle:</b> heterodimer between h48f-yso1 and yccs <b>PDB header:</b> chaperone

79	<a href="#">c1qupA</a>	Alignment	not modelled	64.6	15	<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
80	<a href="#">c2uval</a>	Alignment	not modelled	58.7	26	<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
81	<a href="#">d1jaka1</a>	Alignment	not modelled	57.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
82	<a href="#">c6je8A</a>	Alignment	not modelled	56.9	24	<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
83	<a href="#">c5oarB</a>	Alignment	not modelled	56.3	19	<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
84	<a href="#">c2vkzH</a>	Alignment	not modelled	56.1	24	<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
85	<a href="#">d1yhta1</a>	Alignment	not modelled	53.7	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
86	<a href="#">d1umdb1</a>	Alignment	not modelled	53.6	33	<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
87	<a href="#">c4h04B</a>	Alignment	not modelled	53.2	29	<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
88	<a href="#">c3nsnA</a>	Alignment	not modelled	52.6	24	<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
89	<a href="#">c2yl8A</a>	Alignment	not modelled	52.2	19	<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
90	<a href="#">c3gh7A</a>	Alignment	not modelled	51.2	24	<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
91	<a href="#">c2ylaA</a>	Alignment	not modelled	50.9	24	<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
92	<a href="#">d1qbaa3</a>	Alignment	not modelled	50.1	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
93	<a href="#">d1nowa1</a>	Alignment	not modelled	50.0	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
94	<a href="#">c3m7iA</a>	Alignment	not modelled	49.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase in complex with thiamine2 diphosphate, ribose-5-phosphate(pyranose form) and magnesium ion
95	<a href="#">d2gjxa1</a>	Alignment	not modelled	49.5	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
96	<a href="#">d1itza2</a>	Alignment	not modelled	49.5	26	<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
97	<a href="#">d1ik6a1</a>	Alignment	not modelled	47.8	37	<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
98	<a href="#">c1nouA</a>	Alignment	not modelled	47.6	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
99	<a href="#">c2gjxE</a>	Alignment	not modelled	47.5	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
100	<a href="#">d2bi7a1</a>	Alignment	not modelled	46.1	16	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> UDP-galactopyranose mutase, N-terminal domain
101	<a href="#">d1w85b1</a>	Alignment	not modelled	45.8	30	<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
102	<a href="#">c2gvsA</a>	Alignment	not modelled	45.8	25	<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
103	<a href="#">d1r9ja1</a>	Alignment	not modelled	45.0	19	<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
104	<a href="#">c1m04A</a>	Alignment	not modelled	44.7	19	<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 (glcnac)



105	<a href="#">d1kx9b_</a>	Alignment	not modelled	44.5	25	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Chemosensory protein Csp2 <b>Family:</b> Chemosensory protein Csp2
106	<a href="#">c6ezrA_</a>	Alignment	not modelled	44.4	24	<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
107	<a href="#">d2ozlb1</a>	Alignment	not modelled	44.3	26	<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
108	<a href="#">c3lmyA_</a>	Alignment	not modelled	43.3	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
109	<a href="#">d1n8va_</a>	Alignment	not modelled	43.0	25	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Chemosensory protein Csp2 <b>Family:</b> Chemosensory protein Csp2
110	<a href="#">c3rpmA_</a>	Alignment	not modelled	41.9	19	<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
111	<a href="#">c3rcnA_</a>	Alignment	not modelled	41.8	14	<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
112	<a href="#">c4pysB_</a>	Alignment	not modelled	41.1	29	<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
113	<a href="#">d2r8oa1</a>	Alignment	not modelled	41.0	22	<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
114	<a href="#">d1qpa2</a>	Alignment	not modelled	39.7	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
115	<a href="#">c2yswB_</a>	Alignment	not modelled	39.3	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5
116	<a href="#">d1qs0b1</a>	Alignment	not modelled	39.1	30	<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
117	<a href="#">c3eypB_</a>	Alignment	not modelled	37.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-l-fucosidase; <b>PDBTitle:</b> crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
118	<a href="#">d1gpua2</a>	Alignment	not modelled	35.9	25	<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
119	<a href="#">c1qbaA_</a>	Alignment	not modelled	35.4	14	<b>PDB header:</b> glycosyl hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitobiase; <b>PDBTitle:</b> bacterial chitobiase, glycosyl hydrolase family 20
120	<a href="#">c2wqjK_</a>	Alignment	not modelled	34.8	13	<b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> tumor protein p73; <b>PDBTitle:</b> crystal structure of a truncated variant of the human p73 tetramerization domain