







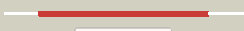
























# Phyre2

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Description	RVBD3107c_agpS_3475375_3476958
Date	Thu Aug 8 16:20:28 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4bc9C_</a>	 Alignment		100.0	27	<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
2	<a href="#">c2uuvC_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> alkyldihydroxyacetonephosphate synthase; <b>PDBTitle:</b> alkyldihydroxyacetonephosphate synthase in p1
3	<a href="#">c3pm9A_</a>	 Alignment		100.0	20	<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
4	<a href="#">c1ahuB_</a>	 Alignment		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
5	<a href="#">c5fxpA_</a>	 Alignment		100.0	16	<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
6	<a href="#">c1wveB_</a>	 Alignment		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
7	<a href="#">c1f0xA_</a>	 Alignment		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.
8	<a href="#">c4oaalB_</a>	 Alignment		100.0	15	<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
9	<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
10	<a href="#">c4ml8C_</a>	 Alignment		100.0	15	<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)
11	<a href="#">c6f73B_</a>	 Alignment		100.0	12	<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

12	<a href="#">c6f74B_</a>	Alignment		100.0	10	<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
13	<a href="#">c3vteA_</a>	Alignment		100.0	14	<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="#">c6c80B_</a>	Alignment		100.0	14	<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
15	<a href="#">c2bvfA_</a>	Alignment		100.0	14	<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)
16	<a href="#">c2exrA_</a>	Alignment		100.0	15	<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
17	<a href="#">c3w8wA_</a>	Alignment		100.0	18	<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
18	<a href="#">c4ud8B_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fad-binding and bbe domain-containing protein; <b>PDBTitle:</b> atbbe15
19	<a href="#">c3rjaA_</a>	Alignment		100.0	12	<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	12	<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="#">c3tstjA_</a>	Alignment	not modelled	100.0	13	<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
22	<a href="#">c5l6fA_</a>	Alignment	not modelled	100.0	14	<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
23	<a href="#">c3fwaA_</a>	Alignment	not modelled	100.0	13	<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
24	<a href="#">c4fdoA_</a>	Alignment	not modelled	100.0	14	<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="#">c3d2hA_</a>	Alignment	not modelled	100.0	14	<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
26	<a href="#">c1zr6A_</a>	Alignment	not modelled	100.0	14	<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
27	<a href="#">c5d79B_</a>	Alignment	not modelled	100.0	13	<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
28	<a href="#">c3popD_</a>	Alignment	not modelled	100.0	15	<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 <b>PDB header:</b> oxidoreductase

29	<a href="#">c5i1wD_</a>	Alignment	not modelled	100.0	16	<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
30	<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
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="#">c2y3rC_</a>	Alignment	not modelled	100.0	15	<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	15	<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	12	<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	15	<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="#">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
37	<a href="#">d1wvfa2</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> FAD-linked oxidases, N-terminal domain
38	<a href="#">d1f0xa2</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="#">d1w1oa2</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> 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="#">d1uxya1</a>	Alignment	not modelled	100.0	14	<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="#">c4jayC_</a>	Alignment	not modelled	100.0	20	<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+
44	<a href="#">c4pytA_</a>	Alignment	not modelled	100.0	19	<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
45	<a href="#">c2yvsa_</a>	Alignment	not modelled	100.0	20	<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
46	<a href="#">c1hskA_</a>	Alignment	not modelled	99.9	16	<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
47	<a href="#">d1e8ga1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
48	<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
49	<a href="#">d1wvfa1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
50	<a href="#">c3i99A_</a>	Alignment	not modelled	99.9	11	<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
51	<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-acetylenolpyruvoylglucosamine reductase; <b>PDBTitle:</b> crystal structure of udp-n-acetylenolpyruvoylglucosamine reductase2 (murb) from mycobacterium tuberculosis
52	<a href="#">d1f0xa1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> D-lactate dehydrogenase
53	<a href="#">c2gquA_</a>	Alignment	not modelled	99.7	16	<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	99.0	16	<b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Cytokinin dehydrogenase 1
55	<a href="#">c5y6qB</a>	Alignment	not modelled	97.8	21	<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
56	<a href="#">d1ffvc2</a>	Alignment	not modelled	97.6	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
57	<a href="#">c5g5hB</a>	Alignment	not modelled	97.6	17	<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
58	<a href="#">c1n62C</a>	Alignment	not modelled	97.5	22	<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="#">c1ffuF</a>	Alignment	not modelled	97.5	18	<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
60	<a href="#">d1n62c2</a>	Alignment	not modelled	97.4	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
61	<a href="#">c1t3qF</a>	Alignment	not modelled	97.3	24	<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="#">d1t3qc2</a>	Alignment	not modelled	97.2	24	<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
63	<a href="#">c3hrdC</a>	Alignment	not modelled	97.2	25	<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
64	<a href="#">d1v97a6</a>	Alignment	not modelled	97.1	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
65	<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
66	<a href="#">c3etrM</a>	Alignment	not modelled	97.1	14	<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
67	<a href="#">c3b9jl</a>	Alignment	not modelled	97.0	14	<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
68	<a href="#">c4zohB</a>	Alignment	not modelled	97.0	19	<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
69	<a href="#">c1rm6E</a>	Alignment	not modelled	96.8	25	<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
70	<a href="#">d1jroa4</a>	Alignment	not modelled	96.7	18	<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	96.7	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
72	<a href="#">d1rm6b2</a>	Alignment	not modelled	96.5	25	<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	96.2	14	<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="#">c3zyvA</a>	Alignment	not modelled	95.0	11	<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)
75	<a href="#">c4uhxA</a>	Alignment	not modelled	92.6	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
76	<a href="#">d2i0ka1</a>	Alignment	not modelled	92.5	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Cholesterol oxidase
77	<a href="#">c6je8A</a>	Alignment	not modelled	79.6	38	<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
78	<a href="#">d1jaka1</a>	Alignment	not modelled	79.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
79	<a href="#">c5oarB</a>	Alignment	not modelled	78.1	38	<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
80	<a href="#">c4h04B</a>	Alignment	not modelled	78.0	33	<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
81	<a href="#">d1yhta1</a>	Alignment	not modelled	77.9	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
82	<a href="#">d1nowa1</a>	Alignment	not modelled	77.1	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
83	<a href="#">d1qbaa3</a>	Alignment	not modelled	77.0	43	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
84	<a href="#">c3nsnA</a>	Alignment	not modelled	77.0	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
85	<a href="#">d2gjxa1</a>	Alignment	not modelled	76.5	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
86	<a href="#">c1nouA</a>	Alignment	not modelled	76.1	33	<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
87	<a href="#">c3rcnA</a>	Alignment	not modelled	76.0	29	<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 aurescens
88	<a href="#">c3gh7A</a>	Alignment	not modelled	75.9	29	<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
89	<a href="#">c2yl8A</a>	Alignment	not modelled	75.7	29	<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="#">c1m04A</a>	Alignment	not modelled	75.6	14	<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)
91	<a href="#">c6ezrA</a>	Alignment	not modelled	75.4	29	<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
92	<a href="#">c2gjxE</a>	Alignment	not modelled	74.6	33	<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
93	<a href="#">c2ylaA</a>	Alignment	not modelled	74.5	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
94	<a href="#">c1no8A</a>	Alignment	not modelled	73.5	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> aly; <b>PDBTitle:</b> solution structure of the nuclear factor aly rbd domain
95	<a href="#">d1no8a</a>	Alignment	not modelled	73.5	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
96	<a href="#">c3lmyA</a>	Alignment	not modelled	73.4	33	<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
97	<a href="#">c2mzqA</a>	Alignment	not modelled	73.3	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-strand telomeric dna-binding protein gbp2; <b>PDBTitle:</b> nmr structure of the rrm3 domain of gbp2
98	<a href="#">c1qbaA</a>	Alignment	not modelled	73.1	43	<b>PDB header:</b> glycosyl hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitobiase; <b>PDBTitle:</b> bacterial chitobiase, glycosyl hydrolase family 20
99	<a href="#">c3rpmA</a>	Alignment	not modelled	72.3	29	<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="#">c4pysB</a>	Alignment	not modelled	72.1	33	<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
101	<a href="#">c2epoB</a>	Alignment	not modelled	68.3	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
102	<a href="#">c2dnoA</a>	Alignment	not modelled	68.1	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trinucleotide repeat containing 4 variant; <b>PDBTitle:</b> solution structure of rna binding domain in trinucleotide2 repeat containing 4 variant
103	<a href="#">c4wikA</a>	Alignment	not modelled	63.9	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> splicing factor, proline- and glutamine-rich; <b>PDBTitle:</b> human splicing factor, construct 2
104	<a href="#">c2dqaA</a>	Alignment	not modelled	63.5	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa0430 protein; <b>PDBTitle:</b> solution structure of the rna recognition motif in kiaa04302 protein
105	<a href="#">d1fhta</a>	Alignment	not modelled	63.0	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
						<b>PDB header:</b> lyase

106	<a href="#">c2yswB_</a>	Alignment	not modelled	61.5	19	<b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinatase; <b>PDBTitle:</b> crystal structure of the 3-dehydroquinatase from aquifex2 aeolicus vf5
107	<a href="#">c5ac4A_</a>	Alignment	not modelled	61.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-beta-d-glucosaminidase; <b>PDBTitle:</b> gh20c, beta-hexosaminidase from streptococcus pneumoniae in complex2 with galnac
108	<a href="#">d2bi7a1</a>	Alignment	not modelled	60.7	18	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> UDP-galactopyranose mutase, N-terminal domain
109	<a href="#">d1x5oa1</a>	Alignment	not modelled	60.2	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
110	<a href="#">c6n2nA_</a>	Alignment	not modelled	58.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate flavodoxin/ferredoxin oxidoreductase domain <b>PDBTitle:</b> crystal structure of 2-oxoglutarate:ferredoxin oxidoreductase from2 magnetococcus marinus
111	<a href="#">d2k3ka1</a>	Alignment	not modelled	58.0	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
112	<a href="#">c2fy1A_</a>	Alignment	not modelled	57.4	17	<b>PDB header:</b> structural protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding motif protein, y chromosome, family 1 member <b>PDBTitle:</b> a dual mode of rna recognition by the rbmy protein
113	<a href="#">c1qapA_</a>	Alignment	not modelled	56.8	11	<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
114	<a href="#">c2mztA_</a>	Alignment	not modelled	55.9	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein hrb1; <b>PDBTitle:</b> nmr structure of the rrm3 domain of hrb1
115	<a href="#">c6em5o_</a>	Alignment	not modelled	55.7	18	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l16-a; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
116	<a href="#">c1jk9D_</a>	Alignment	not modelled	55.2	11	<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
117	<a href="#">c2i38A_</a>	Alignment	not modelled	52.5	22	<b>PDB header:</b> rna binding protein/chimera <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein consists of immunoglobulin g-binding protein <b>PDBTitle:</b> solution structure of the rrm of srp20
118	<a href="#">c6r5kH_</a>	Alignment	not modelled	52.4	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> polyadenylate-binding protein, cytoplasmic and nuclear; <b>PDBTitle:</b> cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
119	<a href="#">d2ftsa3</a>	Alignment	not modelled	51.4	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
120	<a href="#">d1di6a_</a>	Alignment	not modelled	51.3	13	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like