














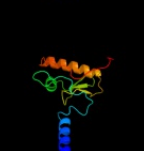



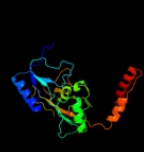




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1mbbA</a>	 Alignment		100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uridine diphospho-n-acetylenolpyruvylglucosamine <b>PDBTitle:</b> oxidoreductase
2	<a href="#">c3i99A</a>	 Alignment		100.0	50	<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="#">c1hskA</a>	 Alignment		100.0	29	<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
4	<a href="#">c2gguA</a>	 Alignment		100.0	30	<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
5	<a href="#">dluxya2</a>	 Alignment		100.0	99	<b>Fold:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Superfamily:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
6	<a href="#">dluxya1</a>	 Alignment		100.0	100	<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
7	<a href="#">dlhska1</a>	 Alignment		100.0	25	<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
8	<a href="#">dlhska2</a>	 Alignment		100.0	36	<b>Fold:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Superfamily:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
9	<a href="#">c3fwaA</a>	 Alignment		99.9	11	<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
10	<a href="#">c2uuuC</a>	 Alignment		99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> alkyl dihydroxyacetonephosphate synthase; <b>PDBTitle:</b> alkyl dihydroxyacetonephosphate synthase in p1
11	<a href="#">c3d2hA</a>	 Alignment		99.9	11	<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="#">c3bw7A_</a>	Alignment		99.9	12	<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
13	<a href="#">c2bvfa_</a>	Alignment		99.9	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)
14	<a href="#">c3pm9A_</a>	Alignment		99.9	17	<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
15	<a href="#">c1wveB_</a>	Alignment		99.9	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
16	<a href="#">c1zr6A_</a>	Alignment		99.9	13	<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
17	<a href="#">c1i19B_</a>	Alignment		99.9	14	<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
18	<a href="#">c3popD_</a>	Alignment		99.9	13	<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
19	<a href="#">c2exra_</a>	Alignment		99.9	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)2 from arabidopsis thaliana at5g21482
20	<a href="#">c2wdwB_</a>	Alignment		99.9	11	<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
21	<a href="#">c2y3rC_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> taml; <b>PDBTitle:</b> structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
22	<a href="#">c1ahuB_</a>	Alignment	not modelled	99.9	18	<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
23	<a href="#">c2vfvA_</a>	Alignment	not modelled	99.9	20	<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
24	<a href="#">c2ipiD_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> aclacinomycin oxidoreductase (aknox); <b>PDBTitle:</b> crystal structure of aclacinomycin oxidoreductase
25	<a href="#">d1wvfa2</a>	Alignment	not modelled	99.9	16	<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
26	<a href="#">c1f0xA_</a>	Alignment	not modelled	99.9	14	<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 peripheral2 membrane respiratory enzyme.
27	<a href="#">c3js8A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> solvent-stable cholesterol oxidase
28	<a href="#">d1e8ga2</a>	Alignment	not modelled	99.9	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
						<b>Fold:</b> FAD-binding/transporter-associated domain-like

29	<a href="#">d2i0ka2</a>	Alignment	not modelled	99.9	16	<b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> FAD-linked oxidases, N-terminal domain
30	<a href="#">d1w1oa2</a>	Alignment	not modelled	99.9	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
31	<a href="#">d1f0xa2</a>	Alignment	not modelled	99.9	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
32	<a href="#">c2yvsA_</a>	Alignment	not modelled	99.5	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
33	<a href="#">d1n62c2</a>	Alignment	not modelled	98.4	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
34	<a href="#">d1ffvc2</a>	Alignment	not modelled	98.3	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
35	<a href="#">c1n62C_</a>	Alignment	not modelled	98.3	14	<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
36	<a href="#">d3b9jb2</a>	Alignment	not modelled	98.2	10	<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
37	<a href="#">c3hrdC_</a>	Alignment	not modelled	98.2	15	<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
38	<a href="#">c1ffuF_</a>	Alignment	not modelled	98.1	14	<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
39	<a href="#">d1v97a6</a>	Alignment	not modelled	98.1	11	<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
40	<a href="#">c1t3qF_</a>	Alignment	not modelled	98.1	19	<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
41	<a href="#">c3etrM_</a>	Alignment	not modelled	98.0	12	<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 with2 lumazine
42	<a href="#">c3b9jl_</a>	Alignment	not modelled	98.0	12	<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
43	<a href="#">d1rm6b2</a>	Alignment	not modelled	97.9	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
44	<a href="#">d1t3qc2</a>	Alignment	not modelled	97.9	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
45	<a href="#">c1wygA_</a>	Alignment	not modelled	97.9	11	<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)
46	<a href="#">c2w3rG_</a>	Alignment	not modelled	97.7	14	<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
47	<a href="#">c1rm6E_</a>	Alignment	not modelled	97.5	19	<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
48	<a href="#">d1jroa4</a>	Alignment	not modelled	97.4	10	<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
49	<a href="#">c1xtyD_</a>	Alignment	not modelled	65.8	15	<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-trna2 hydrolase
50	<a href="#">d1q7sa_</a>	Alignment	not modelled	64.1	21	<b>Fold:</b> Peptidyl-tRNA hydrolase II <b>Superfamily:</b> Peptidyl-tRNA hydrolase II <b>Family:</b> Peptidyl-tRNA hydrolase II
51	<a href="#">d1rlka_</a>	Alignment	not modelled	60.6	15	<b>Fold:</b> Peptidyl-tRNA hydrolase II <b>Superfamily:</b> Peptidyl-tRNA hydrolase II <b>Family:</b> Peptidyl-tRNA hydrolase II
52	<a href="#">c2d3kA_</a>	Alignment	not modelled	55.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> structural study on project id ph1539 from pyrococcus2 horikoshii ot3
53	<a href="#">c2zv3E_</a>	Alignment	not modelled	54.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
54	<a href="#">c2r47C_</a>	Alignment	not modelled	53.9	24	<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

55	<a href="#">c2l1nA_</a>	Alignment	not modelled	52.7	14	<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
56	<a href="#">d3erja1</a>	Alignment	not modelled	48.3	10	<b>Fold:</b> Peptidyl-tRNA hydrolase II <b>Superfamily:</b> Peptidyl-tRNA hydrolase II <b>Family:</b> Peptidyl-tRNA hydrolase II
57	<a href="#">c2qiWA_</a>	Alignment	not modelled	40.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pep phosphonmutase; <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
58	<a href="#">c3ih1A_</a>	Alignment	not modelled	39.1	18	<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
59	<a href="#">c2ze3A_</a>	Alignment	not modelled	32.5	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dfa0005; <b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
60	<a href="#">dlik6a1</a>	Alignment	not modelled	31.6	19	<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
61	<a href="#">c2yswB_</a>	Alignment	not modelled	30.5	9	<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
62	<a href="#">c3dfeA_</a>	Alignment	not modelled	27.3	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
63	<a href="#">clik6A_</a>	Alignment	not modelled	26.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase; <b>PDBTitle:</b> 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
64	<a href="#">c1bplB_</a>	Alignment	not modelled	26.5	20	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,4-glucan-4-glucanohydrolase; <b>PDBTitle:</b> glycosyltransferase
65	<a href="#">d1jaka1</a>	Alignment	not modelled	24.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
66	<a href="#">c2ylaA_</a>	Alignment	not modelled	24.3	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
67	<a href="#">d1hx0a2</a>	Alignment	not modelled	23.6	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
68	<a href="#">c2hjpA_</a>	Alignment	not modelled	23.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonopyruvate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
69	<a href="#">c2yl8A_</a>	Alignment	not modelled	23.2	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
70	<a href="#">d1ybha1</a>	Alignment	not modelled	23.2	22	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
71	<a href="#">d1w85b1</a>	Alignment	not modelled	22.7	19	<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
72	<a href="#">d1umdb1</a>	Alignment	not modelled	22.4	19	<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
73	<a href="#">c3mt1B_</a>	Alignment	not modelled	22.3	11	<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
74	<a href="#">d1yhta1</a>	Alignment	not modelled	22.2	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
75	<a href="#">d2bdua1</a>	Alignment	not modelled	21.2	29	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Pyrimidine 5'-nucleotidase (UMPH-1)
76	<a href="#">d2ozlb1</a>	Alignment	not modelled	21.1	19	<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
77	<a href="#">c2grvC_</a>	Alignment	not modelled	21.0	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> lpqw; <b>PDBTitle:</b> crystal structure of lpqw
78	<a href="#">d2pgca1</a>	Alignment	not modelled	20.6	36	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Marine metagenome family DABB3
79	<a href="#">c1bplA_</a>	Alignment	not modelled	20.3	14	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-glucan-4-glucanohydrolase; <b>PDBTitle:</b> glycosyltransferase
80	<a href="#">d1ne9a1</a>	Alignment	not modelled	19.6	19	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> FemXAB nonribosomal peptidyltransferases

81	<a href="#">d2bfdb1</a>	Alignment	not modelled	19.6	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
82	<a href="#">d1jaea2</a>	Alignment	not modelled	19.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
83	<a href="#">d1nowa1</a>	Alignment	not modelled	18.9	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
84	<a href="#">c3gh7A_</a>	Alignment	not modelled	18.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-hexosaminidase; <b>PDBTitle:</b> crystal structure of beta-hexosaminidase from paenibacillus2 sp. ts12 in complex with galnac
85	<a href="#">d3dhpa2</a>	Alignment	not modelled	18.6	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
86	<a href="#">d2gjxa1</a>	Alignment	not modelled	18.6	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
87	<a href="#">d1qs0b1</a>	Alignment	not modelled	18.1	15	<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
88	<a href="#">c1zlpA_</a>	Alignment	not modelled	18.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> petal death protein; <b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
89	<a href="#">c3nsnA_</a>	Alignment	not modelled	17.9	14	<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
90	<a href="#">c1hvxA_</a>	Alignment	not modelled	17.6	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> bacillus stearothermophilus alpha-amylase
91	<a href="#">c1nouA_</a>	Alignment	not modelled	17.5	24	<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
92	<a href="#">c2gjxE_</a>	Alignment	not modelled	17.4	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
93	<a href="#">d1gcya2</a>	Alignment	not modelled	17.1	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
94	<a href="#">d1qbaa3</a>	Alignment	not modelled	17.1	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
95	<a href="#">c1m8oB_</a>	Alignment	not modelled	16.9	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> platele integrin beta3 subunit: cytoplasmic <b>PDBTitle:</b> platelet integrin alfa1b-beta3 cytoplasmic domain
96	<a href="#">d1ps9a1</a>	Alignment	not modelled	16.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
97	<a href="#">c3rcnA_</a>	Alignment	not modelled	16.7	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 aurescens
98	<a href="#">c1m04A_</a>	Alignment	not modelled	16.5	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)
99	<a href="#">c2g0cA_</a>	Alignment	not modelled	16.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dbpa; <b>PDBTitle:</b> structure of the rna binding domain (residues 404-479) of the bacillus2 subtilis yxin protein