

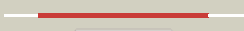


























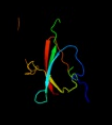



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wyhA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase; PDBTitle: structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
2	c3lvtA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 38; PDBTitle: the crystal structure of a protein in the glycosyl hydrolase2 family 38 from enterococcus faecalis to 2.55a
3	c1htyA_	 Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase ii; PDBTitle: golgi alpha-mannosidase ii
4	c2ow7A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase 2; PDBTitle: golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thionibicyclo[4.3.0]nonan-7,8-diol chloride
5	d3bvua3	 Alignment		100.0	19	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: alpha-mannosidase
6	c1o7dA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
7	d3bvua2	 Alignment		100.0	13	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: alpha-mannosidase, C-terminal domain
8	d1k1xa3	 Alignment		100.0	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: 4-alpha-glucanotransferase, N-terminal domain
9	c1o7dD_	 Alignment		100.0	12	PDB header: hydrolase Chain: D: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
10	c1k1yA_	 Alignment		99.9	14	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
11	c1o7dC_	 Alignment		99.9	11	PDB header: hydrolase Chain: C: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation

12	d3bvua1	Alignment		99.9	15	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: alpha-mannosidase, domain 2
13	c1o7dB_	Alignment		99.5	14	PDB header: hydrolase Chain: B: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
14	c2b5dX_	Alignment		99.5	14	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
15	c1ufaa_	Alignment		99.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tt1467 protein; PDBTitle: crystal structure of tt1467 from thermus thermophilus hb8
16	c3n92A_	Alignment		99.3	17	PDB header: transferase Chain: A: PDB Molecule: alpha-amylase, gh57 family; PDBTitle: crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
17	d2b5dx2	Alignment		99.3	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
18	d1ufaa2	Alignment		99.0	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
19	c1o7dE_	Alignment		98.6	17	PDB header: hydrolase Chain: E: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
20	c3qbuD_	Alignment		98.1	12	PDB header: hydrolase Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of putative peptidoglycan deacetylase (hp0310) from2 helicobacter pylori
21	c3rxzA_	Alignment	not modelled	97.9	14	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
22	d1z7aa1	Alignment	not modelled	97.6	11	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: PA1517-like
23	c3s6oD_	Alignment	not modelled	97.2	12	PDB header: hydrolase Chain: D: PDB Molecule: polysaccharide deacetylase family protein; PDBTitle: crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
24	c2cliA_	Alignment	not modelled	97.1	18	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan glcnac deacetylase; PDBTitle: structure of streptococcus pneumoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
25	c1w17A_	Alignment	not modelled	97.0	17	PDB header: hydrolase Chain: A: PDB Molecule: probable polysaccharide deacetylase pdaa; PDBTitle: structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
26	c2vyoA_	Alignment	not modelled	95.2	13	PDB header: hydrolase Chain: A: PDB Molecule: chitoooligosaccharide deacetylase; PDBTitle: chitin deacetylase family member from encephalitozoon2 cuniculi
27	d1nyla_	Alignment	not modelled	94.8	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
28	d2j13a1	Alignment	not modelled	93.5	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase

29	d2clia1		Alignment	not modelled	93.3	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
30	d2iw0a1		Alignment	not modelled	91.7	12	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
31	c2iw0A		Alignment	not modelled	91.0	9	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: structure of the chitin deacetylase from the fungal 2 pathogen colletotrichum lindemuthianum
32	c3dcdA		Alignment	not modelled	86.2	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: galactose mutarotase related enzyme; PDBTitle: x-ray structure of the galactose mutarotase related enzyme q5fk7 from2 lactobacillus acidophilus at the resolution 1.9a. northeast3 structural genomics consortium target lar33.
33	d2cc0a1		Alignment	not modelled	79.0	20	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
34	dlnofa1		Alignment	not modelled	77.5	16	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
35	c2w3zA		Alignment	not modelled	76.7	20	PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
36	c3cc1B		Alignment	not modelled	64.9	11	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-n-acetyl galactosaminidase; PDBTitle: crystal structure of a putative alpha-n-acetyl galactosaminidase2 (bh1870) from bacillus halodurans c-125 at 2.00 a resolution
37	d1m53a1		Alignment	not modelled	64.4	12	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
38	d1uoka1		Alignment	not modelled	59.5	10	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
39	d2c71a1		Alignment	not modelled	58.5	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
40	c3q1nA		Alignment	not modelled	52.0	28	PDB header: isomerase Chain: A: PDB Molecule: galactose mutarotase related enzyme; PDBTitle: crystal structure of a galactose mutarotase-like protein (lse1_2598)2 from lactobacillus casei atcc 334 at 1.61 a resolution
41	c1qw9B		Alignment	not modelled	51.7	8	PDB header: hydrolase Chain: B: PDB Molecule: alpha-l-arabinofuranosidase; PDBTitle: crystal structure of a family 51 alpha-l-2 arabinofuranosidase in complex with 4-nitrophenyl-ara
42	d1tsja		Alignment	not modelled	49.9	38	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase
43	c3blcB		Alignment	not modelled	49.3	7	PDB header: chaperone,protein transport Chain: B: PDB Molecule: inner membrane protein oxaa; PDBTitle: crystal structure of the periplasmic domain of the escherichia coli2 yidc
44	c3ik2A		Alignment	not modelled	48.9	13	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase a; PDBTitle: crystal structure of a glycoside hydrolase family 44 endoglucanase2 produced by clostridium acetobutylium atcc 824
45	c1zjaB		Alignment	not modelled	47.3	12	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
46	d1u69a		Alignment	not modelled	46.6	38	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase
47	d1ekja		Alignment	not modelled	46.2	10	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
48	d1u7ia		Alignment	not modelled	45.0	44	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase
49	c3omsA		Alignment	not modelled	44.6	53	PDB header: transferase Chain: A: PDB Molecule: phnb protein; PDBTitle: putative 3-demethylubiquinone-9 3-methyltransferase, phnb protein,2 from bacillus cereus.
50	c2q48A		Alignment	not modelled	43.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein at5g48480; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at5g48480
51	d1xy7a		Alignment	not modelled	43.9	22	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Hypothetical protein At5g48480
52	d1r9ja3		Alignment	not modelled	42.8	40	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
53	c3kr6B		Alignment	not modelled	41.3	5	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: inner membrane protein oxaa;

53	c3u5vB_	Alignment	not modelled	41.9	9	PDBTitle: 1.8 angstrom crystal structure of the periplasmic domain of2 the membrane insertase yidc PDB header: unknown function
54	c3l20A_	Alignment	not modelled	38.8	33	Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from staphylococcus aureus
55	d1wzla2	Alignment	not modelled	38.6	13	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
56	d2ieaa3	Alignment	not modelled	38.2	25	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
57	d1u6la_	Alignment	not modelled	37.4	27	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase
58	c2ze0A_	Alignment	not modelled	36.3	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
59	c3a5vA_	Alignment	not modelled	34.3	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of alpha-galactosidase i from mortierella vinacea
60	c2a5hC_	Alignment	not modelled	34.1	15	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
61	c1ktbA_	Alignment	not modelled	33.2	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: the structure of alpha-n-acetylgalactosaminidase
62	c2jgdA_	Alignment	not modelled	32.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoglutarate dehydrogenase e1 component; PDBTitle: e. coli 2-oxoglutarate dehydrogenase (e1o)
63	c1nofA_	Alignment	not modelled	32.2	16	PDB header: hydrolase Chain: A: PDB Molecule: xylanase; PDBTitle: the first crystallographic structure of a xylanase from2 glycosyl hydrolase family 5: implications for catalysis
64	d1j0ha2	Alignment	not modelled	31.7	13	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
65	c2yicC_	Alignment	not modelled	31.3	18	PDB header: lyase Chain: C: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form)
66	d1itza3	Alignment	not modelled	30.8	45	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
67	c1r46B_	Alignment	not modelled	30.0	10	PDB header: hydrolase Chain: B: PDB Molecule: alpha-galactosidase a; PDBTitle: structure of human alpha-galactosidase
68	c1uokaA_	Alignment	not modelled	28.6	10	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
69	d1gpua3	Alignment	not modelled	28.0	45	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
70	c3fw6A_	Alignment	not modelled	28.0	10	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of celm2, a bifunctional glucanase-2 xylanase protein from a metagenome library
71	c2a5vB_	Alignment	not modelled	25.6	14	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase (carbonate dehydratase) (carbonic PDBTitle: crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
72	c3gtnA_	Alignment	not modelled	25.3	17	PDB header: hydrolase Chain: A: PDB Molecule: glucuronoxylanase xync; PDBTitle: crystal structure of xync from bacillus subtilis 168
73	d1ldda_	Alignment	not modelled	24.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: SCF ubiquitin ligase complex WHB domain
74	c1m53A_	Alignment	not modelled	23.3	12	PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
75	c3mwxA_	Alignment	not modelled	23.2	12	PDB header: isomerase Chain: A: PDB Molecule: aldose 1-epimerase; PDBTitle: crystal structure of a putative galactose mutarotase (bsu18360) from2 bacillus subtilis at 1.45 a resolution
76	c1gviA_	Alignment	not modelled	23.0	9	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
77	c2dh3A_	Alignment	not modelled	21.3	11	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
78	d1vi0a2	Alignment	not modelled	21.2	9	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
						Fold: Glycosyl hydrolase domain

79	d1qw9a1	Alignment	not modelled	20.4	15	Superfamily: Glycosyl hydrolase domain Family: Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
80	d1j5sa	Alignment	not modelled	19.7	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like
81	d1v5ma	Alignment	not modelled	19.6	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
82	c2w3nA	Alignment	not modelled	19.1	9	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase 2; PDBTitle: structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
83	c2y2wC	Alignment	not modelled	18.8	8	PDB header: hydrolase Chain: C: PDB Molecule: arabinofuranosidase; PDBTitle: elucidation of the substrate specificity and protein2 struture of abfb, a family 51 alpha-l-arabinofuranosidase3 from bifidobacterium longum.
84	d1j6wa	Alignment	not modelled	18.0	17	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
85	c2vkzH	Alignment	not modelled	17.6	16	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
86	d2r8oa3	Alignment	not modelled	17.5	30	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
87	c2hihB	Alignment	not modelled	17.3	30	PDB header: hydrolase Chain: B: PDB Molecule: lipase 46 kda form; PDBTitle: crystal structure of staphylococcus hyicus lipase
88	c2xt6B	Alignment	not modelled	17.2	19	PDB header: lyase Chain: B: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
89	c2k6xA	Alignment	not modelled	16.7	40	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
90	c3nreB	Alignment	not modelled	15.7	10	PDB header: isomerase Chain: B: PDB Molecule: aldose 1-epimerase; PDBTitle: crystal structure of a putative aldose 1-epimerase (b2544) from2 escherichia coli k12 at 1.59 a resolution
91	c2g28A	Alignment	not modelled	15.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
92	d1lpbb2	Alignment	not modelled	15.1	36	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
93	d1nlna	Alignment	not modelled	15.1	24	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Adenain-like
94	d1rp1a2	Alignment	not modelled	14.4	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
95	c1ygaA	Alignment	not modelled	14.3	14	PDB header: isomerase Chain: A: PDB Molecule: hypothetical 37.9 kda protein in bio3-hxt17 PDBTitle: crystal structure of saccharomyces cerevisiae yn9a protein,2 new york structural genomics consortium
96	d1etha2	Alignment	not modelled	13.7	36	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
97	d1vioa2	Alignment	not modelled	13.4	12	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
98	c2o1sC	Alignment	not modelled	13.2	25	PDB header: transferase Chain: C: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
99	d1hpla2	Alignment	not modelled	12.6	45	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain