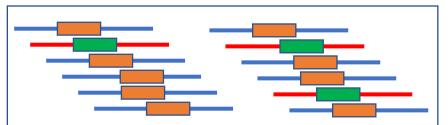
### Proteins of CAZy family (e.g., GH1:

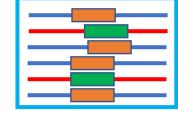
http://www.cazy.org/GH1.htm

### workflow of dbCAN-sub HMM construction

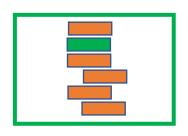
proteins of a CAZy family (e.g., GH1)

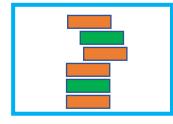


GH1\_e0 GH1\_e1

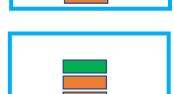


proteins of eCAMI subfamilies (e.g., GH1\_e0)





dbCAN GH1 domains of proteins of GH1\_e0 (hmmscan)



dereplicated dbCAN GH1 domains (cd-hit 95% sequence identity)

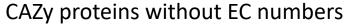




multiple sequence alignment and HMM (mafft & hmmbuild)



CAZy proteins with EC numbers



#### **Notes:**

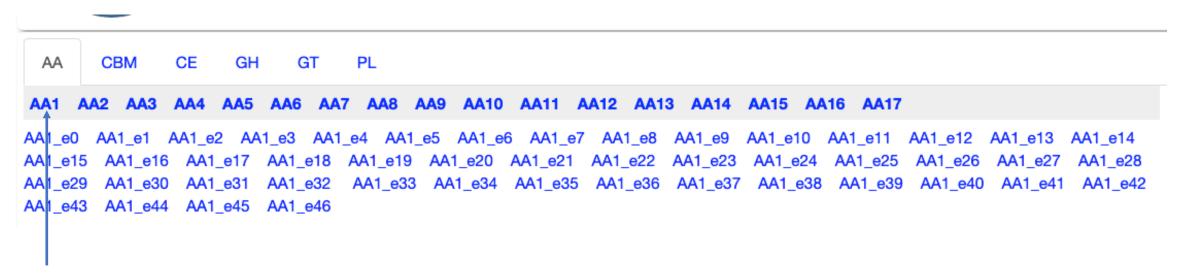
- 1. some proteins do not contain the dbCAN domain (rare but possible)
- 2. some domains are removed after cd-hit
- 3. not all subfamilies have CAZy proteins with EC numbers
- 4. only subfamilies with sequence count >=4 after cd-hit are used for HMM construction



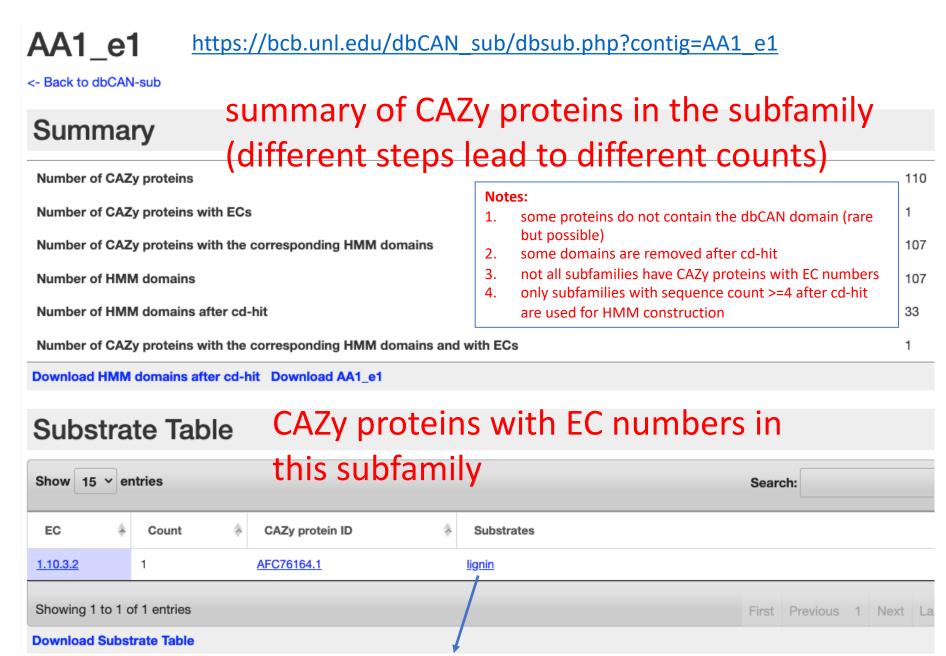
Database of CAZyme subfamilies for substrate annotation



click each tab to access the six CAZyme classes all families of the selected class are shown click on each family will expand to show the subfamilies



click on AA1 to show all subfamilies of AA1 the subfamilies were classified by eCAMI: <a href="https://github.com/yinlabniu/eCAMI">https://github.com/yinlabniu/eCAMI</a> these subfamilies are named with an "e" in them, e.g., AA1\_e0 (e means eCAMI) click on each subfamily will open a new page



# Search dbCAN-sub @ the dbCAN meta server

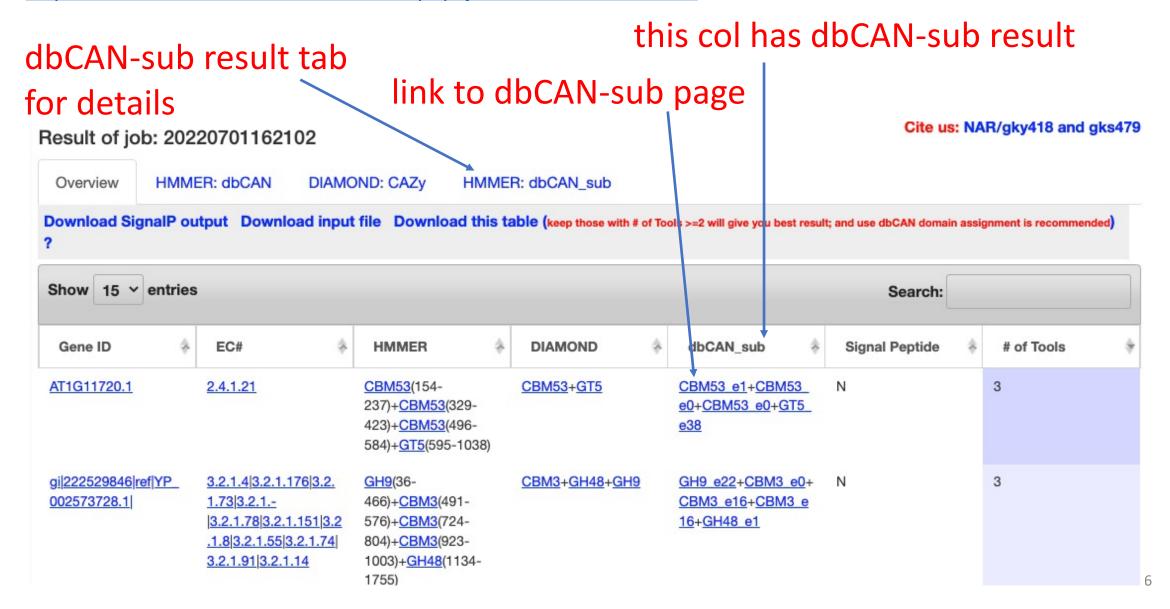
https://bcb.unl.edu/dbCAN2/blast.php

# check here to search dbCAN-sub for substrate prediction

Choose Sequence Type:  Protein sequence (example)? O Nucleotide sequence (example)?  Select Which Tools To Run  HMMER: dbCAN (E-Value < 1e-15, coverage > 0.35) DIAMOND: CAZy (E-Value < 1e-102)  CGCFinder (Distance <= 2, signature genes = CAZyme+TC)?  Just paste some sequences here (note: only FASTA format please!!!)  Try example sequences		/	
Select Which Tools To Run  WHMMER: dbCAN (E-Value < 1e-15, coverage > 0.35)  DIAMOND: CAZy (E-Value < 1e-102)  HMMER: dbCAN-sub (E-Value < 1e-15, coverage > 0.35)  HMMER: dbCAN-sub (E-Value < 1e-15, coverage > 0.35)  Just paste some sequences here (note: only FASTA format please!!!)	Choose Sequence Type:		
✓ HMMER: dbCAN (E-Value < 1e-15, coverage > 0.35) ✓ DIAMOND: CAZy (E-Value < 1e-102) ✓ HMMER: dbCAN-sub (E-Value < 1e-15, coverage > 0.35) CGCFinder (Distance <= 2, signature genes = CAZyme+TC)? ✓ Just paste some sequences here (note: only FASTA format please!!!)	● Protein sequence (example) ? ○ Nucleotide sequence (example) ?		
CGCFinder (Distance <= 2, signature genes = CAZyme+TC)?  ▼ Just paste some sequences here (note: only FASTA format please!!!)	Select Which Tools To Run	$m{\psi}$	
		E-Value < 1e-102) HMMER: dbCAN-sub (E-Value < 1e-15, coverage > 0.35)	
Try example sequences	▼ Just paste some sequences here (note: only FASTA format pl	ease!!!)	
	Try example sequences		//

# Search dbCAN-sub @ the dbCAN meta server

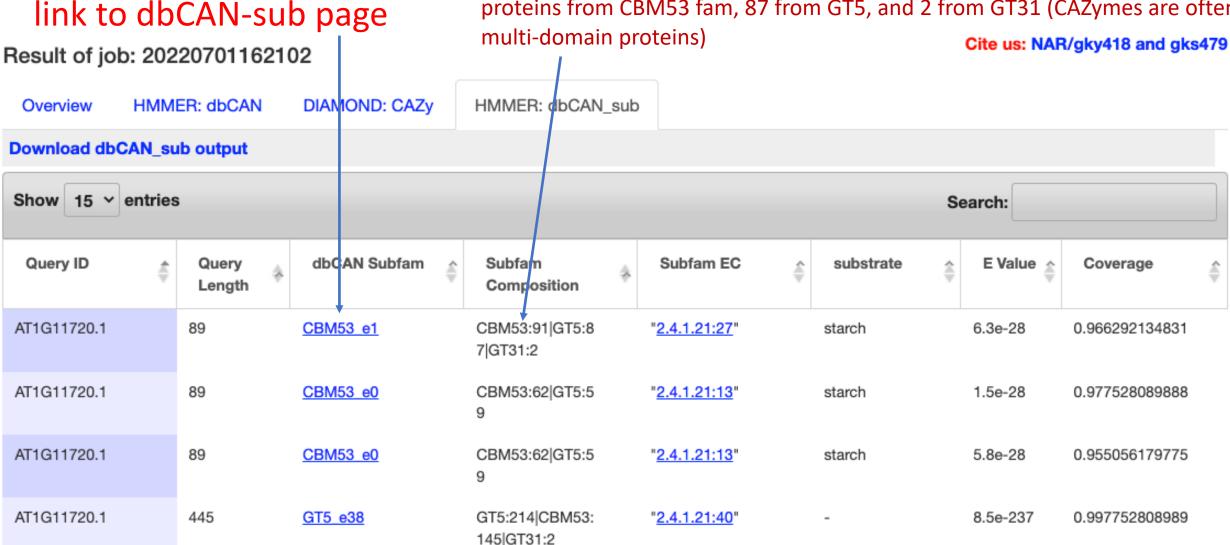
https://bcb.unl.edu/dbCAN2/blastation.php?jobid=20220701162102



### dbCAN-sub result tab for details

# these are the seq composition of CBM53 e1 HMM

CBM53:91 GT5:87 GT31:2 means the CBM53\_e1 subfam contains 91 CAZy proteins from CBM53 fam, 87 from GT5, and 2 from GT31 (CAZymes are often



## CBM53\_e1 sequence composition is described in the dbCAN-sub webpage

