

## File S2: Sequences and alignment of alpha glucuronidases (GH67)

>Blastobotrys.raffinosifermentans ARAD1D23848  
MCIDFTMQFLLPLPVSLGFLGLAAANGIDGWLRYAPLPCNHQCKSELPGSIVALNSTQSSPIYVAGAE LQKGLKSIYQQADVSHDKCDSSSSSVVIGTVAQYDRSCGPVKDA  
IPQLDADGFWIDTRGDQIRILGNSNERGALYGTFEYLSMIAQGNMSKVAYATNPASAPLRWTNEWDNMDGSIERGYGSSSIFFANGTVVEDLTRVQQYGRLLASLRINTVVINNV  
NANASLLTSEN1KGLGVRADTFRPWGIQVAAALNFASPKTYGGLTDFDLDDSVIKFWSNITDSIYTVQVPDFAGYLVKASSEGGQPGPSTYNRTLSDAANLFANALEPYGGVVM  
FRAFVYDQLNESNWDADRAKAAVDYFKPLDGGKFKDNVVVQIKYGPIDFQVREPASPLFANLPNTNTAIELEITQEYLGQQSHLVYLAPLWKELLDLFDLRADNKSSSKVQDVVTG  
KRFNRLLGGFAGVNVVNGSNSNWLGSLSMSNLYAYGRLAWNPAADPRSILQDWIRLTFGMDEKVVNVITQMSMESWPAYENYSGNLGIQTLTDILYTHYGPNPASQDNNGWGQ  
WTRADHNTIGMDRTVSNGTGYSGQYVSEIAAMYENIETTPDNLLLWFHHVNYTQPLKSGKTVIQHFYDAHYDGAETANSFPAMWQTLKGKIDDERYDHLRHLREYQAGHSLVW  
RDAIVNFYHNLSGIGDTSKRVGYPWR1EAEDMTLDGKYKPYTVSPFETASGSVAIVTSTNTVTGTASTHVNFPSPGKYDLAINYYDLYGGQSQWKVYLNDKKIGEWQGNMENVL  
SHNPSIYLDGHSATRIKFKDYNVVKGDVLKIVGTPDGI EPAPLDYVAFPLPGGIID

>Trichomonascus.ciferrii\_KAA8917114.1+KAA8917113.1  
MNLPEIENIALNHSETSPVFTAGNEVLRGLEGIFDHHASVKHDGCGSRSNVVIGTAHAFKSSCTGVIVPEIEEGFWLSINGSSVKIVGQNDRGALYGAFEYLGMMQAQGNFTAVD  
YVTNPDPQIRWVNQWDFDGTIERGYEGPSIFFANYSIVDDLGRANEYARLLASIRVNGI VVNVNANETLLKDENIIGLARIADVFRPWGIPIGISLNF AAPKDLGGLETFD  
PLDQKVIQFWQDRSDTIYKLIPLDLAGYLVKGDSEGGEGPLTYNRTLADGANLFANA1KKYGGIVMYRAFVYEKLNKTDWKS DRAKAAYDYFQPLDGGKFDENVVQVQYKGPIDF  
QVREAISPLFGSLRHTNVAVELQITQEYLGQQCHLVYLPPLWRTVWDFDLRTDNESTLVSEVVSRRFRNRPLAGSAAVVNVGTNDT: :MIDAITTMSMNSWSAYEKYSGNLGI  
QTLADILYTHFGPNPQSMDDNNGWGQWTRSFHETVGMDRRTVENGTGYTGQYPPEVAALYEDVTTTPDDL LLLWFHHVPTYTHRPKSSNKTVIQHFYDHSHYEGAEMANEFLT LWESL  
EGKIDTQRYHETLFRQKYQAGHSI VWRDAINN FYNNISGILDEAGRVRGHPWR1EAEEMHLDGYELYTVSPFEMASNSTAIVTSSNATSGTASIIIPFEDGKYDIAIGYYDLF  
DGKAQWEATINNKLGSWTGDNEDHLGHEQSR YLDGHTATRITFRNIKVNNGDELKVKGTPNGIEPAPLDYVAFPLNGIID

>Penicillium.rokeforti\_XP\_038928484.1 CAZyme family GH67  
MRTLFFVSLGFAAAENGLNGWLRYASLPCSGQCHYNLPSSISILNATETSPVYVAGTELQNLKGIYKGSVQVTHNCN1SSVVVGTVDQYRKSCGAVNSVPELEEDGFWLDT  
KGGNVQILGQNERGALYGTFEYLSMLAQGNFSKVAYATNPASAPIRWVNQWDNMDGRIERGYGGPSIFFKDGQIVDDLTRVAGYARLLASIRINAVVINNVNADATLLNPTNLD  
GVARIADVFRPYGIQVGLSLNFASPKTYGGLSTFDPLDTSVIAWWSNITQIYDLVPDMAGYLVKADSEGGQPGPQTYNRTLADAANLFAKEVQPYGGIVMYRAFVYNQNLNESV  
WTDRAKAAAEFFKDL DGEFDDNVVQIKYGPIDFQIREPASALFANLFNTSM AIELQVTQEYLGQQSHLVYIAPLWKTILDTDLRV DHQPSLVRDIVAGKRFNRRLGGSAAV  
VNVGTNTTWLGSLSMSNLYAYGRLAWNPAADQDILQDWIRLTFGLDRKVLGTITRMSMESWPAYEQYSGNLGIQTLTDILYTHYGPSPASQDNNGWQWTRADQTSIGMDR  
TVANGTGFSGQYVDEIAAMYENIETTPDDL LLLWFHHVKYTHRLHSGKTVIQHFYDEHYSGAETAQTFLTQWKLHGKIDTERTYNNHVRHFLDYQSGHSI VWRDAINNFYNL SG  
IPDESKRAGHHPWR1EAEEDMELDGYEAYTVSPFETASGSVAIVTTSNNTAGTASTKIKFPSGT YDLAVNYYDVYGGQSRWKIYLN DHEIGQWVGNS E DVLSTHTPSIYLDGHS A  
IRIKFRGVKIHKGNTLKI VGM PNGTEFAPLDYVALLPAGIVD

>Rasamsonia.emersonii SAL89189.1 Glucuronidase  
MRRLLLLASAALVAAENGLDGWLRYAPLPGASRYLHDLPSISIVSLNASETSPVYVAGSELQKGLQGIFGKQVSI SHQNCNASSSIVVGTVDEYSKLCGSSAALPELEQDGFWL  
STKGNVSQILGRNERGALYGAFEYLSMLAQGNFSQVAYANNPRAPIRWVNQWDNLDGSIERGYGGASIFFENGGVVSNLTRA AQYARLLASIGLNAVVINNVNANASILT PQN  
IEGLGRIADVFRPYGVQLALSLNFASPTIIGGLSTYDPLDPSVIAWWTNVTDQLYQRI PDFAGYLVKADSEGGQPGPLTYNRTL AQGANLFAKPLQPYGGIVMFR AFVYNQ LNE  
SDWKADRAKAAAEFFQGLDGGQFDDNVVQIKYGPIDFQVREPTSPLFAHLRNTSTAIELEITQEYLGQQCHLVYLPPLWKT VLD FDLRV DQKPSLVRDIITGQRFNR TLGGSA  
GVNVGTNTTWLGSLSMSNLYAYGRLAWNPAADPQSVLQDWIRLTFGLDRSVIDTITQMSMESWPAYENYSGNLGIQTLTDILYTHFGPNPASQDNNGWGQWTRADHTS TGM  
DRTVWNGTYTGQYPPEVAAMYENIDTTPDNLLVLFHHVNYTHRLHSGKTVIQHFYDAHYSGAETAQTFLTMWESLKGKIDDERYDNDVHFR LTYQAGHSI VWRDAINNFYNL  
SGIPDEAKRVGNHHPWRVEAESMTLSGYKTYAVNPFETASNNTAIVT TTNSTVGTATT KLEYPSGTYDLAVNYYDMYGGKSHWQVYLN NRKIGEWVGNS E DLTGHTPSIYLDGH  
SATRITFRGVKIEKGDELKIVGTPDGV EPAPLDYVSVLPEGVVD

>Aspergillus.fumigatus Af293\_XP\_753219.1 alpha-glucuronidase  
MWSGIPIFALLSSIGIAAAETGLDGWLRYASVPCNGNCQRALPSHIVTLNSTRSSPVYVAGQELQDGLHQILGKHASVKSTGCSTDSSII VGTVEAYRQVCNAGRQVPQFDVD  
GFWLSIREKSVLIVGQSERGALYGAYEYLSMLAQGNFSQVSYATSPHAPIRWVNQWDNMDGSIERGYGGPSIFFKDGVI RQDLSRVQQYARLLASVRINGIIVNNVNANASLL  
MPSNMDGLARIADVFRPYGIRVIGISLNFASPTLGNLSTYDFDSSVIAWGNVTDQLYARI PDMAGYLVKANSEGQPGPTTYNRTLADGANMFARALKPYGGVVMFRAFVYD  
HHISEDNWNDRANAADVDFKPLDGGKFDNDNVVQIKYGPIDFQVREPASPLFANLYKTNNTAIELEITQEYLGQQSHLVYLPPLWQTILGFDLRVDQKPSLVRDIISGQRFDRP  
LGGWA AVNVGTNSTWLGSLSMSNLYAYGRLAWEPTLDS E DIVQDWIRLTFGLDRRI VDTLTQMSMESWPAYENYSGNLGIQTLTDILYTHYGPNPASQDGNWGQWTRADH  
LSIGMDRTVKNGTKFSGQYPAEVAAMYENIETTPDNLLLWFHHVNYTQRLHSGKTVIQHFYDAHYTGAETAQT FVVSQWESLRERIDAERYQHVLTRLIYQAGHSI VWRDAINN  
FYHNLBSIADEKQRVGHHPWRVEAEDMQLDGYVPYAVSPFETASNNTAIVTASN GTTGTASATLDPKTGT YDLGINYYDMYGGKSHWTVYLNDRV VVGWQGNSE DVLSTHTPSI  
YLDGHSATRITFRDVKIHKGDR LKIVGKPDGV EPAPLDYV VVLP PGIVD

>Aspergillus.fischeri NRRL 181\_XP\_001259234.1 alpha-glucuronidase  
MWSGIPVFALLSSIGIAAAENGLDGWLRYASVPCNGNCQRALPSHIVTLNSTKSSQVYVAGQELQDGLHQILGKHASVKSTGCSTDSSII VGTVEAYRQVCNTGSQAPELDVD  
GFWLSIRGKSVQIVGQTERGALYGAYEYLSMLAQGNFSQVSYATSPHAPIRWVNQWDNMDGSIERGYGGPSIFFKDGVI PQDLSRVKQYARLLASVRINGIIVNNVNANASLL  
MPSNMDGLARIADVFRPYGIRVIGISLNFASPTLGNLSTYDFDSSVIAWGNVTDQLYARI PDMAGYLVKANSEGQPGPTTYNRTLADGANMFARALKPHGGRVVMFRAFVYD  
HHISEDNWNDRANAADVDFKPLDGGKFDNDNVVQIKYGPIDFQVREPASPLFANLYKTNNTAIELEITQEYLGQQSHLVYLPPLWQTILGFDLRVDQKPSLVRDIISGQRFDRP  
LGGWA AVNVGTNTTWLGSLSMSNLYAYGRLAWEPTLDS E DIVQDWIRLTFGLDRRVLDTLTQMSMESWPAYENYSGNLGIQTLTDILYTHYGPNPASQDGNWGQWTRADH  
LSIGMDRTVKNGTKFSGQYPAEVAAMYENIETTPDNLLMLWFHHVNYTQRLHSGKTVIQHFYDAHYDGAETAQT FVVSQWESLRERIDAERYQHVLARLIYQAGHSI VWRDAINN  
FYHNLBSIADEKERVGYHPWRVEAEDMQLDGYVPYAVSPFETASNNTAIVTASN GTTGTASATLDPKTGT YDLGINYYDMYGGKSHWTVYLNDRV VVGWQGNSE DVLSTHTPSI  
YLDGHSATRITFRDVKIHKGDR LKIVGEPDGV EPAPLDYAVVLP RGIVD

>Coniochaeta.ligniaria NRRL 30616\_OIW35663.1 putative alpha-glucuronidase A  
MRNILLVLLSAGLAAEDGLSGWLRYAPLSCGRSSHLSLPQTIVALNTTISSPVYTAGQELQKGLQGI FAKQVKISDQTTKSSSVVVGSLAQYIKATGNSDVP SLEEDGYWLS  
VKGDSVQIVGQNERGALYGAFEYLSMLAQGNFADVAKVSNPSAPIRWTNEWDNMDGSI ERGFAGPSIFFANGVVVDDLTRVAEYARLLASIGINGIIINN VNANATTLSTQNI  
RGLGRVADAMRPYGVQIGISLNFASPSQSGGLSTFDPLDASVIKFWTDITNQIYQQVPDFAGYLVKANSEGQPGPITYNRTLADGANLFAKAIKPHGGIVMFR AFVYDQLNES  
DWHADRADA AVNYFKPLDGEFDDNVVQIKYGPIDFQVREPASPLFANIPKTNNTAIELEITQEYLGQQCHLVYLPPLWKT VLD FDLKVDGQPSLVRDIVSGERFKRPLGGYAG  
VVNVGTNSTWLGSLSMSNLYAYGRLAWDPTSDAQAILQDWIRLTFGLNRIVVDITKMSMDSWPAYENYSGNLGIQTLTDILYTHFGPNPASQDNNGWGQWTRADHNLGMD  
RTVSNGTGFAGQYPAEVAAYVESLEITPDNLLLWFHHVPTYTYLHEGKTVIQHFYDAHYSGAETAQT FPTLWEG LKGKID DQRYEEVLFRLKYQAGHSI VWRDAISEFYFNKS  
SIPDQANRVGNHHPWRVEAESMQLSGYKVTA VNP FETASNFKAVTSSNNTAGTATAKLNFP SGTYDLAINYYDIIGGRARYEVYLN DKLVGKWTGDNEDKLGH TPSTFLDGH S  
ATRITFGGVKVETGDTLKIVGTPDGT ELAPLDYVAVLPSGVID

>Aureobasidium.pullulans\_AAR87862.1 alpha glucuronidase  
MQLTLTFLALFGLALAE TGLDGWLRYAALPSSISWSPVKHIVVLTNTETSPVYTAGQELQRGIQSILGQNCRFSTNKPDESII VGTLDAYVAAYGNFSQSVNLKEDGFWLSTE  
NNTVQIVGQNERGALYGAFEYLSMLAQANFSTVAYVSNPDAPIRWVNQWDNLDGSIERGYGGASIFFANGTVIVNDLTRVAEYARLLASVGINAIVINN VNANASILSPQNI DG  
VGRIADTMRPYGVQIGLSLYFASPTSGVQGANLTTFDPLDPGVVTWGNVTDQIYERIPDMAGYLVKANSEGQPGPITYNRTLAEGANLFA RALQPHGGRVLFRAFVYNQNL  
ESDWRADRANAADVDFKPLDGGKFDNDNVVQIKYGPIDFQVREPASPLFANLFHTNTAIELEITQEYLGQQTHLVYLPPLWDTVLGDFDMRIDNETSLVRDIIAGRTFNRSLGGY  
AAVVNVGTNQTWLGSLSMSNFYAYGRLAWNPTEDTTKIHEDWTRLTFGLDQNVVDTTI HMALESWPAYENYSGNLGIQTLTDILYTHFGPNPQSQDNNGWGQWTRADHTTIG  
MDRTVSNGTGYSGTYTPEVAAMYENIETTPDNLLLWFHHVNYTQKLHSGKTVIQHFYDAHYAGADTAQT FPEQWQTLAGKIDSQR FDEQLYRLKYQAGHSLVWRDAIVNFYHN  
ISGLADENVRGVNHPYRIEABSMNTLNGYBPYAVSPFETASDYAVTSDNSTTGSVSTR LHPFAGTYDVGVNFDYMYGGISKYEMLINNKTVATWAGDSENYLGH TPTSIYLDG  
HSARRITFDVTVKEGDTLEIVGIPNGIEPAPLDYV VVLP KGMID



Alignments were performed with the Multalin server (<http://multalin.toulouse.inra.fr/multalin/>). The *B. raffinosifermentans* ARAD1D23848 predicted protein was aligned with *Penicillium roqueforti* XP\_038928484.1, *Rasamsonia emersonii* SAL89189.1, *Aspergillus fumigatus* Af293 XP\_753219.1, *Aspergillus fischeri* NRRL 181 XP\_001259234.1, *Coniochaeta ligniaria* NRRL 30616 OIW35663, *Aureobasidium pullulans* AAR87862.1 and the two *Trichomonascus ciferrii* KAA8917114.1 and KAA8917113.1 conserved proteins.

Amino acids 21 to 701 of the *B. raffinosifermentans* Agul protein correspond to the COG3661 conserved domain of the alpha glucuronidase AGUA2 family.

Amino acids 705 to 839 of the *B. raffinosifermentans* Agul protein correspond to the Carbohydrate Binding Module 6 (CBM6) and CBM35\_like superfamily (cd02795).

E in positions 705 and 707 and D in position 835 of the *B. raffinosifermentans* Agul protein are the three conserved residues that bind metal ion in the module (Nurizzo et al.; 2002).

N-glycosylation sites predicted in *B. raffinosifermentans* Agul protein, at positions 55, 196, 286, 317, 349, 441, 533, 616, and 688.