

Figure S1

FIGURE S1: Sequence alignment of the GH62 subfamilies. Subfamilies are numbered on the right hand side with the first representative of the family been *PaAbf62A* and *UmAbf62A* for subfamily 1 and 2, respectively. Secondary structure elements are represented in the top of the page. Um_maydi stand for *Ustilago maydis*, and Po_anser for *Podospora anserina*. Accession numbers are indicated for each protein. pSript was used to generate this picture (<http://esript.ibcp.fr/ESPrript/ESPrript>)(45).

Structural characterization of GH62 α -L-arabinofuranosidases

		β 20	β 21	η 4	β 22	η 5	β 23		
<i>Us_maydi</i>	EAK85571	→	→	→	→	→	→		
<i>Po_anser</i>	CAP62336	→	→	→	→	→	→		
	3.2.1.55	279	289	299	309	319	329		
1	<i>Po_anser</i>	CAP62336	3.2.1.55	DEKLLIDPCN	IRFMYQGM	DPSA	GG EYVHALPWR	LGFIHNNPAC	
	<i>Am_medit</i>	AEK42553	DISHGEMIRAGT	DOTLLTIDPCR	IRVLYQGR	DPAS	GG DVNSLPWR	LGLLTQTNATC	
	<i>Am_medit</i>	ADJ45772	DISHGEMIRAGT	DOTLLTIDPCR	IRVLYQGR	DPAS	GG DVNSLPWR	LGLLTQTNATC	
	<i>Pi_indic</i>	CCA70773	DISHGEAIRTQV	DOTMSISGCG	IRVLYQGL	APGS	SG DVNSLPLA	PPRSSHSDK...	
	<i>Pi_indic</i>	CCA70772	DISHGEAIRDQV	DOTMSLNGCG	MRYLYQGL	APGS	SG DVNSLPWR	LGLLTQTN.C	
	<i>Pi_indic</i>	CCA70771	DISHGEAIRSQV	DOTMSISGCG	IRVLYQGL	APGS	SG DVNSLPWR	LGLLTQTN.C	
	un ACQ07729		DISHGELIRTQT	DOTMTISPCK	LOVLYQGL	SPSA	GG DVLLPWK	LGLLTQTNSAC	
	un ACQ05660		DISHGEMVRSQV	DOTMTISPCK	LRVLYQGL	SPTA	TG DVNSLPWR	LALLTQTNSAC	
	un_bacte	AFY23018	DISHGEMVIRAGT	DOMHEISSCR	MOVLYQGM	APGS	GG DVHRLPWK	LGLLTQTNSAC	
	<i>Co_clner</i>	BAK14423	3.2.1.55	DISHGELIRSGN	DOTLIPSPCN	LRVLYQGL	DPNS	GG DVNSLPWK	LGLLTQTNSAC
	<i>Ac_mirum</i>	ACU37207	DISHGELVRSGT	DOTMEINPCK	LSVLYQGL	DPNA	SG DVHRLPWK	LGLLTQTNSPC	
	<i>St_bingc</i>	AD113053	DISHGELVRAGY	DOTLTINPCK	MOVLYQGM	NPNA	SG DVHRLPWK	LGLLTQTNSCT	
	<i>Cl_sachc</i>	AGF55270	RVSHGELRSGI	NOKLEINDINK	VDFLIQGS	TDMN	V.AVEKKIWN	LGIIKNYK...	
	<i>So_cellu</i>	AGP41089	RVSHGELIRAGV	NOKLEINDINK	VDFLIQGN	LNLIS	GP.PYQQLP	WDLGVRINYAAG	
	<i>Cl_cellu</i>	ACL75596	NVSHGELIRAGY	NOKLEINDINK	VDFLIQGT	TNMM	A.AEQ0IWD	LDGLIRNYEGS	
	<i>Cl_cellu</i>	ACL75590	NVSHGELIRAGY	NOKLEINDINK	VDFLIQGT	TNMM	A.AEQ0IWD	LDGLIRNYEGS	
	<i>Cl_BHL1100</i>	AEV65176	NVSHGELIRAGY	NOKLEINDINK	VDFLIQGT	TDMS	P.EYQ0IWN	LDGLIRNY	
	<i>Cl_BHL1100</i>	AEV65171	NVSHGELIRAGY	NOKLEINDINK	VDFLIQGT	TDMS	P.EYQ0IWD	LDGLIRNYTGSF	
	<i>Te_turne</i>	ACR14088	QTSHGEMIRDGY	DEKMLVLDPCN	MOFLYQGV	DLNG	FNG.NVGERPYH	IGVLKQK...	
	<i>So_cellu</i>	CAN98023	DISHGEMVRSQS	DERMTINACN	MOFLYQGR	DPNA	GG AVERLPYK	LGLLITLTK...	
	<i>So_cellu</i>	CAN98020	DISHGELIRSGH	DEKMTIDPCD	LRFLYQGR	DPKW	GG DVGKLPYR	LGMLTLQK...	
	<i>Te_turne</i>	ACR13062	3.2.1.55	DISHGEMVRSAGH	DOFETIDPCN	LRFLYQGS	PPGS	GG DVHRLPWK	LGLLTQTNSAC
	<i>So_cellu</i>	CAN94755	DISHGEMVRSAGH	DOFETIDPCN	LRFLYQGR	NPNA	GG DVNSLPYR	LGLLVNLN	
	<i>So_cellu</i>	CAN94755	DISHGELVRDGN	DETATIDTCN	LOFLYQGR	NPSS	GG EYVHALPWR	LGLLKAVR...	
	<i>Op_terra</i>	ACB73617	DISHGELLRDGN	DETMTLDPSR	LYFLYQGR	RRELTTP	DP.SYDLPYQ	LALLQSDR...	
	<i>Op_terra</i>	ACB76517	DISHGELLRDGN	DETMTIDPDH	LYFLYQGR	GDAPA	GT.EYVHALPWR	LGLLQSTR...	
	<i>Am_medit</i>	ADJ49532	DISHGELIRITGY	DOTMEIDPCH	LQLLYQGV	NPNS	TNVP.SYDLPYQ	LGLLTQTN.PC	
	<i>Am_medit</i>	AF081241	DISHGELIRITGY	DOTMEIDPCH	LQLLYQGV	NPNS	TNVP.SYDLPYQ	LGLLTQTN.PC	
	<i>Le_macul</i>	CBX95362	STSHGELIRSDV	DQKLIKPTSG	IRFMYQGI	DPAA	SA.TYVHALPWR	LGLLTQDA...	
	<i>St_viola</i>	AEM84965	DISHGELIRITGN	DOTMTINPCR	QOFLYQGM	NPSA	GG DVNSLPWR	LGLLTQTNATC	
2	<i>Us_maydi</i>	EAK85571	DISHGDLIRSNP	DOTMTIDPCR	LQLLYQGR	DKNK	VPPSSV	DALPYR	RGLLTYLGL...
	<i>Sp_reill</i>	CB069122	DISHGDLIRSNP	DOTMTINPCR	LQLLYQGR	SPSA	TTSNV	DALPYR	RGLLTLASA...
	<i>Po_anser</i>	CAP65929	DISHGDLVRSNA	DOFETIDPCN	LQLLYQGR	SGMS	NE.VYVHALPWR	LGLLTLTN...	
	<i>Ma_oryza</i>	EAA47906	DISHGDLVRSNA	DOFETIDPCN	LQLLYQGR	SPNA	GG DVNSLPYR	RGLLTLQ...	
	<i>Ma_oryza</i>	EAA57262	DISHGDLVRSNA	DOFETIDPCN	LQLLYQGR	SPNA	GG DVNSLPYR	RGLLTLQ...	
	<i>Tr_aesti</i>	ABT18331	DISHGELVRTAN	DOFETIDPCN	LQLLYQGR	NPSS	NV.DYVHALPWR	RGLLTLRR...	
	<i>Fu_grami</i>	AAV66346	DISHGELVRTSN	DOFETIDPCN	LQLLYQGR	NPSS	NV.DYVHALPWR	RGLLTLRR...	
	<i>My_therm</i>	AE060934	DISHGDLIRIDA	NHTMPVDPGR	LQLLYQGR	S.GD	SA.DYVHALPWR	RGLLTLQG...	
	<i>As_niger</i>	CAA03159	DISHGDLVRNPP	DOTMTVDPCN	LQLLYQGH	DPNS	GG DVNSLPWK	PGVLTLLQ...	
	<i>As_tubin</i>	CA801408	3.2.1.55	DISHGDLVRNPP	DOTMTVDPCN	LQLLYQGH	DPNS	GG DVNSLPWK	PGVLTLLQ...
	<i>As_niger</i>	CAA03158	3.2.1.55	DISHGDLVRNPP	DOTMTVDPCN	LQLLYQGH	DPNS	GG DVNSLPWK	PGVLTLLQ...
	<i>As_niger</i>	CAK38069	3.2.1.55	DISHGDLVRNPP	DOTMTVDPCN	LQLLYQGH	DPNS	GG DVNSLPWK	PGVLTLLQ...
	<i>Pe_capsu</i>	CAN07245	3.2.1.55	DISHGDLVRSNP	DOTMTIDPCN	LQLLYQGR	NPAA	GG DVNSLPWK	PGVLTLLN...
	<i>Pe_chrysu</i>	CAP86032	DISHGDLVRSNP	DOTMTIDPCN	LQLLYQGR	EPNA	GG DVNSLPWK	PAVLTLLKN...	
	<i>Pe_chrysu</i>	BA671682	3.2.1.55	DISHGDLVRSNP	DOTMTIDPCN	LQLLYQGR	EPNA	GG DVNSLPWK	PAVLTLLKN...
	<i>As_nidul</i>	EAA59562	3.2.1.55	DISHGDLVRSNP	DOTMTIDPCN	LQLLYQGR	EPNA	GG DVNSLPWK	PAVLTLLKN...
	<i>As_nidul</i>	EAA62979	3.2.1.55	DISHGDLVRSNP	DOTMTIDPCN	LQLLYQGR	EPNA	GG DVNSLPWK	PAVLTLLKN...
	<i>As_oryza</i>	BAE62533	DISHGDLVRSNP	DOTMTVDPCN	LQLLYQGR	DPNA	GG DVNSLPWK	PGVLTLLQ...	
	<i>As_oryza</i>	BAE62533	DISHGDLVRSNP	DOTMTVDPCN	LQLLYQGR	DPNA	GG DVNSLPWK	PGVLTLLQ...	
	<i>As_sojae</i>	BA85252	3.2.1.55	DISHGDLVRSNP	DOTMTVDPCN	LQLLYQGR	DPNA	GG DVNSLPWK	PGVLTLLQ...
	<i>Th_terra</i>	AE070954	DISHGDLIRSSA	DOTMTIDPCN	LQLLYQGR	N.GS	GS.TYDLPYR	RGLLTLVG...	
	<i>Bo_fucke</i>	CCD43598	DISHGDLIRSSA	DOTMTIDPCN	LQLLYQGR	NPSS	NG.NYDTPYR	RGVLTLLK...	
	<i>Bi_zeico</i>	AA642252	3.2.1.55	DISHGDLVRVNT	DOTMTVDPCN	LQLLYQGR	APNS	GG DVNSLPWK	PGVLTLLK...
	<i>Ma_oryza</i>	EAA47965	DISHGDLVRSNA	DOFETIDPCN	LQLLYQGR	APNS	GG DVNSLPWK	PGVLTLLR...	
	<i>My_therm</i>	AE059813	DISHGELVRLSA	DOTFTIDPCN	LQLLYQGR	DPSS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ch_luckn</i>	AED84983	3.2.1.55	DISHGELVRLSA	DOTFTIDPCN	LQLLYQGR	DPSS	GG DVNSLPWK	PGVLTLLR...
	<i>Ac_N902-109</i>	AGL18056	DISHGELLRISA	DOTNTIDPCN	LQLLYQGR	ATNS	GG DVNSLPWK	PGVLTLLR...	
	<i>Tr_reese</i>	AAP57750	3.2.1.55	DISHGDLIRSNP	DOTMTIDPCN	LQLLYQGR	ATNS	GG DVNSLPWK	PGVLTLLR...
	<i>St_scabi</i>	CB669407	DISHGDLVRSNP	DOTMTIDPCN	LQLLYQGR	DPNA	NDP.DYVHALPWR	RGVLTLLR...	
	<i>Am_medit</i>	AEK41441	DISHGDLVRTNP	DOTKTVDPCH	LQMLYQGR	DPSS	DGM.DYVHALPWR	RGVLTLLR...	
	<i>Am_medit</i>	ADJ44701	DISHGDLVRTNP	DOTKTVDPCH	LQMLYQGR	DPSS	DGM.DYVHALPWR	RGVLTLLR...	
	<i>Th_bispo</i>	ADG88274	DISHGDLVRTNP	DOTKTVDPCH	LQMLYQGR	ATNS	GG DVNSLPWK	PGVLTLLR...	
	<i>St_venez</i>	CCA60032	DISHGDLVRTNP	DOTKTVDPCH	LQMLYQGR	SPOA	GG DVNSLPWK	PGVLTLLR...	
	<i>St_venez</i>	CCA60030	DISHGELIRAGA	DOTFTIDPCN	LQLLYQGR	DPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ac_mirum</i>	ACU38792	DISHGDLVRQNP	DOTKTVDPCH	LQLLYQGR	DPGA	TG.DYVHALPWR	RGVLTLLR...	
	<i>St_scabi</i>	CB667595	DISHGDLVRDNP	DOTMTVDPCN	LRLLYQGL	SPGTPSNT	PYVHALPWR	RGVLTLLR...	
	<i>St_davaw</i>	CCK27713	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGL	STTTPSGT	PYVHALPWR	RGVLTLLR...	
	<i>Mi_auran</i>	ADL45228	DISHGDLVRTNP	DOTKTVDPCH	LQLLYQGR	NPAA	GG DVNSLPWK	PGVLTLLR...	
	<i>Mi_L5</i>	ADU07461	DISHGDLVRTNP	DOTKTVDPCH	LQLLYQGR	NPAA	GG DVNSLPWK	PGVLTLLR...	
	<i>Ac_S50/110</i>	AEV83900	DISHGDLVRNPP	DOTMTVDPCN	LQLLYQGR	NPAA	GG DVNSLPWK	PGVLTLLR...	
	<i>Ac_N902-109</i>	AGL16784	DISHGDLVRTNP	DOTKTVDPCH	LQLLYQGR	NPAA	GG DVNSLPWK	PGVLTLLR...	
	<i>Ac_S50/110</i>	AEV83930	DISHGDLVRNPP	DOTMTVDPCN	LQLLYQGR	NPAA	GG DVNSLPWK	PGVLTLLR...	
	<i>St_chatt</i>	AAD32559	3.2.1.55	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGR	SPMTFPGT	SYDNLPTG	ILTLKR...
	<i>St_davaw</i>	CCK27711	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGR	SPMTFPGT	SYDNLPTG	ILTLKR...	
	<i>Am_medit</i>	ADJ46583	DISHGDLVRTNP	DOTKTVDPCH	LQLLYQGR	DPSS	GG DVNSLPWK	PGVLTLLR...	
	<i>Am_medit</i>	AEK43384	DISHGDLVRTNP	DOTKTVDPCH	LQLLYQGR	DPSS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ca_acidi</i>	ACU37344	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGR	DPSS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ki_setae</i>	BAJ33148	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGR	SPTA	TG.SYDLPYR	RGVLTLLQ...	
	<i>St_scabi</i>	CBG75744	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGR	SPSA	GG DVNSLPWK	PGVLTLLR...	
	<i>St_lvivid</i>	AA26524	3.2.1.55	DISHGDLVRDNP	DOTMTVDPCN	LQLLYQGR	APNA	GG DVNSLPWK	PGVLTLLR...
	<i>St_coeli</i>	CAA16189	DISHGDLVRDNP	DOTMTVDPCN	LQLLYQGR	SPNA	GG DVNSLPWK	PGVLTLLR...	
	<i>St_davaw</i>	CCK24720	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGR	SPTA	GG DVNSLPWK	PGVLTLLR...	
	<i>St_argen</i>	AGU42410	DISHGDLVRDNP	DOTMTIDPCN	LQLLYQGR	DPAA	GG DVNSLPWK	PGVLTLLR...	
	<i>St_rapam</i>	AGP52116	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGR	SPSA	GG DVNSLPWK	PGVLTLLR...	
	<i>St_hygro</i>	AEV86327	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGR	SPSA	GG DVNSLPWK	PGVLTLLR...	
	<i>St_hygro</i>	AGF60549	DISHGDLVRNPP	DOTMTIDPCN	LQLLYQGR	SPSA	GG DVNSLPWK	PGVLTLLR...	
	<i>Th_terra</i>	AE064662	DISHGDLVRTNP	DOTKTVDPCH	LQLLYQGR	APNS	GG DVNSLPWK	PGVLTLLR...	
	<i>No_dasso</i>	ADH68352	DISHGELIRVTA	DOTMTVDACD	MRFYQGR	SPGS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ac_S50/110</i>	AEV83898	DISHGELVRTNP	DOTMTVDPCN	LQLLYQGR	SPSS	GG DVNSLPWK	PGVLTLLR...	
	<i>C_gilvu</i>	AEI13179	DISHGELLRISA	DOTMTVDPCN	LQLLYQGR	SPSS	GG DVNSLPWK	PGVLTLLR...	
	<i>C_fimi</i>	AE47269	DISHGELIRISA	DOTMTIDPCN	LQLLYQGR	SPSS	GG DVNSLPWK	PGVLTLLR...	
	<i>St_therm</i>	BAB84113	3.2.1.55	DISHGELIRISA	DOTMTVDPCN	LQLLYQGR	DPSS	GG DVNSLPWK	PGVLTLLR...
	<i>Ce_flavi</i>	ADG75907	DISHGELLRISA	DOTMTVDPCN	LQLLYQGR	SPQS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ce_flavi</i>	ADG75732	DISHGELLRISA	DOTMTVDPCN	LQLLYQGR	SPQS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ve_maris</i>	AE847822	DISHGELIRISA	DOTMTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ve_maris</i>	AE847440	DISHGELIRISA	DOTMTVDPCN	LQLLYQGR	APNS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ve_maris</i>	AE847815	DISHGELIRISA	DOTMTVDPCN	LQLLYQGR	APNS	GG DVNSLPWK	PGVLTLLR...	
	<i>St_scabi</i>	CBG74885	DISHGELLRISA	DOTMTVDPCN	LQLLYQGR	SPGS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ac_N902-109</i>	AGL19117	DISHGELVRTSA	DOTMTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>St_bingc</i>	AD106184	DISHGELIRITSP	DOTMTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>St_flavo</i>	ADN07591	DISHGELLRISA	DOTMTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>St_PAMC26508</i>	AGJ52854	DISHGELLRISA	DOTMTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>Ac_misso</i>	BAL88054	DISHGELIRVTA	DOTMTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>Mi_auran</i>	ADL49492	DISHGELIRITTA	DOTFTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>Mi_L5</i>	ADU11518	DISHGELIRITTA	DOTFTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>Mi_auran</i>	ADL46532	DISHGELIRITTA	DOTFTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	
	<i>Mi_L5</i>	ADU10857	DISHGELIRITTA	DOTFTVDPCN	LQLLYQGR	SPNS	GG DVNSLPWK	PGVLTLLR...	

Structural characterization of GH62 α -L-arabinofuranosidases

		β 1		β 2		β 3		
		1	10	20	30	40	50	
<i>Us_maydi</i> EAK85571		LSNQPPSDLP	TTTQWITSTG	PLV	GPKN.DGRGI	AGIKDPTIIL	INGTHHVF	
<i>Po_anser</i> CAP62336 3.2.1.55		LSNQPPSDLP	TTTQWITSTG	PLV	GPKN.DGRGI	AGIKDPTIIL	INGTHHVF	
Am_medit	AEK42553	TLP	SRYSSSSG	PLI	APKSDATHDI	AGIKDPTIVVY	ADGKYHVF	
Am_medit	ADJ45772	TLP	SRYSSSSG	PLI	APKSDATHDI	AGIKDPTIVVY	ADGKYHVF	
P1_indic	CCA70773	TLP	SSFRSSSG	ALV	SPKN.DSRNI	KGIKDP	SIIVYNGKYHVF	
P1_indic	CCA70772	TLP	SSFRSSSG	ALV	SPKN.DSRNI	KGIKDP	SIIVYNGKYHVF	
P1_indic	CCA70771	TLP	SSFRSSSG	ALV	SPKN.DSRNI	KGIKDP	SIIVYNGKYHVF	
un AC007729		TLP	SSFRSSSG	PLV	EPKN.DGRNI	AGIKDPTIVK	VDCTYHVF	
un AC005660		ATGSLP	TSFRSSSTN	ALV	GPKN.DGRNL	AGIKDPTIIE	VDGTYHVF	
un_bacte	AFY23018	ALP	SSFRSSSG	VLI	SPKSDATHNI	LAVKDP	ITVVRHNR	
Co_ciner	BAK14423 3.2.1.55	PAPAPSGKLP	SSFRSSSG	PLI	GPKS.DSRRI	QGIKDP	SIIVYHDGR	
Ac_mirum	ACU37207	GSLP	SSFRSSSG	ALI	GPKPDSSHAT	IVSKDP	SIIVRHNGR	
St_bingc	ADI13053	ALP	GSFSSSSG	ILM	SPKPDSTHNI	AGLKDPTIVVY	YNGKYHVF	
Cl_sacch	AGF55270	AANP	NPTIQV	G.SVCFYNGPTN	AWDA	VSVKDP	SIIVYANGKYH	
So_cellu	AGP41089	AATA	NPTIYVDA	PIL	YKAKAEPYDH	YAVKDP	ITIVYSGGKYH	
Cl_cellu	ACL75596	AANP	NPSWVDE	RVI	FHQCCSPYDY	YAAKDP	ITIVYNGKYLV	
Cl_cellu	ACL75590	AANP	NPSWVDE	RVI	FHQCCSPYDY	YAAKDP	ITIVYNGKYLV	
Cl_BNL1100	AEY65176	AANP	NPSWVDE	RVI	FHQCCSPYDY	YAAKDP	ITIVYNGKYLV	
Cl_BNL1100	AEY65171	AANP	NPSWVDE	RVI	FHQCCSPYDY	YAAKDP	ITIVYNGKYLV	
Te_turne	ACR14088	CGNNTAAP	LISWTSAG	PLI	SPKE	FVAKDP	ITIVYNNQYH	
So_cellu	CAN98023	TCDLPL	TSFRSSSG	PVI	NPKSAAGNF	VSFKDP	ITIVPQKGYH	
So_cellu	CAN98020	PTCDLPL	TSFRSSSG	PVI	NPKSAAGNF	VSFKDP	ITIVPQKGYH	
Ce_japon	ACE85320 3.2.1.55	CELK	APLRITSTG	PLI	SPKN	ISIKDP	SIIVKYNDR	
Te_turne	ACR13064	ELP	GQLSITSTS	PVI	APAO	SSW	ASVKDP	SIIVRYNDR
So_cellu	CAN94755	CGLP	TSFRSSSG	ALV	SPKSDATHNI	IVSKDP	ITVVFNDR	
Op_terra	ACB73617	DGLT	GPFFITSTA	PLI	APVADATHPI	IVSKDP	ITIVYHNGK	
Op_terra	ACB76517	IAALAP	FAMITSTG	PLI	SPVSDTTHSI	IVAKDP	ITIVYNGK	
Am_medit	ADJ49532	NLP	SSFRITDQG	PLI	SAKPVSGHNI	IVSKDP	SIIVRYNG	
Am_medit	AF081241	NLP	SSFRITDQG	PLI	SAKPVSGHNI	IVSKDP	SIIVRYNG	
Le_macul	CBX95362	PLP	RNFSSSSN	VLV	TPKN.DDRNV	AGIKDPTIIO	HNGKYHVF	
St_viola	AEM84965	QLP	GSFQSSSG	QLI	APKPDASHPV	IVSKDP	ITIVQADG	
2 Us_maydi	EAK85571	ALP	TTYRTSSA	PLA	QPKD	GW	VSFKDP	ITIVPYNG
Sp_relli	CBQ69122	ALP	TTYRTSSA	PLA	QPKD	GW	VSFKDP	ITIVPYNG
Po_anser	CAP59529	PGADAACSPL	TSYRWRDSC	ILA	QPKS	GW	VSFKDP	ITIVPQK
Ma_oryza	EAA47906	QCTLPL	TSYRWRDSC	ILA	QPKS	GW	VSFKDP	ITIVPQK
Ma_oryza	EAA37262	QCTLPL	TSYRWRDSC	ILA	QPKS	GW	VSFKDP	ITIVPQK
Tr_aesti	ABT18331	AQCSLPL	TSYRTSSG	PLA	QPKD	GW	VSFKDP	ITIVAPYNG
Fu_grami	AAV66346	QCALP	TSYRTSSG	PLA	QPKS	PF	KNLKD	ITIVAPYNG
My_therm	AE060934	SLP	SSYRTSTG	ALA	QPKS	GW	ANLKD	ITIVPYNG
As_niger	CAA03159	KCALP	SSYRTSTG	ALA	TPKS	GW	TALKD	ITIVVSDG
As_tubin	CAB01408 3.2.1.55	KCALP	SSYRTSTG	ALA	TPKS	GW	TALKD	ITIVVSDG
As_niger	CAA03158 3.2.1.55	KCALP	SSYRTSTG	ALA	TPKS	GW	TALKD	ITIVVSDG
As_niger	CAK38069 3.2.1.55	KCALP	SSYRTSTG	ALA	TPKS	GW	TALKD	ITIVVSDG
Pe_capsu	CAM07245 3.2.1.55	NCALP	STYSRTSTG	ALA	NPKP	GW	TALKD	ITIVVSDG
Pe_chrys	CAP86032	ALP	STYSRTSTG	ALA	NPKS	GW	VALKD	ITIVVSDG
Pe_chrys	BAG11682 3.2.1.55	DCALP	STYSRTSTG	ALA	NPKS	GW	VALKD	ITIVVSDG
As_nidul	EAA59562 3.2.1.55	QCGLP	STYSRTSTG	PLA	EPKD	GW	ASLKD	ITIVAPYNG
As_nidul	EAA62979	QCGLP	STYSRTSTG	PLA	EPKD	GW	ASLKD	ITIVAPYNG
As_oryza	BAE62533	QCGLP	SSYRTSTG	ALA	EPKA	GW	ASLKD	ITIVVSDG
As_oryza	BAE85252 3.2.1.55	QCGLP	SSYRTSTG	ALA	EPKA	GW	ASLKD	ITIVVSDG
Th_erre	AE070954	ALP	SSYRTSTG	ALA	TPKS	GW	VSFKD	ITIVPQK
Bo_fucke	CDC43598	ACALP	SKYSRTSTG	ALA	TPKS	GW	ASLKD	ITIVVSDG
Bi_zeico	AAG42252 3.2.1.55	QSCKLP	TSYRTSSG	ALA	QPKS	GW	ANLKD	ITIVVSDG
Ma_oryza	EAA47965	ALP	STYRTSSG	ALA	QPKN	GW	ASLKD	ITIVANNGR
My_therm	AE059813	QSCCLP	SSYRTSTG	ALA	QPKS	PW	VSFKD	ITIVPQK
ChLuckn	AED84983 3.2.1.55	QSCCLP	SSYRTSTG	ALA	QPKS	PW	VSFKD	ITIVPQK
Ac_N902-109	AGL18056	CALP	TSYRTSTG	PLA	QPKS	GW	ASLKD	ITIVAPYNG
Tr_reese	AAP57750 3.2.1.55	APATCTLP	TSYRTSTG	ALA	SPKS	GW	VSFKD	ITIVVSDG
St_scabi	CBG69407	NCSCLP	TSYRTSTG	PLA	QPKN	GW	VSFKD	ITIVVSDG
Am_medit	AEK41441	ATCTLP	TSYRTSTG	PLA	NPKS	GW	VALKD	ITIVVSDG
Am_medit	ADJ44701	ATCTLP	TSYRTSTG	PLA	NPKS	GW	VALKD	ITIVVSDG
Th_bispo	ADG88274	VTCCLP	TSYRTSTG	PLA	NPKS	GW	VSFKD	ITIVVSDG
St_venez	CA60032	CMLP	TSYRTSTG	ALA	QPKA	GW	ASLKD	ITIVVSDG
St_venez	CA60030	ALP	SSYRTSTG	ALA	EPKA	GW	ASLKD	ITIVVSDG
Ac_mirum	ACU38792	CMLP	SSYRTSTG	ALA	NPKS	GW	LALKD	ITIVVSDG
St_scabi	CBG67595	TLP	TSYRTSTG	PLA	QPKN	GW	VSFKD	ITIVVSDG
St_davaw	CCK27713	ALP	TSYRTSTG	PLA	QPKN	GW	VSFKD	ITIVVSDG
Mi_auran	ADL45228	ALP	TSYRTSTG	ALA	NPKN	GW	VSFKD	ITIVVSDG
Mi_L5 ADU07461		ALP	TSYRTSTG	ALA	NPKN	GW	VSFKD	ITIVVSDG
Ac_SE50/110	AEV83900	CTLP	TSYRTSTG	ALA	QPKS	GW	VALKD	ITIVVSDG
Ac_N902-109	AGL16784	CTLP	SSYRTSTG	ALA	TPKN	GW	TSFKD	ITIVVSDG
Ac_SE50/110	AEV85830	TLP	SSYRTSTG	ALA	QPKN	GW	TSFKD	ITIVVSDG
St_chatt	AAD32559 3.2.1.55	APKSDTCLP	TSYRTSTG	PLA	QPKN	GW	ASLKD	ITIVVSDG
St_davaw	CCK27711	ALP	TSYRTSTG	PLA	QPKN	GW	ASLKD	ITIVVSDG
Am_medit	ADJ46583	CTLP	SSYRTSSG	ALA	QPKN	GW	LSLKD	ITIVVSDG
Am_medit	AEK43384	CTLP	SSYRTSSG	ALA	QPKN	GW	LSLKD	ITIVVSDG
Ca_acidi	ACU73744	SLP	STYRTSTG	ALA	TPQN	GW	VSFKD	ITIVVSDG
Kl_setae	BAJ33148	CMLP	TSYRTSTG	ALA	QPKN	GW	ASVKD	ITIVVSDG
St_scabi	CBG75744	ALP	TSYRTSTG	PLA	QPKN	GW	ASVKD	ITIVVSDG
St_livid	AAC26524 3.2.1.55	TDGTCLP	TSYRTSTG	VLA	QPKS	GW	VALKD	ITIVVSDG
St_coeli	CAA16189	PPTDGTCLP	TSYRTSTG	VLA	QPKS	GW	VALKD	ITIVVSDG
St_davaw	CCK24720	GTCCLP	TSYRTSTG	VLA	QPKN	GW	ASVKD	ITIVVSDG
St_argen	AGU42410	ALP	TSYRTSTG	VLA	QPKN	GW	LALKD	ITIVVSDG
St_rapam	AGP52116	ATSACSLP	TSYRTSTG	VLA	QPKN	GW	VSFKD	ITIVVSDG
St_hygro	AEY86327	SLP	TSYRTSTG	ALA	QPKN	GW	VSFKD	ITIVVSDG
St_hygro	AGF60549	SLP	TSYRTSTG	ALA	QPKN	GW	VSFKD	ITIVVSDG
Th_erre	AE064662	DLP	TTYKWTSTG	ALA	QPKN	GW	TSFKD	ITIVVSDG
No_dasso	ADH68352	CALP	SSYRTSTG	PLA	QPKP	GW	ASLKD	ITIVVSDG
Ac_SE50/110	AEV83898	ALP	SSYRTSTG	ALA	TPKS	GR	VALKD	ITIVVSDG
[C_gilvu]	AEI13179	QLP	SSYRTSTG	ALA	NPKS	GW	ASLKD	ITIVVSDG
Ce_fiml	AE47269	CMLP	TSYRTSTG	ALA	QPKS	GW	ASLKD	ITIVVSDG
St_therm	BAB84113 3.2.1.55	CELPL	TSYRTSTG	ALA	QPKS	GW	VSFKD	ITIVVSDG
Ce_flavi	ADG75907	CELPL	TSYRTSTG	VLA	QPKS	GW	VSFKD	ITIVVSDG
Ce_flavi	ADG75732	NLP	SSYRTSSG	VLA	QPKS	GW	VSFKD	ITIVVSDG
Ve_maris	AEB47822	DLP	SSYRTSSG	VLA	QPKS	GW	VSFKD	ITIVVSDG
Ve_maris	AEB47470	CNLP	SSYRTSSG	VLA	QPKS	GW	VSFKD	ITIVVSDG
Ve_maris	AEB47815	CNLP	SSYRTSSG	VLA	QPKS	GW	VSFKD	ITIVVSDG
St_scabi	CBG74885	DLP	SSYRTSSG	VLA	QPKS	GW	VSFKD	ITIVVSDG
Ac_N902-109	AGL19117	TLP	SSYRTSTG	ALA	TPRS	GW	VSFKD	ITIVVSDG
St_bingc	ADI06184	DLP	TSYRTSTG	ALA	QPKP	GW	VSFKD	ITIVVSDG
St_flavo	ADW07591	DLP	SAYRTSTG	ALA	QPKQ	GW	VSFKD	ITIVVSDG
St_PAMC26508	AGJ52854	SCDLP	SAYRTSTG	ALA	QPKQ	GW	VSFKD	ITIVVSDG
Ac_misso	BAL88054	SLP	TSYRTSTG	ALA	QPKS	GW	VSFKD	ITIVVSDG
Mi_auran	ADL49492	CNLP	SSYRTSSG	VLA	QPKS	GW	VSFKD	ITIVVSDG
Mi_L5 ADU11518		CNLP	SSYRTSSG	VLA	QPKS	GW	VSFKD	ITIVVSDG
Mi_auran	ADL46532	CNLP	SSYRTSSG	VLA	QPKS	GW	VSFKD	ITIVVSDG
Mi_L5 ADU10857		CNLP	SSYRTSSG	VLA	QPKS	GW	VSFKD	ITIVVSDG

Structural characterization of GH62 α -L-arabinofuranosidases

Accession	Gene	Strain	Protein	β4	η1	β5	β6	η2	β7																																																			
<i>Us maydi</i>	EAK85571		...	→	→	→	→	→	→																																																			
<i>Po_anser</i>	CAP62336	3.2.1.55	...	→	→	→	→	→	→																																																			
				60	70	80	90	100	110																																																			
1	<i>Po_anser</i>	CAP62336	3.2.1.55	...Q	SAGY	N	L	V	V	F	F	T	A	D	A	D	A	P	N	A	T	F	F	Y	L	D	D	Q	A	P	L	G	T	G	Y	R	A	A	P	Q	V	F	F	F	A	P	K	L	N	Y	L	V	V	Q	.	N	G			
	<i>Am_medit</i>	AEK42553		...N	AAGY	N	L	V	V	L	S	F	T	D	W	A	Q	A	G	S	A	T	Q	Y	L	D	D	Q	S	G	.	I	G	T	G	Y	R	A	A	P	E	V	F	F	F	A	P	O	K	L	N	Y	L	V	V	Q	.	D	G	
	<i>Am_medit</i>	ADJ45772		...N	AAGY	N	L	V	V	L	S	F	T	D	W	A	Q	A	G	S	A	T	Q	Y	L	D	D	Q	S	G	.	I	G	T	G	Y	R	A	A	P	E	V	F	F	F	A	P	O	K	L	N	Y	L	V	V	Q	.	D	G	
	<i>Pi_indic</i>	CCA70773		...V	ASGY	N	L	V	V	F	S	F	T	D	W	A	Q	A	G	S	A	T	F	F	Y	L	D	D	Q	T	P	.	I	G	S	G	Y	R	A	A	P	Q	V	F	F	F	A	P	O	N	R	N	Y	L	V	V	Q	.	N	G
	<i>Pi_indic</i>	CCA70772		...V	ASGY	N	L	V	V	F	S	F	T	D	W	A	Q	A	G	S	A	T	F	F	Y	L	D	D	Q	T	P	.	I	G	S	G	Y	R	A	A	P	Q	V	F	F	F	A	P	O	N	R	N	Y	L	V	V	Q	.	N	G
	<i>Pi_indic</i>	CCA70771		...V	ASGY	N	L	V	V	F	S	F	T	D	W	A	Q	A	G	S	A	T	F	F	Y	L	D	D	Q	T	P	.	I	G	S	G	Y	R	A	A	P	Q	V	F	F	F	A	P	O	N	R	N	Y	L	V	V	Q	.	N	G
	<i>un AC007729</i>			...T	KSGY	N	L	V	V	F	N	F	K	D	F	S	Q	A	N	A	T	F	F	Y	L	D	D	Q	T	P	.	I	G	S	G	Y	R	A	A	P	Q	V	F	F	F	K	P	H	N	L	N	Y	L	V	F	Q	.	N	G	
	<i>un AC005660</i>			...Q	ASGY	N	L	V	V	F	N	F	T	D	F	N	Q	A	G	N	A	P	F	F	Y	L	D	D	Q	S	G	.	I	G	T	G	Y	R	A	A	P	Q	V	F	F	F	Q	P	H	L	N	Y	L	V	F	Q	.	N	G	
	<i>un_bacte</i>	AFY23018		...N	SAGY	N	M	M	T	T	S	F	G	D	W	S	Q	A	A	S	A	P	H	F	L	D	R	S	G	.	I	G	A	G	Y	R	A	A	P	Q	V	F	F	F	A	P	O	N	R	N	Y	L	V	V	Q	.	T	G		
	<i>Co_ciner</i>	BAK14423	3.2.1.55	...N	KTEG	N	L	V	V	I	S	F	T	D	W	A	Q	A	G	S	A	S	F	F	Y	L	D	D	Q	A	P	.	L	G	T	G	Y	R	A	A	P	Q	V	F	F	F	A	P	O	K	L	N	Y	L	V	V	Q	.	N	G
	<i>Ac_mirum</i>	ACU37207		...T	NGY	N	L	V	V	H	S	F	T	D	W	S	Q	A	A	S	A	P	H	F	L	D	R	S	G	.	I	G	T	G	Y	R	A	A	P	Q	V	F	F	F	A	P	O	R	L	N	Y	L	V	V	Q	.	T	G		
	<i>St_bingc</i>	ADI13053		...S	ASGY	N	L	V	V	L	N	F	S	T	D	W	S	Q	A	A	S	A	P	H	F	L	D	R	S	G	.	I	G	T	G	Y	R	A	A	P	Q	V	F	F	F	A	P	O	R	T	N	Y	L	V	V	Q	.	T	G	
	<i>Cl_sacch</i>	AGF55270		...D	KTKF	Q	M	G	Y	A	S	A	S	T	I	N	G	L	S	A	Q	H	K	L	N	L	N	G	.	N	G	T	G	S	Y	G	A	P	Q	V	F	F	F	M	S	K	O	M	N	Y	L	V	V	Q	.	I	G			
	<i>So_cellu</i>	AGP41089		...N	ASGW	Q	M	L	Y	S	A	T	T	M	E	G	F	R	I	A	P	H	I	V	L	S	R	I	G	.	E	S	F	C	A	P	E	L	F	F	F	E	P	H	N	L	N	Y	L	V	V	Q	.	D	G					
	<i>Cl_cellu</i>	ACL75596		...N	KSGW	Q	M	C	F	T	S	A	S	T	I	S	G	L	K	T	A	P	R	T	Y	M	S	K	I	G	.	E	S	F	C	A	P	E	L	F	F	F	E	P	O	K	L	N	Y	L	V	V	Q	.	D	G				
	<i>Cl_cellu</i>	ACL75590		...N	KSGW	Q	M	C	F	T	S	A	S	T	I	S	G	L	K	T	A	P	R	T	Y	M	S	K	I	G	.	E	S	F	C	A	P	E	L	F	F	F	E	P	O	K	L	N	Y	L	V	V	Q	.	D	G				
	<i>CL_BNL1100</i>	AEY65176		...N	KSGW	Q	M	C	F	T	S	A	S	T	I	A	G	L	K	T	A	P	R	T	Y	M	S	K	I	G	.	E	S	F	C	A	P	E	L	F	F	F	E	P	O	K	L	N	Y	L	V	V	Q	.	D	G				
	<i>CL_BNL1100</i>	AEY65171		...N	KSGW	Q	M	C	F	T	S	A	S	T	I	A	G	L	K	T	A	P	R	T	Y	M	S	K	I	G	.	E	S	F	C	A	P	E	L	F	F	F	E	P	O	K	L	N	Y	L	V	V	Q	.	D	G				
	<i>Te_turne</i>	ACR14088		...D	GNK	S	M	I	O	I	T	.	L	D	N	L	.	A	Q	A	T	T	N	Y	O	P	F	S	P	N	T	.	G	S	S	A	V	A	P	Q	V	F	F	T	P	O	K	N	Y	L	V	V	Q	.	W	P				
	<i>So_cellu</i>	CAN98023		...D	TAGN	G	W	S	V	Y	L	N	F	T	D	F	S	Q	A	A	S	Q	O	H	H	M	A	N	W	.	T	G	G	T	V	A	P	Q	V	F	F	F	R	P	H	N	K	N	Y	L	V	V	Q	.	W	N				
	<i>So_cellu</i>	CAN98020		...D	TAGN	G	W	S	V	Y	L	N	F	T	D	F	S	Q	A	A	S	Q	O	H	H	M	A	N	W	.	T	G	G	T	V	A	P	Q	V	F	F	F	R	P	H	N	K	N	Y	L	V	V	Q	.	W	N				
	<i>So_cellu</i>	CAN98020		...D	TAGN	G	W	S	V	Y	L	N	F	T	D	F	S	Q	A	A	S	Q	O	H	H	M	A	N	W	.	T	G	G	T	V	A	P	Q	V	F	F	F	R	P	H	N	K	N	Y	L	V	V	Q	.	W	N				
	<i>Te_japan</i>	ACE85320	3.2.1.55	...D	TAYR	S	M	.	Y	T	S	F	T	D	W	T	A	Q	A	P	H	I	S	M	N	G	S	R	.	V	G	N	T	V	A	P	Q	V	F	F	F	R	P	H	N	K	N	Y	L	V	V	Q	.	W	A					
	<i>Te_turne</i>	ACR13064		...D	NGL	S	S	G	I	.	Y	M	N	F	S	D	F	T	Q	A	S	A	T	O	N	Y	M	R	N	T	.	V	G	N	T	V	A	P	Q	V	F	F	T	P	O	N	R	N	Y	L	V	V	Q	.	W	G				
	<i>So_cellu</i>	CAN94755		...N	TAGN	.	Q	M	T	Y	L	N	F	T	D	F	S	Q	A	A	S	A	S	H	Y	L	D	R	T	.	G	F	S	G	Y	C	A	P	Q	V	F	F	F	R	P	O	N	K	N	Y	L	V	V	Q	.	S	Q			
	<i>Op_terra</i>	ACB73617		...D	TSGN	.	S	M	T	Y	L	S	F	R	T	W	A	E	A	S	A	A	R	P	Y	L	D	O	N	P	.	N	L	R	G	Y	H	C	A	P	Q	V	F	F	R	P	O	K	N	Y	L	V	V	Q	.	S	H			
	<i>Op_terra</i>	ACB76517		...D	TSGN	.	S	M	T	Y	L	S	F	R	T	W	A	E	A	S	A	A	R	P	Y	L	D	O	N	P	.	N	L	R	G	Y	H	C	A	P	Q	V	F	F	R	P	O	K	N	Y	L	V	V	Q	.	S	H			
	<i>Am_medit</i>	ADJ49532		...D	TSGA	.	S	V	E	Y	H	F	T	D	F	S	Q	A	A	S	Q	Y	H	L	S	D	N	P	N	L	G	H	R	Y	M	A	P	Q	V	F	F	A	P	O	K	N	Y	L	V	V	Q	.	O	G						
	<i>Am_medit</i>	AF081241		...D	TSGA	.	S	V	E	Y	H	F	T	D	F	S	Q	A	A	S	Q	Y	H	L	S	D	N	P	N	L	G	H	R	Y	M	A	P	Q	V	F	F	A	P	O	K	N	Y	L	V	V	Q	.	O	G						
	<i>Le_macul</i>	CBX95362		...K	EAGY	.	S	L	V	V	F	N	F	T	D	F	S	Q	A	A	N	R	A	P	F	F	L	D	Q	S	A	.	I	G	T	G	Y	R	A	A	P	Q	V	F	F	F	A	P	O	K	L	N	Y	L	V	V	Q	.	N	G
	<i>St_viola</i>	AEK965		...N	TSGA	.	S	M	A	Y	T	S	F	T	D	F	S	Q	A	A	S	A	S	H	Y	L	D	R	T	.	G	F	S	G	Y	C	A	P	Q	V	F	F	F	R	P	O	N	K	N	Y	L	V	V	Q	.	T	G			
	<i>Us_maydi</i>	EAK85571		...D	STKY	G	S	M	A	F	S	P	F	K	H	W	A	D	M	A	T	A	T	Q	T	G	M	T	Q	A	.	V																												

Structural characterization of GH62 α -L-arabinofuranosidases

		β12 → →→→ →→→		→ →→→ →→→		β13 → →→→ →→→		→→→ →→→ →→→		β14 → →→→ →→→																																																
		170		180		190		200		210																																																
<i>Us_maydi</i>	EAK85571																																																									
<i>Po_anser</i>	CAP62336	3.2.1.55																																																								
1	<i>Po_anser</i>	CAP62336	3.2.1.55	SDDN	G	Q	L	Y	R	S	E	T	S	I	L	E	F	P	N	G	M	S	D	P	V	T	A	M	Q	D	N	R	N	D	...	L	F	E	A	A	C	V	V	S	L	...	P	D	G	K	...							
	<i>Am_medit</i>	AEK42553		SDDN	G	H	L	Y	R	S	Q	T	S	V	A	N	F	F	E	P	N	G	M	S	D	P	V	I	A	A	Q	D	A	D	R	Y	A	...	L	F	E	A	S	N	V	V	K	V	...	A	G	A	D	Q	...			
	<i>Am_medit</i>	ADJ45772		SDDN	G	H	L	Y	R	S	Q	T	T	L	A	N	F	F	E	P	N	G	M	S	D	P	V	I	A	A	Q	D	A	D	R	Y	A	...	L	F	E	A	S	N	V	V	K	V	...	A	G	A	D	Q	...			
	<i>Pi_indic</i>	CCA78773		SDDN	G	H	L	Y	R	S	Q	T	T	L	A	N	F	F	E	P	N	G	M	S	D	P	V	I	A	A	Q	D	A	D	R	Y	A	...	L	F	E	A	S	N	V	V	K	V	...	A	G	A	D	Q	...			
	<i>Pi_indic</i>	CCA78772		SDDN	G	H	L	Y	R	S	Q	T	T	L	A	N	F	F	E	P	N	G	M	S	D	P	V	I	A	A	Q	D	A	D	R	Y	A	...	L	F	E	A	S	N	V	V	K	V	...	A	G	A	D	Q	...			
	<i>Pi_indic</i>	CCA78771		SDDN	G	H	L	Y	R	S	Q	T	T	L	A	N	F	F	E	P	N	G	M	S	D	P	V	I	A	A	Q	D	A	D	R	Y	A	...	L	F	E	A	S	N	V	V	K	V	...	A	G	A	D	Q	...			
	<i>un</i>	ACQ07729		SDDN	G	H	L	Y	R	S	Q	T	S	L	A	N	F	F	E	P	N	G	M	S	D	P	V	I	A	A	Q	D	S	N	K	N	A	...	L	F	E	A	S	N	V	V	H	T	...	A	G	N	G	E	...			
	<i>un</i>	ACQ05660		SDDN	G	H	L	Y	R	S	Q	T	S	L	A	N	F	F	E	P	N	G	M	S	D	P	V	I	A	A	Q	D	S	N	P	N	N	...	L	F	E	A	S	N	V	V	H	T	...	A	G	N	G	E	...			
	<i>un</i>	bacte	AFY23018	SDDN	G	H	L	Y	R	A	Q	T	T	V	A	N	F	F	E	P	N	G	F	T	N	T	V	M	V	M	S	D	S	N	K	Y	A	...	L	W	E	A	S	N	V	V	K	V	...	Q	G	T	A	N	Q	...		
	<i>Co_ciner</i>	BAK14423	3.2.1.55	SDDN	G	H	L	Y	R	S	Q	T	S	L	A	N	F	F	E	P	N	G	F	N	E	P	V	I	A	M	Q	D	S	N	K	N	R	...	L	F	E	A	A	N	V	R	I	...	D	G	S	N	E	...				
	<i>Ac_mirum</i>	ACU37207		SDDN	G	H	L	Y	R	S	Q	T	S	L	A	N	F	F	E	P	N	G	F	T	N	T	V	I	A	M	Q	D	S	N	R	N	R	...	L	F	E	A	S	N	I	V	K	V	...	A	G	K	N	Q	...			
	<i>St_bingc</i>	ADI13053		SDDN	G	H	L	Y	R	S	Q	T	T	L	A	N	F	F	E	P	N	G	F	T	N	T	V	I	A	A	Q	D	S	N	K	Y	A	...	L	F	E	A	S	N	V	V	K	V	...	Q	G	S	N	Q	...			
	<i>Cl_sacch</i>	AGF55270		TPSD	G	S	H	N	I	Y	C	R	K	T	S	L	A	N	F	F	E	P	N	G	W	G	P	A	T	V	A	...	V	K	D	...	T	F	E	G	A	C	V	V	K	S	...	K	A	D	N	N	...					
	<i>So_cellu</i>	AGP41089		TPDD	G	S	R	R	L	Y	V	R	K	T	A	R	G	S	F	F	P	N	G	W	G	S	P	S	V	A	I	D	T	F	E	G	A	H	V	V	K	S	...	L	A	D	G	Q	...				
	<i>Cl_cellu</i>	ACL75596		TPSD	G	S	G	K	L	Y	M	R	K	T	T	L	A	N	F	F	E	P	N	G	W	S	T	P	T	V	A	V	F	E	G	A	A	V	V	K	S	...	L	A	D	G	Q	...				
	<i>Cl_cellu</i>	ACL75590		TPSD	G	S	G	K	L	Y	M	R	K	T	T	L	A	N	F	F	E	P	N	G	W	S	T	P	T	V	A	V	F	E	G	A	A	V	V	K	S	...	L	A	D	G	Q	...				
	<i>Cl_BNL1100</i>	AEY65176		TPSD	G	S	G	K	L	Y	M	R	K	T	A	L	A	N	F	F	E	P	N	G	W	S	T	P	T	V	S	V	F	E	A	A	V	V	K	S	...	L	A	D	G	Q	...					
	<i>Cl_BNL1100</i>	AEY65171		TPSD	G	S	G	K	L	Y	M	R	K	T	A	L	A	N	F	F	E	P	N	G	W	S	T	P	T	V	S	V	F	E	A	A	V	V	K	S	...	L	A	D	G	Q	...					
	<i>Te_turne</i>	ACR14088		FKDD	G	K	M	Y	N	S	T	P	V	D	N	F	F	E	P	N	G	F	D	P	G	T	T	F	K	V	A	D	I	E	D	S	G	P	T	...	N	I	V	F	E	A	G	N	I	K	T	...	K	N	S	D	Y	...
	<i>So_cellu</i>	CAN98023		SRDD	G	K	L	Y	R	S	K	V	S	I	D	K	F	F	A	...	F	D	G	Y	E	T	V	M	T	A	P	S	A	G	L	...	L	F	E	A	S	N	V	V	K	V	...	D	G	T	N	K	...					
	<i>So_cellu</i>	CAN98020		SRDD	G	K	L	Y	R	S	K	V	S	I	D	K	F	F	A	...	F	D	G	Y	E	T	V	M	S	A	P	S	A	G	L	...	L	F	E	A	S	N	V	V	K	V	...	D	G	S	N	K	...					
	<i>Ce_japon</i>	ACE85320	3.2.1.55	SRDD	G	V	L	Y	S	K	T	L	A	N	F	F	N	...	F	S	G	Y	T	V	M	E	D	H	R	G	N	G	S	Y	...	L	F	E	A	A	N	V	V	K	L	...	D	G	Q	N	R	...						
	<i>Te_turne</i>	ACR13064		SRDD	G	T	L	Y	M	S	K	T	S	I	G	N	F	F	...	F	S	G	Y	T	T	V	M	S	G	A	Q	N	V	...	L	F	E	A	A	N	V	V	K	L	...	K	G	T	D	Q	...							
	<i>So_cellu</i>	CAN94755		TGDD	G	R	M	Y	S	Q	T	T	L	Q	N	F	F	...	F	G	F	P	V	S	I	A	L	Q	D	S	N	R	N	...	L	F	E	G	S	S	V	T	K	I	...	K	G	M	N	K	...							
	<i>Op_terra</i>	ACB73617		SDDY	G	R	F	Y	R	S	R	T	R	V	E	N	F	F	...	F	G	F	E	D	P	V	V	M	Q	D	A	N	R	F	...	L	F	E	G	G	C	V	T	R	...	K	G	L	N	Q	...							
	<i>Op_terra</i>	ACB76517		SDDW	G	R	F	Y	R	S	R	T	K	L	E	D	F	F	...	F	G	F	E	D	P	V	V	M	Q	D	A	N	R	F	...	L	F	E	A	S	C	I	V	R	...	K	G	T	N	E	...							
	<i>Am_medit</i>	ADJ49532		ANDA	G	D	I	F	R	S	Q	T	T	V	A	N	F	F	...	F	G	F	N	T	A	V	V	L	H	D	D	N	R	G	...	L	F	E	A	T	A	V	V	K	L	...	K	G	S	T	S	...						
	<i>Am_medit</i>	AF081241		ANDA	G	D	I	F	R	S	Q	T	T	V	A	N	F	F	...	F	G	F	N	T	A	V	V	L	H	D	D	N	R	G	...	L	F	E	A	T	A	V	V	K	L	...	K	G	S	T	S	...						
	<i>Le_macul</i>	CBX95362		SDDN	G	H	L	Y	R	S	Q	T	A	V	G	E	F	F	...	G	M	S	E	P	V	I	A	Q	D	K	N	D	L	F	E	A	A	T	V	V	S	V	...	G	A	S	S	...					
	<i>St_viola</i>	AEM84965		SDDN	G	H	L	F	R	S	E	T	T	V	G	E	F	F	...	G	F	R	N	T	Q	L	V	L	Q	D	S	K	F	A	...	L	F	E	G	E	A	V	V	R	...	Q	G	T	N	T	...							
	<i>Us_maydi</i>	EAK85571		VADN	G	K	V	Y	R	T	S	M	A	I	G	D	F	F	...	F	S	G	T	A	S	E	V	V	L	S	D	T	Q	A	...	L	F	E	A	V	Q	V	T	V	...	A	G	Q	N	Q	...							
	<i>Sp_reil1</i>	CB069122		CGDN	G	K	V	Y	H	S	K	M	A	I	G	S	F	F	...	F	S	G	T	A	S	E	V	V	L	S	D	T	P	O	K	...	L	F	E	A	V	Q	V	T	V	...	S	G	T	N	Q	...						
	<i>Po_anser</i>	CAP65929		AGDN	G	R	I	Y	S	M	P	L	G	N	F	F	...	N	F	G	T	S	T	I	F	H	G	A	K	N	D	L	F	E	A	V	Q	V	T	L	...	K	D	S	S	P	T	...					
	<i>Ma_oryza</i>	EAA47906		CGDN	G	K	I	Y	R	S	T	M	P	L	G	N	F	F	...	N	F	G	T	S	T	I	F	H	G	A	K	N	D	L	F	E	A	V	Q	V	T												

Structural characterization of GH62 α -L-arabinofuranosidases

		β15		β16		β17		β18		β19																																									
		220		230		240		250		260																																									
<i>Us maydi</i>	EAK85571																																																		
<i>Po_anser</i>	CAP62336	3.2.1.55																																																	
1	<i>Po_anser</i>	CAP62336	3.2.1.55	YLLLV	AI	GT	...	DGH	RM	F	R	S	W	T	A	D	S	I	R	G	P	W	O	G	L	A	N	.	T	E	Q	N	P	W	A	R	S	N	V	Q	F	D	G	D	V	W	T	K			
	<i>Am_medit</i>	AEK42553		YLLLV	AI	GA	...	QGG	R	F	R	S	W	T	S	S	A	I	A	G	P	W	T	P	L	A	D	.	T	E	S	A	P	F	A	G	A	N	V	T	F	P	A	G	Q	.	W	T	T		
	<i>Pi_indic</i>	CA70773		YLLLV	AI	GS	...	NG	R	F	R	S	W	R	S	S	L	T	G	S	W	T	P	L	A	A	.	T	E	S	A	P	F	A	G	A	N	V	T	F	P	A	G	Q	.	W	T	T			
	<i>Pi_indic</i>	CCA70772		YLLLV	AI	GS	...	NG	R	F	R	S	W	K	S	S	L	T	G	S	W	T	P	L	A	A	.	T	E	S	T	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	<i>Pi_indic</i>	CA70771		YLLLV	AI	GS	...	NG	R	F	R	S	W	K	S	S	L	T	G	S	W	T	P	L	A	A	.	T	E	A	N	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	un ACQ07729			YLLLV	AI	GS	...	DG	R	F	R	S	W	T	S	S	L	T	G	S	W	T	P	L	A	A	.	T	E	A	N	P	F	A	R	S	N	V	V	F	.	S	G	T	A	.	W	T	K		
	un ACQ05660			YLLLV	AI	GS	...	DGN	R	F	R	S	W	T	A	P	S	L	T	G	S	W	T	P	L	A	A	.	T	E	A	N	P	F	A	R	S	N	V	V	F	.	S	G	T	A	.	W	T	K	
	un_bacte	AFY23018		YLLLV	AI	GS	...	NGK	R	F	R	S	W	T	A	N	G	I	T	G	S	W	T	P	L	A	A	.	T	E	A	N	P	F	A	R	S	T	N	V	T	F	.	S	G	T	A	.	W	T	K
	Co_ciner	BAK14423	3.2.1.55	YLLLV	AI	GS	...	DGR	R	F	R	S	W	T	S	I	A	G	P	W	T	P	L	A	D	.	Q	E	S	N	P	F	A	R	A	N	V	V	F	.	T	G	N	A	.	W	T	K			
	Ac_mirum	ACU37207		YLLLV	AI	GS	...	DGR	R	F	R	S	W	T	A	P	A	I	A	G	P	W	T	P	L	A	D	.	S	E	S	N	P	F	A	R	A	N	V	T	F	.	P	G	G	Q	.	W	T	K	
	St_bingc	ADT13053		YLLLV	AI	GS	...	DGR	R	F	R	S	W	T	S	S	I	G	S	W	T	P	L	A	A	.	S	E	S	N	P	F	A	R	A	N	V	T	F	.	P	S	G	A	.	W	T	K			
	So_cellu	AGP41089		YMLLV	DM	...		KDN	R	F	R	Y	E	L	H	O	A	S	S	L	G	S	W	T	P	L	A	.	K	W	A	R	S	N	V	T	F	.	P	S	G	A	.	W	T	K					
	So_cellu	AGP41089		YMLLV	DM	...		KDN	R	F	R	Y	E	L	H	O	A	S	S	L	G	S	W	T	P	L	A	.	K	W	A	R	S	N	V	T	F	.	P	S	G	A	.	W	T	K					
	CL_cellu	ACL75596		YMLLV	DM	...		IDG	R	F	R	S	Y	E	L	F	T	S	S	A	G	S	W	T	P	L	A	.	K	W	A	R	S	N	V	T	F	.	P	S	G	A	.	W	T	K					
	CL_cellu	ACL75596		YMLLV	DM	...		IDG	R	F	R	S	Y	E	L	F	T	S	S	A	G	S	W	T	P	L	A	.	K	W	A	R	S	N	V	T	F	.	P	S	G	A	.	W	T	K					
	CL_BNL1108	AEV63176		YMLLV	DM	...		IDG	R	F	R	S	Y	E	L	F	T	S	S	A	G	S	W	T	P	L	A	.	K	W	A	R	S	N	V	T	F	.	P	S	G	A	.	W	T	K					
	CL_BNL1108	AEV63176		YMLLV	DM	...		IDG	R	F	R	S	Y	E	L	F	T	S	S	A	G	S	W	T	P	L	A	.	K	W	A	R	S	N	V	T	F	.	P	S	G	A	.	W	T	K					
	Te_turne	ACR14088		YLLQV	EW	GET	...	ESRR	L	R	S	Y	L	S	T	S	L	D	G	P	W	I	A	H	H	.	D	E	S	A	P	F	A	G	P	E	N	T	T	F	.	N	G	P	A	.	W	T	K		
	So_cellu	CAN98023		YLLLV	AF	.	D	NSP	R	F	R	S	W	T	S	E	S	I	D	G	P	W	A	P	L	A	.	T	K	O	K	P	F	A	G	P	A	N	V	T	F	.	E	G	G	.	W	T	K		
	So_cellu	CAN98020		YLLMV	AY	.	D	NSP	R	F	R	S	W	T	S	E	S	I	D	G	P	W	A	P	L	A	.	T	K	O	K	P	F	A	G	P	A	N	V	T	F	.	E	G	O	.	W	T	K		
	Te_japon	ACE85320	3.2.1.55	YLLMV	AY	.	I	SGP	R	F	R	S	W	T	A	T	S	L	D	G	P	W	T	P	L	A	D	.	T	E	A	N	P	F	A	G	N	V	V	E	S	T	.	G	K	.	W	T	K		
	Ce_turne	ACR13064		YLLLV	GW	QS	...	GPR	F	F	R	A	W	T	S	N	S	L	D	G	P	W	T	A	Y	K	T	.	S	E	S	N	P	F	A	G	N	V	V	E	S	T	.	G	K	.	W	T	K		
	So_cellu	CAN94755		YLLLV	AI	GP	...	TGAR	F	R	F	Y	S	F	T	A	D	R	L	D	G	P	W	T	P	L	A	H	.	T	N	A	P	F	A	G	N	V	V	T	A	P	G	V	A	D	.	W	T	K	
	Op_terra	ACB73617		YLCFI	CI	G	GP	...	TGK	R	F	R	A	F	T	A	D	R	L	D	G	P	W	T	P	L	A	Q	A	N	S	W	D	T	P	F	A	G	P	N	V	T	A	D	.	W	T	K			
	Op_terra	ACB73617		YLCFI	CI	G	GP	...	TGK	R	F	R	A	F	T	A	D	R	L	D	G	P	W	T	P	L	A	Q	A	N	S	W	D	T	P	F	A	G	P	N	V	T	A	D	.	W	T	K			
	Am_medit	ADJ49532		YMLLV	GW	DS	...	VGH	R	V	Y	R	A	W	T	A	P	S	L	G	S	W	T	P	L	A	.	P	F	A	G	L	A	N	V	T	F	.	P	S	G	A	.	W	T	K					
	Am_medit	AF081241		YMLLV	GW	DS	...	VGH	R	V	Y	R	A	W	T	A	P	S	L	G	S	W	T	P	L	A	.	P	F	A	G	L	A	N	V	T	F	.	P	S	G	A	.	W	T	K					
	Le_macul	CBX95362		YLLLV	CI	G	AG	SP	G	G	R	F	R	S	W	T	S	N	S	L	G	S	W	A	P	L	A	.	T	Q	N	P	F	A	G	N	V	V	E	S	T	.	G	K	.	W	T	K			
	St_viola	AEH84965		YLLMV	AI	GS	...	DGR	R	F	R	S	F	T	A	Q	L	D	G	P	W	Q	P	L	A	.	T	E	S	N	P	F	A	G	N	V	V	E	S	T	.	G	K	.	W	T	K				
	Us_maydi	EAK85571		YMLLV	AI	GT	...	NG	R	F	R	S	F	T	A	S	L	D	G	P	W	K	P	V	Q	A	.	S	E	S	A	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	Sp_reli	CB069122		YLMIV	AI	GS	...	NG	R	F	R	S	F	T	A	S	L	D	G	P	W	T	P	L	A	A	.	S	E	S	A	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	Po_anser	CAP65929		YLMIV	AI	GS	...	NG	R	F	R	S	F	T	A	S	L	D	G	P	W	T	P	L	A	A	.	S	E	S	A	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	Ma_oryza	EAA47906		YLMIV	AI	GS	...	NG	R	F	R	S	F	T	A	S	L	D	G	P	W	T	P	L	A	A	.	T	O	N	D	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	Ma_oryza	EAA57262		YLMIV	AI	GS	...	NG	R	F	R	S	F	T	A	S	L	D	G	P	W	T	P	L	A	A	.	T	O	N	D	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	Tr_aesti	ABT18331		YLMIV	AI	GS	...	NG	R	F	R	S	F	T	A	S	L	D	G	P	W	T	P	L	A	A	.	T	E	S	N	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	Fu_grami	AAV66346		YMLLV	AI	GS	...	NG	R	F	R	S	F	T	A	S	L	D	G	P	W	T	P	L	A	A	.	S	E	S	S	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	My_therm	AE060934		YLMIV	AI	GS	...	NG	R	F	R	S	F	T	A	S	L	D	G	P	W	T	P	L	A	A	.	S	E	S	O	P	F	A	G	K	N	V	D	F	.	P	G	G	R	.	W	T	N		
	As_niger	CAA03159		YLMIV	AI	GS	...	TGH	R	F	R	S	F	T	A	S	L	D	G	P	W	T	P	L	A	A	.																								