

SUPPLEMENTARY MATERIAL

Chitinolytic enzymes of the hyperparasite fungus *Aphanocladium album*: genome-wide survey and characterization of a selected enzyme.

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Table S1. HMMER prediction of the main domains in GH18 sequences.

	Id	Length	HMMER					
			LysM	C-R	GH18	CBM	Pept M508	P-E
1	KAJ6787801.1	336			33-313			
2	KAJ6781922.1	445			30-317	415-441		
3	DAA05865	392			31-307	360-388		
4	KAJ6780968.1	757			31-312	378-405	529-732	
5	KAJ6788767.1	324			38-310			
6	KAJ6787922.1	315			30-253			
7	KAJ6780669.1	423			137-380			
8	KAJ6780036.1	330			24-312			

9	KAJ6780631.1	348			13-289			
10	KAJ6787472.1	365			42-298			
11	KAJ6779939.1	369			21-352			
12	KAJ6782108.1	363			1-335			
13	KAJ6782480.1	392			22-380			
14	KAJ6785755.1	574			31-338			
15	DAA05854	492			100-451			
16	KAJ6782844.1	540			157-501			
17	KAJ6786186.1	394			4-349			
18	KAJ6783291.1	428			42-388			
19	KAJ6787487.1	423			39-383			
20	KAJ6785998.1	1832		141-187	202-541			
21	KAJ6779834.1	532			153-493			
22	DAA05857	1533	308-355		520-848			
23	KAJ6783597.1	742			15-358			
24	KAJ6781350.1	671			86-435			
25	KAJ6786554.1	1495			496-844			1380-1481
26	KAJ6789350.1	754			152-343			
27	KAJ6787215.1	1373	403-445		606-949			
28	KAJ6784990.1	1418	349-396	411-476	490-841			
29	KAJ6784672.1	1279	295-337	420-486	501-852			

Legend (Pfam IDs are reported in brackets): LysM=LysM domain (PF01476); C-R=Chitin recognition protein (PF00187); GH18=Glycosyl hydrolases family 18 (PF00704); CBM= Fungal cellulose binding domain (PF00734); Pept_M508= Peptidase M50B-like (PF13398); P-E=Pathogen effector; putative necrosis-inducing factor (PF14856).

Table S2. HMMER prediction of the main domains in GH3 sequences

Id	Length	HMMER				
		WSC	GH3-N	GH3-C	AT	F-III
1	KFG78085	909		28-357		
2	KAJ6788372.1	932		21-350		
3	AGC24356	858		8-336	552-655	
4	KAJ6789110.1	539		6-330		
5	KAJ6787877.1	370		32-364		
6	KAJ6782998.1	369		47-366		
7	KAJ6785893.1	870	32-113	169-461	499-724	
8	KAJ6786934.1	830		5-277	312-703	736-808
9	KAJ6780833.1	760		46-324	369-634	681-747
10	KAJ6787866.1	802		55-341	388-659	717-791
11	KAJ6786079.1	777		85-334	382-642	700-766
12	KAJ6785739.1	893		54-358	419-672	796-870
13	KAJ6782204.1	948		166-420	485-751	868-939
14	KFG84234	879		85-354	414-673	
15	KAJ6788989.1	883		97-356	416-677	804-873

Legend (Pfam IDs are reported in brackets): WSC=WSC domain for carbohydrate binding (PF01822); GH3-N=Glycosyl Hydrolase family 3 N-terminal domain (PF00933); GH3-C=Glycosyl Hydrolase family 3 C-terminal domain (PF01915); AT=Acetyl Transferase (GNAT) family (PF00583); F-III=Fibronectin type III-like domain (PF14310).

Table S3. HMMER prediction of the main domains in GH20 sequences

	Id	Length	HMMER			
			GH20-2	β-AH	GH20	β-AG
1	KAJ6784096.1	848	157-304		307-638	
2	KAJ6785798.1	741	32-167		170-339	
3	KAJ6780494.1	661	48-191			197-508
4	KAJ6785933.1	514	23-92		97-448	
5	KFG80340	620		27-171	193-564	
6	KAJ6783033.1	633		28-184	207-577	
7	KAJ6780076.1	577		16-163	188-528	
8	KAJ6789215.1	751		204-335	360-628	
9	KAJ6787434.1	574		20-161	186-526	
10	KFG85702	579		21-166	191-530	
11	KAJ6780083.1	579		19-165	190-529	

Legend (Pfam IDs are reported in brackets): GH20-2=Glycosyl Hydrolase family 20 domain 2 (PF02838); β-AH=beta acetyl hexoaminidase like (PF14845); GH20=Glycosyl Hydrolase family 20 catalytic domain (PF00728); β-AG=beta-N-acetylglucosaminidase (PF07555).

Table S4. HMMER prediction of the main domains in GH75 sequences

	Id	Length	HMMER	
			GH75	A-L
1	KAJ6785337.1	1093	667-836	877-1092
2	KAJ6783761.1	252	80-249	
3	KAJ6781651.1	299	82-251	
4	BAA12799	304	82-254	
5	KAJ6788818.1	300	81-253	
6	KAJ6786595.1	273	52-234	
7	ADG96019	304	100-244	
8	KAJ6781485.1	256	105-249	
9	AA041660	238	72-235	
10	KAJ6783315.1	232	70-231	
11	KAJ6787168.1	234	70-231	
12	ABY77913	217	53-214	

Legend (Pfam IDs are reported in brackets): GH75=Fungal chitosanase of glycosyl hydrolase group 75 (PF07335); A-L=Alginate Lyase (PF08787).

Table S5. Summary of the Phyre2 analysis for the GH3 sequences of *A. album*

GH3 sequence	Model	Enzyme	Cnf	Cvr	Id	Organism
KAJ6786934.1	3AC0	β-glucosidase	100	97	49	<i>Kluyveromyces marxianus</i>
KAJ6780833.1	4IID	“ “	100	94	47	<i>Aspergillus aculeatus</i>
KAJ6788989.1	5NBS	“ “	100	95	62	<i>Neurospora crassa</i>
KAJ6788372.1	4ZM6	β-N-acetylglucosaminidase	100	89	30	<i>Rhizomucor miehei</i> CAU432
KAJ6782204.1	4IID	β-glucosidase	100	85	46	<i>Aspergillus aculeatus</i>
KAJ6785739.1	4D0J	“ “	100	91	42	<i>Rasamsonia emersonii</i>
KAJ6787866.1	“ “	“ “	100	91	45	“ “
KAJ6785893.1	7VC7	β-xylosidase	100	84	51	<i>Phanerochaete chrysosporium</i>
KAJ6787877.1	6K5J	β-N-acetylglucosaminidase	100	88	31	<i>Paenibacillus</i> sp. str. fpu-7
KAJ6789110.1	4ZM6	“ “	100	94	39	<i>Rhizomucor miehei</i> CAU432
KAJ6782998.1	6K5J	“ “	100	88	31	<i>Paenibacillus</i> sp. str. fpu-7
KAJ6786079.1	4D0J	β-glucosidase	100	93	43	<i>Rasamsonia emersonii</i>

Model = PDB model; Cnf=confidence (%); Cvr=coverage (%)

Table S6. Summary of the Phyre2 analysis for the GH20 sequences of *A. album*

GH20 sequence	Model	Enzyme	Cnf	Cvr	Id	Organism
KAJ6780076.1	3NSN	β-N-acetylglucosaminidase	100	90	31	<i>Ostrinia furnacalis</i>
KAJ6780083.1	“ “	“ “	100	90	31	“ “
KAJ6785933.1	3RCN	“ “	100	93	48	<i>Paenarthrobacter aurescens</i>
KAJ6783033.1	5OAR	“ “	100	79	67	<i>Aspergillus oryzae</i>
KAJ6780494.1	6PV5	GH84 Hydrolase	100	83	32	<i>Clostridium perfringens</i>
KAJ6787434.1	3NSN	β-N-acetylglucosaminidase	100	91	33	<i>Ostrinia furnacalis</i>
KAJ6784096.1	6JQF	“ “	100	72	24	<i>Akkermansia muciniphila</i>
KAJ6785798.1	“ “	“ “	100	82	25	“ “
KAJ6789215.1	3LMY	“ “	100	62	30	<i>Homo sapiens</i>

Model = PDB model; Cnf = confidence (%); Cvr = coverage (%); Id = identity (%)

Figure S1

B

KAJ6780669.1	--TGYEAMA-----QHFRSHFASDPSKQYYMTAAPQC PFTAD-----DE	318
KAJ6788767.1	--TGYLAMT-----KRFRANMAKDASKYYLTAAPQC PFPDQ-----SE	219
KAJ6787801.1	-NQFYPDMI-----AKLRGNFASDSSNQYFITGAPQC PIPEP-----NM	214
KAJ6781922.1	SSQYYQYMI-----AKLRQNFAKDSSKKYYIAGAPQC PIPEP-----NM	211
DAA05865.1	--NNMEPFA-----AELRSOLIDASTSKKFYLSAAPQC CPYPDV-----SD	211
KAJ6780968.1	--NNLPAGF-----AKLRSLMDSAGGKKYYLSAAPQC CVFPDA-----AV	214
	: : : : : : **	
KAJ6780631.1	EVMR--GREVAWYNTQFYCGWGDFSST-----VMYDMMLRKGWAP-----	229
KAJ6787472.1	NTAV--GSKISFYNGQFYSGFGTMART-----DDYVKIVDNGFAA-----	250
KAJ6780036.1	KKYVD-NGRLWWLNMQYYNGDMYCGSG-----DSYGAGTTQGFIAQTDCLNNGLTIGG	260
KAJ6787922.1	TPEI--AGAVDHVWIQFYDTKYCLIGD-----DTFYG-KVRTWSQ-----	248
KAJ6780669.1	ELSL--FQHLDYLVVFQFYNNNCNVGQ-----SGFET-SVRRWSE-----	355
KAJ6788767.1	PLSV--CKL LDYLVVFQFYNNNCNVGQ-----SGFNA-AVKNWSK-----	256
KAJ6787801.1	NEIIT-KAHF DYL FVQFYNNPGC SVD-----GTINFEDWKKNVANT-----	254
KAJ6781922.1	GEIIS-TSQFDWLTVQFYNNNNYTVPCALPINGNAPFNYNNWTSFISTT-----	259
DAA05865.1	ESFLDGQVPFDWNVNFQFYNNNGCGVSHYP-----ADFNWATWDNWAKTV-----	254
KAJ6780968.1	GAALD-AVAFDFVMIQFYNNWCGVSNFQEGASSQNAFNF DVWDWKWAKGS-----	262
	* : *	
KAJ6780631.1	-----EKVVVGLVTNPAN-----GPGFI AWDSLQQTLAIL-RQRPHNFGGIMWEY	274
KAJ6787472.1	-----SKVVA GQLTDPSN-----GGGYIPYSQNLNATII AL-RKKYQIGGVMGWEY	295
KAJ6780036.1	VTIKV PYDKQV PGLPAQPGA-----GGGYM STSDVSSVLNH---NGNLKGLMTWSL	309
KAJ6787922.1	---AVKG-DIYIGATARNTP-----DQVGYLEPHALLTALHKVEAMGLPNYSGAMLWEA	298
KAJ6780669.1	---AIGN TLLVGALASNAD-----KDEGYVDAKTFNSVLGKVAKMNL PN YGGVMLWEA	406
KAJ6788767.1	---GIGNAKLFIGGLASGSD-----GDQGYVDSNTFIKA IKGV EAMNL PN YGGAMLWEA	307
KAJ6787801.1	---PSSAKI FIGVPASPLGATGTESGAKYYLEPTKLASLVGEH--KSDA AFGG VMMWAA	309
KAJ6781922.1	---PSKDAK IFIGVPASTLASNGSPNGATYYATPEQLATIVNDY--KSDAH FGGIMMWAA	314
DAA05865.1	---SANKAKVLIGT PANVGGANAG-----SPTDSQLSGAISLA--KGSSSF GGVM LWDM	305
KAJ6780968.1	---KNPNVKLLLGIPAAPGA--GG-----GYTSGSKLKA INYS--QKYSSF GGVM LWDM	310
	* : : * * *	
KAJ6780631.1	YNSLPGDRERPW EARTMTAMI--RSH-CLAPAPPVATP-PRPEEK-----AAVVDID	324
KAJ6787472.1	FNSQPGGTKEPW KWAQVMTQIL---RPN-APV KLSITTAD-AD---H-----LTNTYE	340
KAJ6780036.1	NWDGSKNWSFGDN-----VKGTLGTA-----	330
KAJ6787922.1	ELAMKN-KNYQKT-----LRAGL-----	315
KAJ6780669.1	ELAAKN-GNYQKK-----IKAEL-----	423
KAJ6788767.1	QLSRNN-GNFAKK-----IRSSL-----	324
KAJ6787801.1	GFS DAN-VNNGCTYAQEAKH IL TTGSAC-----	336
KAJ6781922.1	GFS DS N-VNNGCTYAQEAKH IL VNNGPCGSNGPPP STS PPP STAP PTGT PPS TST	373
DAA05865.1	AQLFT--NQGYL--A--KIVADLGSASSPPP PASTTLQ-----TIT	340
KAJ6780968.1	SQLYS--NNGFL--G---EVLS DISGGPAT T QPP STT QPP GTT QPP GTT-----TTCT	358
	*	
KAJ6780631.1	ADA--PGGEELEI P--APFEYYSDGAEE-----	348
KAJ6787472.1	HTV--SGGSPNARPASPGINYYDMVNA-----	365
KAJ6780036.1	-----	330
KAJ6787922.1	-----	315
KAJ6780669.1	-----	423
KAJ6788767.1	-----	324
KAJ6787801.1	-----	336
KAJ6781922.1	HPC ASHTSSSSPVSSPRGTV PQWQV RNEER RDGEFDANIKKCGGK KYNGPTECVPPFT	433
DAA05865.1	RSS--TASTGPTNPPSGGSVPQWG-----QCGGNGYTGP QCQAPYK	380
KAJ6780968.1	STT--TPASTSTPPP TS GGLDQ YA-----QCGGQG YSGPTVCKAPY T	398
KAJ6780631.1	-----	348
KAJ6787472.1	-----	365
KAJ6780036.1	-----	330
KAJ6787922.1	-----	315
KAJ6780669.1	-----	423
KAJ6788767.1	-----	324
KAJ6787801.1	-----	336
KAJ6781922.1	CVKLGEWWSSCR-----	445
DAA05865.1	CVATSEWWSSCQ-----	392
KAJ6780968.1	CVKQNTLPSRLTSATSSH LHLAQATTLLQ L LPFIALRSV AFTFCDPD PRV HSSPGSLTRA	458
KAJ6780631.1	-----	348

KAJ6787472.1	-----	365
KAJ6780036.1	-----	330
KAJ6787922.1	-----	315
KAJ6780669.1	-----	423
KAJ6788767.1	-----	324
KAJ6787801.1	-----	336
KAJ6781922.1	-----	445
DAA05865.1	-----	392
KAJ6780968.1	AYYQLAKTALLRRFEASYIMAPSFSTSSGILETHNPVRIFGQKPEPSPGLSLASRSLQHP	518
KAJ6780631.1	-----	348
KAJ6787472.1	-----	365
KAJ6780036.1	-----	330
KAJ6787922.1	-----	315
KAJ6780669.1	-----	423
KAJ6788767.1	-----	324
KAJ6787801.1	-----	336
KAJ6781922.1	-----	445
DAA05865.1	-----	392
KAJ6780968.1	NHTQQVTLGVIAAYVVVIAILWNVPYIKNILWPFKMLVIAFHFGHAITAVFTGGRVKSI	578
KAJ6780631.1	-----	348
KAJ6787472.1	-----	365
KAJ6780036.1	-----	330
KAJ6787922.1	-----	315
KAJ6780669.1	-----	423
KAJ6788767.1	-----	324
KAJ6787801.1	-----	336
KAJ6781922.1	-----	445
DAA05865.1	-----	392
KAJ6780968.1	SLDPNEGGVTKMVGGSIAITLPAGYLGSSTIIGALLTFCGFNIVASKIASIVLGVCFLLTL	638
KAJ6780631.1	-----	348
KAJ6787472.1	-----	365
KAJ6780036.1	-----	330
KAJ6787922.1	-----	315
KAJ6780669.1	-----	423
KAJ6788767.1	-----	324
KAJ6787801.1	-----	336
KAJ6781922.1	-----	445
DAA05865.1	-----	392
KAJ6780968.1	WWGKRDWLTVLTVLLAVALLVACWFIFKHAEALRFVVLFIGVMSSLYSVWDICDDLILRKV	698
KAJ6780631.1	-----	348
KAJ6787472.1	-----	365
KAJ6780036.1	-----	330
KAJ6787922.1	-----	315
KAJ6780669.1	-----	423
KAJ6788767.1	-----	324
KAJ6787801.1	-----	336
KAJ6781922.1	-----	445
DAA05865.1	-----	392
KAJ6780968.1	NSSDASVFAKRYGGSSQCWGIIWSIISVLIMAVGIVAGLAAFSQSFAQQQEDSKHFPT	757

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KAJ6779939.1	GDMIAFTAEQVPKISETVDFVNVMTYDLMNRRDTSTDHHSSVS-----	GSLATV	225
KAJ6782108.1	RDLMAFTANTVPKIVKQVDFINIMTYDLINRRDTVVQHHSVA-----	DSRASI	206
KAJ6782480.1	FDGPNGPLSDVSAFAKVVVDYGNLQMODYINGWNSVTGPLAPFNFESGRGA--QVSFVSAI		237
KAJ6785755.1	--PAVLQHIDLAVAESLDFINLQTYNLHHAQPGRSLCPSQLYSMAKDEP---STSTVA		242
KAJ6786186.1	--PDNFQKLNIPGMADYLDFWNILMAYDYAGSWDQVSGHQANLYPCNDNPACTPFSTAAV		239
KAJ6783291.1	--PEKYKKLRLADLGKVLDYINLMAYDYAGWSWSNYTTHNANLYANPQNPNATPFNTEDAV		273
KAJ6787487.1	--PDNYNKLKFAELGVLDYINLMAYDYAGWSWSNYTGH DANIYANPQNPNATPYNTDDAV		273
DAA05854.1	--QOHYKWLDMPAIRYLDLDAWHLMAYDYAGSWDDLSGDQSNVFHDATNPHRTRANSQAV		341
KAJ6782844.1	--PSKYKLLNLGAMDKFVDSWHL MAYDYAGSWDSTTGHQANVYPDPSNTASTKFNTEQAV		391
	: * : * : . : .		
KAJ6779939.1	ETYLSRGMPAAKMNLGFAYAKWFTTKDGATCDQATGCPTAVLEDANGGD-TGK-----		278
KAJ6782108.1	QRYLDRGVPRSMANLGLGYY/KWVMTDP-CERDDILGCPQLLEDPDGSNDLGR-----		259
KAJ6782480.1	DAWTAAGWPAAQLNAGYAFYSLSTTALEDMTKDPT---NQYQPQSSTVPLGKD EASW		292
KAJ6785755.1	GYILSRNFPQAQKLLGIPTFGTSFPGCDGPGQ-----AYDPAE		280
KAJ6786186.1	DYTQNQGVAPDKLVLGMLPYGRAFENCDGIGK-----PFQGVG		277
KAJ6783291.1	KAYVSEGI PANKIVLGMPYGRSFQQTEGIGK-----PYNGIG-----A		313
KAJ6787487.1	QAYINGGV PANKIVLGMPYGRSFQQTEGIGK-----PYNGIG		311
DAA05854.1	NDYVAAGVNPEKIIILGIPLYGRSF MNTDGP GK-----PYEGVG		379
KAJ6782844.1	NDYIAAGIAPEKIIILGLPLYGRSF MQTSGMGQ-----SFNGTG		429
	: * : . : .		
KAJ6779939.1	-----SGAVTFKE-----NYSGAFLNAMNNKGADNEKGGQWYWDASAKV		318
KAJ6782108.1	-----TAAFSWHDN-----VPSELSASFSRALNRGR-YFEDGSYGYWDEQEHR		301
KAJ6782480.1	YDACAGATSNSGTWQWKHLLDQGVLSAPTTASAPWV----RQWDNTTQT PWLFNPQTSI		347
KAJ6785755.1	-----SQMDYLG LPVAGR Q-----EGIDRRRISAYCAGG-PEG		313
KAJ6786186.1	-----QGTWEQGVYDYKKLPLEGAE-----EHQDDASGATYCYNFQSRT		316
KAJ6783291.1	--SFGQGSWENGVWDYKALPAGAT-----VTCDDTAKGCYSYDFSTKE		355
KAJ6787487.1	-----SGSWENGIW DYKALPKAGAT-----VKCDDTAKGCYSYDFSTKE		350
DAA05854.1	-----KGSIEKGVWLYRDLP RPGSV-----VNLRDIIAAYS YDNATRE		418
KAJ6782844.1	-----EGGV EAGVWLYKDL PRPGAT-----VTVDSDVLAAYS YDP KERM		468
	: * : . : .		
KAJ6779939.1	YWTWD TPEFIAKKMTDIVKAKGLGGVMA-----WSLAQDSDHW SH-IKA		361
KAJ6782108.1	WWSFD TPDVIARKMKELVGSMGLGGVFA-----WGLGEDATDFAR-LAA		344
KAJ6782480.1	FISYE DPVSLKV KV-DYAASKGLAGAMV-----WSVNMDSSN-TLLKV		389
KAJ6785755.1	FIAYD NPDTVKEKA-DFCKQKGFW TTPKGAS ADDATPEHWPRCVWGASARSSR-CSLACV		371
KAJ6786186.1	LVTYD TPQLAKTKA-QFIKERGLGGMW-----WESSADKAGGDSL IQT		359
KAJ6783291.1	LISFD TPSMISTKV-EWLKGNGLGGSMF-----WEASADKKGSDSL IGT		398
KAJ6787487.1	LISFD TPAMISTKV-SWLKGKG LGGSMF-----WEASADKKGSDSL I ST		393
DAA05854.1	LVTYD NMETTTLK A-EYLGKKGLGGAVF-----WEASGDRSGDES LIKA		461
KAJ6782844.1	LITYD NKE SANLK A-QYLMKKGLGGAVF-----WDASGDKPGNGS LIST		511
	: * : . : .	*	.
KAJ6779939.1	LQS---GIKS--L-----		369
KAJ6782108.1	TV D---GIR A--LHNSRDAGKDE-----L-----		363
KAJ6782480.1	LRG-----		392
KAJ6785755.1	VTARADKIAAPDLASQQAMATSSADADAASRTSLSPPRNPTAGATE TDTQKRRGVVQQL		431
KAJ6786186.1	VVGEGFGPGA--LKQQENC-----ISYPETKYDNL-----RNGLPDN-		394
KAJ6783291.1	SRQ---GLGS---LDGTQNY-----LHYPNSTYDNI-----KKGMN--		428
KAJ6787487.1	SHQ---GLGS---QDSTQNY-----LDYPN SKYDNI-----KKGMN--		423
DAA05854.1	VAR---KMAL---LDISMNM-----LSYPQSQFSNI-----RNATRW--		492
KAJ6782844.1	LAR---SIWP---LESSQNM-----LEYPKSEYANI-----RANS---		540
	: * : . : .	*	.
KAJ6779939.1	-----		369
KAJ6782108.1	-----		363
KAJ6782480.1	-----		392
KAJ6785755.1	SAADC SVGDDSGAVTSSIAFGGSVPAAAASAEHISSETEQQPPPPP FEPLFALLTNT		491
KAJ6786186.1	-----		394
KAJ6783291.1	-----		428
KAJ6787487.1	-----		423
DAA05854.1	-----		492
KAJ6782844.1	-----		540
	: * : . : .		
KAJ6779939.1	-----		369
KAJ6782108.1	-----		363

KAJ6782480.1	-----	392
KAJ6785755.1	TTGATVHPRIHYIFSDDDTSIPTDTAAHQHGADEHRSVVVALQPPDDHNDGAESNEIHD	551
KAJ6786186.1	-----	394
KAJ6783291.1	-----	428
KAJ6787487.1	-----	423
DAA05854.1	-----	492
KAJ6782844.1	-----	540

KAJ6779939.1	-----	369
KAJ6782108.1	-----	363
KAJ6782480.1	-----	392
KAJ6785755.1	PGALRSGSASQSQDTTIPTTSAA	574
KAJ6786186.1	-----	394
KAJ6783291.1	-----	428
KAJ6787487.1	-----	423
DAA05854.1	-----	492
KAJ6782844.1	-----	540

C

KAJ6785998.1	-----	0
KAJ6779834.1	-----	0
KAJ6783597.1	-----	0
KAJ6789350.1	-----	0
DAA05857.1	-----MPWISPAGGIACWLASATAIVSF---H--G--VSATANEVDA	34
KAJ6784990.1	MQ-----YHTSAALTALAGLGLFPLASGITT-S	27
KAJ6787215.1	MRLTIFTGATLLASTAHVSATVQSLRPVSLAARMSASDFA-NVDGGDDELAALKASA	59
KAJ6784672.1	MRR-----TPSQVAA-----AVSLLASVATAVTESY	26
KAJ6781350.1	-----	0
KAJ6786554.1	-----APSWFNAALGATSVLLSTNALVAASSPSRIGASI	35

KAJ6785998.1	-----	0
KAJ6779834.1	-----	0
KAJ6783597.1	-----	0
KAJ6789350.1	-----	0
DAA05857.1	FSQLNLCPLACSDKS-----PEQWSVYSSFERLSQCQPVLFDLAIHTPINDKTNVL	89
KAJ6784990.1	FGDYADLCPVACTSN-----PSQWTKYHSLDRLLAGCEADLLFDFTNLKQVDSN--TVF	79
KAJ6787215.1	QSAIVKACPEACSELKDGEDGTTGLSLIPDENMLSRCNETMLVDLVVKSK-----DSKAI	114
KAJ6784672.1	QGQYPDDCPQLCEAVGPARGN--WTHVHHKLSSCKNDMIFDFNVHNLVDDPNTILTI	83
KAJ6781350.1	-----	0
KAJ6786554.1	SYRGSERCPRSCADAGADSFA---WDSFRSMDEVDCGNPMLFNFALDRVDEHGRNHRI	92

KAJ6785998.1	-----	0
KAJ6779834.1	-----	0
KAJ6783597.1	-----	0
KAJ6789350.1	-----	0
DAA05857.1	RACTTSPAAGGSQPMASTVK-----REAEACGGSFVESKVPLLISQNPGQ	134
KAJ6784990.1	RTCSLASDAKPPTELAELTSNNK-----LSVDSDCGATVKQQNVTIATSSAGAV	128
KAJ6787215.1	RACMGDYGENVKAFAKADSSKAALCDTPNYNLTSTMSTFSG-----F-PQSIQGTSE	166
KAJ6784672.1	RACTTISNETYD----TRSQFIRDEGSVQSSLV-ISDSCGAKTVKSPLTPRVGNGL--	135
KAJ6781350.1	-----	0
KAJ6786554.1	YACTTSSESFKK----ISQAQVLAEP-----ADEVDAE--FEVGRGD--	129

KAJ6785998.1	-----	0
KAJ6779834.1	-----	0
KAJ6783597.1	-----	0
KAJ6789350.1	-----	0
DAA05857.1	ATAPFGNGLV TILEGLKEYRQKAVATSGCTGDNNIMLGYFDGAVVGTYAGKALSSATIPS	194
KAJ6784990.1	QDQSASTIVSSDIETAAKNLATYLKYH-ASCGSSTLFSKVNNAVVGFYSGADVQQASAAA	187
KAJ6787215.1	GTSEQSFDAKDAISALQQVSRHLQTEEPSCDNVIKFGYSKSAAVGIVFGSEHHHQGLTK	226
KAJ6784672.1	MNRSNSTLSTTDVASAARLQSYINKG-SQCGTTILFAKSGSAVVGHLAGSHITKSSVE	194
KAJ6781350.1	-----	0

KAJ6786554.1	--EDGGIAPEVAVSSLTGFLGQYVRQGLAQNGTTIYGSGFGAAAGLYVGHGLNGGAVSA	187
KAJ6785998.1	-----	0
KAJ6779834.1	-----	0
KAJ6783597.1	-----	0
KAJ6789350.1	-----	0
DAA05857.1	I-VDYLLEEDKEQGSAPFGMIAQICDHDS-DMDHTAGVAVALKADIG-SVQSALLSWNQG	251
KAJ6784990.1	M-----LE-RFGTSLSGPТИLQTCLNSDIGADTTVGVVGNSNLQELGGSLHSSVRAWNG	241
KAJ6787215.1	TVIDEVIKSLEDKG-TSETTGFECHPDRIGADYSAGIILTSAGNLY-KAKDVLATWASG	284
KAJ6784672.1	-----LLDT-FDAQLGQNRLSLEVCGANV-T-SSTFGIAAAEFGSIG-AVQA AVKGWADG	245
KAJ6781350.1	-----	0
KAJ6786554.1	TALQHLEDSVKHANSQGILGVQMC GSDY-DSDHTFGFIATTNGTFC-AIQDAMLSWYGG	245
KAJ6785998.1	-----MGSWSRIFLTTLITPSLGA--ITSW-----PRSVDAPELPGAGTCRAIVSP	45
KAJ6779834.1	-----MRLFRTALLAL-----LAT-----E-----AAASS	20
KAJ6783597.1	-----	0
KAJ6789350.1	-----	0
DAA05857.1	ECAKAQSGTTLRELVISQVPLPS-INAKASNISLAEAPGRKAQALDKV DKGKYCKMRTI-	309
KAJ6784990.1	TCVEGSGTASMPHMLSVLSSTT-----SSNSTTPVAANRRGE CRDTQV-	286
KAJ6787215.1	ACVSSQN-SWMEVTV--RLPPPALKETNTTSNSTASSSNLQSRQLKTLLPRGDCKTTV-	340
KAJ6784672.1	ECLGDGT-ALPRMDLSVLVSTIDK--NATFY--LNGTLA-SRSLKHLPRGDCRTEQV-	296
KAJ6781350.1	-----	0
KAJ6786554.1	DCVKFGT-SDKVKSKAHFASPLM-----SS---IQGSNSTNSTAHFSKRGE CRTVQV-	293
KAJ6785998.1	FDYSAKNRRDDELPVCSADNLTL DNGISSI QSELSLFGR-----	85
KAJ6779834.1	FIEQAIA-SGQLKPSNSHPNS-----KSDASL-A-----	47
KAJ6783597.1	-----	0
KAJ6789350.1	-----	0
DAA05857.1	-----AAGDSCASI A KACKVSV--ADFFKYNGVKG-----	337
KAJ6784990.1	-----HTGDSCGSLATRCGISG-----PDFEKYNSGV-----	313
KAJ6787215.1	-----DKGMGCYDLAKKCGISS--NDLTKYNPQKNCSTLVVDQKVCCSSGT	385
KAJ6784672.1	-----QEHDSCAAVASRCGISV--DDLQKYNGGA-----	323
KAJ6781350.1	-----	0
KAJ6786554.1	-----KQGTGCPELA KMCGISG--PDFTKYNPGK-----	320
KAJ6785998.1	-----QVVGNTDYTCGPDRPKKNKAC-----	106
KAJ6779834.1	-----ATGDSPDYHCRKD KPCALGCC-----	68
KAJ6783597.1	-----	0
KAJ6789350.1	-----	0
DAA05857.1	-----NGNDWCRKLQAGRNICC-----	354
KAJ6784990.1	-----KNLCSTLKDQYVCC-----	328
KAJ6787215.1	LPATI PAGGNGLCKTKEVVVAHDTCGSLAAKCGLTPQDFSKINTK TGLCSSLAPQVN VCC	445
KAJ6784672.1	-----SDWCNKLM PKQHVCC-----	338
KAJ6781350.1	-----	0
KAJ6786554.1	-----TFCNDLMPQHVCC-----	334
KAJ6785998.1	CPKK---TGQCNYGEEACGTSGISPNDVCWSN-----CDA-----	138
KAJ6779834.1	GPLDEGNGICGMGPKFCG-----KGCTSS-----CDQ-----	96
KAJ6783597.1	-----	0
KAJ6789350.1	-----MPELRPKPNEDGSCATYPVDHNDGCSMI AVARQLTVDDLEEFN-KNTWGQGCEA-	54
DAA05857.1	SSGS---SKPLPEANGDCFSYT IKAGDDCS SIGMPWN LTPKDIEGFNQKV TWGWRGCPN-	410
KAJ6784990.1	SSGTL PDHRPKPGSDGSCNVHKIEKNDGCWAIADKFGITQDDIEKF N-KKTWG WAGCDH-	386
KAJ6787215.1	SYGKL PDRRPKPKNADGTAT YTTQPNDCS VIAAKRDLVAKDIEEFN-KNTWG WKGCEI-	503
KAJ6784672.1	GEGLP LDYRPQPNSDGT CANYQIHNDTCYVIADGNYLKSDDIEEMN-KSTWG WSGCEH-	396
KAJ6781350.1	-----	0
KAJ6786554.1	SAGKL PDPYKPKPSKD GSCATVKVEKGLDCSSIGASYGLTKKEIEGFNAKKTWG WNGCDGG	394
KAJ6785998.1	-----KSEC GKN-----AKV-----PGQKCPLNVCCGKW	162
KAJ6779834.1	-----KSECDAG-----WGMQWSKAGPCPLNVCCSEY	123
KAJ6783597.1	-----	0
KAJ6789350.1	-----PMPNPVENAECGP TVPGTKPPPA--GISLADLNQ CPLKVCCNIW	96
DAA05857.1	-LTVG LKICL SKGSPMPAPV SNAV CGPQKPGTVR PESVKDA FELAKL NPCPL NSCCNVW	469
KAJ6784990.1	-LQPDQLICLSTGRPPFLPVEGAKCGPMKPGSKPIAG--DDDYSKVSPCPLNACCDVW	442

KAJ6787215.1	-VFKDFKMCVKGDPPMPAPVSNAVCGPTVPGTPQPPK--GTELKTLNECPLKACCVW	559
KAJ6784672.1	-LQVGQIICLSKGDPMPAQVQGTTCGPQVPGTKRPTD--GTALADLNPCPLNACCDVW	452
KAJ6781350.1	-----MPDPIADAVCGPQVAGTKKPID--MSKISELNPCLNACCDVW	41
KAJ6786554.1	RLWAGTVICVSKGTPPMPSVDPKAVCGPKSGSKPKD--MSKISELNPCLNACCDVW	451
KAJ6785998.1	GFCGMTEDYDAE--DHGA-----TGGCQSNCDQPGPKN-ASDQLNRVIGYYEAWRH	212
KAJ6779834.1	GFCGTTQDFCNGK--KVTS-----P-----SCSAS-AGSANKRIIGYYEGWNH	163
KAJ6783597.1	-----MDIISSA-PPK-EFISIGYFEGYGL	23
KAJ6789350.1	GHCGFSDDFCTVSKSKSGAPGTAALGINGCVSNCGRYIVGSPSAPE-KPLRIGYFEAWNK	155
DAA05857.1	GQCgidALFCTKADGPTGNPGTAPAGSNGCISNCGTIVNNAKPSSGGFRRIGYYEAFNW	529
KAJ6784990.1	GFCGITSDFCTKTPADTGAPGTAKEGTNGCISNCGTDIKSD-PPS-SLMKVAYYEAWNF	500
KAJ6787215.1	GQCGLTDDFCTYAPSKSGAPGTS-LONGCVSSCGRELKKGP-APD-KKMVKVAYFEAWNG	616
KAJ6784672.1	GFCGTTDEFCTKTPSDTGAPGTAKGTCISNCGRDLVNNDKAPD-EFRRVGYYEAFGM	511
KAJ6781350.1	GQCGITDEFCTDT--GTGAPGTAAPNTNGCISNCGTIVKGS--VS-EFRSIAYYEGFSF	96
KAJ6786554.1	GQCGBTDEFCTDT--GNGAPGTAKKDTNGCISNCGTIIITGN--QK-EIRSIAYFEGYAF	506
	.*:.*:.*:.*:	
KAJ6785998.1	DSKQCDMGLDDIPVNSLTHLYFSFAFITPGEYNIVGMNGLPNRLLFTDSLKKNPGLKT	272
KAJ6779834.1	QRSCDTMKPSEIPLGYYTHINFCAFALIHPTQFTIDAMDDKTGSLYREVTGLSKDPLKLV	223
KAJ6783597.1	TQPCDRDVVRTIDVKKYTHIQFAFSTVTANTFEVDMGPTL--NQFYFKQLN---GVKR	77
KAJ6789350.1	NRNCLTMDNH-----	165
DAA05857.1	ERPCLHMESKLSNTDKYTHMHWAEGDIKSD-FSVYINDTH--HQWDGFMGLK---NVKR	582
KAJ6784990.1	DRSCLHMNVDAIKG-DYTHIHFATVDKN-WGVSLDKN-TQKQFNRFKSVK---GPKK	553
KAJ6787215.1	NRPCLHMDVTIDTSLYTHIHFABAEVTRD-YNVDISKVQ--KQFDKFKSMT---GIKK	669
KAJ6784672.1	NRPCMNMGVKEIDVNHYSHIHFABAFTVTAS-FQVDISDSK--EQFGDFVQMK---NIKK	564
KAJ6781350.1	SRKCLYQDALQIDGSQYTHLHFGFDISPD-FQISIGDEMATYEFNNFRFIR---GPKK	151
KAJ6786554.1	NRKCQYQDAFQIDPKKYTHLHFGFTISKD-LKPSIDDYATNYEFGNNFRMIS---GPKR	561
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KAJ6785998.1	IIAVGGWTHNDPGPLQKVFSTMVSTKETRAKFINKLFLRLNAP[DGVDFDW]YPGADDR	332
KAJ6779834.1	WIAIGGWAFNDPGPTQSTFSVLVKAPAAQELFFNSLITFLINNNF[DGV DIDWE]YPAADDR	283
KAJ6783597.1	ILSFGGWTFSTDPATYGIFRTG-VTPEHRQTMANNIAKFIIDQGL[DGV DIDWE]YPAAPDI	136
KAJ6789350.1	-----EI[DGIDIDWE]YPGSY--	180
DAA05857.1	IVSFGGWFSTGVASYDVLRKA-MTPENRGHFVSNVVAFAKKMGI[DGI DLDWE]YPGAPDI	641
KAJ6784990.1	ILSFGGWFSTEPDTYQRRDA-TKAENREKFATNVVKFLNDNSI[DGLDFDWE]YPGAPDI	612
KAJ6787215.1	IISFGGWDFSALPGTFDILREA-VK PANRNVFQNVVKFVKDNGI[DGV DLDWE]YPGAPDI	728
KAJ6784672.1	IISFGGWDSTKPETFQRRDA-TKPENRDAFIASLVDFAKNAI[DGLDFDWE]YPGAPDI	623
KAJ6781350.1	IISFGGWEFSNAPSTYDIFRRG-VQDGNEIILAKNIAKFVNDNGI[DGV DIDWE]YPGA TD	210
KAJ6786554.1	IISFGGWDSTGPDTYTFREG-TKKENRETLATNLAKFVEKYQI[DGIDIDWE]YPSAPDI	620
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KAJ6785998.1	GGVP----EDGVNFTQFLKELEDDENNQPKKYIVSFTAPTSWYLRHFDLKIAIE-HVDY	386
KAJ6779834.1	GGKP----EDFKNFVFSIAKLRARLNASGKDFGLSLTPSSWYMQHFDIILEPYVDW	338
KAJ6783597.1	PGIPAAD-PAEGANYLKF MIALRGV--LPDKDSLFAAPASSWYLKGFP IAIITKIVDY	192
KAJ6789350.1	-----LSASKSVSFAIPAS YWYLKFPIAMMSKRF DY	212
DAA05857.1	PGIPKGL-PSDGP NYLET LRALRK---LPSKYSLSIAVPAS YWYL RPFPIREMSETVDY	697
KAJ6784990.1	PNVPPGS-TDEGSNYLAFLKVLKGK---L DKSKSISIALPSSFWYLQAYPV KELNSVV D Y	668
KAJ6787215.1	PDIPSDD-PHNGVNYYMF LKQLKSA---LG-DKSVSF AAPSSWYMRSPV DLMARDI DY	783
KAJ6784672.1	PDIPP GD-KGE GD NYLEFLKLDLAKA---L PSDKSVSIALPAS YWYL KQYPV KKMADIVDY	679
KAJ6781350.1	PGTPAGDPKTEGINYLKFLVVLKEM---LP-NKSVSIAAPAS YWYL KNPFIKRISQIVDY	266
KAJ6786554.1	PGVPPGD-KSEGKNYLEFLKLLSK---LK-GKSVSIAAPAS YWYL KGFPIKDIGKV VD Y	675
	:*:.*:.*:.*:.*:.*:	
KAJ6785998.1	VNVMSYDLHGVDSSNP-----IGSHIYGHNTLTEMKLA FDLFWRNDVPANKLNMGLG	439
KAJ6779834.1	FNMMTYDIHGTDGTIPS-----LGPRVQAHTNLTEIELAMELLWRNNINPERVTMGLG	392
KAJ6783597.1	VVYMTYDLHGQWDYGNKWTSPGCDTGNCRLSHVNMTETINALSMITKAGPSNKIAVG LT	252
KAJ6789350.1	IVFMT-----DALAMITKAGVPANKIALEIA	238
DAA05857.1	IVYMAYDLHG-----NGNCLRSHVNQTEVVLALSMTKAGVSASKVVVGES	743
KAJ6784990.1	FIYMTYDLHGQWDYDNKFTTPGCGANGNCIRSHVNITEKTS LAMVT KAGLSSNKVV VGS	728
KAJ6787215.1	II FM TYDLHGQWDYGNKWTSPGCDTGNCRLSHVNMTETKDSLIM ITKAGVPTNKV VV GVA	843
KAJ6784672.1	FIYMTYDLHGQWDVGNKYATPDCATGNCLRSHINKTETMDSLI LITKAGVESRKIV VVG IS	739
KAJ6781350.1	II YM TYDLHGQWDAGNPNAQPGCSDGMCLRSQVNLTETMSSLSMITKAGVN SGKVV VGV T	326
KAJ6786554.1	II FM TYDLHGQWDADNKNSQIGCPGGNCLRSHVNL TETRNSLSMITKAGVD SGKVV VGV T	735
	:.:.*:.*:.*:.*:	
KAJ6785998.1	FYGRAFQLADSSCDKPGCLFKGG-----ATKGACSGESGILSYREIREI LDKNK---MTP	491
KAJ6779834.1	FYGRSFTLKDPSC TAPGCPFSGP-----GKPGECTGTGGVLSAGEINRAIKGG---K-M	443

KAJ6783597.1	SYGRSFKMLTSGCTGPMCTFAGP--QSQAKPGRCTGTAGYISQNEIDYVLRNNF--SAQK	308
KAJ6789350.1	TYGRSFKMAKGCGWGPMLFTGTRNRIISNAAEGRCTKTAGYISNAEIQBIIQYGN--VNQK	296
DAA05857.1	SYGRSFKMAKGCTGPLCKFTGANGKSEAAAGRCTNARGYLANAEINEIISKS--GHPKT	802
KAJ6784990.1	SYGRSFRLKLPGCFTPDCFLFTGSPTQSDAFQGRCTNTSGYISNAELKEIADKKYSYVK	788
KAJ6787215.1	SYGRSFKMEKAGCDGPMCKFTGSARVSNAAHGRCTDTGGYISNAEIAEIIDSGK--VTRQ	901
KAJ6784672.1	SYGRSFRMSDPSCGPMCTYTGTRDHSEAYQGRCTGTSGYISNAEMQEIIQDHNYGTIN	799
KAJ6781350.1	SYGRSFAMAEAGCHGAQCKYTGSRLQSNAAKGECTDTSGYISNAEIGKILADPS-RVNEH	385
KAJ6786554.1	AYGRSFAMSDGSCHGPDCFTGTRLHSNANKGECTDTAGYISNAEIKKIADKK-RVVKS	794
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KAJ6785998.1	VHDKEAGVKYLTYNN---DQWVSPFDKETFKQKKDLASDLGLGGFLIWAIQDDAEMSAL	548
KAJ6779834.1	VLDKPSAAQIVTFGG---DQWVSPFDSTSLGLKQKWANEHCIGGLMWAIDLDDGSLLD-	499
KAJ6783597.1	THDAESNSDILVDDT---TEWVASYMDRDTKEKRKELYQALHFLGLTSDWAVIDLRRFSSTG-	364
KAJ6789350.1	WEA--VGSHVLVYND---TEWVAYMDDDKKKRADYFSQSNSFGGTSEWAIDLRRFSSTG-	350
DAA05857.1	WYDKDTASDYLVYND---VEWVAYMSDKTKQSRREWKGLNFLGLTVDWAVIDLQEFNVT-	858
KAJ6784990.1	WYDKDSDSNIMVYGDGPKHDWVAYMDDDVSKRQLDLYKGYNMAGTTDWAVDLAEFLKDD-	847
KAJ6787215.1	WKA--AGSDILVYSG---TEWVAYMSDDTKAERAKFYDSYNFLGTTDWAVDLQDFNGD-	955
KAJ6784672.1	YYDSSSSDLSILEYGDGNAVDWVAYMDELKESRASWVKGGLNFACTSDWAVIDLNDINGGG-	858
KAJ6781350.1	YIDAGSNSNVLVYDN---TEWVAYMTPELRKTRTSIYKGLQMGGTTNWATDLEDFNDVP-	441
KAJ6786554.1	YMDSTSNSNVLVYDN---NQWVAYMDSSVRSIREKLYKGWGMGGSSNNWATDLEDFEDPP	850
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KAJ6785998.1	QAVLDPKPLGDFKSIDKGDDNWTGTNEKCYVTAC-GEGCKAGEIKITDEYCAKKVSTLC	607
KAJ6779834.1	-ALFGNTGHKKRKTRDPKD---NDYNLKCFAGGI-NGG-----	532
KAJ6783597.1	-----PDPSTIDANGPSLLADGLTLKHSSCLPYREIWT-----WD	402
KAJ6789350.1	-----TGMDQQLDESFI-----EIRCDGQYTTFADAVE-----	377
DAA05857.1	-----HTEPPQGGPGAN-----ETGCINVDNMIWDWVNPSEEAAIG	895
KAJ6784990.1	-----GGSPDPTNDPS-----KLCKDAKMSYKKQDI-SPIYFPTY	883
KAJ6787215.1	-----DGDDDDDG-MHGSAD--YFGECTGSYDSLES-L-EKAKDSIPDY	995
KAJ6784672.1	-----GGDDS-DMPDIDMSDG--DNINC PADMAPGSLEDSLANNLPMR	899
KAJ6781350.1	-----DGVKDWANFRLQIKAG--NN-----PLTHAGDRTGNWTKLT	475
KAJ6786554.1	-----KGFPDWGAFTVSLKSR--KD-----PYEDVGKRSGNWTRLD	884
KAJ6785998.1	CPLSGAPDPKDCTWRGGTTRWCNGRCHDDEVMTMSKYGGGHDCWDGQIAHCKSALGEY	667
KAJ6779834.1	-----	532
KAJ6783597.1	-----DAG-----TIAKAPYNWSRFNK-YQKVL-----	424
KAJ6789350.1	-----RA-----LQA-----M-----HDA-----LDR-YKKLVDGGY	398
DAA05857.1	-----CTNILQPSPLSTTVTL-TAYT-----TLT-----LQSGTKLSTSUVVSA-PFSISEVSY	941
KAJ6784990.1	-----GDAL-----TT-----YVV-----IVNLTPHKFKI-----TSTSHY	909
KAJ6787215.1	-----CVDQ-----YA-----TQV-----QQAMLRDAIKRYD-----DLVNGDY	1024
KAJ6784672.1	-----CQAL-----YA-----LDI-----LYNTLEDSLSQLFD-----TNSQDY	927
KAJ6781350.1	-----CDDK-----YW-----TEK-----LDYTPAERWAGLD-----AK-----	499
KAJ6786554.1	-----CTAD-----GA-----TDT-----LHYTSDERWENLD-----AA-----	908
KAJ6785998.1	NVC-KWRGVGEKCHAGELPMTFSGTVLNILEDIAKVILRVVGRAYPLTALTGELLKVLD	726
KAJ6779834.1	-----	532
KAJ6783597.1	-----NN-----YLGKKGQVPLITD---AIWKNFERHSEIHGPREGIRIYL	465
KAJ6789350.1	-----DDKF---NY-----YSNYIKMLVPMQIDE---FMASGKADD-----YF-	430
DAA05857.1	-----QPFID-----YPDLLSKS-DGQM-----ITYNPTPQIT-PD-----PITI-	975
KAJ6784990.1	-----QYDIDFKDV-----YPGSMMQGA-----FSRGNGGSPVDDHA---EIYY-	945
KAJ6787215.1	-----NHYF-----DV-----YAGYVKSQVPSQIED-----FMGSKDAQK-----YF	1056
KAJ6784672.1	-----DDKF---GY-----YEQWVKGIDSRIKD-----FLNFRDDVK-DAPG-----IDFF-	965
KAJ6781350.1	-----DAW-----TDIIND-----WKQYRKERP-----N-----SA-----	520
KAJ6786554.1	-----NAW-----KDMVAD-----WKRYRAKTS-----G-----VN---	929
KAJ6785998.1	ELHLDTKKLYCCPEEEKKWKNCAWYGKPGNC-----FDGHCPDMKTVQITDSYFG	777
KAJ6779834.1	-----	532
KAJ6783597.1	-----NIY-----CDQY-----ALPRKFT-----EKPKEERCNKLNRD	493
KAJ6789350.1	-----TCQGTMGYHC-----SDCQWG-----GCLDSCRAEDCKSGMYTEVKCPDTLKY	476
DAA05857.1	-----RIPDG-----WTVTGGHLASPGSGPGSSSGPSSPAKATSTTS	1014
KAJ6784990.1	-----DVEGTDKK-----FVIRL-----TNND-----	962
KAJ6787215.1	-----KCTETGKPNC-----GSCRYFCEEDDVKNCDRTPGCD-----NKGTRDID	1099
KAJ6784672.1	-----DCKYT-----WGTK-----EGT-----	977
KAJ6781350.1	-----	520
KAJ6786554.1	-----	929

KAJ6785998.1	GGETCGGQLSRVRTFCCESDGE-----PLFLPVPLTNLFHPPDGGVDTDFTLKTDKS	830
KAJ6779834.1	-----	532
KAJ6783597.1	-DVVA--TYRFPGTWF----WSEYYIILCPAFLGKI--PKYQ---FTDLKDL-	534
KAJ6789350.1	----RE--SGVLPHEYRL--MSADYHL-----	495
DAA05857.1	----DG--AGYLLPITFYP----TLSYRI--PSILTPK--PPAP----T-KLPD--	1049
KAJ6784990.1	----KG--TGTFERVICDLRGIGIGSRELNV--PGQ-----VP----L-VITG--	997
KAJ6787215.1	----CP--TDVVQHEFLDSSRL--HNATFNL-----	1122
KAJ6784672.1	----TS--CAGMPHFWDYNDRS--WTVEFIL-----	1000
KAJ6781350.1	----KE--TGAFSQFISYLIB-----	535
KAJ6786554.1	----TG--TALFSEFFANNFN-----	944
KAJ6785998.1	SDHGDSDPNDAAFQFVVLVSPESLQVSLDKRDGSHWDVFECNDSVSEGEHTVRMVCNDHT	890
KAJ6779834.1	-----	532
KAJ6783597.1	KKEADSYP---LLQTE-INR-W--SGTKRGVTMYYEVA-----	565
KAJ6789350.1	---DDIEG---FW----KE-W--AKNTASMSHGWPLM-----	519
DAA05857.1	---NDEHP---IN---TP-S---SSTSSGRPGDGQQS-----	1073
KAJ6784990.1	---SKRAG---FR----SS---L-LVDGKVAGWMQS-----	1019
KAJ6787215.1	---KDHG---FF---KA---IGDKYGINDEWIQF-----	1145
KAJ6784672.1	---KDEKG---FY---DA---LAAQTGIDKDWITF-----	1023
KAJ6781350.1	-----NPPDPHCEDILT-----	547
KAJ6786554.1	-----HTQPIDCGDITV-----	956
KAJ6785998.1	ADSNCHKIGLGHGVPGTILQMPKGCGPGKYAVAKS---MAPAPGK-DHVKL-LPRHL-----	943
KAJ6779834.1	-----	532
KAJ6783597.1	-----HLQDVS-----NNPTCDNNE-----LYDPRRI-----	587
KAJ6789350.1	-----IDCARKSDFYFHYP--KVKDDMKVPNPKD-----	548
DAA05857.1	-SGTPRPPSNGQNPSST-P-KPPGDGPINTQK-----PGDGPDPINT-----QKPPGDG-----	1122
KAJ6784990.1	-IKDTIKD-----RRIKDVVLPGTHDSAMSKISHKL-----	1049
KAJ6787215.1	-SRKTMHVSNGCQYAGT-----HVKECQDKQDSHYYNFPL-ANNDKIHVFNPKDM-----	1193
KAJ6784672.1	--GTKEEPYVCADPSGDAP-LRPGGGAATPCHRLLT-HTLKNYPTKIDDKDIHVGNPKKF-----	1078
KAJ6781350.1	-GNNCRNTFDCKSFKGDK-----SGPAAAL-----	571
KAJ6786554.1	-SSNCRSAVTCDFFTGER-----TGPAAL-----	980
KAJ6785998.1	HLAGLEPVVYELTFDYDFHRVPRDL---GDTQMRIDFSNQEDYWKNIAGSV---NRKR-----	996
KAJ6779834.1	-----	532
KAJ6783597.1	----VLAQGGYDRDYEFHLANAHSWTLSALGMWM-----MKTFLNSDPPMPRGTQIQ-----	636
KAJ6789350.1	----IGKSYNEALDLLKYFKI-----ARSAAI-----YDSLAAEDLLDAISVSAF-----	589
DAA05857.1	----PDPSNAHNT-----PASTKRPG-----DNQH-----PTPTPAPIR-----	1152
KAJ6784990.1	----ITAADSPNTQTQ--GMS---IYN---QLRLG---ARWF-----DLRVI-----	1081
KAJ6787215.1	----IDKGYKNMTTRDDLDL--LLAA---SQYQIG-----MAW---DDAADGTDIPAM-----	1235
KAJ6784672.1	----IEASMTNITALQDSLLS---SYAVAVGLGVYSEG-----KTDVSEIDPVTAAMPVL-----	1126
KAJ6781350.1	----IWNSLVKVSSTY---A---NHLL-PLL-----PLL-----PLLP-----	598
KAJ6786554.1	----IWNSFVQINEMY---A---SYAD-ALG-----NAAAEEKIDPSLD-----	1012
KAJ6785998.1	DVNGRKRLAKRTLEDVGGNPVRWLEEEFRDDHFDFKIASRELQERWFGK-----SILEW-----	1050
KAJ6779834.1	-----	532
KAJ6783597.1	-----QRDGDDGSGDETGN DIV-----DQN-DDFDPSQID--PTEFFWMSRLGYVPNRLHLY-----	685
KAJ6789350.1	-----TYQSAVEK---MDAIV-----KEV-KTIKKN--D--LKE-----FILDF-----	620
DAA05857.1	D----IDC---KDDSC-----TRG-RDCESD-----D-----CL-----	1173
KAJ6784990.1	-----SVHGTAGM---EGDYE-----	1094
KAJ6787215.1	-----SVVSAVDN---MKEIR-----DKG-KEIEKK--E--REQ-----FILNM-----	1266
KAJ6784672.1	-----QLQSID S---MRDIK-----DIG-EKAKEE--K--KKQ-----LIMTI-----	1157
KAJ6781350.1	-----L-LPLLPL--L--PLH-----LLTL-----	613
KAJ6786554.1	-----DFQ-----NTF-APTPPE--K--DNE-----WLTL-----	1033
KAJ6785998.1	--LAALVKPEIRREFT---YKYDDSVTAKLFDESWDCPGSVE---GVNYDGHLLAQAVL-----	1101
KAJ6779834.1	-----	532
KAJ6783597.1	VTLVVLVIPPFPVKYICAHDYGVNTAVVIAK-----RA---NMNIKANAKHIVVV-----	732
KAJ6789350.1	-----ITGVIMLVP-GIGEAL-GPEMA--ATRS-----FLRLLG DVGDA-GTLIYGVVED-----	665
DAA05857.1	-----RG-GDCEG--ENCVEGGKCRGKRCISGGNCK-G-----	1202
KAJ6784990.1	-----FYG--AHVNDEK---MSACIGNTG---QLSLDDIISDINQF-----	1126
KAJ6787215.1	-----VLGILFFIP-FVGEAA-GAAGL--TAV--RT---LCRLIGDLDI-GMTIY GIVEN-----	1312
KAJ6784672.1	-----LTVVFMVLP-FVGEAL-GPIVG--AASSIAR--IALIISEAGNA-AISIKDIVDD-----	1205

KAJ6781350.1	-HLLTLH-----L-LPLLS--ASCLALL---LRFFVHSSLTEPSS-----H---	647
KAJ6786554.1	LDLVSMG---TSMVA-GPFVG---KVI-GK---LPYFVSKIEDAGANALKDKIAS---	1077
KAJ6785998.1	DI-----EVETSFGFTLIVESLTLPLNLDKSYLT-----YN	1133
KAJ6779834.1	-----	532
KAJ6783597.1	VL-VPQQVVLF-----	742
KAJ6789350.1	----PSSGLMRG-----FGAFAAVGLSRSGI-LK---A---SESRRGMS	698
DAA05857.1	----PK-----CKTGGPCEGENCEKGGG-CAKTLFGDCGSGGCQGARCF	1242
KAJ6784990.1	TSENPGEVIFRRLRYMVGIRKVPSLGPIHWGDDWSNL-YDD---FLGRMQKVHNRCLN	1181
KAJ6787215.1	----PSDAF-----GAIFGALLGRALD-----HV-----QLG	1335
KAJ6784672.1	----PTSA-----PFAMILGFIVGAAGAGAGG-S-----RLT	1231
KAJ6781350.1	----RPPLI-----VLCNADDYATA--EDG--KVLYT-----	671
KAJ6786554.1	----TSSTILT-----AITIGSGFIDGSTDDWDPE--AED--HFKNTMSLAMTGWN	1121
KAJ6785998.1	KGRVTGVVTLEALARVT-YEKKKVLNLP-----FPGASFKIPGIATIGPQLTVEGSIDA	1187
KAJ6779834.1	-----	532
KAJ6783597.1	-----	742
KAJ6789350.1	DTEIESGE-----VSGDGSRRAVLIDPTSCIPASGI	728
DAA05857.1	KRDCFGAQ-----CERLTIKPLPKDPKSTPATPPKPT	1275
KAJ6784990.1	IDGDFGAKKMGTTFMDMNEGKGCVIFLLSPTD-FSGNPYR--PQY-----	1222
KAJ6787215.1	KAAKSGRE-----LKRKGID-----D-----	1351
KAJ6784672.1	KVETLGDA-----AAVRGA-----	1245
KAJ6781350.1	-----	671
KAJ6786554.1	KIATFGLR-----DLFNGSD-----SSLN--TLS-----	1143
KAJ6785998.1	SLGMAGLVETKLEIAKWEVRQVMPSTDYKPELIDNSSPS--LDRT-----GDFSGIQKP	1240
KAJ6779834.1	-----	532
KAJ6783597.1	-----	742
KAJ6789350.1	----S-----DPRIAHI-----NKYIRILSITPDNIF-----P	753
DAA05857.1	----CLVD-----CPKLPECVDWPLCHDPCFSAC-----P	1303
KAJ6784990.1	----GLYD-----AGKLVITDDWADTES-----TKDMVNRETKDWQDP	1256
KAJ6787215.1	-----	1364
KAJ6784672.1	-----LK-AEDLA-----KFPARFRELDSQVQKIVKKF-----	1272
KAJ6781350.1	-----	671
KAJ6786554.1	----DLLS-----GGKFAAGKDYGKGSYDQASSKEANKTLEDNLSKTFYAYAIP	1188
KAJ6785998.1	EFYAGVTASGDVTLRLGAAAEF-----GVRFDDWKVDPAAAAVGEVSLTTKF	1289
KAJ6779834.1	-----	532
KAJ6783597.1	-----	742
KAJ6789350.1	V-----	754
DAA05857.1	VYRRPTG-KACTTLQTARDCTEFVSSTRVKTPPTSWSTTRTL CET	1349
KAJ6784990.1	RKFINIH-IAQWLL-----TS-QGIDAVSWDNYYEAMQVN	1289
KAJ6787215.1	-----IRGARMCKL-----	1373
KAJ6784672.1	-----EGKACHL-----	1279
KAJ6781350.1	-----	671
KAJ6786554.1	AIWHASG-HRPFII DTGLSCDKGKA-ED-VKLKGACWKDTWYRLASP-----	1232
KAJ6785998.1	AAGSSTTGTCPFTYGLDVGARLFARAIAPQVFGWGGGEVDLTA KWEKSII EGGTCPDLGP	1349
KAJ6779834.1	-----	532
KAJ6783597.1	-----	742
KAJ6789350.1	-----	754
DAA05857.1	-----MVDCEA-----ADITAT-----TTTTTHTPDP	1372
KAJ6784990.1	-----PLIYS-----	1298
KAJ6787215.1	-----	1373
KAJ6784672.1	-----	1279
KAJ6781350.1	-----	671
KAJ6786554.1	-----DGGYQECAK-----NGCDHVPNP	1250
KAJ6785998.1	IPSKRSLQSLDPPSIDGLSEDHVTRNKSRLGGADLG-----SYSASDVQSMHS---	1398
KAJ6779834.1	-----	532
KAJ6783597.1	-----	742
KAJ6789350.1	-----	754
DAA05857.1	IESV-----GPAPVYYGVWSFGEKEKS-----SMLADEEAYFSALET PMTTTT	1418

KAJ6784990.1	--EMSPTAWPGVLMVDYLGETWYAGHDFAD-TGAELATLAVGLNQY-----	MLSENC	1348
KAJ6787215.1	-----		1373
KAJ6784672.1	-----		1279
KAJ6781350.1	-----		671
KAJ6786554.1	CVECDDDQFKTPSGVDKLGSFYFSQSVHD-LIV--GYVRTGTPNFFSTTSRKLTAKCR		1307
KAJ6785998.1	-----SEEHTSSPAKRGSLVKRGGVYGPAPSLPVGEFFCPSK-DGEKGMC		1443
KAJ6779834.1	-----		532
KAJ6783597.1	-----		742
KAJ6789350.1	-----		754
DAA05857.1	SAEPSTTDDPTETTADGPTSTVGPNVLVCGFALYAAFYRFDIVKM-VGDWVWDDEGHK-		1476
KAJ6784990.1	LSSI-----YPPLLDYPEGYKDKSANKAN---NK-		1374
KAJ6787215.1	-----		1373
KAJ6784672.1	-----		1279
KAJ6781350.1	-----		671
KAJ6786554.1	SVRTWLDNDKENGGSANPNSPDTLKSSLQDDVTTPGFIRMPVCTADRARIWGASSDS-		1366
KAJ6785998.1	VQAYDALAESNEGGVWQNMRKRDTLVPSTIDEN--AVAAHFHDH-----		1486
KAJ6779834.1	-----		532
KAJ6783597.1	-----		742
KAJ6789350.1	-----		754
DAA05857.1	LKKELKGCGALTGWKWyRR-----DDG-----SREA		1502
KAJ6784990.1	IA--GADEEQWNNGIFANGTVIDHP---SPDV-----GVYNGPHKD		1410
KAJ6787215.1	-----		1373
KAJ6784672.1	-----		1279
KAJ6781350.1	-----		671
KAJ6786554.1	AK--NYPCNANAGYDYCGDSTIENQTSDASPDVEDCKEMIRRLEDGRLPKRWPVHGPLEK		1424
KAJ6785998.1	-QRSHGYR---RHVRGEELHELE-KRAKEKLICKACERTCDIS-----ADFPGGQ		1531
KAJ6779834.1	-----		532
KAJ6783597.1	-----		742
KAJ6789350.1	-----		754
DAA05857.1	-RFNLPVFLTACVESAIKSAGGPGLS-----CIFA		1532
KAJ6784990.1	-DAIITYYS-----		1418
KAJ6787215.1	-----		1373
KAJ6784672.1	-----		1279
KAJ6781350.1	-----		671
KAJ6786554.1	QQAIATYESCKFGVTGKGIGHNVDFKVGAQDVIDLVRDSIDKFGGGGKVGSKGTMSCKGN		1484
KAJ6785998.1	LKGKEWGWATKDCGDFNFGSPLLAREPNTDYHTEHVLEAQMIDLFFQYLNKKKKPQPDPK		1591
KAJ6779834.1	-----		532
KAJ6783597.1	-----		742
KAJ6789350.1	-----		754
DAA05857.1	T-----		1533
KAJ6784990.1	-----		1418
KAJ6787215.1	-----		1373
KAJ6784672.1	-----		1279
KAJ6781350.1	-----		671
KAJ6786554.1	IKGQKVNWGLY-----		1495
KAJ6785998.1	PGAAKGDTVSFCYVNVLWDVPAFWPGQDMGGIGKKWDPIMHIAQFPTKTFNKQE		1651
KAJ6779834.1	-----		532
KAJ6783597.1	-----		742
KAJ6789350.1	-----		754
DAA05857.1	-----		1533
KAJ6784990.1	-----		1418
KAJ6787215.1	-----		1373
KAJ6784672.1	-----		1279
KAJ6781350.1	-----		671
KAJ6786554.1	-----		1495
KAJ6785998.1	ALESINTPSKTRAWASGNPWDKGWTNDIADYAKSRIILQKLRSTMGSRIVQSDSTISQ		1711
KAJ6779834.1	-----		532

KAJ6783597.1	-----	742
KAJ6789350.1	-----	754
DAA05857.1	-----	1533
KAJ6784990.1	-----	1418
KAJ6787215.1	-----	1373
KAJ6784672.1	-----	1279
KAJ6781350.1	-----	671
KAJ6786554.1	-----	1495
KAJ6785998.1	TMKTQTD R IGVVLDALDT T LLKANTPAGYTAWEKQDLKDEWHKYMKGQYTTMQSKTRGLV	1771
KAJ6779834.1	-----	532
KAJ6783597.1	-----	742
KAJ6789350.1	-----	754
DAA05857.1	-----	1533
KAJ6784990.1	-----	1418
KAJ6787215.1	-----	1373
KAJ6784672.1	-----	1279
KAJ6781350.1	-----	671
KAJ6786554.1	-----	1495
KAJ6785998.1	NDWLPKLKKAWCSQAEKDKWEAKPTDSGT L KTEKEEHRAFIKAIEDFDTKWNGLAVNNP	1831
KAJ6779834.1	-----	532
KAJ6783597.1	-----	742
KAJ6789350.1	-----	754
DAA05857.1	-----	1533
KAJ6784990.1	-----	1418
KAJ6787215.1	-----	1373
KAJ6784672.1	-----	1279
KAJ6781350.1	-----	671
KAJ6786554.1	-----	1495
KAJ6785998.1	L 1832	
KAJ6779834.1	- 532	
KAJ6783597.1	- 742	
KAJ6789350.1	- 754	
DAA05857.1	- 1533	
KAJ6784990.1	- 1418	
KAJ6787215.1	- 1373	
KAJ6784672.1	- 1279	
KAJ6781350.1	- 671	
KAJ6786554.1	- 1495	

Fig. S1. Clustal alignment of *A. album* GH18 chitinases. The alignment of the 26 *A. album* sequences and the three *H. jecorina* sequences (DAA05865, DAA05854, DAA05857) was subdivided for the subgroups A, B and C (see Figure 1) in order to better indicate the specificities of the three subgroups. Boxed sequences correspond to the conserved motif DXXDXDXE, typical of GH18 sequences. Yellow highlighted C's (in the B sequences) correspond to C residues 46, 93, 185 and 214 in hevamine (P23472), a lysozyme/chitinase identified in rubber tree (*Hevea brasiliensis*). Green highlighted sequences in A and C groups indicate the typical extra α/β region of about 70 amino acids described in plant and fungal Class V chitinases (Taira, 2009, Kamerewerd 2011).

Figure S2

KAJ6787877.1	-----	0
KAJ6782998.1	-----	0
KFG78085.1	-----	0
KAJ6788372.1	-----	0
AGC24356.1	-----	0
KAJ6789110.1	-----	0
KAJ6785893.1	-----MMPSKYNALAVILLASSAYARTCLPAYEAQTSYVG-----CYHDPNSPR	43
KAJ6786934.1	-----	0
KAJ6780833.1	-----	0
KAJ6787866.1	-----	0
KAJ6786079.1	-----	0
KAJ6785739.1	-----	0
KAJ6782204.1	MTSVAKPGDDGLLPSK-----PKYGSEEDSGSDIELEELRDEVAD	42
KFG84234.1	-----	0
KAJ6788989.1	-----	0
 KAJ6787877.1	-----MRI-VEIASSLGLLLA-----	15
KAJ6782998.1	-----MHL-PLTHSLLALTIV-----	15
KFG78085.1	-----MAAAANLPKKPNSS-----	14
KAJ6788372.1	-----MTSNNAN-----	7
AGC24356.1	-----	0
KAJ6789110.1	-----	0
KAJ6785893.1	DLSGPLLTGKL-----NSPQYCANICGAAGYSYSGVEYTVQCFCGYKIESTSIA	97
KAJ6786934.1	DE-----	0
KAJ6780833.1	-----MKSPLNSYCLAGL-----	13
KAJ6787866.1	-----MVAATKLLSVATAGWAVASAAAA-----	23
KAJ6786079.1	-----MLLPLLAGLALVHPA-V-----	16
KAJ6785739.1	-----MVQTT-----ITSVAG-ALALFS-----	18
KAJ6782204.1	LLPGTRPGVSKKRHRRTTEASDHFLARIL---NWRLRKRTVFIVSIVGVVLVLLGGLFG---	96
KFG84234.1	-----MKSLSIFAALLT-AVVDAGLTS-----	22
KAJ6788989.1	-----MKTASFVAAAALLA-VGTDAAHFG-----	22
 KAJ6787877.1	-----THAKPCAGA--ASLDLILAGQHVIYSFPTS-43	
KAJ6782998.1	-----SAASGSVKP--ACDLDILAGQHVIYSWDYTL 44	
KFG78085.1	-----SSSDGSDLDP-----WQNLDWAVGQMLIMGWGDTE 45	
KAJ6788372.1	-----NGAESADIDPI--YQNLDWAIGQTLMGWGDTE 38	
AGC24356.1	-----MTVGN-----DDNLDEKEIGQLLMCGFDGLE 25	
KAJ6789110.1	-----MV-----TPEQRKKVGVQFAVGFHDTT 22	
KAJ6785893.1	QCNAADCPADPSKKCGGNMINIYKINNP-SANPPLSPSFPCDTRPLCSNDVCDTSKIA 156	
KAJ6786934.1	-----	MAD 3
KAJ6780833.1	-----LLPAAVAGRATSPDVYPT--PQGK-GE-----GPWAAAY 44	
KAJ6787866.1	-----ASDGVTNDTYFYGQSPPVYPS--PEMS-SS-----GAWAEAQ 58	
KAJ6786079.1	-----SNQIYFRAEPDAYQNSPEVLP-----PQTS-GQ-----NEWADAF 51	
KAJ6785739.1	-----AQGHASAATASGYDSPAYYPA-----PYGG-WV-----SEWRDSY 52	
KAJ6782204.1	-----WGRYTQTPPDGHSPPWYPC--PRGG-TV-----SQWAESY 128	
KFG84234.1	-----PGHFHKLDARAELATSPPHYP-----PWMPNQA-----PGWEDAY 58	
KAJ6788989.1	-----NN-----TNSNSTEQTGPLAHSPPFYPS-----PWMDPKA-----PGWEDAY 60	
 KAJ6787877.1	STPPAQLVQLTKAGLVGGVILFGENVDAKTAAMD--TLRQAYAASPAPA-LLKKT-TGV 99	
KAJ6782998.1	PGPDELYDLTRAGLVGGVLLYDVHVNKDTPAALA--KLQAAKASPAHK-LLRKQ-SGR 100	
KFG78085.1	VTP--QIKSLIEDHHLGSIIILTAKNLKS--AQETA--KLVQEL-----Q-TIAKN-AGH 91	
KAJ6788372.1	VTP--QIRTLIEDHHLGSIIILTAKNLKS--AQQTA--RLVQEL-----Q-TIAQN-AGH 84	
AGC24356.1	PTP--GIIDLIEHNHLGSIIILFSRNIA-----PKQVQ--KLTHSL-----Q-QIARN-AGH 71	
KAJ6789110.1	VNN--DIKSLIQDYGVGAIVLFKRNVGS--AAELR--TLCRDL-----Q-QLAKD-AGH 68	
KAJ6785893.1	DRAAAIVKVLTLD-----KANNLASSAS-----GS 182	
KAJ6786934.1	LNVEEVLKKTITE-----KVELLSGMSIA-----PAM 31	
KAJ6780833.1	QSARALVGQMTLDE-----KVNIITRGFK-ADN-----ICAGTTGSV 79	
KAJ6787866.1	AKAQLKVSQMTEL-----KVSLTGADSIDN-----GCSGNVANI 94	
KAJ6786079.1	AKAKAMVQMSLEE-----KVSITGGVD-LKS-----GCGSTIAGI 86	
KAJ6785739.1	SKAKKLVDQMSLAE-----KTNITAGTGIFMGKSRLSNQAKASDAAILRCNGNTGSA 104	
KAJ6782204.1	EKAARMVRNMTLAE-----KVNITTGTGWAMG-----LAVGNTGPA 164	
KFG84234.1	KQARDFVSRMTELAE-----KVNLTGWTGMSD-----NCVGNNSGAV 94	
KAJ6788989.1	AKAKAFVSQLTAE-----KVNITTGVGWMGE-----KCVGNVGSV 96	
 KAJ6787877.1	ADA--KFFISTDQ---EGGQVRRMKGEE-----PKL--SPKQMGASADPAAAGKAGG 144	
KAJ6782998.1	DTA--LLIMITNEE--GGTVFNGVHDGG-----PAL--SAKQVGASPDAAAGWQAG 145	
KFG78085.1	PQ---PLLIAVDQ---ENGGVNSLFDED-----YVCQFPSAMGIAATGRVELAYEI-Y 137	
KAJ6788372.1	PQ---PLLIAVDQ---ENGGVNSLFDED-----YVCQFPSAMGIAAAGSPELAYEV-T 130	
AGC24356.1	KR---PLFIAVDQ---ENGVVRLRGD-S-----GTYLPGNMALGALGSSTAARNV-A 115	
KAJ6789110.1	EQ---PLFIGIDQ---ENGLVTRISP-P-----VASQQPGPMLGAAGSLDIASQV-A 113	
KAJ6785893.1	SKIGLPAYQWQNEALHGVAGSTGVQFQSPLGSNFSAA SFPMPI LLSA FDDKMVKDV-A 241	

KAJ6786934.1	PKHGIPSIRMSD-----GPNGVRGTTKFF--NGVPAACFPCGTALGSTFNQELLEKA-G 81
KAJ6780833.1	PRLNWPGMCLHD-----AGNGVRAAELV--N----AWPSALHSGASWDRNLTHQR-G 124
KAJ6787866.1	SRLGFPGMCLSD-----AGNGLRATDFV--S----SFPSGIHVVGASWNKDLAARR-G 139
KAJ6786079.1	PRLKFPGMCLND-----AGNGVRATDYV--S----GFASGIGVGASWNKVLAKQR-G 131
KAJ6785739.1	PRVGFPMCLLED-----GASGIRQADHV-T----AFPDGITAGATFDKELMYQR-G 149
KAJ6782204.1	IYAGFPSLALQD-----GPLGIRFADNA-T----AFPAGITVVGASWNKELMFQR-G 209
KFG84234.1	PRLGLRALCLQD-----GPLGIRLSDYN-S----AFPAGITAGATWSEHLWRDR-G 139
KAJ6788989.1	PRMGLKSLCMQD-----GPLGLRFSDYN-S----AFPVGVTAGASWARHLWRDR-G 141
	: : : :
KAJ6787877.1	AGAAAATLKKFNNNN-----LAPVLGV-YREAGDFLDYYGRSGFNGNSAAAVAAAAPFIKA 198
KAJ6782998.1	VQAAAALKRYNFNVD----LAPVLGV-YRDEGNFLDTGNRSYGTADKVIATLPFIRA 199
KFG78085.1	KATASEIISACGVNLM----LGPVLDV-LNNAR-YQPLGVRSTGDDPQEASQYGLAALNG 190
KAJ6788372.1	KATATEIISACGVNLM----LGPVLDV-LNNAR-YQPLGVRATSDDPQEVSQYGLAAMAG 183
AGC24356.1	MAISKEELLGLGMNWN----LAPVLDV-NNNP-NPViGVRSPGDPEKVAQFASACAKG 166
KAJ6789110.1	GATAEMLGHFGINMN----YAPVGD-NSEPL-NPViGVRSPGDPEKVAQFASACAKG 166
KAJ6785893.1	TIISTEARAFANHGFAGLDFWTNPINP-FRDPR--WGRGMETPGEDSFRISNYVVSLVDG 298
KAJ6786934.1	KTMGDEIAIKSAHLI----LGPTIN-MQRSP--GGRGFESIGEDPFLSGLGAAALVRG 133
KAJ6780833.1	LYMGGEFKKGGINIA----LGPNAGPLGRTPL--GGRNWEGFSVPYLSQLNAETITG 177
KAJ6787866.1	AAMAGEFKKKGVNWL--LGPGVVGPAWRVTL--SGRNWEGFSADPYLSGSLAAQSVAG 192
KAJ6786079.1	VALGENRKKGVNIM----LGPGVGPAAWTVVK--GGRNWEGSSADPYLSGALAAETVVG 184
KAJ6785739.1	VALGKEARGKGVNIL----LGPTVGPIGRKPK--GGRNWEGFGVDPLQATGARQTIG 202
KAJ6782204.1	QAHQGEAREKGINVL----LGPSVGPLGRMPA--GGRNWEGYGPDPYLQGIAAAETRG 262
KFG84234.1	KALGAESRDKGIDIA---LGPGASGPLGRAPT--GGRNAEGFGSDPYLQKGLANTVIG 192
KAJ6788989.1	NAMGSEARDKGVDVI----LGPGASGPLGRLSK--GGRIGEAFGADPYLQGQALANTVTG 194
	*
KAJ6787877.1	QQAAG----VAATA--KHFPGLGAASHDANT-----DTGPVTLEQLSDEIRSIDE 242
KAJ6782998.1	QRERG----ILVSI--KHFPGLGAARKDQNT-----DAAPVTLDVSRADLESIDL 243
KFG78085.1	IRDAG----IAAAG--KHFPSPYGNLDFQGSN----S-APVPIQTLEELSLISAL 233
KAJ6788372.1	IRDAG----IATCG--KHFPSPYGNLDFLGSS-----L-DVPIITQTLEELSLISAL 226
AGC24356.1	YQRKG----VATST--KHFPGHGDTA-TDSH-----L-DVPIVINKTLEELDKTEL 210
KAJ6789110.1	MRENK----VVPCI--KHFPGHGDTA-VDSH-----Y-GLPSIDKSRAQLDAVEL 208
KAJ6785893.1	LQGGINPEFHRTISTC--KHFAYADVESGRQTQN-----DIHPTRQDMADYYL 343
KAJ6786934.1	IQSTG----VVATI--KHFCLNDQEDKRMGV-----QSIVTERALREIYA 172
KAJ6780833.1	IQKAG----VIANI--KHFIAEQETYRRPY----FGVEAASSNVDDKTLHEYYL 222
KAJ6787866.1	IQGOG----VITST--KHFIAEQETNRPD----QDVQSLSSNIDDCKTMHEYYL 237
KAJ6786079.1	VQSQN----VMTSVKKQHYIGNEQELYRSLE-----GDIQAISSNIDDCKTMHEYYL 231
KAJ6785739.1	IQEQQ----VIATI--KHLVGNEQEMYRMYN----PFQQAYSSNIDDRTLHEVYL 247
KAJ6782204.1	IQGEG----VMATI--KHFVANEQEHFRQP----WAWLPHAVSSNVDDRTMHELYA 309
KFG84234.1	IQESG----VIACA--KHFIAEQEHFRQAGESVPRGFNISESLSNVDDKTLHEDYA 244
KAJ6788989.1	IQGAG----VVACA--KHYIANEQEHFRQVGEVSVDRGYDISETILSSNVNDKLMHEYYS 246
	: * :
KAJ6787877.1	APYVGAIA-AGVELVM---MSWA--VYPALDG-RPAGLSNKWVQDELRGRLGFTG--V 291
KAJ6782998.1	RPFQQAIR-AGVDMVM---VYPAVDGAWPAGLSSNPKMDILRGRGLGFRG--V 293
KFG78085.1	VPFRNAIA-TGKLDAM--FVGCGCISNPSMNVG-HACLSDQVVDLLRNELGFKG--V 285
KAJ6788372.1	VPFRNAVA-SGKLDM--FVGCGGLSNPSMNVS-HACLSDQVVDMLRNEMGFRG--V 278
AGC24356.1	VPFKKALE-AGGIACPTSVMVGHM--LLPHFNKDVVSSIAPIEIVRDLRRLRFRGYKG--V 264
KAJ6789110.1	IPFKRAAQ-EGIE---MIMTAHI--AMPQLTGSMDPSTLSPQVLSILRDEFKFDG--V 258
KAJ6785893.1	PMFQCRVDAKVGGSV-----C--AYNSVDGI-PACASSYLLQTVLRDGWNFKEPYNY 393
KAJ6786934.1	MPFQLAVRDNPGAFM-----T--AYNGINGT-FCSENPKYLDGMLRKREWGDG--L 219
KAJ6780833.1	WPFMDGVH-AGVGSVM-----C--SYNRINTT-YGCENSKLMLNGLLKGELAFDG--F 268
KAJ6787866.1	WPFQDAVH-AGSGNIM-----C--SYQRINNS-YGCANSKTLNLKSELGFQG--F 283
KAJ6786079.1	WPFVDLVK-AGTANVM-----C--SYNRLNQT-YACGNSKTLNLKTELGFQG--F 277
KAJ6785739.1	WPFAGIH-AGVGAVM-----T--AYNAVNGS-ACSQNPyLINGILKDELGFQG--F 293
KAJ6782204.1	WPFANAVK-AGVAVSVM-----C--SYNMVNNS-YACGNSKLLNLGILKDELGFQG--F 355
KFG84234.1	WPFADAIR-AGVGSIM-----C--SYNQINNS-YACQNSKLLNLGILKDEMGFQG--F 290
KAJ6788989.1	WPFQDAVK-AGVGSIM-----C--SYNQVNNS-YACQNSKLLNLGILKHEYGFQG--F 292
	: * :
KAJ6787877.1	TITDAMEAGSLKG----FGGAETAKLAAAAGMDLLIASGRNVTQG--DTIRKAVVSGIQ 345
KAJ6782998.1	TITEAMEAGSLP----FGDVEERTKIAVRAGNDLILASGLNVTEG--EVIRKALVEGLK 347
KFG78085.1	AISECLEMEALSH----DLGVQNGVVMAVEAGCDLVLLCRAYDQVL--EAI-KGLKLG 338
KAJ6788372.1	AISECLEMEALSH----DLGVQNGVVMAVEAGCDLVLLCRAYDQVL--EAI-KGLQLGLE 331
AGC24356.1	IITDCLEMDAVKE--TVGTPKGALMALQAGNDMAMI SHTLAQFK--DAP-KVLYSALQ 317
KAJ6789110.1	IMTDCLEMDGIRA--TYGTVEGALLAFQAGVVDNVMICHTYDVQT--AAV-DRICAAL 311
KAJ6785893.1	VVSDCAVDNI FDPHYAKDRVEASALGINAGTDLDCGD-----TY--TNLNQGV 442
KAJ6786934.1	IMSDWYGTYSTND-----AVKAGLDLEMGPS-----RFRGEALQFNAS 258
KAJ6780833.1	VMLDWNAQHNL-N-----SANAGLDMMLMPMG-----GNWGQNLNTNAVR 305
KAJ6787866.1	VVSDWGAQHTGHA-----GALAGMDMAMPNP-----GSFWGDELVKSVK 322
KAJ6786079.1	VVSDWGAQHAL-T-----DAPNGLDMGMPNS-----DPYWGAAALVNAVK 315
KAJ6785739.1	VMSDWLGHMSGVE-----SALAGLDMMDMPGDTQVPLLGYSYWMFELTRSAL 339
KAJ6782204.1	VMSDWLAQQSGV-----SALAGLDMMSMPGDGLGWTGESLWGPQLSRAVL 401
KFG84234.1	VMSDWQAQHGGAA-----TAVAGLDMMSMPGDTE-FNTGYSFWGGNLTLAVI 335
KAJ6788989.1	VMSDWQAQHSGVS-----NAVAGMDMAMPGDTI-FNTGRSYWGGNLTLAVL 337
	* * :

KAJ6787877.1	SGRLSRAQFDEATKRIAAMRSKL-----WA-----	370
KAJ6782998.1	RGEGLRDEFRQATERIIALRKV-----	369
KFG78085.1	NGIITKDRIFTSIRRQVQLKSTCT-----SWAKALN-----P 370	
KAJ6788372.1	NGIITKERIFTSLRRVLHLKASCT-----SWSKALN-----P 363	
AGC24356.1	EGOLDKDETRQSLQRVAQLKDQFL-----NWDDVLQ-----Q 349	
KAJ6789110.1	KDEISQTRIDESLARLSLKLAKFT-----NWDRALQ-----T 343	
KAJ6785893.1	SKLTTEATLDKSLGLRSLALIKGVYFNPP---AQYNR-----476	
KAJ6786934.1	TGKPIHHIDE---RVRAVLKLKVKKVSSL---PIE-----EN-----289	
KAJ6780833.1	NGTVAEARVSDMATRIVASWYLVGQD---N-FPVPGIGMK-----NLT 344	
KAJ6787866.1	NGSPVPESRINDMATRILTTWYQFKQD-EH-FPAPPGVGP-----KDT 363	
KAJ6786079.1	SGSPVPESRTDMAMRIIASWYQLQDDPS-FPAPGIGMP-----GNLT 357	
KAJ6785739.1	NGSPVMTRLNDMATRIVATWYHMGDQGF---PATNFHYNTRDEKGPLYPAAWPESPTT 395	
KAJ6782204.1	NGSLPVSRLDDMTARIVASWYQLGQDDKSRFDRKGPNFSSWTNDKMGYINDGTSSRQEKV 461	
KFG84234.1	NGTPPAYRIDDMAMRIMASFFKVGKPGK---QVPTSFSSTWRTDFGYRQAAKENWEQV 392	
KAJ6788989.1	NGTPPAYRVDDMAMRIMASLFKVGWNVET---AKDTNFFWSRN TYDYRHAAKESMEQV 394	
* :		
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369
KFG78085.1	PGISLLSQLHPHSVSLSRAYDESITVIRDKEKMLPLASSMHPGE-----415	
KAJ6788372.1	PGISLLSQLHPHSLAISRRAFDESITVIRDKEQLLPLARSMPGE-----408	
AGC24356.1	ADLTMGSE--AHATLSKELYDRVPTVVNTNRKNTLPIRPAQTDK-----391	
KAJ6789110.1	STDALDDINARGAKLAHKAYAADATVVRIIDKILPLSTSASTV-----387	
KAJ6785893.1	--LGWADVNTEAQTLAYNAAVKGMTLLKN-DGTLPLSK-----512	
KAJ6786934.1	--GPENTRDTPTETAQRLKIGNESIVLLKNNDLPLFTKEKTLVLPNAKEATYHGGGS 347	
KAJ6780833.1	EPEHLDVARNPESKPLMEGAITGHVLLKNTNNTPFKGKQK-----386	
KAJ6787866.1	KPHKIVDGRDPAAKPVLLDGAVEGHVLVKNTKSTLPLRQ-PK-----404	
KAJ6786079.1	VPHRIIEGRDPADLPVILQGAIESHVLVKNEKSTLPLQS-PK-----398	
KAJ6785739.1	VINENIDVRADH-DIVARQVAQDAITLLKNDAGLLPLSE-ER-----435	
KAJ6782204.1	EVNQYVNAQHNH-SILAREVAEGTVLLKN-SGILPLTR-SGPRTR-----TKHKEGK 511	
KFG84234.1	--NFQVDVRGDH-AAHIRESAAKTVILKN-TGSLPLNK-PK-----429	
KAJ6788989.1	--NFQVDVRANH-ANHIRESGAKGTVILKN-NGALPLNK-PK-----431	
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369
KFG78085.1	ELLLLTPLVKPLPAS-----AMTKS-----435	
KAJ6788372.1	ELLLLTPLVKPLPAS-----SLTKS-----428	
AGC24356.1	-ILFLAA----HV-----PQTL-----403	
KAJ6789110.1	-FVSPGP-----DF-----PVGGG-----400	
KAJ6785893.1	-FLSNVAIIGPWANVTDKMQGNYAGTAPLL-----VNPLDVFQKRWN 554	
KAJ6786934.1	AALRAYYAVTPYEGI---GEKLGQTPTFTVGYATHRFLPILGNQLTDPMNGKQGMWRV 402	
KAJ6780833.1	-ML-----SVF-----GYDAALPETKNTD-----ILFQL 409	
KAJ6787866.1	-MV-----SLF-----GYSAKSPDFFAPGGNLQL-----LQWQL 432	
KAJ6786079.1	-KV-----SIF-----GYSASTPPKWTAQDDT-D-----GTWRF 425	
KAJ6785739.1	-SI-----KVF-----GTDAAKNP-----448	
KAJ6782204.1	VNI-----GIF-----GDDAGP-G-----524	
KFG84234.1	-FL-----AVI-----GEDAGQNS-----442	
KAJ6788989.1	-FL-----AVI-----GEDAGPNP-----444	
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369
KFG78085.1	-----LLESKKTWSQAPTQH-----D 451	
KAJ6788372.1	-----LLDAKNDQSAATGPH-----E 444	
AGC24356.1	-----AVDSE-----KEP-----411	
KAJ6789110.1	-----AVNSG-----DAAHPTR-----V 413	
KAJ6785893.1	VKYVQG-----AD--IDSGNTG-----569	
KAJ6786934.1	FNEVPGTADRKLIDELQFTKTEMHLVDYSNPVNDWVYADMEGLVADEDCTYEIGVVVS 462	
KAJ6780833.1	GYYS-----SQEMAQAVLGEAHDQARG-GTIIS 439	
KAJ6787866.1	GAES-----IDLNEVLAGALGNAANASSIGIN-GTLFG 464	
KAJ6786079.1	GLAP-----V-----FEEDPATSPTCGR-----GTMF 448	
KAJ6785739.1	-----DGPNACADRNCNK-----GTLQ 466	
KAJ6782204.1	-----LGPNCADRGCNE-----GTLGS 542	
KFG84234.1	-----RGPNGCDDRGCDD-----GTLAM 460	
KAJ6788989.1	-----KGPNCGADRGCDD-----GTLAM 462	
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369
KFG78085.1	SWAHKDRE-----RSAIMSSEGVF-----470	
KAJ6788372.1	RWAHRRLD-----RTAHMSSEGVFREFGKTLARYRNEKLHTSY-----483	
AGC24356.1	-----FNSFHASLLK-RHTNLEYIY-----431	
KAJ6789110.1	SWV-----SSSGFGDEIRK-HCAGAAEIRY-----436	
KAJ6785893.1	GFGAA-----574	
KAJ6786934.1	GTAKAFVNDQLIVDNATNQVAGDAFFGSA TREERG-RVEMKKG ETYNFR IFGSAPTYTL 521	
KAJ6780833.1	GGRAAATAPS YIIDPLNAI-----Q-QRAMEDDTWV-----469	

KAJ6787866.1	GCGSGATTTPANAVSLEAI-----K-ARTYRGDTAL-----	494
KAJ6786079.1	AGGSGAITPQDSVSPQQAF-----V-ARAAKDGFTL-----	478
KAJ6785739.1	GWGS GTVD TYLDDPI GAL-----Q-ARVKNVTL-Y-----	495
KAJ6782204.1	GWGS GAVDFPYLVTP ESSL-----S-ATFDLN A N V I S S S L-----	576
KFG84234.1	LWGSGTSQFPYLITPDSAL-----Q-RQAIQDGS R Y E S V L-----	494
KAJ6788989.1	LWGSGTSNFPYLITPDSAL-----Q-QQA IKDGS R Y E S V L-----	496
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369
KFG78085.1	-----LHENLIARASC II I VTADANRN MY QAGF-----	498
KAJ6788372.1	-----TANGV--RPVHENLINRASCIVI F TADANRN LY QAGF-----	518
AGC24356.1	-----NEET----PDLSQ KI QEADW VI IGTANAN LY PFQ VRM-----	464
KAJ6789110.1	-----TDE DPL---TDE QWS KIEGADFL L I LATRN AREAP Y QQKL-----	471
KAJ6785893.1	-----LDAARSS DHII YLGG D IDVENE GH-----	599
KAJ6786934.1	KGDAYVPGHGS LR VGGCKVIDDQE EIKKS VLAKEHD QVII CAGLNAD WET EGA-----	575
KAJ6780833.1	-----NWDTKSFDPPVNPA---SNACLVFINAISTEGWDRDGL-----	504
KAJ6787866.1	-----FHDLAS P SPV DPA---SDVCLVLGN AFACE AYDRPAL-----	529
KAJ6786079.1	-----VQDLTSPQPQV DPA---SDV C VFGN AWAREG ND R PQL-----	513
KAJ6785739.1	-----NTDSVPPSLPKPAD---DDIA I VFISS D A GENT YTV EGN-----	531
KAJ6782204.1	-----SNKK---PSK DLL QA---MDVC I C V FANADAGE GEF FIRWE SV-----	610
KFG84234.1	-----SNY QWA ATQRVVA QP---NVTA VVFVNADSG EGYIEVDGN-----	531
KAJ6788989.1	-----SNYAW PATHDLVSQP---NVTA IVFANS NAGE GYIN VGGN-----	533
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369
KFG78085.1	-----TKHV DMMCM S M HRS RGN K K Q L I V V A V S S P Y D---FAMDKS I G T Y I C T-----	541
KAJ6788372.1	-----TKH VEMM CM S M L R S R G Q K K H L I V V A V S S P Y D---FAMDKS I G T Y I C T-----	561
AGC24356.1	-----VQ-----QA QKLAK R L V V A V M N P Y D---QMCFPQV D T Y L V T-----	498
KAJ6789110.1	-----GLD-----IAQRRSGKT V I S I A T C A P Y D---FLEEP A I K N V I V-----	507
KAJ6785893.1	--DRT---SISWP G N Q N D L I S Q L S N L G K ---PLV I V K F G G Q V D S S L L S N K V N S I V W A-----	651
KAJ6786934.1	--DRA---SMKLP G VLD Q L I A E V A A N P---N T V V V M Q T G T P E E M P-W L S---QTKA V L Q A-----	624
KAJ6780833.1	-----HDD FSD G L V R N V A S K C A---N T I V V V H A S G I R L V D Q W I E H P N V T A I I A-----	550
KAJ6787866.1	-----Q D A Y T D D L V K T V A A S C A---R T V V V L H N A G P R V V D A W I E H D N V T A V I F A-----	575
KAJ6786079.1	-----E D A Y T D M I N A V D R C A---K T V V V F H N A G P R L V D G F V N H P N V T A V I F G-----	559
KAJ6785739.1	H G D R D A S K L Y A W H N G D O L V Q D V A K K Y R---N V I V V V H T V G P L V L E K W I E L P T V K S V L I A-----	587
KAJ6782204.1	AGDRN--D L F L Q R G G D Y L V L A V A E E C G G G K G K T I V V V H A V G P V V M E R W I D H P G I G A V L A A-----	668
KFG84234.1	AGDRK--N L T L W K N G D D L I K N V S S I C H---N T I V V I H S V G P V L V T D W Y Q N P N I S A I V W A-----	585
KAJ6788989.1	E G D R N--N L T L W K N G D D L I R N V S A L C R---N T I V V I H S G G P V L L D E I S K N E N V T A I V W A-----	587
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369
KFG78085.1	FDFTEDA M S A L V R V L V G E I T P I G S M P G T L R K S K K V L K-----SRQH WL V-----	585
KAJ6788372.1	FDFTE N A M A S L V R V L V G E I V K P V G S L P G T L R K S K K V L K-----SRQL WL V-----	605
AGC24356.1	YEY T P P A H E A A V R L I F G E I E T R S R L P I S I P N V D D A I A-----P-ATFIV-----	541
KAJ6789110.1	YEPT L E A F R S A V D I I Y G V D T P R G K L P V A E K K V-----	539
KAJ6785893.1	GYPG Q E G G N A V F D V L T G A A P P A G R L P I T Q Y P K S Y V E N N N I L D M N L R P S N-----GIPG-----	704
KAJ6786934.1	WYGGNET GNC I A D T I F G D S N P S G K L S L S F P K R-L Q D T P A F L N F R-----T E A G R T L Y G E-----	677
KAJ6780833.1	H V P Q D S G R A I V K V L L Y G E A D F S G K L P Y T I A K N-E S D Y A V Y K-P C G L A H K G D T D P Q C D Y T E-----	608
KAJ6787866.1	H L P Q D S G A A L V S L L Y G D A V P S G K L P Y T L A K R-D T D Y P V L K -P S R P E G R F V N F P Q S N T E-----	633
KAJ6786079.1	H L P Q Q A A G D A I V Q L L F G D A N P S G K L P Y T V A K Q-A A D Y G P L L D P Q A S P G-S Q S P Q A Y F Q-----	616
KAJ6785739.1	H L P Q E A G R S L V E V L Y G D V S P N G H P Y S I T H A-E E D M P K S V T D L I N F E L A G K Q A D D Y T E-----	646
KAJ6782204.1	N L P Q Q E S G N A I S T I I F G D A S P S G K L P Y T I G K S-L E D Y G P G A K V M Y T P N-G L V P Q Q D F N E-----	725
KFG84234.1	G L P Q Q E S G N S I T D I I Y G K T S P-G R S P F T W G P T-RE S Y G T D-V L Y K P N N G N G A P Q Q D F T E-----	641
KAJ6788989.1	G Q P Q Q E S G N S I T D I I Y G K T S P-G R T P F T W G A S-E A A Y G N D-V L Y K P N N G K A P Q Q D F T D-----	643
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369
KFG78085.1	E E Y D R A R D Y A G L E D L L K A V H R A S A P D L H F L K S T R A A S M E L H L P N I K E T H F V-----	636
KAJ6788372.1	E E Y D R E R D A T G L D D L L K A I H R S G G S D L D F L A N T S A S A F E L F N T N I K E A H Y V-----	656
AGC24356.1	D D Y R N D D D L D H V T A M W D D I F G-K D W P L R---K D K I N L G L Q R A K L Q K H K-----	585
KAJ6789110.1	-----	539
KAJ6785893.1	R T---Y M W Y---T-----G K P I L P F G Y G L H Y T N F S T S W K T K P S A S Y S I Q A L A-----	745
KAJ6786934.1	D V Y I C Y R Y Y E F A D-----R E V N F P F G H G L S Y T T F G F S D L S V N V A D G K I-----	720
KAJ6780833.1	G O Y L D Y R A F D A K N-----I T P R F E F G Y G L S Y T T F N Y S I S A H-----	648
KAJ6787866.1	G V F T D Y R H F D Q K N-----I T P R F E F G F G L S Y T T F G F G L A N L Q A R R-F D M A S D A L A-----	680
KAJ6786079.1	G V Y T D Y K Y F E Q A H-----I E P R Y E F G F G L S Y T R F D Y S D I V L G A R P N A P T T P P P-----	664
KAJ6785739.1	G L Y I D Y R W L N K Q K-----I K P R Y A F G H G L S Y T K F N L S D A I K K V T S L T K T-P P A R A-----	696
KAJ6782204.1	G V Y V D Y R H F D K F N-----I Q P R F E F G F G L S Y T T F N Y S N L Q L T E V K A K S R L A G E R P A-----	776
KFG84234.1	G S F I D Y R H F D K V A P G-K N S-T G A P I Y E F G H G L S W S T F E Y S N L K V E K R D V R P-M S P P N G-----	696
KAJ6788989.1	G A F F D Y R H F D K E S D G-K P G S D P K A P V Y E F G F G L S W S T F E Y S N L Q V V K K N D R P-Y K P T T G-----	700
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369

KFG78085.1	-----VRNSSTGALYGFVATYFI	-----AGVG-----	658
KAJ6788372.1	-----VRNSSTQALYGFVATYAT	-----GGVG-----	678
AGC24356.1	-----VARDSQGKIVGFVATQIVVVVDNKKHG	-----	611
KAJ6789110.1	-----	-----	539
KAJ6785893.1	-----	-----	745
KAJ6786934.1	-----	-----	720
KAJ6780833.1	-----	-----	648
KAJ6787866.1	-----	-----	680
KAJ6786079.1	-----	-----	664
KAJ6785739.1	AKSGILDYSQKIPDASEGVAPDGFKKLFRYIYSWVQPNEAADAVK	-----DAATKKYPYP	751
KAJ6782204.1	DQANPPDFEDKIPDISEAIFPSIEIRKLKKFIYPYITSASDIKPG	-----VYPY-----P	825
KFG84234.1	KTIAAPTFGNFSTNLKYAFPPSIRYIYQFTYPWLNTTASGKEASGDPHYGQTAEQFLPP	756	
KAJ6788989.1	NSIAAPTFGNFSKDIKYGFPAFHYVKQFIYPWLNTSSGKEASGDSSYGKTADEFLPP	760	
KAJ6787877.1	-----	-----	370
KAJ6782998.1	-----	-----	369
KFG78085.1	-----II-----	GALLVDPSKRNV	672
KAJ6788372.1	-----IL-----	GALFVDPTKRNV	692
AGC24356.1	-----QL-----	MLLMVSPSYQGK	625
KAJ6789110.1	-----	-----	539
KAJ6785893.1	-----SQAGNDPNNALFAN-----LAISVKNTGGEANIASDYVGLFLSSQNAG	-	789
KAJ6786934.1	-----IAIVTVNTGSR-----AGSAVAQMYIEPKQAA	-	748
KAJ6780833.1	-----VRKCVSTTLNELWEVVATLEVSIITNSG-----AVAGHEVAQLYLGIPGA	-	692
KAJ6787866.1	-----EYPTGAVIPGGHADLWDNLVSVTADVTNTGR-----NHTGAEVVQLYLGIPSGG	-	729
KAJ6786079.1	-----EYPSGEIVSGGQKDLWEVLATVKCRLVNNGG-----KVAGAEAVQLYVRFPGM	-	711
KAJ6785739.1	DGYSTEQKPGPRAGGEGGGNPAIWDVAYTLSVKVTNVGN-----KYGGKASVQAYLQFPDDA	-	808
KAJ6782204.1	DG-YDVVKQPPSAAGGGQGHPELWETHVSVQADVGNEGA-----V-GGKVVAQLYISFPNTK	-	880
KFG84234.1	GATDGSPQPLASSGEPPGNRQLWDVVYTVSATITNTGK-----R-VSDEIPQLYISLG	-	809
KAJ6788989.1	NAIDANPQPKHPAGGEPPGNRQLFDVIYEVTATITNTGK-----MTDEVPQLYLSHG	-	813
KAJ6787877.1	-----	-----	370
KAJ6782998.1	-----	-----	369
KFG78085.1	SIGRSLHRRAKLKSLSQRGLKKVQVGMSFPGVFLGIPLDPE-----ANTVKEWFNSNGWDTQFP	731	
KAJ6788372.1	SIGRSLHKRALKTLSQRGIKRVLQGACFPSVFPGIALGVE-----AATVRTWFSNSGWDTQFP	751	
AGC24356.1	GVGTLHDAALEHFR-----EQGADC1KLGSTYPRFPGPDDAOSRKAQAFFSKKGWRMD	-	682
KAJ6789110.1	-----	-----	539
KAJ6785893.1	--PS--PRPNKKLVSYGRAQSIVQGSTQQQLNL-R-----NIAELARSDEN	-	830
KAJ6786934.1	--RI--NRPVKELRGFAKVE-----LEAGASKTVTISEL-----EKYAAAYFDEE	-	789
KAJ6780833.1	--PPKQLRGFEKLG-----LQPRTETGKATF-EL-----TKRDLSQWDVV	-	728
KAJ6787866.1	--GAAAAAPPVQLRGYEKVT-----LQPGETKTASF-AL-----SRRDLSVWNVE	-	772
KAJ6786079.1	--QAKQLRGFEKPT-----LKPGESRSVSF-EL-----TRRELDSVWNTE	-	747
KAJ6785739.1	--GY--ETPIIQLRDFEKTKTIAPIGGSETVKL-QL-----TRKDLWSVWDTV	-	849
KAJ6782204.1	--GV--DFPVRLRGEFEKVVY-----LEPGQTKSVQF-NL-----TRRDLSYWDTT	-	920
KFG84234.1	--GK--NEPVRLRGEFNRIEGIAPGQNVTFRH-EI-----TRREISNWDTA	-	850
KAJ6788989.1	--GE--GEPVRLRGEFDIERIAPGASATFRV-EL-----TRRDISNWDSN	-	854
KAJ6787877.1	-----	-----	370
KAJ6782998.1	-----	-----	369
KFG78085.1	RRLTNMIIHNLPNWVAPEGLLQSIQRANISFDLIHGLENAEVLSLHHVRANANPEVLELYT	791	
KAJ6788372.1	RRLTNMITADLGNWTAPEGLLPTIQRANISFDLIHGLDNADTVLHHVRTESGPEVVELYR	811	
AGC24356.1	DNLVHDLIGDLQDYKVPDKIQARMLKEKIWFGRIKPSETWELYAF-----QQRNFPHWLSTYQ	740	
KAJ6789110.1	-----	-----	539
KAJ6785893.1	--GDKYIYP-----	-----	837
KAJ6786934.1	--RDQWCVES-----	-----	797
KAJ6780833.1	--QQKWLH-----	-----	736
KAJ6787866.1	--RQKWLQP-----	-----	780
KAJ6786079.1	--KQMWLQLR-----	-----	755
KAJ6785739.1	--KQDWVIPTVD-----	-----	859
KAJ6782204.1	--LQNWWMP-----	-----	928
KFG84234.1	--SQNWVITK-----	-----	858
KAJ6788989.1	--AQNWVVT-----	-----	862
KAJ6787877.1	-----	-----	370
KAJ6782998.1	-----	-----	369
KFG78085.1	YA--LSENKTCGIVRAKDPGNLIGTVII-----CRQGSPLVTYIPPLLSD-----GEDVG	840	
KAJ6788372.1	YA--LAETKSCGIVRAKDPAGAIMGTIII-----CRQGSPLSTYIPALRSR-----SENV	860	
AGC24356.1	HHVELGDYQDLIVARQDDENGRVIASLIL-----NTTHVS-HEYRSDLIWTDDKLFGERSG	795	
KAJ6789110.1	-----	-----	539
KAJ6785893.1	--GDYLTLDTTGATAA-----QFKLTGQPAKI-----STLPRK	-	869
KAJ6786934.1	--GEYDVVISDSSAVTEKALRATINVSESYWWSGI-----	-	830
KAJ6780833.1	--GEYKIYVGASSRDIR-----LTGKIVISG	-	760
KAJ6787866.1	--GTYTVWVGTSRNLP-----LKQTLKI	-	802
KAJ6786079.1	--GDYEIYIGRSSSKLP-----LKTYLTI	-	777
KAJ6785739.1	--GGYKVWVGEASDNLG-----TVC SIDSMK-CQSGAKGPV-Q	-	893

KAJ6782204.1	-----GQFSIAVGASSRDLP--LTGTW-----	948
KFG84234.1	-----APKKVFVGSSSRNLP--LSADLN-----	879
KAJ6788989.1	-----APKTIWVGSSSRNLP--LSAKLQ-----	883
KAJ6787877.1	-----	370
KAJ6782998.1	-----	369
KFG78085.1	GI APIV P STP Q A T L V L Q G L A L M G V R Q S K G H R A S K A V L S W I V D D A F E P L V A M G F D I L Q A F	900
KAJ6788372.1	G I V A P T V P P G P L S T L V L Q G L A L M G V R Q C K S H K A S K A V L S W I V D D T S E P L I G M G F E A L Q S F	920
AGC24356.1	G M A C V G V A Q E E R G R G I G I G I V A H A N W L L K Q R G V T K S Y V D W V E L L D F Y S -- R V G Y K T W R S Y	853
KAJ6789110.1	-----	539
KAJ6785893.1	-----S-----	870
KAJ6786934.1	-----	830
KAJ6780833.1	-----	760
KAJ6787866.1	-----	802
KAJ6786079.1	-----	777
KAJ6785739.1	-----	893
KAJ6782204.1	-----	948
KFG84234.1	-----	879
KAJ6788989.1	-----	883
KAJ6787877.1	----- 370	
KAJ6782998.1	----- 369	
KFG78085.1	E E I T N S P E V --- 909	
KAJ6788372.1	E E I T N S P D I F Q N 932	
AGC24356.1	R L G H ----- F -- 858	
KAJ6789110.1	----- 539	
KAJ6785893.1	----- 870	
KAJ6786934.1	----- 830	
KAJ6780833.1	----- 760	
KAJ6787866.1	----- 802	
KAJ6786079.1	----- 777	
KAJ6785739.1	----- 893	
KAJ6782204.1	----- 948	
KFG84234.1	----- 879	
KAJ6788989.1	----- 883	

Figure S2. Clustal alignment of *A. album* GH3 enzymes. The twelve sequences were aligned together with the GH3 β -N-acetylhexosaminidases identified in *R. miehei* (AGC24356) and *M. anisopliae* (KFG78085) and with one *M. anisopliae* GH3 β -glucosidases (KFG84234). Boxed sequences correspond to the conserved motif KHF(I)PGH(L)GXXXXDS(T)H, typical of GH3 sequences.

Figure S3

KAJ6780494.1	-----	-----	0
KAJ6784096.1	MAS-----TQT-----	FGGKRAMTAGSVRPTANYEKPRA	29
KAJ6785798.1	-----	-----	0
KAJ6785933.1	-----	-----	0
KFG80340.1	-----	-----	0
KAJ6783033.1	-----	-----	0
KAJ6780076.1	-----	-----	0
KAJ6789215.1	MYKFVQLFCLFWLFLLTVHALAAGLQDTTTTTGIVVARSHAVTVG-FLPVQRFHHLQA	59	
KAJ6787434.1	-----	-----	0
KFG85702.1	-----	-----	0
KAJ6780083.1	-----	-----	0
KAJ6780494.1	-----	-----	0
KAJ6784096.1	RGAEPGARADKES-----	-----ALHLGQQPGAD	53
KAJ6785798.1	-----	-----	0
KAJ6785933.1	-----	-----	0
KFG80340.1	-----	-----	0
KAJ6783033.1	-----	-----	0
KAJ6780076.1	-----	-----	0
KAJ6789215.1	RDQAAGSSCSSEGQWNCMTNSWQRCAAGRWTMOCAKGTTCAPAGLTNEFRIQHDGSVN	119	
KAJ6787434.1	-----	-----	0
KFG85702.1	-----	-----	0
KAJ6780083.1	-----	-----	0
KAJ6780494.1	-----MLHQQCATALWASI-----	-----VALSLSAT	22
KAJ6784096.1	GARRPDSEEQEAAAADAAAANRDLTGPAAPTAHLWHRR-----RLCRDRWEFAQWNEAFF	109	
KAJ6785798.1	-----	-----MWSS-----	4
KAJ6785933.1	-----	-----	0
KFG80340.1	-----	-----	0
KAJ6783033.1	-----	-----	0
KAJ6780076.1	-----	-----	0
KAJ6789215.1	GNGGPPTTSVA-----ASLGTRTWVSKVGTGFLVLGWWFLRIKFAIHSK	163	
KAJ6787434.1	-----	-----	0
KFG85702.1	-----	-----	0
KAJ6780083.1	-----	-----	0
KAJ6780494.1	ASPI-----V-----GS-----SADAQIDLNGAADSK---SNLPAWPPPQKISGS	61	
KAJ6784096.1	ESDKMHAMVDIKEIIQELTQDLNRNGLSQI--VLSTLACQGGA--ASLIGIPTADYTT	164	
KAJ6785798.1	-----FNL--LSGLLLLDVAL--AHLPGIPTVPFKG	31	
KAJ6785933.1	-----	-----	0
KFG80340.1	-----MR-----FYTSALLAALATVELTSAVTVKVNPLPAPQDVTWG	37	
KAJ6783033.1	-----MRS--QSLSSALLIWL-AAATGLGAAVKVNPLPAPQEITWG	38	
KAJ6780076.1	-----MRL--IVF--STLLA--AA--TALWPVPKEIQTG	26	
KAJ6789215.1	ESSL--GLPSVDVVVFYCFRK--ARSGMHLRIVFVVVASAQ--LA--AALWPVPKHLSTG	214	
KAJ6787434.1	-----MLSFKFLALLALAAIG--QV--NAIWPIPSSLSTG	30	
KFG85702.1	-----MLNNAIIAVAALAALR--PV--DAIWWPVPQQISTG	31	
KAJ6780083.1	-----MRLHSY--LAVALAAS--PV--AALWPIPIDISTG	29	
KAJ6780494.1	GDCAV-----R-L-----	SSEVTIVTGNATDG-----PTIKVIQ	89
KAJ6784096.1	TECK-----RF-----	DLRQVSGIVVDAQHASARDTQGATLIP	197
KAJ6785798.1	DGKK-----TF-----	KLDAVQTIVIDSKYTKTDDKSGTLIP	64
KAJ6785933.1	-----	-----MSLIP	5
KFG80340.1	DSGP-----KHVGW-----LNL--RTNSN-RKSESNTQLVSEAWNRAKAITSLRWVP	82	
KAJ6783033.1	ESGA-----IPVGY-----LTL--RTVNADWSTNDNRIVNDNRAFKAITTIRWVP	84	
KAJ6780076.1	NETVWIGQDIQVSYRHGNNCYVFDFGKNADDHDEITVRAVRGAIARALSTVDEGLIP	86	
KAJ6789215.1	QTILEIGTALKITYNGGSLAWNGQAVDSQ-----NLNDTNIVQGGIARAYNAIESGFVP	269	
KAJ6787434.1	SDVLFISQDIQVTFNGGALSSASS-----GGGGRSTIPDAVARTLDTILKKGFTP	80	
KFG85702.1	QDVLFVDKSIQVTYNGEPMVSYDGRITGETK---ESPSSSSQVVDavarSLTAIFEHGLVP	88	
KAJ6780083.1	NKTLYIDKTINITYNGEPLQYTTGYNPPA---GSSFTSKSIVQGALARSLKAIFFDDGYVP	86	
KAJ6780494.1	AIVAAAGGKATVSPYASGAGAQIF-----	VGTDSENRA-----AADAALKALT	131
KAJ6784096.1	PTLQEFAT--TFA-----SDLASSLGKTNVEAAPRDQ--CIYI-TLDP-QGNY	242	

KAJ6785798.1 PTLHEFGA--TFA-----QDLQEVFNKTVTAKGDKRESN--TIFL-TIDS-DHEF 109
 KAJ6785933.1 ----QPOS---VTPKEG-I-----VE-----LASLDQIV--- 26
 KFG80340.1 QAIQPPIP--KFEFPFT-AGSNDSSSS-----AKSKRNTGGSWLNEVNQVSDW 128
 KAJ6783033.1 QAVEQPIP--KFDPFPG-KNSTSNSKRADAQADAQAGDASASNNWGSRWLNEITVKVDDW 141
 KAJ6780076.1 WKLVPRNELPNHEPSAD-AT-KTYIRKLSIV--QTAVA-----ND--- 122
 KAJ6789215.1 YMLNPPGS--DFEPEPSRA-QI-QGQIKVLVIS--NVRK----- 300
 KAJ6787434.1 WMLREANS--DYEPAIG-SG-KGKVKSALK--RAGKE-----AGGSSSS 119
 KFG85702.1 WMLNPPGS--DFEPALD-DG-AAKVTSLTIK--QTGED-----NATV--- 124
 KAJ6780083.1 WMLHKPGS--HFEPRCG-PNNKNHVRSLTIT--QTGTD-----DAST--- 123

KAJ6780494.1 GDSAKSLTAEGYVLGSGKYNGHPTIVLNGVDTRGTFYAAQTLRQLVGGK----- 180
 KAJ6784096.1 TDAAGRFTHEGYSLTTNS----GVFIAGASPLGAWWATRTVLQQAAIRSQ----TKNV 293
 KAJ6785798.1 LDAAGRSTTEGYTIVAEED---GVTIRGASSLGAWWGTRTLLQQAILGD-----K 156
 KAJ6785933.1 SSDLPTLHPEGYTIDISAA--Q-GVQIKGGSDAGLFYAKQTLRQLLIPPSALRSGARGPWR 83
 KFG80340.1 SADLKGVDESYLTVSAS--SSTVEIAKTVWGAHLAHTTFQQLVIFEG-----GSL 179
 KAJ6783033.1 SADLKGVDESYTVDITSS--SSQVQVTAKTAWGAHLAHTTLQQMVISDG-----RGGL 193
 KAJ6780076.1 -SSLIGPSNESYSLHIETD--G-TASITAVAPSGILRALQTFQLFYLHS----TKQGSY 174
 KAJ6789215.1 -----NNSESYSLHVGDG----NAVINAESTIAVRLAETFTQLFNQHS---SGSYWY 346
 KAJ6787434.1 SRLDFAEMDESYTLDLSSS--G-DATIAANSTVGLLRGLETFQLFYKHS---SGAAVY 172
 KFG85702.1 FKPLAGQVDESYSLHEAN--G-EASIEAVTSTGLVRGLESFTQLFFKHS---SGDAFY 177
 KAJ6780083.1 FKPLAGQRDESYALNVTFD--G-LASIRANSSIGVMRGLETFSQLFFKHS---SGGAWY 176

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KAJ6780494.1 RGPGVGKVRDWPLMPVRGSIEFGYGIWPSHQARMDDQYVFGQHKMNTYVYTPKGDPY--- 237
 KAJ6784096.1 TALPYGHGRDAPGWGMGRGMMLDAGRHWYPKEFLVEMCGYMSYFKQNTFHVLSDNLVTQD 353
 KAJ6785798.1 SAVPGQGDDAPGWSTRGMMLCDGRHFYPKQFLIDMCYSIISFFKQNTFHIHLSNTIVPT 216
 KAJ6785933.1 LPQAQTISDAPSSGLRWRCGMLDVARHFMPSDVLHFIDVLAFHKLNTFHFLHTDDQGWRI 143
 KFG80340.1 IVEQPVTIKDHNPYNPYRGMVDTGRNFISANKIKEQIDGLALSkmnNILHWHTDTQSWPI 239
 KAJ6783033.1 IVEQPVKIKDHNPYNPYRGMVMDSGRNFISVNKLREQIDGLALSkmnNILHWHTDDQSWPI 253
 KAJ6780076.1 TRLAPIHTDAPQFSHRGINLDVARNFYPVKDVLRTIDALAWNKFVNVLHHMTDSQSWPM 234
 KAJ6789215.1 TTLAPVAIEDSPTFPHRGGLIFDVSRERYSVDDVVKHTIDALAMAKLNKLHLSVTNTQSWQV 406
 KAJ6787434.1 TDMAPVSIIRDAPVMPYRALLIDVARHWYEVADIKRTIDGLAMNKLNVLHLHITDTQSWPL 232
 KFG85702.1 TKQAPVSIQDAPRFPHRGVLDDLRSRHFAVDDIKRTIDGLAMNKMNVIHLHITNTQSWPL 237
 KAJ6780083.1 TTQAPVRIADAPKFPHRGMMLDVSRHFAVADIKRTIDGLSMAKMNVLHLHITDTQSWPL 236

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KAJ6780494.1 LRATWRELYGGEDLDKLKELIETANAHVDFTYALSPGLDICYTSGADFNATVAKFEQLR 297
 KAJ6784096.1 YYSYEQAMALEANFRLF---SESG---ALQ-----GLSSPRDV--AYTRADFDEVQ 396
 KAJ6785798.1 YTPD-NYNETYARFRWL---SDSS---EVS-----GLNKHANE--SYTKDDFEDIQ 258
 KAJ6785933.1 DVPQWPRLAEVASSRKR--SMQGTRHDCS-----FDARPHGG--FYTADDLREIV 189
 KFG80340.1 HLEAYPQVT-KD-----AYSGRE--SYSAKDVQDII 267
 KAJ6783033.1 HIDAFPEFT-KD-----AYSERE--IYSANDVADV 281
 KAJ6780076.1 EIPSLPDLAGKG-----AYYAGM--SYTPTDIETIQ 263
 KAJ6789215.1 EIPSFPELTEKG-----TFYSGQ--YYSVDDLHDLY 435
 KAJ6787434.1 EIPALPLLAEKH-----RYAKGL--TYSPADLEDIQ 261
 KFG85702.1 EIPALPKLAEGK-----RYAPGL--TYSQPQAIQEIQ 266
 KAJ6780083.1 EIPALPLLAERH-----AYSKGL--TYSPADIAIDLH 265

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KAJ6780494.1 KLGVSSFYIALDDIPLEFHCDSDKQKYPNTGNY---HWL-----ADAHAFY 340
 KAJ6784096.1 QKCAARGVTVMPEIEAPGHALRIVQWKPQLG-----FHKDPSL 434
 KAJ6785798.1 TKCAQRGVVTIPIPEIEAPGHCLPIVQWRPQIG-----YQGDSL 296
 KAJ6785933.1 AFAAERHVTVPEVNPMPGHMQAAIAAYPELGNTDVEGRSPDAGVWDSWI---SPR--V 243
 KFG80340.1 SYARARGVRVVIPEIDMPGHSASGWQQLDKDIVTCQNSWWS---NDNWPLHTAVQPNPGQ 323
 KAJ6783033.1 SYARARGVRVVPYEIDMPGHSASGWQQYDKDIITCENSWWS---NDNWPLHTAVQPNPGQ 337
 KAJ6780076.1 KYALHRGVTVHIEFDMPGHTTAVSWGYPELVAEEAQPR-----G-RYCAEPPCGT 313
 KAJ6789215.1 TYAVSRGVEIVMGIDMPGHSN-IQHIYPD LGVAYMAHPW-----N-TYCSEPPCGS 484
 KAJ6787434.1 EYGAARGVQVILEIDMPGHVG-IERAYPGLSNAFAQPW-----G-TYCAEPPCGS 310
 KFG85702.1 EYGVARGVQVLLIEDMPGHVG-IDKAYPGLSVAYNEKPY-----D-KYCAQPPCGA 315
 KAJ6780083.1 EYGIHRGVQVILEIDMPGHFG-IERAYPGLSVAYNKRPy-----G-QYCAQPPCGS 314

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KAJ6780494.1 LNRVQKEYIKAHEGLT-DL-ETVP--TNYAGSAPDPYKSEFGKQLDKNIRVQ----- 388
 KAJ6784096.1 LNISHPETIPTMKSIIWQEFLPWFH--TKLVSIGADEYHGTV-ADYNR----- 478
 KAJ6785798.1 LNISHPDITPTMKTIWKEFLPWFH--TSVVSIGADEYKGPE-EDYKR----- 340
 KAJ6785933.1 LNV-SDKTLDFCRSVLVLCDFP--SETVCIGGDECPTYDE-WKASPSVQARMKELGIKT 299
 KFG80340.1 LDVMNPKTYQVVGNVYSELSSKKFS--DDFFHVGGDELQIGC-FNFSKGIRDWFAADPKRT 380
 KAJ6783033.1 LDVLNPKTYKTVEKVAELSHRFS--DDFFHVGGDELQIGC-FNFSKGIRDWFAEDSSRT 394

KAJ6780076.1	LQLNNPAVDDFLDTLFDDMPRVKSYAAYE	HTGGDEVNAQA-YTLDPTMQT---NDRSK 368
KAJ6789215.1	YRLNNNTGVDRFLEKLFDLLPRIAPYASHE	HTGGDEVNANN-CALDPDIRS---GEMSV 539
KAJ6787434.1	LKLNNTDVYKFLDTLFDDLLPRTAPYSSYF	HTGGDEYKASN-SLLDPALRT---DDTSV 365
KFG85702.1	LKLNNTDVENFISTLFDDLLPRLSPYSAYF	HTGGDEYKATN-SLLPDLQT---DNMTL 370
KAJ6780083.1	LRLGNKKVEELDTLFEDLLPRLSPYTAYF	HTGGDEYKANN-SLLSDLQT---NDPAI 369
	:	*
KAJ6780494.1	-WTGEGVFSDKITVDSVVRADSTYVTDKLFIWENDFPVN-DNKPFRL-----F 433	
KAJ6784096.1	-----FVNMTMND-FIR---EQSNKMTMSIWTGTFPPK-YDGTYDNINQNVAIQHWEFFE 525	
KAJ6785798.1	-----FVNEMSA-FMN---EEASKSIRIWTGTFPAVKHAGSPPTTIDSNTIQHWAYLF 388	
KAJ6785933.1	ESALQGWFTDRMA----AHLATRGKRAYGWDEVIEG-YTGP---TEKILVAAWRG-- 346	
KFG80340.1	YFDLNQYWIHDAYPLFMSEENSGKKDRRLIMWEDVVLS-PDAAHNVSKSVIMQSWNNG- 438	
KAJ6783033.1	YFDLNQHWDITSMPIFTSEKNGKKNRRLIMWEDVVLS-PDAAAHNVSVDVIMQSWNNG- 452	
KAJ6780076.1	IRAQIQQKMDRDNH----AHVRKAGLTPIVWEEMILLE-WNLTL-PLDVVVQWTWRG-- 416	
KAJ6789215.1	VQPLMQKMFVNQVH----KIIRKGLTPIVWEEMETINV-WNVT-L-PKDTLVQSWRG-- 587	
KAJ6787434.1	LKPLLHAFLQHVH----GKIRQHGMPFVWEEMVGQ-WGAP--LPTNDTIIQWTWFG-- 414	
KFG85702.1	LQPLLQRFLDHAH----NNIRGHGLPIVWEEMVEE-WAAD--V-GNDTVVQAWLG-- 418	
KAJ6780083.1	LQPLLQRFLDHAH----GKIRELGLVPMVWEEMINE-WNAT--V-GKDVVVQSWFG-- 417	
	:	*
KAJ6780494.1	LNPLTERATDLYKHMIGFTSNPMVQSYASMIALGNYGD-----471	
KAJ6784096.1	DKPLTDYIQNNYSVINSDDTY----YVNVKYSSESYPALPLDKTSADPSVPGGGP--- 577	
KAJ6785798.1	DNPYEDYIKNNYSVINSDEMY----YIVMKDG-PYGRKINTDITFTGN--PDGHGP-- 437	
KAJ6785933.1	PGPTAIAARRGFVDVTCPDVN----AYLDYRQSD----D----PGEPTPVGI---- 386	
KFG80340.1	VANIDKLTAKGYDVIVSSADF----MYLDCGNGGYVTNDPRYNAPQSNPDATGATFSFN 493	
KAJ6783033.1	ITNIGKLTEQGYDVIVSSADF----LYLDCGFGGYVTNDPRYNQ-QENPDPTGATPSFN 506	
KAJ6780076.1	DAIAIAETVKQGYKALVGNKAS----WYLNCGMGSWYNAAN-----GAEFK 457	
KAJ6789215.1	GAT-PSLAKAGYKVIDSSSSY----YLYNCGRGAFVVDYQD-----GSSLQ 627	
KAJ6787434.1	AESVQKYARAGYRVIDTSYDA----YYLDCGRGSWVDYAD-----SAV-S 454	
KFG85702.1	SASVAKLAAAGHKVIDSTFDI----YYLDCGRGQWLDFKD-----GPSLD 459	
KAJ6780083.1	QDKVKELAEGHKVIVSSSDS----YYLDCGRGEFIDYEN-----GPDFQ 458	
	:	*
KAJ6780494.1	-----YSWNSPAYNPQDSWAASI-----QELAGKDQGIHSALLA---FADING 511	
KAJ6784096.1	-----WYPHFNAKKA-----SDNPQRSEPRVLGSIVPLWNDFGQNATVASEAAYY 622	
KAJ6785798.1	-----WYPNIFNLSNPD-----NSNPKSKNNKLIQGAISPLWNDHGANTSVYSEAYY 482	
KAJ6785933.1	-----LLTLENVYSFEPVPAGLTPEE-ARHIVGAQVNWVEHMESARRVQ--YM 432	
KFG80340.1	YGGPGGSWCAPYKTWQRIYDYDFTA-NLTSQ-AKHIIGAAAPLWSEQVDDA-VIS--SK 548	
KAJ6783033.1	YGGIGGGSWCAPYKTWQRIYDYDFTQ-GLSEAQ-AKHIIGASAPLWSEQVDDT-IIS--GK 561	
KAJ6780076.1	QQYPFNDYCSPVKNWRLVYAFDPLA-GVPANL-TDLVLGGEVHLWSEQADGV-NVD--GL 512	
KAJ6789215.1	NAYPFTDWCAPAKNWRYVMHTPTD-GVDARH-AQNVVGGEVAIFSETVDA-SLD--VI 682	
KAJ6787434.1	PGTTFNSWCDPFKNWHIVYNHDPFA-GLEGSAAKVVGGEVALWSETIDGA-TFD--QI 510	
KFG85702.1	AYAYPFADYCSPTKNWRLIYSHDPVE-NMTAEA-AANVIGGEAVVTEMIDPV-SLD--TL 514	
KAJ6780083.1	GAYPFTDWCAPTKNWRLIYAQDPRA-GVSEEA-AENVIGGELPLWTETIDTT-SLD--SI 513	
	:	*
KAJ6780494.1	NWPYRNNTESAPQLSKDIDAFWAARKSSQKQSDSALASRLTLIA-SIPDLLPG----- 563	
KAJ6784096.1	AWREG-----LPAVADKQWGGLTNRAQFDAVFPQVQPYAPGQNLDRAPISPAGETIL 674	
KAJ6785798.1	AWRDG-----IPALADKHGGNLTDQYSNWFSKLLAKIPAQTLLERIIPSQ-NTIF 533	
KAJ6785933.1	VYPR-----ACAFAEVAWGKTKHEHGSF---EDFRKRLEDKHLARLD-----AL 472	
KFG80340.1	MWPR-----AAALAELEVWSGNKDPKTGLKRTTYLTQRILN-----583	
KAJ6783033.1	MWPR-----AAALGELTWSGNKDPKTGKRTTFTQRILN-----596	
KAJ6780076.1	LWPR-----AAAAAEVLSGRHDAGGQNRSQVDAAPRLAE-----547	
KAJ6789215.1	LWPR-----AAAAGEIWWSGRKDENGTDRSVWHPRLSE-----717	
KAJ6787434.1	AWPR-----ASAGGEIWWSGRKDASGNLRSQYHARPRLAE-----545	
KFG85702.1	AWPR-----AAAAGEAWWSGRKDGEGNLRSVFTARPRLEE-----549	
KAJ6780083.1	VWPR-----AAAAGESWWSGRYDADGKNRSMYDARPRLSE-----548	
	:	*
KAJ6780494.1	-MAMKPF---AADVAPWSTVAMQWAKASQHMISIMIAIDAGDKST-ADSEY----- 609	
KAJ6784096.1	QYNFASIPGHVVKDAKGNGHDAKTTCTMDRTALAIRPGCDVTLPFGAKGRDYTLSTVKL 734	
KAJ6785798.1	SYDLRKVKGSVADKSGNKYDAKTTCKGADDGIMSTDCDITTPWSSKGRNYKLSLTLNM 593	
KAJ6785933.1	HVNYRP---QTGPRPWDGRPDAPGYPQSREHR---LAEIEKM-----TAELRL 514	
KFG80340.1	---FRE---YLVANGIGAAMPLVKYCLQPHP---ACDLYYN-----QTAVQ- 620	
KAJ6783033.1	---FRE---YLVANGIGATPLVKYCFQPHP---ACDLYYD-----QEAVK- 633	
KAJ6780076.1	---MRE---RMVLGGVQAGPQMVFCQKMDAR---ECIF-----577	
KAJ6789215.1	---MRH---RMLARGVKGATVTHWCEQHALE---ECTSGYS-----G---- 751	
KAJ6787434.1	---MRE---RMLARGIVGGTIAPGFCLQSELG---ACV-----574	
KFG85702.1	---MRE---RMLARGVRGAVISQLFCGQSPL-----DCAA-----579	

KAJ6780083.1 ---MRE---RMLARGVRGAPITQLWCDQADTI-----DCSSE----- 579

KAJ6780494.1	-----	NAAQEWEKTKAKTVSSLRDD	630	
KAJ6784096.1	DQDMRGQNATILTGTDSALLLPTLTLYASNNYYPLNLTI	PVNWRVDI	-----TIRGK	787
KAJ6785798.1	DKLTDETNTTLVAGSDSTLMLTPNVTLFASGIYYRLNKTI	PLQSWVRL	-----EINGD	646
KAJ6785933.1	-----		-----	514
KFG80340.1	-----		-----	620
KAJ6783033.1	-----		-----	633
KAJ6780076.1	-----		-----	577
KAJ6789215.1	-----		-----	751
KAJ6787434.1	-----		-----	574
KFG85702.1	-----		-----	579
KAJ6780083.1	-----		-----	579

KAJ6780494.1	GKVVPNSTITPTTGDGVFDAFIANATALYNDQ-----		661	
KAJ6784096.1	GNQTFGAMKPA--GGFFEEEFQTVMGIVGKRLHWDTIAVEAPLGKLGFTGMLRNLT	L	845	
KAJ6785798.1	GPKTFASAFNEKGDIIFSKEEFLTEMSYYGQPLRWHEMAIEAPIHQITGWQGKVRF	TL	706	
KAJ6785933.1	-----		-----	514
KFG80340.1	-----		-----	620
KAJ6783033.1	-----		-----	633
KAJ6780076.1	-----		-----	577
KAJ6789215.1	-----		-----	751
KAJ6787434.1	-----		-----	574
KFG85702.1	-----		-----	579
KAJ6780083.1	-----		-----	579

KAJ6780494.1	-----	661
KAJ6784096.1	NRG-----	848
KAJ6785798.1	TDGMGDKPGDSFATRGLPSAPILIAALAVALCLGL	741
KAJ6785933.1	-----	514
KFG80340.1	-----	620
KAJ6783033.1	-----	633
KAJ6780076.1	-----	577
KAJ6789215.1	-----	751
KAJ6787434.1	-----	574
KFG85702.1	-----	579
KAJ6780083.1	-----	579

Figure S3. Clustal alignment of *A. album* GH20 enzymes. The nine sequences were aligned together with the GH20 β -N-acetylhexosaminidases identified in *M. anisopliae* (KFG803409 and KFG85702). Boxed sequences correspond to the conserved motif H(N)XGA(C/G/M)DEA(I/L/V/Y), typical of GH20 sequences.

Figure S4

KAJ6781485.1	-----	0
BAD08218.2	-----	0
ADG96019.1	-----	0
BAA92250.1	-----	0
ABZ88800.1	-----	0
EAL84291.1	-----	0
AAO41660.1	-----	0
CAE54966.1	-----	0
AJG44374.1	-----	0
KAJ6787168.1	-----	0
ABY77913.1	-----	0
KAJ6783315.1	-----	0
AFG33049.1	-----	0
KAJ6786595.1	-----	0
KAJ6788818.1	-----	0
ABX57824.1	-----	0
BAA12799.1	-----	0
KAJ6781651.1	-----	0
KAJ6785337.1	MLESFEGDDADSDVDSAAMATILWGRAVEQEDDILLWSLSSIINLHELGLASSHELGIA	60
KAJ6783761.1	-----	0
KAJ6781485.1	-----	0
BAD08218.2	-----	0
ADG96019.1	-----	0
BAA92250.1	-----	0
ABZ88800.1	-----	0
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KAJ6787168.1	-----	0
ABY77913.1	-----	0
KAJ6783315.1	-----	0
AFG33049.1	-----	0
KAJ6786595.1	-----	0
KAJ6788818.1	-----	0
ABX57824.1	-----	0
BAA12799.1	-----	0
KAJ6781651.1	-----	0
KAJ6785337.1	GPPASMAEIAPIFAPSSFDAIQVKINSIGHLSYLSQLAHPSYHSNFEQGLVESALS	120
KAJ6783761.1	-----	0
KAJ6781485.1	-----	0
BAD08218.2	-----	0
ADG96019.1	-----	0
BAA92250.1	-----	0
ABZ88800.1	-----	0
EAL84291.1	-----	0
AAO41660.1	-----	0
CAE54966.1	-----	0
AJG44374.1	-----	0
KAJ6787168.1	-----	0
ABY77913.1	-----	0
KAJ6783315.1	-----	0
AFG33049.1	-----	0
KAJ6786595.1	-----	0
KAJ6788818.1	-----	0
ABX57824.1	-----	0
BAA12799.1	-----	0
KAJ6781651.1	-----	0
KAJ6785337.1	ARTAIMFSVTYFQQSHRYISLVHRPSFGSQDTSTALLAVAFAGSTRSPPKDDVLCVRSL	180
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KAJ6781485.1	-----	0

BAD08218.2	-----	0
ADG96019.1	-----	0
BAA92250.1	-----	0
ABZ88800.1	-----	0
EAL84291.1	-----	0
AAO41660.1	-----	0
CAE54966.1	-----	0
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KAJ6783315.1	-----	0
AFG33049.1	-----	0
KAJ6786595.1	-----	0
KAJ6788818.1	-----	0
ABX57824.1	-----	0
BAA12799.1	-----	0
KAJ6781651.1	-----	0
KAJ6785337.1	ARLLEEFVFQHLERLIVNANSMNRSRELLETLAAAILVYQIQFMSAAAALQRMRTSRLP	240
KAJ6783761.1	-----	0

KAJ6781485.1	-----	0
BAD08218.2	-----	0
ADG96019.1	-----	0
BAA92250.1	-----	0
ABZ88800.1	-----	0
EAL84291.1	-----	0
AAO41660.1	-----	0
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ABY77913.1	-----	0
KAJ6783315.1	-----	0
AFG33049.1	-----	0
KAJ6786595.1	-----	0
KAJ6788818.1	-----	0
ABX57824.1	-----	0
BAA12799.1	-----	0
KAJ6781651.1	-----	0
KAJ6785337.1	ALISAARKMGLFTTKHKAGLGSVVISADLSLTMPHMATALFTA VARWQKLWQENLRALSG	300
KAJ6783761.1	-----	0

KAJ6781485.1	-----	0
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ABZ88800.1	-----	0
EAL84291.1	-----	0
AAO41660.1	-----	0
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AFG33049.1	-----	0
KAJ6786595.1	-----	0
KAJ6788818.1	-----	0
ABX57824.1	-----	0
BAA12799.1	-----	0
KAJ6781651.1	-----	0
KAJ6785337.1	KAIKKGGIEKYPTCSFFCIWAENQTPSCQQNILNTKLKSKAKA ALSAIANYPQLHLEL	360
KAJ6783761.1	-----	0

KAJ6781485.1	-----	0
BAD08218.2	-----	0
ADG96019.1	-----	0
BAA92250.1	-----	0

ABZ88800.1	-----	0
EAL84291.1	-----	0
AAO41660.1	-----	0
CAE54966.1	-----	0
AJG44374.1	-----	0
KAJ6787168.1	-----	0
ABY77913.1	-----	0
KAJ6783315.1	-----	0
AFG33049.1	-----	0
KAJ6786595.1	-----	0
KAJ6788818.1	-----	0
ABX57824.1	-----	0
BAA12799.1	-----	0
KAJ6781651.1	-----	0
KAJ6785337.1	DLASSTSIMTFAAEFAKQFNGQINIFIKNPGGVPDNHDHSEDGYERQFSMNYLGQFQLFS	420
KAJ6783761.1	-----	0
KAJ6781485.1	-----	0
BAD08218.2	-----	0
ADG96019.1	-----	0
BAA92250.1	-----	0
ABZ88800.1	-----	0
EAL84291.1	-----	0
AAO41660.1	-----	0
CAE54966.1	-----	0
AJG44374.1	-----	0
KAJ6787168.1	-----	0
ABY77913.1	-----	0
KAJ6783315.1	-----	0
AFG33049.1	-----	0
KAJ6786595.1	-----	0
KAJ6788818.1	-----	0
ABX57824.1	-----	0
BAA12799.1	-----	0
KAJ6781651.1	-----	0
KAJ6785337.1	MLKDALLSSATAASPSRLINVSSTRHKRGPITDGIINVKKEDYDAFDSYCQSCTAAVYL	480
KAJ6783761.1	-----	0
KAJ6781485.1	-----	0
BAD08218.2	-----	0
ADG96019.1	-----	0
BAA92250.1	-----	0
ABZ88800.1	-----	0
EAL84291.1	-----	0
AAO41660.1	-----	0
CAE54966.1	-----	0
AJG44374.1	-----	0
KAJ6787168.1	-----	0
ABY77913.1	-----	0
KAJ6783315.1	-----	0
AFG33049.1	-----	0
KAJ6786595.1	-----	0
KAJ6788818.1	-----	0
ABX57824.1	-----	0
BAA12799.1	-----	0
KAJ6781651.1	-----	0
KAJ6785337.1	ASEMERRYGAPRIFTDVAAAISSDVLHKDMRGRYLEDVFVSI PAAETKYPDILGYAEHT	540
KAJ6783761.1	-----	0
KAJ6781485.1	-----MLVKSI-----ASLA 10	
BAD08218.2	-----MPIKSF-----ASRL 10	
ADG96019.1	-----MMTY-----SRLI 8	
BAA92250.1	-----M---H-----FAGI 6	
ABZ88800.1	-----M---R-----LSEI 6	
EAL84291.1	-----M---R-----LSEI 6	
AAO41660.1	-----M---R-----LSEI 6	

CAE54966.1	-----M-----R-----LSEI 6
AJG44374.1	-----MR-----Y-----LATA 7
KAJ6787168.1	-----M-----L-----FSLS 6
ABY77913.1	-----0
KAJ6783315.1	-----MR-----S-----ATVI 7
AFG33049.1	-----MKTAA-----ITSL 9
KAJ6786595.1	-----0
KAJ6788818.1	-----MASL-----RSTL 8
ABX57824.1	-----MPSL-----RNTL 8
BAA12799.1	-----MPSL-----RNTL 8
KAJ6781651.1	-----MKT-----ASIL 8
KAJ6785337.1	YDEQRAKDLWKFTKELLGHDTGLFPYAFTSFNTVAAQYRDI PDMMRVTT-----KIAL 593
KAJ6783761.1	-----MK-----ASLA 6

KAJ6781485.1	ALSGIAAAAGPIRASVPTNVGSKYN---KPNAGPPGDWFSGDSSLPIISKASA---V-S 63
BAD08218.2	A-LSLA---ICGTAMGQKVNGADYN---KPDGGPPAKFFQASSSIPIVAAIQA---A-A 58
ADG96019.1	PFALFA---LFGTGLAQTVDGSKFN---KPDGGPPGSYFAAGSSIPVAALQSA---A-A 57
BAA92250.1	VAIALA---TGATAYDLPENLKQ-IYE---KH-KGKCSK-----ELQGG---YDN 46
ABZ88800.1	LTVVAL---TGATAYNLPNNLNEQ-IYD---KH-K-GKCSK-----VLAGK---FTN 45
EAL84291.1	LTVVAL---TGATAYNLPNNLQK-IYD---KH-K-GKCSK-----VLAGK---FTN 45
AAO41660.1	LTVVAL---TGATAYNLPNNLQK-IYD---KH-K-GKCSK-----VLAGK---FTN 45
CAE54966.1	LTVVAL---TGATAYNLPNNLQK-IYD---KH-K-GKCSK-----VLAGK---FTN 45
AJG44374.1	AVLAGA--GLASAYSVPANLQQ-IYN---KH-KTGTTCQN-----KLQDG---FSD 47
KAJ6787168.1	TVAALG--AVASAYDLPDNLRS-LYQ---AH-INGECRS-----ALSDP---FNT 46
ABY77913.1	-----YQLPANLKK-IYD---SH-KSGTCSK-----KLSSA---FSG 29
KAJ6783315.1	TLAALG--SLASGYQLPAKLKS-LYD---QH-KSGSCSK-----KLAGP---FNG 47
AFG33049.1	AVAALA--APALAYDIPDNVQA-FYD---KVKKGGDCTG-----SDLKG---FYA 52
KAJ6786595.1	-----MRA-LVN---I-----TW-----HVGAQLARNA 20
KAJ6788818.1	LLSL-A--AVAAARDVPSNRD-FYN---SVRGKGQCSN-----KLKSG---FHS 48
ABX57824.1	LASLLA--ASVSARDVPANVKS-FKD---SIIKQGSCKS-----TLATG---FYS 49
BAA12799.1	LASLLA--ASVSGRDVPANVKT-FKD---SIIKQGSCKS-----TLATG---FFS 49
KAJ6781651.1	FASLLA--SPVLRGRQVPQNVRD-LYN---SIRAQKSCHN-----ELKGG---FYS 49
KAJ6785337.1	TASLLA--LNSYARDVPSNIRD-LYN---SIRARGQCSN-----VLKGG---FYS 634
KAJ6783761.1	ILSLLA--TGALSREVPANVKS-LYK---SIRSKGQCSK-----VLKTG---FFS 47

KAJ6781485.1	KMSKTPKDASYIILSND-NHKKATIHSDWANLSKGA-AYAFVA [REDACTED] IDSH----- 115
BAD08218.2	KASKVPSHATYPIG--QGSTKSTIHSWDWAGFSEGA-AFSFIA [REDACTED] LNHG----- 109
ADG96019.1	KARTPVPDATYPINGDNGAKKVTIHSWDWAKFDKGA-AYVWIA [REDACTED] IDYK----- 110
BAA92250.1	GHSHDGKFSY--CGDIP-----NAIYLHSSKNGGQYA [REDACTED] ANRH-----AGK 92
ABZ88800.1	GDASQGKFSY--CGDIP-----GAIFISSSK---GYT [REDACTED] ANNS-----AGK 88
EAL84291.1	GDASQGKFSY--CGDIP-----GAIFISSSK---GYT [REDACTED] ANNS-----AGK 88
AAO41660.1	GDASQGKFSY--CGDIP-----GAIFISSSK---GYT [REDACTED] ANNS-----AGK 88
CAE54966.1	GDASQGKFSY--CGDIP-----GAIFISSSK---GYT [REDACTED] ANNS-----AGK 88
AJG44374.1	GISPGPT-SAY--CGDIQ-----GAIFLHSSANGQYD [REDACTED] ANNS-----GGD 92
KAJ6787168.1	G-----AVY--CGDIP-----NAIFLKG---PNGEYD [REDACTED] ANNS-----AGD 83
ABY77913.1	G-----AVY--CGDLP-----NAIFLKG---KAGNYD [REDACTED] ANNS-----AGE 66
KAJ6783315.1	G-----ASY--CGDIN-----NAIFLKG---N-GNYD [REDACTED] ANRT-----GGA 83
AFG33049.1	-EEGGSKNFGY--CQKYF-----TNKG-FYLKG---SGSKLA [REDACTED] DQDG---IDSR 98
KAJ6786595.1	-DQITRADMSY--CGDHL-----DDLGVVYLQG---P-GKFS [REDACTED] AQGGPQDDGR 68
KAJ6788818.1	-IEGDDGSFSY--CGDHM-----NDYRVVYLQG---KGGQLV [REDACTED] IQHGPADDGR 97
ABX57824.1	-SDGDSGTYSY--CGDHV-----KDYNVIYLQG---KNGKLV [REDACTED] IQGSPADDGR 98
BAA12799.1	-SDGDSGTYSY--CGDHV-----KDYNVIYLQG---KNGKLV [REDACTED] VQGSPADDGR 98
KAJ6781651.1	-QEGLDSKNFGY--CGDHL-----SDYGYIMYLQG---KNGQLV [REDACTED] ALGD--GDGS 96
KAJ6785337.1	-QEGLDSKNFGY--CGDHL-----ASDGIVYLQG---THGNLV [REDACTED] ALGE--GDGS 681
KAJ6783761.1	-SEDDSKDFSY--CGDHL-----ESDGILYIQG---KGGKLT [REDACTED] ILSK--KHGE 94

* . :*:***

KAJ6781485.1	CKGNDD--GETHTDFG-----ALAAYEVFPVVIPNKFASEHEK-----ELAG 155
BAD08218.2	CKGNPD--GQKETNWG-----ALSAYEVFPFIVIPQEFLDANKG-----TLKG 149
ADG96019.1	CKGNPD--GQHQTNFG-----ALAAYEVFFFVIPDRFGTKYAK-----QLPG 150
BAA92250.1	CSNDHS--GQGETTRWKDEVQKL--GIDDDLDANIHPYVVFGNENDDGDDPEFDPRKHGMEP 148
ABZ88800.1	CANDPS--GQGETAFKSDVKKF--GISLDLDANIHPYVVFGNED---HSPKFKPQSHGMQP 141
EAL84291.1	CANDPS--GQGETAFKSDVKKF--GISLDLDANIHPYVVFGNED---HSPKFKPQSHGMQP 141
AAO41660.1	CANDPS--GQGETAFKSDVKKF--GISLDLDANIHPYVVFGNED---HSPKFKPQSHGMQP 141
CAE54966.1	CANDPS--GQGETAFKSDVKKF--GISLDLDANIHPYVVFGNED---HSPKFKPQSHGMQP 141

KAJ6787168.1	-	234
ABY77913.1	-	217
KAJ6783315.1	-	232
AFG33049.1	-	249
KAJ6786595.1	NGG-----DGCSWDGHAGASCTRAQDCADQLTCVKGKCA-----	273
KAJ6788818.1	GGGNP-----PPSGGNCSWAGHCEGASCKNENDCSDSLVCKSGKCSR-----	300
ABX57824.1	SGGT-----TPPPTCSWPGHCQGATCKTGDDCSDDLICTNGKCSPP-----	300
BAA12799.1	NNGGGD-----TGGGSGNTCSWPGLCQGAACKTGDDCSDDLICTKGKCSPP-----	304
KAJ6781651.1	GGS-NP-----GNPGNPPSCSWQGHCLGAKCSSLDDCDGNLQC-----KS--	294
KAJ6785337.1	DTGSNPTSTTASPGRPTNSPPP-----NENLNPKCAPGGNFDLGYFNLQLPVGGPDIISKQ	898
KAJ6783761.1	-	252
KAJ6781485.1	-	256
BAD08218.2	WEGHCKGATCSS--NDDCSDELACIS-G----ICSVDNGVETCE-----	351
ADG96019.1	-	304
BAA92250.1	-	245
ABZ88800.1	-	238
EAL84291.1	-	238
AAO41660.1	-	238
CAE54966.1	-	238
AJG44374.1	-	242
KAJ6787168.1	-	234
ABY77913.1	-	217
KAJ6783315.1	-	232
AFG33049.1	-	249
KAJ6786595.1	-	273
KAJ6788818.1	-	300
ABX57824.1	-	300
BAA12799.1	-	304
KAJ6781651.1	-HK-CSQ-----	299
KAJ6785337.1	LQG-CNGYTGDTFFTDXSSGEMVLLAPGNPDLTGATTSGSAHCRTELREVIHSSGANAA	957
KAJ6783761.1	-	252
KAJ6781485.1	-	256
BAD08218.2	WEGHCEGASCSS---HDDCDGNLACKNGKCSA-----	380
ADG96019.1	-	304
BAA92250.1	-	245
ABZ88800.1	-	238
EAL84291.1	-	238
AAO41660.1	-	238
CAE54966.1	-	238
AJG44374.1	-	242
KAJ6787168.1	-	234
ABY77913.1	-	217
KAJ6783315.1	-	232
AFG33049.1	-	249
KAJ6786595.1	-	273
KAJ6788818.1	-	300
ABX57824.1	-	300
BAA12799.1	-	304
KAJ6781651.1	-	299
KAJ6785337.1	WSPKGNTNTVTMKVVKSDDGTHGTAIGQVFASEASKPLAEMYSPSGDIVVGVKPDEDS	1017
KAJ6783761.1	-	252
KAJ6781485.1	-	256
BAD08218.2	-	380
ADG96019.1	-	304
BAA92250.1	-	245
ABZ88800.1	-	238
EAL84291.1	-	238
AAO41660.1	-	238
CAE54966.1	-	238
AJG44374.1	-	242
KAJ6787168.1	-	234
ABY77913.1	-	217
KAJ6783315.1	-	232

AFG33049.1	-----	249
KAJ6786595.1	-----	273
KAJ6788818.1	-----	300
ABX57824.1	-----	300
BAA12799.1	-----	304
KAJ6781651.1	-----	299
KAJ6785337.1	NQVVTKLGNVSVGTKFTYVLNYSDDKLSISINGKTTALDTFNWDSPACYFKSGNYNQGKS	1077
KAJ6783761.1	-----	252
KAJ6781485.1	-----	256
BAD08218.2	-----	380
ADG96019.1	-----	304
BAA92250.1	-----	245
ABZ88800.1	-----	238
EAL84291.1	-----	238
AAO41660.1	-----	238
CAE54966.1	-----	238
AJG44374.1	-----	242
KAJ6787168.1	-----	234
ABY77913.1	-----	217
KAJ6783315.1	-----	232
AFG33049.1	-----	249
KAJ6786595.1	-----	273
KAJ6788818.1	-----	300
ABX57824.1	-----	300
BAA12799.1	-----	304
KAJ6781651.1	-----	299
KAJ6785337.1	ATSSEVRIYSIDVVHK	1093
KAJ6783761.1	-----	252

Figure S4. Clustal alignment of *A. album* GH75 enzymes. The eight sequences were aligned together with the GH75 chitosanases characterized in fungi (http://www.cazy.org/GH75_characterized.html) with the exception of the sequence EAQ87617 which is not complete. Boxed sequences correspond to the conserved motifs N(D)M(L)DIDCD and YGIWGD, typical of GH75 sequences.

Figure S5

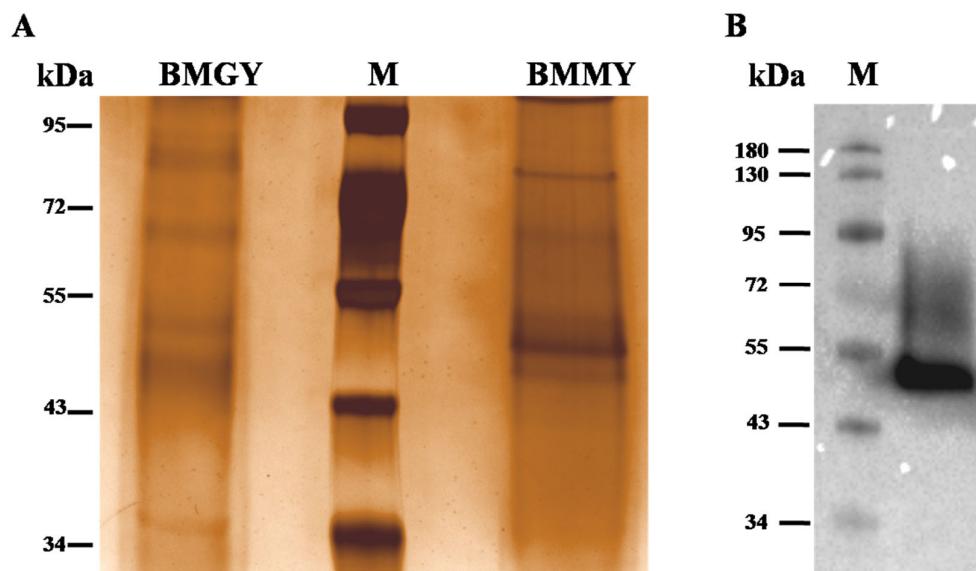


Figure S5. Expression of recombinant Chi1 mature protein. (A) SDS-PAGE on 15% biphasic polyacrylamide gel, M: Marker Protein (Thermo Scientific); BMGY (Buffered Glycerol-complex Medium): clone growth not induced with methanol; BMMY (Buffered Methanol-complex Medium): clone growth induced with methanol. Gel stained with silver staining. (B) Western blot of culture medium after expression in *Pichia pastoris* cells.

Figure S6

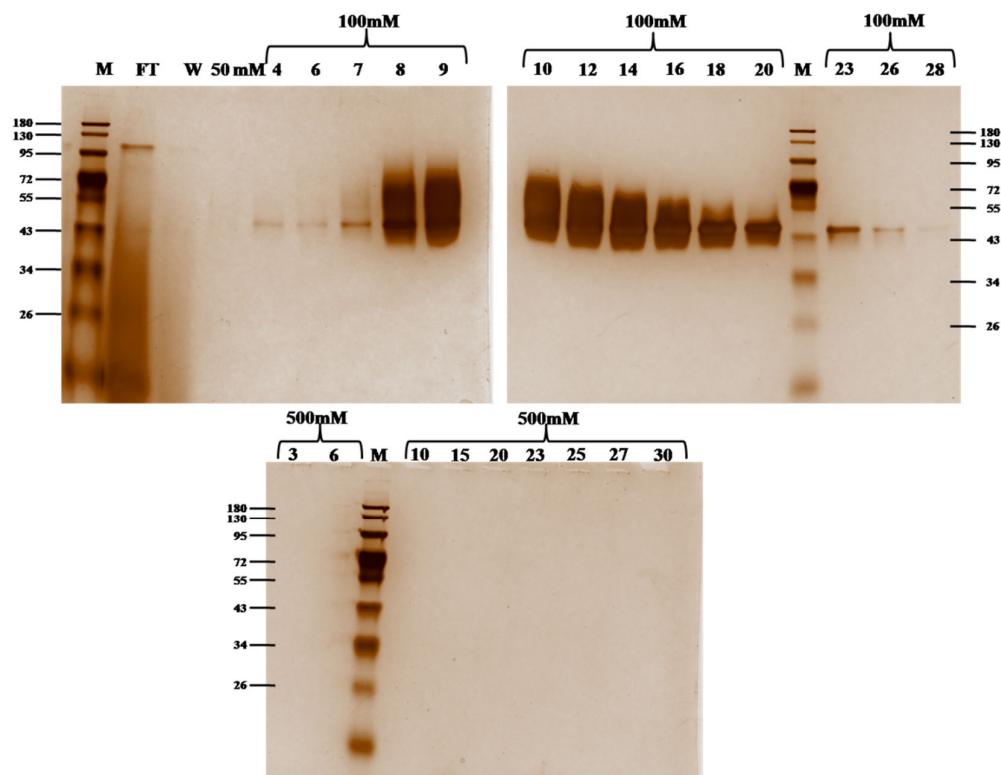


Figure S6. SDS-PAGE (15% polyacrylamide gel) analysis of chromatographic fractions. M: Marker PageRuler Prestained Protein Ladder (Thermo Scientific); FT: flow-through; W: washing fraction; 50 mM: fraction eluted with 50 mM imidazole EB; 100mM: fractions eluted with 100 mM imidazole EB; 500 mM: fractions eluted with 500 mM imidazole EB. Gels stained with silver staining.

Figure S7

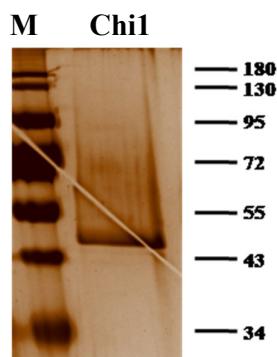


Figure S7. SDS-PAGE (15% polyacrylamide gel) of the purified Chi1 recombinant protein. M: Marker PageRuler Prestained Protein Ladder (Thermo Scientific). Chi1: purified recombinant Chi1 protein after dialysis. Gel stained with silver staining.