

SUPPLEMENT

Mapping and characterization of target-site resistance to cyclic ketoenol insecticides in cabbage whiteflies, *Aleyrodes proletella* (Hemiptera: Aleyrodidae)

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Table S1. Samples of *Aleyrodes proletella* adults collected in different European countries and preserved in ethanol (70% v/v) for pyrosequencing diagnostic.

Year	Sample-ID	Country	Venue	Host
2019	NAR2019-131	Netherlands	Mijnsherenland	Brussels sprouts
	NAR2019-132	Netherlands	Klaaswaal	Brussels sprouts
	NAR2019-148	Poland	Warsaw	Unknown
	NAR2019-149	Poland	Warsaw	Unknown
	NAR2019-150	Netherlands	Schagerbrug	Green cabbage
	NAR2019-151	Netherlands	Oosternijkerk	Broccoli
	NAR2019-162	Switzerland	Zollikofen	Brussels sprouts
	NAR2019-163	Spain	Andalucia	Broccoli
	NAR2019-164	Spain	Murcia	Broccoli
	NAR2019-165	Spain	Murcia	Broccoli
	NAR2019-166	Spain	Murcia	Broccoli
	NAR2019-183	Spain	La Rioja	Cauliflower
2020	NAR2020-119	Belgium	Roeselare	Brussels sprouts
	NAR2020-120	Belgium	Lier	Brussels sprouts
	NAR2020-121	Belgium	Kruishoutem (Kruisem)	Brussels sprouts
	NAR2020-122	Netherlands	Den Bommel	Brussels sprouts
	NAR2020-123	Netherlands	Oud-Beijerland	Brussels sprouts
	NAR2020-124	Netherlands	Heerjansdam	Brussels sprouts
2021	NAR2021-048	Spain	Picassent	Cabbage
	NAR2021-049	Spain	Picassent	Cabbage
	NAR2021-050	Spain	Alzira	Cabbage
	NAR2021-051	Spain	Simat de la Valldigna	Cabbage
	NAR2021-052	Spain	Algemesi	Cabbage
	NAR2021-053	Spain	Alzira	Cabbage
	NAR2021-054	Spain	Manuel	Cabbage
	NAR2021-055	Spain	Simat de la Valldigna	Cabbage
	NAR2021-060	Spain	Finca Las Cabecicas Lorca	Cabbage
	NAR2021-061	Spain	Lorca	Cabbage
	NAR2021-110	Netherlands	Den Bommel	Brussel sprouts
	NAR2021-111	Netherlands	Hellevoetsluis	Brussel sprouts
	NAR2021-112	Netherlands	Mijnsheerenland	Brussel sprouts
	NAR2021-113	Netherlands	Bruinisse	Cabbage
	NAR2021-114	Netherlands	Zeewolde	Cabbage
	NAR2021-115	Netherlands	Den Bommel	Cabbage
	NAR2021-116	Netherlands	Hellevoetsluis	Cabbage
	NAR2021-117	Netherlands	Mijnsheerenland	Cabbage
	NAR2021-120	Netherlands	Sexbierum	Cabbage
	ALTHFL_DEU21_0001	Germany	Hannover	Savoy cabbage
	ALEUPR_DEU21_0002	Germany	Hannover	Savoy cabbage

Table S2. Primer pairs used for RT-qPCR analysis of *Aleyrodes proletella* acetyl-CoA carboxylase (ACC) expression levels.

Primer	Forward primer (5' to 3')	Reverse primer (5' to 3')	Amplicon, bp
ACC	AGGTACGGCGCCAGATTATG	AACCACTGTCGTTGCTAGG	121
<i>Actin</i>	CGGTCGTACCACTGGTATCG	AAACGGAGGATGGCATGAGG	99
<i>ATP</i>	AAGTCAACCACCGAGTCAGC	TGAAGACCTTTCTGCCGAGC	129
<i>HSP-90</i>	AGCTCTCCGTGCTAAAGCTG	CTGATCATGCGGTGAATGCG	147

Table S3. Primer pairs used for *Aleyrodes proletella* acetyl-CoA carboxylase (ACC) genotyping by pyrosequencing.

Primer	Forward primer (5' to 3')	Reverse primer (5' to 3')	Amplicon, bp
ACC A2083V	TGTGGATGAGTTACGTGTTTACAA	[btn]GGGGTTAATGGTGGGATCAACTA	
ACC A2083V_seq	AGAGGAGGAGCTTGG		106

Table S4. Genotyping by pyrosequencing of alcohol-preserved individuals of *Aleyrodes proletella* for the presence of the A2083V mutation in the ACC carboxyltransferase (CT) domain. Genotypes: A/A, susceptible homozygotes; A/V, heterozygotes; V/V, resistant homozygotes.

Sample	Country	Year	Genotype (%)		
			A/A	A/V	V/V
NAR2019-131	Netherlands	2019	100	0	0
NAR2019-132	Netherlands	2019	100	0	0
NAR2019-148	Poland	2019	100	0	0
NAR2019-149	Poland	2019	90	10	0
NAR2019-150	Netherlands	2019	100	0	0
NAR2019-151	Netherlands	2019	100	0	0
NAR2019-162	Switzerland	2019	0	0	100
NAR2019-163	Spain	2019	100	0	0
NAR2019-164	Spain	2019	100	0	0
NAR2019-165	Spain	2019	100	0	0
NAR2019-166	Spain	2019	100	0	0
NAR2019-183	Spain	2019	100	0	0
NAR2020-119	Belgium	2020	100	0	0
NAR2020-120	Belgium	2020	100	0	0
NAR2020-121	Belgium	2020	100	0	0
NAR2020-122	Netherlands	2020	0	0	100
NAR2020-123	Netherlands	2020	0	30	70
NAR2020-124	Netherlands	2020	0	50	50
NAR2021-048	Spain	2021	100	0	0
NAR2021-049	Spain	2021	100	0	0
NAR2021-050	Spain	2021	100	0	0
NAR2021-051	Spain	2021	100	0	0
NAR2021-052	Spain	2021	100	0	0
NAR2021-053	Spain	2021	100	0	0
NAR2021-054	Spain	2021	0	100	0
NAR2021-055	Spain	2021	20	80	0
NAR2021-060	Spain	2021	100	0	0
NAR2021-061	Spain	2021	100	0	0
NAR2021-110	Netherlands	2021	0	10	90
NAR2021-111	Netherlands	2021	0	0	100
NAR2021-112	Netherlands	2021	0	10	90
NAR2021-113	Netherlands	2021	0	10	90
NAR2021-114	Netherlands	2021	100	0	0
NAR2021-115	Netherlands	2021	0	10	90
NAR2021-116	Netherlands	2021	0	0	100
NAR2021-117	Netherlands	2021	0	0	100
NAR2021-120	Netherlands	2021	100	0	0
ALTHFL_DEU21_0001	Germany	2021	30	40	30
ALEUPR_DEU21_0002	Germany	2021	0	60	40

Figure S1. Partial nucleotide sequence of a cDNA fragment of the carboxyltransferase (CT) domain of *Aleyrodes proletella* ACC harboring the mutation site A2083 (red). Annealing positions for primers for pyrosequencing diagnostics of the mutation site A2083V are indicated by blue arrows.



Figure S2. Translation of GenBank Acc. No. GJYF01046828.1 representing the amino acid sequence of ACC of *Aleyrodes proletella* strain 3/19. The protein sequences of ACC in strains 3/19, 4/19, 5/20 and 6/19 are identical. Strains 2/20 and SPI-2/20 have A2084V (shown in red).

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1  MEGDTGPKTN NVNFIVGDDG QDGEIANGLI NTISEEDERK ENRDSFSPSGN
51  GPTGLISNSS SYNMMFGLAE RRKRLRPSMS QGTVIHQRLD DKDFTVGTPE
101 EFVKRFKGTR VINKVLIANN GIAAVKCMRS IRRWSYEMFK NERAVRFVVM
151 VTPEDLKANA EYIKMADHYV PVPGGTNNNN YANVELIVDI ALRTQVQAVW
201 AGWGHASENP KLPELLHKNN IAFIGPPEKA MWALGDKIAS SIVAQTAEIP
251 TLPWSGSELT AQYSGKKIKI SSDLYKKGCV SSVEEGLRSA HKIGFPIMIK
301 ASEGSGGKGI RKVEAAEEFP NLFRQVQSEV PGSPIFIMKL ARCARHLEVQ
351 LLADQYGNAI SLFGRDCSIQ RRHQKIIEEA PAVIAEPDVF ENMEKAAVRL
401 AKMVGYSAG TVEYLYDPSE GQYFFLELNP RLQVEHPCTE MVADVNLPA
451 QLQIAMGLQL NCIKDIRLLY GESPWGDNYI DFDEPRHKPQ PWGHVIAARI
501 TSENPDEGFK PSSGTVQELN FRSSKNVWGY FSVAASGGLH EFADSQFGHC
551 FSWGENREQA RENLVIALKE LSIRGDFRTT VEYLITLLET ESFQINTIDT
601 AWLDLLISER VQSEKPDVLL GVMCGALHIA DRKVCDAFQN FQTSLEGRQI
651 QGCNTLDHNV QVELIHDGLK YKVHATKSLG NSYFLVMNGS FKEIELHRLS
701 DGGILLSVDG SSFTTYMREE VDRYRIVIGN LTCVFEEKEND PSLLRSPSAG
751 KLISYLIEDG GHVSKGQAYA EIEVMKMMVT LTANESGLVT FAKRPGAVLD
801 AGSLIGTLEL DDPSLVSKAL DYKGEFFELD VSTPMVGEKL NHAHNHYRQM
851 LDNILAGFCL PDPYHLVRLR EVIEKFMSSL RDPSPLELLEL QEVISSISGR
901 IPISVEKKIR KLMTLYERNI TSVLAQFPSQ QIAGVIDSHA ATLQKRSDRD
951 GFFLTQGVIV QLVQRYRNGI RGRMKSASVHE LLRQYYEVES QFQQGHYDKC
1001 VMAIREKFKD DMAAVTSTIF SHGQVAKKNM LVTMLIDHLW SNEPGLTDEL
1051 ATTNLNELTSL NRSEHSRVAL RSRQVLIAAH QPAYELRHNQ MESIFLSAVD
1101 MYGHDFHPEN LQKLIQSETS IFDILHDFFY HTNRAVCNAA LEVYVRRVYI
1151 SYELTCLQHL ELSGEVPLVQ FQFLLPSSHP NRQKVTDPSS PIIADSPETE
1201 EPPSSTPTII HSYQRTGCMA AFESFDQFES YYDEILDLLD ELSPSTISPR
1251 IMEALSGSE SRMSTSINVS LSVGDNPRPP GLEDGLQVEP IHILCIAVKD
1301 NGDLEDEKLS KLLGDFCAKH REELKEKSIR RITFLALNRR QFPKLFTFRN
1351 CDFVEDRIY RHLEPGMAFQ LELNRMKTYH LEALPTSNRK MYLYLGRAKV
1401 AKGQEVTDNR FFIRSIIRHS DLITKEASFE YLQNEGERVL LEAMDELEVA
1451 FSHPLARTRD CNHIFLNFPV TVIMDSAKIE ESVTNMVMRY GARLWKLRVL
1501 QAELRMTIRT SPNSKTTNVR LCLANDSGYY LDICLYKEVV DPKTGIIKLE
1551 SYGSKQGPLH GLPTAIPYVT KDYLQKQRFQ AQSAGTTYCH DIPDMFRQMV
1601 ERQWKEFIEQ RPNDGIVKPS QLMDYVELVL EDDHLVEQKR LAGENTIGMV
1651 AWRITLNTPE YPDGREIIVI ANDITVRIGS FGPEEDLVFD LASKIARQMK
1701 VPRIYIAANS GARIGLAEV KSLFRVAVED PDEPDKGLKY LYLSTEDFIK
1751 ISACNSVRAI LIEDEGEARY KITDIIGKED GLGVENLRYA GMIAGETSEA
1801 YREIVTISMV SCRAIGIGAY LVRLGQRFVQ VENSIIITG YSALNKLGR
1851 EVYASNNQLG GIQIMYNNGI SHKTEPRDLG GIYSIVKWLK YIPKDKYSPV
1901 PVIKPADPVD REVGYMPTKT PYDPRWMIAG RYSPNNSNEW ESGFFDEGSW
1951 EEVMQPPAQV VVVGRRARLG IPMGVIAVET RTVEVKLPAD PANLDSEAKT
2001 LSQAGQVWFP DSAFKTAQAI KDFEHEDLPL IIFANWRGFS GGMKDMYEQV
2051 MKFGAYIVDE LRVKQPVII YIPNGELRG GAWAVVDPTI NPRHMEMYAD
2101 PESRGGVLEP EGIVEIKFRE KDILKTMHRI DQVIVPLKQK LAVPDLSPPE
2151 KAEVENQIVE REQYLKPMYH QVAIHFAHLH DTPERMMEKG VIHNIVPWRK
2201 SRTLLHWRVK RLLLENQIKC NLLKVQPQMD NGQAQAMLRR WFVEDKGTST
2251 AYLWENNESV VAWLMSQLSP DGSISPNSIV ANNIRCVQRD ALINQIKTSM
2301 EESPDVAQDA VVEMFQTLA NERSEVLRKL SHLETISKPE PQS

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Figure S3. Multiple alignment of ACCase of *Bemisia tabaci*, *Myzus persicae*, predicted ACCase amino acid sequence of *Trialeurodes vaporariorum* and of five strains of *Aleyrodes proletella*, 2/20 (GenBank accession no. GJYF01020973.1; identical to SPI-2/20), 3/19 (GJYF01046828.1), 4/19 (GJYF01092380.1), 5/20 (GJYF01105771.1) and 6/19 (GJYF01137039.1). The carboxyltransferase (CT) domain (PF01039.35) is highlighted in yellow (AA 1658-2210). Previously described mutations E645K (*T. vaporariorum*; Karatolos et al., 2012) and A2083V (*B. tabaci*; Lueke et al., 2020) are highlighted in blue.

	1				50
BEMITA_QJQ31013	MEGETGQKAN	NVNFIVGDDG	QDGEIPNGIN	T..ISEEDER	ERRENRDSFP
MYZUPE_XP_022181497	~~~MSSETSG	GVNFIVGDED	GVDQAPAEIV	NGELMKALEA	EKHENTDSFP
TRIAVA_ACCase	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
2/20 & SPI-2/20	MEGDTGPKTN	NVNFIVGDDG	QDGEIANGLI	N..TI.SEED	ERKENRDSFP
3/19	MEGDTGPKTN	NVNFIVGDDG	QDGEIANGLI	N..TI.SEED	ERKENRDSFP
4/19	MEGDTGPKTN	NVNFIVGDDG	QDGEIANGLI	N..TI.SEED	ERKENRDSFP
5/20	MEGDTGPKTN	NVNFIVGDDG	QDGEIANGLI	N..TI.SEED	ERKENRDSFP
6/19	MEGDTGPKTN	NVNFIVGDDG	QDGEIANGLI	N..TI.SEED	ERKENRDSFP
	51				100
BEMITA_QJQ31013	SGNG.PTGII	SSSSSYKDMF	GLAERRKRLR	PSMSQGTVIH	QRLLDKDFTV
MYZUPE_XP_022181497	LGKETRMGVT	SNSSSYNNMF	GLTEKRKRLR	PSMSQGNVIH	QRLTEKDFNV
TRIAVA_ACCase	~~~~~	~~~~~	~~~~~	~~MSQGTVIH	QRLLDKDFTV
2200	SGNG.PTGLI	SNSSSYNNMF	GLAERRKRLR	PSMSQGTVIH	QRLLDKDFTV
319	SGNG.PTGLI	SNSSSYNNMF	GLAERRKRLR	PSMSQGTVIH	QRLLDKDFTV
419	SGNG.PTGLI	SNSSSYNNMF	GLAERRKRLR	PSMSQGTVIH	QRLLDKDFTV
520	SGNG.PTGLI	SNSSSYNNMF	GLAERRKRLR	PSMSQGTVIH	QRLLDKDFTV
619	SGNG.PTGLI	SNSSSYNNMF	GLAERRKRLR	PSMSQGTVIH	QRLLDKDFTV
	101				150
BEMITA_QJQ31013	GTPEEFVKRF	KGTRVINKVL	IANNGLIAAVK	CMRSIRRWSY	EMFKNERAVR
MYZUPE_XP_022181497	STPEEFVKRF	KGTRVINKVL	IANNGLIAAVK	CMRSVRRWSY	EMFRNERAVR
TRIAVA_ACCase	GTPEEFVKRF	KGTRVINKVL	IANNGLIAAVK	CMRSIRRWSY	EMFKNERAVR
2200	GTPEEFVKRF	KGTRVINKVL	IANNGLIAAVK	CMRSIRRWSY	EMFKNERAVR
319	GTPEEFVKRF	KGTRVINKVL	IANNGLIAAVK	CMRSIRRWSY	EMFKNERAVR
419	GTPEEFVKRF	KGTRVINKVL	IANNGLIAAVK	CMRSIRRWSY	EMFKNERAVR
520	GTPEEFVKRF	KGTRVINKVL	IANNGLIAAVK	CMRSIRRWSY	EMFKNERAVR
619	GTPEEFVKRF	KGTRVINKVL	IANNGLIAAVK	CMRSIRRWSY	EMFKNERAVR
	151				200
BEMITA_QJQ31013	FVVMVTPEDL	KANA EYIKMA	DHYVPVPGGT	NNNNYANVEL	IVDIALRTQV
MYZUPE_XP_022181497	FVVMVTPEDL	KANA EYIKMA	DHYVPVPGGT	NNNNYANVEL	IVNIAIRSQV
TRIAVA_ACCase	FVVMVTPEDL	KANA EYIKMA	DHYVPVPGGT	NNNNYANVEL	IIDIATRTQV
2200	FVVMVTPEDL	KANA EYIKMA	DHYVPVPGGT	NNNNYANVEL	IVDIALRTQV
319	FVVMVTPEDL	KANA EYIKMA	DHYVPVPGGT	NNNNYANVEL	IVDIALRTQV
419	FVVMVTPEDL	KANA EYIKMA	DHYVPVPGGT	NNNNYANVEL	IVDIALRTQV
520	FVVMVTPEDL	KANA EYIKMA	DHYVPVPGGT	NNNNYANVEL	IVDIALRTQV
619	FVVMVTPEDL	KANA EYIKMA	DHYVPVPGGT	NNNNYANVEL	IVDIALRTQV
	201				250
BEMITA_QJQ31013	QAVWAGWGHA	SENPKLPELL	HKNNIAFIGP	PEKAMWALGD	KIASSIVAQT
MYZUPE_XP_022181497	QAVWAGWGHA	SENPELPKLL	DKNKIAFIGP	PEKAMFALGD	KIASSIVAQT
TRIAVA_ACCase	QAVWAGWGHA	SENPKLPELL	HKNNIAFIGP	PEKAMWALGD	KIASSIVAQT
2200	QAVWAGWGHA	SENPKLPELL	HKNNIAFIGP	PEKAMWALGD	KIASSIVAQT
319	QAVWAGWGHA	SENPKLPELL	HKNNIAFIGP	PEKAMWALGD	KIASSIVAQT
419	QAVWAGWGHA	SENPKLPELL	HKNNIAFIGP	PEKAMWALGD	KIASSIVAQT
520	QAVWAGWGHA	SENPKLPELL	HKNNIAFIGP	PEKAMWALGD	KIASSIVAQT

619	QAVWAGWGHA	SENPKLPELL	HKNNIAFIGP	PEKAMWALGD	KIASSIVAQT
	251			300	
BEMITA_QJQ31013	AEIPTLPWSG	SELTAQYSGR	KIKISSELYK	RGCVSSVEEG	LRSQKIGFP
MYZUPE_XP_022181497	AEIPTLPWSG	SGVVGHYSGK	KIEIGPDLYK	KGCVASIEEG	LVSAEKVGYP
TRIAVA_ACCase	AEIPT.....ISSELYK	KGCVQNVVEG	LRSQKIGFP
2200	AEIPTLPWSG	SELTAQYSGK	KIKISSDLYK	KGCVSSVEEG	LRSQKIGFP
319	AEIPTLPWSG	SELTAQYSGK	KIKISSDLYK	KGCVSSVEEG	LRSQKIGFP
419	AEIPTLPWSG	SELTAQYSGK	KIKISSDLYK	KGCVSSVEEG	LRSQKIGFP
520	AEIPTLPWSG	SELTAQYSGK	KIKISSDLYK	KGCVSSVEEG	LRSQKIGFP
619	AEIPTLPWSG	SELTAQYSGK	KIKISSDLYK	KGCVSSVEEG	LRSQKIGFP
	301			350	
BEMITA_QJQ31013	VMIKASEGGG	GKGIRKVESS	EEFPNLFQV	QSEVPGSPIF	IMKLARCARH
MYZUPE_XP_022181497	IMIKASEGGG	GKGIRKVENT	EEFPNAYQV	QAEVPGSPIF	IMKLAKCARH
TRIAVA_ACCase	VMVKASEGGG	GKGIRKVESS	EEFPNLFQV	QAEVPGSPIF	IMKLARCARH
2200	IMIKASEGGG	GKGIRKVEAA	EEFPNLFQV	QSEVPGSPIF	IMKLARCARH
319	IMIKASEGGG	GKGIRKVEAA	EEFPNLFQV	QSEVPGSPIF	IMKLARCARH
419	IMIKASEGGG	GKGIRKVEAA	EEFPNLFQV	QSEVPGSPIF	IMKLARCARH
520	IMIKASEGGG	GKGIRKVEAA	EEFPNLFQV	QSEVPGSPIF	IMKLARCARH
619	IMIKASEGGG	GKGIRKVEAA	EEFPNLFQV	QSEVPGSPIF	IMKLARCARH
	351			400	
BEMITA_QJQ31013	LEVQLLADQY	GNAISLFGRD	CSIQRRHQKI	IEEAPAVIAE	PEIFEDMEKA
MYZUPE_XP_022181497	LEVQLLADQY	GNAISLFGRD	CSIQRRHQKI	IEEAPAVIAE	PSVFEEMERA
TRIAVA_ACCase	LEVQLLADQY	GNAISLFGRD	CSIQRRHQKI	IEEAPAVIAE	PEVFEAMEKA
2200	LEVQLLADQY	GNAISLFGRD	CSIQRRHQKI	IEEAPAVIAE	PDVFENMEKA
319	LEVQLLADQY	GNAISLFGRD	CSIQRRHQKI	IEEAPAVIAE	PDVFENMEKA
419	LEVQLLADQY	GNAISLFGRD	CSIQRRHQKI	IEEAPAVIAE	PDVFENMEKA
520	LEVQLLADQY	GNAISLFGRD	CSIQRRHQKI	IEEAPAVIAE	PDVFENMEKA
619	LEVQLLADQY	GNAISLFGRD	CSIQRRHQKI	IEEAPAVIAE	PDVFENMEKA
	401			450	
BEMITA_QJQ31013	AVRLAKMVG	VSAGTVEYLY	DPSEGQYFFL	ELNPRLQVEH	PCTEMVADV
MYZUPE_XP_022181497	AVRIAKMVG	VSAGTVEYLY	DT.DGNYYFL	ELNPRLQVEH	PCTEMVSDV
TRIAVA_ACCase	AVRLAKMVG	VSAGTVEYLY	DPSEGQYFFL	ELNPRLQVEH	PCTEMVADV
2200	AVRLAKMVG	VSAGTVEYLY	DPSEGQYFFL	ELNPRLQVEH	PCTEMVADV
319	AVRLAKMVG	VSAGTVEYLY	DPSEGQYFFL	ELNPRLQVEH	PCTEMVADV
419	AVRLAKMVG	VSAGTVEYLY	DPSEGQYFFL	ELNPRLQVEH	PCTEMVADV
520	AVRLAKMVG	VSAGTVEYLY	DPSEGQYFFL	ELNPRLQVEH	PCTEMVADV
619	AVRLAKMVG	VSAGTVEYLY	DPSEGQYFFL	ELNPRLQVEH	PCTEMVADV
	451			500	
BEMITA_QJQ31013	LPAAQLQVAM	GLQLHCKDI	RVLYGESPWG	DSLIDFDQPR	HKPQPWGHVI
MYZUPE_XP_022181497	LPAAQLQISM	GLALNCIKDI	RLLYSESANG	DSYIDFDAPR	HKPHPWGHVI
TRIAVA_ACCase	LPAAQLQIAM	GLPLNCIKDI	RLLYGESPWG	DNLIDFDEPR	HKPQPWGHVI
2200	LPAAQLQIAM	GLQLNCIKDI	RLLYGESPWG	DNYIDFDEPR	HKPQPWGHVI
319	LPAAQLQIAM	GLQLNCIKDI	RLLYGESPWG	DNYIDFDEPR	HKPQPWGHVI
419	LPAAQLQIAM	GLQLNCIKDI	RLLYGESPWG	DNYIDFDEPR	HKPQPWGHVI
520	LPAAQLQIAM	GLQLNCIKDI	RLLYGESPWG	DNYIDFDEPR	HKPQPWGHVI
619	LPAAQLQIAM	GLQLNCIKDI	RLLYGESPWG	DNYIDFDEPR	HKPQPWGHVI
	501			550	
BEMITA_QJQ31013	AARITSENP	EGFKPSSGT	QELNFRSSKN	VWGYFSVAAS	GGLHEFADSQ
MYZUPE_XP_022181497	AARITSENP	EGFKPSSGT	QELNFRSSKN	VWGYFSVAAS	GGLHEFADSQ
TRIAVA_ACCase	AARITSENP	EGFKPSSGT	QELNFRSSKN	VWGYFSVAAS	GGLHEFADSQ
2200	AARITSENP	EGFKPSSGT	QELNFRSSKN	VWGYFSVAAS	GGLHEFADSQ
319	AARITSENP	EGFKPSSGT	QELNFRSSKN	VWGYFSVAAS	GGLHEFADSQ
419	AARITSENP	EGFKPSSGT	QELNFRSSKN	VWGYFSVAAS	GGLHEFADSQ

520	AARITSENP	EGFKPSSGT	QELNFRSSKN	VWGYFSVAAS	GGLHEFADSQ
619	AARITSENP	EGFKPSSGT	QELNFRSSKN	VWGYFSVAAS	GGLHEFADSQ
	551				600
BEMITA_QJQ31013	FGHCFSWGEN	REQARENLVI	ALKELSIRGD	FRTTVEYLIT	LLETESFQIN
MYZUPE_XP_022181497	FGHCFSWGEN	REQARENLVI	ALKELSIRGD	FRTTVEYLIT	LLETESFQSN
TRIAVA_ACCase	FGHCFSWGEN	REQARENLVI	ALKELSIRGD	FRTTVEYLIT	LLETESFQIN
2200	FGHCFSWGEN	REQARENLVI	ALKELSIRGD	FRTTVEYLIT	LLETESFQIN
319	FGHCFSWGEN	REQARENLVI	ALKELSIRGD	FRTTVEYLIT	LLETESFQIN
419	FGHCFSWGEN	REQARENLVI	ALKELSIRGD	FRTTVEYLIT	LLETESFQIN
520	FGHCFSWGEN	REQARENLVI	ALKELSIRGD	FRTTVEYLIT	LLETESFQIN
619	FGHCFSWGEN	REQARENLVI	ALKELSIRGD	FRTTVEYLIT	LLETESFQIN
	601				650
BEMITA_QJQ31013	TIDTAWLDVL	IAEKVQSEKP	DILLGVMCGA	LHIADRRVTD	AFQNFQTSLE
MYZUPE_XP_022181497	TIDTAWLDLL	ISERVQSEKP	DIFLGVICGG	LHIADRKISE	SFQNFQTSLE
TRIAVA_ACCase	TIDTAWLDVL	IAQKVPSEKP	DILLGVMCGA	LHIADRKVTD	AFQNFQTSLE
2200	TIDTAWLDLL	ISERVQSEKP	DVLLGVMCGA	LHIADRKVCD	AFQNFQTSLE
319	TIDTAWLDLL	ISERVQSEKP	DVLLGVMCGA	LHIADRKVCD	AFQNFQTSLE
419	TIDTAWLDLL	ISERVQSEKP	DVLLGVMCGA	LHIADRKVCD	AFQNFQTSLE
520	TIDTAWLDLL	ISERVQSEKP	DVLLGVMCGA	LHIADRKVCD	AFQNFQTSLE
619	TIDTAWLDLL	ISERVQSEKP	DVLLGVMCGA	LHIADRKVCD	AFQNFQTSLE
	651				700
BEMITA_QJQ31013	RGQIQGSNTL	DHNVQVELIN	DGLKYKVHAT	KSGPNSYFLV	MNGSFKEIEL
MYZUPE_XP_022181497	RGQVLSANTL	DHHVSVELIN	GGYKYKVQVT	KSGLNSYFLI	MNGSFKEIEV
TRIAVA_ACCase	RGQIQGSNTL	DHHLSVELIH	DGLKYRVHAT	KSGANSYFLV	MNGSFKEIEL
2200	RGQIQGCNTL	DHNVQVELIH	DGLKYKVHAT	KSGLNSYFLV	MNGSFKEIEL
319	RGQIQGCNTL	DHNVQVELIH	DGLKYKVHAT	KSGLNSYFLV	MNGSFKEIEL
419	RGQIQGCNTL	DHNVQVELIH	DGLKYKVHAT	KSGLNSYFLV	MNGSFKEIEL
520	RGQIQGCNTL	DHNVQVELIH	DGLKYKVHAT	KSGLNSYFLV	MNGSFKEIEL
619	RGQIQGCNTL	DHNVQVELIH	DGLKYKVHAT	KSGLNSYFLV	MNGSFKEIEL
	701				750
BEMITA_QJQ31013	HRLSDGGILL	SVDSSSFTTY	MREEVDYRI	VIGNQTCVFE	KENDPSLLRS
MYZUPE_XP_022181497	HRLSDGGILL	SLDGSSFTTY	MREEVDYRI	VIGNQTCVFD	KENDPSLFRS
TRIAVA_ACCase	HRLSDG....EVDYRI	VIGNQTCVFE	KENDPSLLRS
2200	HRLSDGGILL	SVDGSSFTTY	MREEVDYRI	VIGNLTCVFE	KENDPSLLRS
319	HRLSDGGILL	SVDGSSFTTY	MREEVDYRI	VIGNLTCVFE	KENDPSLLRS
419	HRLSDGGILL	SVDGSSFTTY	MREEVDYRI	VIGNLTCVFE	KENDPSLLRS
520	HRLSDGGILL	SVDGSSFTTY	MREEVDYRI	VIGNLTCVFE	KENDPSLLRS
619	HRLSDGGILL	SVDGSSFTTY	MREEVDYRI	VIGNLTCVFE	KENDPSLLRS
	751				800
BEMITA_QJQ31013	PSAGKLLSFL	IEDGGHVSKG	QAYAEIEVMK	MVMTLTASEN	GNVTFAKRPG
MYZUPE_XP_022181497	PSAGKLISFL	IEDGGQVKKG	QPYAEIEVMK	MVMTLTATEN	GRVYYSKRPG
TRIAVA_ACCase	PSAGKLISFL	IEDGGHVAKG	AAYAEIEVMK	MVMTLTANES	GLVTFAKRPG
2200	PSAGKLISYL	IEDGGHVSKG	QAYAEIEVMK	MVMTLTANES	GLVTFAKRPG
319	PSAGKLISYL	IEDGGHVSKG	QAYAEIEVMK	MVMTLTANES	GLVTFAKRPG
419	PSAGKLISYL	IEDGGHVSKG	QAYAEIEVMK	MVMTLTANES	GLVTFAKRPG
520	PSAGKLISYL	IEDGGHVSKG	QAYAEIEVMK	MVMTLTANES	GLVTFAKRPG
619	PSAGKLISYL	IEDGGHVSKG	QAYAEIEVMK	MVMTLTANES	GLVTFAKRPG
	801				850
BEMITA_QJQ31013	AVLDAGSLIA	TLEDDPSLV	TKALDYKGQF	PELDVSTPTV	GEKLNHAHNH
MYZUPE_XP_022181497	AVLDAGSLIA	TLEDDPSLV	TKAIEYKGQF	LELDGTSIHY	GESLNNIHTC
TRIAVA_ACCase	AVLDAGSLIA	TLEDDISLV	TKALDYKGQF	PELDVSTPMV	GDKLNHAHNH
2200	AVLDAGSLIG	TLEDDPSLV	SKALDYKGEF	PELDVSTPMV	GEKLNHAHNH
319	AVLDAGSLIG	TLEDDPSLV	SKALDYKGEF	PELDVSTPMV	GEKLNHAHNH

419	AVLDAGSLIG	TLELDDPSLV	SKALDYKGEF	PELDVSTPMV	GEKLNHAHNNH
520	AVLDAGSLIG	TLELDDPSLV	SKALDYKGEF	PELDVSTPMV	GEKLNHAHNNH
619	AVLDAGSLIG	TLELDDPSLV	SKALDYKGEF	PELDVSTPMV	GEKLNHAHNNH
	851				900
BEMITA_QJQ31013	YRQMLDNILA	GYCLDPYHL	VRLREVIEKF	MSSLRDPSLP	LLELQEVISS
MYZUPE_XP_022181497	YRQMLDNILA	GYCLPEPYHL	VRLREVIEKF	MNSLRDPSLP	LLELQEVISS
TRIAVA_ACCase	YRQMLDNILA	GYCLDPYHL	VRLREVIEKF	MSSLRDPSLP	LLELQEVISS
2200	YRQMLDNILA	GFCLDPYHL	VRLREVIEKF	MSSLRDPSLP	LLELQEVISS
319	YRQMLDNILA	GFCLDPYHL	VRLREVIEKF	MSSLRDPSLP	LLELQEVISS
419	YRQMLDNILA	GFCLDPYHL	VRLREVIEKF	MSSLRDPSLP	LLELQEVISS
520	YRQMLDNILA	GFCLDPYHL	VRLREVIEKF	MSSLRDPSLP	LLELQEVISS
619	YRQMLDNILA	GFCLDPYHL	VRLREVIEKF	MSSLRDPSLP	LLELQEVISS
	901				950
BEMITA_QJQ31013	ISGRIPISVE	KKIRKLMTRY	ERNITSVLAQ	FPSQQIASVI	DSHAATLQKR
MYZUPE_XP_022181497	ISGRIPKAVD	KKIKSLMKLY	ERNITSVLAQ	FPSQQIAAII	DGHAATLQKR
TRIAVA_ACCase	ISGRIPISVE	KKIRKLMTRY	ERNITSVLAQ	FPSQQIASVI	DSHAATLQKR
2200	ISGRIPISVE	KKIRKLMTRY	ERNITSVLAQ	FPSQQIAGVI	DSHAATLQKR
319	ISGRIPISVE	KKIRKLMTRY	ERNITSVLAQ	FPSQQIAGVI	DSHAATLQKR
419	ISGRIPISVE	KKIRKLMTRY	ERNITSVLAQ	FPSQQIAGVI	DSHAATLQKR
520	ISGRIPISVE	KKIRKLMTRY	ERNITSVLAQ	FPSQQIAGVI	DSHAATLQKR
619	ISGRIPISVE	KKIRKLMTRY	ERNITSVLAQ	FPSQQIAGVI	DSHAATLQKR
	951				1000
BEMITA_QJQ31013	SDRDGFFLTT	QGIVQLVQRY	RNGIRGRMKS	AVHELLRQYY	EVESQFQQGH
MYZUPE_XP_022181497	TDRDSFFQTT	QGIVQLVQRY	RNGIRGRMKS	AVHELLKQYY	EVESQFQHGS
TRIAVA_ACCase	SDRDGFFLTT	QGIVQLVQRY	RNGIRGRMKS	AVHELLRQYY	EVESQFQQGH
2200	SDRDGFFLTT	QGIVQLVQRY	RNGIRGRMKS	AVHELLRQYY	EVESQFQQGH
319	SDRDGFFLTT	QGIVQLVQRY	RNGIRGRMKS	AVHELLRQYY	EVESQFQQGH
419	SDRDGFFLTT	QGIVQLVQRY	RNGIRGRMKS	AVHELLRQYY	EVESQFQQGH
520	SDRDGFFLTT	QGIVQLVQRY	RNGIRGRMKS	AVHELLRQYY	EVESQFQQGH
619	SDRDGFFLTT	QGIVQLVQRY	RNGIRGRMKS	AVHELLRQYY	EVESQFQQGH
	1001				1050
BEMITA_QJQ31013	YDKCVTAIRE	KFKDDMAAVT	GTIFSHGQVA	KKNMLVTMLI	DHLWSNEPGL
MYZUPE_XP_022181497	YDKCATALRD	RYKDDMAAVT	STIFSHTQVA	KKNMLVTMLI	DHLWSNEPGL
TRIAVA_ACCase	YDKCVTAIRE	KFKDDMAAVV	GTIFSHGQVA	KKNMLVTMLI	DHLWSNEPGL
2200	YDKCVMAIRE	KFKDDMAAVT	STIFSHGQVA	KKNMLVTMLI	DHLWSNEPGL
319	YDKCVMAIRE	KFKDDMAAVT	STIFSHGQVA	KKNMLVTMLI	DHLWSNEPGL
419	YDKCVMAIRE	KFKDDMAAVT	STIFSHGQVA	KKNMLVTMLI	DHLWSNEPGL
520	YDKCVMAIRE	KFKDDMAAVT	STIFSHGQVA	KKNMLVTMLI	DHLWSNEPGL
619	YDKCVMAIRE	KFKDDMAAVT	STIFSHGQVA	KKNMLVTMLI	DHLWSNEPGL
	1051				1100
BEMITA_QJQ31013	TDELATTLINE	LTSLNRSEHS	RVALRARQVL	IAAHQPAYEL	RHNQMESIFL
MYZUPE_XP_022181497	TDELAATLINE	LTSLNRSEHS	RVALRARQVL	IAAHQPAYEL	RHNQMESIFL
TRIAVA_ACCase	TDELATTLINE	LTSLNRSEHS	RVALRARQVL	IAAHQPAYEL	RHNQMESIFL
2200	TDELATTLINE	LTSLNRSEHS	RVALRSRQVL	IAAHQPAYEL	RHNQMESIFL
319	TDELATTLINE	LTSLNRSEHS	RVALRSRQVL	IAAHQPAYEL	RHNQMESIFL
419	TDELATTLINE	LTSLNRSEHS	RVALRSRQVL	IAAHQPAYEL	RHNQMESIFL
520	TDELATTLINE	LTSLNRSEHS	RVALRSRQVL	IAAHQPAYEL	RHNQMESIFL
619	TDELATTLINE	LTSLNRSEHS	RVALRSRQVL	IAAHQPAYEL	RHNQMESIFL
	1101				1150
BEMITA_QJQ31013	SAVDMYGHDF	HPENLQKLIQ	SETSIFDILH	DDFFYHTNRAV	CNAALEVYVR
MYZUPE_XP_022181497	SAVDMYGHDF	HPENLQKLIQ	SETSIFDILH	DDFFYHSNRAV	CNAALEVYVR
TRIAVA_ACCase	SAVDMYGHDF	HPENLQKLIQ	SETSIFDILH	DDFFYHTNRAV	CNAALEVYVR
2200	SAVDMYGHDF	HPENLQKLIQ	SETSIFDILH	DDFFYHTNRAV	CNAALEVYVR

319	SAVDMYGHDF	HPENLQKLIQ	SETSIFDILH	DDFYHTNRAV	CNAALEVYVR
419	SAVDMYGHDF	HPENLQKLIQ	SETSIFDILH	DDFYHTNRAV	CNAALEVYVR
520	SAVDMYGHDF	HPENLQKLIQ	SETSIFDILH	DDFYHTNRAV	CNAALEVYVR
619	SAVDMYGHDF	HPENLQKLIQ	SETSIFDILH	DDFYHTNRAV	CNAALEVYVR
	1151				1200
BEMITA_QJQ31013	RVYISYELTC	LKHLELTEEV	PLVQFQFLLP	SSHPNRQVRV	DSASPGRDAP
MYZUPE_XP_022181497	RVYISYDLTC	LQHLELSGEI	PLVHFQFLLP	SSHPNRQQNK	INSGAN...G
TRIAVA_ACCase	RVYISYDLTC	LQHLELSGEI	PLVQFQFLLP	SSHPNRQKVT	DSSPIKADTP
2200	RVYISYELTC	LQHLELSGEV	PLVQFQFLLP	SSHPNRQKVT	DPSSPIIAD.
319	RVYISYELTC	LQHLELSGEV	PLVQFQFLLP	SSHPNRQKVT	DPSSPIIAD.
419	RVYISYELTC	LQHLELSGEV	PLVQFQFLLP	SSHPNRQKVT	DPSSPIIAD.
520	RVYISYELTC	LQHLELSGEV	PLVQFQFLLP	SSHPNRQKVT	DPSSPIIAD.
619	RVYISYELTC	LQHLELSGEV	PLVQFQFLLP	SSHPNRQKVT	DPSSPIIAD.
	1201				1250
BEMITA_QJQ31013	..ETDMTASA	APTVIHSYQR	TGCMAAFESF	DQFESYYDEI	LDLLDEL.SP
MYZUPE_XP_022181497	SENLESPKT	PLPYIPTYQR	TGCMAAFESF	TQFEQYFDEI	LDIMEDLSSP
TRIAVA_ACCase	PPEIEAGQSS	APTIIHSYQR	TGCMAAFESF	DQFESYYDEI	LDLLDDLMS
2200	SPETEEPPSS	TPTIIHSYQR	TGCMAAFESF	DQFESYYDEI	LDLLDEL.SP
319	SPETEEPPSS	TPTIIHSYQR	TGCMAAFESF	DQFESYYDEI	LDLLDEL.SP
419	SPETEEPPSS	TPTIIHSYQR	TGCMAAFESF	DQFESYYDEI	LDLLDEL.SP
520	SPETEEPPSS	TPTIIHSYQR	TGCMAAFESF	DQFESYYDEI	LDLLDEL.SP
619	SPETEEPPSS	TPTIIHSYQR	TGCMAAFESF	DQFESYYDEI	LDLLDEL.SP
	1251				1300
BEMITA_QJQ31013	STVSPRIMEA	LESGSES RMS	TSINVSLSD	.TORPAGGEE	GLQVEPIHIL
MYZUPE_XP_022181497	VYVSPRIIDA	LESGSESRLS	SSLNVSLSLG	DQRPPD..QE	NVEIEPCHIL
TRIAVA_ACCase	STVSPRIMEA	LESGSES RMS	TSINVSLSVS	DNPRPPGLEE	GLQVEPIHIL
2200	STISPRIMEA	LESGSES RMS	TSINVSLSVG	DNPRPPGLED	GLQVEPIHIL
319	STISPRIMEA	LESGSES RMS	TSINVSLSVG	DNPRPPGLED	GLQVEPIHIL
419	STISPRIMEA	LESGSES RMS	TSINVSLSVG	DNPRPPGLED	GLQVEPIHIL
520	STISPRIMEA	LESGSES RMS	TSINVSLSVG	DNPRPPGLED	GLQVEPIHIL
619	STISPRIMEA	LESGSES RMS	TSINVSLSVG	DNPRPPGLED	GLQVEPIHIL
	1301				1350
BEMITA_QJQ31013	CIAVKDNGDL	EDDKLSKMF	DFCAKNRDEL	KEKSIRRITF	LALNRRQFPK
MYZUPE_XP_022181497	CIAMKDTGNM	EDDKLGKMYE	EFCQRRREEL	KKRSIRRITF	LALNRRQFPK
TRIAVA_ACCase	CIAVKDNGDL	EDDKLSKLLG	DFCARHRDEL	KEKSIRRITF	LALNRRQFPK
2200	CIAVKDNGDL	EDEKLSKLLG	DFCAKHREEL	KEKSIRRITF	LALNRRQFPK
319	CIAVKDNGDL	EDEKLSKLLG	DFCAKHREEL	KEKSIRRITF	LALNRRQFPK
419	CIAVKDNGDL	EDEKLSKLLG	DFCAKHREEL	KEKSIRRITF	LALNRRQFPK
520	CIAVKDNGDL	EDEKLSKLLG	DFCAKHREEL	KEKSIRRITF	LALNRRQFPK
619	CIAVKDNGDL	EDEKLSKLLG	DFCAKHREEL	KEKSIRRITF	LALNRRQFPK
	1351				1400
BEMITA_QJQ31013	LFTFRNCDNF	VEDRIYRHLE	PGMAFQLELN	RMKTYHLEAL	PTSNRKMYLY
MYZUPE_XP_022181497	LFTYRNYEDF	AEDRIYRHLE	PGMAFQLELN	RMRTYELEAL	PTSNRKMYLY
TRIAVA_ACCase	LFTFRNCDNF	VEDRIYRHLE	PGMAFQLELN	RMKTYHLEAL	PTSNRKMYLY
2200	LFTFRNCDNF	VEDRIYRHLE	PGMAFQLELN	RMKTYHLEAL	PTSNRKMYLY
319	LFTFRNCDNF	VEDRIYRHLE	PGMAFQLELN	RMKTYHLEAL	PTSNRKMYLY
419	LFTFRNCDNF	VEDRIYRHLE	PGMAFQLELN	RMKTYHLEAL	PTSNRKMYLY
520	LFTFRNCDNF	VEDRIYRHLE	PGMAFQLELN	RMKTYHLEAL	PTSNRKMYLY
619	LFTFRNCDNF	VEDRIYRHLE	PGMAFQLELN	RMKTYHLEAL	PTSNRKMYLY
	1401				1450
BEMITA_QJQ31013	LGKAKVAKGQ	EVTDYRFFIR	SIIRHSDLIT	KEASFEYLQN	EGERVLLLEAM
MYZUPE_XP_022181497	LGKAKVPRGQ	VVTDYRFFIR	SIIRHQDLIT	KEASFEYLQN	EGERVLLLEAM
TRIAVA_ACCase	LGKAKVAKGQ	EVTDYRFFIR	SIIRHSDLIT	KEASFEYLQN	EGERVLLLEAM

2200	LGRAKVAKGQ	EVTDFRFFIR	SIIRHSDLIT	KEASFEYLQN	EGERVLLLEAM
319	LGRAKVAKGQ	EVTDFRFFIR	SIIRHSDLIT	KEASFEYLQN	EGERVLLLEAM
419	LGRAKVAKGQ	EVTDFRFFIR	SIIRHSDLIT	KEASFEYLQN	EGERVLLLEAM
520	LGRAKVAKGQ	EVTDFRFFIR	SIIRHSDLIT	KEASFEYLQN	EGERVLLLEAM
619	LGRAKVAKGQ	EVTDFRFFIR	SIIRHSDLIT	KEASFEYLQN	EGERVLLLEAM
	1451			1500	
BEMITA_QJQ31013	DELEVAFSHP	LAKRTDCNHI	FLNFVPTVIM	DSAKIEESVT	NMVMRYGPRL
MYZUPE_XP_022181497	DELEVAFSHP	HARRTDCNHI	FLNFVPTVIM	DPAKIKESVT	NMVMRYGPRL
TRIAVA_ACCase	DELEVAFSHP	LAKRTDCNHI	FLNFVPTVIM	DSAKIEESVT	NMVMRYGPRL
2200	DELEVAFSHP	LARRTDCNHI	FLNFVPTVIM	DSAKIEESVT	NMVMRYGARL
319	DELEVAFSHP	LARRTDCNHI	FLNFVPTVIM	DSAKIEESVT	NMVMRYGARL
419	DELEVAFSHP	LARRTDCNHI	FLNFVPTVIM	DSAKIEESVT	NMVMRYGARL
520	DELEVAFSHP	LARRTDCNHI	FLNFVPTVIM	DSAKIEESVT	NMVMRYGARL
619	DELEVAFSHP	LARRTDCNHI	FLNFVPTVIM	DSAKIEESVT	NMVMRYGARL
	1501			1550	
BEMITA_QJQ31013	WKLRLVQAEL	RMTIRASPNA	KTTNVRLCLA	NDSGYLDIC	LYKEVDPKT
MYZUPE_XP_022181497	WKLRLVQAEL	RMTIRPSPTS	KTSNVRLSLA	NGSGYHLDIC	LYKEITDSKL
TRIAVA_ACCase	WKLRLVQAEL	RMTIRASPNS	KTTNVRLCLA	NDSGYLDIC	LYKEVDPKT
2200	WKLRLVQAEL	RMTIRTSPNS	KTTNVRLCLA	NDSGYLDIC	LYKEVDPKT
319	WKLRLVQAEL	RMTIRTSPNS	KTTNVRLCLA	NDSGYLDIC	LYKEVDPKT
419	WKLRLVQAEL	RMTIRTSPNS	KTTNVRLCLA	NDSGYLDIC	LYKEVDPKT
520	WKLRLVQAEL	RMTIRTSPNS	KTTNVRLCLA	NDSGYLDIC	LYKEVDPKT
619	WKLRLVQAEL	RMTIRTSPNS	KTTNVRLCLA	NDSGYLDIC	LYKEVDPKT
	1551			1600	
BEMITA_QJQ31013	GIKLESYGS	KQGPHGLPV	ATPYVTKDYL	QQKRFQAQSA	GTTYCHDIPD
MYZUPE_XP_022181497	GMIKFESYES	KQGPHGLPV	STPYVTKDFL	QQKRFQAQSA	GTTYVVDIPD
TRIAVA_ACCase	GIKLESYGS	KQGPVHGLPV	SLPYVTKDYL	QQKRFQAQSA	GTTYCHDIPD
2200	GIKLESYGS	KQGPHGLPT	AIPYVTKDYL	QQKRFQAQSA	GTTYCHDIPD
319	GIKLESYGS	KQGPHGLPT	AIPYVTKDYL	QQKRFQAQSA	GTTYCHDIPD
419	GIKLESYGS	KQGPHGLPT	AIPYVTKDYL	QQKRFQAQSA	GTTYCHDIPD
520	GIKLESYGS	KQGPHGLPT	AIPYVTKDYL	QQKRFQAQSA	GTTYCHDIPD
619	GIKLESYGS	KQGPHGLPT	AIPYVTKDYL	QQKRFQAQSA	GTTYCHDIPD
	1601			1650	
BEMITA_QJQ31013	MFRQMVERQW	KEHIDQRPDD	GIVKPAQLMD	FAELVLEEDH	LVEQKRLPGE
MYZUPE_XP_022181497	MFRQMIETLW	QEYILEHPND	GVLKSSLVFD	YVELVVEDNH	LIEQKRFSGE
TRIAVA_ACCase	MFRQMVERQW	KEHIEQRPND	GIVKPSQLMD	FVELVMEEDH	LIEVKRLSGE
2200	MFRQMVERQW	KEFIEQRPND	GIVKPSQLMD	YVELVLEDDH	LVEQKRLAGE
319	MFRQMVERQW	KEFIEQRPND	GIVKPSQLMD	YVELVLEDDH	LVEQKRLAGE
419	MFRQMVERQW	KEFIEQRPND	GIVKPSQLMD	YVELVLEDDH	LVEQKRLAGE
520	MFRQMVERQW	KEFIEQRPND	GIVKPSQLMD	YVELVLEDDH	LVEQKRLAGE
619	MFRQMVERQW	KEFIEQRPND	GIVKPSQLMD	YVELVLEDDH	LVEQKRLAGE
	1651			1700	
BEMITA_QJQ31013	NNVGMVAWRI	TLNTPEYPDG	RDIIIVIANDI	TVRIGSFGPE	EDLVFDLASK
MYZUPE_XP_022181497	NTAGMVAWRF	TMHTPEYPSG	RDIIIVIANDL	TVNIGSFGPQ	EDIVFDLASK
TRIAVA_ACCase	NNVGMVAWRI	TLNTPEYPDG	RDIIIVIANDI	TVRIGSFGPE	EDIVFDLASK
2200	NTIGMVAWRI	TLNTPEYPDG	REIIVIANDI	TVRIGSFGPE	EDLVFDLASK
319	NTIGMVAWRI	TLNTPEYPDG	REIIVIANDI	TVRIGSFGPE	EDLVFDLASK
419	NTIGMVAWRI	TLNTPEYPDG	REIIVIANDI	TVRIGSFGPE	EDLVFDLASK
520	NTIGMVAWRI	TLNTPEYPDG	REIIVIANDI	TVRIGSFGPE	EDLVFDLASK
619	NTIGMVAWRI	TLNTPEYPDG	REIIVIANDI	TVRIGSFGPE	EDLVFDLASK
	1701			1750	
BEMITA_QJQ31013	IARQRKIPRI	YIAANS GARI	GLAE EVKSLF	RV AWEDPDEP	DKGFKYLYLS
MYZUPE_XP_022181497	EARRKKIPRI	YISANS GARI	GLAE EIKSLF	NV AWEDPSDP	EKGFKYLYLT

TRIAVA_ACCase	IARARKIPRI	YIAANSGARI	GLAEVKSFL	RVAWEDPDEP	DKGFKYLYLS
2200	IARQMKVPRI	YIAANSGARI	GLAEVKSFL	RVAWEDPDEP	DKGLKYLYLS
319	IARQMKVPRI	YIAANSGARI	GLAEVKSFL	RVAWEDPDEP	DKGLKYLYLS
419	IARQMKVPRI	YIAANSGARI	GLAEVKSFL	RVAWEDPDEP	DKGLKYLYLS
520	IARQMKVPRI	YIAANSGARI	GLAEVKSFL	RVAWEDPDEP	DKGLKYLYLS
619	IARQMKVPRI	YIAANSGARI	GLAEVKSFL	RVAWEDPDEP	DKGLKYLYLS
BEMITA_QJQ31013	TEDFTKISSC	NSVHAILIED	EGEARYKITD	IIGKEDGLGV	ENLRYAGMIA
MYZUPE_XP_022181497	PDDYGKLAGQ	NSVEAELIED	EGEPYKLT	IIGKDFGYGV	ENLKFAGMIA
TRIAVA_ACCase	TEDFTKISSL	NSVHAILIED	EGEARYKITD	IIGKEDGLGV	ENLRYAGMIA
2200	TEDFIKISAC	NSVRAILIED	EGEARYKITD	IIGKEDGLGV	ENLRYAGMIA
319	TEDFIKISAC	NSVRAILIED	EGEARYKITD	IIGKEDGLGV	ENLRYAGMIA
419	TEDFIKISAC	NSVRAILIED	EGEARYKITD	IIGKEDGLGV	ENLRYAGMIA
520	TEDFIKISAC	NSVRAILIED	EGEARYKITD	IIGKEDGLGV	ENLRYAGMIA
619	TEDFIKISAC	NSVRAILIED	EGEARYKITD	IIGKEDGLGV	ENLRYAGMIA
BEMITA_QJQ31013	GETSEAYREI	VTISMVSCRA	IGIGAYLVRL	GQRVIQVENS	HIILTGYSAL
MYZUPE_XP_022181497	GETSRAYQDI	VTISMVTCRA	IGIGAYLVRL	GQRVIQIENS	HIILTGYSAL
TRIAVA_ACCase	GETSEAYREI	VTISMVSCRA	IGIGAYLVRL	GQRVIQVENS	HIILTGYSAL
2200	GETSEAYREI	VTISMVSCRA	IGIGAYLVRL	GQRVIQVENS	HIILTGYSAL
319	GETSEAYREI	VTISMVSCRA	IGIGAYLVRL	GQRVIQVENS	HIILTGYSAL
419	GETSEAYREI	VTISMVSCRA	IGIGAYLVRL	GQRVIQVENS	HIILTGYSAL
520	GETSEAYREI	VTISMVSCRA	IGIGAYLVRL	GQRVIQVENS	HIILTGYSAL
619	GETSEAYREI	VTISMVSCRA	IGIGAYLVRL	GQRVIQVENS	HIILTGYSAL
BEMITA_QJQ31013	NKLLGREVYA	SNNQLGGIQI	MYNNGVSHKT	EPRDLGDIYS	IVKWL SYIPK
MYZUPE_XP_022181497	NKLLGREVYA	SNNQLGGIQI	MYNNGVSHKT	EARDLDGVYR	ILKWL SYIPK
TRIAVA_ACCase	NKLLGREVYA	SNNQLGGIQI	MHNNGVSHKT	EPRDLGDIYS	IVKWLAFVPK
2200	NKLLGREVYA	SNNQLGGIQI	MYNNGISHKT	EPRDLGDIYS	IVKWLGYIPK
319	NKLLGREVYA	SNNQLGGIQI	MYNNGISHKT	EPRDLGDIYS	IVKWLGYIPK
419	NKLLGREVYA	SNNQLGGIQI	MYNNGISHKT	EPRDLGDIYS	IVKWLGYIPK
520	NKLLGREVYA	SNNQLGGIQI	MYNNGISHKT	EPRDLGDIYS	IVKWLGYIPK
619	NKLLGREVYA	SNNQLGGIQI	MYNNGISHKT	EPRDLGDIYS	IVKWLGYIPK
BEMITA_QJQ31013	DKLSPVPVIK	PADPIDREVG	YMPTKTPYDP	RWMLAGRYSP	.NNSNEWESG
MYZUPE_XP_022181497	TKESPLPVIK	SVDSVERDID	YVPTKVPYDP	RWMIAGKE..	.DTNGHWESG
TRIAVA_ACCase	DKMSPVPVLK	PADPVDREVG	YMPTKTPYDP	RWMLAGHFSF	LDSSNEWESG
2200	DKYSPVPVIK	PADPVDREVG	YMPTKTPYDP	RWMIAGRYSP	.NNSNEWESG
319	DKYSPVPVIK	PADPVDREVG	YMPTKTPYDP	RWMIAGRYSP	.NNSNEWESG
419	DKYSPVPVIK	PADPVDREVG	YMPTKTPYDP	RWMIAGRYSP	.NNSNEWESG
520	DKYSPVPVIK	PADPVDREVG	YMPTKTPYDP	RWMIAGRYSP	.NNSNEWESG
619	DKYSPVPVIK	PADPVDREVG	YMPTKTPYDP	RWMIAGRYSP	.NNSNEWESG
BEMITA_QJQ31013	FFDEGSWEEV	MQPWAQTVVV	GRARLGGIPM	GVIAVETRTV	EVKLPADPAN
MYZUPE_XP_022181497	FFDKGSWDEI	MQPWAQTVVC	GRARLGGIPV	GVIAVETRTV	EVTLPADPAN
TRIAVA_ACCase	FFDEGTWEEV	MQPWAQTVVV	GRARLGGIPM	GVIAVETRTV	ELKWPADPAN
2200	FFDEGSWEEV	MQPWAQTVVV	GRARLGGIPM	GVIAVETRTV	EVKLPADPAN
319	FFDEGSWEEV	MQPWAQTVVV	GRARLGGIPM	GVIAVETRTV	EVKLPADPAN
419	FFDEGSWEEV	MQPWAQTVVV	GRARLGGIPM	GVIAVETRTV	EVKLPADPAN
520	FFDEGSWEEV	MQPWAQTVVV	GRARLGGIPM	GVIAVETRTV	EVKLPADPAN
619	FFDEGSWEEV	MQPWAQTVVV	GRARLGGIPM	GVIAVETRTV	EVKLPADPAN
BEMITA_QJQ31013	LDSEAKTLSQ	AGQVWFPDSA	YKTAQAIKDF	EHEDLPLIIF	ANWRGFSGGM

MYZUPE_XP_022181497	LDSEKTVSQ	AGQVWFPDSA	YKTSQAIKDF	AHEDLPLFIF	ANWRGFSGGM
TRIAVA_ACCase	LDSEAKTLSQ	AGQVWFPDSA	YKTAQAIKDF	QHEDLPLIIF	ANWRGFSGGM
2200	LDSEAKTLSQ	AGQVWFPDSA	FKTAQAIKDF	EHEDLPLIIF	ANWRGFSGGM
319	LDSEAKTLSQ	AGQVWFPDSA	FKTAQAIKDF	EHEDLPLIIF	ANWRGFSGGM
419	LDSEAKTLSQ	AGQVWFPDSA	FKTAQAIKDF	EHEDLPLIIF	ANWRGFSGGM
520	LDSEAKTLSQ	AGQVWFPDSA	FKTAQAIKDF	EHEDLPLIIF	ANWRGFSGGM
619	LDSEAKTLSQ	AGQVWFPDSA	FKTAQAIKDF	EHEDLPLIIF	ANWRGFSGGM

	2051		A2083V	2100
BEMITA_QJQ31013	KDMYEQVMKF	GAYIVDELRV	YKQPVIIYIP	PNGELRGGAW
MYZUPE_XP_022181497	KDMYEQIMKF	GAYIVDELRL	YNQPIITYIP	PFGE LRGGAW
TRIAVA_ACCase	KDMYEQVMKF	GAYIVDELRL	YKQPVIIYIP	PNGELRGGAW
2200	KDMYEQVMKF	GAYIVDELRV	YKQPVIIYIP	PNGELRGGAW
319	KDMYEQVMKF	GAYIVDELRV	YKQPVIIYIP	PNGELRGGAW
419	KDMYEQVMKF	GAYIVDELRV	YKQPVIIYIP	PNGELRGGAW
520	KDMYEQVMKF	GAYIVDELRV	YKQPVIIYIP	PNGELRGGAW
619	KDMYEQVMKF	GAYIVDELRV	YKQPVIIYIP	PNGELRGGAW

	2101			2150
BEMITA_QJQ31013	HMEMYADPES	RGGVLEPEGI	VEIKFREKDI	LKTMHRIDQV
MYZUPE_XP_022181497	HIEMYADPES	RGGVLEPEGI	VEIKFREKDI	LKSINRIDTN
TRIAVA_ACCase	YMEMYADPES	RGGVLEPEGI	VEIKFREKDI	LKTMHRIDQI
2200	HMEMYADPES	RGGVLEPEGI	VEIKFREKDI	LKTMHRIDQV
319	HMEMYADPES	RGGVLEPEGI	VEIKFREKDI	LKTMHRIDQV
419	HMEMYADPES	RGGVLEPEGI	VEIKFREKDI	LKTMHRIDQV
520	HMEMYADPES	RGGVLEPEGI	VEIKFREKDI	LKTMHRIDQV
619	HMEMYADPES	RGGVLEPEGI	VEIKFREKDI	LKTMHRIDQV

	2151			2200
BEMITA_QJQ31013	TDISPEEKAD	VESRIVEREQ	YLKPMYHQA	VHFADLHDTF
MYZUPE_XP_022181497	ASPTPEEA	IEKNVAERIS	VLKPIYHQA	IHFADLHDTF
TRIAVA_ACCase	PDISPEEKAE	VENQIVEREQ	YLKPMYHQA	VHFADLHDTF
2200	PDISPEEKAE	VENQIVEREQ	YLKPMYHQA	IHFADLHDTF
319	PDISPEEKAE	VENQIVEREQ	YLKPMYHQA	IHFADLHDTF
419	PDISPEEKAE	VENQIVEREQ	YLKPMYHQA	IHFADLHDTF
520	PDISPEEKAE	VENQIVEREQ	YLKPMYHQA	IHFADLHDTF
619	PDISPEEKAE	VENQIVEREQ	YLKPMYHQA	IHFADLHDTF

	2201			2250
BEMITA_QJQ31013	DIVPWRKSRT	ILHWRVKRLL	LENQIKSNLL	KVQPQMDGQ
MYZUPE_XP_022181497	DIVQWKKSRN	TLYWRVKRLL	LQNQIQKVIT	KSNDTIQDDV
TRIAVA_ACCase	DIVPWRKSRS	IIHWRMKRLL	LENQIKSNLI	RVQPQLDDGQ
2200	NIVPWRKSRT	LLHWRVKRLL	LENQIKCNLL	KVQPQMDNGQ
319	NIVPWRKSRT	LLHWRVKRLL	LENQIKCNLL	KVQPQMDNGQ
419	NIVPWRKSRT	LLHWRVKRLL	LENQIKCNLL	KVQPQMDNGQ
520	NIVPWRKSRT	LLHWRVKRLL	LENQIKCNLL	KVQPQMDNGQ
619	NIVPWRKSRT	LLHWRVKRLL	LENQIKCNLL	KVQPQMDNGQ

	2251			2300
BEMITA_QJQ31013	EDIGTTTAYL	WENNESVWSW	LMGQLS.PDG	SISPNSIVAN
MYZUPE_XP_022181497	EDKGTASYL	WDNNQAVVQW	LTSQLEDSDG	TIVADSLIGN
TRIAVA_ACCase	EDKGTTTAYL	WENNESVWSW	LMTQLS.PDG	SISPNSIVAN
2200	EDKGTTTAYL	WENNESVVAW	LMSQLS.PDG	SISPNSIVAN
319	EDKGTTTAYL	WENNESVVAW	LMSQLS.PDG	SISPNSIVAN
419	EDKGTTTAYL	WENNESVVAW	LMSQLS.PDG	SISPNSIVAN
520	EDKGTTTAYL	WENNESVVAW	LMSQLS.PDG	SISPNSIVAN
619	EDKGTTTAYL	WENNESVVAW	LMSQLS.PDG	SISPNSIVAN

2301				2350
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BEMITA_QJQ31013	INQIKSMEE	SPDVAQDAVV	EMFQTLSASE	RSEVLRKLSH	LETISKPEPQ
MYZUPE_XP_022181497	INQVKSTIND	TPEVTSDVIM	GMFQSLSEMQ	RLDLIHNLTQ	ATSIGNVKLN
TRIAVA_ACCase	INQIKSMEE	SPDVAQDAVV	EMFQALSSSE	RSEVLRKLSH	LEMINSSEPQ
2200	INQIKSMEE	SPDVAQDAVV	EMFQTLSANE	RSEVLRKLSH	LETISKPEPQ
319	INQIKSMEE	SPDVAQDAVV	EMFQTLSANE	RSEVLRKLSH	LETISKPEPQ
419	INQIKSMEE	SPDVAQDAVV	EMFQTLSANE	RSEVLRKLSH	LETISKPEPQ
520	INQIKSMEE	SPDVAQDAVV	EMFQTLSANE	RSEVLRKLSH	LETISKPEPQ
619	INQIKSMEE	SPDVAQDAVV	EMFQTLSANE	RSEVLRKLSH	LETISKPEPQ

	2351
BEMITA_QJQ31013	S~
MYZUPE_XP_022181497	S~
TRIAVA_ACCase	NS
2200	S~
319	S~
419	S~
520	S~
619	S~