

	1	10	20	30	40	50	60
lac1338	MNRRDFLVTTSAATLFPRIALASAPVELVAQPVNAQILPEGEPATPMLGFNGGTPGPVLR						
4F7K_A
WP_106610581.1
WP_035257147.1
WP_058289265.1
WP_054463654.1
MBA84203.1
MBT24881.1
OIQ43611.1
WP_167685249.1

	70	80	90	100	110	120
lac1338	ARQGEVFDIRFQNQIGEGL	V HWHGLR	I DNAMDGVPGMTQDVV	E AGGEFE	YSFRAPDAGT	
4F7K_A
WP_106610581.1	.	V HWHGLR	I DNAMDGVPGMTQDVV	NAGGEFE	YRFRAPDAGT	
WP_035257147.1	.	V HWHGLR	I DNAMDGVPGMTQDVV	E AGDGFE	YRFRAPDAGT	
WP_058289265.1	.	V HWHGLR	I DNAMDGVPGMTQDVV	EVDAEFA	YRFRAPDAGT	
WP_054463654.1	.	V HWHGLR	S DNAMDGVPGLTQDVV	E AGSEFA	YRFRAPDAGT	
MBA84203.1	.	V HWHGLR	I DN TMDGVPGMTQGVV	S AGDAFA	YRFRAPDAGT	
MBT24881.1	.	V HWHGLR	I NNAMDGVPGMTQDVV	E KGGELG	YRFRAPDAGT	
OIQ43611.1	.	V HWHGLR	S DNAMDGVPGLTQDIV	QSGDHFD	YRFRAPDAGT	
WP_167685249.1	.	V HWHGLR	S DNAMDGVPGLTQDIV	QSGDHFD	YRFRAPDAGT	

	130	140	150	160	170	180
lac1338	F WYHS HNRSWEQVA	K GLYGPLIVEEP	T PPDVDHDLLIMIDDWR	I TE NGVLAGDFENMRDQ		
4F7K_A	F WYHS HNRSWEQVA	K GLYGPLIVEEP	T PPDVDHDLLIMIDDWR	I TE NGVLAGDFENMRDQ		
WP_106610581.1	F WYHS HNRSWEQVA	K GLYGPLIVEEP	T PPDVDHDLLIMIDDWR	I TE NGVLAGDFENMRDQ		
WP_035257147.1	F WYHS HNRSWEQVA	K GLYGPLIVEEP	T PPDVDHDLLIMIDDWR	I TE NGVLAGDFENMRDQ		
WP_058289265.1	F WYHS HNRSWEQVA	K GLYGPLIVEEP	T PPDVDHDLLIMIDDWR	I TE NGVLAGDFENMRDQ		
WP_054463654.1	F WYHS HNRSWEQVA	K GLYGPLIVEEP	T PPDVDHDLLIVLIMDDWR	MTE AGT LADGFENMHDQ		
MBA84203.1	F WYHA HNRSWEQVA	R GLYGPLIVEEQ	T PPDVDHDLLIVLIMDDWR	MTE AGT LAEGFENMHDQ		
MBT24881.1	F WYHA HNRSWEQVA	R GLYGPLIVEEQ	T PPDVDHDLLIVLIMDDWR	MTE AGT LAEGFENMHDQ		
OIQ43611.1	F WYHS HNRSWEQVA	R GLYGPLIVEEQ	T PPDVDHDLLIVLIMDDWR	MTD SGT LADDFFDNRHHDQ		
WP_167685249.1	F WYHS HNRSWEQVA	R GLYGPLIVEEQ	T PPDVDHDLLIVLIMDDWR	MTD SGT LADDFFDNRHHDQ		

	190	200	210	220	230	240
lac1338	A HQGR LGNFARA LVEP	V TP VRRGDR VRLRLINVATDRIFP	V ELEG VEGKVVALDGMP	I VD		
4F7K_A	A HQGR LGNFARA LVEP	V TP VRRGDR VRLRLINVATDRIFP	V ELEG VEGKVVALDGMP	I VD		
WP_106610581.1	A HQGR LGNFARA HVEP	V PRQVRGDR VRLRLINVATDRIFP	V ELEG VEGKVVALDGMP	L ES		
WP_035257147.1	A HQGR LGNFARA HVEP	V PRQVRGDR VRLRLINVATDRIFP	V ELEG VEGKVVALDGMP	L ES		
WP_058289265.1	A HQGR LGNFARA LVEP	S TP VRRGDR VRLRLINVATDRIFP	V ELEG VEGKVVALDGMP	L VS		
WP_054463654.1	A HQGR LGNYARA LVEP	S TP VRRGDR VRLRLINVATDRIFP	V ELEG VEGKVVALDGMP	L SD		
MBA84203.1	A HQGR LGNFARA LIVPS	S TP PARRGDRL RLRLLINVATDRIFP	V ELEG VEGKVVALDGMP	L GR		
MBT24881.1	A HQGR LGNFARA LIVPS	S TP PARRGDRL RLRLLINVATDRIFP	V ELEG VEGKVVALDGMP	L GR		
OIQ43611.1	A HQGR LGNFARA LIVPS	S TP PARRGDRL RLRLLINVATDRIFP	V ELEG VEGKVVALDGMP	L VS		
WP_167685249.1	A HQGR GMGNFARA I INTKA P VQTDRDL RLRLLINVATDRIFP	I DLDI GIEGKVVALDGMP	L AE			

	250	260	270	280	290	300
lac1338	P QEF S GLI LAPAQR ADIIADVI	T DAP I G FVFP TRDGPYL LGE	I PVKGANNT	T RQPS EI PAL		
4F7K_A	P QEF S GLI LAPAQR ADIIADVI	T DAP I G FVFP TRDGPYL LGE	I PVKGANNT	T RQPS EI PAL		
WP_106610581.1	L QEL S GLI LAPAQR ADIIADVI	S ATSATAS FAFPT RDGPYL LGE	I PVVEGSNIT	T RQPS EI STL		
WP_035257147.1	P QEMSGL II LAPAQR ADIIADVI	S AFVSPTRDGPYL LGE	I PVVEGANNT	T RQPS EI SVL		
WP_058289265.1	P QEL LSS II LAPAQR ADIIADVI	S TSDPQIA FMFPT QDGPYL LGE	I PVVEDANTER	T RQPS EI SAL		
WP_054463654.1	P HEI SDF I LAPAQR DIIADVI	S SDQVIA FVFPT RDGPYL LGE	V PVVA GENT	T RQPS VV RAL		
MBA84203.1	P QEI LSGVL LAPAQR ADIIADVI	S VVSDAPVIA FVFRT QDGPYL LGE	I PVVEGVNSMRQASEISAL			
MBT24881.1	P QEL SGLV LAPAQR ADIIADVI	S VVSDAPVIA FVFRT QDGPYL LGE	I PVVEGVNSMRQASEISAL			
OIQ43611.1	P QEL SDLV LAPAQR ADIIADVI	S VVSDANSV SI FPLPTRDAPVYL LGE	I QVEGKNTRR QPTDIP TL			
WP_167685249.1	P QDI SGLV LAPAQR ADIIADVI	S SDNVQ FVFPT RDDPYV LGE	I ALEGTNNN RAA SDI LPL			

	310	320	330	340	350	360
lac1338	P PN EVT SPDMG SAVS LTL TM EGGA MRS MMQ GMMGG	D I WA FNQ QSL TD TP LHSF ERGQT				
4F7K_A	P PN EVT SPDMG SAVS LTL TM EGGA MRS MMQ GMMGG	D I WA FNQ QSL TD TP LHSF ERGQT				
WP_106610581.1	T QNEVASPDM DNA IS LTL TM EGGA MRS MMQ GMMDDW	N I WA FNQ QSL TD TP LHSF ERGQT				
WP_035257147.1	T QNEI ASPDM DNA IS LTL TM EGGA MRS MMQ GMMGG	D I WA FNQ QSL TD TP LHSF ERGKT				
WP_058289265.1	L PNEV T QPD LD NAVS LTL TM EGGA MRS MMQ GMMGG	D I WA FNQ QSL TD TP FHL FERGQT				
WP_054463654.1	P ANET A QPD MG NAI PLTL TM QGGAM SRR MMQ GMAGG	G I WA FNQ QSL TD TP FHL FERGQT				
MBA84203.1	P PNEMA Q PDM DNA IS LTL TM EGGA MRS MMQ GMMGG	N I WA FNQ QSL TD TP HAFERGQT				
MBT24881.1	P PNEMA Q PDM DNA IS LTL TM EGGA MRS MMQ GMMGG	N I WA FNQ QSL TD TP HAFERGQT				
OIQ43611.1	P PN KAV RPD MG NAVS LTL TM EGGA MRS MMQ GMMGG	E I WAL NGQ SGLKD TP FHSF ENGQT				
WP_167685249.1	P VN TMA Q PDL DNA IS LTL TM EGGA MRS PRSSS . LT	D I WG FNQ QSL NDAP FHSF ERGQT				

	3 7 0	3 8 0	3 9 0	4 0 0	4 1 0	4 2 0
lac1338	ARI R I V N D T R F P H G I H L H G H H F F E V G A D G N L G A L R D T T L V D A G E T R D I V C V F D N P G N W L L					
4F7K_A	ARI R I V N D T R F P H G I H L H G H H F F E V G A D G N L G A L R D T T L V D A G E T R D I V C V F D N P G N W L L					
WP_106610581.1	ARI R I V N D T R F P H G I H L H G H H F F E L G L D G S Q G A F R D T T L V D A G K S R D I V C V F D N P G R W L L					
WP_035257147.1	ARI R I V N D T R F P H G I H L H G H H F F E V G A D G N L G A L R D T T L V D A D E T R D I V C V F G N P G R W L L					
WP_058289265.1	ARI R I V N D T R F P H G I H L H G H H F F E V R A D N N L G A F R D T T L V D A G E A R D I V C V F D N P G K W L L					
WP_054463654.1	ARI R I V N D T S F A H G I H L H G H H F F E V E A D G D L G A L R D T T L V D A G E T R D I V C V F D N P G R W L L					
MBA84203.1	ARI R I V N D T R F P H G I H L H G H H F F E V E T D G T L G A L R D T T L V D A G E S R D I V C V F D N P G K W L L					
MBT24881.1	ARI R I V N D T R F P H G I H L H G H H F F E V E T D G T L G A L R D T T L V D A G E S R D I V C V F D N P G K W L L					
OIQ43611.1	ARI R I V N D T R F A H G I H L H G H H F F E V G G D S L G A F R D T T L V E P G E T R D I V C V F D N P G K W L L					
WP_167685249.1	ARI S M V N D T R F P H G I H L H G H H F F E V Q A D G M L G A F R D T T L V T P G E T R D I L C I F D N P G K W L L					

	4 3 0
lac1338	H C H M L G H Q A A G M K T W V E V A
4F7K_A	H C H M L G H Q A A G M K T W V E V A L E H H H H H
WP_106610581.1	H C H M L G H Q A A G M K T W V E V V
WP_035257147.1	H C H M L G H Q A A G M K T W V E V A
WP_058289265.1	H C H M L G H Q A A G M K T W V E V V
WP_054463654.1	H C H M L G H Q A A G M K T W V E V V
MBA84203.1	H C H M L G H Q A A G M K T W V Q V T
MBT24881.1	H C H M L G H Q A A G M K T W V Q V T
OIQ43611.1	H C H M L G H Q A A G M K T W V E V V
WP_167685249.1	H C H M L G H Q A A G M K T W L E V S