

	1					50
E2_5	MRGSHHHHHH	GSDLGKKLLE	AARAGQDDEV	RILMANGADV	NARDFWGHTP	
E2_17	MRGSHHHHHH	GSDLGKKLLE	AARAGQDDEV	RILMANGADV	NAMDYYGSTP	
E3_5	MRGSHHHHHH	GSDLGKKLLE	AARAGQDDEV	RILMANGADV	NATDNDGYTP	
E3_19	MRGSHHHHHH	GSDLGKKLLE	AARAGQDDEV	RILMANGADV	NAEDTYGDTP	
E4_2	MRGSHHHHHH	GSDLGKKLLE	AARAGQDDEV	RILMANGADV	NADDQHGNTP	
E4_8	MRGSHHHHHH	GSDLGKKLLE	AARAGQDDEV	RILMANGADV	NARDRDGNTP	
Consensus	MRGSHHHHHH	GSDLGKKLLE	AARAGQDDEV	RILMANGADV	NA <u>XDXXG</u> XTP	

	51					100
E2_5	LHLAATEGHL	EIVEVLLKYG	ADVNDARDAAG	FTPLHLAADN	GHLEIVEVLL	
E2_17	LHLAAYNGHL	EIVEVLLKNG	ADVNAKDFQG	ETPLHLAANN	GHLEIVEVLL	
E3_5	LHLAASNGHL	EIVEVLLKNG	ADVNASDLTG	ITPLHLAAAT	GHLEIVEVLL	
E3_19	LHLAARVGHL	EIVEVLLKNG	ADVNALDFSG	STPLHLAAKR	GHLEIVEVLL	
E4_2	LHLAASKGHL	EIVEVLLKHG	ADVNaNDTNG	TTPLHLAAQA	GHLEIVEVLL	
E4_8	LHLAADMGHL	EIVEVLLKNG	ADVNAADDVTG	FTPLHLAAVW	GHLEIVEVLL	
Consensus	LHLA <u>AXXG</u> HGL	EIVEVLLK <u>ZG</u>	ADVNA <u>XDXXG</u>	<u>XTPLHLA</u> <u>AXX</u>	GHLEIVEVLL	

	101					150
E2_5	KNGADVNA..	
E2_17	KNGADVNA..	
E3_5	KHGADVNAVYD	NDGHTPLHLA	AKYGHLEIVE	VLLKHGADVNA	A.....	
E3_19	KYGADVNAADD	TIGSTPLHLA	ADTGHLEIVE	VLLKYGADVNA	A.....	
E4_2	KHGADVNASD	ELGSTPLHLA	ATHGHLEIVE	VLLKYGADVNA	ADDTVGITPL	
E4_8	KNGADVNAID	TIGYTPLHLA	ANNGHLEIVE	VLLKNGADVNA	AHDTNGVTPL	
Consensus	K <u>ZG</u> ADVNA <u>XD</u>	<u>XXGXT</u> PLHLA	<u>AXXG</u> HLEIVE	VLLK <u>ZG</u> ADVNA	<u>AXDXXGXT</u> PL	

	151					199
E2_5QDKFGK	TAFDISIDNG	NEDLAEILQ	
E2_17QDKFGK	TAFDISIDNG	NEDLAEILQ	
E3_5QDKFGK	TAFDISIDNG	NEDLAEILQ	
E3_19QDKFGK	TAFDISIDNG	NEDLAEILQ	
E4_2	HLAAFFGHLE	IVEVLLKYGA	DVNAQDKFGK	TAFDISIDNG	NEDLAEILQ	
E4_8	HLAAHEGHLE	IVEVLLKYGA	DVNAQDKFGK	TAFDISIDNG	NEDLAEILQ	
Consensus	HLA <u>AXXG</u> HLE	IVEVLLK <u>ZG</u> A	DVNAQDKFGK	TAFDISIDNG	NEDLAEILQ	