

	1	10	20	30	40	50	60		
<i>CMLV_M96_18</i>	MSSIRFIA	GLYLISVFGN	CHE	DPYYQPFDKL	NLDIYTYEDLV	PYTVNDL	PNPNDDTTS	SVFK	64
<i>HSPV9_023</i>	MSSIRFIA	GLGLIFVLVGN	CHD	DPYYQPFNKL	NLDIYTYEDLV	PYTVDN	.....	DTTSFVK	57
<i>CPXV_GRI_C12L</i>	MSSIRFIA	GLGLISVLVGN	CHD	DPYYQPFDKL	NLDIYTYEDLV	PYTVNDL	LPNPNDTTS	SVFK	64
<i>CPXV_BRI_028</i>	MTAIRFIA	GLGLISVFGN	CRV	DPYYQPFDKL	NLDIYTYEDLV	PYTVNDL	LPNPNDTTS	SVFK	65
<i>CPXV_GER91_026</i>	MSSIRFIA	GLYLISVIFGN	CHD	DPYYQPFDKL	NLDIYTYEDLV	PYTVNDL	PNPNDDTTS	SVFK	64
<i>VACV_WR_C8L</i>	MSSIRFIA	GLYLISVIFGN	CHE	DPYYQPFNKL	NLDIYTYEDLV	PYTVDN	.....	DTTSFVK	57

  

	70	80	90	100	110	120		
<i>CMLV_M96_18</i>	IYFKNFWITVMTKW	CASFIDTVSLY	ISHDNLN	IOFYTRDEY	DTQSEDK	GTIDVKAR	CNHLTKRE	129
<i>HSPV9_023</i>	IYFKNFWITVMTKW	CAPFIDTVSVY	TSHDNLN	IEFYTRDEY	DTQSEDK	GTIDVKAR	CNHLTKRE	122
<i>CPXV_GRI_C12L</i>	IYFKNFWITVMTKW	CAPFIDTVSVY	TSHDNLN	IOFYTRDEY	DTQSEDK	GTIDVKAR	CNHLTKRE	129
<i>CPXV_BRI_028</i>	IYFKNFWITVMTKW	CAPFIDTVSVY	TSHDNLN	IOFYTRDEY	DTQSEDK	GTIDVKAR	CNHLTKRE	130
<i>CPXV_GER91_026</i>	IYFKNFWITVMTKW	CAPFIDTVSVY	TSHDNLN	IEFYTRDEY	DTQSEDK	GTIDVKAR	CNHLTKRE	130
<i>VACV_WR_C8L</i>	IYFKNFWITVMTKW	CAPFIDTVSVY	TSHDNLN	IEFYTRDEY	DTQSEDK	GTIDVKAR	CNHLTKRE	122

  

	130	140	150	160	170	180	
<i>CMLV_M96_18</i>	VIVTQKEAYRYS	LSDDLSC	FDSDLDLEIDL	IE NSTDTTVLKS	YELMLP	KRAKTSIHN	182
<i>HSPV9_023</i>	VIVTQKEAYRYS	LSDDLSC	FDSDLDLEIDL	IE NSTDTTVLKS	YELMLP	KRAKTSIHN	177
<i>CPXV_GRI_C12L</i>	VIVTQKEAYRYS	LSDDLSC	CFDSDLDLEIDL	IE NSTDTTVLKS	YELMLP	KRAKTSIHN	182
<i>CPXV_BRI_028</i>	VIVTQKEAYRYS	LSDDLSC	CFDSDLDLEIDL	IE NSTDTTVLKS	YELMLP	KRAKTSIHN	185
<i>CPXV_GER91_026</i>	VIVTQKEAYRYS	LSDDLSC	CFDSDLDLEIDL	IE NSTDTTVLKS	YELMLP	KRAKTSIHN	184
<i>VACV_WR_C8L</i>	VIVTQKEAYRYS	LSDDLSC	CFDSDLDLEIDL	IE NSTDTTVLKS	YELMLP	KRAKTSIHN	177

**Figure S11.** Sequence alignment of the C8 family members. Cysteine residues are boxed in yellow. Predicted N-linked glycosylation sites are boxed in blue.