Okamoto et al Supplemental Material

Legends to the Supplementary Figures

Figure S1: Sequence alignment of all 6 identified M11L orthologs

Residues marked in cyan are located in the binding grove of M11L are conserved between M11L and SPPV14. Green indicates residues that are located in the binding grove of M11L are conserved between M11L and SPPV14 and appear as a group to determine anti-apoptotic activity within the 6 M11L orthologs. Magenta indicates residues that are different between DPV83gp022 and DPV84gp022. & indicate additional residues that are conserved in all 6 M11L orthologs and are located in the M11L binding groove. * indicates residues fully conserved across all sequences, : highly conserved and . relatively conserved residues.

Figure S2: The putative SPPV14 binding grove

Ribbon diagram of M11L (green) bound to the Bak BH3 peptide (yellow, N-terminus at bottom); PDB:2JBY (1). Highlighted in cyan are four M11L residues (I37, Y41, A82 and F122) that are strictly conserved across a family of related poxvirus sequences. Highlighted in magenta are four M11L residues (M52, T67, L68, A71) that display sequence variation between functionally active and inactive proteins described here (see Discussion). Particular constellations of these four residues can be correlated with prosurvival activity.

Figure S3: SPPV14 does not inhibit Fas-induced cell death

Bax/Bak ($bax^{-/-}/bak^{-/-}$) deficient or wild-type MEFs infected with retrovirus carrying M11L, SPPV14 or B14 were treated with (A) FasL (100 ng/mL) alone or additionally, with (B) cycloheximide (1 µg/mL) and anti-FLAG antibody (2 µg/mL). Cell viability was determined by propidium iodide (PI) exclusion at each time point. Data represent means ± SD from 2 independent experiments.

SM References

1. Kvansakul M, van Delft MF, Lee EF, Gulbis JM, Fairlie WD, Huang DC, *et al.* A structural viral mimic of prosurvival Bcl-2: a pivotal role for sequestering proapoptotic Bax and Bak. *Mol Cell* 2007 Mar 23; **25**(6): 933-942.

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м11т.	MMSRLKTAVYDYLNDVDITECTEMDLLCOLSNCCDFTNETYAKNYDTLYDIMERDILS	58
SPPV14	MDNCNYNTEKVI.NVYI.RDI.RTESI.NNNEI.ETI.TMTRECCEVTKKDYKTEFNEI.CNFTI.ONNVK	63
GP011L	MSRLKEVVYTYLNGGDITECTEIDLLCOLVNCCNFINNTYAKNYDVLCDIMERDILS	57
LD17	MDNCNYNIEKVLNVYLRDLRIESLNNNELAILIMIRECCEVIKKDYKTEFNEICNFILRNNVK	63
SPV12L	MYKKYNSNVCIRNVLYVYLKYNTINKLSRYERMIYTKIKNOCEAIKYRYCNDFNSVTCILEYDENK	66
DPV83qp022	MEAAIEFDEIVKKLLNIYINDICTTGEKRLLNNYEKSILDRIYKSCEYIKKNYELDFNSMYNQININDIT	70
DPV84qp022	MEAAIEFDEIVKKLLNIYINDICT <mark>M</mark> GEKRLLNNYEKSILDRIYKSCEYIKKNYELDFNSMYNQININDIT	70
51	······································	
	&	
M11L	YNIVNIKN <mark>TL</mark> TF <mark>A</mark> LR-DASPS <mark>V</mark> KL <mark>A</mark> TLT <mark>L</mark> LASVIKKLNKIQHTDAAMFSEVIDGIVAEEQQVIG <mark>F</mark>	122
SPPV14	SCYDINDVKN <mark>II</mark> IE <mark>T</mark> INSDFRPS <mark>V</mark> IL <mark>A</mark> SIS <mark>L</mark> LSIIIKKKKDENNEVVDDDLALNELINKFSSYQKDIIS <mark>F</mark>	133
GP011L	YNIENIKK <mark>AL</mark> GF <mark>A</mark> LL-DASPSVKLATLALLSIILKKLNKIRHTEACVFSDVIDGITAEENKVIGF	121
LD17	SCYDINDVKN <mark>II</mark> IE <mark>T</mark> INSDFRPSVILASISLLSIIIKKKKNENNEVVNDDLALNELINTFSSYQKDIISF	133
SPV14	YIDNVHK <mark>EV</mark> IS <mark>I</mark> LLSDSRPSIKLAAISLLSIIIDKLICRNIRIAKYIIDDIINIISEDGIYIILF	131
DPV83gp022	TSDIKS <mark>KI</mark> IE <mark>A</mark> LLIDSRPSVKLATLSFISLIAEKWG-EKNR <mark>A</mark> KIMEILSNEIVEKISNNGKDFIDF	135
DPV84gp022	TSDIKS <mark>KI</mark> IE <mark>S</mark> LLIDSRPSVKLATLSFISLIAEKWG-EKNR <mark>T</mark> KIMEILSNEIVEKISNNGKDFIDF	135
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M1 1 T		
	IQKKCKINTTIINVRSGGCKISVILTAAVVG-FVAIGILKWIRGT 100	
SPPV14		
GPUIIL	IQEKIKINTTIINKKSKLPVILSTAMVATLIVIGVIKWKKGT 103	
DIVIS and 22		
MDV8/ap22		
HI VO49PZZ	TOWDODI''DDI''DII'NILKIII'GAILGIIAIIICAILLAGII- 1/3	

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