

TBE40/E	1	MESRGRRCPEMISVLGPISGHVLKAVFSRGDTPVLPHETRLLQTGIHVRVSQPSLILVSQ
AD169	1	MESRGRRCPEMISVLGPISGHVLKAVFSRGDTPVLPHETRLLQTGIHVRVSQPSLILVSQ

TBE40/E	61	YTPDSTPCHRGDNQLQVQHTYFTGSEVENVSVNVHNPTGRSICPSQEPMSIYVYALPLKM
AD169	61	YTPDSTPCHRGDNQLQVQHTYFTGSEVENVSVNVHNPTGRSICPSQEPMSIYVYALPLKM

TBE40/E	121	LNIP ^{PS} IN ^{VH} HYPSAAERKHRHLPVADAVIHASGKQMWQARLTVSGLAWTRQQNQWKEPDV
AD169	121	LNIP ^{PS} IN ^{VH} HYPSAAERKHRHLPVADAVIHASGKQMWQARLTVSGLAWTRQQNQWKEPDV

TBE40/E	181	YYTSAFVFPTKDVALRHVVCAHELVCSEMENTRATKMQVIGDQYVKVYLESFCEDVPSGKL
AD169	181	YYTSAFVFPTKDVALRHVVCAHELVCSEMENTRATKMQVIGDQYVKVYLESFCEDVPSGKL

TBE40/E	241	FMHVTLGSDVEEDLTMTTRNPQPFMRP ^{HER} NGFTVLC ^{PK} NMI ^{IK} PGKISHIMLDVAFTSHE
AD169	241	FMHVTLGSDVEEDLTMTTRNPQPFMRP ^{HER} NGFTVLC ^{PK} NMI ^{IK} PGKISHIMLDVAFTSHE

TBE40/E	301	HFGLLCPKSIPGLSISGNLLMNGQQIFLEVQAIRETVELRQYDPVAALFFFDIDLLLQRG
AD169	301	HFGLLCPKSIPGLSISGNLLMNGQQIFLEVQAIRETVELRQYDPVAALFFFDIDLLLQRG

TBE40/E	361	PQYSEHPTFTSQYRIQGKLEYRHTWDRHDEGAAQGDDDVWTSGSDSDEELVTTER ^{RK} ^{TPRV}
AD169	361	PQYSEHPTFTSQYRIQGKLEYRHTWDRHDEGAAQGDDDVWTSGSDSDEELVTTER ^{RK} ^{TPRV}

TBE40/E	421	TGGGAMAGASTSAG ^{RKR} KSASSATACTSGVMTRGRLKAESTVAPEEDTDEDSDNEIHNPA
AD169	421	TGGGAMAGASTSAG ^{RKR} KSASSATACTSGVMTRGRLKAESTVAPEEDTDEDSDNEIHNPA

TBE40/E	481	VFTWPPWQAGILARN ^{LVP} MVATVQ ^Q GNLKYQE ^{FF} WDANDIYRIFAELEGVWQ ^{PAA} Q ^P ^{KRR}
AD169	481	VFTWPPWQAGILARN ^{LVP} MVATVQ ^Q GNLKYQE ^{FF} WDANDIYRIFAELEGVWQ ^{PAA} Q ^P ^{KRR}

TBE40/E	541	R ^{HR} Q ^E ALPGPCIASTP ^{KK} HRG M ^{ESS} AKRKMDP ^{DN} PDEGPSSK ^{VPR} PETPVTKATTFLQTM
AD169	541	R ^{HR} Q ^D ALPGPCIASTP ^{KK} HRG M ^{ESS} AKRKMDP ^{DN} PDEGPSSK ^{VPR} PRPETPVTKATTFLQTM
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TBE40/E	601	LRKEVNSQLSLGDPLFP ^E LA ^E ESLKT ^F EQVTEDCNENPEKDVLAELVKQIKVRVDMVR ^{HR}
AD169	601	LRKEVNSQLSLGDPLFP ^E LA ^E ESLKT ^F EQVTEDCNENPEKDVLAELVKQIKVRVDMVR ^{HR}

TBE40/E	661	I ^{KEH} MLKKYTQTEEKFTGAFNMMGGCLQNALDILDKVHEPF ^E EMKCI ^{GL} TMQSMYENYIV
AD169	661	I ^{KEH} MLKKYTQTEEKFTGAFNMMGGCLQNALDILDKVHEPF ^E EMKCI ^{GL} TMQSMYENYIV

TBE40/E	721	PEDKREMWMACIKELHDVTKGAANKLGGALKAKARAKD ^{EL} K ^{RK} MIYMCYRNIEFFTKNS
AD169	721	PEDKREMWMACIKELHDVSKGAANKLGGALQAKARAKD ^{EL} R ^{RR} KMMYMCYRNIEFFTKNS

TBE40/E	781	AFPKTTNGCSQAMAALQNL ^P QCSPDEIMAYAQKIFKILDEERDKVLTHIDHIFMDILTTC
AD169	781	AFPKTTNGCSQAMAALQNL ^P QCSPDEIMAYAQKIFKILDEERDKVLTHIDHIFMDILTTC

TBE40/E	841	VETMCNEYKVTSDACMM TM YGSISLLSEFCRVLCCY ^{IL} EETS ^{SV} MLAKRPLITKPEVINVM
AD169	841	VETMCNEYKVTSDACMM TM YGGISLLSEFCRVLCCY ^{VL} EETS ^{SV} MLAKRPLITKPEVISVM

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TBE40/E  901  KRRIEEICKMVFQAQYILGADPLRVCSPSVDDLRAIAEESDEEDAIAAYTLATAGASSSDS
AD169    901  KRRIEEICKMVFQAQYILGADPLRVCSPSVDDLRAIAEESDEEEAIVAYTLATAGVSSSDS
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TBE40/E  961  LVSPPEPVPATIPLSSVIVAENSDQEESQSDDEEQEEGAQEEQEDTVSVKSEPVSEIEE
AD169    961  LVSPPEPVPATIPLSSVIVAENSDQEESQSDDEEEEGAQEEREDTVSVKSEPVSEIEE
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TBE40/E  1021 VASEEEEDGAEEPTTSGGKSTHPMVTRSKADQ
AD169    1021 VAPEEEEDGAEEPTASGGKSTHPMVTRSKADQ
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Suppl. Fig. 1. Alignment of pp65 and IE1 of HCMV strain TBE40/E and AD169. The primary amino acid sequences of pp65 (GenBank: ABV71605.1 and DAA00180.1) and IE1 (GenBank: ABV71636.1 and DAA00112.1) from the HCMV strains TBE40/E and IE1 were aligned using SIM [1]. Identical amino acids are indicated by asterisks (*). The fusion site of the HCMV pp65-IE1 fusion protein is indicated as a vertical line (|). HCMV pp65 and IE1 epitopes, which were investigated in this study, are marked green and yellow, respectively. The bipartite nuclear localization signal of HCMV pp65 consisting of motif A-B and C-D [2] is marked violet. The N-terminal nuclear localization signal [3] and the STAT2-binding domain [4] of HCMV IE1, which are absent in the pp65-IE1 fusion protein, are marked red.

References

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- [3] Lee HR, Huh YH, Kim YE, Lee K, Kim S, Ahn JH. N-terminal determinants of human cytomegalovirus IE1 protein in nuclear targeting and disrupting PML-associated subnuclear structures. *Biochem Biophys Res Commun* 2007;356:499-504.
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