



Supplementary materials

Review

The cytomegalovirus protein kinase pUL97: host interactions, regulatory mechanisms and antiviral drug targeting

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Table S1. Viral proteins coimmunoprecipitated in complex with pUL97-Flag using lysates of HCMV-infected HFFs*

		IP: mAb/pAb-Flag						
		pUL97-Flag						
Gene	Description	I	I	III	IV	mean	pUL97	
UL83 ¹	65 kDa phosphoprotein pp65	584	611	403	458	514	13	
UL97 ¹	Serine/threonine protein kinase UL97	141	105	170	173	147	-	
UL25	Phosphoprotein 85	98	81	67	73	80	3	
MCP	Major capsid protein	78	37	59	65	60	4	
RIR1	Ribonucleoside-diphosphate reductase large subunit-like protein	58	56	45	49	52	b.c.	
UL44 ¹	DNA polymerase processivity subunit	59	41	44	51	49	5	
UL32	Large structural phosphoprotein	54	23	37	47	40	-	
IRS1	Protein IRS1	36	26	29	24	29	b.c.	
UL48	Large tegument protein deneddylase	23	15	35	44	29	-	
UL47	Inner tegument protein	27	13	21	29	23	-	
TRS1	Protein HHLF1	24	18	21	24	22	b.c.	
UL35	Protein UL35	23	24	17	14	20	-	
TRX2	Triplex capsid protein 2	21	9	15	18	16	-	
NEC2 ¹	Nuclear egress protein 2 pUL50	18	13	17	13	15	b.c.	
UL26	Tegument protein UL26	13	11	17	13	14	-	
UL112/UL113	Early phosphoprotein p84	7	9	18	17	13	-	
UL82	Protein pp71	15	4	14	13	12	-	
UL104	Portal protein	14	13	9	8	11	-	
DBP	Major DNA-binding protein	24	5	5	8	11	-	
UL84	Protein UL84	8	5	10	14	9	-	
UL43	Tegument protein UL43	14	5	3	8	8	-	
TRX1	Triplex capsid protein 1	12	3	6	7	7	-	
CVC1	Capsid vertex component 1	8	7	6	6	7	-	
NEC1 ¹	Nuclear egress protein 1 pUL53	7	5	8	5	6	b.c.	
UL29	Protein UL29/UL28	5	5	b.c.	4	5	-	
US22	Early nuclear protein HWLF1	8	9	b.c.	5	7	b.c.	
UL69 ¹	mRNA export factor ICP27 homolog	52	37	24	27	35	8	
IR11	Viral Fc-gamma receptor-like protein IR11	15	9	9	6	10	b.c.	
UL98	Alkaline nuclease	4	3	7	6	5	-	
UL54	DNA polymerase catalytic subunit	3	-	10	4	6	-	
UL103	Cytoplasmic envelopment protein 1	4	b.c.	b.c.	b.c.	4	-	
UL24	Protein UL24	4	b.c.	4	4	4	-	
UL70	DNAprimase	3	b.c.	b.c.	-	3	-	
UL122	Viral transcription factor IE2	4	b.c.	6	5	5	-	
TRM3	Tripartite terminase subunit 3	b.c.	b.c.	4	3	4	-	
UL94	Cytoplasmic envelopment protein 2	-	b.c.	4	b.c.	4	-	
US20	Membrane protein US20	b.c.	b.c.	3	b.c.	3	-	
CVC2	Capsid vertex component 2	b.c.	-	b.c.	3	3	-	

*HFFs were infected with HCMV AD169-UL97(Mx4)-Flag (expressing the large isoform M1 of pUL97 C-terminally tagged with Flag) and harvested 4 d p.i. for immunoprecipitation (IP) of protein complexes and their subsequent analysis by mass spectrometry. The four columns I-IV present the number of peptides identified in four replicates. Flag-specific monoclonal and polyclonal antibodies were used for IP as indicated. All WSC values were corrected against the negative control value obtained by IP with a rabbit Fc fragment. Flag-specific IP using lysates from HCMV AD169-infected cells expressing untagged pUL97 served as an additional negative control. For a description of the methods for the proteomic analysis, see previous reports on similar investigations [51, 77]. Cut-off criteria were chosen as follows: (i) \geq 20% IP control and (ii) > 15-fold above Flag neg. control, in either of the two samples pUL97-Flag or pUL97. ¹Known interactors and/or phosphorylated substrates of pUL97 in bold letters; b.c., below cut-off (cut-off \geq 3 WSC); WSC, weighted spectral counts.





Table S2. Cyclins, CDKs and additional cellular proteins in complex with pUL97-Flag using lysates of HCMV-infected HFFs: the selection of scored proteins was performed according to their previously published properties of putative pUL97 interaction *

		IP: mAb/pAb-Flag						
Gene								
	Description	I	II	III	IV	mean	pUL97	
LMNA ³	Prelamin-A/C	71	58	22	26	44	6	
IFI16 ¹	Interferon gamma-inducible protein 16	10	10	9	7	9		
CDC5L ³	Cell division cycle 5-like protein	4	4	4	5	4	-	
EMD ²	Emerin	28	18	4	b.c.	17	b.c.	
LMNA ¹	Lamin A/C	9	5	3	b.c.	6	b.c.	
LRRFIP2 ³	Leucine-rich repeat flightless-interacting protein 2	6	6	b.c.	-	6	-	
RBL1 ³	Retinoblastoma-like protein 1	6	1	10	7	6		
LEMD3 ³	Inner nuclear membrane protein Man1	3	-	-	-	3	-	
CDK1 ¹	Cyclin-dependent kinase 1	b.c.	b.c.	15	8	11	-	
CCNT1 ¹	Cyclin T1	-	b.c.	4	3	4	-	
RB1 ¹	Retinoblastoma-associated protein	b.c.	b.c.	3	b.c.	3	-	
CCNB1 ¹	Cyclin B1, G2/mitotic-specific cyclin	-	-	4	3	4	-	
CDK9 ¹	Cyclin-dependent kinase 9	b.c.	b.c.	3	b.c.	3	-	
CDC20 ³	Cell division cycle protein 20 homolog		b.c.	4	3	4	-	
PPIB ³	Peptidyl-prolyl cis-trans isomerase B	b.c.	b.c.	b.c.	32	32	b.c.	
FKBP3 ³	Peptidyl-prolyl cis-trans isomerase FKBP3	-	-	-	8	8	-	
CDK5RAP2 ³	CDK5 regulatory subunit-associated protein 2	-	-	b.c.	3	3	-	

*HFFs were infected with HCMV AD169-UL97(Mx4)-Flag (expressing the large isoform M1 of pUL97 C-terminally tagged with Flag) and harvested 4 d p.i. for IP of protein complexes and their subsequent analysis by mass spectrometry. The four columns I-IV present the number of peptides identified in four replicates. Flag-specific monoclonal and polyclonal antibodies were used for IP as indicated. All WSC values were corrected against the negative control value obtained by IP with a rabbit Fc fragment. Flag-specific IP using lysates from HCMV AD169-infected cells expressing untagged pUL97 served as an additional negative control. For a description of the methods for the proteomic analysis, see previous reports on similar investigations [51, 77]. Cut-off criteria were chosen as follows: (i) \geq 20% IP control and (ii) > 15-fold above Flag neg. control, in either of the two samples pUL97-Flag or pUL97. ¹Known interactors and/or phosphorylated substrates of pUL97 in bold letters; ²known components of pUL97-associated complexes; ³putatively associated proteins; b.c., below cut-off (cut-off \geq 3 WSC); WSC, weighted spectral counts.





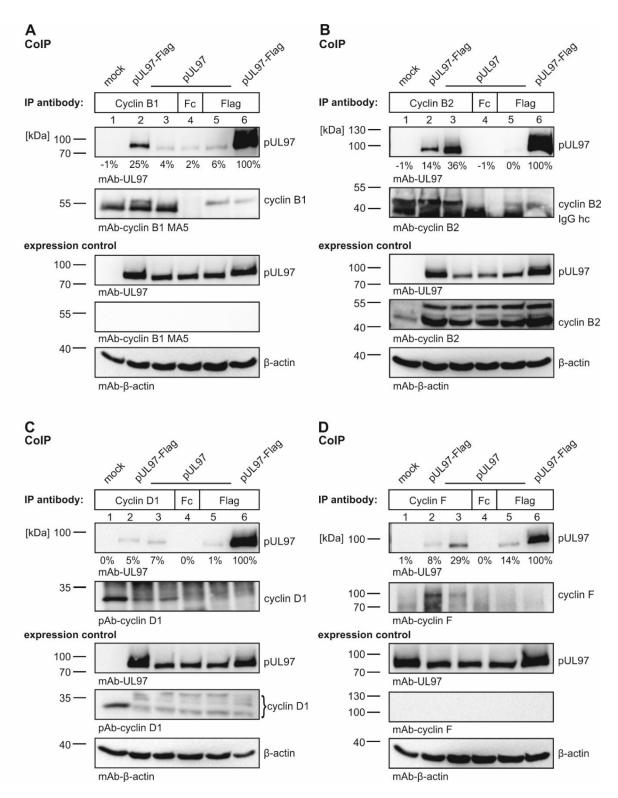
Cyclin type	pUL97-Flag	pUL97 % IP	Flag neg.	pUL97-Flag	pUL97 x-fold Flag neg.	Flag neg.
Cyclin B1	20.7	1.3	0.8	27.3	1.7	1.0
Cyclin B2	16.3	40.5	0.6	28.6	71.0	1.0
Cyclin D1	8.9	11.2	4.9	1.8	2.3	1.0
Cyclin F	7.1	24.3	14.0	0.5	1.7	1.0
Cyclin K	20.9	23.7	-1.5	20.9	23.7	1.0
Cyclin L2a	5.4	16.7	1.4	3.8	11.7	1.0
Cyclin Y	6.0	18.5	-0.5	6.0	18.5	1.0

Table S3. Quantities of pUL97 detected by cyclin-specific coimmunoprecipition analysis (CoIP/Wb)*

*Signal intensities of CoIP/WB experimentation (partly depicted by Figure S1) were quantitated densitometrically using Aida Image Analyzer v.4.23 (mean values of densitometrical dermination in quadruplicate, i.e. performing quantitation duplicates each of two independent Wbs). Direct pUL97-Flag IP via Flag-antibody was set to 100% and values corrected against the rabbit Fc fragment negative control by subtraction. Flag-specific IP using lysates from HCMV AD169-infected cells expressing untagged pUL97 (Flag neg.) served as an additional negative control. Cut-off criteria were chosen as follows: (i) IP % values >20% of IP control (positive, +) or value 15-20% of IP control (slightly positive, ±) and >15-fold above Flag neg. control, at least in one of the samples pUL97-Flag or pUL97.











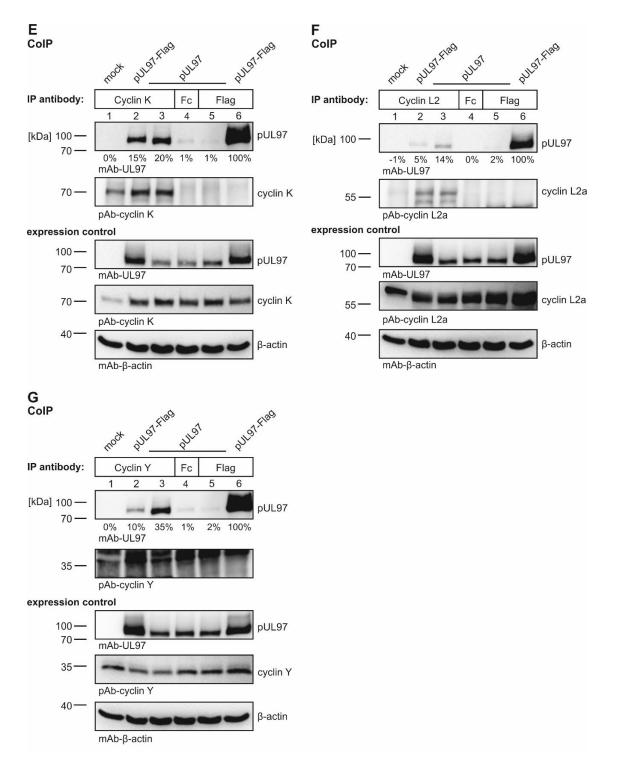


Figure S1. Representative series of primary data of the CoIP/Wb analysis of pUL97-cyclin interactions (see Table S3 for densitometrical quantitation and Table 2 presenting summarized data of various determinations of pUL97-cyclin interaction). HFFs were infected with HCMV strain AD169 (expressing untagged pUL97) or the recombinant virus AD169-UL97(Mx4)-Flag (expressing the large isoform M1 of pUL97 C-terminally tagged with Flag). CoIPs were performed with a specificity of the individually used IP antibodies as indicated, **(A)** cyclin B1, **(B)** cyclin B2, **(C)** cyclin D1, **(D)** cyclin F, **(E)** cyclin K, **(F)** cyclin L2a and **(G)** cyclin Y. Fc, antibody Fc fragment used as a negative control.