

## Supporting information

### **Cyclins B1, T1 and H differ in their molecular mode of interaction with cytomegalovirus protein kinase pUL97**

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Running title: *Differential mode of cyclins' interaction with vCDK pUL97*

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#### **Supplemental Table S1**

Mass spectrometry data of pUL97 phosphosites from Analyses I and II as presented in Table 3.

**Table S1****Mass spectrometry raw data of pUL97 phosphosites from Analyses I and II as presented in Table 3**

Samples for Analysis I were prepared from HFF cells infected with HCMV AD169 for 5 days. Six 175 cm<sup>2</sup> flasks per sample were harvested and used for upscaling pUL97-IP. IP samples have been used for two runs of phosphosite mass spectrometry analysis, virion-derived pUL97. Samples for Analysis II were prepared from gradient-purified HCMV AD169 HB15 or UL97ΔK355 virions, respectively.

<b>Analysis I</b>				
<b>Run I</b>				
<b>pUL97 Peptide</b>	<b>Score</b>	<b>PTM Probability</b>	<b>Residue</b>	<b>Prot Loc</b>
AAGEQQQPPSLVGTGVHR	70,06	99,84321	S	386
GSAASGDGYHGLR	69,93	99,743026	S	142
ALFTGGSDPDSVSGVR	121,91	99,47842	S	180
ALFTGGSDPDSVSGVR	85,43	99,19151	T	177
ALFTGGSDPDSVSGVR	85,43	99,19151	S	180
ALFTGGSDPDSVSGVRGGR	58,52	98,94308	S	180
RALFTGGSDPDSVSGVR	46,49	96,70893	T	177
RALFTGGSDPDSVSGVR	46,49	96,70893	S	180
RALFTGGSDPDSVSGVR	56,16	89,25548	S	180
ALFTGGSDPDSVSGVR	58,23	72,14349	S	185
ALFTGGSDPDSVSGVR	58,23	72,14349	S	180
VGGVDAVLEENDVELRAESQDSAVASGPGR	66,88	39,342076	S	239
ALFTGGSDPDSVSGVRGGR	31,03	35,443994	S	187
ALFTGGSDPDSVSGVRGGR	31,03	35,443994	T	177
RPVVPSTSSRGSAAASGDGYHGLR	36,88	19,636643	S	133

  

<b>Run II</b>				
<b>pUL97 Peptide</b>	<b>Score</b>	<b>PTM Probability</b>	<b>Residue</b>	<b>ProtLoc.</b>
DGEKEDAASDKENLR	105,6	100	S	121
GSAASGDGYHGLR	74,92	100	S	139
GSAASGDGYHGLR	74,92	100	S	142
ALFTGGSDPDSVSGVR	144,29	99,99815	S	180
AESQDSAVASGPGR	51,1	99,964035	S	239
RALFTGGSDPDSVSGVR	144,6	99,90375	S	180
ALFTGGSDPDSVSGVRGGR	80,82	99,90005	S	180
AESQDSAVASGPGR	85,83	99,819547	S	232
AAGEQQQPPSLVGTGVHR	69,07	99,70235	S	386
GSAASGDGYHGLR	122,12	99,681854	S	142
RALFTGGSDPDSVSGVR	101	97,61795	T	177
RALFTGGSDPDSVSGVR	101	97,61795	S	180
ALFTGGSDPDSVSGVR	122,18	96,13632	T	177
ALFTGGSDPDSVSGVR	122,18	96,13632	S	180

ALFTGGSDPSDSVSGVRGGR	67,97	94,74132	T	177
ALFTGGSDPSDSVSGVRGGR	67,97	94,74132	S	180
SASLGTTTQGWDPPLR	112,42	89,81314	S	13
RPVVPSTSSR	66,86	88,700634	S	135
SASLGTTTQGWDPPLRRPSR	44,88	86,84324	S	13
ALFTGGSDPSDSVSGVR	108,3	77,43492	T	177
ALFTGGSDPSDSVSGVR	108,3	77,43492	S	183
RPVVPSTSSRGSAAASGDGYHGLR	67,56	74,8651	S	139
RPVVPSTSSRGSAAASGDGYHGLR	67,56	74,8651	S	142
CVAVFQETGTAR	38,44	74,297535	T	504
ALFTGGSDPSDSVSGVR	130,3	70,99193	T	177
RALFTGGSDPSDSVSGVRGGR	25,55	69,59055	S	180
RPVVPSTSSRGSAAASGDGYHGLR	81,7	49,894965	S	142
RPVVPSTSSRGSAAASGDGYHGLR	81,7	49,894965	S	139
RPVVPSTSSRGSAAASGDGYHGLR	81,7	49,894965	S	133
ALFTGGSDPSDSVSGVRGGR	80,63	49,750978	S	185
ALFTGGSDPSDSVSGVRGGR	80,63	49,750978	S	180
ALFTGGSDPSDSVSGVRGGR	26,26	47,008517	S	185
RPVVPSTSSRGSAAASGDGYHGLR	82,31	40,128493	S	139
RPVVPSTSSRGSAAASGDGYHGLR	82,31	40,128493	S	136
RPVVPSTSSRGSAAASGDGYHGLR	71,25	21,381325	S	133

## Analysis II

### HB15 wild-type

pUL97 Peptide	Score	PTM Probability	Residue	ProtLoc.
DGEKEDAASDKENLR	88,29	100	S	121
GSAASGDGYHGLR	113,86	99,99875	S	142
ALFTGGSDPSDSVSGVR	137,68	99,885895	S	180
ALFTGGSDPSDSVSGVR	106,98	98,7356	S	185
SASLGTTTQGWDPPLR	83,86	52,892834	S	13

### UL97ΔK355

pUL97 Peptide	Score	PTM Probability	Residue	ProtLoc.
DGEKEDAASDKENLR	80,04	100	S	121