

Supplementary Information

Table S1. Conserved putative phosphorylation sites and the respective candidate kinase in the C-terminal region of L4-22K (**A**) and L4-33K (**B**) of different serotypes. The prediction was performed by using the NetPhosK 1.0 Server.

A		
Conserved Putative P-Site	Adenovirus Serotype	Candidate Kinase
S118	Ad12	
S126	Ad3	
S116	Ad11	
S126	Ad5	PKC
S90	Ad9	
S117	Ad4	
S132	Ad41	
B		
Conserved Putative P-Site	Adenovirus Serotype	Candidate Kinase
T146	Ad12	
T175	Ad3	
T167	Ad11	
T168	Ad5	PKC
T114	Ad9	
T154	Ad4	
T158	Ad41	
S167	Ad12	
S196	Ad3	
S188	Ad11	
S189	Ad5	PKA, PKC
S135	Ad9	
S175	Ad4	
S179	Ad41	
S170	Ad12	
S199	Ad3	
S191	Ad11	
S192	Ad5	PKC
S138	Ad9	
S178	Ad4	
S182	Ad41	

Table S1B. *Cont.*

Conserved Putative P-site	Adenovirus Serotype	Candidate Kinase
T172	Ad12	
T201	Ad3	
T193	Ad11	
T194	Ad5	PKA
T140	Ad9	
T180	Ad4	
T184	Ad41	
T187	Ad12	
T216	Ad3	
T208	Ad11	
T209	Ad5	cdc2
T155	Ad9	
T195	Ad4	
T199	Ad41	
S202	Ad12	PKC, PKA
T231	Ad3	PKC
T223	Ad11	PKC
T224	Ad5	PKC
T170	Ad9	PKC
T210	Ad4	PKC
S214	Ad41	PKA

Table S2. Quantitative analysis of the kinases and the putative target phosphorylation sites of L4-22K (**A**) and of L4-33K (**B**) of different serotypes. The putative targets were detected by NetphosK 1.0 analysis. The kinases with the highest number of targets for each serotype are shown in bold. The number of potential kinases and potential targets with the respective % of the total number of amino acids of each protein are indicated.

A							
Kinase	Ad12	Ad3	Ad11	Ad5	Ad9	Ad4	Ad41
	L4-22K	L4-22K	L4-22K	L4-22K	L4-22K	L4-22K	L4-22K
ATM	3	2	1	1	1	1	1
cdc2	2	0	3	2	0	3	2
cdk5	1	0	0	4	0	0	2
CKI	3	1	2	1	1	3	2
CKII	5	5	5	5	2	5	7
DNAPK	2	3	3	2	1	3	5
GSK3	1	2	1	2	0	0	2
INSR	0	0	0	1	0	0	0
PKA	2	2	2	1	0	4	0
PKB	0	0	1	0	0	0	0
PKC	11	13	13	8	1	8	5
PKG	0	1	0	1	0	1	1
p38MAPK	0	3	1	4	0	1	1
RSK	0	1	2	0	0	1	0
SRC	0	0	0	1	0	1	0
Potential kinases	30	33	34	33	6	31	28
and % of the tot length	(16.30%)	(16.58%)	(17.80%)	(17.01%)	(4.38%)	(17.32%)	(14.51%)
Target residues and %	19	24	22	22	3	21	19
of the length	(10.33%)	(12.06%)	(11.52%)	(11.34%)	(2.19%)	(11.73%)	(9.84%)
Tot residues	184	199	191	194	137	179	193

B							
Kinase	Ad12	Ad3	Ad11	Ad5	Ad9	Ad4	Ad41
	L4-33K	L4-33K	L4-33K	L4-33K	L4-33K	L4-33K	L4-33K
ATM	2	1	0	1	1	1	1
cdc2	3	3	2	4	1	4	3
cdk5	2	0	0	3	0	0	2
CKI	3	1	2	1	1	3	2
CKII	5	5	6	6	2	6	5
DNAPK	1	2	2	2	1	3	4
GSK3	1	0	0	2	0	0	2
PKA	5	5	6	5	2	6	3
PKB	1	0	1	0	0	0	0
PKC	19	20	25	15	6	17	10
PKG	0	4	1	3	0	4	3
p38MAPK	0	1	0	3	0	0	0
RSK	0	2	3	0	0	1	0

Table S1B. *Cont.*

Kinase	Ad12	Ad3	Ad11	Ad5	Ad9	Ad4	Ad41
	L4-33K	L4-33K	L4-33K	L4-33K	L4-33K	L4-33K	L4-33K
SRC	0	0	0	1	0	0	0
Potential kinases	42	44	48	46	14	45	35
and % of the tot length	(20.39%)	(18.72%)	(21.15%)	(20.18%)	(8.05%)	(21.03%)	(16.06%)
Target residues and %	28	32	35	33	10	31	25
of the length	(13.59%)	(13.62%)	(15.42%)	(14.47%)	(5.75%)	(14.49%)	(11.47%)
Tot residues	206	235	227	228	174	214	218