

Supplementary Table S1. Putative phosphorylation sites in SV40 and HPyV LTA_g and their protein kinase. Putative protein kinases were predicted using the algorithm NetPhos3.1 [1,2]. Protein kinase consensus motifs are based on [3-7]. Proven phosphorylation sites are shown in grey.

residue	Protein kinase	Consensus motif	Sequence in LTA _g	score
S10	PKA	K/RK/RXS/T	NREESLQLM	0.749
S22	CKI CDK1	D/E(X)XS/T LPXSPXKK	GLERSAWGN	0.510 0.503
T57	PKC	R/KR/KR/K/FSFRR	KKMNTLYKK	0.842
T85	CKII	D/ED/ED/ES/TD/ED/E	TEIPTYGTD	0.534
T88	CKII	D/ED/ED/ES/TD/ED/E	PTYGTDEWE	0.583
S111	CKII	D/ED/ED/ES/TD/ED/E	EEMPSSDDE	0.638
S112	CKII	D/ED/ED/ES/TD/ED/E	EMPSSDDEA	0.723
S120	ATM CKI	L/SSQE/D D/E(X)XS/T	ATADSQHST	0.556 0.549
S123	PKC	R/KR/KR/K/FSFRR	DSQHSTPPK	0.666
T124	PKC CDK5 p38 ^{MAPK} GSK3	R/KR/KR/K/FSFRR S/TPXK/H/R PXS/TP S/TXXS/T	SQHSTPPK	0.727 0.603 0.523 0.502
T163	PKC	R/KR/KR/K/FSFRR	FAIYTTKEK	0.750
T182	PKC	R/KR/KR/K/FSFRR	KYSVTFISR	0.829
S189	PKA RSK	K/RK/RXS/T RXRXXS/T	SRHNSYNHN	0.606 0.515
T199	p38 ^{MAPK} CDK5	PXS/TP S/TPXK/H/R	LFFLTPHRH	0.567 0.535
S206	PKA PKG	K/RK/RXS/T R/KR/KXS/T	RHRVSAINN	0.748 0.556
T237	PKC	R/KR/KR/K/FSFRR	YSALTRDPF	0.762
S242	CKII PKC	D/ED/ED/ES/TD/ED/E R/KR/KR/K/FSFRR	RDPFSVIEE	0.617 0.586
S247	CKI DNAPK	D/E(X)XS/T QXS/TQE/D	VIEESLPGG	0.574 0.502
T265	CKI	D/E(X)XS/T	EAEETKQVS	0.516
S269	PKC	R/KR/KR/K/FSFRR	TKQVSWKV	0.597
T280	CKII	D/ED/ED/ES/TD/ED/E	YAMETKCDD	0.504
S330	PKC	R/KR/KR/K/FSFRR	IFADSKNQK	0.826
T343	PKC	R/KR/KR/K/FSFRR	QAVDTVLAK	0.844
S352	PKA	K/RK/RXS/T	KRVDLSQLT	0.835
T362	PKC	R/KR/KR/K/FSFRR	EQMLTNRFN	0.722
T379	CKII	D/ED/ED/ES/TD/ED/E	MFGSTGSAD	0.521
S381	CKII	D/ED/ED/ES/TD/ED/E	GSTGSADIE	0.566
Y414	EGFR	XXEXYYXX	KCMVYNIPK	0.505
T434	PKC	R/KR/KR/K/FSFRR	SGKTTLAAA	0.593
T478	CKII	D/ED/ED/ES/TD/ED/E	DVKGTGGES	0.563
S482	CKII	D/ED/ED/ES/TD/ED/E	TGGESRDLP	0.503
S504	PKC	R/KR/KR/K/FSFRR	YLDGSVKVN	0.869
T518	PKG	R/KR/KXS/T	LNKRTQIFP	0.548
T527	CKII PKG	D/ED/ED/ES/TD/ED/E R/KR/KXS/T	PGIVTMNEY	0.520 0.517
Y531	SRC	EEDVYGXV	TMNEYSVPK	0.501
S560	CKII	D/ED/ED/ES/TD/ED/E	CLERSEFLL	0.528
S571	PKA PKC	K/RK/RXS/T R/KR/KR/K/FSFRR	RIIQSGIAL	0.804 0.698
S591	CDK1	LPXSPXKK	EFAQSIQSR	0.509
S594	PKC	R/KR/KR/K/FSFRR	QSIQSRIVE	0.601

S608	CKI	D/E(X)XS/T	DKEFSLSVY	0.518
S610	PKC	R/KR/KR/K/F \underline{S} FRR	EFSL \underline{S} VYQK	0.776
S632	CKII	D/ED/ED/ES/TD/ED/E	WLRN \underline{S} DDDD	0.697
S639	CKII	D/ED/ED/ES/TD/ED/E	DDED \underline{S} QENA	0.648
	CKI	D/E(X)XS/T		0.606
	DNAPK	QXS/TQE/D		0.603
	ATM	L/ \underline{S} \underline{S} QE/D		0.599
S657	CKII	D/ED/ED/ES/TD/ED/E	NMED \underline{S} GHET	0.598
S661	CKII	D/ED/ED/ES/TD/ED/E	SGHET \underline{G} IDS	0.567
S665	DNAPK	QXS/TQE/D	TGID \underline{S} QSQG	0.635
	ATM	L/ \underline{S} \underline{S} QE/D		0.577
S667	DNAPK	QXS/TQE/D	IDSQ \underline{S} QGSF	0.604
	PKC	R/KR/KR/K/F \underline{S} FRR		0.601
	ATM	L/ \underline{S} \underline{S} QE/D		0.585
	CDK1	LPX \underline{S} PXKK		0.520
S670	CDK1	LPX \underline{S} PXKK	QSQ \underline{S} FFQAP	0.581
	PKC	R/KR/KR/K/F \underline{S} FRR		0.568
S677	DNAPK	QXS/TQE/D	APQ \underline{S} QSVH	0.637
	CDK1	LPX \underline{S} PXKK		0.560
	ATM	L/ \underline{S} \underline{S} QE/D		0.534
S679	PKC	R/KR/KR/K/F \underline{S} FRR	Q \underline{S} QSVH \underline{D} H	0.537
Y687	EGFR	XXEY \underline{Y} YXX	HNQPYHICR	0.550
T694	PKC	R/KR/KR/K/F \underline{S} FRR	CRGFT \underline{C} FKK	0.757
T701	p38 ^{MAPK}	PXS/T \underline{P}	KKPPT \underline{P} PPPE	0.555
	GSK3	\underline{S} /TXXS/T		0.519

Prediction based on motifs for the protein kinases ATM, CDK1, CDK5, CKI, CKII, CaMKII, DNAPK, EGFR, GSK3, INSR, p38^{MAPK}, PKA, PKB, PKC, PKG, RSK, and SRC.

BKPyV

residue	Protein kinase	Consensus motif	Sequence in LTag	score
T57	PKC	R/KR/KR/K/F \underline{S} FRR	KRMV \underline{T} LYKK	0.798
S78	CKII	D/ED/ED/ES/TD/ED/E	FGTW \underline{S} SSEV	0.582
T84	CKII	D/ED/ED/ES/TD/ED/E	SEVPT \underline{Y} GTE	0.554
Y85	SRC	EEDV \underline{Y} GXV	EVGT \underline{Y} GTEE	0.531
T87	CKII	D/ED/ED/ES/TD/ED/E	PTYGT \underline{E} EWE	0.547
S95	CKII	D/ED/ED/ES/TD/ED/E	ESWW \underline{S} SFNE	0.511
S96	PKC	R/KR/KR/K/F \underline{S} FRR	SWW \underline{S} FN \underline{E} K	0.563
	CKII	D/ED/ED/ES/TD/ED/E		0.541
	CKI	D/E(X)XS/T		0.529
	CDK1	LPX \underline{S} PXKK		0.507
S114	CKII	D/ED/ED/ES/TD/ED/E	DMFA \underline{S} DEEA	0.687
S122	ATM	L/ \underline{S} \underline{S} QE/D	ATAD \underline{S} QHST	0.555
	CKI	D/E(X)XS/T		0.550
S125	PKC	R/KR/KR/K/F \underline{S} FRR	DSQH \underline{S} T \underline{P} PK	0.666
T126	PKC	R/KR/KR/K/F \underline{S} FRR	SQHST \underline{P} PKK	0.727
	CDK5	\underline{S} /TPXK/H/R		0.603
	p38 ^{MAPK}	PXS/T \underline{P}		0.523
	GSK3	\underline{S} /TXXS/T		0.502
S142	PKG	R/KR/KX \underline{S} /T	KDFP \underline{S} DLHQ	0.548
S149	PKC	R/KR/KR/K/F \underline{S} FRR	HQFL \underline{S} QAVF	0.749
	DNAPK	QXS/TQE/D		0.614
	ATM	L/ \underline{S} \underline{S} QE/D		0.598
T165	PKC	R/KR/KR/K/F \underline{S} FRR	FAVYT \underline{T} KEK	0.685
	PKG	R/KR/KX \underline{S} /T		0.503

T166	PKC	R/KR/KR/K/F <u>S</u> FRR	AVYT <u>T</u> KEKA	0.541
T184	PKC	R/KR/KR/K/F <u>S</u> FRR	KYSV <u>T</u> FISR	0.829
T201	CDK5 p38 ^{MAPK}	<u>S</u> /TPXK/H/R	IFFL <u>T</u> PHRH	0.579
		PX <u>S</u> / <u>T</u> P		0.572
S208	PKA	K/RK/RX <u>S</u> / <u>T</u>	RHV <u>S</u> AINN	0.748
	PKG	R/KR/KX <u>S</u> / <u>T</u>		0.544
T239	PKC	R/KR/KR/K/F <u>S</u> FRR	YSAL <u>T</u> RDY	0.559
T245	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	DPYH <u>T</u> IEES	0.590
S271	PKC	R/KR/KR/K/F <u>S</u> FRR	TKQV <u>S</u> WKLI	0.629
T282	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	YAVET <u>K</u> CED	0.628
Y299	INSR	<u>Y</u> XXM	LEFQY <u>N</u> VEE	0.505
S332	PKC	R/KR/KR/K/F <u>S</u> FRR	IFAE <u>S</u> KNQK	0.845
S337	PKA	K/RK/RX <u>S</u> / <u>T</u>	KNQK <u>S</u> ICQQ	0.506
T345	PKC	R/KR/KR/K/F <u>S</u> FRR	QAVD <u>T</u> VLAK	0.844
T354	PKA	K/RK/RX <u>S</u> / <u>T</u>	KRVD <u>T</u> LHMT	0.669
	PKG	R/KR/KX <u>S</u> / <u>T</u>		0.551
T358	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	TLHM <u>T</u> REEM	0.578
T364	PKC	R/KR/KR/K/F <u>S</u> FRR	EEM <u>L</u> TERFN	0.563
T435	PKC	R/KR/KR/K/F <u>S</u> FRR	DSGK <u>T</u> TLAA	0.543
T480	PKC	R/KR/KR/K/F <u>S</u> FRR	DVKG <u>T</u> GAES	0.684
	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E		0.598
S484	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	TGAES <u>K</u> DLP	0.546
S506	PKC	R/KR/KR/K/F <u>S</u> FRR	YLDG <u>S</u> VKVN	0.869
	CDK1	LPX <u>S</u> PXKK		0.515
T520	PKG	R/KR/KX <u>S</u> / <u>T</u>	LNKR <u>T</u> QIFP	0.548
T529	PKG	R/KR/KX <u>S</u> / <u>T</u>	PGLV <u>T</u> MNEY	0.553
S558	PKA	K/RK/RX <u>S</u> / <u>T</u>	YLRK <u>S</u> LNQS	0.605
	RSK	RXR <u>X</u> S/ <u>T</u>		0.501
S573	PKA	K/RK/RX <u>S</u> / <u>T</u>	RILQSGMTL	0.821
S596	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	TDIQ <u>S</u> RIVE	0.501
S607	PKA	K/RK/RX <u>S</u> / <u>T</u>	ERLD <u>S</u> EISM	0.695
	RSK	RXR <u>X</u> S/ <u>T</u>		0.551
	PKG	R/KR/KX <u>S</u> / <u>T</u>		0.509
S610	CDK1	LPX <u>S</u> PXKK	DSEI <u>S</u> MYTF	0.515
T613	PKC	R/KR/KR/K/F <u>S</u> FRR	ISMY <u>T</u> FSRM	0.752
S615	PKC	R/KR/KR/K/F <u>S</u> FRR	MYTF <u>S</u> RMKY	0.658
T631	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	ILD <u>T</u> REED	0.629
S636	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	REED <u>S</u> ETED	0.687
T638	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	EDSE <u>T</u> EDSG	0.591
	CKI	D/E(X)X <u>S</u> / <u>T</u>		0.532
	CDK1	LPX <u>S</u> PXKK		0.526
S641	CKI	D/E(X)X <u>S</u> / <u>T</u>	ETED <u>S</u> GHGS	0.569
S645	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	SGHG <u>S</u> STES	0.621
S646	CDK1	LPX <u>S</u> PXKK	GHG <u>S</u> TESQ	0.515
T647	PKC	R/KR/KR/K/F <u>S</u> FRR	HG <u>S</u> TESQS	0.639
	CDK1	LPX <u>S</u> PXKK		0.551
S649	DNAPK	QX <u>S</u> / <u>T</u> QE/D	SST <u>E</u> SQSQC	0.647
	ATM	L/ <u>S</u> <u>S</u> QE/D		0.527
S651	DNAPK	QX <u>S</u> / <u>T</u> QE/D	TESQ <u>S</u> QCSS	0.586
S654	CDK1	LPX <u>S</u> PXKK	QSQC <u>S</u> SQVS	0.552
S655	DNAPK	QX <u>S</u> / <u>T</u> QE/D	SQC <u>S</u> SQVSD	0.590
S667	DNAPK	QX <u>S</u> / <u>T</u> QE/D	PAED <u>S</u> QRSD	0.522
	ATM	L/ <u>S</u> <u>S</u> QE/D		0.512
S674	DNAPK	QX <u>S</u> / <u>T</u> QE/D	SDPH <u>S</u> QELH	0.634
	ATM	L/ <u>S</u> <u>S</u> QE/D		0.623

T691	p38 ^{MAPK}	PXS/TP	KRPKTTPPPK	0.534
	GSK3	S/TXXXS/T		0.524
	CDK5	S/TPXK/H/R		0.514

JCPyV

residue	Protein kinase	Consensus motif	Sequence in LTA _g	score
T84	CKII	D/ED/ED/ES/TD/ED/E	SEVPTTYGTD	0.509
T87	CKII	D/ED/ED/ES/TD/ED/E	PTVPTYGTD	0.566
T96	CKII	D/ED/ED/ES/TD/ED/E	SWWNTTFNEK	0.534
S114	CKII	D/ED/ED/ES/TD/ED/E	EMFASDDEN	0.699
S121	DNAPK ATM	QXS/TQE/D	ENTGSQHST	0.634
		L/S ₂ QE/D		0.627
S124	PKC	R/KR/KR/K/F ₂ FRR	GSQHSTPPK	0.699
T125	CDK5	S/TPXK/H/R	SQHSTTPPKK	0.659
	PKC	R/KR/KR/K/F ₂ FRR		0.647
	GSK3	S/TXXXS/T		0.503
S148	PKC	R/KR/KR/K/F ₂ FRR	HAFLSQAVF	0.748
	DNAPK	QXS/TQE/D		0.614
	ATM	L/S ₂ QE/D		0.582
S159	PKC	R/KR/KR/K/F ₂ FRR	RTVASFAVY	0.785
T164	PKC	R/KR/KR/K/F ₂ FRR	FAVYTTKEK	0.685
T165	PKC	R/KR/KR/K/F ₂ FRR	AVYTTKEKA	0.541
T183	PKC	R/KR/KR/K/F ₂ FRR	KYSVTFISR	0.829
T200	p38 ^{MAPK} CDK5	PXS/TP	LEFLTTPHRH	0.567
		S/TPXK/H/R		0.547
S207	PKA PKG	K/RK/RXS/T	RHRVSAINN	0.756
		R/KR/KXS/T		0.556
S248	CKI	D/E(X)XS/T	VVEESIQGG	0.544
S270	PKC	R/KR/KR/K/F ₂ FRR	TKQVSWKLV	0.597
	PKA	K/RK/RXS/T		0.505
T281	CKII	D/ED/ED/ES/TD/ED/E	YALETKCED	0.577
Y322	SRC	EEDVYGXV	HEKHYYNAQ	0.502
Y323	EGFR	XXEXYYXX	EKHYYNAQI	0.554
S331	PKC	R/KR/KR/K/F ₂ FRR	IFADS ₂ KNQK	0.722
T344	PKC	R/KR/KR/K/F ₂ FRR	QAVDTVA ₂ AK	0.816
S353	PKA PKG	K/RK/RXS/T	QRVD ₂ SIHMT	0.598
		R/KR/KXS/T		0.514
T357	CKII	D/ED/ED/ES/TD/ED/E	SIHMTREEM	0.590
T435	PKC	R/KR/KR/K/F ₂ FRR	SGKTTLAAA	0.593
T479	CKII	D/ED/ED/ES/TD/ED/E	DVKG ₂ TGAES	0.590
S483	CKII	D/ED/ED/ES/TD/ED/E	TGAESRDLP	0.536
S488	PKC	R/KR/KR/K/F ₂ FRR	RDLP ₂ SGHGI	0.549
S493	CDK1	LPXSPXKK	GHG ₂ ISNLDC	0.529
S505	PKC	R/KR/KR/K/F ₂ FRR	YLDG ₂ SVKVN	0.569
T519	CDK1	LPXSPXKK	QNKRTQVFP	0.513
T528	CKII	D/ED/ED/ES/TD/ED/E	PGIVTMNEY	0.520
S533	CDK1	LPXSPXKK	MNEYSVPR ₂ T	0.516
S557	RSK	RXRXS/T	YLRKSLSCS	0.541
S559	PKA	K/RK/RXS/T	RKSLSCSEY	0.575
S561	CKII	D/ED/ED/ES/TD/ED/E	SLSCSEYLL	0.521
S572	PKA	K/RK/RXS/T	RILOSGMTL	0.824
S609	CDK1	LPXSPXKK	DLEISMYTF	0.515
Y611	EGFR	XXEXYYXX	EISMYTFST	0.515
S614	PKC	R/KR/KR/K/F ₂ FRR	MYTFSTMKA	0.731

T615	PKC	R/KR/KR/K/F <u>S</u> FRR	YTF <u>S</u> T <u>M</u> KAN	0.911
S635	CKII	D/ED/ED/ES/TD/ED/E	REED <u>S</u> EAED	0.699
S640	CKI	D/E(X)X <u>S</u> /T	EAED <u>S</u> G <u>H</u> G <u>S</u>	0.542
S644	CKII	D/ED/ED/ES/TD/ED/E	SG <u>H</u> G <u>S</u> STES	0.621
S645	CDK1	LPX <u>S</u> PXKK	G <u>H</u> G <u>S</u> STESQ	0.505
T646	PKC	R/KR/KR/K/F <u>S</u> FRR	H <u>G</u> SSTESQS	0.639
S648	DNAPK	QX <u>S</u> /TQE/D	SSTESQSQC	0.647
S650	DNAPK	QX <u>S</u> /TQE/D	TESQSQCF <u>S</u>	0.586
S654	DNAPK	QX <u>S</u> /TQE/D	SQCF <u>S</u> QVSE	0.520
T664	ATM	L/ <u>S</u> <u>S</u> QE/D	SGADTQENC	0.517
	CKII	D/ED/ED/ES/TD/ED/E		0.513
T648	p38 ^{MAPK}	PX <u>S</u> /TP	KKPKTPPPK	0.548
	GSK3	<u>S</u> /TXXS/T		0.520

KIPyV

residue	Protein kinase	Consensus motif	Sequence in LTag	score
S6	CKII	D/ED/ED/ES/TD/ED/E	DKTLT <u>R</u> EEA	0.518
S65	CDK1	LPX <u>S</u> PXKK	KLQD <u>S</u> VSSV	0.514
S82	CDK1	LPX <u>S</u> PXKK	NIWQ <u>S</u> SQIP	0.516
S83	DNAPK	QX <u>S</u> /TQE/D	IWQSSQIPT	0.574
	ATM	L/ <u>S</u> <u>S</u> QE/D		0.533
T90	p38 ^{MAPK}	PX <u>S</u> /TP	PTYGT <u>P</u> DL	0.540
S98	ATM	L/ <u>S</u> <u>S</u> QE/D	DEWWSQFNT	0.633
	DNAPK	QX <u>S</u> /TQE/D		0.605
T102	CKII	D/ED/ED/ES/TD/ED/E	SQFN <u>T</u> YWEE	0.699
S113	DNAPK	QX <u>S</u> /TQE/D	RCNE <u>S</u> MPSS	0.543
S116	PKC	R/KR/KR/K/F <u>S</u> FRR	ESMP <u>S</u> SPKR	0.633
S117	CDK5	<u>S</u> /TPXK/H/R	SMP <u>S</u> SPKRS	0.635
	GSK3	<u>S</u> /TXXS/T		0.535
S121	PKG	R/KR/KX <u>S</u> /T	SPKR <u>S</u> AP <u>E</u> E	0.612
	CKII	D/ED/ED/ES/TD/ED/E		0.590
S130	DNAPK	QX <u>S</u> /TQE/D	EPSC <u>S</u> QATP	0.621
	ATM	L/ <u>S</u> <u>S</u> QE/D		0.586
T133	p38 ^{MAPK}	PX <u>S</u> /TP	CSQATPPKK	0.565
	CDK5	<u>S</u> /TPXK/H/R		0.525
S144	DNAPK	QX <u>S</u> /TQE/D	AFDAS <u>L</u> E <u>E</u> P	0.558
S161	PKC	R/KR/KR/K/F <u>S</u> FRR	HAVF <u>S</u> NKCI	0.899
T172	PKC	R/KR/KR/K/F <u>S</u> FRR	FVVHTTREK	0.836
	CKII	D/ED/ED/ES/TD/ED/E		0.521
S191	PKC	R/KR/KR/K/F <u>S</u> FRR	KYQC <u>S</u> FISK	0.778
T208	p38 ^{MAPK}	PX <u>S</u> /TP	IFFLT <u>P</u> HKH	0.585
	CDK5	<u>S</u> /TPXK/H/R		0.539
S215	PKA	K/RK/RX <u>S</u> /T	KHRV <u>S</u> AINN	0.758
	PKG	R/KR/KX <u>S</u> /T		0.569
S228	PKC	R/KR/KR/K/F <u>S</u> FRR	HCTV <u>S</u> FLFC	0.720
S303	PKC	R/KR/KR/K/F <u>S</u> FRR	YLLGS <u>Y</u> IRF	0.771
T309	CKII	D/ED/ED/ES/TD/ED/E	IRFAT <u>K</u> PEE	0.530
S318	CKII	D/ED/ED/ES/TD/ED/E	CEKCSKNDD	0.509
T324	PKC	R/KR/KR/K/F <u>S</u> FRR	NDDAT <u>H</u> KRV	0.886
T350	DNAPK	QX <u>S</u> /TQE/D	KNACTQ <u>A</u> ID	0.525
Y362	EGFR	XXEXY <u>Y</u> YXX	AERR <u>Y</u> NCVT	0.522
T366	PKC	R/KR/KR/K/F <u>S</u> FRR	YNCV <u>T</u> LTRK	0.878
T368	PKC	R/KR/KR/K/F <u>S</u> FRR	CVTL <u>T</u> RKKL	0.883
T374	PKC	R/KR/KR/K/F <u>S</u> FRR	KKLLT <u>K</u> RFK	0.940

S400	PKA	K/RK/RXS/T	LYMASIAWY	0.510
T405	PKC	R/KR/KR/K/F _S FRR	IAWYTGLNK	0.766
S440	PKA	K/RK/RXS/T	GPINS _G KTT	0.528
S528	PKG	R/KR/KXS/T	VNKR _S QIFP	0.514
T537	CKII PKG	D/ED/ED/ES/TD/ED/E R/KR/KXS/T	PGIVTMNEY	0.563 0.537
T546	PKC	R/KR/KR/K/F _S FRR	CIPETVAVR	0.591
T558	PKC	R/KR/KR/K/F _S FRR	TVMFTIKRN	0.883
S566	DNAPK	QXS/TQE/D	NLRESLEKT	0.532
T570	CDK5 GSK3	S/TPXK/H/R S/TXXS/T	SLEKTPQLL	0.649 0.501
S575	PKC ATM	R/KR/KR/K/F _S FRR L/SSQE/D	PQLLSQRIL	0.650 0.518
S581	PKC PKA	R/KR/KR/K/F _S FRR K/RK/RXS/T	RILHSGIAM	0.672 0.589
S596	CKII	D/ED/ED/ES/TD/ED/E	YRPVSDFDE	0.556
S604	CKII	D/ED/ED/ES/TD/ED/E	EEIQSNVVY	0.528
T620	PKC	R/KR/KR/K/F _S FRR	YIGLIEFAT	0.590
T630	PKC	R/KR/KR/K/F _S FRR	QMNVTTNGKN	0.675

WU

residue	Protein kinase	Consensus motif	Sequence in LTag	score
T4	CDK1	LPXSPXKK	MDKTLSRN	0.505
S6	PKC CKII	R/KR/KR/K/F _S FRR D/ED/ED/ES/TD/ED/E	DKTLSRNEAA	0.621 0.547
T32	PKC	R/KR/KR/K/F _S FRR	PLMRITKYL	0.512
S36	PKC	R/KR/KR/K/F _S FRR	TKYL _S KCKE	0.638
S57	PKA PKC	K/RK/RXS/T R/KR/KR/K/F _S FRR	KKLN _S LYLK	0.681 0.620
S82	CDK1	LPXSPXKK	EVWSSSQIP	0.529
S83	DNAPK ATM CDK1	QXS/TQE/D L/SSQE/D LPXSPXKK	VWSSSQIPT	0.588 0.519 0.505
T90	CDK5 p38 ^{MAPK}	S/TPXK/H/R PXS/TP	PTYGTDPWD	0.552 0.506
Y95	EGFR	XXEXYYXX	PDWDYWWSQ	0.550
S98	ATM DNAPK	L/SSQE/D QXS/TQE/D	DYWW _S QFNS	0.639 0.605
S102	CKII	D/ED/ED/ES/TD/ED/E	SQFNSYWEE	0.701
S117	GSK3 CKI p38 ^{MAPK}	S/TXXS/T D/E(X)XS/T PXS/TP	EMPKSPGET	0.540 0.522 0.519
T121	CDK5 p38 ^{MAPK}	S/TPXK/H/R PXS/TP	SPGETPTKR	0.591 0.522
T126	CKII	D/ED/ED/ES/TD/ED/E	PTKRTREDD	0.511
S136	DNAPK ATM	QXS/TQE/D L/SSQE/D	EPQCSQATP	0.612 0.537
T139	p38 ^{MAPK} CDK5	PXS/TP S/TPXK/H/R	CSQATPPKK	0.571 0.515
S152	DNAPK	QXS/TQE/D	ATDASLSFP	0.561
S154	PKC	R/KR/KR/K/F _S FRR	DASLSFPKE	0.670
S164	DNAPK	QXS/TQE/D	EEFVSQAVF	0.585

	ATM	L/SSQE/D		0.562
T180	PKC	R/KR/KR/K/F _S FRR	FVIHTTKEK	0.815
	CKII	D/ED/ED/ES/TD/ED/E		0.553
T181	PKC	R/KR/KR/K/F _S FRR	VIHTTKEKA	0.525
T187	PKC	R/KR/KR/K/F _S FRR	EKAETLYKK	0.759
S194	PKC	R/KR/KR/K/F _S FRR	KKLLSKFKC	0.842
S202	PKG	R/KR/KXS/T	CNFA _S RHSY	0.543
S205	PKA	K/RK/RXS/T	ASRHSYYNT	0.830
	DNAPK	QXS/TQE/D		0.552
T216	p38 ^{MAPK}	PXS/TP	VFILT _P FRH	0.654
	CDK5	S/TPXK/H/R		0.507
S223	PKA	K/RK/RXS/T	RHRV _S AVNN	0.725
Y247	EGFR	XXEXYYXX	VNNAYGLYS	0.513
T254	PKC	R/KR/KR/K/F _S FRR	YSRMT _R DPF	0.542
T259	CKII	D/ED/ED/ES/TD/ED/E	RDPFT _L CEE	0.620
Y280	SRC	EEDVYGXV	AEDLYGEFK	0.552
S293	CKII	D/ED/ED/ES/TD/ED/E	WKAL _S EFAL	0.518
S326	CDK1	LPXSPXKK	EKCNS _N NEDA	0.539
	CKII	D/ED/ED/ES/TD/ED/E		0.507
S351	PKC	R/KR/KR/K/F _S FRR	SDSK _S SQKNV	0.601
S371	PKA	K/RK/RXS/T	RRVDS _L LNMS	0.757
T394	PKC	R/KR/KR/K/F _S FRR	KMDK _T IKGE	0.681
T451	PKC	R/KR/KR/K/F _S FRR	SGKT _T VAAA	0.763
S509	CDK1	LPXSPXKK	GNGMS _N NLDN	0.547
S521	PKC	R/KR/KR/K/F _S FRR	YLDG _S VKVN	0.869
S535	PKG	R/KR/KXS/T	LNKR _S QIFP	0.545
T544	PKG	R/KR/KXS/T	PGIV _T MNEY	0.546
	CKII	D/ED/ED/ES/TD/ED/E		0.506
T561	PKC	R/KR/KR/K/F _S FRR	RFHK _T VLFT	0.538
T565	PKC	R/KR/KR/K/F _S FRR	TVLFT _P PKRH	0.783
	p38 ^{MAPK}	PXS/TP		0.533
S573	PKC	R/KR/KR/K/F _S FRR	HLKE _S LDKT	0.807
T577	CDK5	S/TPXK/H/R	SLDK _T PELM	0.651
	GSK3	S/TXXS/T		0.520
	p38 ^{MAPK}	PXS/TP		0.502
S588	PKC	R/KR/KR/K/F _S FRR	RVLQ _S GMCI	0.701
	PKA	K/RK/RXS/T		0.585
S603	PKA	K/RK/RXS/T	CRPV _S DFHP	0.644
T627	PKC	R/KR/KR/K/F _S FRR	YIGL _T EFAD	0.534

MCPyV

residue	Protein kinase	Consensus motif	Sequence in LTag	score
Y24	INSR	YXXM	APNCYGNIP	0.568
S37	PKC	R/KR/KR/K/F _S FRR	AFKR _S CLKH	0.567
	PKG	R/KR/KXS/T		0.521
T57	PKC	R/KR/KR/K/F _S FRR	MELN _T LWSK	0.571
S60	PKC	R/KR/KR/K/F _S FRR	NTLW _S KFQQ	0.654
Y85	EGFR	XXEXYYXX	EAPIYGTK	0.524
T87	PKC	R/KR/KR/K/F _S FRR	PIYG _T TKFK	0.918
T88	PKC	R/KR/KR/K/F _S FRR	IYGT _T KFKE	0.660
S100	PKC	R/KR/KR/K/F _S FRR	SGGF _S FGKA	0.687
	CKI	D/E(X)XS/T		0.542
S116	PKC	R/KR/KR/K/F _S FRR	HGTN _S SRK	0.761
S118	CDK1	LPXSPXKK	TNSR _S RKPS	0.508

S122	PKB PKG RSK	RXR <u>X</u> *X*S/TF/L R/KR/KX <u>S</u> /T RXRX <u>X</u> S/T	SRKP <u>S</u> SNAS	0.638 0.628 0.577
S123	PKC	R/KR/KR/K/F <u>S</u> FRR	RKP <u>S</u> SNASR	0.656
S126	CDK1	LPX <u>S</u> PXKK	SSNA <u>S</u> RGAP	0.523
S131	CDK1	LPX <u>S</u> PXKK	RGAP <u>S</u> GSSP	0.521
S133	CDK1	LPX <u>S</u> PXKK	APSG <u>S</u> SPPH	0.601
S134	CDK5 CDK1 p38 ^{MAPK} GSK3	<u>S</u> /TPXK/H/R LPX <u>S</u> PXKK PX <u>S</u> /TP <u>S</u> /TXXS/T	PSG <u>S</u> SPPHS	0.636 0.554 0.506 0.502
S138	DNAPK GSK3	QX <u>S</u> /TQE/D <u>S</u> /TXXS/T	SPPH <u>S</u> QSSS	0.636 0.502
S140	CDK1	LPX <u>S</u> PXKK	PHSQ <u>S</u> SSSG	0.591
S141	CKI	D/E(X)X <u>S</u> /T	HSQ <u>S</u> SSSGY	0.563
S142	CDK1	LPX <u>S</u> PXKK	SQ <u>S</u> SSSGYG	0.536
S147	PKC CDK1	R/KR/KR/K/F <u>S</u> FRR LPX <u>S</u> PXKK	SGYG <u>S</u> FSAS	0.741 0.507
S149	CDK1	LPX <u>S</u> PXKK	YGSF <u>S</u> ASQA	0.596
S151	DNAPK ATM CDK1	QX <u>S</u> /TQE/D L/SSQE/D LPX <u>S</u> PXKK	SFS <u>A</u> SQASD	0.637 0.622 0.531
S156	DNAPK CDK1	QX <u>S</u> /TQE/D LPX <u>S</u> PXKK	QASD <u>S</u> QSRG	0.598 0.559
S175	CDK1	LPX <u>S</u> PXKK	PTSS <u>S</u> GSSS	0.500
S177	CKII CDK1 CKI	D/ED/ED/ES/ <u>T</u> D/ED/E LPX <u>S</u> PXKK D/E(X)X <u>S</u> /T	SSSG <u>S</u> SSRE	0.536 0.516 0.513
S178	PKC CKII	R/KR/KR/K/F <u>S</u> FRR D/ED/ED/ES/ <u>T</u> D/ED/E	SSG <u>S</u> SSREE	0.684 0.572
S179	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	SGSS <u>S</u> REET	0.605
T184	CDK1	LPX <u>S</u> PXKK	REET <u>T</u> NSGR	0.531
S186	PKC	R/KR/KR/K/F <u>S</u> FRR	ETT <u>N</u> SGRES	0.581
S190	PKA	K/RK/RX <u>S</u> /T	SGRES <u>T</u> PN	0.604
S191	PKA RSK	K/RK/RX <u>S</u> /T RXRX <u>X</u> S/T	GRES <u>T</u> PNG	0.685 0.503
T192	CDK1	LPX <u>S</u> PXKK	RES <u>T</u> PNGT	0.503
T196	CDK1	LPX <u>S</u> PXKK	TPNG <u>T</u> DVPR	0.503
S197	PKC	R/KR/KR/K/F <u>S</u> FRR	PNG <u>T</u> SVPRN	0.666
S202	PKA	K/RK/RX <u>S</u> /T	VPRN <u>S</u> SRTD	0.576
S203	PKA	K/RK/RX <u>S</u> /T	PRN <u>S</u> SRTDG	0.671
T205	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	NSSR <u>T</u> DGTW	0.508
S217	DNAPK CDK1	QX <u>S</u> /TQE/D LPX <u>S</u> PXKK	FCDE <u>S</u> LSSP	0.570 0.528
S219	CKII CDK1	D/ED/ED/ES/ <u>T</u> D/ED/E LPX <u>S</u> PXKK	DESL <u>S</u> SPEP	0.628 0.524
S220	p38 ^{MAPK}	PX <u>S</u> /TP	ESL <u>S</u> SPEPP	0.535
S225	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	PEPP <u>S</u> SSEE	0.673
S226	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	EPP <u>S</u> SSEEP	0.664
S227	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	PPSS <u>S</u> EEPE	0.620
S235	GSK3	<u>S</u> /TXXS/T	EEPP <u>S</u> SRSS	0.507
S238	CDK1	LPX <u>S</u> PXKK	PSSR <u>S</u> SPRQ	0.553
S239	CDK5 p38 ^{MAPK} GSK3 PKC	<u>S</u> /TPXK/H/R PX <u>S</u> /TP <u>S</u> /TXXS/T R/KR/KR/K/F <u>S</u> FRR	SSR <u>S</u> SPRQP	0.717 0.579 0.516 0.505

S245	CDK1	LPXSPXKK	RQPPSSSAE	0.577
S246	CKII	D/ED/ED/ES/TD/ED/E	QPPSSSAEE	0.618
S247	CDK1	LPXSPXKK	PPSSSAEEA	0.543
S253	CKII	D/ED/ED/ES/TD/ED/E	EEASSSQFT	0.520
	CDK1	LPXSPXKK		0.520
S254	ATM	L/SSQE/D	EASSSQFTD	0.605
	CKII	D/ED/ED/ES/TD/ED/E		0.575
	DNAPK	QXS/TQE/D		0.564
	CKI	D/E(X)XS/T		0.552
	CDK1	LPXSPXKK		0.505
T257	CKII	D/ED/ED/ES/TD/ED/E	SSQFTDEEY	0.600
Y261	SRC	EEDVYGXV	TDEEYRSSS	0.541
S263	CKII	D/ED/ED/ES/TD/ED/E	EEYRSSSFT	0.502
S264	CKI	D/E(X)XS/T	EYRSSSFTT	0.524
	PKA	K/RK/RXS/T		0.510
S265	CKI	D/E(X)XS/T	YRSSSFTTP	0.590
	PKA	K/RK/RXS/T		0.578
T267	PKC	R/KR/KR/K/FSFRR	SSSFTTPKT	0.886
T268	CDK5	S/TPXK/H/R	SSFTTPKTP	0.678
	p38 ^{MAPK}	PXS/TP		0.514
T271	CDK5	S/TPXK/H/R	TTPKTTPPF	0.610
	p38 ^{MAPK}	PXS/TP		0.526
	GSK3	S/TXXS/T		0.510
S276	PKC	R/KR/KR/K/FSFRR	PPPF _S RKRK	0.829
S284	PKC	R/KR/KR/K/FSFRR	KFGGSRSSA	0.632
	CDK1	LPXSPXKK		0.527
S287	CDK1	LPXSPXKK	GSRSSASSA	0.554
S290	PKC	R/KR/KR/K/FSFRR	SSASSASSA	0.623
S292	CDK1	LPXSPXKK	ASSASSASF	0.527
S293	CDK1	LPXSPXKK	SSASSASFT	0.527
T297	PKC	R/KR/KR/K/FSFRR	SASFTSTTP	0.681
T299	CDK5	S/TPXK/H/R	SFTSTPPKP	0.748
	PKC	R/KR/KR/K/FSFRR		0.729
	p38 ^{MAPK}	PXS/TP		0.506
S320	CKII	D/ED/ED/ES/TD/ED/E	PIDLSDYLS	0.509
S324	PKC	R/KR/KR/K/FSFRR	SDYL _S HAVY	0.619
S329	PKC	R/KR/KR/K/FSFRR	HAVY _S NKTV	0.721
T341	CKII	D/ED/ED/ES/TD/ED/E	AIYTTSDKA	0.543
S342	PKC	R/KR/KR/K/FSFRR	IYTTSDKAI	0.852
	CKII	D/ED/ED/ES/TD/ED/E		0.504
T375	CDK1	LPXSPXKK	LLFITLSKH	0.514
S377	PKC	R/KR/KR/K/FSFRR	FITL _S KHRV	0.842
	CDK1	LPXSPXKK		0.502
S382	PKA	K/RK/RXS/T	KHRV _S AIKN	0.693
	PKG	R/KR/KXS/T		0.566
	PKC	R/KR/KR/K/FSFRR		0.514
T390	PKC	R/KR/KR/K/FSFRR	NFCSTFCTI	0.567
S501	PKC	R/KR/KR/K/FSFRR	LFYESKSQK	0.712
T514	PKC	R/KR/KR/K/FSFRR	QAADTVLAK	0.697
	CDK1	LPXSPXKK		0.501
T527	CKII	D/ED/ED/ES/TD/ED/E	MLEMTIRTEM	0.513
T580	PKC	R/KR/KR/K/FSFRR	IQLLTENIP	0.619
S601	PKC	R/KR/KR/K/FSFRR	SGKTSFAAA	0.614
S647	DNAPK	QXS/TQE/D	KGQNSLNKD	0.514
S675	CDK1	LPXSPXKK	AVAVSLEKK	0.503
T694	PKG	R/KR/KXS/T	PCIVTANDY	0.627

T703	PKC	R/KR/KR/K/F <u>S</u> FRR	FIPK <u>T</u> LIAR	0.652
S709	PKC	R/KR/KR/K/F <u>S</u> FRR	IARF <u>S</u> YTLH	0.582
T711	PKC	R/KR/KR/K/F <u>S</u> FRR	RFSY <u>T</u> LHFS	0.698
S723	PKA	K/RK/RX <u>S</u> /T	NLRD <u>S</u> LDQN	0.576
S738	PKA	K/RK/RX <u>S</u> /T	RILQ <u>S</u> GTTL	0.682
T741	CDK1	LPX <u>S</u> PXKK	QSGT <u>T</u> LLLC	0.549
S772	PKC	R/KR/KR/K/F <u>S</u> FRR	QILQ <u>S</u> EISY	0.788
T806	CKII CKI	D/ED/ED/ES/ <u>T</u> D/ED/E	GPEE <u>T</u> EETQ	0.608
		D/E(X)X <u>S</u> /T		0.606
T809	DNAPK CKI	QX <u>S</u> /TQE/D	ETE <u>E</u> TQDSG	0.597
		D/E(X)X <u>S</u> /T		0.520
S812	CKI	D/E(X)X <u>S</u> /T	ETQD <u>S</u> GTFS	0.506
T814	PKC	R/KR/KR/K/F <u>S</u> FRR	QD <u>S</u> G <u>T</u> FSQ	0.705
S816	ATM DNAPK	L/ <u>S</u> <u>S</u> QE/D	SGT <u>F</u> <u>S</u> Q	0.663
		QX <u>S</u> /TQE/D		0.620

*=polair amino acids

HPyV6

residue	Protein kinase	Consensus motif	Sequence in LTag	score
S20	PKA	K/RK/RX <u>S</u> /T	LIGL <u>S</u> MACW	0.631
	CDK1	LPX <u>S</u> PXKK		0.532
T65	PKC	R/KR/KR/K/F <u>S</u> FRR	KLNA <u>T</u> LRDQ	0.572
S73	ATM	L/ <u>S</u> <u>S</u> QE/D	QM <u>S</u> <u>S</u> SPTWC	0.520
T75	PKC CDK1	R/KR/KR/K/F <u>S</u> FRR	SSSPT <u>W</u> CFS	0.661
		LPX <u>S</u> PXKK		0.503
S90	p38 ^{MAPK} GSK3 CDK5	PX <u>S</u> /TP	PQYG <u>S</u> PGWE	0.538
		<u>S</u> /TXXX <u>S</u> /T		0.508
		<u>S</u> /TPXK/H/R		0.502
Y110	SRC	EEDVY <u>G</u> XV	DEDLY <u>C</u> DEH	0.546
S116	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	DEHL <u>S</u> ASEE	0.731
S118	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	HLSA <u>S</u> EEED	0.704
S131	ATM DNAPK	L/ <u>S</u> <u>S</u> QE/D	GEGN <u>S</u> QDSK	0.623
		QX <u>S</u> /TQE/D		0.616
T139	CDK5 p38 ^{MAPK}	<u>S</u> /TPXK/H/R	KYSC <u>T</u> PPKK	0.583
		PX <u>S</u> /TP		0.552
T178	CKII CKI	D/ED/ED/ES/ <u>T</u> D/ED/E	FVSY <u>T</u> TLEK	0.594
		D/E(X)X <u>S</u> /T		0.538
T179	CKI	D/E(X)X <u>S</u> /T	VSY <u>T</u> TLEKW	0.510
T185	DNAPK	QX <u>S</u> /TQE/D	EKWE <u>T</u> LYDK	0.560
Y187	SRC	EEDVY <u>G</u> XV	WETLY <u>D</u> KLQ	0.505
T199	PKC	R/KR/KR/K/F <u>S</u> FRR	NAVFT <u>G</u> AYK	0.721
T216	p38 ^{MAPK} CDK5	PX <u>S</u> /TP	LYCI <u>T</u> PRRH	0.634
		<u>S</u> /TPXK/H/R		0.531
S223	PKA	K/RK/RX <u>S</u> /T	RHRV <u>S</u> AMLN	0.721
S246	PKG	R/KR/KX <u>S</u> /T	AVLK <u>S</u> AECY	0.506
S264	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	VIQE <u>S</u> KAEG	0.581
S271	CKII CDK1	D/ED/ED/ES/ <u>T</u> D/ED/E	EGLH <u>S</u> YDFQ	0.546
		LPX <u>S</u> PXKK		0.503
S278	CKII PKC	D/ED/ED/ES/ <u>T</u> D/ED/E	FQEG <u>S</u> KKEE	0.668
		R/KR/KR/K/F <u>S</u> FRR		0.554
S290	PKC	R/KR/KR/K/F <u>S</u> FRR	NQVA <u>S</u> FASD	0.667
T295	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	FASD <u>T</u> DLTD	0.548
S316	PKC	R/KR/KR/K/F <u>S</u> FRR	NDPA <u>S</u> CMKC	0.714

S368	PKC	R/KR/KR/K/F <u>S</u> FRR	LMLE <u>S</u> TRQD	0.595
T396	CDK1	LPX <u>S</u> PXKK	GVEIT <u>Q</u> LLG	0.520
T413	PKC	R/KR/KR/K/F <u>S</u> FRR	QPSFT <u>T</u> TKLK	0.791
T414	CDK1	LPX <u>S</u> PXKK	PSFT <u>T</u> TKLKE	0.538
S421	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	KEIL <u>S</u> ILTE	0.503
T424	CKI	D/E(X) <u>X</u> S/ <u>T</u>	LSIL <u>T</u> ENIP	0.506
T445	PKC	R/KR/KR/K/F <u>S</u> FRR	SGKT <u>T</u> LAAA	0.543
T464	p38 ^{MAPK}	PX <u>S</u> / <u>T</u> P	NVNC <u>I</u> PDKI	0.510
T489	p38 ^{MAPK}	PX <u>S</u> / <u>T</u> P	DVKG <u>T</u> PMAN	0.536
T497	DNAPK	QX <u>S</u> / <u>T</u> QE/D	NTNL <u>T</u> QGCG	0.579
T503	CDK1	LPX <u>S</u> PXKK	GCGM <u>T</u> NLDN	0.517
T538	PKG	R/KR/KX <u>S</u> / <u>T</u>	PSVIT <u>C</u> NEY	0.508
T547	PKC	R/KR/KR/K/F <u>S</u> FRR	VIPCT <u>V</u> KAR	0.898
T575	PKC	R/KR/KR/K/F <u>S</u> FRR	CVLM <u>S</u> KRLL	0.716
T583	CDK1	LPX <u>S</u> PXKK	LQKG <u>T</u> TLLA	0.529
S618	PKA	K/RK/RX <u>S</u> / <u>T</u>	ERWV <u>S</u> FGMY	0.716
T624	PKC CKII	R/KR/KR/K/F <u>S</u> FRR D/ED/ED/ES/ <u>T</u> D/ED/E	GMVQ <u>T</u> MKEN	0.781 0.536
T637	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	IDPF <u>T</u> INLV	0.513
T654	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	ENDE <u>T</u> NDST	0.505
S657	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	ETND <u>S</u> TQES	0.583
T658	DNAPK ATM CDK1	QX <u>S</u> / <u>T</u> QE/D L/ <u>S</u> <u>S</u> QE/D LPX <u>S</u> PXKK	TND <u>S</u> <u>T</u> QESG	0.636 0.577 0.512
S661	CKI	D/E(X) <u>X</u> S/ <u>T</u>	STQ <u>E</u> SGIGS	0.510
S665	DNAPK	QX <u>S</u> / <u>T</u> QE/D	SGIG <u>S</u> MHSM	0.518

HPyV7

residue	Protein kinase	Consensus motif	Sequence in LTag	score
S38	PKC PKA	R/KR/KR/K/F <u>S</u> FRR K/RK/RX <u>S</u> / <u>T</u>	VRLASKKYH	0.921 0.508
S73	RSK p38 ^{MAPK}	RXR <u>X</u> S/ <u>T</u> PX <u>S</u> / <u>T</u> P	QRSG <u>S</u> PMWH	0.537 0.500
S79	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	MWHY <u>S</u> SDEV	0.572
S80	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	WHY <u>S</u> SDEVR	0.504
S91	CDK5 p38 ^{MAPK} GSK3	<u>S</u> / <u>T</u> PXK/H/R PX <u>S</u> / <u>T</u> P <u>S</u> / <u>T</u> XXS/T	PPYG <u>S</u> PAWD	0.587 0.524 0.508
Y110	SRC	EEDVY <u>G</u> XV	DEDLY <u>C</u> TEE	0.539
T112	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	DLYC <u>T</u> EELS	0.564
S116	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	TEEL <u>S</u> SSDE	0.708
S117	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	EEL <u>S</u> SSDEE	0.753
S118	CKII CDK1	D/ED/ED/ES/ <u>T</u> D/ED/E LPX <u>S</u> PXKK	EL <u>S</u> SSDEEE	0.733 0.510
S136	ATM DNAPK	L/ <u>S</u> <u>S</u> QE/D QX <u>S</u> / <u>T</u> QE/D	EEGC <u>S</u> QDSK	0.598 0.531
S142	PKC	R/KR/KR/K/F <u>S</u> FRR	DSKY <u>S</u> ATPP	0.515
T144	p38 ^{MAPK} CDK5	PX <u>S</u> / <u>T</u> P <u>S</u> / <u>T</u> PXK/H/R	KYSAT <u>P</u> PKQ	0.549 0.543
S163	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	PECL <u>S</u> EFLS	0.505
T183	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	FLCY <u>T</u> TYEK	0.505
Y207	EGFR	XXEY <u>Y</u> YXX	FIGAY <u>N</u> CV	0.523
S213	PKA	K/RK/RX <u>S</u> / <u>T</u>	CVDS <u>G</u> ALV	0.568
S221	CDK1	LPX <u>S</u> PXKK	VFFI <u>S</u> GSRH	0.523

S223	PKC CDK1	R/KR/KR/K/F <u>S</u> FRR LPX <u>S</u> PXKK	FISG <u>S</u> RHRV	0.698 0.546
S228	PKA	K/RK/RX <u>S</u> / <u>T</u>	RHRV <u>S</u> AILN	0.732
T239	PKC	R/KR/KR/K/F <u>S</u> FRR	KKHCTV <u>S</u> FI	0.505
S241	PKC	R/KR/KR/K/F <u>S</u> FRR	HCTV <u>S</u> FIMV	0.850
S276	CKII CDK1	D/ED/ED/ES/ <u>T</u> D/ED/E LPX <u>S</u> PXKK	GGLHSYDFQ	0.560 0.533
S283	PKC	R/KR/KR/K/F <u>S</u> FRR	FQEAS <u>K</u> KDD	0.518
T303	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	DMEL <u>T</u> DVLL	0.507
S328	PKC	R/KR/KR/K/F <u>S</u> FRR	KCLK <u>S</u> VKAH	0.913
T347	PKC	R/KR/KR/K/F <u>S</u> FRR	KLKFTAKNQ	0.780
S373	PKC	R/KR/KR/K/F <u>S</u> FRR	LMME <u>S</u> TRKD	0.571
S382	PKC	R/KR/KR/K/F <u>S</u> FRR	LMVM <u>S</u> FKKQ	0.753
T401	CDK1	LPX <u>S</u> PXKK	GVEIT <u>Q</u> LIG	0.524
S426	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	KEML <u>S</u> YLVE	0.525
Y427	INSR	<u>Y</u> XXM	EMLS <u>Y</u> LVEN	0.500
T450	PKC	R/KR/KR/K/F <u>S</u> FRR	SGKT <u>T</u> LAAA	0.543
S470	PKC	R/KR/KR/K/F <u>S</u> FRR	VNC <u>S</u> SDKIN	0.611
T494	p38 ^{MAPK}	PX <u>S</u> / <u>T</u> P	DVKGT <u>I</u> PLPN	0.524
T533	PKC	R/KR/KR/K/F <u>S</u> FRR	HINK <u>T</u> SQLF	0.734
S534	CDK1	LPX <u>S</u> PXKK	INK <u>T</u> SQLF	0.542
T543	PKG CKII	R/KR/KX <u>S</u> / <u>T</u> D/ED/ED/ES/ <u>T</u> D/ED/E	PCIIT <u>C</u> NEY	0.609 0.521
Y547	INSR	<u>Y</u> XXM	TCNEY <u>A</u> IPT	0.502
T551	PKC	R/KR/KR/K/F <u>S</u> FRR	YAIPT <u>T</u> VKA	0.621
T552	PKC	R/KR/KR/K/F <u>S</u> FRR	AIPT <u>T</u> VKAR	0.861
S602	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	WEPV <u>S</u> DFVE	0.645
S624	PKC	R/KR/KR/K/F <u>S</u> FRR	EQWV <u>S</u> YGMF	0.543
S630	PKC	R/KR/KR/K/F <u>S</u> FRR	GMFQ <u>T</u> MKEN	0.692
S637	PKC	R/KR/KR/K/F <u>S</u> FRR	ENIL <u>S</u> GKDP	0.506
S655	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	TEENT <u>R</u> ETQ	0.507
T658	DNAPK	QX <u>S</u> / <u>T</u> QE/D	NTRET <u>Q</u> EST	0.617
S661	CKI	D/E(X)X <u>S</u> / <u>T</u>	ETQEST <u>E</u> SG	0.593
T662	CKI	D/E(X)X <u>S</u> / <u>T</u>	TQEST <u>E</u> SGI	0.530
S664	CKI CDK1	D/E(X)X <u>S</u> / <u>T</u> LPX <u>S</u> PXKK	ESTESGIGS	0.600 0.508
S668	DNAPK	QX <u>S</u> / <u>T</u> QE/D	SGIG <u>S</u> MNN	0.599

TSPyV

residue	Protein kinase	Consensus motif	Sequence in LTag	score
S6	CKII CKI	D/ED/ED/ES/ <u>T</u> D/ED/E D/E(X)X <u>S</u> / <u>T</u>	DKFL <u>S</u> REES	0.598 0.577
S10	PKA DNAPK	K/RK/RX <u>S</u> / <u>T</u> QX <u>S</u> / <u>T</u> QE/D	SREES <u>L</u> ELM	0.660 0.503
S38	PKC PKA	R/KR/KR/K/F <u>S</u> FRR K/RK/RX <u>S</u> / <u>T</u>	HKKM <u>S</u> LKYH	0.921 0.565
S53	PKA	K/RK/RX <u>S</u> / <u>T</u>	PEKM <u>S</u> RLNQ	0.611
Y67	EGFR SRC	XXEXY <u>Y</u> YXX EEDV <u>Y</u> GXV	QEGY <u>N</u> ARQ	0.629 0.513
S76	CDK1	LPX <u>S</u> PXKK	EFPT <u>S</u> FSSQ	0.519
S79	ATM DNAPK	L/ <u>S</u> QE/D QX <u>S</u> / <u>T</u> QE/D	TSF <u>S</u> QHDV	0.602 0.571

	CKI	D/E(X)XS/T		0.549
T85	DNAPK	QXS/TQE/D	HDVPTQDGR	0.552
S98	PKA	K/RK/RXS/T	YGHP\$WASW	0.502
S127	CKII	D/ED/ED/ES/TD/ED/E	FCHE\$TIPS	0.514
S136	CDK5 p38 ^{MAPK} GSK3	S/TPXK/H/R	DESR\$PSPT	0.539
		PXS/TP		0.521
		S/TXXXS/T		0.502
S138	CDK5 GSK3 p38 ^{MAPK}	S/TPXK/H/R	SRSP\$PTPG	0.725
		S/TXXXS/T		0.520
		PXS/TP		0.503
T140	CDK5 GSK3	S/TPXK/H/R	SPSPTPGPS	0.651
		S/TXXXS/T		0.540
T145	ATM	L/\$SQE/D	PGP\$TQFSE	0.553
S163	GSK3	S/TXXXS/T	PPED\$PGCT	0.503
S170	PKC	R/KR/KR/K/\$F\$FRR	CTQ\$SFSAT	0.552
T174	CDK5 p38 ^{MAPK}	S/TPXK/H/R	SFSATPPKP	0.699
		PXS/TP		0.567
S181	PKG PKA	R/KR/KXS/T	KPKK\$KYDS	0.637
		K/RK/RXS/T		0.525
S209	PKA	K/RK/RXS/T	NKTL\$SFLI	0.542
S210	PKC PKA	R/KR/KR/K/\$F\$FRR	KTL\$SFLIY	0.752
		K/RK/RXS/T		0.502
T215	CKII	D/ED/ED/ES/TD/ED/E	FLIYTNEK	0.584
T216	CDK1 CKII	LPX\$PXKK	LIYTNEKA	0.538
		D/ED/ED/ES/TD/ED/E		0.533
S239	PKA	K/RK/RXS/T	KSRH\$FQEG	0.625
T250	p38 ^{MAPK} CDK5	PXS/TP	VFLMTPGKH	0.628
		S/TPXK/H/R		0.589
S257	PKA	K/RK/RXS/T	KHRV\$AIKN	0.715
S270	PKC	R/KR/KR/K/\$F\$FRR	HCTV\$FLIC	0.745
S298	CKI	D/E(X)XS/T	LLEE\$KPGI	0.566
T322	PKC	R/KR/KR/K/\$F\$FRR	WNLLTDFAV	0.595
S351	PKC	R/KR/KR/K/\$F\$FRR	PSIC\$KCTK	0.654
T354	PKC	R/KR/KR/K/\$F\$FRR	CSKCTKKAL	0.908
T380	PKC	R/KR/KR/K/\$F\$FRR	KECKTQKTA	0.524
T383	PKG	R/KR/KXS/T	KTQKTACQQ	0.539
S403	PKC	R/KR/KR/K/\$F\$FRR	KLIE\$TRKE	0.759
T421	CKII	D/ED/ED/ES/TD/ED/E	FEKLIDEFG	0.527
S440	CKII	D/ED/ED/ES/TD/ED/E	VAWYSCLFE	0.515
T479	PKC	R/KR/KR/K/\$F\$FRR	SGKTTFAAA	0.704
S537	CDK1	LPX\$PXKK	GQGV\$NLDN	0.532
S549	PKC	R/KR/KR/K/\$F\$FRR	HLDG\$VKVD	0.870
S563	PKG	R/KR/KXS/T	VNKR\$QIFP	0.514
T572	PKG	R/KR/KXS/T	PCLVTMNEY	0.565
T593	p38 ^{MAPK} CDK1	PXS/TP	VLNFTPKHN	0.577
		LPX\$PXKK		0.511
S600	PKC	R/KR/KR/K/\$F\$FRR	HNLRSCLQV	0.622
S605	PKA CKII	K/RK/RXS/T	CLQV\$DYLL	0.649
		D/ED/ED/ES/TD/ED/E		0.510
Y607	EGFR	XXEXYYXX	QVSDYLLTE	0.583
T610	PKC	R/KR/KR/K/\$F\$FRR	DYLLTERIL	0.534
S636	CKII	D/ED/ED/ES/TD/ED/E	MFSE\$IKED	0.575
Y643	INSR	YXXM	EDVKYWKDI	0.511
S687	CKII CKI	D/ED/ED/ES/TD/ED/E	EEEF\$ETND	0.610
		D/E(X)XS/T		0.603

S689	CKII	D/ED/ED/ES/TD/ED/E	EFSE <u>T</u> NDSG	0.530
S696	ATM	L/SSQE/D	SGFQT <u>Q</u>	0.523

HPyV9

residue	Protein kinase	Consensus motif	Sequence in LTA _g	score
S6	CKII DNAPK	D/ED/ED/ES/TD/ED/E QXS/TQE/D	DQTL <u>S</u> LEEK	0.622 0.505
S28	PKC	R/KR/KR/K/F <u>S</u> FRR	WGNL <u>S</u> LMKK	0.521
Y34	EGFR	XXE <u>X</u> Y <u>Y</u> YXX	MKKAY <u>K</u> TVS	0.515
T36	PKC	R/KR/KR/K/F <u>S</u> FRR	KAYK <u>T</u> VSKI	0.831
S38	PKC	R/KR/KR/K/F <u>S</u> FRR	YKTV <u>S</u> KIYH	0.837
S75	PKC	R/KR/KR/K/F <u>S</u> FRR	SNCG <u>S</u> SSSQ	0.590
S76	CDK1	LPX <u>S</u> PXKK	NCG <u>S</u> SSQG	0.607
S77	CDK1	LPX <u>S</u> PXKK	CGSS <u>S</u> SQGY	0.503
S78	ATM DNAPK CDK1 CKI	L/SSQE/D QXS/TQE/D LPX <u>S</u> PXKK D/E(X)XS/T	GSS <u>S</u> SQGY	0.640 0.627 0.546 0.504
S83	CDK1 CKII PKG	LPX <u>S</u> PXKK D/ED/ED/ES/TD/ED/E R/KR/KXS/T	QGY <u>S</u> DSPY	0.544 0.508 0.504
S85	CDK1	LPX <u>S</u> PXKK	YYSD <u>S</u> PYFT	0.558
T91	CDK5 p38 ^{MAPK}	<u>S</u> /TPXK/H/R PXS/ <u>T</u> P	YFTE <u>T</u> PFSY	0.613 0.561
S94	CKII	D/ED/ED/ES/TD/ED/E	ETPF <u>S</u> YCER	0.547
S130	CKII	D/ED/ED/ES/TD/ED/E	SETI <u>S</u> SSDD	0.627
S131	CKII	D/ED/ED/ES/TD/ED/E	ETI <u>S</u> SSDDE	0.620
S132	CKII	D/ED/ED/ES/TD/ED/E	TISS <u>S</u> DDEN	0.710
S149	CKII	D/ED/ED/ES/TD/ED/E	PSSA <u>S</u> ASED	0.510
S151	CKII	D/ED/ED/ES/TD/ED/E	SASA <u>S</u> EDPD	0.624
S163	DNAPK CDK1 ATM	QXS/TQE/D LPX <u>S</u> PXKK L/SSQE/D	EAGS <u>S</u> QSSF	0.614 0.559 0.520
S166	CKI	D/E(X)XS/T	SSQS <u>S</u> FTCT	0.545
T168	PKC	R/KR/KR/K/F <u>S</u> FRR	QSS <u>F</u> ICTPP	0.585
T170	CDK5 PKC p38 ^{MAPK}	<u>S</u> /TPXK/H/R R/KR/KR/K/F <u>S</u> FRR PXS/ <u>T</u> P	SFTC <u>T</u> PPKR	0.759 0.626 0.551
T181	CDK5 GSK3	<u>S</u> /TPXK/H/R <u>S</u> /TXXS/T	PEPNT <u>T</u> PEDF	0.548 0.516
S199	PKC	R/KR/KR/K/F <u>S</u> FRR	HAIYSNKT <u>M</u>	0.688
T210	CKII	D/ED/ED/ES/TD/ED/E	FLIY <u>T</u> TVEK	0.514
T211	PKC	R/KR/KR/K/F <u>S</u> FRR	LIYT <u>T</u> VEKS	0.792
T221	PKC	R/KR/KR/K/F <u>S</u> FRR	QLYR <u>T</u> VEKS	0.822
S258	PKA PKG	K/RK/RXS/T R/KR/KXS/T	KHRV <u>S</u> AVKH	0.655 0.532
S271	PKC	R/KR/KR/K/F <u>S</u> FRR	QCTF <u>S</u> FIHC	0.794
T331	PKA	K/RK/RXS/T	EAKI <u>T</u> DVLL	0.531
S351	PKC	R/KR/KR/K/F <u>S</u> FRR	PGTC <u>S</u> KCEK	0.667
S357	PKC PKG	R/KR/KR/K/F <u>S</u> FRR R/KR/KXS/T	CEKK <u>S</u> HKFH	0.664 0.560
S378	PKC	R/KR/KR/K/F <u>S</u> FRR	LFLE <u>S</u> KSQK	0.619
S380	ATM	L/SSQE/D	LESK <u>S</u> QKNI	0.512
T404	CKII	D/ED/ED/ES/TD/ED/E	LVECT <u>R</u> MEL	0.543

	PKA	K/RK/RXS/T		0.516
S435	PKA	K/RK/RXS/T	LRWMSGVAW	0.818
	CDK1	LPXSPXKK		0.512
T459	PKC	R/KR/KR/K/F _S FRR	LQLVTTSQP	0.752
T460	PKC	R/KR/KR/K/F _S FRR	QLVTTSQPK	0.533
S461	DNAPK	QXS/TQE/D	LVTTSQPKK	0.631
S476	PKA	K/RK/RXS/T	GPINSGKTT	0.532
T480	PKC	R/KR/KR/K/F _S FRR	SGKTTLASA	0.512
S550	PKC	R/KR/KR/K/F _S FRR	HLDGTIKVN	0.873
S564	PKG	R/KR/KXS/T	VNKR _S QIFP	0.514
T573	PKG	R/KR/KXS/T	PVIMTMNEY	0.593
	DNAPK	QXS/TQE/D		0.509
T597	PKC	R/KR/KR/K/F _S FRR	FHCKTYLKQ	0.700
S606	CKII	D/ED/ED/ES/TD/ED/E	SLEKSDLIE	0.552
	CDK1	LPXSPXKK		0.531
S616	PKA	K/RK/RXS/T	RILNSGYTI	0.768
Y618	EGFR	XXEXYYXX	LNSGYTILL	0.512
T634	p38 ^{MAPK}	PXS/TP	VDSFTPQVQ	0.519
S653	PKA	K/RK/RXS/T	ERHV _S ITQF	0.730
T655	ATM	L/SSQE/D	HVSITQFGN	0.534

HPyV10

residue	Protein kinase	Consensus motif	Sequence in LTag	score
S6	CKII	D/ED/ED/ES/TD/ED/E	DRVLSRDEV	0.576
	RSK	RXRXXS/T		0.540
	CKI	D/E(X)XS/T		0.502
T37	PKC	R/KR/KR/K/F _S FRR	KYROTCLKL	0.696
S60	PKC	R/KR/KR/K/F _S FRR	NELFSKMYT	0.531
Y63	INSR	YXXM	FSKMYTTIE	0.522
T64	PKC	R/KR/KR/K/F _S FRR	SKMYTTIEK	0.639
Y76	SRC	EEDVYGXV	EGEVYFPAK	0.516
Y85	EGFR	XXEXYYXX	GNPTYGTPE	0.573
	SRC	EEDVYGXV		0.523
T87	p38 ^{MAPK}	PXS/TP	PTYGTPEWD	0.530
S106	CKII	D/ED/ED/ES/TD/ED/E	DEDLSCNES	0.539
S114	CKII	D/ED/ED/ES/TD/ED/E	SFAPSD _S EEE	0.726
S122	DNAPK	QXS/TQE/D	EPGPSQSAS	0.575
S124	CDK1	LPXSPXKK	GPSQSASQT	0.500
S126	DNAPK	QXS/TQE/D	SQSASQTAN	0.625
T134	PKC	R/KR/KR/K/F _S FRR	NDTNTPKKR	0.808
	p38 ^{MAPK}	PXS/TP		0.518
S142	PKA	K/RK/RXS/T	RPRESSSNS	0.805
S143	PKB	RXRXX*XS/TF/L	PRESSNST	0.771
	RSK	RXRXXS/T		0.541
S146	CKI	D/E(X)XS/T	SSSNSTCTP	0.559
	CDK1	LPXSPXKK		0.511
T147	PKC	R/KR/KR/K/F _S FRR	SSNSTCTPP	0.605
T149	CDK5	S/TPXK/H/R	NSTCTPPKR	0.645
	p38 ^{MAPK}	PXS/TP		0.621
S182	PKA	K/RK/RXS/T	KTLN _S FVLY	0.583
	PKC	R/KR/KR/K/F _S FRR		0.513

T187	PKC	R/KR/KR/K/F <u>S</u> FRR	FVLYT <u>T</u> TREK	0.872
S209	PKA	K/RK/RX <u>S</u> /T	AMFY <u>S</u> LHEF	0.598
	PKG	R/KR/KX <u>S</u> /T		0.544
	CKII	D/ED/ED/ES/TD/ED/E		0.512
S217	PKA	K/RK/RX <u>S</u> /T	FDGD <u>S</u> LLFG	0.645
	CDK1	LPX <u>S</u> PXKK		0.557
S224	PKC	R/KR/KR/K/F <u>S</u> FRR	FLL <u>S</u> SGKHR	0.772
S230	PKA	K/RK/RX <u>S</u> /T	KHRV <u>S</u> AIKN	0.653
	PKG	R/KR/KX <u>S</u> /T		0.583
	CDK1	LPX <u>S</u> PXKK		0.570
T263	CDK5	<u>S</u> /TPXK/H/R	ALCKT <u>P</u> FKL	0.555
	p38 ^{MAPK}	PX <u>S</u> /T <u>P</u>		0.503
S271	ATM	L/ <u>S</u> <u>S</u> QE/D	LIKQ <u>S</u> QEHG	0.602
	DNAPK	QX <u>S</u> /TQE/D		0.574
	PKA	K/RK/RX <u>S</u> /T		0.523
T279	CKII	D/ED/ED/ES/TD/ED/E	GLSKT <u>D</u> FCF	0.648
S325	CKII	D/ED/ED/ES/TD/ED/E	VEGC <u>S</u> KCEQ	0.549
S377	PKC	R/KR/KR/K/F <u>S</u> FRR	LILE <u>S</u> TREH	0.655
T378	CDK1	LPX <u>S</u> PXKK	ILE <u>S</u> TREHL	0.517
T432	PKC	R/KR/KR/K/F <u>S</u> FRR	IKAMT <u>E</u> NVP	0.511
T453	PKC	R/KR/KR/K/F <u>S</u> FRR	SGKT <u>T</u> VAAA	0.711
S504	DNAPK	QX <u>S</u> /TQE/D	GSNS <u>S</u> LLTPG	0.562
	CKI	D/E(X)X <u>S</u> /T		0.543
T506	p38 ^{MAPK}	PX <u>S</u> /T <u>P</u>	NSSLT <u>P</u> GMG	0.549
S512	CDK1	LPX <u>S</u> PXKK	GMGMS <u>N</u> LDN	0.525
T547	PKG	R/KR/KX <u>S</u> /T	PGIIT <u>M</u> NDY	0.537
Y551	INSR	<u>Y</u> XXM	TMNDY <u>F</u> IPP	0.505
T564	PKC	R/KR/KR/K/F <u>S</u> FRR	RMIKT <u>I</u> NFR	0.669
S576	DNAPK	QX <u>S</u> /TQE/D	FLRN <u>S</u> LEKN	0.574
S591	PKA	K/RK/RX <u>S</u> /T	RIVQ <u>S</u> GVTL	0.763
T659	DNAPK	QX <u>S</u> /TQE/D	ADEDT <u>Q</u> QDS	0.501
S667	ATM	L/ <u>S</u> <u>S</u> QE/D	SGIN <u>S</u> Q	0.660
	DNAPK	QX <u>S</u> /TQE/D		0.649
	CKII	D/ED/ED/ES/TD/ED/E		0.507

STLPyV

residue	Protein kinase	Consensus motif	Sequence in LTA _g	score
S6	PKC	R/KR/KR/K/F <u>S</u> FRR	DQAL <u>S</u> RAEA	0.659
	CKII	D/ED/ED/ES/TD/ED/E		0.622
S23	PKA	K/RK/RX <u>S</u> /T	LPED <u>S</u> WGNV	0.517
S31	PKC	R/KR/KR/K/F <u>S</u> FRR	VPLI <u>S</u> YRYR	0.832
S38	PKB	RXR*X <u>S</u> /TF/L	YRQK <u>S</u> KIYH	0.806
	PKC	R/KR/KR/K/F <u>S</u> FRR		0.745
	RSK	RXRXX <u>S</u> /T		0.580
	PKG	R/KR/KX <u>S</u> /T		0.575
S71	CKII	D/ED/ED/ES/TD/ED/E	QNLRS <u>S</u> SEN	0.553
	CDK1	LPX <u>S</u> PXKK		0.537
S72	PKA	K/RK/RX <u>S</u> /T	NLR <u>S</u> SENE	0.615
	CDK1	LPX <u>S</u> PXKK		0.524
S73	RSK	RXRXX <u>S</u> /T	LR <u>S</u> SENE	0.519
T87	p38 ^{MAPK}	PX <u>S</u> /T <u>P</u>	GQYGT <u>P</u> AWE	0.561
T106	CKII	D/ED/ED/ES/TD/ED/E	EDDLT <u>C</u> NES	0.624
S114	CKII	D/ED/ED/ES/TD/ED/E	SFNC <u>S</u> DDEG	0.715
S122	PKC	R/KR/KR/K/F <u>S</u> FRR	GTSAS <u>Q</u> KRK	0.876

	DNAPK CDK1	QXS/TQE/D LPXSPXKK		0.573 0.515
S130	PKC	R/KR/KR/K/F _S FRR	KFPD _S STQN	0.512
T132	DNAPK PKC	QXS/TQE/D R/KR/KR/K/F _S FRR	PDSSTQNST	0.608 0.563
S135	PKC	R/KR/KR/K/F _S FRR	STQNSTPPK	0.641
T136	CDK5	S/TPXK/H/R	TQNSTPPKK	0.585
S163	PKC	R/KR/KR/K/F _S FRR	HAVF _S NKTS	0.812
Y173	INSR	YXXM	CFCIYT _T IE	0.518
T174	PKC CKII PKG	R/KR/KR/K/F _S FRR D/ED/ED/ES/TD/ED/E R/KR/KXS/T	FCIYT _T IEK	0.586 0.529 0.503
Y183	INSR	YXXM	GNELYTVIG	0.509
T184	PKC CDK1	R/KR/KR/K/F _S FRR LPXSPXKK	NELYTVIGP	0.655 0.526
S196	PKA	K/RK/RXS/T	SMFI _S CHSY	0.516
S217	PKA PKG	K/RK/RXS/T R/KR/KXS/T	KHRV _S ALKN	0.596 0.505
S249	RSK PKA	RXRXS/T K/RK/RXS/T	YRLCSAPFA	0.537 0.516
T255	PKC	R/KR/KR/K/F _S FRR	PFAVT _K QSR	0.795
S258	PKG PKA	R/KR/KXS/T K/RK/RXS/T	VTQ _S SRPEG	0.562 0.547
S264	DNAPK CKII ATM	QXS/TQE/D D/ED/ED/ES/TD/ED/E L/SSQE/D	PEGL _S QAEF	0.586 0.580 0.575
S277	PKC	R/KR/KR/K/F _S FRR	NSKPSVNWQ	0.540
S306	CKII	D/ED/ED/ES/TD/ED/E	YLD _F SESPE	0.508
S308	CKI CKII	D/E(X)XS/T D/ED/ED/ES/TD/ED/E	DFSE _S PENC	0.546 0.527
T317	PKC	R/KR/KR/K/F _S FRR	EKCKT _E ELKH	0.546
S323	ATM	L/SSQE/D	LKHHS _S QFHE	0.512
Y330	EGFR SRC	XXEY _Y YXX EEDVY _G XV	HEKEY _N NAK	0.543 0.515
S339	PKA PKC	K/RK/RXS/T R/KR/KR/K/F _S FRR	LFRDSKTQK	0.760 0.664
S364	CKII	D/ED/ED/ES/TD/ED/E	LILE _S TRED	0.547
T365	CDK1	LPXSPXKK	ILEST _E REDL	0.506
S401	PKC	R/KR/KR/K/F _S FRR	VAWL _S LLFN	0.567
T422	CDK5	S/TPXK/H/R	MVIN _T PKKR	0.582
T440	PKC	R/KR/KR/K/F _S FRR	SGKT _T VAAA	0.711
T485	PKC	R/KR/KR/K/F _S FRR	VKGQ _T EGKT	0.588
S502	PKC	R/KR/KR/K/F _S FRR	NNLD _S LRDH	0.612
S524	PKG	R/KR/KXS/T	LNKR _S QIFP	0.545
T533	CKII	D/ED/ED/ES/TD/ED/E	PGIIT _M NEY	0.540
Y537	INSR	YXXM	TMNEY _N VPL	0.506
T542	PKC	R/KR/KR/K/F _S FRR	NVPL _T ILAR	0.516
S577	PKC PKA	R/KR/KR/K/F _S FRR K/RK/RXS/T	RIVQ _S GKTL	0.693 0.505
S597	CKII	D/ED/ED/ES/TD/ED/E	VFHSS _I HED	0.552
T608	PKC PKG	R/KR/KR/K/F _S FRR R/KR/KXS/T	IWKE _T LTKY	0.711 0.540
T610	PKC	R/KR/KR/K/F _S FRR	KETL _T KYVS	0.655
T641	CKII	D/ED/ED/ES/TD/ED/E	ICED _T ENNE	0.530
T646	DNAPK	QXS/TQE/D	ENNE _T QDSA	0.623

	CKII	D/ED/ED/ES/TD/ED/E		0.523
T653	CKII	D/ED/ED/ES/TD/ED/E	SAFCTQDSD	0.558
S656	CKII	D/ED/ED/ES/TD/ED/E	CTQDSDNE	0.655

NJPyV

residue	Protein kinase	Consensus motif	Sequence in LTA _g	score
S8	CKII	D/ED/ED/ES/TD/ED/E	VLEKSDKEM	0.608
Y34	EGFR	XXEXYYXX	MKTAYKRAS	0.531
S38	PKC	R/KR/KR/K/F _S FRR	YKRA _S KIYH	0.880
	PKA	K/RK/RX _S /T		0.516
S57	PKC	R/KR/KR/K/F _S FRR	MLLN _S SLWQK	0.616
S76	CKII	D/ED/ED/ES/TD/ED/E	SEVF _S DSYG	0.559
	CDK1	LPX _S PXKK		0.520
Y79	INSR	YXXM	FSD _S YGSAN	0.580
	SRC	EEDVY _G XV		0.532
	EGFR	XXEXYYXX		0.526
Y88	INSR	YXXM	FRKRYASWC	0.510
S90	PKB	RXR _X *X*S/TF/L	KRYA _S WCSS	0.856
	RSK	RXRXX _S /T		0.579
	PKA	K/RK/RX _S /T		0.555
	PKC	R/KR/KR/K/F _S FRR		0.510
S94	PKC	R/KR/KR/K/F _S FRR	SWC _S SVFTN	0.596
S101	CKII	D/ED/ED/ES/TD/ED/E	TNEK _S DSRA	0.532
S112	GSK3	S/TXXS/T	HCDE _S PISS	0.519
S115	CKII	D/ED/ED/ES/TD/ED/E	ESPI _S SSSD	0.565
S116	CKII	D/ED/ED/ES/TD/ED/E	SPI _S SSSDE	0.665
S117	CKII	D/ED/ED/ES/TD/ED/E	PI _S SSSDEE	0.737
S118	CKII	D/ED/ED/ES/TD/ED/E	ISS _S SSDEED	0.722
	CKI	D/E(X)X _S /T		0.517
T124	CDK1	LPX _S PXKK	EEDE _T QSSG	0.554
Y129	EGFR	XXEXYYXX	QSSGYN _S SFP	0.562
T135	PKC	R/KR/KR/K/F _S FRR	SFP _T ISTPT	0.553
T137	CDK5	S/TPXK/H/R	PFT _S ITPTS	0.634
	p38 ^{MAPK}	PX _S /TP		0.568
T139	CDK5	S/TPXK/H/R	TSTPT _S PTS	0.609
	p38 ^{MAPK}	PX _S /TP		0.590
T142	PKC	R/KR/KR/K/F _S FRR	PTP _S ISTAS	0.751
S146	ATM	L/SSQE/D	TSTA _S QEV	0.646
	DNAPK	QXS/TQE/D		0.643
S169	PKC	R/KR/KR/K/F _S FRR	SGSS _S AGR	0.724
T174	CKII	D/ED/ED/ES/TD/ED/E	AGRNTETER	0.603
T176	CKII	D/ED/ED/ES/TD/ED/E	RNTETERES	0.587
	PKC	R/KR/KR/K/F _S FRR		0.566
S180	CDK5	S/TPXK/H/R	TERES _S PPKR	0.684
	GSK3	S/TXXS/T		0.512
T188	PKA	K/RK/RX _S /T	RRRG _T EDLD	0.804
	RSK	RXRXX _S /T		0.558
S194	DNAPK	QXS/TQE/D	DLDG _S YTDS	0.566
	CKI	D/E(X)X _S /T		0.557

	CDK1	LPXSPXKK		0.522
T196	CKII	D/ED/ED/ES/TD/ED/E	DGSYTDSQT	0.512
S198	DNAPK ATM	QXS/TQE/D L/SSQE/D	SYTDSQTSF	0.614 0.546
T200	PKC	R/KR/KR/K/F _S FRR	TDSQTSFAS	0.730
S201	CKI	D/E(X)XS/T	DSQTSFAST	0.506
S204	PKC	R/KR/KR/K/F _S FRR	TSFASTPPK	0.534
T205	CDK1 PKC	LPXSPXKK R/KR/KR/K/F _S FRR	SFASTPPKQ	0.737 0.631
S213	RSK GSK3	RXRXXS/T S/TXXXS/T	QKRKSPDSP	0.531 0.503
S216	CDK5 GSK3 p38 ^{MAPK}	S/TPXK/H/R S/TXXXS/T PXS/TP	KSPDSPSDL	0.567 0.533 0.503
S234	PKC	R/KR/KR/K/F _S FRR	HAIFSNKTV	0.793
T237	PKC	R/KR/KR/K/F _S FRR	FSNKTVNAF	0.563
T246	PKC	R/KR/KR/K/F _S FRR	ILYSTLEKA	0.657
S251	PKA	K/RK/RXS/T	LEKASLLYE	0.528
S266	PKA	K/RK/RXS/T	IEFKSLHKL	0.573
S292	PKA PKG	K/RK/RXS/T R/KR/KXS/T	KHRVSAMKN	0.650 0.501
S328	DNAPK	QXS/TQE/D	KPPFSQVKA	0.530
S339	CKII	D/ED/ED/ES/TD/ED/E	DGLFSYDEE	0.632
Y396	EGFR	XXEXYYXX	KAHDYHKAH	0.555
S412	PKC	R/KR/KR/K/F _S FRR	EACKSQRSI	0.651
S415	PKA	K/RK/RXS/T	KSQRSICNQ	0.513
T433	CKII	D/ED/ED/ES/TD/ED/E	RLLLTSTR	0.528
S435	CKII	D/ED/ED/ES/TD/ED/E	LLTESTREE	0.551
T510	PKC	R/KR/KR/K/F _S FRR	SGKTTFAAA	0.704
S568	CDK1	LPXSPXKK	GQGISNLDN	0.550
T603	PKG CKII	R/KR/KXS/T D/ED/ED/ES/TD/ED/E	PCVMTMNEY	0.654 0.514
Y607	SRC	EEDVYGVXV	TMNEYFMPQ	0.506
S618	PKA PKC CKI	K/RK/RXS/T R/KR/KR/K/F _S FRR D/E(X)XS/T	FVRFSLKLD	0.759 0.592 0.511
S625	PKA	K/RK/RXS/T	LDFVSRPNL	0.553
T636	p38 ^{MAPK}	PXS/TP	AVDKTPGLV	0.542
T650	PKA	K/RK/RXS/T	QKGLTLFLL	0.599
T659	CDK1 CDK5	LPXSPXKK S/TPXK/H/R	LIWYTPVKK	0.532 0.500
S667	PKA CKII	K/RK/RXS/T D/ED/ED/ES/TD/ED/E	KFAVSLQEE	0.630 0.565
T703	CKII	D/ED/ED/ES/TD/ED/E	ESPLTDLID	0.604

QPyV

residue	Protein kinase	Consensus motif	Sequence in LTag	score
S6	PKA RSK CKII	K/RK/RXS/T RXRXXS/T D/ED/ED/ES/TD/ED/E	DRLLSRDEV	0.587 0.580 0.578
S20	PKA CDK1	K/RK/RXS/T LPXSPXKK	LIGLSMSNW	0.718 0.577
S22	CDK1	LPXSPXKK	GLSM _S NWGN	0.531
T65	PKC	R/KR/KR/K/F _S FRR	KFAATMRDQ	0.835

S70	PKA	K/RK/RXS/T	MRDQSSGNP	0.764
S79	CKII	D/ED/ED/ES/TD/ED/E	IWHFSSEEV	0.533
T91	CDK5 p38 ^{MAPK} GSK3	S/TPXK/H/R	PPYGTPEWD	0.583
		PXS/TP		0.548
		S/TXXS/T		0.500
Y110	SRC	EEDVYGXV	DEDLYCTEE	0.539
S116	CKII	D/ED/ED/ES/TD/ED/E	TEELSASDE	0.622
S118	CKII CDK1	D/ED/ED/ES/TD/ED/E LPXSPXKK	ELSADEEQ	0.683
				0.524
T123	CKII	D/ED/ED/ES/TD/ED/E	DEEQTAEDP	0.635
S132	ATM DNAPK CDK1	L/SSQE/D	EEGCSQNSK	0.565
		QXS/TQE/D		0.536
		LPXSPXKK		0.519
Y137	EGFR	XXEXYYXX	QNSKYSATP	0.514
S138	PKG	R/KR/KXS/T	NSKYSATPP	0.520
T140	CDK5 p38 ^{MAPK}	S/TPXK/H/R PXS/TP	KYSATPPKQ	0.593
				0.543
T179	PKC CKII	R/KR/KR/K/FSFRR D/ED/ED/ES/TD/ED/E	FVCYTMEK	0.532
				0.502
S184	PKA	K/RK/RXS/T	TMEKSLMLY	0.546
S209	PKA	K/RK/RXS/T	CNDGSGSIV	0.592
S219	PKC CDK1	R/KR/KR/K/FSFRR LPXSPXKK	MITGSRHRP	0.795
				0.581
S224	PKA PKG	K/RK/RXS/T R/KR/KXS/T	RHRPSAILN	0.719
				0.532
S230	PKC CDK1	R/KR/KR/K/FSFRR LPXSPXKK	ILNASKKYC	0.870
				0.534
T235	PKC	R/KR/KR/K/FSFRR	KKYCTVSFS	0.631
S237	PKC	R/KR/KR/K/FSFRR	YCTVSFSLV	0.598
T260	PKC	R/KR/KR/K/FSFRR	GPNFTVIRE	0.591
S265	PKA	K/RK/RXS/T	VIRE\$REGG	0.572
S272	CDK1 CKII	LPXSPXKK D/ED/ED/ES/TD/ED/E	GGLH\$YDFQ	0.575
				0.549
S279	PKC	R/KR/KR/K/FSFRR	FQEASKKFF	0.518
S343	PKG	R/KR/KXS/T	KLFK\$AKVNQ	0.520
T352	DNAPK	QXS/TQE/D	RGIA\$QAAD	0.635
S360	PKC RSK	R/KR/KR/K/FSFRR RXRXXS/T	DRVLSARRV	0.673
				0.573
S369	PKC	R/KR/KR/K/FSFRR	MMIESTRVD	0.579
T414	PKC	R/KR/KR/K/FSFRR	MPSFTTKLK	0.748
T415	PKC	R/KR/KR/K/FSFRR	PSFTTKLKE	0.676
T445	PKC	R/KR/KR/K/FSFRR	NSGKTTVAA	0.555
T446	PKC	R/KR/KR/K/FSFRR	SGKTIVAAG	0.529
S466	PKC	R/KR/KR/K/FSFRR	VNCSSDKIN	0.611
T526	PKC PKG	R/KR/KR/K/FSFRR R/KR/KXS/T	ERKHTNKVS	0.751
				0.530
S530	CDK1	LPXSPXKK	TNKV\$QLFP	0.512
T539	PKG	R/KR/KXS/T	PCIITCNDY	0.516
Y543	INSR	YXXM	TCNDYAI\$PR	0.545
T548	PKC	R/KR/KR/K/FSFRR	AIPRTVKAR	0.851
S598	CKII	D/ED/ED/ES/TD/ED/E	WEPV\$EFVE	0.628
Y621	SRC	EEDVYGXV	RWVTYGM\$YQ	0.507
Y639	SRC	EEDVYGXV	KDPFYGVIM	0.553
S644	CKII PKA	D/ED/ED/ES/TD/ED/E K/RK/RXS/T	GVIM\$DINE	0.577
				0.534

T653	DNAPK ATM	QXS/TQE/D L/SSQE/D	IVEETQEST	0.603 0.505
S656	CKI	D/E(X)XS/T	ETQESTESG	0.517
T657	CKI	D/E(X)XS/T	TQESTESGV	0.575
S659	CKI	D/E(X)XS/T	ESTESGVGS	0.597
S663	CKI	D/E(X)XS/T	SGVGSMET	0.536
	DNAPK	QXS/TQE/D		0.525
	CKII	D/ED/ED/ES/TD/ED/E		0.525

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Supplementary Table S2. Putative phosphorylation sites in SV40 sTA_g and human polyomaviruses and their protein kinase. The algorithm NetPhos3.1 was used to predict protein kinases [1,2]. The protein kinase consensus motifs are based on [3-7].

SV40

residue	Protein kinase	Consensus motif	Sequence in sTA _g	score
S10	PKA	K/RK/RXS/T	REES	0.749
S22	CKI CDK1	D/E(X)XS/T LPXSPXKK	ERS GLERSAWGN	0.510 0.503
T57	PKC	R/KR/KR/K/FSFRR	KKMNT	0.842
T81	CDK1	LPXSPXKK	FWDAT _{EV} FA	0.511
S87	CKI	PS/GS/TPXR/K	VFASSLNPG	0.509
Y96	EGFR	XXEXYYXX	VDAM _Y CKQW	0.532
S108	PKA	K/RK/RXS/T	KKMS	0.653
T167	PKC	R/KR/KR/K/FSFRR	IIGQT _{TY} R	0.755
T168	PKC	R/KR/KR/K/FSFRR	IIGQT _{TY} R	0.654

BKPyV

residue	Protein kinase	Consensus motif	Sequence in sTA _g	score
T57	PKC	R/KR/KR/K/FSFRR	KRMNTLYKK	0.798
S78	CKII	D/ED/ED/ES/TD/ED/E	FGTWSSSEV	0.584
S79	CDK1	LPXSPXKK	FGTWSSSEV	0.506
S80	CDKI CKII	LPXSPXKK D/ED/ED/ES/TD/ED/E	FGTWSSSEV FGTWSSSEV	0.525 0.518
S102	PKC	R/KR/KR/K/FSFRR	WPIC _S KKPS	0.727
S106	PKC PKA	R/KR/KR/K/FSFRR K/RK/RXS/T	SKKPS _{VH} CP SKKPS _{VH} CP	0.603 0.534
T165	p38 ^{MAPK}	PXS/TP	IGET _{TP} FRD	0.556

JCPyV

residue	Protein kinase	Consensus motif	Sequence in sTA _g	score
S79	CDK1	LPXSPXKK	GTWNSSEVG	0.506
T103	PKC	R/KR/KR/K/FSFRR	PNCATNP _{SV}	0.512
S128	PKA	K/RK/RXS/T	KFLRSSPLV	0.545
S129	PKA CDK1	K/RK/RXS/T LPXSPXKK	KFLRSSPLV KFLRSSPLV	0.596 0.503
T151	DNAPK ATM	QXS/TQE/D L/SSQE/D	GCDLTQEAL	0.617 0.564

KIPyV

residue	Protein kinase	Consensus motif	Sequence in sTA _g	score
S6	CKII	D/ED/ED/ES/TD/ED/E	DKT _{LS} REEA	0.518
S65	CDK1	LPXSPXKK	KLQDS _V VSV	0.514
S83	DNAPK CDK1	QXS/TQE/D LPXSPXKK	IWQSSQVYC	0.591 0.520
Y102	EGFR	XXEXYYXX	VNAI _Y GEYY	0.643
Y105	EGFR SRC	XXEXYYXX EEDV _Y GXV	IYGE _Y YEAY	0.527 0.508
Y106	SRC INSR	EEDV _Y GXV YXXM	YGE _Y YEAYI	0.529 0.523
Y109	EGFR	XXEXYYXX	YYEAYIMKQ	0.543

S133	PKC	R/KR/KR/K/F <u>S</u> FRR	HCIL <u>S</u> KYHK	0.755
T170	PKC	R/KR/KR/K/F <u>S</u> FRR	ISMQ <u>T</u> FFFW	0.722

WUPyV

residue	Protein kinase	Consensus motif	Sequence in sTag	score
T4	CDK1	LPX <u>S</u> PXKK	MDK <u>T</u> LSRN	0.505
T32	PKC	R/KR/KR/K/F <u>S</u> FRR	PLMR <u>T</u> KYLS	0.512
S36	PKC	R/KR/KR/K/F <u>S</u> FRR	TKYL <u>S</u> KCKE	0.638
S57	PKA	K/RK/RX <u>S</u> / <u>T</u>	KKLN <u>S</u> LYLK	0.681
	PKC	R/KR/KR/K/F <u>S</u> FRR		0.620
S81	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	DEVW <u>S</u> SSQV	0.566
S82	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	DEVW <u>S</u> SSQV	0.544
S83	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	DEVW <u>S</u> SSQV	0.618
	DNAPK	QX <u>S</u> / <u>T</u> QE/D		0.603
	CDK1	LPX <u>S</u> PXKK		0.531
	CKI	PS/G <u>S</u> / <u>T</u> PXR/K		0.530
Y106	EGFR	XXEXY <u>Y</u> YXX	VGEV <u>Y</u> GDVF	0.507
	SRC	EEDV <u>Y</u> GXV		0.507
T174	PKC	R/KR/KR/K/F <u>S</u> FRR	ISAE <u>T</u> FFYW	0.767
	CKI	PS/G <u>S</u> / <u>T</u> PXR/K		0.550
T185	PKC	R/KR/KR/K/F <u>S</u> FRR	IIFL <u>T</u> TMQG	0.545

MCPyV

residue	Protein kinase	Consensus motif	Sequence in sTag	score
Y24	INSR	<u>Y</u> XXM	APNC <u>Y</u> GNIP	0.568
S35	PKC	R/KR/KR/K/F <u>S</u> FRR	AFKR <u>S</u> CLKH	0.567
	PKG	R/KR/KX <u>S</u> / <u>T</u>		0.521
T57	PKC	R/KR/KR/K/F <u>S</u> FRR	MELN <u>T</u> LWSK	0.571
S60	PKC	R/KR/KR/K/F <u>S</u> FRR	NTLW <u>S</u> KFQQ	0.654
S80	PKC	R/KR/KR/K/F <u>S</u> FRR	FDEV <u>S</u> TKFP	0.608
	CKI	PS/G <u>S</u> / <u>T</u> PXR/K		0.538
T81	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	DEV <u>S</u> TKFPW	0.563
T90	PKC	R/KR/KR/K/F <u>S</u> FRR	EEG <u>T</u> LKDY	0.677
S117	PKA	K/RK/RX <u>S</u> / <u>T</u>	QLRD <u>S</u> KCAC	0.592
S123	PKC	R/KR/KR/K/F <u>S</u> FRR	CACI <u>S</u> CKLS	0.635
S132	PKC	R/KR/KR/K/F <u>S</u> FRR	RQH <u>C</u> SLKTL	0.657
T135	PKC	R/KR/KR/K/F <u>S</u> FRR	CSL <u>K</u> TLKQK	0.922
T143	PKG	R/KR/KX <u>S</u> / <u>T</u>	KNCL <u>T</u> WGEC	0.501
T172	CKII	D/ED/ED/ES/ <u>T</u> D/ED/E	WWQK <u>T</u> LEET	0.589
Y178	EGFR	XXEXY <u>Y</u> YXX	EETD <u>Y</u> CLLH	0.514

HPyV6

residue	Protein kinase	Consensus motif	Sequence in sTag	score
S20	PKA	K/RK/RX <u>S</u> / <u>T</u>	LIGL <u>S</u> MACW	0.631
	CDK1	LPX <u>S</u> PXKK		0.532
T65	PKC	R/KR/KR/K/F <u>S</u> FRR	KLNAT <u>L</u> RDQ	0.572
S73	ATM	L/ <u>S</u> <u>S</u> QE/D	QM <u>S</u> SSPTWC	0.520
T75	PKC	R/KR/KR/K/F <u>S</u> FRR	SS <u>S</u> PTWCFS	0.661

S80	CKII	D/ED/ED/ES/TD/ED/E	WCFSS <u>EV</u> SD	0.505
S83	CKII	D/ED/ED/ES/TD/ED/E	SSEVS <u>DD</u> WG	0.597
T91	PKC	R/KR/KR/K/F <u>S</u> FRR	GIPL <u>T</u> VGEF	0.727
S117	CDK1	LPXSPXKK	QQGIS <u>S</u> CKC	0.518
S118	PKC	R/KR/KR/K/F <u>S</u> FRR	GGIS <u>S</u> CKCL	0.671
S176	CDK5	<u>S</u> /TPXK/H/R	IYQ <u>S</u> PLDW	0.509

HPyV7

residue	Protein kinase	Consensus motif	Sequence in sTag	score
S38	PKC PKA	R/KR/KR/K/F <u>S</u> FRR K/RK/RX <u>S</u> /T	VRLAS <u>K</u> KYH	0.921 0.508
S73	RSK p38 ^{MAPK}	RXRX <u>S</u> /T PX <u>S</u> /TP	QRSG <u>S</u> PMWH	0.537 0.500
S79	CKII	D/ED/ED/ES/TD/ED/E	MWHY <u>S</u> SDEV	0.585
S80	CKII	D/ED/ED/ES/TD/ED/E	WHY <u>S</u> SDEV	0.534
S84	CKII	D/ED/ED/ES/TD/ED/E	SDEV <u>S</u> FWDI	0.530
T91	CKII	D/ED/ED/ES/TD/ED/E	DIEL <u>T</u> VGEF	0.527
S168	CKI	PS/G <u>S</u> /TPXR/K	RSEE <u>S</u> FMWW	0.536
S173	PKA	K/RK/RX <u>S</u> /T	FMWW <u>S</u> HIIF	0.515
T179	p38 ^{MAPK}	PX <u>S</u> /TP	IIFQ <u>T</u> PMDV	0.517

TSPyV

residue	Protein kinase	Consensus motif	Sequence in sTag	score
S6	CKII CKI	D/ED/ED/ES/TD/ED/E PS/G <u>S</u> /TPXR/K	DKFL <u>S</u> REES	0.598 0.517
S10	PKA DNAPK	K/RK/RX <u>S</u> /T QX <u>S</u> /TQE/D	SREE <u>S</u> LELM	0.660 0.503
S38	PKC PKA	R/KR/KR/K/F <u>S</u> FRR K/RK/RX <u>S</u> /T	HKKM <u>S</u> LKYH	0.921 0.565
S53	PKA	K/RK/RX <u>S</u> /T	PEKM <u>S</u> RLNQ	0.611
Y67	EGFR SRC	XXEXY <u>Y</u> YXX EEDV <u>Y</u> GXV	QEGI <u>Y</u> NARQ	0.629 0.513
S76	CDK1	LPXSPXKK	EFPT <u>S</u> FSSQ	0.560
S78	CDK1	LPXSPXKK	PTSF <u>S</u> SQVG	0.515
S79	ATM DNAPK	L/SSQE/D QX <u>S</u> /TQE/D	TSF <u>S</u> SQVGS	0.673 0.572
S83	CKII CDK1	D/ED/ED/ES/TD/ED/E LPXSPXKK	SQVG <u>S</u> WYWE	0.511 0.508
Y85	EGFR	XXEXY <u>Y</u> YXX	VGSW <u>Y</u> WEAN	0.501
S92	CKI PKG	PS/G <u>S</u> /TPXR/K R/KR/KX <u>S</u> /T	ANLI <u>S</u> LKEY	0.546 0.528
T125	PKC	R/KR/KR/K/F <u>S</u> FRR	CKCL <u>T</u> CKIG	0.589
S173	CDK1	LPXSPXKK	LWAW <u>S</u> CIVG	0.563

HPyV9

residue	Protein kinase	Consensus motif	Sequence in sTag	score
S6	CKII DNAPK	D/ED/ED/ES/TD/ED/E QX <u>S</u> /TQE/D	DQTL <u>S</u> LEER	0.622 0.505
S28	PKC	R/KR/KR/K/F <u>S</u> FRR	WGNL <u>S</u> LMKK	0.521
Y34	EGFR	XXEXY <u>Y</u> YXX	MKK <u>A</u> YKTVS	0.515
T36	PKC	R/KR/KR/K/F <u>S</u> FRR	KAYK <u>T</u> VSKI	0.831

S38	PKC	R/KR/KR/K/F <u>S</u> FRR	YKTV <u>S</u> KIYH	0.873
S76	CDK1	LPX <u>S</u> PXKK	NCG <u>S</u> <u>S</u> <u>S</u> <u>S</u> QV	0.548
S78	DNAPK ATM	QX <u>S</u> /TQE/D L/ <u>S</u> <u>S</u> QE/D	G <u>S</u> <u>S</u> <u>S</u> <u>S</u> QVAW	0.603 0.529
T113	PKC	R/KR/KR/K/F <u>S</u> FRR	PDCIT <u>Y</u> NKP	0.727
Y114	EGFR	XXEXY <u>Y</u> YXX	DCIT <u>Y</u> NKPS	0.502
S118	PKA	K/RK/RX <u>S</u> /T	YNKP <u>S</u> CCCI	0.603
S132	PKC	R/KR/KR/K/F <u>S</u> FRR	QQHK <u>S</u> TKIN	0.898
T133	PKC PKG	R/KR/KR/K/F <u>S</u> FRR R/KR/KX <u>S</u> /T	QHK <u>S</u> TKINK	0.861 0.547
S179	PKA	K/RK/RX <u>S</u> /T	NMDL <u>S</u> LLRL	0.579

HPyV10

residue	Protein kinase	Consensus motif	Sequence in sTag	score
S6	CKII RSK CKI	D/ED/ED/ES/TD/ED/E RXRX <u>S</u> /T PS/G <u>S</u> /TPXR/K	DRVLSRDEV	0.576 0.540 0.502
T37	PKC	R/KR/KR/K/F <u>S</u> FRR	KYRQT <u>C</u> LKL	0.714
S60	PKC	R/KR/KR/K/F <u>S</u> FRR	NELF <u>S</u> KMYT	0.531
Y63	INSR	<u>Y</u> XXM	FSKM <u>Y</u> TTIE	0.522
T64	PKC	R/KR/KR/K/F <u>S</u> FRR	SKMYT <u>T</u> IEK	0.639
Y76	SRC	EEDV <u>Y</u> GXV	EGEV <u>Y</u> FPAK	0.518
T90	CKI	PS/G <u>S</u> /TPXR/K	DDVV <u>T</u> LGDV	0.520
S98	CKII	D/ED/ED/ES/TD/ED/E	VLGP <u>S</u> FEEK	0.514
Y105	EGFR INSR	XXEXY <u>Y</u> YXX <u>Y</u> XXM	EKII <u>Y</u> IWPL	0.611 0.517
Y163	INSR	<u>Y</u> XXM	QEF <u>G</u> YTSFF	0.521
S195	PKC CKI	R/KR/KR/K/F <u>S</u> FRR PS/G <u>S</u> /TPXR/K	VSYF <u>S</u> FILG	0.638 0.512

STLPyV

residue	Protein kinase	Consensus motif	Sequence in sTag	score
S6	PKC CKII	R/KR/KR/K/F <u>S</u> FRR D/ED/ED/ES/TD/ED/E	DQALS <u>R</u> AEA	0.659 0.622
S23	PKA	K/RK/RX <u>S</u> /T	LPED <u>S</u> WGNV	0.517
S31	PKC	R/KR/KR/K/F <u>S</u> FRR	VPLI <u>S</u> YRYR	0.832
S38	PKB PKC RSK PKG	RXR <u>X</u> *X*S/TF/L R/KR/KR/K/F <u>S</u> FRR RXRX <u>S</u> /T R/KR/KX <u>S</u> /T	YRQK <u>S</u> KIYH	0.806 0.745 0.580 0.575
S71	CKII CDK1	D/ED/ED/ES/TD/ED/E LPX <u>S</u> PXKK	QNR <u>S</u> SEN	0.553 0.537
S72	PKA CDK1	K/RK/RX <u>S</u> /T LPX <u>S</u> PXKK	NLR <u>S</u> SENE	0.615 0.524
S73	RSK	RXR <u>X</u> <u>S</u> /T	LR <u>S</u> SENE	0.519
T90	CDK1	LPX <u>S</u> PXKK	LLSD <u>T</u> FTLG	0.522
T92	CKI	PS/G <u>S</u> /TPXR/K	SDT <u>F</u> TLGDL	0.592
S103	CDK1	LPX <u>S</u> PXKK	PQF <u>E</u> SKVIF	0.536
T111	PKC	R/KR/KR/K/F <u>S</u> FRR	FIWPT <u>C</u> AKC	0.502
T119	PKG	R/KR/KX <u>S</u> /T	CRYRT <u>F</u> CKC	0.645
T145	PKG	R/KR/KX <u>S</u> /T	KPCV <u>T</u> WGEC	0.538
S167	PKC PKA	R/KR/KR/K/F <u>S</u> FRR K/RK/RX <u>S</u> /T	FTKT <u>S</u> LHAW	0.722 0.525

X*=polar amino acid

NJPyV

residue	Protein kinase	Consensus motif	Sequence in sTag	score
S8	CKII	D/ED/ED/ES/TD/ED/E	VLEKSDKEM	0.608
Y34	EGFR	XXEXY [*] YXX	MKTAYKRAS	0.531
S38	PKC	R/KR/KR/K/FSFRR	YKRASKIYH	0.880
	PKA	K/RK/RXS/T		0.518
S57	PKC	R/KR/KR/K/FSFRR	MLLN [*] SLWQK	0.616
S78	CDK1	LPXSPXKK	VCQV [*] FSDC	0.551
S80	CDK1	LPXSPXKK	QVSFSDCYD	0.543
S85	CDK1	LPXSPXKK	DCYDSLLK	0.520
S86	PKC	R/KR/KR/K/FSFRR	CYDSLLKC	0.506
S92	p38 ^{MAPK}	PXS/TP	LKCCSPKVF	0.509
	CDK1	LPXSPXKK		0.505
S103	p38 ^{MAPK}	PXS/TP	LFLR [*] PQCL	0.584
	CDK5	S/TPXK/H/R		0.526
T138	PKA	K/RK/RXS/T	KRCLTWGNC	0.786
	PKG	R/KR/KXS/T		0.538
	PKC	R/KR/KR/K/FSFRR		0.524
T157	PKC	R/KR/KR/K/FSFRR	GLRETWKTf	0.692

QPyV

residue	Protein kinase	Consensus motif	Sequence in sTag	score
S6	PKA	K/RK/RXS/T	DRLLSRDEV	0.587
	RSK	RXRXS/T		0.580
	CKII	D/ED/ED/ES/TD/ED/E		0.578
S20	PKA	K/RK/RXS/T	LIGLSMSNW	0.718
	CDK1	LPXSPXKK		0.577
S22	CDK1	LPXSPXKK	GLSMSNWGN	0.531
T65	PKC	R/KR/KR/K/FSFRR	KFAATMRDQ	0.835
S70	PKA	K/RK/RXS/T	MRDQSSGNP	0.764
S79	CKII	D/ED/ED/ES/TD/ED/E	IWHFSSEEV	0.547
S80	CKII	D/ED/ED/ES/TD/ED/E	WHFSSEEVs	0.500
T173	DNAPK	QXS/TQE/D	FEWWTQITY	0.561
T179	DNAPK	QXS/TQE/D	IYGTQMDV	0.549
	ATM	L/SSQE/D		0.501

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Supplementary Figure S1. Alignment of LTag from SV40 and HPyVs. The known phosphorylation sites in SV40 are shown in grey and conserved residues are highlighted in green. Clustal was used for alignment [1].

Alphaviruses

SV	MDKVLNREESLQ LMDLLGLERSAWGNIPLMRKAYLKKCKEFHPDKGGDEEKMKKMNTLYK	60
TS	MDKFLSREESLELMDLLQIPRH CYGNFALMKINHKKMSLKYHPDKGGDPEKMSRLNQLWQ	60
H9	MDQTLSLEERNE LMDLLQLTRA AWGNLSLMKKAYKTVSKIYHPDKGGNPEKMQR LNELFQ	60
MC	MDLV LNRKEREALCKLLEIAPNCYGNIPLMKAAFKRSC LKHHHPDKGGNPVIMMELNTLWS	60
NJ	MEKVLEKSDKEMLI ELLGIPRYAYGNFPI MKTAYKRASKIYHPDKGGSSEKMMLLNSLWQ	60
	*: * . .: * .** : .:***: *: . . .*****. * : * *..	
SV	KMEDGVKYAHQPDFGG-----FWDAT EIPT YGTDEWEQW---WNAFN	99
TS	KLQEG IYNARQE-FPTSFSSQH--DVPT-----QDGRDIPPYGHPSWASW---WESFN	107
H9	KLQVTLL EIRSN-CGSSSSQGYSDSPYFTETPF SYCERKNEDPEGGSWGKW---WREFV	116
MC	KFQQNIHKLRSD-FSMFDEV D---EA-----PIYGTTFKFEW---WRSGG	98
NJ	KFQEG LIEVRDS-EVFSD-----SYGSANFRKRYASWCSSV	95
	*:: : :. .: . *	
SV	E-----	100
TS	QEW D-----	111
H9	NK-----	118
MC	FSFGKAYEYGP NPHGTNSRSRKPSSNASRGAPSGSSPPHSQSSSSGYGSFSASQASDSQS	158
NJ	FTNEKSD-----SRA---DLHCDESP ISSSSDEEDETQSSGYNSFPFTSTP----	138
SV	-----ENLFCSEEM	109
TS	-----NLFDTMQDPDLFCHEST	128
H9	-----EYDDLFCSETI	129
MC	RGPDI PPEHH EPTSSSGSSSREETTNSGRESSTPNGTSVPRNSSRTDGTWEDLFCDESL	218
NJ	-----	138
SV	PSSDDEAT-----	117
TS	IP SDES R-----SP-----SPTPGPSTQFSEENSRR-----RRAAPP----	160
H9	SSSDDEN-----NP-----GPSAPPPSSAS-----A-----SEDPDP----	156
MC	SSPEPPSSS EEP EPPSRSSPRQPPSSSAEEASSSQFTDEEYRSSSFTTPKTPPPFSRK	278
NJ	---TP-STSTASQEVPPPFSEPFQFP ESSSASGSSSAGRNT-----ETERESP PKRRR	186
SV	-----ADSQHSTPPKKK--RKVEDPKDFPSELLSFLSHAVFSNRTLACFAI	161
TS	-----EDSPGCTQSSFSATPPKPKKSKYDSVPNDFPDMLRPFLSNAVYSNKTLS SFLI	213
H9	-----EEEAGSSQSSFTCTPPKRKKPE-PNTPEDFPMCLYSFLSHAIYSNKT MNCF LI	208
MC	RKFGGSRSSASSASSASFTSTPPKPKKNRETPVPTDFPIDLS DYLSHAVYSNKT VSCFAI	338
NJ	G--TEDLDGSYTD SQTSFASTPPKQKR-KSPDSPSDLPSCLFDFVSHAIFSNKTVNAFIL	243
	* .**** * . * *: * * :*: *: *: *: *	
SV	YTTKEKAALLYKKIMEK-----YSVT FISRHSYN-----HNILFFLTPHRHRVSAINNY	211
TS	YTTNEKA EYLYKKLDKFN-----PEFKSRHSFQE-----GSMVFLMTPGKHRVSAIKNL	262
H9	YTTVEKSKQLYRTVEKSKIKVDFKAI FLYKDDGIE-----GGLLYFITLGKHRVSAVKHF	263
MC	YTTSDKAI ELYDKIEKFV-----DFKSRHACEL-----GCILLFITLSKHRVSAIKNF	387
NJ	YSTLEKASLLYEKIDKFKI-----EFKSLHLKLT EGANVGGLV LVTIAKHRV SAMKNF	297
	: *: * * .: : * . : : .*: :*****::	
SV	AQKLCTFSFLICKGVNKEYLMYSALTRDPFSVIEESLP GGLKEHDFNP EEA EETKQVSWK	271
TS	CVTHCTV SFLLCKAVIKQVECYRCMCSEPFKLLEESKPGIF-EYEF--NEENGKPVVNW N	319
H9	CVAQCTFSFIHCKAVIKPLELYRALGKPPFKLLEENKPGVS-MFDF--QEEKE-QAVNWQ	319
MC	CSTFCTISFLICKGVNKMPEM YNNLCKPPYKLLQENKP-LL-NYEF--QEKEKEASCNWN	443
NJ	CQQFCTV SF LICKVVLKPLECYQCLCKPPFSQVKANKDGLF-SYDF--ED-KKEENCNWN	353
	. **.**: ** * * * : * :. :. . .: * : : : *	
SV	LVTEYAMETKCD DVL LLLGMYLEFQYSFEMCLKCIKKEQPSHYKYHEKH YANAAIFADSK	331
TS	LLTDFAVTNRLDDPLLIMAHYLDFAE EPSICSKCTKKALKAHYNYHSLH HKNAKLFKECK	379
H9	EICNYAVEAKITDVL LLLGIYLDFAVEPGTCSKCEKSKHKFHYNYHSHKHANACLFLESK	379
MC	LVAEFACEYELDDHFII LAHYLDFA-KPFP CQKCENSR LKPKHAHEAHSNAKLFYESK	502

NJ	KVAEFAVLADIDDPILLI LAHYLDFA-QPFPCLKEHQK-TKAHDYHKAHHENAVLFEACK : : :* * : : : . ** : * : . * . * : ** : * . *	411
SV	NQKTICQQAVDQVLAQKRVDSLQLTREQMLTNRFNLDLDRMDIMFGSTGSADIEEWMAGV	391
TS	TQKTACQQAADVMAKQRLKLIESTRKELEERFKLMFEKLTDE---FGQIKILQYMAGV	436
H9	SQKNICQQAVDQVLAQKRLKLVECTRMELLEDRFIQLFDEMEDFL--HGEIEILRWMSGV	437
MC	SQKTICQQAADTVLAKRRLEMLEMTRTEMLCKKFKKHLERLRDL----DTIDLLYYMGGV	558
NJ	SQRSICNQASDIVLAKRRLLLTESTREELLAMCFQKQLKALQAL----DTLEIYDHMAGV . * . . * : ** * * : * : * : : ** : : * * : . : . : * . **	467
SV	AWLHCLLPKMDSVVYDFLKCMVYNIPKKRYWLFKGPIDSGKTTLAAALLELCGGKALNVN	451
TS	AWYSCLFENIDEVVTIKILKLVENVPKKRNCLFRGPINSKGTTFAAALMNFLGGKTLNVN	496
H9	AWYTILLDNSWDVFQKILQLVTTSQPKKRNI LFKGPINSKGTTLASAFMHFFDGGKALNIN	497
MC	AWYCCLFEEFEKKLQKIIQLLTENIPKYRNIWFKGPINSKGTSFAAALIDLLEGKALNIN	618
NJ	AWYANLFENFDDILFQILKLLTQNI PKQRNIFRGPVNSKGTTFAAALVDLLGGRSLNVN ** * : : . . . : : : . . ** * * : ** : : ** : : ** : : : * : ** : *	527
SV	LPLDRLNFELGVAIDQFLVVFEDVKGTTGGESRDLPSSQGINNLDNLRDYL DGSVKVNLEK	511
TS	CPADKLPFELGCAIDQFVVFEDVKGQIALNKKLQPGQGVSNLDNLRDHL DGSVKVDLER	556
H9	CPAEKLSFELGCAIDQFCVLLDDVKGQITLNKHLQPGQGVNNLDNLRDHL DGTIKVNLEK	557
MC	CPSDKLPFELGCALDKFMVVFEDVKGQNSLNKDLQPGQGINNLDNLRDHL DGAVAVSLEK	678
NJ	CPADKLNLFELGCAIDRFVVFEDVKGQNMNLNKKLQPGQGISNLDNMRDYL DGAVPVNLEK * : : * ** * * : * : * * : : : ** * . : . * ** : . ** : : ** : : ** : : * . ** :	587
SV	KHLNKRQIFPPGIVTMNEYSVPKTLQARFVKQIDFRPKDY LKHCLERSEFLLEKRIIQS	571
TS	KHVNKRSQIFPPCLVTMNEYLLPETIFTRFAYVLNFTPKHNLRSCLQVSDYLLTERILQD	616
H9	KHVNKRSQIFPPVIMTMNEYLLPPTVGVRFALHIHFHCKTYLKQSLEKSD-LIEKRILNS	616
MC	KHVNKKHQIFPPCIVTANDYFIPKTLIARFSYTLHFSPKANLRDSLDQNM EIRKRRILQS	738
NJ	KHMNKR SQVFPPCVMTMNEYFMPQTLFVRFS LKLDVSRPNLQSAVDKTPGLVANRILQK ** : ** : * : ** : : * * : * * : . * : * : : : : . : : . ** : : .	647
SV	GIALLLMLIWYRPVAEFAQSIQSRIVEWKERLDKEFSLSVYQKMKFNVAMGIGVLDWLRN	631
TS	GVTIALLLVWYCPITMFSESIKEDVKYWKDILCKYMGHTNFATLLLNVEEGK DPLDSVVI	676
H9	GYTILLLLWYNPVDSTFPKVQEYVVKWKEILERHVSITQFGNIQQNILDGKDPLHGIVI	676
MC	GTTLCLLIWCLPDTTFKPCLQEEIKNWKQILQSEISYGKFCQMIENVEAGQDPLL NILI	798
NJ	GLTLFLLLIWYTPVKKFAVSLQEEIANWKCIIEKTVSHSDFCKMLENIEVGESPLTDLID * : : * * : * * : : . : * * : . . : : * : * . * :	707
SV	SDDDDDEDQENADKNEDGGEKNMEDSGHETGIDSQSQGSFQAPQSSQSVHDHNQPYHICR	691
TS	EVEDEEEEF-SET-----NDSGFQ----TQ-----	697
H9	EEQA-----	680
MC	EEEGPEETE---ET-----QDSGTF---SQ-----	817
NJ	EGDN----- . :	711
SV	GFTCFKKPPTPPPEPET 708	
TS	----- 697	
H9	----- 680	
MC	----- 817	
NJ	----- 711	

Betapolyomaviruses

SV	MDKVLNREESLQ LMDLLGLERSAWGNIPLMRKAYLK KCKEFHPDKGGDEEKM KKMNTLYK	60
BK	MDKVLNREESMELMDLLGLERAAGWNLPLMRKAYLRKCKEFHPDKGGDEDKMKRMNTLYK	60
JC	MDKVLNREESMELMDLLGLDRSAWGNIPVMRKAYLK KCKELHPDKGGDEDKMKRMNFLYK	60
KI	MDKTL SREEAKQLMQLLCLDMSCWGNLPLMRQYLVKCKEYHPDKGGNEESMKLLNSLYL	60
WU	MDKTL SRNEAKELMQLLGLDMTCWGNLPLMRKYLSKCKEFHPDKGGNEEKMKLLNSLYL	60
	.*.*.*: : **:* * : .::*:* * * * * * * * * * * : .: * * : * *	
SV	KMEDGVKYAHQPD--FGGFWDAT EIP TYGTDEWEQW WNAFNE--ENLFCSEEMPSSDDE	115
BK	KMEQDVKVAHQPD--FG-TWSSSEVPTYGTEEWESWSSSFNEKWDEDLFCHEDMFASDEE	117
JC	KMEQGVKVAHQPD--FG-TWNSSEVPTYGTEEWESW WNTFNEKWDEDLFCHEEMFASDDE	117
KI	KLQDSVSSVHDLNEEEDNIWQSSQIPT YGTPDLDEWWSQFNTYWEEELRCNESMPSSPKR	120
WU	KLQECVSTVHQLNEEEDVWSSSQIPT YGTPDWYDWWWSQFNSYWEEELRCNEEMPKSPGE	120
	*::: * . .*: : . * .:::***** : : * . * * * : * * * . * *	
SV	AT-----ADSQHSTPPKKKR--KVEDPKDFPSELLSFLSHAVFSNRTLACFAIYT	163
BK	AT-----ADSQHSPPKKKR--KVEDPKDFPSDLHQFLSQAVFSNRTLACFAVYT	165
JC	NT-----GSQHSPPKKKK--KVEDPKDFPVDLHAFLSQAVFSNRTVASFAVYT	164
KI	S-----APEEPPSCSQAPPPKKK--HAFDASLEFPKELLE FVSHAVFSNKCITCFV VHT	172
WU	TPTKRTREDDEEPQCSQAPPPKKKKDNATDASLSFPKELEEFVSQAVFSNRTLTA FVIHT	180
	.:::***** : . * * : * * : * * * * : : .: * .: *	
SV	TKEKAALLYKKIMEKYSVTFISRHSYNHNILFFLT PHRHRVSAINNYAQKLCTFSFLIC	223
BK	TKEKAQILYKKLMEKYSVTFISRHCAGHNIFFLT PHRHRVSAINNFCQKLCTFSFLIC	225
JC	TKEKAQILYKKLMEKYSVTFISRHGFGGHNILFFLT PHRHRVSAINNYCQKLCTFSFLIC	224
KI	TREKGEVLYKKLLQKYQCSFISKHAFYNTVLIFFLT PHKHRVSAINNFCKGHCTVSFLFC	232
WU	TKEKAETLYKKLLSKFKCNFASRHSYNTALVFILT PFRHRVSAVNNFCKGYCTISFLFC	240
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SV	KGVNKEYLMYSALTRDPFSVIEESLPGGLKEHDFNPEEAE---ETKQVSWKLVTEYAMET	280
BK	KGVNKEYLLYSALTRDPYHTIEESIQGGLEKHDNFNPEEPE---ETKQVSWKLITEYAVET	282
JC	KGVNKEYLFYSALCRQPYAVVEESIQGGLEKHDNFNPEEPE---ETKQVSWKLV TQYALET	281
KI	KGVNPNPYGLYSRMC RKP FNLC EENIPGGLKENEFNPEDLFGE PKEPSLSWNQIANFALEF	292
WU	KGVNNAYGLYSRMT RPF T LCEENIPGGLKENDFKAEDLYGEFKD-QLNWKALSEFALEL	299
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SV	KCDDVLLLLGMYLEFQYSFEMCLKCIKKEQPSHYKYEKHYANAAIFADSKNQKTICQQA	340
BK	KCEDVFLLLGMYLEFQYNVEECKKCKQKQDPYHFYHEKH FANATIFAESKNQKSICQQA	342
JC	KCEDVFLLMGMYLDFQENPQQCKKCEKKDQPNHFNHHEKHYNAQIFADSKNQKSICQQA	341
KI	DIDDVYLLGSYIRFATKPEECEKCSKNDDATHKRVHVQN HENAVLLQESKSLKNACTQA	352
WU	GIDDVYLLGLYLQLSIKVEECEKCSNEDATHNRLHMEHQKNALLFSDSKSQKNVCQQA	359
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SV	VDTVLA KRVDLSQLTREQMLTNRFNLDLRMDIMFGSTGSADIEEWMAGVAWLHCLLPK	400
BK	VDTVLA KRVDTLHMTREEMLT ERFNHLDKMDLIFGAHGN AVLEQY MAGVAWLHCLLPK	402
JC	VDTVA AKQRVDSIHMTREEMLVERFNFLDKMDLIFGAHGN AVLEQY MAGVAWIHCLLPQ	401
KI	IDRVIA ERRYNCVTLTRKKLLTKRFKKLFNEMDKIV--GERKILLYMASIAWYTGLNKK	410
WU	IDVVI AKRRVDSL NMSREDLLARRFEKILDKMDKTIK--GEQDVLLY MAGVAWYLG LNGK	417
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SV	MDSVYDFL KCMVYNI PKKRYWLFKGPIDSGKTTLAAALLELCGGKALNVNLP LDRLNFE	460
BK	MDSVIFDFLHCIVFNVPKRRYWLFKGPIDSGKTTLAAGLLDL CGGKALNVNLP MERLTFE	462
JC	MDTVIYDFL KCIVLNIPKKRYWLFKGPIDSGKTTLAAALLDL CGGKSLNVNMP LERLNFE	461
KI	IDELVVRFLKLIVDNKPKHRYWLFKGPINS GKTTLATALLNL CGGKALNINIPSEKLPFE	470
WU	IDELVYRLK VIVENVPKKRYWVFGPINS GKTTVAAALLDL CGGKALNINIPADRLNFE	477
	: * : : * : : * * * * * * * * * * : * * * * * * * * * * : * * *	
SV	LGVAIDQFLVVFEDVKGTGGESRDLPSGQGINNLDNLRDYLDG SVKVNLEKKHLNKR TQI	520
BK	LGVAIDQYMVVFEDVKGTGAESKDLPSGHGINNLD SLRDYLDG SVKVNLEKKHLNKR TQI	522
JC	LGVGIDQFMVVFEDVKGTGAESRDLPSGHGISNLDC LRDYLDG SVKVNLERKHQNKRTQV	521
KI	LGVALDQYMVVFEDVKQIGIEKQLPSGNGVNNLDNLRDYLDGCVEVNLEKKHVNKR SQI	530
WU	LGVAIDQFTVVFEDVKGVQVDNKLLPSGNGMSNLDNLRDYLDG SVKVNLEKKHLNKR SQI	537
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SV	FPPGIVTMNEYSVPKTLQARFVKQIDFRPKDYLKHCLERSEF LLEKRIIQSGIALLLMLI	580

BK	FPPGLVTMNEYVPVKTLQARFVRQIDFRPKIYLRKSLQNSEFLLEKRILQSGMTLLLLLI	582
JC	FPPGIVTMNEYSVPRTLQARFVRQIDFRPKAYLRKSLSCSEYLLLEKRILQSGMTLLLLLI	581
KI	FPPGIVTMNEYCIPETVAVRFEKTMFTIKRNLRESLEKTPQLLSQRILHSGIAMLLLLLI	590
WU	FPPGIVTMNEYLVPATLAPRFHKTVLFTPKRHLKESLDKTPELMVKRVLQSGMCILIMLI	597
	****:***** :* *: ** : : * * *...*. : *: :*:**: :*:**	

SV	WYRPVAEFAQSIQSRIVEWKERLDKEFSLSVYQKMKFNVAMGIGVLDWLRNSDDDDDED	640
BK	WFRPVADFATDIQSRIVEWKERLDSEISMYTFSRMKYNICMGKCILDITREEDSETED	642
JC	WFRPVADFAAAIHERIVQWKERLDLEISMYTFSTMKANVGMGRPILDFPREEDSEAED	641
KI	WYRPVSDFDEEIQSNVVYWKEVLNDNYIGLTEFATMQMNVNKGKNILEKWFE-----	641
WU	WCRPVSDFHPCIQAKVVYWKELLDKYIGLTEFADMQMNVTNGCNILEKHNA-----	648
	* ***:~* *: .:* *** ** :.: : *: *: * :*:	

SV	ENADKNEDGGEKNMEDSGHETGIDSQSQGSF-----QAPQSSQSVHHDNQPYHICRGFT	694
BK	-----HGSSTESQSQCSSQVSDTSAPAEDSQRSDPHSQELHLCKGFQ	684
JC	-----HGSSTESQSQCFVSEASGAD-----TQENCTYHICKGFQ	677
KI	-----	641
WU	-----	648

SV	CFKKPPPPPEPET	708
BK	CFKRPKPPPK---	695
JC	CFKKPKPPPK---	688
KI	-----	641
WU	-----	648

Deltapolyomavirus

H6	MDRLLAREEVKELMNLIGLSMACWGNLPLMQQKIRLACKKYHPDKGGDPEKMQRNLNLKE	60
H7	MDKLLGRDEVKELMELIGLNMACWGNLPLIQHKVRLASKKYHPDKGGDPQKMQRNLNLKD	60
Q	MDRLLSRDEVNELMQLIGLSMSNWGNLPLIQHKVREACKKHHHPDKGGDPEKMQRNLNLKD	60
SV	MDKVLNREESLQLMDLLGLERSAWGNIPLMRKAYLKKCKEFHPDKGGDEEKMKKMNTLYK	60
H10	MDRVLSRDEVKELMALLSLNTAAWGNIPLMQYKYRQTCLKLHPDKGGDGEKMKRLNELFS	60
STL	MDQALSRAEAKELMGLLGLPEDSWGNVPLISYRYRQKSKIYHPDKGGNEETMKRLTELYS *: * * * : * * *: . * * * * : . : * : . * .	60
H6	KLNATLRDQMSSS--PTWCFSS-EVRPPPYQYSPGWQWADFNRGWDEDEDLYCDEHLSA	117
H7	KLQATLRDQRSGS--PMWHYSSDEVPPPPYGPSPAWDQWWQDFNKGWD-EDLYCTEELSS	117
Q	KFAATMRDQSSGN--PIWHFSSEEVPPPPYGTPEWDKWWHDFNRGW-EDLYCTEELSA	117
SV	KMEDGVKYAHQPDFGGFW----DATEIPTYGTDWEQWNAFNE----ENLFCSEEMP	111
H10	KMYTTIEKLRR-GEVYF----PAKGNPTYGTPEWDQWEEFNRGWD-EDLSCNESFAP	113
STL	RMQNTLQNLRSS-SENEN----VFPPGGQYGTPAWEQWEEFNQPF-DDLTCNESFNC : : : . * * : * : * * * . : * * * :	113
H6	SEEDN-----VD-----PGEQNSQDSKYSCTPPKKRKPNPAPNDFPSCLDHLYLSHA	164
H7	SDEEPAASASVN-----PEEGCSQDSKYSATPPKQKKPNPAPQDFPECLSEFLSHA	169
Q	SDEEQT-----ED-----PEEGCSQNSKYSATPPKQKKPNPAPQDFPECINEYLSHA	165
SV	SDDEATADSQH-----STPPKKRKVEDPKDFPSELLSFLSHA	149
H10	SDEEPPGPSQASQNTANDTNTPKKRPRESSSNSTCTPPKRPRNFNPVDFPEVLLLEFLSNA	173
STL	SDDEGTSASQK-----RKFPDSSTQNSTPPKKNKPADPTDFPAELETFLSHA *: * * * : : * * * * : : * * * :	160
H6	TLGNKCYTCFVSYTTLEKWETLYDKLQSAFNAVFTGAYKCDNTGAILYCITPRRHRVSA	224
H7	TLGNKCYTCFLCYTTYEKSMLLYEKLGVFENALFIGAYNCVDGSGALVFFISGSRHRVSA	229
Q	TLGNKCYNCFCVYTTMEKSLMLYDKLNNEFNALFIGNYKCDGSGSIVYMITGSRHRPSA	225
SV	VFSNRTLACFAIYTTKEKAALLYKKIMEKYSVTFISRHNS--YNHNILFFLTPHRHRVSA	207
H10	IFSNTLNSFCVLYTTREKQGFLEYKVPKFKAMFYSLHEF--DGDSLFLLLSGKHRVSA	231
STL	VFSNKTNSFCVIYTTIEKGNELYTVGPKFKSMFISCHSY--NTCCILFMILAGKHRVSA : . * : . * * * * * : : . * . : . : : : : * * *	218
H6	MLNALSKCCTISFLLIKAVLKSACCYMALQGDEFTVIOESKAEGHLSYDFQEGSK--KEE	282
H7	ILNACKKHCTVSFIMVKAVLKNAECYKALQDSKFAVLRESKEGGLHSYDFQEASK--KDD	287
Q	ILNASKKYCTVSFSLVKAVLKNAECYKALQGNFTVIRESREGGLHSYDFQEASK--KDD	283
SV	INNVAQKLCTFSFLICKGVNKEYLMSALTRDPFSVIEESLPGGLKEHDFNPEEAETKQ	267
H10	IKNYCSNLCTVSFLLVKGCLKAYECYALCKTPFKLIKQSQEHLGSLKTDFCEEEEK--DKV	289
STL	LKNFCAALCSISFVLVKSLKPYECYRLCSAPFAVTKQSRPEGLSQAEFMEQEN-SKPS : * : * : * : * : * : * : * : * : *	277
H6	CDWNQVASFASDSDLTDCLALLGYIEFANDPASCCKKGVKV--HKHHEVHFHNAQLF	340
H7	CDWNFVADFAADMELTDVLLIMGYMEFATEPSLCPKCLKSVKA--HQHHEKHWANAKLF	345
Q	CDWNAVEAFALANDLTDPLIMGYLEFAAEPSLCQCKKGVKA--HKCHELQWSNAKLF	341
SV	VSWKLVTHEYAMETKDDVLLLLGMYLEFQYSFEMCLCKIKKEQPSHYKYHEKHANAAIF	327
H10	VNWQQICEFAVEVQCEDPLLLMGMLLDFAKDVEGCSKCEQKKLKHYYKFHEAQNINSKLF	349
STL	VNWQQICEFAVQFNCEPLLLMGIYLDSESPENCEKCKT-ELKHHSQFHEKEYNNAKLF : * : : * : . * * : * : * : . * * : * * : * : *	336
H6	KAAKNQKSIAQQACDRVAAQRRVLMLESTRQDLVLQAFKKQFKILAEQY--AGGVEITQL	398
H7	KTAKNQKGIAQQAADRVLAARRVLMLESTRKDLVMVSFKKQFKVLAEQF--GGGVEITQL	403
Q	KSAKNQRGIAQQAADRVLSARRVMMIESTRVDLVMAFKKQFQVLNDQF--AGGVEITQL	399
SV	ADSKNQKTICQQAVDTVLAKKRVDLSQLTREQMLTNRFNDLLDRMDIMFGSTGSADIEEW	387
H10	KDCKNQKTICQQATDWVTAQRRLILESTREHLLVLRFKHMFEEKMEDI---CGEVEICQY	406
STL	RDSKTQKTLCQQACDWVCAKRRVLILESTREDLLVIRFKQVLKEMQDI---AGEVEILRY : . * : : . * * * : : * : : * : : * : : *	393
H6	LGAVAWLDCLQPSFTTKLKEILSILTENIPKKRNVLFKGPINSGKTTLAAAILDLVGGVS	458
H7	IGAVAWLDCLLPQFTTIKIKEMLSYLVENTPKRNNLLFKGPINSGKTTLAAAILDLGGVA	463
Q	LGAVAWLDCLMPSTTKLKEMLTLLVQNYAKRNNLLFKGPINSGKTTVAGIMDLLGGVA	459
SV	MAGVAWLHCLLPKMDSVVYDFLKCMVYNIPKKRYWLFKGPIDSGKTTLAAALLELCGGKA	447
H10	MAGVAWLSLLMPHFDEIILFIIKAMTENVPKRRYVLFKGPINSGKTTVAAAILDLGGKT	466
STL	MAGVAWLSLLFNHFDDIVLEIIRTMTVINTPKRRYVLFKGPINSGKTTVAAAILDLGGRT : . * * * * : : : : . * * * * * * * * * * * * * * *	453
H6	LNVNCTPDKINFELGCAIDKFMCVIEDVKGTP-MANTNLTQCGMTNLDNLRDYLDCGVP	517
H7	LNVNCSSDKINFELGCAIDKYMVVIDVKGTP-LPNTDLPSGVGMANLDNMRDYLDCGVP	522

Q	LNVNCSDDKINFELGCAIDKMLVVFEDVKGQP-LPNTDLPAGVGMANLDNLRDHLDDGCVF	518
SV	LNVLNPLDRLNFELGVAIDQFLVVFEDVKGTG-GESRDLPSPGQGINNLDNLRDYLDDGCVK	506
H10	LNVNCPDPDKLAFEIGCAIDEYMVVFEDVKGQNEGSNSSLTPGMGMSNLDNLRDHLDDGCVK	526
STL	LNINCPPEKVNFEELGCAIDFEMVVFEDVKGQTEGK-TNLTSGMGMNLDNLRDHLDDGCVK	512
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H6	VNMERKHLNPKVSQLFPPSVITCNEYVIPCTVKARIARGYYFLHKPCLQKCLKD-CVLMSK	576
H7	VNLERKHINKTSQLFPPCIITCNEYAIPPTVKARVAKGYFFLHKPLKKSOLDANPILMKK	582
Q	VNLERKHTNPKVSQLFPPCIITCNDYAIPTVKARVAKGYFFIHKPNLKKCLDVNPILMQK	578
SV	VNLEKKHLNKRQTQIFPPGIIVTMNEYSVPKTLQARFVKQIDFRPKDYLKHCLERSEFLLEK	566
H10	VNLEKKHVNKKSQIFPPGIITMNDYFIPPTLQARMIKTINFRPKFLRNSLEKNSELLRK	586
STL	VNLEKKHLNKRKQIFPPGIITMNEYNVPLTILARMVKVINFRPKHYLKKSLVNNELLHR	572
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H6	RLLQKGTTLAALIWWEPVEDFMEELQEDVVNWKQTFERWVSFGMYQTMKENILAGIDPF	636
H7	RLLQKGTTLAALIWWEPVSDFVEEIQEEVVNWKQTFEQWVSYGMFQTMKENILSGKDPF	642
Q	RLLQKGVTLAALIWWEPVSEFVEEIQEDVVNWKQTFERWVTYGYQDMKQNILAGKDPF	638
SV	RIIQSGIALLLMLLIWYRPVAFQAQSIQSRIVEWKERLDKEFSLSVYQKMKFNVAMGIGVL	626
H10	RIVQSGVTLLLLLCCWWQPVIAFHPEIHDNVRYWKETIEKYVPFGMYHDIRRNIESGEDPL	646
STL	RIVQSGKTLMLLMWWQPVKVFHSSIHEDVKIWKETLTKYVSIGMFHDMQRNIQNGDDPL	632
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H6	TNVLVDESFFVQPPQEND-ETN-----DSTQESGIGSMHSM-----	669
H7	EGVLINDPTE---ENT-RET-----QESTESGIGSMNN-----	671
Q	YGVIMSDIN---EIV-EET-----QESTESGVGSMET-----	666
SV	DWLRNSDDDDDEDSQENADKNEDGGEKNMEDSGHETGIDSQSQGSFQAPQSSQSVHHDNQF	686
H10	KDILICVDADEDQQDSGINSQ-----	668
STL	KNILICEDTENNETQDSAFCTQDSDNE-----	659
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H6	-----	669
H7	-----	671
Q	-----	666
SV	YHICRGFTCFKKPPTPPPEPET	708
H10	-----	668
STL	-----	659

Supplementary Figure S2. Alignment of the HPyV and SV40 sTag. The Alphapolyomaviruses are shown in pink, the Betapolyomaviruses in yellow, and the Deltapolyomaviruses in turquoise. Conserved and partially conserved S, T and Y are highlighted in red, green, and blue, respectively.

SV40	MDKVLNREESLQMDLLGLERSAWGNIPLMRKAYLKKCKEFHPDKGGDEEKMKKMNTLYK	60
BKPyV	MDKVLNREESMELMDLLGLERAAGNPLMRKAYLRKCKEFHPDKGGDEEDKMKRMNTLYK	60
JC	MDKVLNREESMELMDLLGLDRSAWGNIPVMRKAYLKKCKELHPDKGGDEEDKMKRMNTLYK	60
KI	MDKTLRSREAAQQLMQLLCLDMSCWGNLPLMRQYLVKCKEYHPDKGGNEESMKLLNSLYL	60
WU	MDKTLRSNEAKELMQLLGLDMTCWGNLPLMRTRYLSKCKEFHPDKGGNEEKMKKLNLSLYL	60
NJ	MEKVLKSDKEMLIELGIPRYAYGNFPIMKTAYKRASKIYHPDKGGSSEKMMLLNSLWQ	60
TS	MDKFLSREESLELMDLLQIPRHCGYGNFALMKINHKKMSLKYHPDKGGDPEKMSRLNQLWQ	60
MC	MDLVNLRKEREALCKLLEIAPNCYGNIPLMKAAFKRSCLKHHHPDKGGNPVIMMELNTLWS	60
H6	MDRLAREEVKELMNLIGLSMACWGNLPLMQQKIRLACKKYHPDKGGDPEKMQRNLNLKE	60
H7	MDKLLGRDEVKELMELIGLNMACWGNLPLIQHKVRLASKKYHPDKGGDPQKMQRNLNLKD	60
Q	MDRLSRDEVNELMQLIGLSMSNWGNLPLIQHKVREACKKHHHPDKGGDPEKMQRNLNLKD	60
H9	MDQTLSEERNELMDLLQLTRAAGNLSLMKKAYKTVSKIYHPDKGGNPEKMQRNLNELFQ	60
H10	MDRVLRSDEVKELMALLSLNTAAWGNIPLMQYKYRQTCLKLHPDKGGDGEKMKRLNELFS	60
STL	MDQALSRAEAKELMGLLGLPEDSWGNVPLISYRYRQKSKIYHPDKGGNEETMKRLTTELYS	60
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SV40	KMEDGVKYAHQPD--FGGFWDATVFA[S]S-----LNPGV-----DAM[CKQWP	101
BKPyV	KMEQDVKVAHQPD--FGT-WSSSEV-CAD----FPLCP-----DTL[CKEWP	99
JC	KMEQGVKVAHQPD--FGT-WNSSEV-GCD----FPPNS-----DTL[CKEWP	99
KI	KLQDSVSSVHDLNEEEDNIWQSSQV[CKDLCCN----KFRLVNAIYGE-YYEAYIMKQWD	115
WU	KLQECVSTVHQLNEEEDVWSSSQV[ELCCNFPPRK[RLVGEVYGD-VFEEYILKDWD	119
NJ	KFQEGLEIVRDE[---VCQVSFSD[-----DS[LLKCCSPKVFHELF-LRSP	104
TS	KLQEGTYNARQEF---PTSF-SSQVGSW----YWEANLISLKEYFGKKKYDENVIKHW	111
MC	KFQQNIHKLRSDF---SMFDEVS--[KF-----PW-EE[GLKDYMQS-GYNARFCRGP	108
H6	KLNATLRDQMSSS---PTWCFSSSEV[DD-----W-GIPLTVGEFLGP-EFHKKKVWDFC	109
H7	KLQATLRDQSGS---PMWHYSSDEVSF-----W-DIELTVGEFLGP-EFNRKKVWNYN	109
Q	KFAATMRDQSSGN---PIWHFSSEVSF-----W-DLQLTVGEFLGV-EFNRKKLWNFE	109
H9	KLQVTLLEIRSNC---GSSS--SQVAV[-----FWDENFRTLGAFLGE-KFNQRIIGYP	109
H10	KMYTTIEKLRE-----GEVYFPAKVG[-----FIDDVTLGDVLGP-SFEKKIYIWP	108
STL	RMQNTLQNLRSSS---ENENVFPPVRML-----LLSD[FTLGDLLGP-QFESKVIIFIWP	110
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SV40	ECAKMS[ANCICLLCLLRMKHENRK----LYRKDPLVWVDC[CFDCFRMWFGDLDC-EG	155
BKPyV	ICSKKPS-VHCPCLMCQLRLRHLNRK----FLRKEPLVWIDC[CFIDFTQWFGDLDT-EE	153
JC	NCATNPS-VHCPCLMCMLKLRHRNRK----FLRSSPLVWIDC[CFDCFRQWFGCDLT-QE	153
KI	VCIHGYN-HEQCICILSKYHKEY---KIYRKPPVWIEC[CKC[RECFFFPIS-MQ	169
WU	ICLKGFY-YLCNCFYCFLDKRHKQKY---KIFRKPPMWIEC[CKC[REWFGFEIS-AE	173
NJ	QCLLKGP-TSCSCITSCLYNQHRQIK---LCGKKRCLTWGNCFCFSCFILWFGGLRET-WK	159
TS	QCAEKAL-KECKCLTCKIGLQHYVYK---QMHQKKCVWGEFC[CKC[CAWFGEDLYCLD	167
MC	CMLKQLRDSKACISCKLSRQHCSLK---TLKQKNCLTWGEFC[CKC[QCFILWFGFPPT-WE	164
H6	LCVQQGI-SSCKCLHCLLKKEHKKQV---EINLGKPTIWGKCWC[CKC[CLWFGLPVE-AD	164
H7	LCVLQGL-RACCCIHCILKRKHKKAKKEYAKDHRGPLLWGKCWCFC[CKC[LDWFGVERS-EE	167
Q	LCVLQGL-RACCCILHCLLRKHKKLAKQMAKDQKGPLVWGHWCFC[CKC[QWFGEDKN-KE	167
H9	DCITYN-KPSCCIVCLLKQQHKSTK---INKKKPCLVWGEFC[CKC[LLWFGFPED-FT	164
H10	LCASDLLRHKCGVCCLLKQHRNDK---LAKQKQCLVWGEFC[CKC[FLWFGQFEG-YT	164
STL	TCACRYRTFCKCICILKRQHDEIK---QVRKKPCVTWGEFC[CKC[FLWFGCDFT-KT	166
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SV40	TLLWCDIIGQTT[RDCLKL-----	174
BKPyV	TLQWVQIIGETPFRDLKL-----	172
JC	ALHCWEKVLGDT[RDCLKL-----	172
KI	TFFFWKVIIFNTEIRAVQPLLR-----	191
WU	TFFYWKKIIFLT[MQVGL[LR-----	194
NJ	TFEIWKHVIAQMPAALLQL[PSLF-----	183
TS	SLWAW[SCIVGEVDFHLVNL[LRVNQGFNWGK-----	198
MC	SFDWWQKTLEE[TD[CLLHLHLF-----	186
H6	SFMWW[SHIYQ[PLDWLGI[TEKLIWW-----	190
H7	SFMWW[SHIIFQ[IPMDVLNLWGQLNLL-----	193
Q	SFEWW[QIYGT[QMDVINIWQINLL-----	193
H9	SFNYW[LLMRNMDLSLLRLWTELGF-----	189
H10	SFFWWKHIMHN[TEFDLLCLLGELILWVSYSFILGKSHLWDS	206
STL	SLHAWKHVMFNLDLDLLMFKQLNLVSFSF-----	195
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