

Supplemental Data

Table 1.

Peptide number	Sequence	Kinase	Barrett / Squamous
183	SSLKSRKRA		2.46
152	KRPSKRAKA	PKC	2.39
164	SSKRAK	PKC	2.25
995	RQRKSRRTI	PKC	2.11
926	KYRKSSLKS		2.07
195	LRGRSFMNN	PKA	1.85
389	SRTASFSES	PKB	1.77
650	EDTLDSDDD	CKII	1.75
23	SPRKSPKKS	sperm-specific histone kinase	1.73
179	RKQISVRGL	PK	1.73
239	KASASPRRK	sperm-specific	1.67
369	SLRASTSKS	S6K	1.66
368	RSGYSSPGS		1.66
34	RKRSAKE	PKA,PKG	1.65
1062	SPRKSPRKS	sperm-specific	1.65
900	AAASFKAAR	PKC	1.61
201	HMRSSMSGGL	PKA	1.55
316	RGKSSSYSK	PKC	1.52
566	RRATPA		1.51
1096	AAASFKAAR	PKC	1.51
45	KRAKAKTAKKR	PKC	1.50
941	DPTMSKSKK	PKC	1.49
352	DAGASPVEK	PKC	1.49
380	PLTPSGEAP	Src	1.49
356	EGTHSTKRG	PKC	1.48
351	GSRGSGSSV	PKA	1.47
30	TLASSFKRR	PKC	1.46
793	ALGISYGRK	PKC	1.46
833	LTRRASFSAQ	PKA	1.45
807	SPKKSPRKA	sperm-specific	1.45
705	ARKKSSAQL	PKA	1.44
364	GEINTEDDD	CKII	1.44
231	VIKRSRKR	CDK	1.43
180	AGTTYAL	MHCK	1.43
348	KRPSIRAKA	PKC	1.43
169	RLSPSPTSQ	CDK	1.42
969	LGSALRRR		1.40
166	AVDRYIAIT	IR	1.39
1044	RRLSSLRAS	S6K	1.38
244	KRSGSVYEP	PKA	1.37
1110	REILSRRPS	GSK3	1.36
574	YKNDYYRKR		1.36
167	DPLLYRFP	PKC	1.36
1033	EQEYEDPD	Lyn,Syk	1.35
189	VKRGISGL	H4-PK-I,PKA	1.35
154	PYKFPSSPLRIPGZ	na	1.33
349	NPGFYVEAN	EGFR	1.32
1149	RKRKSSQAL	PKA	1.31
827	KAKTTKGRP		1.31
151	ESSNYMAPY	PDGFR	1.30
551	GTVPDNDID	GRK2,GRK5	1.30

337	KLRRSSSVG	PKA,PKC	1.29
571	RKFSSARPE	PKA	1.28
362	AVDGYVKPQ	Lyn,Src,JAK2	1.28
188	PQPEYVNQP	erbB2	1.27
786	KRPSNRAKA	PKC	1.25
158	GGRDSRSGS	PKA,PKC	1.25
1063	RRRASVA	PKA,PKC	1.25
156	DAHKSKRQH	CKII	1.24
915	GRGLSLSR	PKA	1.20
49	KRKQGSVRGL	PhK,PKA	1.16
127	TAYGTRRHL	PKC	1.12
747	GTRLSLARM	PKA,PKC	1.12
1076	KKDVTVPKA		0.84
602	EKESSNDST	GRK	0.82
951	DNLYYWDQD	erbB2	0.82
260	RRRASQLKI	PKC	0.81
453	GRILTLPRS	PKC	0.80
3	EDNEYTARQ	Src	0.79
689	EEQEYVQTV	EGFR	0.77
307	EENVSVDDT	CKII	0.77
696	DLPLSPSAF	MAPK	0.77
259	EPAVSPLLP	CDK	0.76
427	VHNRSKINL	AMP-PK	0.76
539	QLIDSMANS	Raf1	0.75
254	AQDTYL VLD	Lyn,JAK2	0.74
517	LGEGTP		0.74
232	SPVKSPEAK		0.73
1040	FLTEYVATR		0.73
834	HRQETVEAL	CaM-II	0.73
716	TRQTSVSGQ	CaM-II	0.73
531	PINGSPRTP	CDK	0.73
208	GMGTSVERA	PDK	0.73
33	SPGEYVNIE	IR	0.72
1080	MPGETPPLS	GSK3	0.72
284	STGIYEALE	Src	0.71
512	RGAI SAEVY	PKG	0.71
500	DLPMSPRTL	JAK1,Src	0.71
734	LIEDAEYTA	Lck,Fyn,Fes,Yes	0.70
1067	PSPKYPGPQ		0.69
102	ERTNSLPPV	PKA	0.69
516	SGYSSPGSP		0.68
533	KLINSIADT		0.67
311	NDITSL	tropomyosin kinase	0.67
805	ESVDYVPML	PDGFR	0.66
69	DGHEYIYVD	PDGFR	0.66
400	GHQGTVPSD	GRK5	0.66
529	SVFSSPSAS	CDK	0.65
591	EDA ESEDEE		0.65
393	HDALSGSGN	CKI	0.65
880	KKIDSFASN	PKC	0.65
709	RKISASEA		0.64
673	SRKGSFGFH	PKA,PKC	0.64
76	PRRASATSS	? CKI	0.64
501	GDLQSAEFH		0.64
536	SRQLSSGVS	MAPKAPK2	0.64
1068	SSVLYTAVQ	PDGFR	0.64
94	LSVSSLPGL	CKI	0.64

409	NVFSSPGGT	CDK	0.63
246	HSSSQGGG	PKA,PKC	0.63
444	EEELYLEPL		0.63
1051	RDDTYTAHA	Abl	0.63
111	EEPQYEEIP	Src	0.62
97	KVPQTPLHT	MAPK	0.61
261	SFTTTAERE	AFK	0.61
519	TAESSQAEE	CKII	0.60
921	STSVSAVAS	GRK	0.60
819	VGPGYLGSG		0.59
255	DIPESQMEE	CK,CKII	0.59
62	EEDLSDENI	CKII	0.59
1059	TPPLSPIDM	ERT,PK	0.58
1058	STNEYMDMK	PI3K,CHK	0.57
66	KQISVR	PK	0.57
919	PASPSPQRQ	CDK	0.55
1001	ESSYSYEEI		0.54
41	LSDDSFIED	CKII	0.52
143	QASSTPLSP	CDK	0.50
610	YTRFSLARQ	PKC	0.50
510	DLFGSDDEE	CKII	0.49
83	STNDSL	GRK5	0.47

Peptide substrates with significantly altered phosphorylation in Barrett's esophagus versus normal squamous esophagus. The fold induction of each substrate, their corresponding protein kinases and chip peptide number are provided.

Table 2.

Peptide number	Sequence	Kinase	Barrett / Cardia
955	LRRGSLG	PKA,H4-PK	2.34
214	RRASI	PKA,PKC	2.23
573	LRRASLG	PKA,H4-PK	2.07
625	LRRASLGAA	PKA,H4-PK	2.06
174	LRRASLAG	PKA	2.04
650	EDTLDSDDD	CKII	2.02
941	DPTMSK K K K K	PKC	1.99
804	DDAYS DTET	CKI	1.88
1093	RRRRAASVA	PKC	1.87
534	LDDQYTSSS		1.87
958	RRASLG		1.83
1151	LRRATLG	PKA,H4-PK	1.79
694	GRRESLTSF	PKA,PKG	1.79
588	QRRTSVSGE	PKA	1.78
152	KRPSKRAKA	PKC	1.73
134	SRRSSLGSL	PKA	1.72
891	ARTKRSGSV	PKA	1.71
890	GRPITPPRN	CDK	1.69
784	QRRTSLTGS	PKA	1.69
747	GTRLSLARM	PKA,PKC	1.67
566	RRATPA		1.65
917	VTRSSAVRL		1.62
977	SRSRSRSPG	RS	1.61
1110	REILSRRPS	GSK3	1.60
552	EGSAYEEVP	EGFR	1.59
1145	ADSFSLHDA	CKI	1.59
1078	LYSGSEGDS		1.59
972	PPRRSSIRN		1.56
946	RVLESFRAA	PKC	1.56
898	SIYSSDDDE	CKII	1.56
769	LRRASGG	PKA,H4-PK	1.56
177	TVTRSYRSV	PKC	1.55
915	GRGLSLSR	PKA	1.55
959	AAVDTSSSEI	CKII	1.55
951	DNLYYWDQD	erbB2	1.54
949	ADSFSLNDA	CKI	1.54
498	GRRQSLIED	PKA,PKC,Cam-II	1.52
688	MRRNSFTPL	PKA	1.51
187	TTPLSPTRL	CDK	1.51
294	PRRRTRRAS	PKA	1.51
1137	DPPGTEFV	beta-ARK	1.50
759	LRRPSLG	PKC	1.50
146	LLQDSVDFS	CaM-II	1.50
911	SYPLSPLSD	MAPK	1.49
20	DDINSYEA W		1.49
103	IRRASTIEM	PKA,CaM-II	1.49
167	DPLLTYRFP	PKC	1.49
835	LRRFSLATM	PKA	1.49
705	ARKKSSAQL	PKA	1.48
973	RTKGSGSV	PKA	1.48
813	SSSNTIRRP	PKC	1.48
549	DRLVSARSV	PKC	1.48
276	VPRTPGGRR	MAPK	1.48
901	ARKFSSARP	PKA	1.47

692	NDSVYANWM		1.46
967	SSEESIISQ	CKI	1.45
768	LRRASLDG	PKA,H4-PK	1.43
928	SRLHSVRER		1.43
23	SPRKSPKKS	sperm-specific histone kinase	1.43
865	RAAASRARQ	PKC	1.42
256	FPRASFGSR	PKA	1.42
18	RRASL	PKA	1.41
244	KRSGSVYEP	PKA	1.40
128	TRRISQTSQ	CaM-II	1.40
275	TRAPSRTAS	MFPK	1.39
752	RRPTPA	PKA	1.38
556	RRPTVA	PKA	1.37
935	ESMESYEVS		1.37
807	SPKKSPRKA	sperm-specific	1.37
453	GRILTLPRS	PKC	1.36
719	GTKRSGSV	PKA	1.36
1169	RTGRSGSV	PKA	1.36
37	LRRFSLATM	PKA	1.36
135	PETVYEVAG	Src	1.35
481	TPAISPSKR		1.35
929	KNDKSKTWQ	IR	1.32
905	RAKRSGSV	PKA	1.32
846	EDSTYYKAS	FAK	1.32
444	EEELYLEPL		1.31
282	LSGFSFKKS	PKC	1.31
1154	RGYSLG	PKA	1.31
731	PLRRTLVA	AMP-PK,CKI,PKA,PK	1.28
1149	RKRKSSQAL	PKA	1.25
1106	SSKRA	PKC	1.25
885	EEQEYIKTV	EGFR	1.24
141	KLSPSPSSR	CDK	1.24
956	RRSVSEAAL	AMP-PK,CaM-II	1.23
836	EEEAYGWMD	Src	1.21
1160	RKRTLRL	PKC	1.21
1146	ATRRSYVSS	PKA,PKC	1.20
728	KQGSGRGL	PK	1.20
857	TKRSGSV	PKA	1.19
220	RRAASVA	PKA,PKC	1.18
348	KRPSIRAKA	PKC	1.18
260	RRRASQLKI	PKC	1.18
1044	RRLSSLRAS	S6K	1.17
374	YDKEYYSVH	Met	1.17
1045	SFKKSFKLS	PKC	0.94
24	RRKASGP	PKA	0.91
575	SSEITTKDL	CKII	0.89
542	EILNSPEKA	AKT	0.88
652	RRPTSPVSR		0.85
169	RLSPSPTSQ	CDK, cdc2 kinase	0.85
274	STSKSESSQ	S6K	0.84
829	PLSKTLVSSL	AMP-PK,CKI,PKA,PK	0.84
28	LRRAS	PKA	0.84
702	SKAGSLGNI	PKA	0.83
1012	YRKGLKSR		0.82
691	IREESPPHS		0.82
644	PYKFPSSPLRIPGZ		0.81
491	IGSVSEDNS	CaM-II	0.81

661	VKRGSGL	H4-PK-I	0.80
380	PLTPSGEAP	Src	0.80
501	GDLQSAEFH		0.80
539	QLIDSMANS	Raf1	0.79
176	THERSPSPS	proline-rich kinase	0.79
124	SIDEYFSEQ	Tyk2	0.78
640	EEEEYMPME	Src	0.78
641	EQFSTVKGV	GRK5	0.78
699	EEKGSPLNA		0.77
156	DAHKSKRQH	CKII	0.77
197	HDLSSEMFN		0.77
667	TPQVSDTMR	PKA	0.77
529	SVFSSPAS	CDK	0.76
38	PRPASVPPS	DYRK	0.76
540	IVYKSPVVS		0.76
1122	KYLASASTM	CaM-II	0.75
796	GKTDYMGEA	IR	0.75
286	LYSSSPGGA	CDK	0.74
218	YVTTSTRTY	PKC	0.74
297	EETQTQDQP	ds-DNA	0.74
119	GAFSTVKGV	RK	0.74
616	KGYSLG		0.74
651	ENQASEEED	CKII	0.74
414	YTTNSPSKI	CDK	0.74
620	YRLPSNVDQ	CRYS-K	0.73
482	LVVASAGPT		0.73
344	KGGYSQAA		0.73
812	KEAKSD	CKII	0.73
985	HHHATPSPP	GSK3	0.72
882	PAAPSPGSS	MAPK	0.72
653	SFMDSSGLG		0.72
531	PINGSRTP	CDK	0.72
841	GNGDYMPMS	IR	0.71
800	SAYGSVKAY	PKC	0.71
895	EEKESNDS	GRK	0.70
74	RRKMSRGLP	PKA	0.70
990	DDPSYVNVQ	Fyn,Lck,IR,PDGFR	0.70
798	EKEISDDEA	CKII	0.70
75	SEVPYREVQ	JNK2	0.69
823	SSNEYMDMK	PI3-KINASE	0.69
880	KKIDSFASN	PKC	0.69
609	ETAESSQAE	CKII	0.68
299	IRQASQAGP	CaM-II	0.68
502	GSEEYMNMD	IR	0.68
723	PASQTPNKT	CDK	0.68
602	EKESNDST	GRK	0.68
232	SPVKSPEAK		0.68
991	EVEKSPVKS		0.68
727	PGPQSPGSP		0.67
791	PYKFPSSPLRIPGZ		0.67
52	EEGISQESS	CKII	0.67
432	TKAASEKKT	PKC	0.67
84	VRTFTHEVV	CDK	0.67
974	KRAASPRKS	sperm-specific	0.67
95	SRHSSPHQS	GSK3, CKII	0.67
646	APVASPAAP	MAPK	0.67
830	QSGMTEYVA	MAPK	0.67

730	LASSSKEEN		0.67
888	NDSTSVSAV	GRK	0.67
1030	HRQETVDAL	CaM-II	0.66
613	RPPGFSPFR		0.66
519	TAESSQAE	CKII	0.66
1121	KKRFSFKKS	PKC	0.66
271	SETKTEEEE	CKII	0.65
878	KRKQISVAGL	PK	0.65
679	PTRHSRVAE	PKA	0.65
822	PRHLSNVSS	PKA	0.65
61	GRLSSMAMI	CaM-II	0.65
1164	PKKGSKKAV	PKA	0.65
67	SLKDH	PKC	0.65
795	EYVQTVKSS	PKC	0.64
1040	FLTEYVATR		0.64
817	SNVSTGSI	GSK3	0.63
840	PYKFPSSPLRIPGZ		0.63
984	ELSNIAMG	IR	0.63
986	KTETSQVAP	RK	0.63
60	FPVSYSSSG	Ret	0.63
425	SPALTGDEA	CKII	0.62
82	SPSSPTHE	proline-rich kinase	0.62
91	PVSPSLVQG	GRK	0.61
834	HRQETVEAL	CaM-II	0.61
630	PSAPSPQPK	CDK	0.60
794	DDSGSAMSG	GRK	0.60
400	GHQGTVPSPD	GRK5	0.60
819	VGPGYLGSG		0.55
1170	KQSPSSSPT	PKC	0.55
598	DEAATKTQT	MHCK	0.54
66	KQISVR	PK	0.53
393	HDALSGSGN	CKI	0.51
618	TKKTSFVNF	PKA	0.44
589	HATPSPPVD	GSK3	0.43

Peptide substrates with significantly altered phosphorylation in Barrett's esophagus

versus gastric cardia. The fold induction of each substrate, their corresponding protein kinases and chip peptide number are provided.