

Supplementary Materials for

Genome to Kinome: Species-Specific Peptide Arrays for Kinome Analysis

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Table SA1. Protein names and target amino acids for peptides on the bovine array.

Table SA2. Peptide sequences printed on the bovine peptide array.

13	12	11	10	9
IRF-3(S385/6)	IRAK-1(T209)	Akt1(S129)	IL2RB(Y536)	WASP(Y291)
CTNNB1(S675)	IRAK-1(T100)	ERK3(S189)	IL2RB(Y364)	Syk(Y525/6)
CTNNB1(Y142)	FADD(S194)	ERK2(Y205)	IL-10R-A(Y496)	Cot(S400)
CTNNB1(T41)	HIF2A(T840)	ERK1(T202/4)	IKK- β (Y199)	CaMK2- α (T286)
CTNNB1(S33)	HIF1A(T796)	TBK1(S172)	IKK- β (Y188)	smMLCK(S1773)
STAT6(Y641)	XIAP(S87)	Jak3(Y981)	HMGAI(T52)	MKP-1(S359)
STAT5B(Y699)	BATF(T48)	Jak2(Y1007/8)	LEF-1(S166)	MKP-1(S323)
STAT5B(S731)	NFAT4(S163/5)	Jak1(Y1022/3)	LEF-1(T155)	MKP-1(S296)
STAT4(S721)	NFAT2(S294)	JNK1(S377)	DOCK2(Y209/212)	PLCB1(S887)
STAT4(Y693)	NFAT2(S245)	p38- α (Y323)	CBP(S2063)	PLCB1(T333/4/6)
STAT3(S727)	NFAT1(S326)	p38- α (T179/Y181)	DNA-PK(T2638)	BLNK(Y96)
STAT3(Y705)	NFAT1(S168)	axin-1(S486)	DNA-PK(T2609)	BLNK(Y72)
STAT2(Y690)	Smad4(T277)	Notch 2(S2070)	PKR(T446)	DAPP1(Y139)
STAT1(S727)	Smad3(S422/3/5)	Notch 2(T1808)	Btk(Y550)	RelB(S573)
STAT1(Y701)	Smad3(S208)	GSK3- β (Y216)	Btk(Y222)	APE1(S289)
IKK-G(S43)	Smad2(S255)	GSK3- β (S9)	ITK(Y512)	Tyk2(Y1054/5)
IKK-G(S31)	Smad2(T8)	Elk-1(T417)	FAK(Y397)	p70S6Kb(S473)
NFKB-p105(S907)	Smad1(S462/3/5)	Elk-1(S389)	TAK1(S192)	CXCR4(Y157)
NFKB-p105(S337)	ATF-4(S245)	Fos(T232)	TAK1(T184)	CCR5(S336/7)
NFKB-p65(S536)	ATF-2(T513/5)	Casp8(S347)	PKA α (S338)	CCR2(Y139)
NFKB-p65(S311)	ATF-2(S44)	Casp3(S150)	PKA α (T195/7)	IL7R(Y449)
NFKB-p65(S276)	IRF-5(S437)	IRAK-1(S568)	Akt3(T447)	IL1A(S87)
NFKB-p100(S870/2)	IRF-3(S402/T404)	IRAK-1(T387)	Akt3(S120)	IL-16(S143/4)
NFKB-p100(S866/Y868)	IRF-3(S396)	IRAK-1(S376)	Akt1(Y326)	IL4R(Y713)

13	12	11	10	9	8	7
IARQGGASSENTVD	LHEICQGHDFSEEL	SGSPGENSGAEEMEV	LTLNTDAYLSLQELQ	RETSKVYDFIEKGT	TSRIRTQSFSLQERH	EGRNPGFYVEANPMP
QDYKKRLSVELTSSL	LRARDJITAWHPPAP	YSHKGHLSLEGVLTKW	SCFTNQGYFFHHLPD	ALRADENYKKAQTHG	PELCGPGSPPALTPG	IGTAEPPDYGALYEGR
AVVNLINYODDAELA	QSGSANPGSFTAOWDS	IMLNSKGYTKSIDIW	LPALAKGYVQODPPE	EDQPRCQSLDSALFE	GKESLIGYRLTADSR	KLAEGSAEYEEVPTSV
HSGATTTAPLSGKG	YLLPELTRYDCEVNV	HTGFLTEWATRWR	ELLEQQKYTVTVDYW	SCMHROETVDCLKFF	NTTTSFGYDKPHVLV	RTSSKKGTLRYMSPSEQ
QSYLDGSIHSGATTT	ESGLPQLTSYDCEVN	EDDEQFVSLYGTEEY	SFVGTLYLAPELLE	GLSGRKSSTGSPTSP	VGLLKLASPELERLI	YIDFREYEDLKWEF
MKGDRGRGYVPATIKM	IGRHRRVSPNCRFIN	LPLDKEYVVVREPGQ	KEPSEVPTKRRPRGR	SALSVALQSPITTS	KNSDLLTSPDVGLLK	TGSLDNEYLYIDFRE
TAKAVDGYVKPQIKQ	QKSRQRTQKADTLH	VLPQDKEYYKKEPG	TYSDEHFSPGSHPSH	HCSAEAGSPAMAVLD	AAEERRKSHEAEVLK	GILPRQRYFKQNCSSQ
TYMDQAFSPAFCPOP	SYRESSLSPPASSI	ALETKEYYTKDDR	SHAVHPLTPLITYSD	KQRRSIISPNFSFMG	KELEKRASGQAFELI	QVFSRSESTQPLLDS
PSDLLPMSPSVYAVL	POGSPRVSTDDTWL	GVRGQPSPLGAAVI	MSKDDQPDYGMYSRIS	HSQPAPGSVKAPAKT	GYPVRTYTHEVVTLW	STVWHSGYRHRQVPSV
TEKGDGKYVPSVFIPI	PSTSPRTSVTEESWL	DEPVADPYDQSFESR	PPRSISPGALODLLR	INSSHNTLYTAGQLA	EKIGEGTYGVVYKAR	KLCDFGVSGQLDSM
NTIDLPMSPRTLDSL	PPKMWKTSPDPSPVSV	RHTDDEMTGYVATRW	MAGQVRATQQQLDFT	EEAGDDSYEPPEVEQ	CSIESDIYAEIPDET	ENTEDQYSLVEDDED
DPGSAAPYLKTKFIC	YREPLCLSPASSGSS	MRTPGCQSPGPGHRS	LTPMFVETQASQSTL	SDDDFDSDYENPDEHS	GSPSRAYTHQVVTRW	ARDIKNDSNVVVKGN
NPEERKKYLKHKLIF	GSRTAPYTPNLPHHQ	DEYNVTPSPGTVLT	LKNDETRTSKKGTLR	KVEEPSIYESVRVHT	VDLACTPTDVRDVINI	CNDSTNEYMDMKPGV
TDNLLPMSPEEFDEV	LTMGSPSIRCSSVSV	RTPSLALTPPQAEQE	RVYLDDEYTSVSGSK	AGFGGGLLSPGPEAT	MLRRRNASMQRTGVV	EEANYHLYGRMIDRR
DGPKGTGYIKTELIS	DAGSPNLSPNPMSPT	RGEFNVSYCSRYR	LKKVVALYDYMIPMNA	DYFLLSHSLLPALCD	SELLRSGSSPNLNMG	HIGLDSSSISGSGPGD
PAMLHVPSEQGTPET	ELSPITLSPVNHSLD	SGRPRTTSFAESCCKP	RFVLLDDQYTSSTGTK	A/PEGHEYYCYVREDDG	PGPTRRHYQPYAPAR	EMRERLGTGGFGNVC
QDMLGEESSLKGKAM	MSSILPFTPPVVKRL	ISVDGFSTPVLSPG	TPPETDDYAEIIDEE	PPSGTKKSKRGRGRP	MVQEAKEYKAEDEVQ	PPGSTKRSPYEEVSA
QAHSPLPSPASTRQQ	LTMGSPHNPISSVSV	LSPAPRSI LAKLSFQ	HMTNNKGSAAWMAPE	LLAEKVYVGVWLPA	RALSRQLSSGVSEIQ	PGESDGGYMDMSKDE
FVQLRRKSDLTSEP	SRGSPNKSLLSPGAL	GGLPEAATPESEEF	GTACDIQTHMTNNKG	EAPERVSSVYTRSTG	EDDPEATYTTSGGKI	VSSDGHHEYVDPMQ
SGDEDFSSIADVDFS	IVADQTPPTFRFLKN	FTGLKCPSLIGKPKI	EEEEIRV/SINEKCGK	ILLTIDRYLAIVHAV	TYVDPHTYEDPNQAV	DIMINDSNVYVKNAR
RTYETFKSIMKKSPPF	FGPARNDSVIVADQIT	FRGDYCRSLTGKPKL	R/VKGRTWLTCGTPEY	GSSQEEAYTMSSFY	QLKPLKTYVDPHTYE	ESYEGNSYTFIDPTQ
SMQLRRPSPDRELSEP	FSGELWSADSIRLQ	WQPLAAPSGASAQAA	TAQTTTTPEKYEDE	ILKRRRLSNQNFID	LDNFDGTYETQGGKI	RGEPHVTRRTPDYFL
DSAYGSGSVEQEAEK	NSDPLSLTPDQYMAC	RTRTVRGTALYLPPEE	EEERMINCSPTSOIDN	SSIKORISSFEFFSS	PAVPRRPSADILHR	RNRVYRDSVSPDHSRI
STEVKEDSAYGSSQSV	NTVDLHISNSDPLSL	GSSPSSQSSMVARQT	E/VLEDNDYGRAVDWW	LNGHIYSALTCILC	LRRLRPRTRRVKSES	TGDYIPGTTETHMAPE