

Supplementary Materials

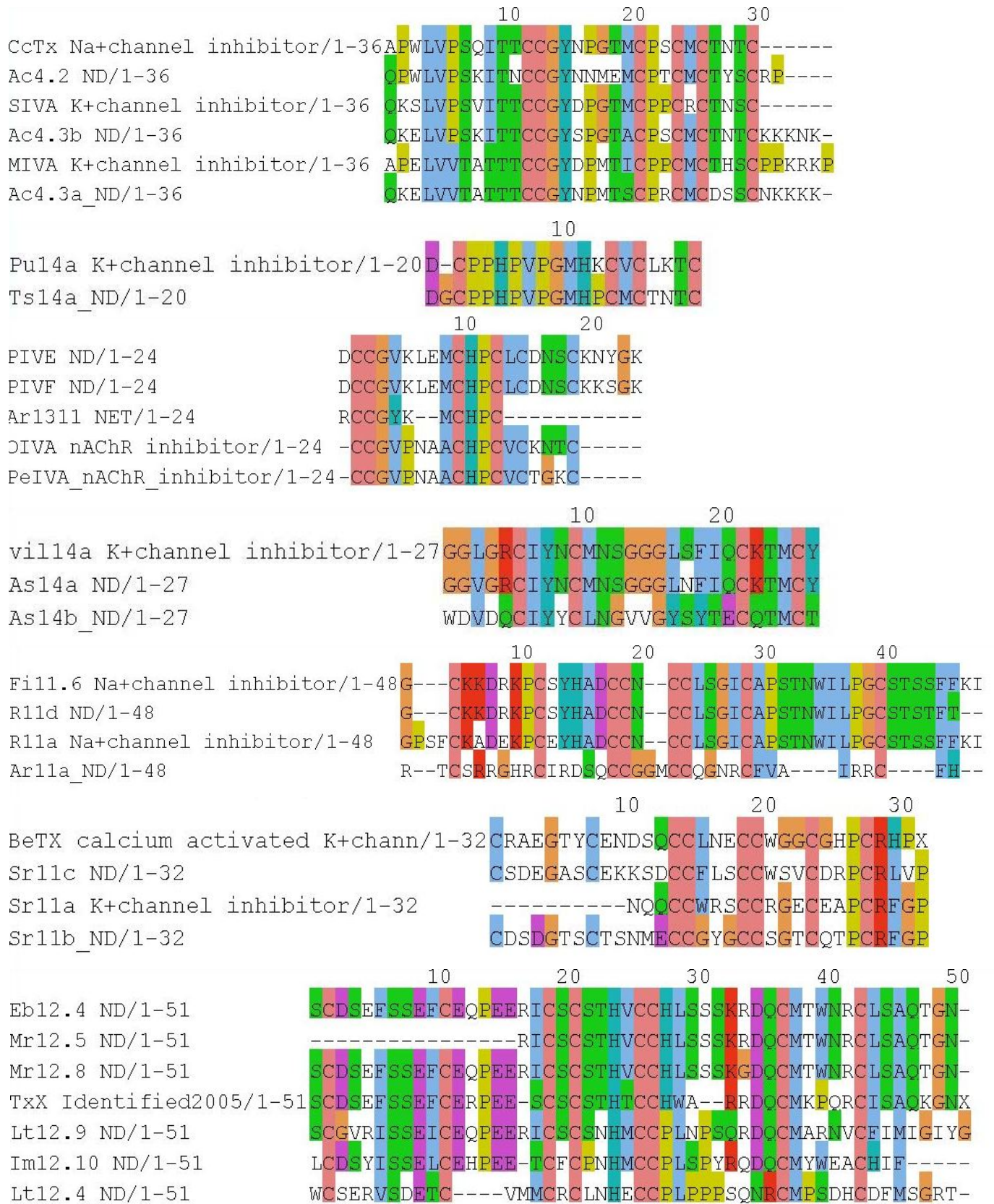
Table S1. *Conus* peptides identified from 1 January 2007 to 31 August 2011.

Peptide	Gene Superfamily and Cysteine framework	Type	Sequence	Predicted target
Ts14a	A superfamily XIV [connectivity I-III, II-IV]	α 1-conotoxin	DGCPPHPVPGMHPCMCTNTC	nAChR
alpha-conotoxin	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GGCCSHPACQNNPDYC	nAChR
Lp1.1	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GCCARAACAGIHQELC	nAChR
Lp1.10	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	NDCCHNAPCRNNHPGIC	nAChR
Lp1.4	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GCCSHPACSGNHQELCD	nAChR
Lp1.6a	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	QFCCGHYDCDFIPNVC	nAChR
Lp1.6b	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	QICCGYGDCGFVPNVCV	nAChR
Lp1.7	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GMWDECCDDPPCRQNNMEHCPAS	nAChR
Lp1.8	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GVWDECKDPQCRQNHMQHCPAR	nAChR
Lp1.9	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	CCSDSDCNANHPDMCS	nAChR
Mr1.1	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GCCSHPACSVNNPDIC	nAChR
Mr1.2	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GCCSNPPCYANNQAYCN	nAChR
Mr1.3	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GCCSHPACRVHYPHVCY	nAChR
Pu1.1	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	QNCCNVPGCWAKYKHL C	nAChR
Pu1.2	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GGCCSYPPCIANNPLC	nAChR
Qc α L-1	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	TVRRFCSDPPCRISNPESCGW	nAChR
Qc α L-2	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	TVRGFCSDPSCRFGNPELCDW	nAChR
Qc1.1a	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	DECCPDPPCKASNPDLCDWRS	nAChR
Qc1.1b	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	NECCDNPPCKSSNPDLCDWRS	nAChR
Qc1.1c	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	DDCCPNPPCKASNPDLCDWRS	nAChR

Qc1.2	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	QCCANPPCKHVNC	nAChR
Qc1.4a	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	DGCCSNPSCSVNNPDIC	nAChR
Qc1.4b	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	DGCCPNPSCSVNNPDIC	nAChR
Qc1.5	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GCCSNPACSVNHPELC	nAChR
Qc1.6	A superfamily I [connectivity I-III, II-IV]	α -conotoxin	GCCSNPTCAGNNGNIC	nAChR
Ac4.2	A superfamily IV [connectivity I-V, II-III, IV-VI]	κ -conotoxin	QPWLVPISKITNCCGYNNMEMCPTCMCT YSCR	K ⁺ channel
Ac4.3a	A superfamily IV [connectivity I-V, II-III, IV-VI]	κ -conotoxin	QKELVVTATTTCCGYNPMTSCPRCMCD SCNKKKK	K ⁺ channel
Ac4.3b	A superfamily IV [connectivity I-V, II-III, IV-VI]	κ -conotoxin	QKELVPSKITTCGYSPTACPSMCTNT CKKKNK	K ⁺ channel
Ar11a	I1 superfamily XI [connectivity I-IV, II-VI, III-VII, V-VIII]	ι -conotoxin	RTCSRGRHRCIRDSQCCGGMCCQGNRC FVAIRRCFH	Na ⁺ channel
R11d	I1 superfamily XI [connectivity I-IV, II-VI, III-VII, V-VIII]	ι -conotoxin	GCKKDRKPCSYHADCCNCLSGICAPSTN WILPGCSTSTFT	Na ⁺ channel
Eb12.4	I2 superfamily <u>XII</u>	E-conotoxin	SCDSEFSSEFCEQPEERICSCSTHVCCHLSS SKRDQCMTWN RCLSAQTGN	ND
Im12.10	I2 superfamily <u>XII</u>	E-conotoxin	LCDSYISSELCEHPEETCFPNHMCCLSP YRQDQCMYWEA CHIF	ND
Lt12.4	I2 superfamily <u>XII</u>	E-conotoxin	WCSEVSDETVMCMCRCLNHECCPLPP PSQNRCMPSDHCDF MSGRT	ND
Lt12.9	I2 superfamily <u>XII</u>	E-conotoxin	SCGVRISSEICEQPEERICSCSNHMCPLN PSQRDQCMARN VCFIMIGIYG	ND
Mr12.5	I2 superfamily <u>XII</u>	E-conotoxin	RICSCSTHVCCHLSSSKRDQCMTWNRCL SAQTGN	ND
Mr12.8	I2 superfamily <u>XII</u>	E-conotoxin	SCDSEFSSEFCEQPEERICSCSTHVCCHLSS SKGDQCMTWN RCLSAQTGN	ND
Sr11b	I2 superfamily XI [connectivity I-IV, II-VI, III-VII, V-VIII]	κ -conotoxin	CDSDGTSCSTNMECCGYGCCSGTCQTPC RFGP	K ⁺ channel
Sr11c	I2 superfamily XI [connectivity I-IV, II-VI, III-VII, V-VIII]	κ -conotoxin	CSDEGASCEKKSDCCFLSCCWSVCDRPCR LVP	K ⁺ channel

Ca11a	I3 superfamily XI [connectivity I-IV, II-VI, III-VII, V-VIII]	I-conotoxin	AWPCGGVVRASCSRHDDCCGSLCCFGTST GCRVAVRPCW	
Ca11b	I3 superfamily XI [connectivity I-IV, II-VI, III-VII, V-VIII]	I-conotoxin	ALLCGGTHARCNRDNDCCGSLCCFGTCIS AFVPC	
Pr3a	III [connectivity I-IV, II-V, III-VI]	μ-conotoxin	CCNWPCSFGCIPCCY	Na ⁺ channel
Pr3b	III [connectivity I-IV, II-V, III-VI]	μ-conotoxin	ERVCCGYOMSCKSRACKOSYCC	Na ⁺ channel
PIVE	IV [connectivity I-V, II-III, IV-VI]	κ-conotoxin	DCCGVKLEMCHPCLCDNSCKNYGK	ND
PIVF	IV [connectivity I-V, II-III, IV-VI]	κ-conotoxin	DCCGVKLEMCHPCLCDNSCKKSGK	ND
Sr7a	O1 superfamily VI/VII [connectivity I-IV, II-V, III-VI]	conotoxin	CLQFGSTCFLGDDDICCSGECFYSGGTFGI CS	ND
Ca8a	S superfamily VIII	conotoxin	GCSGTCHRREDGKCRGTCDCSGYSYCRC GDAHFFYRGCTCTC	ND
Pu5.1	T superfamily V [connectivity I-III, II-IV]	T-1 conotoxin	SCCPSPTSCCPW	ND
Pu5.2	T superfamily V [connectivity I-III, II-IV]	T-1 conotoxin	GCCEDKTCCFI	ND
Pu5.3	T superfamily V [connectivity I-III, II-IV]	T-1 conotoxin	SCCPEEPCCFW	ND
Pu5.4	T superfamily V [connectivity I-III, II-IV]	T-1 conotoxin	SCCPEEITCCPW	ND
Pu5.5	T superfamily V [connectivity I-III, II-IV]	T-1 conotoxin	ECCPQSPPCCHYYYYGSW	ND
Pu5.6	T superfamily V [connectivity I-III, II-IV]	T-1 conotoxin	CCPRKIWCCMIP	ND
Vi1359	T superfamily V [connectivity I-III, II-IV]	T-1 conotoxin	ZCCITIECCRI	ND
Vi1361	T superfamily V [connectivity I-III, II-IV]	T-1 conotoxin	ZCCPTMPECCRI	ND
Sr5.4	T superfamily V [connectivity I-III, II-IV]	T-1-conotoxins	IINWCCLVFYQCC	ND
Sr5.5	T superfamily V [connectivity I-III, II-IV]	T-1-conotoxins	IINWCCLTFYQCC	ND
Sr5.6	T superfamily V [connectivity I-III, II-IV]	T-1-conotoxins	IMAGCCPRFYQCCYP	ND
Sr5.7	T superfamily V [connectivity I-III, II-IV]	T-1-conotoxins	IINWCCLIFYQCCL	ND
Vi15a	V superfamily XV	V-conotoxin	DCTTCAGEECCGRCTCPWGDNCSCIEW	5-HT ₃ receptor
Pr6a	VI/VII [connectivity I-IV, II-V, III-VI]	conotoxin	TCLARDELCGASFLSNFLCCDGLCLLICV	ND
Pr6b	VI/VII [connectivity I-IV, II-V, III-VI]	conotoxin	FGSFIOCAHKGEOCTICCROLRCHEEKTO	ND

	II-V, III-VI]		TCV	
Pr6c	VI/VII [connectivity I-IV, II-V, III-VI]	conotoxin	DQCTYCGIYCCPPKFCTSSGCRSP	ND
Pr6d	VI/VII [connectivity I-IV, II-V, III-VI]	conotoxin	YGNFOTCSETGEDCSAMHCCRSMTCRN NICAD	ND
De7b	VI/VII [connectivity I-IV, II-V, III-VI]	δ -conotoxin	DCIPGGENCDFRPPYRCCSGYCILLCA	Na ⁺ and/or Ca ²⁺ channel
Mr1e	X [connectivity I-IV, II-III]	α -conotoxin	CCHSSWCKHLC	nAChR
As14a	XIV [connectivity I-III, II-IV]	κ -conotoxin	GGVGRCIYNCMNSGGGLNFIQCKTMCY	K ⁺ channel
As14b	XIV [connectivity I-III, II-IV]	κ -conotoxin	WDVDQCIYYCLNGVVGYSYTECQTMCT	K ⁺ channel
Qc16a	XVI	conotoxin	DCQPCGHNVC	
P21a	XXI	conotoxin	SCCIQKTLECLENYOGQASQRAHYCQQD ATTNCODTYFYGCCPGYATCMSINAGNV RSAFDKCINRLCFDPGH	AMPA receptor
Ca16a	Y superfamily XVII	conotoxin	CGGTGDSCNEOAGELCCRRCLKVNSRCC PTTDGC	ND

Figure S1. Multiple alignments of predicted conotoxin targets.

CalTx Ca²⁺channel inhibitor/1-13 NCPAGCRSQGCCM
 Qc16a_ND/1-13 DCQP-CGHNVCC-

Con-ikot-ikot AMPA/1-87 SGPADCCRMKECCTDFVNECLQRYSGREDKFVSFCYEAATVTC-GSFNEIVGCCYGYQCMIRVVKPNSLSGAHEACKTVSCGNPCA
 P21a_ND/1-87 -----SCCIQKTLLECLNNMOGASQRAHYCQDDATNCDITY--YFGCCPGYATCMS--INAGNVRSAFDKICINRLCFDPGH

Mu-hexatoxin-Mq2a Na⁺channel i/1-46 GGCIKWNHSCQTITLKCCKGKCVVCYCHTPWGTNCRCDRTRLFCTED
 Omega-plectoxin-Pt1a Ca²⁺chann/1-46 ADCSATGDTCDHTK-KCCDDCYTCRCGTPWGANCRCDDYYKARCDT-
 Vi15a_ND/1-46 -DCT-----TCAGEE--CCGRG-TC-----PWGDNCSCEIW-----

RIIIj K⁺channel inhibitor/1-29 -LPPCCTE--PKKHCFAPACKYKE-CCKS
 PrIIIE nAChR inhibitor/1-29 -AARCCT---YHGSLKEKCRKY-CCGR
 PIIIA Na⁺channel inhibitor/1-29 -QRLCCG---FPKSCRSRQCKPHR-CC--
 Pr3b ND/1-29 -ERVCCG---YOMSCKSRACKOSY-CC--
 BuIIIA Na⁺channel inhibitor/1-29 VTDRCK---GKRECG-RWCRDHSRCC--
 BuIIIB Na⁺channel inhibitor/1-29 VGERCKN--GKRGCG-RWCRDHSRCC--
 BuIIIC Na⁺channel inhibitor/1-29 IVDRCCNKGNKGKRGCS-RWCRDHSRCC--
 SIIIA Na⁺channel inhibitor/1-29 --ZNCCN-----GGCSSKWCRDHARCC--
 SIIIB Na⁺channel inhibitor/1-29 --ZNCCN-----GGCSSKWCKGHARCC--
 TIIIA Na⁺channel inhibitor/1-29 -RHGCCGGO---KGCSSECRPQH-CC--

TxO1 Ca²⁺channel inhibitor/1-32 -CLDAGEVCDIFFP---TCC-GYCILLFCA--
 De7b ND/1-32 DCIPGGENCDFVRPY--RCCSGYCILLCA--
 PnVIA Ca²⁺channel inhibitor/1-32 GCLEVDYFCGIPFANNGLCSSGNCVFV-CTPQ
 Pr6a_ND/1-32 TCLARDEL CGASFLSNFLCCDGLCLLI-CV--

Lt5d Na⁺channel inhibitor/1-16 ---DCCPAKLLCCN-P
 Pu5.6 ND/1-16 ----CCPRKIWCCMIP
 Vi1359 ND/1-16 ---ZCCITIFECCRI-
 Vi1361 ND/1-16 ---ZCCPTMPECCRI-
 Pu5.3 ND/1-16 ---SCCPEE-PCCFW-
 Pu5.4 ND/1-16 ---SCCPEEITCCPW-
 Pu5.1 ND/1-16 ---SCCPSPTSCCPW-
 Pu5.2 ND/1-16 ---GCCEDK-TCCFI-
 Sr5.4 ND/1-16 IINWCCLVFYQCC---
 Sr5.7 ND/1-16 IINWCCLIFYQCCL--
 Sr5.5 ND/1-16 IINWCCLTIFYQCC---
 Sr5.6_ND/1-16 IMAGCCPRFYQCCYP-