Orphan Bioactive Peptides

NEWLY IDENTIFIED IN THE REGULATED SECRETORY PATHWAY (RSP) USING PEPTIDOMICS

Snapshot peptidomics of the regulated secretory pathway

Neurons and endocrine cells have the regulated secretory pathway (RSP), in which precursor proteins undergo proteolytic processing by prohormone convertase (PC) 1/3 or 2 to generate bioactive peptides. While motifs for PC-mediated processing have been described (R/K-Xn-R/K, n=0, 2, 4, 6), actual processing sites cannot be predicted from amino acid sequences alone. We hypothesized that discovery of bioactive peptides would be facilitated by experimentally identifying signal sequence cleavage sites and processing sites. However, in vivo and in vitro peptide degradation, which is widely recognized in peptidomics, often hampers processing site determination. To obtain sequence information about peptides generated in the RSP on a large scale, we applied a brief exocytotic stimulus (2 min) to cultured endocrine cells and analyzed peptides released into supernatant using LC-MSMS. Of note, 387 of the 400 identified peptides arose from 19 precursor proteins known to be processed in the RSP, including nine peptide hormone and neuropeptide precursors, seven granin-like proteins, and three processing enzymes (PC1/3, PC2, and peptidyl-glycine alpha-amidating monooxygenase). In total, 373 peptides were informative enough to predict processing sites in that they have signal sequence cleavage sites, PC consensus sites or monobasic cleavage sites. Several monobasic cleavage sites identified here were previously proved to be generated by PCs. Thus, our approach helps to predict processing sites of RSP precursor proteins and will expedite the identification of unknown bioactive peptides hidden in precursor sequences.

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PHOENIX PHARMACEUTICALS, INC. 330 BEACH ROAD, BURLINGAME CA, 94010, USA PHONE: (650) 558-8898 EMAIL: info@phoenixpeptide.com WWW.PHOENIXPEPTIDE.COM PHOENIX EUROPE GMBH VIKTORIASTRASSE 3-5, D-76133 KARLSRUHE, GERMANY PHONE: +49-721-1611950 EMAIL: germany@phoenixpeptide.com WWW.PHOENIXPEPTIDE.COM

	Validation												manual										manual				standard						
	Precursor	Salli	5	VGF	c	CI	VGF	t o	VGF	TMSB4X	P02	TMSB10	CGRP	SgIII	VGF	VGF		GRP	CGRP	SST	CT/CGRP	CGRP	PC2	Sgl		Soll Inco	9	VGF	VGF	CT	C1	ll B	CGRP
(maiRo	C-term	RKAGCKNFFW RELSAERPLN	C-term	RSPOPPPAP	C-term	AN	RNSEPQDEGE	z	RGARNSEPOD	C-term	RKKRGYRDIN	C-term	GRRDLOA	KKTYPPENKP	RASWGEFQAR	RASWGEFQAR	KKTYPPENKP	RGNHWAVGHL	NFVPTNVGSK	C-term	LAALVQDYVQ	RSGGWKNNF	KAKRRRSLHH	6)KRFPVGPPKN	GRARDMSSUL	KRIVSSI	Cterm	C-term	GRROAEATRO	GKKRDMSSDL	KKRDMSSDLE		KRCGNLSTCM KRACDTATCV
ומכוווול מו מוס ווומלמו למלוומכת ומוכמסכת מו באסמלוממות להמתה הווימומוונית המלוות בד - ממוו מוס ו מי ד המתה להמוי מוויוומנים אותו	Sequence	SANSNPAMAPRE FPKPGGSQDKSLHN h Sq III . Dredro (20-33)	DMSSDLERDHRPHVSMPONAN h Katacalcin, Met (0)16	NAPPEPVPPPRAAPATHV h VGF, prepro (485-503)	DMSSDLERDHRPHVSMPQNAN h Katacalcin	DMSSDLERDHRPHVSMPQN h Katacalcin (1-19)	APPGRPEAQPPPLSSEHKEPVAGDAVPGPKDGSAPEVRGA h VGF, Prepro(23-62) RNSEPQDEGE	DMSSDLERDHRPHVSMPQNA h Katacalcin (1-20)	APPGRPEAQPPPLSSEHKEPVAGDAVPGPKDGSAPEV h VGF, prepro (23-59)		VKMALQQEGFD h PC2, prepro (95-105)	Ac-ADKPDMGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSEIS	NFVPTNVGSKAF-NH2 h CGRP I / II (26-37)-NH2	FPKP GGSQDKSLHNRELSAERPLNEQIAEAEEDKI h Sg III, prepro (20-54)				VPLPAGGGTVLTKMYP			APFRSALESSPADPATLSEDEARLL h CT / CGRP I / II, Pro (1-25)	ACDTATCVTHRLAGLLS h CGRP I/ II (1-17) h PC2, prepro (26-75)	ERPVFTNHFL VELHKGGEDKARQVAAEHGFGVRKLPFAEGLYHFYHNGLA	VPGQGSSEDDLGEEEQIEQAIKEHLNQGSSQETDKLAPVSh Sgli, prepro (527-566)KRFPVGPPKN	CONLETCOTUBI A QUENTRET FROM A GOVERPENTZ IL CARCIONIN ACOTATO/ATUBI AGUI SPECIOA A MANINELISTIN VOERA E NUMERA FOOD I	GUKEDVDI SKMRDFINKOADAVVEKALI DKEFAFAL N SA III DEPUD (436-461)	intect ubjourtin		RPESALLGGSEAGERLLQQGLAQVEA-NH2 h VGF, prepro (281-306)		CGNLSTCMLGTYTQDFNKFHTFPQTAIGVGAPG h Sg III prepro (426-468)	GNKEDYDLSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL	APFRSALESS PAD PATUSEDE ARULLAALVOD YVOMKAS ELEGE GEREGSSUDSPRS APFRSALESS PAD PATUSEDE ARULLAALVOD YVOMKAS ELEGE GEREGSRIIAO
	Expect. N-term value	3.30E-05 QDEMRLELQR 0.025 Signal	0.0009 IGVGAPGKKR	0.0000033 EVEEKRKKK	0.00031 IGVGAPGKKR	0.03 IGVGAPGKKR	5.40E-09 Signal	0.00033 IGVGAPGKKR	0.00024 Signal	5.10E-07 M	0.00022 HKQQLERDPR	3.80E-10 M	0.86 LSRSGGVVKN	0.0055 Signal	5.70E-09 RDFSPSSAKR	1.70E-06 RDFSPSSAKR	8.50E-07 GSQDKSLHNR	0.011 Signal	(2.50E-07) EGSRIJAQKR	(4.90E-05) NPAMAPRERK	8.60E-08 Signal	(1.20E-07) EGSRIJAQKR	0.19 Signal	1.50E-08 EIINSNQVKR	(0.00048) SSLUSPRSKK	1 40E-06 IEWI KKHDKK	2.2 E+02	2.40E-08 YPGREAQARR	0.00031 GVAAPFPKAR	(1.30E-05) SSLDSPRSKR	(0.0003) SSLDSPRSKR	1.10E-14 WLKKHDKK	2.50E-11 Signal 1.60E-12 Signal
	Score	74 48	8	8	8	\$	119	8	12	100	89	131	38	8	118	83	95	8	(88)	(02)	106	(88)	4	112	(10)	05	-	112	8	(78)	64	11	143
	Base peak intensity	4.33E+06 4.74E+06	2.78E+06	1.17E+07	1.29E+07	4.65E+06	1.96E+07	7.48E+06	9.82E+06	1.58E+07	2.66E+06	5.12E+06	7.21E+06	2.37E+06	4.07E+06	4.51E+06	2.56E+06	3.70E+06	2.39E+06	4.71E+06	2.47E+06	3.57E+06	2.13E+06	3.73E+06	2.28E+05	2.61F+06	3.09E+07	2.51E+07	4.27E+06	2.68E+07	9.68E+06	7.83E+06	3.95E+07 3.91E+07
ndo.	Mass error (ppm)	0.27	0.40	0.76	1.26	0.87	0.31	0.67	1.45	1.23	0.03	1.22	0.74	0.84	1.06	0.73	0.95	0.46	(-1.20)	(-0.79)	-0.55	(-1.10)	0.89	-1.15	(90.1-)	1020	0.94	0.13	(-0.82)	(-1.57)	(-1.68)	0.0	1.41
	Mr(Calc)	1243.5615 1510.7528	2451.0655	1914.0112	2435.0706	2249.9906	3950.9875	2321.0277	3666.8278	4960.4862	1264.6122	4933.5229	1278.6721	3931.9663	3406.6865	3389.6600	2283.1230	1599.8695	(2642.3381)	(1752.7753)	2642.3187	(1844.8873)	5687.9079	4349.0419	(3000 0006)	(Dece: 2000)	8559.6167	3705.8346	2677.4147	(3531.6374)	(3589.6429)	4992.5178	6056.0436
	N	0 0	4	3	4	3	9	3	5	9	2	0	2	5	5	4	3	2	4	2	3	en 10	80	4	n 4	0 W	12		3	e	en 1	60 0	00
2	(bedo)	622.7882 504.5915	613.7738	639.0115	609.7757	751.0048	659.5054	774.6837	734.3736	827.7560	633.3134	823.2621	640.3438	787.4012	682.3453	848.4229	762.0490	800.9424	632.5773	819.3663	881.7797	577.2836	711.9964	1088.2665	760 2000	R30.0130	714.3080	742.1743	883.4781	1139.5341	1158.8690	833.0936	1037.1808
	RT (min)	8.85 9.72	12.55	13.51	13.59	13.68	13.79	14.01	14.42	14.94	14.94	15.46	15.70	16.14	16.30	17.37	17.60	18.64	19.65	19.79	19.91	20.25	20.33	20.37		21 16	21.50	21.52	21.55	21.90	21.93	22.25	23.69

Identity of the major peptides released on exocytosis (base peak intensities beyond 2E+06 in the Fig. 2 base peak chromatogram)

Amino acid sequence of human Secretogranin II

MAEAKTHWLG AALSLIPLIF LISGAEAASF QRNQLLQKEP DLRLENVQKF PSPEMIRALE YIENLRQQAH KEESSPDYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ AENEPQSAPK ENKPYALNSE KNFPMDMSDD YETQQWPERK LKHMQFPPMY EENSRDNPFK RTNEIVEEQY TPQSLATLES VFQELGKLTG PNNQKRERMD EEQKLYTDDE DDIYKANNIA YEDVVGGEDW NPVEEKIESQ TQEEVRDSKE NIEKNEQIND EMKRSGQLGI QEEDLRKESK DQLSDDVSKV IAYLKRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRNLQI PPEDLIEMLK TGEKPNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYPKTPG RAGTEALPDG LSVEDILNLL GMESAANQKT SYFPNPYNQE KVLPRLPYGA GRSRSNQLPK AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVPGQ GSSEDDLQEE Human Secretogrann II, Prepro (527-56).

KAEKGREHIA KRAMENM

April 06, 2009, Phoenix Pharmaceuticals

Amino acid sequence of human Secretogranin III

	human Cara	· /20		retogranin III, prepro (35-54)				
	numan Secre	togranin III, prepro (20	-33)						
	-	hu	man Secretogranin III	prepro (20-54)	-				
MGFLGTGTWI	lvlvlpiqa <mark>f</mark>	PKPGGSQDKS	LHNRELSAER	PLNEQIAEAE	EDKI KKTYPP				
ENKPGQSNYS	FVDNLNLLKA	ITEKEKIEKE	RQSIRSSPLD	NKLNVEDVDS	TKNRKLIDDY				
DSTKSGLDHK	FQDDPDGLHQ	LDGTPLTAED	IVHKIAARIY	EENDRAVFDK	IVSKLLNLGL				
ITESQAHTLE	DEVAEVLQKL	ISKEANNYEE	DPNKPTSWTE	NQAGKIPEKV	TPMAAIQDGL				
AKGENDETVS	NTLTLTNGLE	RRTKTYSEDN	FEELQYFPNF	YALLKSIDSE	KEAKEKETLI				
TIMKTLIDFV	KMMVKYGTIS	PEEGVSYLEN	LDEMIALQTK	NKLEKNATDN	ISKLFPAPSE				
KSHEETDSTK	EEAAKMEKEY	GSLKDSTKDD	NSNPGGKTDE	PKGKTEAYLE	AIRKNIEWLK				
KHDKK<mark>GNKED</mark>	YDLSKMRDFI	NKQADAYVEK	GILDKEEAEA	IKRIYSSL					
human Secretogranin III, prepro (426-468)									

human Secretogranin III, prepro (426-451)

April 06, 2009, Phoenix Pharmaceuticals

MGFQKFSPFL ALSILVLLQA GSLHAAPFRS ALESSPADPA TLSEDEARLL LAALVQDYVQ DMSSDLERDH RPHVSMPQNA N h Katacalcin h Katacalcin (1-20) h Katacalcin (1-19) April 06, 2009, Phoenix Pharmaceuticals Amino acid sequence of human Prepro-Calcitonin-related Peptide I (CGRP I) h CT / CGRP I / CGRP II, Pro (1-25) human CGRP I, prepro (26-80) -MGFQKFSPFL ALSILVLLQA GSLHA<mark>APFRS ALESSPADPA TLSEDEARLL</mark> LAALVQDYVQ MKASELEQEQ EREGSRIIAQ KR<mark>ACDTATCV THRLAGLLSR SGGVVKN</mark>NFV PTNVGSKAFG --RRRRDLQA huma CGRP I (1-25) human CGRP I (1-17) h CGRP I

April 06, 2009, Phoenix Pharmaceuticals

Amino acid sequence of human Prepro-Calcitonin-related Peptide II (CGRPII)

h CT/CGRP I / CGRPII, Pro (1-25)

human 200 - 200 - 100 - 201

MGFRKFSPFL ALSILVLYQA GSLQAAPFRS ALESSPDPAT LSKEDARLLL AALVQDYVQM KASELKQEQE TQGSSSAAQK RACNTATCVT HRLAGLLSRS GGMVKSNFVP TNVGSKAFGR RRRDLQA h CGRP I/ CGRP II (26-37)

h CGRP II

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Amino acid Sequence of Human PC2

		-	human PC	2, Prepro (26-7	5)
MKGGCVSQWK	AAAGFLFCVM	VFASA <mark>ERPVF</mark>	TNHFLVELHK	GGEDKARQVA	AEHGFGVRKL
PFAEGLYHFY	HNGLAKAKRR	RSLHHKQQLE	RDPR <mark>VKMALQ</mark>	QEGFD RKKRG	YRDINEIDIN
MNDPLFTKQW	YLINTGQADG	TPGLDLNVAE	human PC2, pre AWELGYTGKG		DYLHPDLASN
YNAEASYDFS	SNDPYPYPRY	TDDWFNSHGT	RCAGEVSAAA	NNNICGVGVA	YNSKVAGIRM
LDQPFMTDII	EASSISHMPQ	LIDIYSASWG	PTDNGKTVDG	PRELTLQAMA	DGVNKGRGGK
GSIYVWASGD	GGSYDDCNCD	GYASSMWTIS	INSAINDGRT	ALYDESCSST	LASTFSNGRK
RNPEAGVATT	DLYGNCTLRH	SGTSAAAPEA	AGVFALALEA	NLGLTWRDMQ	HLTVLTSKRN
QLHDEVHQWR	RNGVGLEFNH	LFGYGVLDAG	AMVKMAKDWK	TVPERFHCVG	GSVQDPEKIP
STGKLVLTLT	TDACEGKENF	VRYLEHVQAV	ITVNATRRGD	LNINMTSPMG	TKSILLSRRP
RDDDSKVGFD	KWPFMTTHTW	GEDARGTWTL	ELGFVGSAPQ	KGVLKEWTLM	LHGTQSAPYI
DQVVRDYQSK	LAMSKKEELE	EELDEAVERS	LKSILNKN		

Amino acid sequence of human prepro-Calcitonin

MKASELEQEQ EREGSSLDSP RSKRCGNLST CMLGTYTQDF NKFHTFPQTA IGVGAPGKKR

RELATED PRODUCTS

Catalog No.	Product Name	Standard Size
007-75	PC2, prepro (26-75) (Human)	100 ug
014-03	Calcitonin (Human)	500 µg
014-07	Calcitonin, Gly, (Human)	100 ug
014-08	Calcitonin, Met (O)8, (Human)	100 ug
014-41	Calcitonin/CGRP I/ II, Pro (1-25) (Human)	100 ug
015-28	CGRP (1-17) (Human)	200 ug
015-29	CGRP (1-25) (Human)	100 µg
015-02	CGRP (Human)	200 µg
015-30	CGRP I/II (26-37) (Human)	200 ug
015-07	CGRP II (Human)	200 µg
015-31	CGRP, Pro (1-54) (Human)	100 ug
014-32	Katacalcin (1-19) (Human)	200 ug
014-33	Katacalcin (1-20) (Human)	200 ug
014-12	Katacalcin / C-Procalcitonin / PDN-21	500 μg
014-13	Katacalcin, Met (O)16, (Human)	200 ug
007-76	PC2, prepro (95-105) (Human)	200 ug
004-99	Secretogranin II, prepro (527-566) (Human)	100 ug
004-84	Secretogranin III, prepro (20-33) (Human)	200 ug
004-85	Secretogranin III, Prepro (20-54) (Human)	100 ug
004-86	Secretogranin III, prepro (35-54) (Human)	100 ug
004-98	Secretogranin III, prepro (426-461) (Human)	100 ug
004-87	Secretogranin III, prepro (426-468) (Human)	100 ug
007-67	VGF, prepro (177-206) (Human, Rat)	100 ug
007-66	VGF, prepro (23-59) (Human, Rat)	100 ug
007-65	VGF, prepro (23-62) (Human, Rat)	100 ug
007-69	VGF, prepro (281-306) (Human, Rat)	100 ug
007-71	VGF, prepro (485-503) (Human, Rat)	100 ug
007-70	VGF, prepro (586-615) (Human, Rat)	100 ug

		Blast sequenc	es of rat and h	uman VGF	
Rat Human	1 1	MKALRLSASA	LFCFLLLIRG LFC-LLLING F, Prepro (23-62) —	LGAAPPGRSD LGAAPPGRPE	30 29
Rat Human	31 30	VYPPPLGSEH AQPPPLSSEH	NGQVAEDAVS KEPVAGDAVP repro (23-59)	RPKDDSVPEV GPKDGSAPEV	<mark>60</mark> 59
Rat	<mark>61</mark>	RAARNSEPQD	QGELFQGVDP	RALAAVLLQA	<mark>90</mark>
Human	60		EGELFQGVDP	RALAAVLLQA	89
Rat	<mark>91</mark>	LDRPASPPAV	PAGSQQGTPE		120
Human	90	LDRPASPPA-	PSGSQQGPEE		118
Rat	121	VRSQTHSLPA	SEIQASAVAP	PRPQTQDNDP	150
Human	119	VRSQTHSLPA	PESPEPA-AP	PRPQTPENGP	147
Rat Human	151 148	EADDRSEELE EASDPSEELE h VGF, prepr	ALASLLQELR	DFSPSNAKRQ DFSPSSAKRQ	180 177
Rat	181	Q <mark>etaaaetet</mark>	RTHTLTRVNL	ESPGPERVWR	210
Human	178	Qetaaaetet	RTHTLTRVNL	ESPGPERVWR	207
Rat	<mark>211</mark>	ASWGEFQARV	PERAPLPPSV	PSQFQARMSE	240
Human	208	ASWGEFQARV	PERAPLPPPA	PSQFQARMPD	237
Rat Human	241 238	NVPLPETHQF SGPLPETHKF	GEGVSSPKTH GEGVSSPKTH	LGETLTPLSK LGEALAPLSK - NERP-1	270 267
Rat Human	271 268	AYQSLSAPFP AYQGVAAPFP	KVRRLEGSFL KARRPESALL	GGSEAGERLL GGSEAGERLL NERP-2	300 297
Rat	301	QQGLAQVEAG		AAQEERLADL	330
Human	298	QQGLAQVEAG		AAQEERLADL	327
Rat	331	ASDLLLQYLL	QAGARQRDLG	GRGLQETQQE	360
Human	328	ASDLLLQYLL	QGGARQRGLG	GRGLQEAAEE	357
Rat	361	RENEREEEAE	QERRGGGEDE	VGEEDEEAAE	390
Human	358	RESAREEEEA	EQERRGGEER	VGEEDEEAAE	387
Rat	391		ARQNALLFAE	EEDGEAGAED	420
Human	388		ARQNALLFAE	EEDGEAGAED	417
Rat	421	KRSQEEAPGH	RRKDAEGTEE	GGEEDDDDEE	450
Human	418	KRSQEETPGH	RRKEAEGTEE	GGEE-EDDEE	446
Rat Human	451 447	MDPQTIDSLI MDPQTIDSLI		DDVVSIIEEV DDVVSIIEEV (485-503)	480 476
Rat	481	<mark>EEKRKRKKNA</mark>	PPEPVPPPRA	APAPTHVRSP	510
Human	477	EEKRKRKK <mark>NA</mark>	PPEPVPPPRA	APAPTHVRSP	506
Rat Human	511 507	QPPPPAPA QPPPPAPAPA	RDELPDWNEV RDELPDWNEV	LPPWDREEDE LPPWDREEDE - TLQP-21	538 536
Rat	539	VFPPGPYHPF	PNYIRPRTLQ	PPASSRRRHF	568
Human	537	VYPPGPYHPF	PNYIRPRTLQ	PPSALRRRHY	566
Rat	569	HHALPPARHH	<mark>PDLEAQARRA</mark>	QEEADAEERR	598
Human	567	HHALPPSRHY	PGREAQARR <mark>A</mark>	QEEAEAEERR	596
Rat	<mark>599</mark>	LQEQEELENY	IEHVLLHRP	617	
Human	597	LQEQEELENY	IEHVLLRRP	615	

h VGF, prepro (586-615) ----->

Rat TLQP-21 peptide was identified by Bartolomucci A., et al. PNAS, 2006, 103, 14584-14589 Nov. 03, 2006, Phoenix Pharmaceuticals, Inc. July. 09, 2007, Phoenix Pharmaceuticals, Inc.