

**Appendix A: Details of companies and distributors****Table A.1:** Companies and distributors.

<b>Company</b>	<b>City</b>	<b>Country</b>
Amersham Pharmacia Biotech	Freiburg	Germany
Applied Biosystems	Foster City, CA	USA
BD Biosciences Discovery Labware	Franklin Lakes, NJ	USA
Becton-Dickinson <b>GmbH</b>	Heidelberg	Germany
Biochrom AG	Berlin	Germany
Biogenesis Ltd.	Poole	UK
Bio-Rad Laboratories	Munich	Germany
Calbiochem	San Diego	USA
Carl Roth GmbH	Karlsruhe	Germany
Carl Zeiss Mikroskopie	Göttingen	Germany
Clontech Laboratories	Palo Alto, CA	USA
E. Merck AG	Karlsruhe	Germany
Eppendorf	Hamburg	Germany
Falcon	Heidelberg	Germany
Glaswarenfabrik Karl Hecht KG	Sondheim	Germany
GFL Gesellschaft für Labortechnik mbH	Burgwedel	Germany
GIBCO Invitrogen Corporation	Karlsruhe	Germany
Gramsch Laboratories	Schwabhausen	Germany
Hoefer Inc.	San Francisco, CA	USA
Invitrogen GmbH	Karlsruhe	Germany
Kendro	Osterode	Germany
Linaris	Wertheim-Bettingen	Germany
MICROM International GmbH	Walldorf	Germany
Millipore GmbH	Eschborn	Germany
Miltenyi Biotec	Bergisch Gladbach	Germany
Nunc GmbH	Wiesbaden	Germany
OCT Miles Inc.	Elkhart	IN
Peninsula Laboratories Inc.	Belmont, CA	USA
Pharmacia Biotech	Hørsholm	Denmark
Pharmingen	Heidelberg	Germany
ProGen Biotechnik GmbH	Heidelberg	Germany
QIAGEN	Hilden	Germany
R & D Systems GmbH	Wiesbaden	Germany
Rhodia Organic Fine Limited	Bristol	UK
Roche Diagnostics Corporation	Mannheim	Germany
Santa Cruz Biotechnology	Heidelberg	Germany
Serotec	Oxford	UK
Shimadzu Europa GmbH	Duisburg	Germany
Sigma-Aldrich	Taufkirchen	Germany

Table A.1 continued

<b>Company</b>	<b>City</b>	<b>Country</b>
TIBMOLBIOL	Berlin	Germany
Vector Laboratories Inc.	Burlingame, CA	USA
Wallac Distribution GmbH	Freiburg	Germany

## Appendix B: Sequence alignments of RT-PCR products

		→SIG	
PanT <sup>+</sup> LN cells:	138	atgccgagattctgctacagtcgctcaggggccctgctgctggccctcctgcttcagacc	197
NM_139326:	122	atgccgagattctgctacagtcgctcaggggccctgctgctggccctcctgcttcagacc	181
		SIG ←	
PanT <sup>+</sup> LN cells:	198	tccatagacgtgtggagctggtgcctggagaagcagccagtgccaggacctcaccacgga	257
NM_139326:	182	tccatagacgtgtggagctggtgcctggag-agcagccagtgccaggacctcaccacgga	240
		Exon 2 ↔ Exon 3	
PanT <sup>+</sup> LN cells:	258	aagcaacctgctggcttgcattccgggctgcagactcgacctctcggcggagacgcccgt	317
NM_139326:	241	aagcaacctgctggcttgcattccgggctgcagactcgacctctcggcggagacgcccgt	300
PanT <sup>+</sup> LN cells:	318	gtttccaggcaacggagatgaacagcccttgactgaaaatccccggaagtacgtcatggg	377
NM_139326:	301	gtttccaggcaacggagatgaacagcccttgactgaaaatccccggaagtacgtcatggg	360
PanT <sup>+</sup> LN cells:	378	tcacttccgctgggaccgcttcggccccagaaaacagcancagtgctggnggctcagcgca	437
NM_139326:	361	tcacttccgctgggaccgcttcggccccagaaaacagcagcagtgctggcggctcagcgca	420
PanT <sup>+</sup> LN cells:	438	naggcgtgctggaggaagagacggcggggggagatggccgtccggagccaagtccacggga	497
NM_139326:	421	gaggcgtgctggaggaagagacggcggggggagatggccgtccggagccaagtccacggga	480
		→ACTH	
PanT <sup>+</sup> LN cells:	498	gggcaagcgctcctactccatggagcacttccgctggggcaagccggt-ggcaagaagc-	555
NM_139326:	481	gggcaagcgctcctactccatggagcacttccgctggggcaagccggtgggcaagaagcg	540
PanT <sup>+</sup> LN cells:	556	gcgccctgtgaaggtgtaccccaatgtccccgaaaacgagtcggccgaggccttttcct	615
NM_139326:	541	gcgccctgtgaaggtgtaccccaatgtcgccgagaacgagtcggccgaggcc-tttccc	599
		ACTH ←	
PanT <sup>+</sup> LN cells:	616	tagagttcaagag	628
NM_139326:	600	tagagttcaagag	612

Fig. A.1 Sequence alignment of lymphocyte-derived POMC Ex2-3G transcripts with *Rattus norvegicus* data base POMC. 1.5 µg DNA of cloned RT-PCR products were sequenced. Sequence data string obtained from PanT<sup>+</sup> LN cells (POMC Ex2-3G) was aligned with data bank rat POMC mRNA (Accession # NM\_139326). Sequence identity was 97% (483of 493 bases, Gaps = 4 of 493). Strands compared were Plus / Plus.

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→ SIG ←
PanT- LN cells: 38 cgtgtggagctggtgcctggagagcagccagtgccaggacctcaccacggaaagcaacct 97
|||||
NM_139326: 69 cgtgtggagctggtgcctggagagcagccagtgccaggacctcaccacggaaagcaacct 128
Exon 2 ↔ Exon 3
PanT- LN cells: 98 gctggcttgcacccgggctgcagactcgacctctcggcggagacgcccgtgtttccagg 157
|||||
NM_139326: 129 gctggcttgcacccgggctgcagactcgacctctcggcggagacgcccgtgtttccagg 188

PanT- LN cells:158 caacggagatgaacagcccttgactgaaaatccccggaagtacgtcatgggtcacttccg 217
|||||
NM_139326: 189 caacggagatgaacagcccttgactgaaaatccccggaagtacgtcatgggtcacttccg 248

PanT- LN cells:218 ctgggaccgcttcggcccagaaaacagcagcagtgctggcggctcagcgcagaggcgtgc 277
|||||
NM_139326: 249 ctgggaccgcttcggcccagaaaacagcagcagtgctggcggctcagcgcagaggcgtgc 308

PanT- LN cells:278 ggaggaagagacngcggggggagaattgnccttccgganccaagtccacgggagggcaag 337
|||||
NM_139326: 309 ggaggaagagacngcggggggaga-tggcctccggagccaagtccacgggagggcaag 366
→ ACTH
PanT- LN cells:338 cgctcctactccatggagcacttccgctggggcaagccggtgggcaagaagcggcgcct 397
|||||
NM_139326: 367 cgctcctactccatggagcacttccgctggggcaagccggtgggcaagaagcggcgcct 426
ACTH ←
PanT- LN cells:398 gtgaaggtgtacccaatgtcgccgagaacgagtcggccgaggcctttccctagagttc 457
|||||
NM_139326: 427 gtgaaggtgtacccaatgtcgccgagaacgagtcggccgaggcctttccctagagttc 486

PanT- LN cells:458 aagagggagctggaaggcgagcancctgatggcttggagcacgtcctggagccggatacc 517
|||||
NM_139326: 487 aagagggagctggaaggcgagcagcctgatggcttggagcacgtcctggagccggatacc 546

PanT- LN cells:518 ganaaggccgacgggcctatcgggtggagcacttcc-ctggggcaaccgcccaggac 576
|| |
NM_139326: 547 gagaaggccgacgggcctatcgggtggagcacttccgctggggcaaccgcccaggac 606
→ END
PanT- LN cells:577 aagcgctacgggtggcttcatgacctccgagaagagccagac-cccctggtgac-ctcttc 634
|||||
NM_139326: 605 aagcgctacggcggcttcatgacctccgagaagagccagacgcccctggtgacgctcttc 666
END ←
PanT- LN cells:635 aagaac-ccatcatcaanaacgc-cacaa-aanggccagtgag 674
|||||
NM_139326: 667 aagaacgcatcatcaagaacgcgcacaagaaggccagtgag 709

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Fig. A.2 Sequence alignment of lymphocyte-derived POMC Ex2-3E transcripts with *Rattus norvegicus* data base POMC. DNA (1.5 µg) of cloned RT-PCR products were sequenced. Sequence data string obtained from PanT<sup>-</sup> LN cells (POMC Ex2-3E) was aligned with data bank rat POMC mRNA (Accession # NM\_139326). Sequence identity was 97% (626 of 643 bases, Gaps = 8 of 643). Strands compared were Plus / Plus.

## Appendix C: Sequence alignments of nested RACE-PCR products

	→ Exon 1	
PanT+	AAAACGNGAGGNGACGGAGGAGAAAAGAGGTTAAGGAGCAGTGANTAAGAGAGGCCACTG	60
PT	AAAACGGGAGGCGACGGAGGAGAAAAGAGGTTAAGGAGCAGTGACTAAGAGAGGCCACTG	60
	Exon 1 ←→ Exon 2 → SIG	
PanT+	AACATCTTCGTCTCAGAGAGCTGCCTTTCCGCGACAGAGCCTCAGCCACCTGGAAGATG	120
PT	AACATCTTCGTCTCAGAGAGCTGCCTTTCCGCGACAGAGCCTCAGCCACCTGGAAGATG	120
	SIG ←	
PanT+	ATAGACGTGTGGAGCTGGTGCCTGGAGAGCAGCCAGTGCCAGGACCTCACCCACGGAAAG	240
PT	ATAGACGTGTGGAGCTGGTGCCTGGAGAGCAGCCAGTGCCAGGACCTCACC-ACGGAAAG	240
	190      200      210      220      230      240	
	Exon 2 ←→ Exon 3	
PanT+	CAACCTGCTGGCTTGCATTCCGGGCCTGCAGAC-TCGACCCTNTCGGCGGAGACGCC	297
PT	CAACCTGCTGGCTTGCATTCCGGGCCTGCAGACNTCGACC-TNTCGGCGGAGACGCC	297

Fig. A.3 Sequence alignment of N-RACE-PCR products from CD3<sup>+</sup> LN cells and pituitary. 5'-N-RACE 3 products from CD3<sup>+</sup> LN cells and pituitary were sequenced. Data strings of 297 and 296 bp, respectively, were aligned using GeneStream Align. Sequences showed 98% identity.

PanT2+	AGCAAGTAGATTGGGATGCAATAGCAGCTTGGTGCAGGATGTTGGCAGGACCTCGGGGGT	60
PanT3-	-----	
PanT2+	CCACATTGCTGGGCCTGATGGCCTCGAGGCATAAACTGGCACCCTAGAGGGCAGGGATG	120
PanT3-	-----CAGGGATG	8
	Intron B ←→ Exon 3	
PanT2+	GTGGCCACAGGAGCTGGCTTGGCTCACACATTGGGCCTCCCTACAGGCTTGCATCCGGGC	180
PanT3-	GTGGCCACAGGAGCTGGCTTGGCTCACACATTGGGCCTCCCTACAGGCTTGCATCCGGGC	68
PanT2+	CTGCAGACTCGACCTCTCGGCGGAGACGCCCGTGTTCAGGCAACGGAGATGAACAGCC	240
PanT3-	CTGCAGACTCGACCTCTCGGCGGAGACGCCCGTGTTCAGGCAACGGAGATGAACAGCC	128
PanT2+	CTTGACTGAAAATCCCCG	258
PanT3-	CTTGACTGAAAATCCCCG	146

Fig. A.4 Sequence alignment of two truncated POMC fragments from LN cells. 5'-N-RACE 3 products from separated LN cells (CD3<sup>+</sup>, lane 2 and CD3<sup>-</sup>, lane 5; Fig. 4.19 B) were sequenced. Alignment of the two sequence data strings of 258 and 146 bp, respectively, shows heterogeneous parts of intron B (underlined in grey).