

DEPARTMENT OF PATHOLOGY  
UNIVERSITY OF HELSINKI  
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# **NEUROENDOCRINE TUMORS: THE QUALITY OF PROGNOSTIC AND PREDICTIVE MARKERS**

**Satu Maria Remes**

ACADEMIC DISSERTATION

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with the permission of the Faculty of Medicine of the University of Helsinki,  
in Auditorium 2 at the Haartman Institute, Haartmaninkatu 3, Helsinki,  
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# LIST OF ORIGINAL PUBLICATIONS

This thesis is based on the following publications.

- I Pulkkinen V, Ezer S, Sundman L, Hagström J, Remes S, Söderhäll C, Greco D, Haglund C, Kere J, and Arola J: Neuropeptide S receptor 1 (NPSR1) activates cancer-related pathways and is widely expressed in neuroendocrine tumors. *Virchows Arch.* (2014) 465:173–183. Erratum in: *Virchows Arch.* (2014) 465:251.
- II Remes SM, Leijon H, Vesterinen T, Louhimo J, Pulkkinen V, Ezer S, Kere J, Haglund C\*, and Arola J\*: PCSK2 expression in neuroendocrine tumors points to a midgut, pulmonary or pheochromocytomas-paraganglioma origin. *APMIS.* (2020) Aug 14. doi: 10.1111/apm.13071. Online ahead of print.
- III Remes SM, Leijon HL, Vesterinen TJ, Arola JT\*, and Haglund CH\*: Immunohistochemical Expression of Somatostatin Receptor Subtypes in a Panel of Neuroendocrine Neoplasias. *J Histochem Cytochem.* (2019) 67:735–743.
- IV Remes SM, Tuominen VJ, Helin H, Isola J, and Arola J: Grading of neuroendocrine tumors with Ki-67 requires high-quality assessment practices. *Am J Surg Pathol.* (2012) 36:1359–1363.

\* indicates an equal contribution.

The publications are referred to in the text by their roman numerals.

## ABBREVIATIONS

5-HIAA	5-hydroxyindole-5-acetic acid
ACTH	Adrenocorticotrophic hormone
AI	Artificial intelligence
AJCC	American Joint Committee on Cancer
ANN	Artificial neural network
AP	Alkaline phosphate
AR	Antigen retrieval
CDX2	Caudal-type homeobox 2
CGA	Chromogranin A
CNS	Central nervous system
CT	Computed tomography
DAB	3,3'-diaminobenzidine
DHFR	Dihydrofolate reductase
DLL3	Delta-like 3
DMEM	Dulbecco's modified Eagle's medium
DOTA	1,4,7,10-tetraazacyclodecane-1,4,7,10-tetraacetic acid
ENETS	European Neuroendocrine Tumor Society
FBS	Fetal bovine serum
FDG	Fluorodeoxyglucose
FNA	Fine-needle aspiration
GEP-NEN	Gastroenteropancreatic neuroendocrine neoplasias
GI	Gastrointestinal
GST	Glutathione S transferase
GUI	Graphical user interface
HE	Hematoxylin-eosin
HER2	Human epidermal growth factor receptor 2
HIER	Heat-induced epitope retrieval
HPF	High-power field
HRP	Horseradish peroxidase
HUSLAB	Department of Pathology, Helsinki University Hospital
IHC	Immunohistochemistry or immunohistochemical
IMP3	Insulin-like growth factor II mRNA-binding protein 3
INSM1	Insulinoma-associated protein 1
ISH	<i>In situ</i> hybridization
ISL1	Insulin gene enhancer-binding protein islet 1
LCNEC	Large-cell neuroendocrine carcinoma



MEN1	Multiple endocrine neoplasias type 1
MEN2	Multiple endocrine neoplasias type 2
MRI	Magnetic resonance imaging
NE	Neuroendocrine
NEC	Neuroendocrine carcinoma
NEN	Neuroendocrine neoplasias
NET	Neuroendocrine tumor
NGS	Next-generation sequencing
ngTMA	Next-generation tissue microarray
NPSR1	Neuropeptide S receptor 1
NPS	Neuropeptide S
NSE	Neuro-specific enolase
OS	Overall survival
PAX8	Paired-box 8
PC	Prohormone convertase
PCSK2	Proprotein convertase subtilisin/kexin type 2
PET	Positron emission tomography
PGL	Paraganglioma
PHEO	Pheochromocytoma
PI	Proliferation index
ROI	Region of interest
SCLC	Small-cell lung cancer
SEER	Surveillance, Epidemiology, and End Results registry
SSA	Somatostatin analog
SSTR	Somatostatin receptor
SYP	Synaptophysin
TMA	Tissue microarray
TNM	Tumor, node and metastasis
TTF1	Thyroid transcription factor 1
UICC	Union for International Cancer Control
VHL	von Hippel-Lindau
WHO	World Health Organization
WSI	Whole-slide imaging

## ABSTRACT

Neuroendocrine tumors (NETs) are derived from neuroendocrine (NE) cells. NETs can appear in a variety of organs because of the disseminated nature of NE cells. NETs show histomorphological similarities independent of the tumor origin, with prognoses varying between different NETs depending upon the primary tumor location and tumor grade.

The diagnosis of an NET is confirmed by the immunohistochemical (IHC) expression of common NE markers including chromogranin A (CGA) and synaptophysin (SYP). The proliferation marker Ki-67 plays a central role in tumor grading in NETs. In practice, all of these markers are determined using IHC, whereby the reliable assessment of staining is crucial. High-quality diagnostics require careful technical verification of protocols and a full understanding of the target antigen.

This thesis aims to identify new diagnostic IHC markers for NETs and to improve the interpretation of staining. Particular focus in this study lies on validating IHC for these new NE markers and verifying the ability of image analysis to reproduce quantitative scores.

The primary study cohort consisted of 91 neuroendocrine neoplasias (NENs) from 12 different primary sites including primary tumor - metastatic pairs. Additional cohorts of tumors from a specific site of origin were used for further study. A multi-NET tissue microarray (TMA) was constructed using TMA technology. The specificity of the primary antibodies was first confirmed using known positive control tissues. Proper staining protocols were used for the IHC staining of multi-NET TMAs. In addition, image analysis using the ImmunoRatio software was used to assess the proliferation labeling index for grading purposes.

All NETs except the pheochromocytomas (PHEOs) expressed neuropeptide S receptor 1 (NPSR1) and its ligand neuropeptide S (NPS). The expression of proprotein convertase subtilisin/kexin type 2 (PCSK2) was found primarily in the small intestine and appendicular NETs, PHEOs, and paragangliomas (PGLs), and half of the typical and atypical pulmonary carcinoids. NETs from other primary locations were negative. In metastases, the expressions of NPSR1 and PCSK2 were comparable to those of the primary tumor.

Different primary antibody clones for somatostatin receptors (SSTRs) varied in terms of staining results. Not all clones could localize in the correct cell components in positive control tissues. The UMB clones exhibited a good staining pattern in the cell membranes. Five SSTRs showed individual and varying profiles in NENs of different origins.

The assessment of Ki-67 using conventional human scoring showed interobserver variation resulting in different gradings. Thus, grading using image analysis proved more reproducible and, thus, more reliable than traditional human analysis.

**In conclusion,** most NENs express NPSR1 widely. Instead, only midgut NENs, PHEOs, PGLs, and some of the lung carcinoids expressed PCSK2. These antibodies can be used in the panel of NE markers and for screening metastatic NENs from an unknown primary tumor. Expression analysis of SSTRs in formalin-fixed paraffin embedded sections, detected using validated IHC methods, may guide therapeutic planning with different somatostatin analogs (SSAs). Image analysis of the proliferation index (PI) is a preferable method for the high-quality grading of NENs.

# 1 INTRODUCTION

Neuroendocrine neoplasias (NENs) represent a heterogeneous group of rare tumors arising from neuroendocrine (NE) cells (Andrew et al. 1998, Rosai 2011) distributed across the human body (Rekhtman 2008). The endocrine system comprises the endocrine organs (pituitary and parathyroid), single disseminated NE cells (gastrointestinal tract) as well as clustered NE cells (islet of Langerhans). The NE cells produce and secrete a variety of hormones that participate in normal physiological functions (de Herder 2007).

The incidence of NENs has increased markedly in recent decades (Dasari et al. 2017). Clinical symptoms can be absent or nonspecific leading to delayed diagnosis with metastatic disease. Thus, NENs are quite frequently diagnosed from small biopsies of a metastatic tumor with an unknown primary.

Immunohistochemical (IHC) markers are used to verify the NE nature of a tumor. Chromogranin A (CGA) and synaptophysin (SYP) represent the most commonly used NE-specific biomarkers in the diagnosis of NENs (Perren et al. 2017). However, knowledge of the primary tumor location is also needed for the management of disease (Oronsky et al. 2017, Milione et al. 2018). In this situation, location-specific IHC markers can be helpful. Tumor grade, which relates to the proliferation activity of the tumor, carries a major prognostic significance, while also guiding treatment options (Cavalcanti et al. 2016). Thus, the grading of NENs is based on the quantitative analysis of Ki-67-positive nuclei on IHC slides or counting the mitotic figures on hematoxylin-eosin (HE) stained slides (Klöppel et al. 2017a).

The growing incidence of NENs (Dasari et al. 2017) has driven attempts to find new potential markers that could serve as crucial diagnostic tools indicative of the treatment response as well as disease prognosis. Discovery of new reliable NE markers is needed since no single primary antibody used today is fully specific (Agaimy et al. 2013, Zimmermann et al. 2016). Markers pointing towards the primary tumor location from a tissue specimen are remarkably valuable, since the primary tumor can be small and, thus, undetectable during imaging (Oronsky et al. 2017). In addition, accurate grading of NENs affects the prognosis, requiring further quality development (Klöppel et al. 2017a, Cavalcanti et al. 2016). The treatment and management of NENs using somatostatin analogs (SSAs) has proved efficient (Qian et al. 2016). The efficacy of SSAs is based on the existence of somatostatin receptors (SSTRs) on the tumor cell membrane, further stressing the importance of the analysis of the SSTR profile in different NENs. Therefore, technical verification and validation of prognostic and predictive markers are needed for the management of NE tumor patients.

## 2 REVIEW OF THE LITERATURE

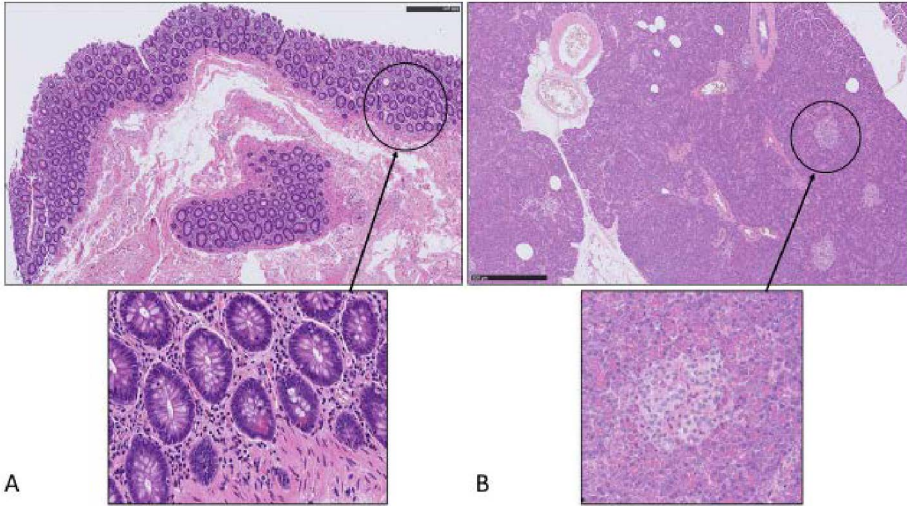
### 2.1 NORMAL ENDOCRINE SYSTEM

The endocrine system comprises a complex of neuroendocrine (NE) cells with the ability to produce hormones. Most of these hormones are peptides, which are synthesized from precursors via post-translational modification along the secretory pathway. These prohormones are transported into the rough endoplasmic reticulum, where they undergo cleavage and modification mediated by various enzymes (Montuenga et al. 2003). Then, the peptide precursors move into the Golgi apparatus, where they are further processed and eventually packed and stored as secretory granules (Montuenga et al. 2003). Hormones coordinate diverse physiological and behavioral functions such as growth, development, and biorhythms. For example, the parathyroid hormone and calcitonin regulate blood calcium levels; insulin and glucagon regulate blood sugar by lowering or raising blood glucose levels. The NE cell of the adrenal medulla releases adrenaline and noradrenaline as a response to stress. Hormonal actions follow exocytosis to the vascular system.

The word *neuroendocrine* implies that NE cells possess two different elements, components similar to neurons and classic endocrine cells (Rekhtman 2008). The small vesicles found in the cytoplasm of an NE cell (Klöppel 2007) refer to “neuro”, while the “endocrine” refers to the NE cell’s ability to secrete and release different hormones in response to stimulation (Montuenga et al. 2003, Rekhtman 2008). Despite the ultrastructural similarity of neurons and NE cells, they differ in terms of cell structure (no processes) and the signaling mode (Rekhtman 2008). Highly condensed cytoplasmic vesicles represent the characteristic feature of NE cells at the electron microscopic level (Klöppel 2007).

Disseminated, single or clustered NE cells are found in almost every anatomic site, as illustrated in Figure 1. Scattered NE cells are usually found within the epithelial linings, and are widespread and diverse in the gastrointestinal (GI) tract, which comprises the stomach, small intestine, appendix, colon, and rectum (Montuenga et al. 2003, Klöppel et al. 2007). In the respiratory system, NE cells are found in the bronchi (Montuenga et al. 2003). NE cells are also present although in lower numbers, for example, in the thymus, thyroid gland (calcitonin-producing cells), skin (Merkel cells), and urogenital and biliary tract (Montuenga et al. 2003, Klöppel 2007). The pancreas contains clusters of endocrine cells, referred to as the so-called islets of Langerhans (Klöppel 2007). Classic endocrine glands are formed by groups of endocrine cells, such as the pituitary, pineal, parathyroid, and adrenal gland, namely, the adrenal medulla (Klöppel 2007).

In addition, NE cells have different embryological origins according to their location. They are derived either from the neural crest (chromaffin cells of the adrenal medulla and extra-adrenal paraganglia, and thyroid C cells) or from an endodermal origin (the GI track and the pancreas) (Andrew et al. 1998, Rosai 2011). Table 1 summarizes the terminology associated with a NE system.



**Figure 1.** Neuroendocrine (NE) cells are widespread in the human body. Single NE cells (A) are found in the epithelium of the small intestine and aggregates of NE cells (B) appear in the pancreatic islet of Langerhans. Scale bar = 500  $\mu\text{m}$ .

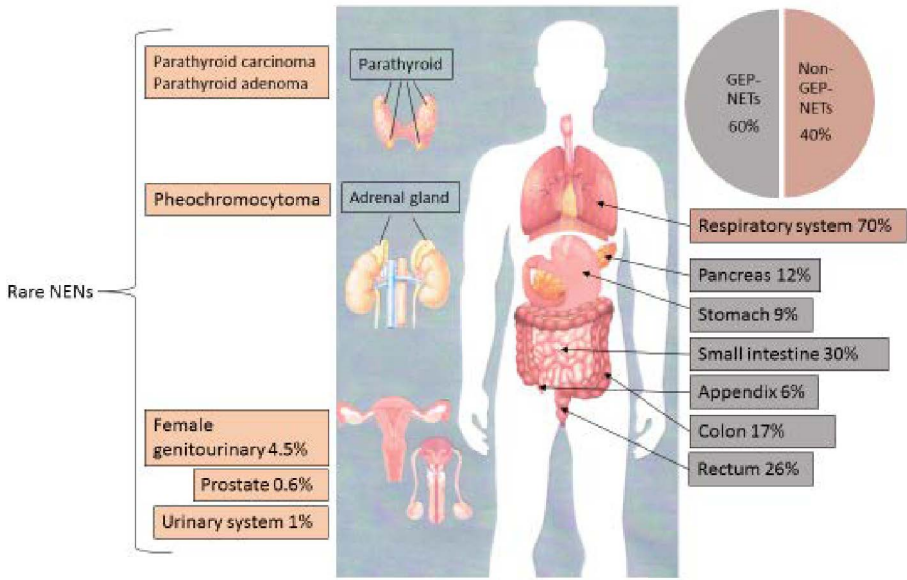
**Table 1.** Terminology associated with the neuroendocrine (NE) system. Modified from Montuenga et al. (2003).

TERMINOLOGY	DEFINITION
Clear cell, Kultschitzky, Chromaffin, Enterochromaffin	Synonyms for NE
Acidophilic, Argentaffin, Argyrophil	Descriptive name by staining
Endocrine cells	Functional term
Neuroendocrine cells	A cell having a neuroendocrine phenotype
Neuroendocrine phenotype	NE granules, secretory vesicle proteins, hormones, peptides
Endocrine secretory granules	Electron dense, small vesicles containing peptides
Diffuse neuroendocrine system	Refers to the widespread location of the neuroendocrine cells

## 2.2 NEUROENDOCRINE NEOPLASIAS

Neuroendocrine neoplasias (NENs) comprise a large, diverse group of NE tumors. NENs are characterized as well-differentiated or poorly differentiated tumors (Rindi et al. 2018). Well-differentiated NENs feature the morphological hallmarks of NE differentiation, including monotonous nuclei with finely speckled chromatin, and typically strongly express NE markers (Rekhtman 2008). Poorly differentiated carcinomas, subdivided into small- and large-cell neuroendocrine carcinomas (NECs) according to the nuclear size, are highly aggressive tumors often with barely detectable NE features (Rekhtman 2008, Klöppel et al. 2017a, Washington 2019).

The diagnostic challenge of NENs lies in the heterogeneity of these tumors. The morphological and behavioral features depend on the location of the primary NEN. In addition, NEN incidence rates vary depending upon the primary tumor location. NENs occur frequently in the GI tract (62-67%) and in the bronchopulmonary system (22-27%) (Oronsky et al. 2017). In the GI, NENs are mostly found in the small intestine (30%) (Frilling et al. 2012). In the lung, the majority of NENs are high-grade, poorly differentiated tumors, comprising small-cell lung cancer (SCLC) (79%), large-cell neuroendocrine carcinoma (LCNEC) (16%), typical carcinoids (5%), and atypical carcinoids (0.5%) (Rindi et al. 2018). Thymic NENs are rare, constituting about 2% to 5% of thymic epithelial tumors (Ströbel et al. 2015). Genitourinary, male and female genital organ NENs, and breast NENs are extremely rare (Oronsky et al. 2017, Rindi et al. 2018). Some NEN types have specific names. These include Merkel cell carcinoma of the skin, a high-grade, poorly differentiated tumor as well as medullary carcinoma of the thyroid, pheochromocytoma (PHEO) of the adrenal gland, and extra adrenal paraganglioma (PGL) (Rekhtman 2008, Delellis et al. 2017, Busam et al. 2018). PHEOs and PGLs are distinct from other NENs because they are not epithelial. Figure 2 illustrates the anatomical distribution of different NENs (Frilling et al. 2012, Oronsky et al. 2017). Table 2 lists the World Health Organization (WHO) classification of NENs with different primary origins (E. Brambilla 2015, Klöppel et al. 2017b, Busam et al. 2018, Washington 2019).



**Figure 2.** Distribution of neuroendocrine neoplasms (NENs). NENs primarily stem from a gastroenteropancreatic (GEP-NEN) origin (top-left). Non-GEP-NENs are primarily located in the respiratory system. NENs metastasize frequently in the liver. Modified from Frilling et al. (2012) and Oronsky et al. (2017).



**Table 2.** World Health Organization (WHO) classification of neuroendocrine neoplasias (NENs). Modified from E. Brambilla (2015), Klöppel et al. (2017b), Busam et al. (2018), and Washington (2019).

ORGAN	WHO CLASSIFICATION		WHO
LUNG THYMUS	Carcinoid tumors	Typical carcinoids	2015
		Atypical carcinoids	
	Large-cell carcinoma		
	Small-cell carcinoma		
STOMACH	Neuroendocrine tumor (NET)	G1 NET	2019
		G2 NET	
		G3 NET	
	Neuroendocrine carcinoma (NEC)	Large-cell NEC	
		Small-cell NEC	
	Mixed neuroendocrine–non-neuroendocrine neoplasm		
Hormone producing neuroendocrine neoplasms: histamine-producing enterochromaffin-like-cell NET (Type 1-3), somatostatin-producing D-cell NET, gastrin-producing G-cell NET, and serotonin-producing enterochromaffin NET			
PANCREAS	Well-differentiated pancreatic neuroendocrine tumors (NET)	PanNET G1	2017
		PanNET G2	
		PanNET G3	
	Poorly differentiated pancreatic neuroendocrine carcinoma (NEC)	Large-cell NEC	
		Small-cell NEC	
	Mixed neuroendocrine–non-neuroendocrine neoplasm		
Hormone producing neuroendocrine neoplasms: insulinoma, glucagonoma, somatostatinoma, gastrinoma, VIPoma, serotonin-producing tumor, and ACTH-producing tumor			
SMALL INTESTINE	Neuroendocrine tumor (NET)	NET G1	2019
		NET G2	
		NET G3	
	Neuroendocrine carcinoma (NEC)	Large-cell NEC	
		Small-cell NEC	
	Mixed neuroendocrine–non-neuroendocrine neoplasm		
Hormone producing neuroendocrine neoplasms: gastrinoma, somatostatinoma, enterochromaffin-cell carcinoid			
APPENDIX	Neuroendocrine tumor (NET)	NET G1	2019
		NET G2	
		NET G3	
	Neuroendocrine carcinoma (NEC)	Large-cell NEC	
		Small-cell NEC	
	Mixed neuroendocrine–non-neuroendocrine neoplasm		
Hormone producing neuroendocrine neoplasms: L-cell tumor, glucagon-like peptide-producing tumor, PP/PYY-producing tumor, enterochromaffin-cell carcinoid, and serotonin-producing carcinoid			
COLON AND RECTUM	Neuroendocrine tumor (NET)	NET G1	2019
		NET G2	
		NET G3	
	Neuroendocrine carcinoma (NEC)	Large-cell NEC	
		Small-cell NEC	
	Mixed neuroendocrine–non-neuroendocrine neoplasm		
Hormone producing neuroendocrine neoplasms: L-cell tumor, glucagon-like peptide-producing tumor, PP/PYY-producing tumor, enterochromaffin-cell carcinoid, and serotonin-producing tumor			
THYROID	Medullary thyroid carcinoma		2017

2 REVIEW OF THE LITERATURE

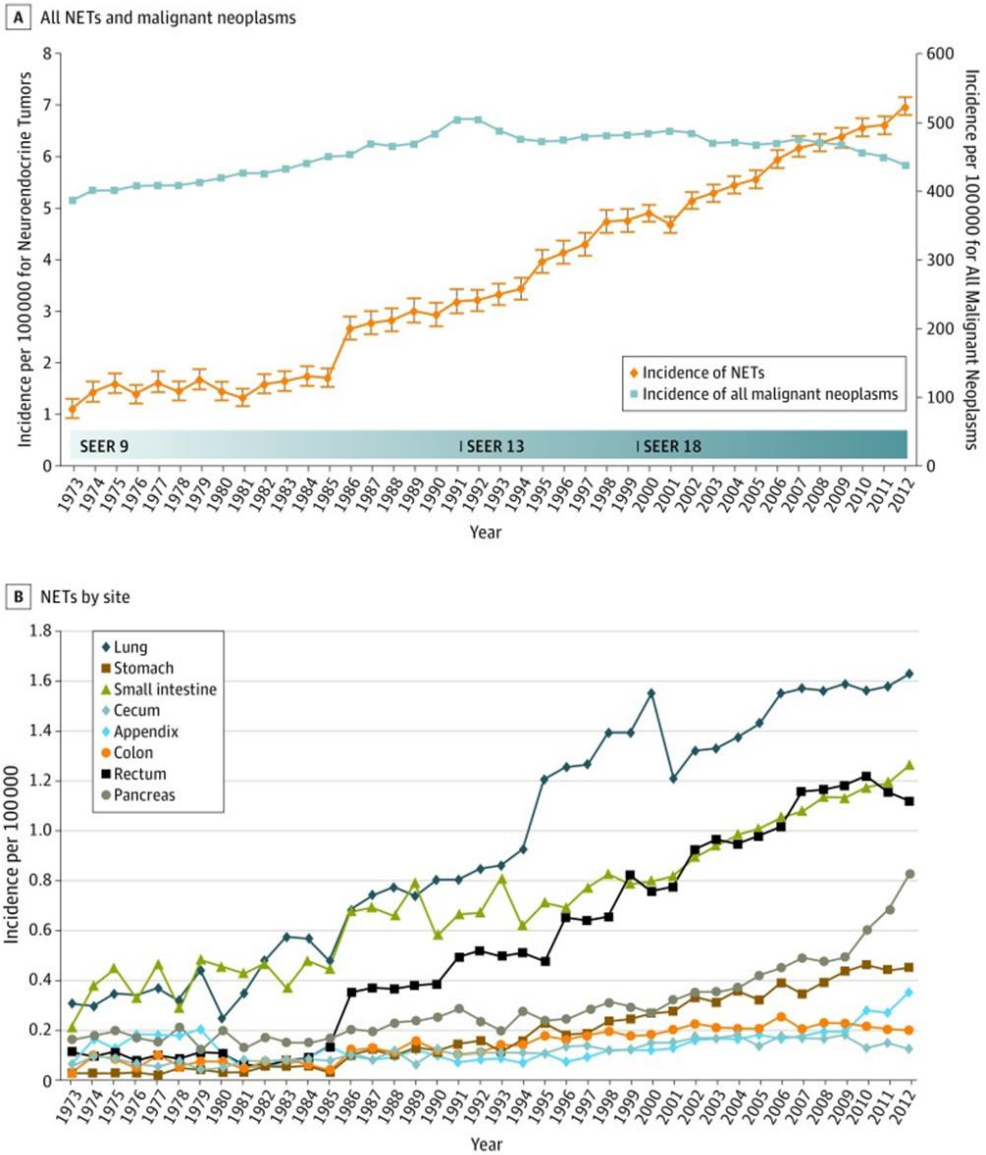
PARATHYROID	Adenoma		2017
	Carcinoma		
ADRENAL MEDULLA	Pheochromocytoma		2017
EXTRA-ADRENAL PARAGANGLIOMA	Head and neck paragangliomas	Carotid body paraganglioma	2017
		Jugulotympatic paraganglioma	
		Vagal paraganglioma	
		Laryngeal paraganglioma	
	Sympathetic paragangliomas		
SKIN	Merkel cell carcinoma		2018

## 2.2.1 INCIDENCE

The incidence of NENs represents about 0.5% of all newly diagnosed malignant neoplasms (Oronsky et al. 2017). The incidence of NENs (Figure 3) for most anatomical sites, stages, and grades is increasing. The rate of NENs increased 6.4-fold from 1973 to 2012 (1.09 to 6.98 per 100 000) in the Surveillance, Epidemiology and End-Results (SEER) 18 registry (Dasari et al. 2017). The highest incidence rates were found in the lung (1.49 per 100 000) and gastroenteropancreatic (GEP) sites (3.56 per 100 000) (Dasari et al. 2017). The incidence rate of neuroendocrine tumors (NETs) with an unknown primary site is 0.84 per 100 000 individuals (Dasari et al. 2017). There is no apparent explanation, but most likely owing to the detection of early-stage disease through more sophisticated diagnostic methods. A comparison of the incidence rates between genders follows a similar distribution (Dasari et al. 2017). Yet, little is known about the environmental, ethnic, genetic or other predisposing risk factors influencing the development of NENs (Leoncini et al. 2017).

NENs can develop sporadically or in association with hereditary syndromes. Most NENs are sporadic, including 80% of GEP–NENs, 95% of pulmonary NENs, 65% of PHEOs and PGLs, and 75% of medullary thyroid carcinomas (Crona and Skogseid 2016). In hereditary syndromes, tumors occur at a younger age and often arise multifocally in multiple organs. A genetic syndrome is behind approximately 20% of all NENs (Crona and Skogseid 2016). At least ten hereditary syndromes (Table 3) including NEN are recognized (Klöppel and Lloyd 2017). The classic syndromes consist of multiple endocrine neoplasias type 1 and 2 (MEN1 and MEN2) and von Hippel-Lindau (VHL).

MEN1 is an autosomal dominantly inherited syndrome in which the *MEN1* gene mutates (Wermer 1954). Over 1000 mutations have been recognized, often leading to the truncation of the menin protein (Crona and Skogseid 2016). Carriers of *MEN1* experience tumors of the parathyroid (95%), pituitary gland (20–40%), and pancreatic/duodenum NENs (40–80%) (Crona and Skogseid 2016). MEN2, in comparison, features subtypes A and B, from which subtype A accounts for 80% of all cases. A mutation of the proto-oncogene *RET* (Mulligan et al. 1993) results in the activation of the RAS/MAPK and PI3K/AKT signalling pathways leading to medullary thyroid carcinoma (90–100%) and tumors of the adrenal medulla (20–80%) (Crona and Skogseid 2016). VHL increases the risk of various tumors, including PGLs and pancreatic NETs (Klöppel and Lloyd 2017). This syndrome is caused by the inactivation of the *VHL* tumor-suppressor gene resulting in the truncation of the VHL protein and the dysregulation of hypoxia-inducible factors (Nordstrom-O'Brien et al. 2010).



**Figure 3.** Incidence rates for neuroendocrine tumors (NETs) compared to all malignancies (A) and by NET origin (B) from 1973 to 2012. Figure adapted from Dasari et al. (2017) in accordance with the terms and conditions stipulated by Elsevier and the Copyright Clearance Center.

**Table 3.** Hereditary syndromes associated with neuroendocrine neoplasias (NENs). Modified from Klöppel and Lloyd (2017).

INHERITED SYNDROM	GENE MUTATION	NENs	OTHER LESIONS
Multiple endocrine neoplasias type 1	MEN1	<ul style="list-style-type: none"> <li>✓ Parathyroid adenomas</li> <li>✓ Pituitary tumors</li> <li>✓ Duodenal tumors</li> <li>✓ Pancreatic tumors</li> </ul>	Adrenal cortical lesions, cutaneous lesion, central nervous system (CNS), soft tissue and breast lesions
Multiple endocrine neoplasias type 2	RET	<ul style="list-style-type: none"> <li>✓ Medullary thyroid carcinoma</li> <li>✓ Pheochromocytoma</li> <li>✓ Paranglioma</li> <li>✓ Parathyroid adenomas</li> </ul>	Hirschsprung disease, cutaneous lichen amyloidosis
Multiple endocrine neoplasias type 4	CDKN1B	<ul style="list-style-type: none"> <li>✓ Parathyroid adenomas</li> <li>✓ Pituitary tumors</li> <li>✓ Pancreatic tumors</li> <li>✓ Cervix tumors</li> <li>✓ Bronchial tumors</li> <li>✓ Stomach tumors</li> </ul>	
Hyperparathyroidism-jaw tumor syndrome	CDC73	<ul style="list-style-type: none"> <li>✓ Parathyroid carcinoma</li> <li>✓ Parathyroid adenoma</li> </ul>	Fibro-osseous lesions of the mandible and maxilla
von Hippel-Lindau syndrome	VHL	<ul style="list-style-type: none"> <li>✓ Pheochromocytoma</li> <li>✓ Paranglioma</li> <li>✓ Pancreatic tumors</li> </ul>	Hemangioblastomas of CNS and retinas, clear-cell renal carcinoma and cysts
Familial paraganglioma-pheochromocytoma syndromes	SDHB SDHC SDHD	<ul style="list-style-type: none"> <li>✓ Pheochromocytoma</li> <li>✓ Paranglioma</li> </ul>	
Neurofibromatosis type 1	NF1	<ul style="list-style-type: none"> <li>✓ Pheochromocytoma</li> <li>✓ Paranglioma</li> <li>✓ Pancreatic tumors</li> <li>✓ Duodenal tumors</li> </ul>	Multiple neurofibromas, café-au-lait spots, freckling of the axilla and/or groin, bone dysplasia, gliomas, gastrointestinal stromal tumors
Carney complex	PRKA-R1A	<ul style="list-style-type: none"> <li>✓ Pituitary tumors</li> <li>✓ Thyroid tumors</li> </ul>	Adrenal cortical lesions, lentiginosis, myxomas
McCune-Albright syndrome	GNAS	<ul style="list-style-type: none"> <li>✓ Parathyroid adenomas</li> <li>✓ Hyperfunctioning syndromes</li> </ul>	Café-au-lait spots, fibrous dysplasia
DICER1 syndrome	DICER1	<ul style="list-style-type: none"> <li>✓ Thyroid tumors</li> <li>✓ Pituitary blastoma</li> <li>✓ Ovarian sertoli cell tumors</li> </ul>	Cystic nephroma, pleuropulmonary blastoma
Glucagon cell hyperplasia and neoplasias	GCGR	<ul style="list-style-type: none"> <li>✓ Pancreatic tumors; glucagon cell</li> </ul>	

## 2.2.2 CLINICAL PRESENTATION

The clinical presentation of NENs varies depending upon the stage and site of the tumor, as well as the tumor's hormonal activity. Patients may be asymptomatic or symptoms can be nonspecific. Thus, NENs are typically found incidentally.

### 2.2.2.1 *Functioning neuroendocrine neoplasms*

If tumor cells release hormones, patients may suffer from symptoms related to the secreted hormone (de Herder 2007). These tumors are syndromic or functioning NENs (Klöppel et al. 2017b). Functioning NENs are named according to the hormone produced, such as insulinomas, glucagonomas, gastrinomas, somatostatinomas, VIPomas, and serotonin or adrenocorticotrophin (ACTH)-producing NENs (Klöppel et al. 2017b, Washington 2019). For example, the autonomic secretion of insulin causes the hypoglycemic syndrome and the overexpression of gastrin causes the Zollinger–Ellison syndrome. The production of serotonin causes the classical carcinoid syndrome with flushing, sweating, and diarrhea. Carcinoid syndrome usually requires the presence of liver metastases to manifest. Table 2 summarizes the terms and locations of the functioning NENs, while Table 4 provides examples of hormone-producing cell types.

### 2.2.2.2 *Nonfunctioning neuroendocrine neoplasms*

Most NENs, however, are asymptomatic. These NENs can be clinically silent for years until late presentation due to the tumor load or symptoms related to metastasis. These tumors are called non-syndromic or nonfunctioning NENs (Klöppel et al. 2017b, Washington 2019). Clinical presentations due to the tumor load or location include pain, weight loss, GI bleeding or obstruction. On average, the diagnosis of a nonfunctioning NEN is more often delayed and misdiagnosed leading to the development of local invasion and metastases.

## 2.2.3 BIOCHEMICAL MARKERS

Preliminary diagnosis of NENs is usually based on elevated levels of NE differentiation-specific and hormone-specific biochemical markers. These tumor markers can be analyzed from different body fluids, such as urine and serum. Biochemical markers can be divided into general NE markers and tumor type-specific markers (Oberg et al. 2017). The most commonly used markers

are serum chromogranin A (CGA) and urinary 5-hydroxyindole-5-acetic acid (5-HIAA), a metabolite of serotonin (Aluri and Dillon 2017). Circulating CGA is quite nonspecific, with a sensitivity and specificity of around 60% to 90% (Oberg et al. 2017, Hofland et al. 2018). Serotonin and 5-HIAA are markers of serotonin secretion, typically suggesting a primary tumor location of the small intestine (Frilling et al. 2012, Aluri and Dillon 2017). Neuro-specific enolase (NSE) is a relevant biochemical marker to diagnose high-grade NENs (Oberg et al. 2017). Biochemical markers are used not only in diagnosis, but also in the follow-up of tumor patients. Elevated levels of markers may indicate disease recurrence.

**Table 4.** Hormone-producing neuroendocrine neoplasias (NENs), specific hormones with the hormone-producing cell type and anatomic location. Modified from Klöppel et al. (2017b).

NEN TYPE	HORMONE	CELL TYPE	ORGAN
ACTH-producing NENs	ACTH	Basophils	✓ Pituitary gland, anterior pituitary
Medullary carcinoma	Calcitonin	C cells	✓ Thyroid
Gastrinoma	Gastrin	Gastrin cells	✓ Pancreas ✓ Stomach pyloric antrum ✓ Small intestine Duodenum
Insulinoma	Insulin	Beta cells	✓ Pancreas, islet of Langerhans
Glucagonoma	Glucagon	Alpha cells	✓ Pancreas, islet of Langerhans
Serotonin-producing NENs	Serotonin	Enterochromaffin cells Kulchitsky cells	✓ GI tract ✓ Lung
Somatostatinoma	Somatostatin	Delta cells	✓ Pancreas ✓ Stomach pyloric antrum ✓ Small intestine Duodenum
VIPoma	Vasointestinal polypeptide	Nerves	✓ GI tract ✓ Pancreas

## 2.2.4 IMAGING

Various imaging methods form the basis of NEN diagnostics (Maxwell and Howe 2015). The detection sensitivity and specificity of imaging varies depending upon the anatomical location and NEN type. Nuclear imaging techniques play an additional role in selecting treatment options and during follow-up to detect recurrent disease (Sundin et al. 2017).

### **2.2.4.1 Radiological examination**

Computed tomography (CT) and magnetic resonance imaging (MRI) are methods which yield detailed information from tissue structures. Contrast-enhanced CT of the neck-thorax-abdomen and pelvis is the primary imaging method for patients with signs and symptoms of a NET (Sundin et al. 2017).

In CT, the mean sensitivity and specificity to detecting NETs are 82% and 86%, respectively, with the lesion-based sensitivity and specificity standing at 77% to 85% and 71% to 85%, respectively (Gabriel et al. 2007, Ruf et al. 2011, Veit-Haibach et al. 2011, Sundin et al. 2017). CT is useful in the context of an unknown primary tumor (Maxwell and Howe 2015). MRI with contrast enhancement is the preferred method for the visualization of the liver, metastases and primary pancreatic NETs (Maxwell and Howe 2015, Sundin et al. 2017). The mean MRI sensitivity and specificity in the diagnosis of pancreatic NENs stand at 70% to 75% and 98% to 100%, respectively (Brenner et al. 2012, Mayerhoefer et al. 2013, Schmid-Tannwald et al. 2013, Sundin et al. 2017).

### **2.2.4.2 Nuclear imaging**

Nuclear imaging utilizes short-lived radioactive substances linked to different molecules (Pauwels et al. 2018). Combining CT and nuclear imaging procedures carries a complementary role to NEN imaging (Maxwell and Howe 2015, Sundin et al. 2017).

Somatostatin receptor (SSTR) scintigraphy benefits the isotope-labeled somatostatin analogs (SSAs) which bind to SSTRs. OctreoScan™ imaging of SSTRs is based on the use of the <sup>111</sup>Indium-labelled conjugate of octreotide, which binds especially to SSTR subtype 2. Upon binding and internalization, the bound radioisotope ligand allows for the imaging of tumors expressing SSTRs (Frilling et al. 2012, Pauwels et al. 2018). Positron emission topography (PET) is an isotope imaging method that observes the metabolic processes in organs and possible tumors. PET utilizes common radioligands, fluoride-18 and gallium-68, linked to different chelators, including 1,4,7,10-tetraazacyclododecane-1,4,7,10-tetraacetic acid (DOTA) and fluorodeoxyglucose (FDG) (Pauwels et al. 2018). Combining PET/CT with <sup>68</sup>Ga-labeled SSAs is optional for the OctreoScan, providing a higher sensitivity (Maxwell and Howe 2015).

The choice of imaging method depends on the differentiation of the tumor. The expression of SSTRs is lower in high-grade NENs (Schmid et al. 2012). Therefore, these tumors have a lower uptake isotope-labeled ligand and are less visible in imaging (Maxwell and Howe 2015, Olsen et al. 2016). PET/CT with <sup>18</sup>F-FDG is more suitable for poorly differentiated NECs than well-differentiated NETs



because NECs grow more actively (Frilling et al. 2012). Slow-growing, well-differentiated NETs have a lower metabolic rate and do not uptake metabolic 18F-FDG so readily (Frilling et al. 2012). Positivity in 18F-FDG-PET/CT predicts poor survival (Binderup et al. 2010, Johnbeck et al. 2016, Majala et al. 2019).

While a variety of imaging techniques have improved the visualization of NEN lesions, some GEP–NENs can remain undetected (Schott et al. 2011, Frilling et al. 2012). A study of the imaging sensitivity of small micrometastases in the liver by Elias et al. (2010) found an MRI detection rate of 33%, a CT detection rate of 21%, and an ultrasonography detection rate of 22% (Elias et al. 2010), highlighting the limitations of current imaging techniques. SSTR scintigraphy carries a detection sensitivity of 60% to 80% and PET carries a mean sensitivity of 88% to 93% (Sundin et al. 2017). If lesions fall under the limits of resolution, as very small tumors, they may remain undetected during imaging (Frilling et al. 2012). The histological or hormonal type of NEN (gastrinomas and insulinomas) may also influence the imaging sensitivity (Frilling et al. 2012, Sundin et al. 2017).

## **2.2.5 PATHOLOGY**

The cornerstone of diagnosing NEN is the histopathological analysis of a tumor specimen (Perren et al. 2017). Specimens are mainly formalin-fixed and paraffin-embedded tissue. Gross examination and histopathology data provide information on the tumor size, invasiveness, resection margins, and the possible presence of local metastases, thus the criteria for the tumor, node, and metastasis (TNM) classification (Klöppel et al. 2009).

### **2.2.5.1 Cytology**

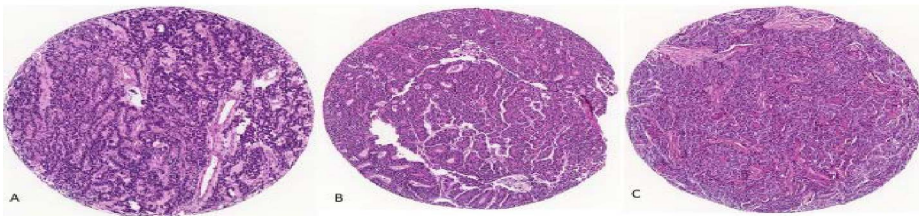
Fine-needle aspiration (FNA) is used for the microscopic examination of cells from a suspicious tissue structure. The reliability of FNA depends on the representativeness of the tumor cells in the sample. In cytological preparation, NENs have a plasmacytoid appearance characterized by an eccentrically placed nucleus and a typical NE-type chromatin (Klöppel et al. 2017b). Cytological samples are commonly taken from organs where histological biopsies prove difficult to collect (the pancreas and thyroid gland) (Klöppel et al. 2017b). Diagnosis relying on FNA is less reliable compared to diagnosis based on a core-needle biopsy. For example, the tumor grade cannot be determined from a cytological sample and, in general, immunohistochemistry (IHC) does not work as well as when analyzing formalin-fixed tissues (Vinayek et al. 2014).

### 2.2.5.2 Histopathology

NEN diagnosis can be made from a histological tissue specimen of the primary tumor or from a metastatic lesion (Perren et al. 2017). The specimen can be a core-needle biopsy, endoscopic biopsy or surgical specimen.

Common nuclear features are characteristic for NENs. Tumor cells are usually monotonic, while the nuclei are uniform and round with smooth nuclear membranes. Chromatin is evenly dispersed showing a characteristic “salt-and-pepper” appearance without prominent nucleoli. The cytoplasm is finely granular corresponding to dense-core granules (Rekhtman 2008, Schmitt et al. 2016). The cellular features of NENs are better distinguished in well-differentiated NENs than in poorly differentiated NECs.

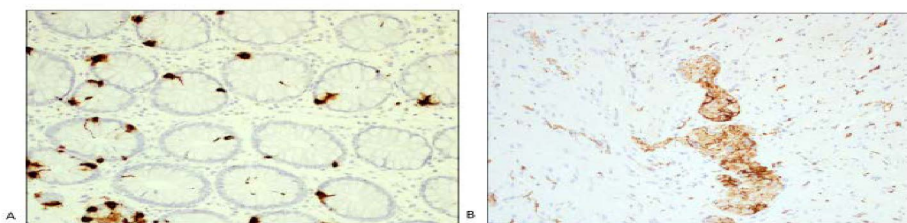
Depending upon the primary site, NENs feature different histological growth patterns (Rekhtman 2008, Schmitt et al. 2016). Classic patterns (Figure 4) characteristic of well-differentiated tumors include 1) a trabecular pattern which forms long nests and cords of cells separated by fibrous septa; 2) a glandular pattern which forms gland structures with lumens; 3) a solid pattern featuring a non-organoid growth pattern; and 4) a pseudorosette or rosette-forming pattern, whereby tumor cells grow around vessels (Schmitt et al. 2016). In a poorly differentiated NEC, the architecture of the growth pattern is often diffuse (Rekhtman 2008).



**Figure 4.** Neuroendocrine neoplasias feature various histological growth patterns: A) trabecular, B) glandular, and C) solid-growth patterns.

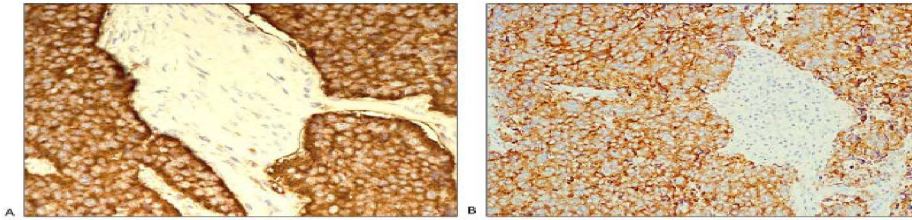
### 2.2.5.3 Neuroendocrine phenotype

The neuroendocrine phenotype is confirmed through IHC (Rekhtman et al. 2008, Perren et al. 2017). Most NENs, except PHEOs and PGLs, are positive for pan-cytokeratin, indicating an epithelial origin for the tumor. Common NE markers (Figures 5 and 6) are CGA and synaptophysin (SYP) (Schmitt et al. 2016). Chromogranins are a family of glycoproteins including types A, B, and C, comprising the majority of soluble proteins in the neurosecretory granules of NE cells (Doblinger et al. 2003, Klöppel 2007). SYP is a glycoprotein, part of the synaptic vesicles of neurons and NE cells (Klöppel 2007). SYP is a broad-spectrum NE marker with a high sensitivity for identifying the NE nature of a tumor, but possessing a lower specificity than CGA (Gut et al. 2016, Perren et al. 2017).



**Figure 5.** Chromogranin A (A) and synaptophysin (B) are expressed in normal neuroendocrine cells and nerves.

The specificity of NE markers varies. The histological differentiation of NENs influences the expression levels of CGA and SYP; well-differentiated NETs unlike poorly differentiated NECs express NE markers abundantly. Well-differentiated NENs are commonly diffusely positive for SYP, although the expression of CGA is often heterogeneous (Perren et al. 2017) since the expression level of CGA correlates with the number of secretory granules (Gut et al. 2016). In poorly differentiated NECs, the staining intensities of the NE markers typically decrease (Schmitt et al. 2016). The application of less-specific NE markers, such as CD56 and neuro-specific enolase (NSE), is not recommended, because CD56 is often expressed in non-NENs and NSE is a typical neural marker (Perren et al. 2017). However, recently identified insulinoma-associated protein 1 (INSM1) is a good NE marker for NECs (Fujino et al. 2017). Table 5 summarizes the typical markers expressed in NENs.



**Figure 6.** Neuroendocrine neoplasias express A) chromogranin A and (B) synaptophysin.

### ***Proprotein convertase subtilisin/kexin type 2***

Proprotein convertases (PCs) are a large family of nine enzymes responsible for the activation of different peptides, proteins, and growth factors (Seidah and Prat 2012). Within the PC family, proprotein convertase subtilisin/kexin type 2 (PCSK2) takes part in the hormonal processing of the regulated secretory pathway of NE cells (Li et al. 2003). PCSK2 is stored in the dense core secretory granules of a normal NE cell (Portela-Gomes et al. 2004, Seidah and Prat 2012). Hormones such as somatostatin, glucagon, and insulin as well as CGA are processed by PCSK2 (Doblinger et al. 2003, Portela-Gomes et al. 2008). PCSK2 was discovered two decades ago, and many NENs from different origins have exhibited PCSK2 positivity (Scopsi et al. 1995, Kajiwara et al. 1999, Kimura et al. 2000, Tomita 2001).

**Table 5.** Neuroendocrine markers localized in the secretory granules, cytoplasm, cell membrane or nuclei of the neuroendocrine cell. Modified from Portela-Gomes et al. (2004).

<b>I Secretory granule proteins</b>
a) Core-related proteins Hormones: insulin, glucagon, serotonin, vasoactive intestinal polypeptide Chromogranin A Proprotein convertase subtilisin/kexin type 2
b) Membrane-related proteins Synaptophysin
<b>II Cytosolic proteins</b>
Neuro-specific enolase
Protein Gene Product 9.5
<b>III Cell membrane</b>
Somatostatin receptors
<b>IV Nuclei</b>
Insulinoma-associated protein 1

### 2.2.5.4 Tumor differentiation and grading

According to the WHO classification, NENs fall into the categories of well-differentiated NETs and poorly differentiated NECs (Klöppel et al. 2017a, Washington 2019). NEN grading is based on the proliferation activity of the tumor cells. The proliferation index (PI), assessed using Ki-67 IHC, is the most important marker for tumor grading together with the mitotic index of the tumor cells. The Ki-67 PI is evaluated from the areas of highest nuclear labeling, referred to as hotspots, including 500 to 2000 tumor cells (Rindi et al. 2006, Rindi et al. 2007, Klimstra et al. 2010, Klöppel et al. 2017a, Klimstra et al. 2019). The nuclear expression of Ki-67 is observed during the active phases of the cell cycle, but not during the resting phase (van Dierendonck et al. 1989). For NEN grading, any level of positivity should be considered a positive finding (Brown and Gatter 1990, Lopez et al. 1991). Grades 1 and 2 in GI and pancreatic NENs are well-differentiated NETs with low mitotic and proliferation activity (Klöppel et al. 2017b, Washington 2019). Grade 3 can be a well-differentiated tumor or a poorly differentiated carcinoma (Klöppel et al. 2017b, Washington 2019). Different NEN types have organ-specific criteria for grading, as summarized in Table 6 (E. Brambilla 2015, Busam et al. 2018, Rindi et al. 2018).

**Table 6.** WHO tumor grading for specific neuroendocrine neoplasm (NENs) according to the proliferation index (PI) and mitotic count. Modified from E. Brambilla (2015), Klöppel et al. (2017b), and Washington (2019). \*Indicates the normative classification. High-power field (HPF)

WHO	NENs	PI KI-67	MITOTIC COUNT
2019	Gastrointestinal NENs	NET, G1 well-differentiated	<3%
		NET, G2 well-differentiated	3–20%
		NET, G3 well-differentiated	>20%
		NEC, small-cell type NEC, large-cell type	>20%
2015	Pulmonary NENs	Small-cell carcinoma	50–100%*
		Large-cell carcinoma	40–80%*
		Typical carcinoids	≥5%*
		Atypical carcinoids	≥20%*
2017	Pancreatic NENs	PanNET, G1 well-differentiated	<3%
		PanNET, G2 well-differentiated	3–20%
		PanNET, G3 well-differentiated	>20%
		PanNEC G3, small-cell type PanNEC G3, large-cell type	>20%
	Endocrine organs	Parathyroid adenoma	≤4%*
		Parathyroid carcinoma	6–8%*

## 2.2.6 CLASSIFICATION

Classifying tumors forms the basis of determining prognosis, disease management, and follow-up of patients. The classification of NENs relies on WHO guidelines and TNM staging proposed by the European Neuroendocrine Tumor Society (ENETS) (Rindi et al. 2006, Rindi et al. 2007, Pavel and de Herder 2017), the American Joint Committee on Cancer (AJCC), and the Union for International Cancer Control (UICC) (Brierley et al. 2017).

### 2.2.6.1 *World Health Organization*

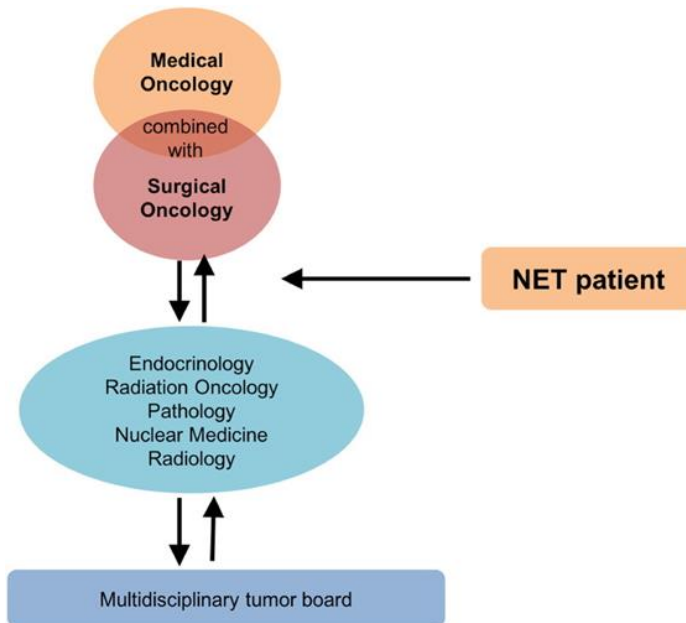
In 1963, Williams and Sandler separated NETs according to embryological tumor origin into the foregut, midgut, and hindgut types (Williams and Sandler 1963), while WHO classifications began in the 1980s (Williams et al. 1980). In 1995, Capella and co-workers proposed the first unified classification model for lung, pancreatic, and GI NETs taking into consideration the potential malignancy of the tumor based on histological criteria (Capella et al. 1995). The WHO classifications continue to aim towards predicting clinical outcomes; the proliferation activity of a tumor seems to carry prognostic significance in NENs (Capella et al. 1995, Solcia et al. 2000, Klöppel et al. 2017a, Klimstra et al. 2019).

### 2.2.6.2 *Tumor-Node-Metastasis*

TNM staging relies on the size of the tumor, the status of the regional lymph nodes, and the absence or presence of metastases. AJCC/UICC staging applies to well-differentiated NENs of the GI tract (G1 and G2 of the gastric, small intestine, appendix, and colorectum), including the pancreas (Brierley et al. 2017). High-grade (G3) NECs follow the same criteria as adenocarcinomas of the respective tumor location (Brierley et al. 2017). The AJCC/UICC staging of Merkel cell carcinoma relies on its own separate classification criteria (Brierley et al. 2017). TNM classification of pulmonary carcinoids complies with the rules governing lung tumors (Brierley et al. 2017).

## 2.2.7 MANAGEMENT

As a heterogeneous tumor type, NENs require multidisciplinary medical teams (Figure 7) for management with the goals of slowing down tumor growth, controlling hormonal symptoms, and improving the quality of life (Oronsky et al. 2017).



**Figure 7.** Neuroendocrine tumors (NETs) require a multidisciplinary healthcare team. Image from Oronsky et al. (2017), reproduced here in accordance with Elsevier Inc., Creative Commons Attribution-NonCommercial-No Derivatives License (CC BY NC ND).

### 2.2.7.1 Surgery

The tumor location and extent of disease play crucial roles in therapeutic planning. Surgery represents first-line treatment for NENs. Indications for surgery depend upon the tumor size, location, histological grade, metastases, and the patient's clinical symptoms. In general, radical resection is preferred, although patients with advanced or nonresectable disease may receive palliative surgery to decrease the tumor burden and to help control hormonal symptoms (Oronsky et al. 2017)

### **2.2.7.2 Medical therapy**

Medical management aims to relieve clinical symptoms and suppress tumor growth and progression given the late diagnostic status of most NETs (Oronsky et al. 2017). Therapy for NENs includes treatment with SSAs and alpha interferons, primarily indicating treatment of functioning NENs causing clinical and hormone-related syndromes (Zandee and de Herder 2018).

#### ***Somatostatin analogs***

Somatostatin is a hormone with a broad range of inhibitory actions, including regulating hormone secretion and cell proliferation (Theodoropoulou and Stalla 2013). Somatostatin binds SSTRs, G-protein-linked receptors, with a single polypeptide chain that passes through the cell membrane seven times.

SSAs are structurally similar to biological somatostatins. Octreotide (Sandostatin) and lanreotide (Somatuline) are synthetic long-acting SSAs, which inhibit growth and the progression of an SSTR-positive tumor (Figure 8). SSAs also reduce clinical symptoms (carcinoid syndrome), thereby improving the quality of life of patients with well-differentiated NENs (Frilling et al. 2012). By comparison, SSAs are ineffective in poorly differentiated NECs due to the lower expression of SSTRs (Schmid et al. 2012).

Octreotide and lanreotide have a high affinity to SSTR2, SSTR3, and SSTR5 (Theodoropoulou and Stalla 2013). More recent analog pasireotide (Signifor), a multi-receptor SSA, binds with a higher affinity to SSTR5 and SSTR1-3 (Vitale et al. 2018). In disseminated disease, analog therapy represents the first-line medical treatment (Rinke et al. 2009, Oronsky et al. 2017).

#### ***Interferon***

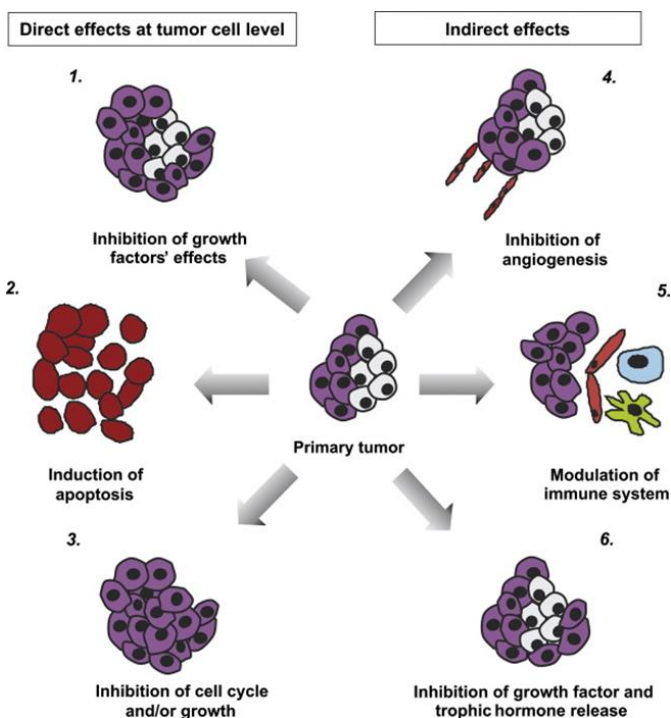
Interferon alpha treatment is recommended as second-line medical therapy after disease progression during treatment on SSAs (Zandee and de Herder 2018). Cytokine, interferone alpha provides palliative effects in functional NENs with a low PI, by stabilizing the disease in 50% of patients (Oronsky et al. 2017). Interferon alpha also carries potential side effects, thereby limiting its use in practice (Mirvis et al. 2014).



### Other medical treatments

Other oncological medical treatments include anti-proliferative agent everolimus and vascular endothelial growth factor receptor inhibitor sunitinib. The RADIANT 1–4 trials studied the effects of everolimus in NETs revealing their safety and efficacy in well-differentiated NETs (Pusceddu et al. 2016). Sunitinib was studied in pancreatic NETs by Raymond et al. (2011). In a study of 171 patients with advanced, well-differentiated pancreatic NETs, sunitinib increased progression-free survival from 5.5 to 11.4 months (Raymond et al. 2011). These target therapy agents are registered for progressive, metastatic, pancreatic and small intestine NETs (Zandee and de Herder 2018).

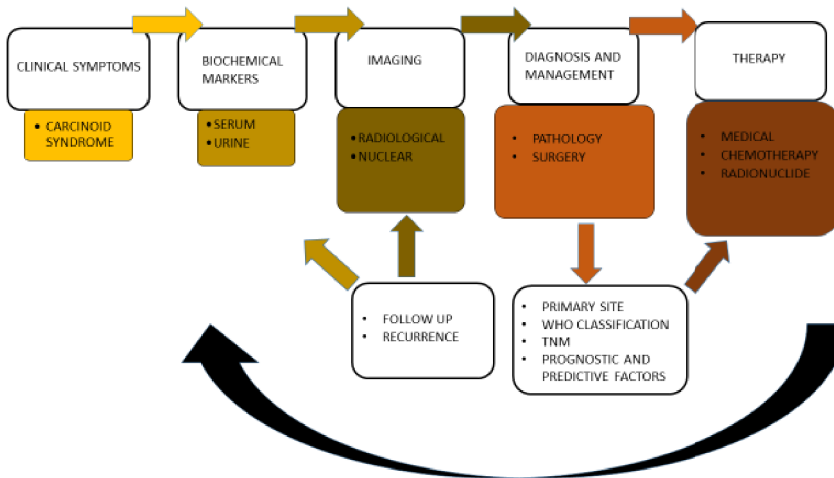
For the treatment of poorly differentiated NECs, chemotherapy remains the first-line treatment (Eriksson et al. 2009, Oronsky et al. 2017). High-grade tumors respond better to cytotoxic chemotherapy compared to low-grade tumors, since the tumor cells divide more aggressively. Chemotherapy for NECs includes treatment with combinations of streptozotocin plus doxorubicin and/or 5-fluorouracil, cisplatin plus etoposide, and dacarbazine (Garcia-Carbonero et al. 2017).



**Figure 8.** Somatostatin analog therapy has antiproliferative effects on tumor cells. The direct mechanisms (1-3) associate with the inhibition of the cell cycle and the induction of apoptosis. The indirect mechanisms (4-6) include inhibition of the vascularization, the secretion of tumor-promoting signals, and the production of growth factors. Image from Theodoropoulou and Stalla (2013) in accordance with the terms and conditions provided by Elsevier and Copyright Clearance Center.

### 2.2.7.3 Peptide receptor radionuclide therapy

Peptide receptor radionuclide therapy (PRRT) utilizes radio-labelled (lutetium-177 and yttrium-90) synthetic SSAs for systemic radiotherapy (Theodoropoulou and Stalla 2013). PRRT provides a safe and effective treatment option for disseminated GEP–NETs, where adequate densities of specific SSTRs are found (Hicks et al. 2017). Other potential NENs for PRRT include lung NETs, PHEOs, and PGLs (Werner et al. 2018). The NETTER-1 trial involved 229 patients with metastatic small intestine NETs (Strosberg et al. 2017). Treatment with  $^{177}\text{Lu}$ -DOTATATE improved progression-free survival and a 60% lower risk of death compared to the octreotide long-acting repeatable group (Hicks et al. 2017, Strosberg et al. 2017). Figure 9 summarizes the steps for NEN diagnosis and management.



**Figure 9.** Overview of the clinical investigations, diagnostics, and treatment steps in the management of neuroendocrine neoplasms.

### 2.2.8 PROGNOSIS

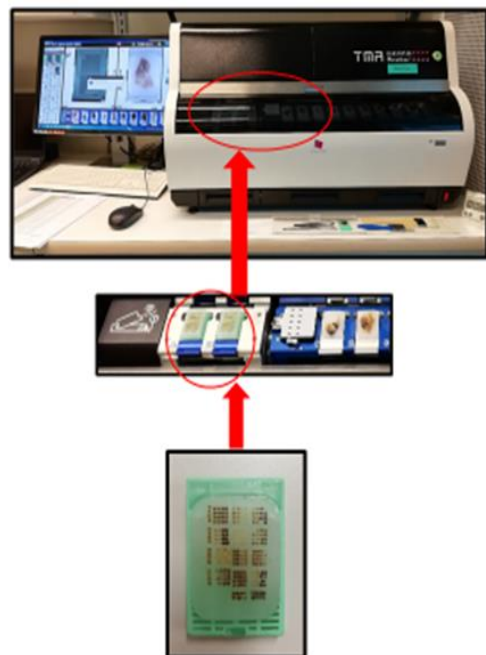
The overall survival (OS) for all types of NENs has improved over time, with a current median OS for all NEN patients of 9.3 years (Dasari et al. 2017). Tumor stage, grade, and primary tumor site all affect OS. Localized NETs accompany a better OS than distant NETs ranging from >30 years to 12 months, and G1 NETs have the highest median OS, while G3 and G4 NETs have the poorest OS irrespective of tumor site (Dasari et al. 2017). When survival is evaluated according to tumor site, appendiceal and rectal NETs feature the best median OS (>30 and 24.6 years, respectively) and NETs from the lung and pancreas (5.5 and 3.6 years, respectively) have the worst median OS (Dasari et al. 2017).

## 2.3 NEUROENDOCRINE TUMOR RESEARCH

In recent decades, the diagnosis and management of NENs have experienced impressive improvements. Tissue microarray (TMA) technology enables the examination of a large number of tissue samples on one slide. The simultaneous study of multiple histological samples began with the “sausage technique” in 1986 (Battifora 1986). Juha Kononen developed the first version of the modern TMA technique in 1998 by introducing a punch instrument that allowed for the rigorous placement and relocalization of individual tissue cores (Kononen et al. 1998). Currently, computer-assisted TMA technology allows for a more detailed orientation of punches through the annotation of digital images to navigate the punching sites (Zlobec et al. 2014). The TMA platform remains the method of choice when novel NE markers are studied in large tumor cohorts (Schmid et al. 2012, Qian et al. 2016, Bellizzi 2020).

### 2.3.1 TISSUE MICROARRAY

The type of TMA varies depending upon the study focus. TMA can be constructed using normal tissues with or without tumor material. Tumor tissue TMAs are further classified as 1) multitumor arrays used to screen for a large number of tumors of different origins and subtypes; 2) progression arrays to assess various diagnostic stages of a particular tumor type; or 3) prognostic arrays for patients with a known clinical outcome (Ramya et al. 2018). Normal tissue TMAs commonly serve as the control material or the verification array (Packeisen et al. 2003).



**Figure 10.** An automated array includes a computer and a connection to a scanner. The tissue microarray instrument holds the donor and receipt blocks.

### **2.3.1.1 Tissue microarray technique**

The construction of a TMA begins with the selection of a tissue cohort (normal tissue, tumor tissue or both). After reviewing the original material, the area of interest is marked on the slide (hematoxylin and eosin, HE) and defined on the corresponding region of the paraffin block (Kononen et al. 1998, Zlobec et al. 2014). The construction of an array can be manual, semi-manual or automatic. Core needles are available in varying diameters, ranging from 0.6 mm to 2.0 mm (Ramya et al. 2018). The appropriate areas from the donor block are punched and relocalized into the ready-made holes on the recipient block. The resulting array block needs warming in an incubator to seal the tissue core holes, after which the block is ready. Tissue data with the coordinates are documented (Kononen et al. 1998, Zlobec et al. 2014).

### **2.3.1.2 Next-generation tissue microarray**

Next-generation TMA (ngTMA) represents a new approach to constructing TMAs, relying on digitalization, and automated arraying (Zlobec et al. 2013). The digitalization of slides allows for a more accurate annotation of the desired tissue area for punching compared to conventional arraying, while slides can be viewed from a computer screen rather than via a microscope, factors rendering ngTMA advantageous (Zlobec et al. 2014).

Digitalization allows for the accurate selection of the region of interest (ROI) for TMA (Zlobec et al. 2013). For example, this may include the selection of areas covering various distances from the tumor border, the areas of tumor-infiltrating lymphocytes, vascularization or tumor budding or the neural and vascular invasion. Selected areas are annotated digitally allowing for notes and for the differentiation of various annotations and to record the information provided into a logbook (Zlobec et al. 2014).

In automated arraying (Figure 10), recipient blocks are placed into the TMA instrument together with empty donor blocks. A camera takes a picture of the recipient blocks, and objective slides are scanned for viewing and annotations. Pictures from these two images are overlapped allowing for the precise drilling of the tissue cores. The instrument prepares the donor block according to the instructions provided by the user, including the size, number, and place of the tissue cores in the block, and the total number of prepared TMA blocks.

## 2.3.2 NEUROENDOCRINE TUMOR MARKERS

The morphological examination of tumor cells is supported by the IHC expression of specific markers, as illustrated in Table 7. Differential diagnoses include the primary diagnostic categories following the subclassification of a neoplasm (Bellizzi 2013, Conner and Hornick 2015).

### 2.3.2.1 *Markers for the primary location*

NETs from various anatomical sites share similar histomorphological features. Predicting the tumor origin is not always possible from an HE slide. Moreover, identifying the primary tumor site from metastatic tissues is important for managing and choosing medical treatment. For example, the primary site of gastric and colon tumors carries a worse OS when disease disseminates (Chan et al. 2017, Dasari et al. 2017). Drug trials have indicated that different NETs, particularly pancreatic NENs, respond differently to chemotherapeutic agents compared to other GI NETs (Kulke et al. 2011, Chan et al. 2017). Primary site-specific IHC markers can be helpful in clinical settings characterized by unknown primary tumors (Schmitt et al. 2016).

**Table 7.** First-line classification of tumors supported by cell line-specific IHC markers addressing tumor origin. Modified from Jackson and Blythe (2008), Koo et al. (2012), Li et al. (2015), Schmitt et al. (2016), and Zhao et al. (2019).

CARCINOMA - EPITHELIAL ORIGIN	SARCOMA - MESENCHYMAL ORIGIN	LYMPHOMA - HEMATOPOIETIC ORIGIN	MELANOMA - MELANOSYTIC ORIGIN	NEUROENDOCRINE - NEUROENDOCRINE ORIGIN
MAJOR DIAGNOSTIC CATEGORIES				
Cytokeratin	Vimentin	CD45	CD3	S100 HMB-45 Melan A
			CD20	
CLASSIFICATION BY CELL ORIGIN				
<b>Lung:</b> Thyroid transcription factor 1, napsin, serotonin				
<b>Thyroid and parathyroid:</b> Calsitonin, thyroid transcription factor 1, thyroglobulin, parathyroid hormone				
<b>Gastrointestinal tract and pancreas:</b> Caudal-type homeobox 2, serotonin, villin, insulin gene enhancer-binding protein islet 1, paired-box 8				
<b>Adrenal gland, cortex, and medulla:</b> Melan A, inhibin alpha, calretinin				
<b>Liver:</b> Hepatocyte specific antigen				
<b>Kidney and urinary tract:</b> Renal cell carcinoma, uroplakin III				
<b>Breast and prostate:</b> Gross cystic disease fluid protein-15, mammaglobin, estrogen receptor, prostata specific antigen, prostata specific membrane antigen				

### ***Caudal-type homeobox 2***

Caudal-type homeobox 2 (CDX2) is a transcription factor that influences the development of the small and large intestines and differentiates the epithelial cells of the intestine and pancreas (James and Kazenwadel 1991). CDX2 is expressed in the small intestine and colorectum as well in the pancreatic ducts (Moskaluk et al. 2003), and is used as a diagnostic marker for intestinal origin in adenocarcinomas and NENs. In NENs, CDX2 has exhibited a specificity for a midgut origin (Moskaluk et al. 2003, Koo et al. 2012) among both primary and metastatic tumors with a sensitivity of 87% to 89% and a specificity of 94% to 100% (Koo et al. 2012). While NENs from the midgut exhibit intense IHC staining for CDX2, its expression in foregut and hindgut NENs remains weaker and patchy (Bellizzi 2013).

### ***Thyroid transcription factor 1***

Thyroid transcription factor 1 (TTF1) plays a role in the morphogenesis of the lung and thyroid gland (Lazzaro et al. 1991). TTF1, a homeodomain-containing transcription factor, is expressed by lung type II pneumocytes and thyroid follicular and C cells (Lazzaro et al. 1991). Thyroid neoplasms and C cell–derived medullary carcinomas are positive for TTF1 (Kato et al. 2000). Pulmonary adenocarcinomas and NENs widely express TTF1 (Bellizzi 2013). NENs of other anatomical localizations are mostly TTF1 negative. Small-cell carcinomas of the prostate and lung are morphologically similar. In a study of 95 prostatic small-cell NECs, Wang et al. (2008) observed TTF1 positivity in 52.3% of cases (Wang and Epstein 2008). Agoff et al. (2000) reported similar results, identifying TTF1 positivity in extrapulmonary small cell carcinomas (Agoff et al. 2000). In comparison, Ordonez et al. (2000) reported TTF1 negativity for all studied small-cell NECs from the prostate (Ordonez 2000). Conflicting reports regarding TTF1 positivity indicate that TTF1 is not only specific to lung origin (Ordonez 2000, Wang and Epstein 2008).

### ***Insulin gene enhancer-binding protein islet 1 and paired-box 8***

Transcription factor insulin gene enhancer-binding protein islet 1 (ISL1) mediates the development of islet cells in the pancreas (Gierl et al. 2006). ISL1 detects pancreatic primary and metastatic NENs with an overall sensitivity of 88% (Graham et al. 2013). While ISL1 is sensitive to a pancreatic tumor origin, it is not specific. Furthermore, according to Graham et al., 89% of duodenal and 100% of rectal NENs are also positive for ISL1 (Graham et al. 2013). Interestingly, 25/25 of Merkel cell carcinoma expressed ISL1 in a study including a total of 124 NENs from different origins (Agaimy et al. 2013). Yet, ISL1 positivity has not been identified in gastric NENs (Bellizzi 2013, Graham et al. 2013). Pulmonary atypical carcinoids and SCLC, however, have demonstrated a variable positivity for ISL1 (Koo et al. 2012, Agaimy et al. 2013). The broad spectrum of possible NENs expressing ISL1 has remained a disappointment when trying to clarify the unknown primary location.

In addition, paired-box 8 (PAX8) positivity has been demonstrated in NENs. Like ISL1, PAX8 is positive in primary NENs of the pancreas (74–88%) and the rectum (9–79%) (Sangoi et al. 2011, Koo et al. 2013). PAX8 positivity in pulmonary NENs and gastric NENs is negligible (10–23%), while ileal NENs show PAX8 negativity (Sangoi et al. 2011, Koo et al. 2012).

### 2.3.2.2 Prognostic and predictive markers

#### *Ki-67*

Ki-67 represents the most essential prognostic marker for NENs. As such, together with the mitotic count, Ki-67 defines the grade of NENs (Klöppel et al. 2017a, Klimstra et al. 2019), and Ki-67 expression in tumor cells correlates with the clinical behavior of NENs (McCall et al. 2013, Warth et al. 2013, van Velthuysen et al. 2014).

The gene *MK167*, localized in chromosome 10, encodes the Ki-67 protein (Fonatsch et al. 1991). Ki-67 is present only in actively proliferating cells (Gerdes et al. 1983), constantly present in the S, G<sub>2</sub>, M, and G<sub>1</sub> phases, but absent in the G<sub>0</sub> phase of the cell cycle (Gerdes et al. 1984). Ki-67 is a nonhistone protein (Gerdes et al. 1991) associated with the chromosomes and nucleolar structures leading to a special, intranuclear staining pattern throughout the cell cycle (van Dierendonck et al. 1989, Verheijen et al. 1989, Isola et al. 1990).

#### *Somatostatin receptors*

Five SSTRs have been characterized in humans. The SSTR<sub>1–5</sub> genes are located on chromosomes 14q13, 17q24, 22q13.1, 20p11.2, and 16p13.3, respectively (Theodoropoulou and Stalla 2013). SSTR<sub>1</sub>, 2, 3, and 4 are closely related in size and structure, unlike SSTR<sub>5</sub> which also exists as truncated isoforms with four to five transmembrane domains (Duran-Prado et al. 2009). Patel et al. (1993) identified two distinct splicing variants of SSTR<sub>2</sub> in humans, named SSTR<sub>2A</sub> and SSTR<sub>2B</sub> (Patel et al. 1993). SSTR<sub>1</sub>, 2, 3, and 4 selectively bind to somatostatin-14, while SSTR<sub>5</sub> prefers somatostatin-28 (Theodoropoulou and Stalla 2013), derived from pro-somatostatin precursor (Schally et al. 1980). The expression of SSTRs predicts the response to SSA therapy (Gatto et al. 2013, Pokuri et al. 2016). Different NENs are known to express SSTRs. The majority of NENs co-express multiple SSTR subtypes with SSTR<sub>2</sub> representing the dominant subtype (Schmid et al. 2012, Hankus and Tomaszewska 2016). A study of 151 PHEOs and PGLs demonstrated that SSTR<sub>2</sub> and SSTR<sub>3</sub> were the most abundant subtypes, whereas subtypes SSTR<sub>1</sub>, SSTR<sub>4</sub>, and SSTR<sub>5</sub> were often negative (Leijon et al. 2019). In a study of parathyroid neoplasms by Storvall et al. (2019), receptors 1 through 5 expressed in parathyroid NENs, with the lowest expression accompanying adenomas and the strongest found in carcinomas (Storvall et al. 2019).

SSTR expression also associates with clinical outcome. Qian et al. (2016) indicated that a high SSTR<sub>2</sub> expression associates with a better OS, especially



in ileal NENs (Qian et al. 2016). Vesterinen et al. (2019) studied a cohort of 178 pulmonary carcinoids and found that negativity for SSTR1 and SSTR2 and positivity for SSTR3 and SSTR4 associated with a shorter disease-specific survival (Vesterinen et al. 2019). In addition, poorly differentiated NENs express lower amounts of SSTRs compared to well-differentiated NENs (Schmid et al. 2012).

### **2.3.2.3 Recent novel markers**

#### ***Insulinoma-associated protein 1***

Insulinoma-associated protein 1 (INSM1), expressed by various NENs, is a key regulator of NE cell development in the pancreas and GI tract (Gierl et al. 2006). Studies by Fujino et al. (2017) and Abe et al. (2019) indicated that INSM1 is a stable NE marker for poorly differentiated NECs. Rectal NENs and SCLC, which often lack CGA positivity (Klöppel et al. 2009), express INSM1 (Fujino et al. 2017). In addition, INSM1 is a useful marker in cytological samples of SCLC (Abe et al. 2019).

#### ***Insulin-like growth factor II mRNA-binding protein 3***

Insulin-like growth factor II mRNA-binding protein 3 (IMP3) overexpresses in the lung, colon, and gastric adenocarcinomas and associates with tumor progression (Beljan Perak et al. 2012, Okada et al. 2012). Er et al. (2017) studied IMP3 expression in GEP–NENs. IMP3 expression correlated positively with the tumor size, grade, and stage, increasing in poorly differentiated NENs (Er et al. 2017).

#### ***Delta-like 3***

Molecular profiling of tumors is becoming increasingly common. George et al. (2018) and Hermans et al. (2019) indicated that delta-like 3 (DLL3) expression is related to the mutational status of STK11/KEAP1 in pulmonary LCNECs (George et al. 2018, Hermans et al. 2019). In addition, Hermans et al. (2019) observed a DLL3 protein-level expression in 74% of LCNEC samples (Hermans et al. 2019). DLL3 falls within the Notch family, an intensively studied pathway candidate for a therapeutic target. The high prevalence of positivity at the protein level in LCNECs and the low level of DLL3 in healthy tissue may predict the potential of DLL3-targeted therapy (Hermans et al. 2019).

### ***Neuropeptide S receptor 1***

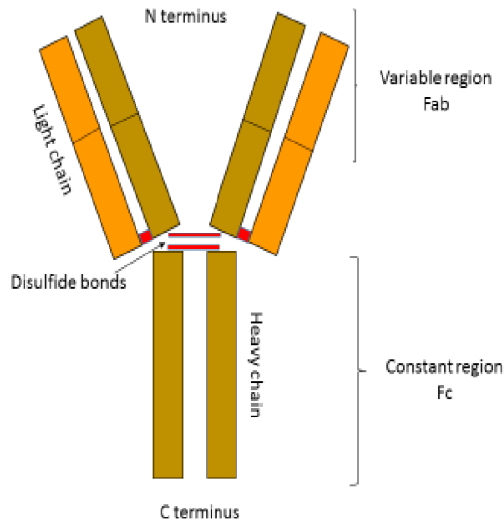
Neuropeptide S receptor 1 (NPSR1) is a G protein–coupled receptor that associates with inflammatory conditions in the intestine (D'Amato et al. 2007, Sundman et al. 2010). NPSR1 is expressed as two different splice variants (Vendelin et al. 2005) inducing signaling upon ligand neuropeptide S (NPS) stimulation. The ligand NPS appears to regulate the production of a range of NE cell hormones (Sundman et al. 2010). Furthermore, NPS appears to play a regulatory role in cell growth in cultured human colon cancer cells (Reinscheid et al. 2005). In 2010, Sundman et al. (2010) showed that the NE cells of the small intestine expressed both the receptor NPSR1 and its ligand NPS at the protein level, indicating their possible role in intestinal functions (Sundman et al. 2010).

## **2.4 QUALITY REQUIREMENTS OF IMMUNOHISTOCHEMISTRY**

The strength of IHC lies in the possibility of visually analyzing target proteins and their cellular distribution. Classification, phenotyping, the assessment of prognostic and predictive markers all rely on IHC. As new biomarkers are identified and their role in predicting prognosis and treatment becomes increasingly essential, understanding the quality of the IHC methodology becomes crucial (Matos et al. 2010, Kim et al. 2016).

### **2.4.1 PRIMARY ANTIBODY**

The primary antibody (Figure 11) defines the recognition of the target protein. Antibodies are glycoproteins produced by the plasma cells in the immune system. In IHC, the most common subtypes of immunoglobulins consist of IgG and IgM (Lipman et al. 2005, Saper 2009). The Fab fragment of an antibody represents the unique structure of the immunoglobulin, which recognizes the antigen. Antibodies are either polyclonal or monoclonal depending upon the type of antigen recognition and production (Schacht and Kern 2015).



**Figure 11.** The structure of the antibody molecule. The immunoglobulin molecule has two light chains (orange) and two heavy chains (brown) joined by sulfur bridges. The variable region (Fab fragment) is involved in antigen binding comprising one light chain and one heavy chain segment on the N-terminal side. Modified from Buchwalow and Böcker (2010).

#### 2.4.1.1 Polyclonal and monoclonal antibodies

The clone of an antibody impacts the staining outcome. Hybridoma technology generates stable cell lines (Kohler and Milstein 1975, Margulies 2005) that secrete defined primary antibody clone with a specificity to a unique part of the target molecule epitopes (Kohler and Milstein 1975, Spieker-Polet et al. 1995, Weber et al. 2017). A polyclonal antibody comprises multiple immunoglobulins that recognize the same antigen with different epitopes. Thus, polyclonal antibodies have a higher affinity and better sensitivity, but are less specific (Lipman et al. 2005, Saper 2009). For example, polyclonal PAX8 is used for staining well-differentiated pancreatic NENs (Haynes et al. 2011, Sangoi et al. 2011). Based on gene expression studies, human islet cells do not contain detectable levels of the PAX8 transcript (Lorenzo et al. 2011). Instead, another member of the PAX family, PAX6, seems to serve as the key regulator of pancreatic islet development (Sander et al. 1997). The polyclonal PAX8 antibody is raised against the N-terminal peptide which contains the DNA binding domain conserved in all members of the family (Lang et al. 2007), consequently recognizing a part of the endogenous PAX6 (Lorenzo et al. 2011). Instead, the monoclonal antibody of PAX8 recognizes the C-terminal region of the protein and staining pancreatic NENs with

monoclonal PAX8 leads to negative staining results (Lorenzo et al. 2011, Tacha et al. 2013).

#### **2.4.1.2 Rabbit and mouse monoclonal antibodies**

Depending upon the animal in which the antibody is produced, different clones have demonstrated a variable sensitivity. Antibodies produced in a rabbit have a higher affinity to antigens than antibodies raised in a mouse (Weber et al. 2017, Huang et al. 2006). TTF1 is an important marker for lung origin in NENs (Lin et al. 2007, Zhao et al. 2019). In pulmonary NENs, the rabbit monoclonal antibody SPT24 demonstrated a stronger IHC reactivity than the mouse monoclonal antibody 8G7G3/1 (La Rosa et al. 2010). Findings from Roge et al. (2019) indicated that rabbit monoclonal clones yielded higher PI values compared to mouse monoclonal clones of Ki-67. Buonocore et al. (2019) also reported similar results with cytological samples from SCLS (Buonocore et al. 2019). However, some studies have demonstrated an unexpected antigen reactivity and coincidental positivity with rabbit monoclonal antibodies in tumors traditionally considered as negative (Comperat et al. 2005, Galloway and Sim 2007, Matoso et al. 2010). According to Ibrahim et al.'s (2008) findings, rabbit monoclonal SP2 yielded a false-positive progesterone receptor staining of a breast tumor, lymphocytes, and endothelial cells compared to other clones of the same antigen (Ibrahim et al. 2008).

The cut-off points of the PI separate the G1 through G3 groups in NENs (Table 6), underscoring the challenge and importance of selecting the primary antibody clone. The preferred clone for PI assessment in NENs is MIB-1 (Klöppel et al. 2017a), which recognizes a highly conserved amino acid sequence from the antigen (Gerdes et al. 1991). Furthermore a comparison of different SSTR2 clones indicated that cell membrane positivity is clone-dependent, where UMB1 clone correlated best with  $^{125}\text{I}$ -[Tyr<sup>3</sup>]-octreotide autoradiography compared to SS-80 or R2-88 clones (Körner et al. 2012).

## **2.4.2 EFFECTS OF TECHNICAL ISSUES ON STAINING QUALITY**

### **2.4.2.1 Tissue fixation**

Tissue fixation aims to preserve the tissue morphology. The type of fixative and the quality of the fixation (under- versus overfixation) significantly impact the staining quality (Meyer and Hornickel 2010, Paavilainen et al. 2010).

Furthermore, pre-analytical factors affect the accuracy of the prognostic and predictive markers (Taylor and Levenson 2006, Engel and Moore 2011). For instance, Khoury et al. (2009) reported a weakened expression of estrogen and progesterone receptors with progressive ischemia (Khoury et al. 2009). The cell membrane receptor human epidermal growth factor receptor 2 (HER2) appeared vulnerable to underfixation leading to the weaker expression of the HER2 antigen on the cell membrane (Goldstein et al. 2003, Moatamed et al. 2011). SSTR2 is a prognostic marker in NENs (Brunner et al. 2017). When studying SSTR2, Körner et al. (2012) observed peripheral but not central IHC staining of UMB1, particularly in large NEN specimens (Körner et al. 2012), pointing towards the impact of poor fixation. Overfixation does not carry the same detrimental effect on antigenicity (Goldstein et al. 2003).

Fixation can be performed using different chemicals, whereby 10% buffered formalin represents the so-called universal fixative (Howat and Wilson 2014, Schacht and Kern 2015). The choice of fixative may influence the detection of antigens. As an example, Buonocore et al. (2019) tested the immunoreactivity of different Ki-67 clones using different fixatives. CytoLyt-fixed cell blocks exhibited lower PI values than parallel formalin-fixed cell blocks which lost up to 70% of the staining intensity and immunoreactivity with the MIB-1 clone (Buonocore et al. 2019).

#### **2.4.2.2 *Antigen retrieval***

Antibody-antigen recognition depends on the compatibility of structures. Formaldehyde fixation masks the epitopes that an antibody recognizes (Fox et al. 1985, Matos et al. 2010). To recover the tissue antigenicity, tissue sections must be subjected to antigen retrieval (AR) (Shi et al. 2007, Schacht and Kern 2015), thereby increasing the sensitivity and intensity of IHC staining (Shi et al. 1991, Pileri et al. 1997). The selection of the optimal AR method is antibody-dependent (Pileri et al. 1997, Ramos-Vara and Beissenherz 2000). A comparison of different heat-induced epitope retrieval (HIER) techniques yielded an SSTR2 positivity in NENs, but the rate of false-negative staining increased under suboptimal AR, preferring high temperatures and a pH 9.0 buffer (Körner et al. 2012).

#### **2.4.2.3 *Blocking of background staining***

Endogenous enzyme activity and unspecific binding of the primary antibody may cause background staining. If endogenous enzymes are present in cells and

tissues, they may react with label substrates used in IHC detection. Endogenous peroxidase activity appears in erythrocytes, monocytes, hepatocytes, and the kidney (Buchwalow and Böcker 2010). Also, nonspecific binding of Fc fragments of an antibody as well as noncovalent interactions may cause background staining. Phagocytes, lymphocytes, and follicular dendritic cells express the Fc receptor on their cell membranes, to which the Fc fragments of primary antibodies can bind (Jackson and Blythe 2008, Kim et al. 2016).

Nonspecific background staining can be blocked with blocking reagents. Endogenous peroxidase activity is frequently blocked with a 3% hydrogen peroxidase solution (Streefkerk 1972, Radulescu and Boenisch 2007). The insufficient quenching of endogenous peroxidase activity may associate with false-negative or false-positive IHC results (Radulescu and Boenisch 2007). For example, some antigens can be destroyed by high concentrations of hydrogen peroxidase (Kim et al. 2016). Most NENs are highly vascular tumors needing endogenous peroxidase blocking. The unspecific binding of Fc fragments is blocked with normal serum (Burry 2011). Protein blocks such as bovine serum albumin inhibit unspecific binding with the charged groups and epitope-like fragments (Burry 2011).

### 2.4.3 THE ROLE OF DETECTION METHODS

The selection of the detection system greatly impacts the technical details related to the IHC staining quality. Two principal detection methods are employed: direct and indirect (Carson and Cappellano 2015). In the direct method, the primary antibody is labeled with, for example, horseradish peroxidase (HRP) or alkaline phosphatase (AP) enzymes (Nakane and Pierce 1966). In the indirect method, a secondary linking antibody is tagged with a label (Schacht and Kern 2015, Kim et al. 2016), representing a present-day technique for visualization.

#### 2.4.3.1 *Avidin-biotin detection*

The avidin-biotin method is an indirect technique, in which a biotin-labeled linking antibody binds to an unconjugated primary antibody followed by binding of an enzyme-labeled biotin-avidin complex (Hsu et al. 1981). The presence of endogenous biotin is a potential source of nonspecific staining (Bussolati and Leonardo 2008, Kim et al. 2016). For example, under proper detection conditions Iezzoni et al. (1999) discredited the claim for inhibin positivity in hepatocellular carcinomas (Iezzoni et al. 1999). Under AR conditions at a high temperature, paraffin sections may be exposed to biotin artifacts (Buchwalow and Böcker 2010).

### **2.4.3.2 Polymer-conjugated detection**

The dextran monomer or polymer technology is biotin-free. Using Envision (Agilent) technology, a secondary linking antibody is conjugated to a labeled polymer chain consisting of dozens of HRP molecules (Sabattini et al. 1998, Kammerer et al. 2001). The OptiView™ (Roche) technology is a three-step detection method with a bridging technique using haptens (Jasani et al. 1981). The hapten-conjugated antibody linker is recognized by an enzyme-labeled tertiary antibody, named a multimer. Each multimer includes seven HRP molecules conjugated through multimer arms (<http://reagent-catalog.roche.com>). Using polymer-conjugated detection in a series of GEP–NENs, Schmid et al. (2012) found frequent SSTR1–2 (42% and 63%) and SSTR5 (65%) positivity, whereas SSTR3 and SSTR4 (6% and 32%) were less detectable (Schmid et al. 2012). Kulaksiz et al. (2002) detected higher levels of positivity with SSTR3 ranging from 71% to 79% compared to the 6% positivity reported by Schmid et al. (2012). Moreover, autoradiography studies by Reubi et al. (2001) indicated that GEP–NENs predominantly express SSTR1 and SSTR2 followed by SSTR5 (Reubi et al. 2001), in agreement with results reported by Schmid et al. (2012). The technical conditions in Kulaksiz et al.'s (2002) study may have contributed to the SSTR3 positivity they observed, although that study did not include biotin-rich tissue-derived NENs (Kulaksiz et al. 2002). Yet, NENs naturally vary in terms of SSTR expression (Hankus and Tomaszewska 2016).

## **2.5 ANTIBODY VALIDATION**

Validation creates the baseline for the quality assessment of markers (Torlakovic et al. 2017). Prior knowledge (Reubi 2014) of expected staining patterns (nuclear, cytoplasmic or membranous) and the cellular location of the antigen assist in the assessment of validation steps (Gown 2016).

### **2.5.1 STEPS TO QUALITY ASSURANCE**

Technical validation includes several variables. In a comparison of different AR methods, primarily comparing HIER buffers with pH 6 and pH 9, combined with using different antibody dilutions provides evidence for the best combination of the protocol settings (Howat et al. 2014). The serial dilution of a concentrated antibody will result in a strong specific labeling with minimal or no background staining (Hladik and White 2008). For example, a study by Copete et al. (2011) showed that half of the false-negative or false-positive stainings were

inappropriately calibrated (Copete et al. 2011). Other variables, such as antibody incubation times and temperatures, are also options to consider during validation (Howat et al. 2014). The expression levels of an antigen determine the choice of the detection method.

The appropriate protocol settings are determined by positive and negative tissue sections ensuring that low-expression tumors are not missed and false-positive results are minimized (Hewitt et al. 2014, Gown 2016). If possible, the positive tissue control should match the tissue under investigation (Burry 2011, Torlakovic et al. 2015), thus normal NE cells represent a proper positive control for the investigation of NEN.

## 2.5.2 THE VALUE OF CONTROLS

Controls are used to confirm the reliability of the staining result (Burry 2000). Controls include a) primary antibody controls showing the specific binding to the target antigen, and b) secondary reagent and label controls to confirm that the resulting color precipitate is from an antigen-primary antibody-complex, not from reaction products (Burry 2011).

### 2.5.2.1 *Primary antibody controls*

Primary antibody controls confirm that an antibody is binding to its correct antigen. A positive normal tissue component or cell known to express the antigen of interest serves as a good primary antibody control (Hewitt et al. 2014). This positive control can be found in the specimen (internal positive control) or can be expressed in a separate tissue (external positive control) (Hewitt et al. 2014, Torlakovic et al. 2015). A negative control is an internal or external tissue component assumed to be negative for the corresponding antigens, thus not expressing the molecule of interest (Hewitt et al. 2014, Torlakovic et al. 2014).

Different genetic approaches can confirm the specificity of the primary antibody. In knockout animals, the expression of a specific protein is blocked using gene manipulation, thus serving as the negative control (Burry 2011). Transfected HEK293 cell lines have been used to demonstrate the stable expression of a specific SSTR subtype (Fischer et al. 2008, Lupp et al. 2011, Lupp et al. 2012, Schmid et al. 2012). In addition Western blotting represents a typical method to determine the binding of the primary antibody to its target molecule by labelling the correct molecular weight target protein.

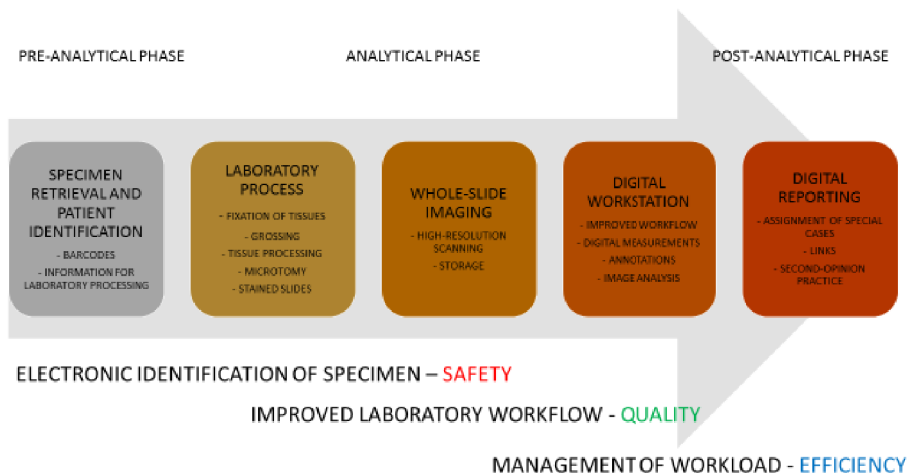


### 2.5.2.2 Secondary reagent control

Controlling the detection reagents serves to confirm that the labelling seen after IHC detection is caused by reactions between antibody complexes rather than the unspecific binding of secondary reagents (Burry 2011, Hewitt et al. 2014). Nonspecific binding can result from charged groups in the cells and tissues or from the Fc fragment of a detection antibody (Buchwalow and Böcker 2010). This can be controlled by excluding the primary antibody.

## 2.6 DIGITAL PATHOLOGY

Digital pathology offers multiple advances including consultation, re-reviewing, education, image analysis, archiving, and quality assurance (Pantanowitz 2010, Griffin and Treanor 2017). The adaptation of digital pathology in routine practice is challenging not only given the technical investments, but also because of other costs (Griffin and Treanor 2017). Figure 12 summarizes the potential steps to digital pathology in the diagnostic laboratory workflow.



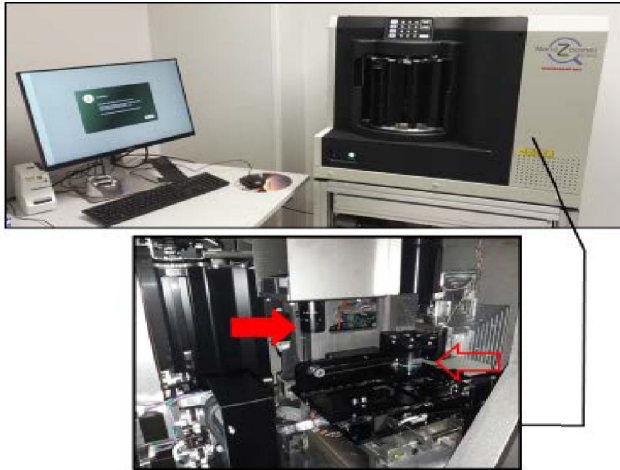
**Figure 12.** Phases of digital pathology in the laboratory workflow process. Modified from Griffin and Treanor (2017).

### 2.6.1 BASICS OF IMAGE ANALYSIS

“Image analysis” refers to quantitative analysis in an objective manner. It allows for the recording of diagnostic information from digitalized slides (whole-slide image (WSI) or digital pictures) in a precise and reproducible manner using analytical tools (Aeffner et al. 2019). Image analysis begins with the identification of the ROI. After defining the ROI, analytical algorithms are configured for the accurate segmentation (Aeffner et al. 2019) to classify cells, typically as either positive or negative based on the staining result (Bankhead et al. 2017, Lykkegaard Andersen et al. 2018). Using segmentation algorithms, different tissue compartments and cell structures are artificially separated. However, nontumor cells along with poor fixation and tissue processing may compromise segmentation (Kwon et al. 2019). In breast cancer studies, cytokeratin-based recognition of tumor cells has provided better recognition of tumor areas and assessment of Ki-67 (Roge et al. 2016, Koopman et al. 2018, Valkonen et al. 2020). In virtual double staining, parallel slides are digitally aligned and fused to one image, from which algorithms automatically detect ROIs and the segment antigen of interest (Roge et al. 2016, Koopman et al. 2018, Lykkegaard Andersen et al. 2018).

Algorithms typically employ fixed or adaptive thresholding. Normally, user-configurable parameters include the color and object size threshold (Zarella et al. 2019). Using graphical icons and tools, the user can interpret the image, guide the analytical process, and evaluate the result of the analysis (Tuominen et al. 2010, Aeffner et al. 2019). This fine adjustment is often included in order to improve accuracy via human interaction. In an analysis of Ki-67 in breast cancer, Kwon et al. (2019) identified discrepancies in the image analysis compared to the visual assessment when the final PI data from an image analysis was not confirmed by a pathologist (Kwon et al. 2019). Furthermore, a study of pancreatic NENs by Reid et al. (2015) highlighted the importance of optimizing image analysis algorithms given that the software was unable to distinguish Ki-67-positive tumor cells from nontumor cells without manual thresholding (Reid et al. 2015).

Digital imaging consists of four key steps: 1) scanning, 2) storing, 3) editing, and 4) viewing images (Pantanowitz 2010). WSI includes the digitalization of slides by scanning (Figure 13), during which the image is captured in a tile- or inline-scanning fashion to generate the final digital image (Zarella et al. 2019). A high-magnification lens together with a high-resolution camera yield good and reliable digital images, but with large file sizes (2 gigabytes). The JPEG, JPEG 2000 or LZW-tiff formats represent the most common packing strategies, although depending upon the compression algorithm, information may be lost during processing (Zarella et al. 2019).

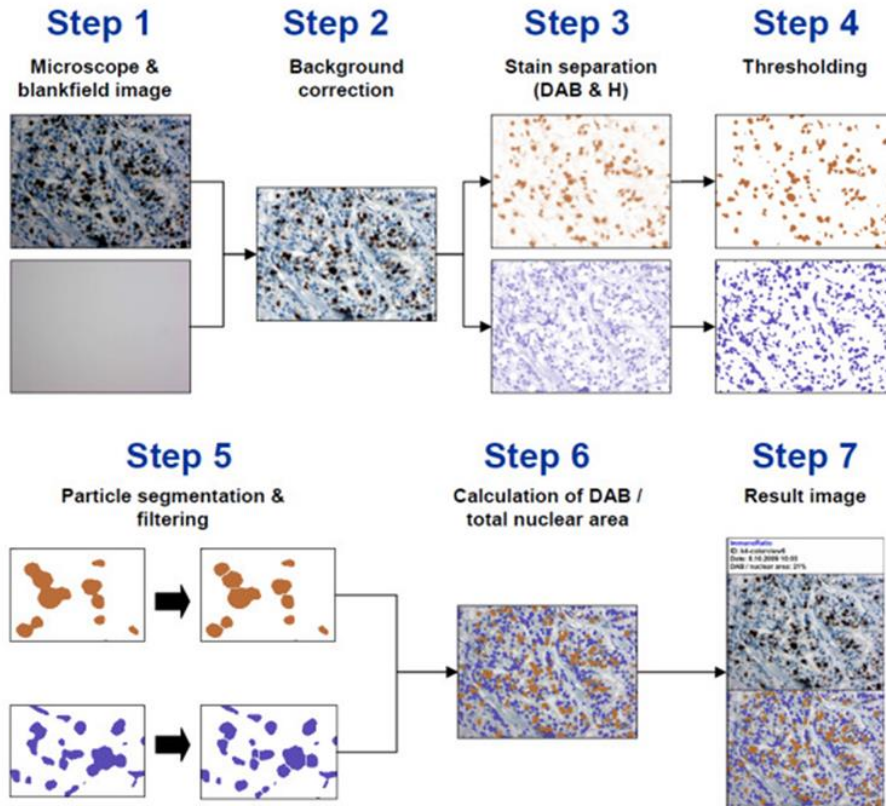


**Figure 13.** Whole-slide scanners are connected to computers with software that sends commands to the scanner. Inside the scanner are the slide stage, the objective lens (right arrow), and the digital camera (solid red arrow on the left).

The accuracy of digital images is appropriate for diagnostic purposes (Snead et al. 2016, Mukhopadhyay et al. 2018). Kaemmerer et al. (2014) compared the SSTR status among 25 NEN patients, comparing manual and digitalized slides in the evaluation of SSTRs, finding a comparable reliability (Kaemmerer et al. 2014). The key elements in high-quality image analysis include high-resolution images (meaning  $0.25 \mu\text{m}/\text{pixel}$  equivalent to a 40x objective magnification), the selection of algorithms and ROIs, and the subjective expertise of the pathologist capable of correlating results with relevant clinical data ensuring an appropriate diagnostic interpretation (Griffin and Treanor 2017, Aeffner et al. 2019).

### ***ImmunoRatio***

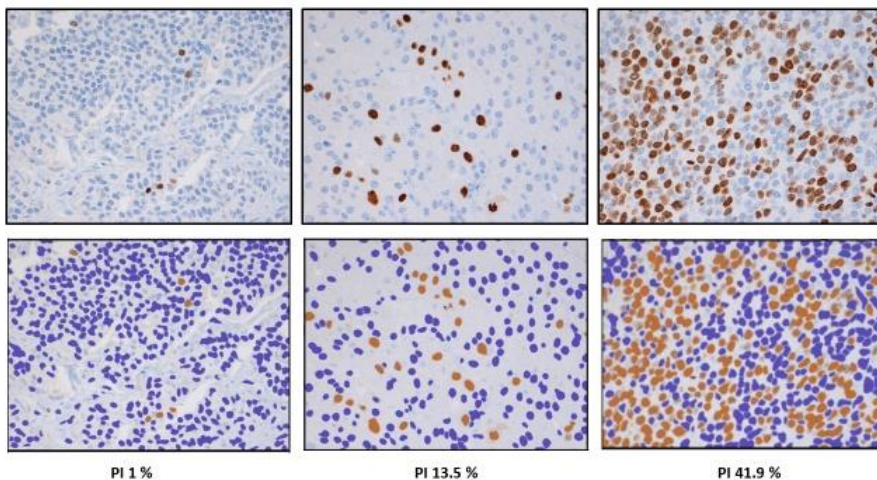
ImmunoRatio image analysis software, originally developed for the quantitative analysis of nuclear breast cancer markers, is based on the ImageJ platform (Tuominen et al. 2010). Analysis uses the digital images taken from the ROI and requires a light microscope with a digital camera. ImmunoRatio includes different algorithms that separate, filter, and combine the image information (Figure 14).



**Figure 14.** Process flowchart of the ImmunoRatio analysis algorithm. Image taken from Tuominen et al. (2010), reprinted in accordance with BioMed Central Ltd. Creative Commons Attribution License (CC BY 2.0).

ImmunoRatio's operational principle is based on the color deconvolution algorithm (Ruifrok and Johnston 2001), which differentiates staining components (DAB and hematoxylin) as separate images by analyzing the absorption spectra of the stains. During this process, the software calculates the intensity of the colors (red, green, and blue) per pixel, quantifying the optical density of a given stain. After separation, components are processed using a mean filter and the adaptive IsoData algorithm thresholding (Ridler and Calvard 1978) to minimize the possible background staining in the images. The binarized components are processed with a median filter to smooth the outline of the nuclei. By using the watershed algorithm (Beucher and Mayer 1993), the nuclei of both stain components are segmented, and then small particles and thin cells are removed. The PI in ImmunoRatio is provided by the percentage of the DAB-stained nuclear area (DAB component) out of the total (DAB and hematoxylin components)

nuclear area (Tuominen et al. 2010). At the end of image processing, the DAB and hematoxylin components are overlaid on the original image and the result is presented as a pseudo-colored image together with the original digital image (Figure 15) (Tuominen et al. 2010). While the DAB density cannot accurately reflect the abundance of the protein in the nuclei, ImmunoRatio's ability to discriminate between positively and negatively stained nuclei (van der Loos 2008) has proved useful in the assessment of breast cancer markers (Tuominen et al. 2010).



**Figure 15.** ImmunoRatio algorithms process digital images (top row) and display the result as a pseudo-colored image (bottom row) with the calculated proliferation index (PI).

## 2.6.2 QUANTITATIVE CALCULATION OF KI-67

The most common evaluation of Ki-67 is the semi-quantitative counting of PI, referred to as eyeballing. Conventional eyeballing is subjective to interobserver and interlaboratory variability (Mengel et al. 2002, Blank et al. 2015, Reid et al. 2015, Cottenden et al. 2018). For accurate assessment, digital pathology has been introduced to analyze the prognostic and predictive markers (Tuominen et al. 2010, Tuominen et al. 2012, Stalhammar et al. 2018, Wang et al. 2019).

Studies using digital image analysis have provided evidence of the accuracy and objectivity of the interpretation of Ki-67 (Tang et al. 2012, Volynskaya et al. 2019). A semi-automated analysis of Ki-67 by Basile et al. (2019) indicated that the calculation of Ki-67 from scanned slides using image analysis software tools proved more accurate than eyeballing (Basile et al. 2019). Reid et al.

(2015) compared different Ki-67 counting methods finding that the accuracy and reproducibility of the camera-captured/printed-image method was highest (81.7%) and the interobserver variability was lowest (43%). The newest classification of GEP–NENs prefers the camera-captured/printed-image method (Klöppel et al. 2017a, Klimstra et al. 2019).

### 2.6.3 ARTIFICIAL INTELLIGENCE AND DEEP LEARNING

Publicly or commercially available image analysis software programs are based on the differentiation of a stained target using a color deconvolution algorithm (Ruifrok and Johnston 2001) or require parallel virtually combined sections (Roge et al. 2016, Koopman et al. 2018, Lykkegaard Andersen et al. 2018) for accurate analysis. These actions require human supervision.

In recent years, artificial intelligence (AI) and deep learning methods have emerged as the primary approaches to medical analysis (Niazi et al. 2019). Broadly, AI refers to machine-based technology that performs specific activities as intelligently as “humans” (Aeffner et al. 2019). Deep learning is a specific field of AI, which is a subset of machine learning where deep learning utilizes artificial neural networks (ANNs) to make their own determination of the output (Khosravi et al. 2018). ANNs are a set of connected layers with defined pathways regarding how data are moved and distributed through a system (Aeffner et al. 2019). The output of ANNs results from many independent steps consisting of calculations, weighting, and assessing (Aeffner et al. 2019, Niazi et al. 2019).

As the utilization of WSI expands, a large volume of digital tissue data becomes more available for AI (Niazi et al. 2019). The emergence of graphic processing units during the millennium has further advanced AI (Aeffner et al. 2019). Machine learning and ANN methods have recently become popular in pathology as well. Pathological approaches include the identification of tumor cells, the tumor microenvironment, and histological features, as well as predicting clinical outcomes (Beck et al. 2011, Luo et al. 2017, Ström et al. 2020).

### **3 AIMS OF THE STUDY**

This thesis aimed to identify novel IHC markers and the best interpretation processes for the diagnosis of NENs. In doing so, this thesis primarily focuses on the quality of techniques, their validation as well as the objective interpretation of staining results, which could provide the best results for diagnosing and managing NEN patients.

The detailed aims were:

1. To identify novel and specific neuroendocrine markers by studying NPSR1 and its ligand NSP expression in a large cohort of different types of NENs.
2. To identify novel and specific neuroendocrine markers by studying PCSK2 expression in a large cohort of different types of NENs.
3. To test different SSTR clones and define the appropriate IHC protocol for SSTR1–5 subtype detection for different NENs.
4. To define a reproducible Ki-67 scoring for grading NENs.

## 4 MATERIAL AND METHODS

### 4.1 TUMOR MATERIAL

The tumor material was collected from the archives of the Department of Pathology (HUSLAB) at Helsinki University Hospital, and comprised primary NENs from 12 different primary sites and nine metastatic tumors.

In studies I, II, and III, we used a multi-NET TMA including tumors from 1997 through 2010. Additional tumor cohorts consisting of PHEOs and PGLs (collected 1995–2004) and pulmonary carcinoid tumors (collected 1990–2013) were used in study II. Study IV comprised a total of 51 pancreatic and small intestine NETs collected from 2003 through 2009. Histopathological diagnoses were confirmed from HE-, CGA-, and SYP-stained slides by an endocrine pathologist. Table 8 summarizes the demographic characteristics for the patients from whom tumor material was extracted.

**Table 8.** Tumor cohorts in studies I through IV.

ORIGIN OF TUMORS	N	GENDER (M:F)	AGE (IN YEARS)	STUDY
MULTI-NET TMA				
RECTUM	6	1:4	43–75	Studies I, II, and III
THYROID	5	2:3	29–59	
LUNG	16	4:12	35–85	
THYMUS	1	0:1	43	
APPENDIX	8	3:5	17–77	
SKIN	4	3:1	68–91	
SMALL INTESTINE	6	4:2	53–75	
PARATHYROID	5	1:4	19–78	
GASTRIC MUCOSA	8	4:4	49–87	
PANCREAS	13	4:9	23–77	
PHEOCHROMOCYTOMA	5	3:2	36–67	
PARAGANGLIOMA	5	2:3	45–82	
METASTASES	9	5:4	43–74	
Total	n = 91	n = 36:54		
ADDITIONAL TMA-TUMOR MATERIAL				
PHEOCHROMOCYTOMA	32	14:18	17–69	Studies II
PARAGANGLIOMA	4	3:1	31–48	
PULMONARY CARCINOIDS	38	18:21	19–84	
Total	n = 94			
WHOLE-SLIDE TUMOR MATERIAL				
SMALL INTESTINE	20	8:12	30–78	Studies II and IV
PANCREAS	31	9:22	12–79	Study IV
Total	n = 51			



## 4.2 TISSUE MICROARRAY

Representative tumor areas were annotated from HE slides to construct the multi-NET TMA (studies I, II, and III). Tumor tissue cores of 1-mm in diameter were taken using a semiautomated TMA instrument (Beecher Instruments, Silver Spring, MD, USA) from both the border and the middle area of each tumor. In total, six cores per tumor were extracted, comprising three parallel blocks with double punches. In study II, a pulmonary carcinoid-TMA block series was constructed with a TMA Grandmaster (3DHistech, Budapest, Hungary) covering 1-mm double punches from the outside, middle, and border of the tumor with a normal bronchus yielding seven punches per tumor sample.

## 4.3 IMMUNOHISTOCHEMISTRY

For IHC, 3- $\mu$ m-thick tissue sections were cut onto TOMO® adhesion microscope slides (Matsunami, Bellingham, WA, USA). Deparaffinization was completed in xylene followed by a graded-alcohol series or in the staining instrument with the EZ Prep buffer (Ventana, Tucson, AZ, USA) depending upon the IHC protocol. Standard protocols for stainings were based on biotin-free polymer detection kits: Envision (Agilent, Santa Clara, CA, USA), UltraVIEW or OptiVIEW DAB (Ventana, Tucson, AZ, USA). Depending upon the staining instrument, the Autostainer 480 (LabVision Thermo Scientific, Cheshire, UK) or the BechMark XT (Ventana, Tucson, AZ, USA), endogenous peroxidase was blocked with the Dako REAL Peroxidase-Blocking Solution (Agilent, Santa Clara, CA, USA) for 5 min or with the Inhibitor dispenser (Ventana, Tucson, AZ, USA) as part of the kit for 4 min before primary antibody incubation. Table 9 presents the detailed data on the primary antibodies we used.

**Table 9.** Details of the primary antibodies.

PRIMARY ANTIBODY	CATALOG NUMBER, SUPPLIER	CLONE	SPECIES	STUDY
Ki-67	M7240, Agilent	MIB-1	Mouse	I, II, and IV
NPSR1-A	Quattromed	CREQRSQDSRMTFRERTER*	Mouse	I
NPSR1-N	Quattromed	TEGSFDSSGTGQTLDSSPVA*	Mouse	I
NPS	Abcam	Polyclonal	Rabbit	I
SSTR1	MCA5924, AbDSerotec	sstr1	Mouse	III
	ab137083, Abcam	UMB7	Rabbit	
SSTR2	ab134152, Abcam	UMB1	Rabbit	III
SSTR3	MCA5921, Bio-RAD	sstr3	Mouse	III
	20696-1-AP, Proteintech Europe	Polyclonal	Rabbit	
	ab137026, Abcam	UMB5	Rabbit	
SSTR4	MCA5922, AbD Serotec	sstr4	Mouse	II
SSTR5	MCA5923, Bio-RAD	sstr5	Mouse	III
	ab109495, Abcam	UMB4	Rabbit	
PCSK2	HPA048851, Sigma-Aldrich	Polyclonal	Rabbit	II
Chromogranin A	A0430, Agilent	Polyclonal	Rabbit	I, II, and III
Serotonin	M0758, Agilent	5HT-H209	Mouse	II
Synaptophysin	Novocastra	27G12	Mouse	I and II

\* Syntetic peptide

In the Autostainer, the secondary antibody polymer was incubated for 30 min, while the DAB substrate mix (Agilent, Santa Clara, CA, USA) was incubated for 10 min at room temperature. Washes were completed using 1XPBS with 0.5% Tween 20 (Acros, Geel, Antwerp, Belgium) following incubation. Using the BenchMark XT, we incubated the secondary antibody for 8 min in the UltraVIEW DAB protocol and 8 to 12 min in the OptiVIEW DAB including incubations of different linkers. The DAB chromogen with the substrate and copper was incubated for 8 and 4 minutes, respectively. Washes were completed using the Reaction Buffer (Ventana, Tucson, AZ, USA) according to the instrument's instructions. The slides were counterstained with Mayer's hematoxylin (Lillie's Modification; Agilent, Santa Clara, CA, USA) and mounted with the Eukitt® quick-hardening mounting medium (Sigma-Aldrich, Saint Louis, MO, USA).

### 4.3.1 SPECIFICITY STUDIES OF PRIMARY ANTIBODIES

#### 4.3.1.1 *Neuropeptide S receptor 1*

The epitope specificity of NPSR1-A and NPSR1-N primary antibodies (study I) were analyzed using the recombinant NPSR1 protein. The recombinant protein fused with either red (NPSR1-A-pDsRed) or green (NPSR1-B-GFP) fluorescent protein was transfected with the COS-7 (African green monkey kidney fibroblast) cell line. This cell line was grown in Dulbecco's modified Eagle's medium containing (DMEM) GlutaMAX-I (Invitrogen), fetal bovine serum (FBS), and 100 U/ml penicillin together with 100 mg/ml streptomycin in a humid +37°C incubator. After 24 h of seeding,  $4-5 \times 10^4$  cells on 24-well plates were transfected with recombinant full-length NPSR1 constructs fused with either pDsRed or GFP fluorescent protein. Incubation followed fixation with 4% paraformaldehyde. The cell lines for the NPSR1-A antibody staining were permeabilized with 0.1% Triton X-100 in 1XPBS. The cells for NPSR1-N staining remained untreated. Primary antibodies were incubated for 1 h. Binding of the primary antibodies were visualized after washes with secondary antibodies labeled with either green (FITC) or red (TRITC) tags, respectively. Colocalization was examined using a conventional fluorescent microscope. A yellow color in the overlay images indicated the colocalization of protein and antibodies.

The epitope specificity of the NPSR1 antibodies was also analyzed with 10% SDS-PAGE and bacterial lysate immunoblots. NPSR1-A and NPSR1-N fragments expressed pGEX 4 T-3 glutathione-S-transferase (GST) and dihydrofolate reductase (DHFR). Monoclonal antibodies against C-terminus and N-terminus expressed a band of the correct molecular size.

#### 4.3.1.2 *Proprotein convertase subtilisin/kexin type 2*

The specificity of the PCSK2 antibody (study II) was confirmed using Western blot analysis of fresh-frozen PHEOs stored at -70°C. The tissue was homogenized and lysed with an LSB buffer (Bio-Rad, Hercules, CA, USA) and titrated to volumes of 2 µl, 5 µl, and 10 µl. The tissue homogenate was subjected to 10% SDS-PAGE and immunoblotted onto the Immobilon-FL Transfer Membrane (Merck Millipore, Burlington, MA, USA). The blots were incubated overnight at +4°C with PCSK2 (Sigma-Aldrich, Saint Louis, MO, USA), diluted to 1:1000, followed by the Alexa Fluor 680-conjugated secondary goat anti-rabbit antibody (1:10 000), and enhanced with Odyssey (LI-COR Biosciences, Lincoln, NE, USA) for chemiluminescence detection. PCSK2 revealed a clear band migrating at an expected size of 70 565 Da.

**Table 10.** Scoring criteria.

NPSR1-A, NPSR1-N & NPS STUDY I	PCSK2 & SSTR5 STUDIES II, III	SSTR5 STUDY III	Ki-67 STUDY IV
Cytoplasmic / Membranous	Cytoplasmic	Membranous	PI from "hot spots"
0 = No staining	0 = No staining	0 = No staining	<2% (G1)
1 = Mild	1 = Mild	1 = Weak (<10%)	2–20% (G2)
2 = Moderate	2 = Moderate	2 = Weak to moderate (≥10%)	>20% (G3)
3 = Strong	3 = Strong	3 = Moderate to strong	
		4 = Strong, complete circumferential (>95%)	

#### 4.3.1.3 Somatostatin receptors

The validation of different SSTR clones (study III) was based on the assessment of the staining profile of normal NE cells in the small intestine and pancreas. Different pretreatment buffers (Tris-EDTA pH 9.0, citrate pH 6.0, CC1), antibody dilutions (1:50–1:7000), primary antibody incubation times (30–60 min), detection systems (Envision, UltraVIEW DAB, and OptiVIEW DAB), and staining platforms (LabVision and BenchMark XT) were tested. The criteria for acceptable staining results included the correct staining pattern and the cellular location in the positive control tissues according to the reviewed literature with no or minimal background staining.

#### 4.3.2 SCORING

Two different researchers independently scored samples in each study, whereby we selected the highest consensus score for statistical analysis. We considered scores of 2 to 4 for a membranous pattern (study III) and intensity levels of 2 and 3 for cytoplasmic staining (study II, III) as appropriate. The serotonin staining (study II) was interpreted as positive or negative. Table 10 describes the scoring criteria.

Ki-67 (in study IV) was assessed conventionally according to the WHO 2010 guidelines using microscopic manual counting. Hot spots were chosen and at least 500 to 2000 cells were counted. The tumor material was reassessed independently by one person. The reassessed PI values and corresponding tumor grades were compared to the original values. Any variation in the conventional assessment practice between the two observers was evaluated blindly from a series of 20 tumors. The observers chose the hot spots independently.

### 4.3.3 IMMUNORATIO

The Ki-67 PI (studies I, II, and IV) was assessed using the image analysis software ImmunoRatio ([jvsmicroscope.uta.fi/immunoratio/](http://jvsmicroscope.uta.fi/immunoratio/)). Digital images were taken with a Nikon Eclipse 80i light microscope (40x objective) connected to a Digital Sight DS-5M (Nikon) digital camera and the NIS-Elements F 3.0 image capture software. In studies I and II, one digital image (JPEG format, resolution 1280 x 960 pixels) was captured from every tumor tissue core from the most proliferative area covering 50% of the core. In study IV, five different image fields were captured as digital images (JPEG format, resolution 1280 x 960 pixels) from the hot spots of each tumor covering a total of 2000 cells. A blank field image was included for each capture round to balance the uneven illuminations in the final digital images. Using ImmunoRatio's Advanced Mode setting, threshold values for studies I and II (hematoxylin -10 and DAB 10) and study IV (hematoxylin +10 and DAB -30) were adjusted without a correction equation. We used consistent settings in the image analysis after light exposure (manual exposure, 10 ms, gain 1) and the thresholds were considered adequate.

## 4.4 NEUROPEPTIDE S INDUCTION OF CANCER-RELATED PATHWAYS IN THE SH-SY5Y CELL LINE

We used the human neuroblastoma cell line (SH-SY5Y) to study the downstream targets of the NPS–NPSR1 signaling pathway (study I) using the HGUI133plus2 Array (Affymetrix). The SH-SY5Y cells were placed in the DMEM-GlutaMAX-I incubation medium with FBS, 100 U/ml penicillin, and 100 mg/ml streptomycin at +37°C in a humid incubator. Cells were transfected with NPSR1-A-GFP plasmid using the FuGENE reagent (Roche) and stable clones were selected with 500 µg/ml G418. The RNA was extracted using the RNeasy® Plus Mini Kit (Qiagen) and the cDNA was synthesized with TaqMan Reverse Transcription Reagents (Biosystems). Then, 100 nM NPS-treated cells were compared to untreated cells. We also compared the parental SH-SY5Y cells with and without NPS treatment. Upregulated genes for the transcripts of the MAPK pathway were studied using real-time quantitative PCR for time course and dose responsiveness.

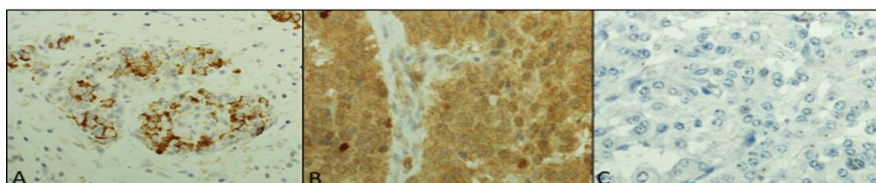
## 4.5 STATISTICAL ANALYSIS

In studies I and IV, correlations between the marker expression and the Ki-67 PI and PI values across different assessment methods were analyzed using two-tailed tests and the Pearson's correlation ( $r$ ). In study IV, the Cohen's kappa ( $\kappa$ ) was calculated to evaluate the agreement of the tumor grade across different assessment conditions. In study II, the Fisher's exact test was used to study the correlations between the tumor origin and marker expression. We considered  $p < 0.5$  (study I),  $p < 0.001$  (study II), and  $p < 0.01$  (study IV) as statistically significant. Statistical analyses were performed using IBM's SPSS version 17.0 (SPSS Inc., Chicago, IL, USA).

## 5 RESULTS

### 5.1 NEUROPEPTIDE S RECEPTOR 1 AND NEUROPEPTIDE S EXPRESSION IN NEUROENDOCRINE TUMORS (STUDY I)

In study I, NPSR1 and NPS were widely expressed in normal NE cells and NENs from various origins (Figure 16). Normal NE cells of the small intestine and islet cells of the pancreas expressed NPSR1. The majority of NENs expressed NPSR1 and NPS. That is, gastric, small intestine, appendicular, rectal, pancreatic, pulmonary, and thymic NENs as well as parathyroid adenomas and carcinomas, medullary carcinomas, and PGLs showed a strong reactivity to NPSR1-N, NPSR1-A, and NPS. All markers were negative or weakly positive in PHEOs. Colon adenocarcinomas were negative for NPSR1. Table 11 summarizes the NPSR1 staining in NENs.



**Figure 16.** Pancreatic islets (A) expressed neuropeptide S receptor 1 (NPSR1). Most neuroendocrine neoplasias (NENs) were positive for NPSR1, including pancreatic NENs (B), although paragangliomas (C) were negative.

In metastatic NENs, the expressions of NPSR1-N and NPSR1-A were similar between primary tumors and metastatic tumors. G1 through G3 tumors of the pancreas and small intestine exhibited similar expression levels of NPSR in primary tumors and in corresponding metastases.

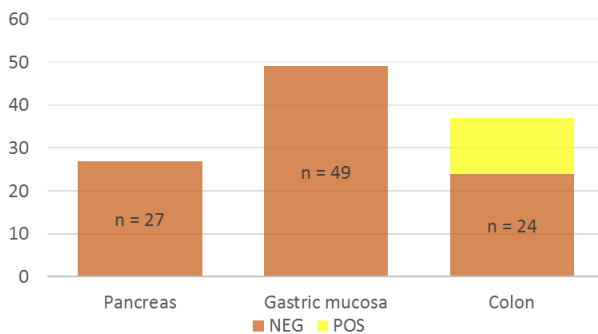
NPSR1 antibodies showed epitope specificity in the immunoblot and fluorescent studies. Immunoblotting with NPSR1 fragments in the bacteria lysate indicated that antibodies recognized the correct size epitopes. The colocalization of the expressed green fluorescent NPSR1 fusion protein with TRITC-labelled anti-NPSR1-N suggested that the full-length NPSR1 protein was recognized by the NPSR1-N antibody. FITC-labelled anti-NPSR1-A colocalized with the red fluorescent NPSR1 fusion protein exhibiting antibody binding to the full-length NPSR1 protein.

NPS-treated SH-SY5Y cells yielded an upregulation of 552 and downregulation of 184 transcripts with 1.25 and 0.75 cut-offs, respectively. The upregulated genes belonged primarily to the MAPK pathway, circadian activity, focal adhesion, transforming growth factor  $\beta$ , and cytokine–cytokine interactions. The expression of the MAPK pathway genes (GADD45A–MYC and NR4A1–NFKB1) peaked at 3 h and 6 h, respectively. NPS treatment of the parental SH-SY5Y induced minor changes in the gene expression due to endogenous NPSR1.

## 5.2 THE EXPRESSION OF PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 2 (STUDY II)

In study II, we found PCSK2 expression (Table 11) mainly in midgut NENs (12/12), PHEOs (4/5), and PGLs (3/5), as well as in some typical and atypical pulmonary carcinoids (4/8). NENs from the thymus, gastric mucosa, pancreas, rectum, thyroid, and parathyroid were negative. Using an additional tumor cohort, PCSK2 was positive in 20/20 small intestine NENs, 13/19 typical and 9/19 atypical pulmonary carcinoids, 24/32 PFEOs, and 3/4 PGLs. The results across these two different staining rounds were similar.

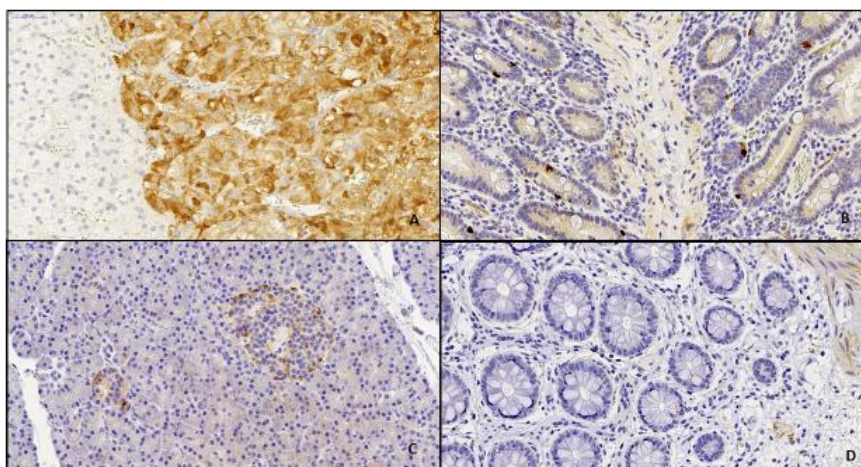
The expression level of PCSK2 in metastatic NENs was comparable to the level found in the primary tumor. Pulmonary carcinoids (n = 5) and a small intestine NEN (n = 1) that were strongly PCSK2 positive exhibited a strong positivity in the corresponding metastatic tumors as well, whereas pulmonary carcinoids (n = 6) and pancreatic NENs (n = 4) that were PCSK2 negative exhibited negative staining in metastatic tumors. None of the pancreatic or gastric adenocarcinomas stained with PCSK2, but one-third of the colon adenocarcinomas were positive for PCSK2 (Figure 17).



**Figure 17.** Proprotein convertase subtilisin/kexin type 2 positivity in adenocarcinomas of the pancreas, gastric mucosa, and colon.



The validity of the PCSK2 primary antibody was confirmed in normal NE cells (Figure 18). The NE cells of the small intestine and adrenal medulla were strongly positive for PCSK2. The gastric, bronchial, thyroid C cells, and pancreatic islet cells were positive, but at a lower intensity. The NE cells of the large intestine were negative. Table 11 summarizes the PCSK2 staining for different NENs.



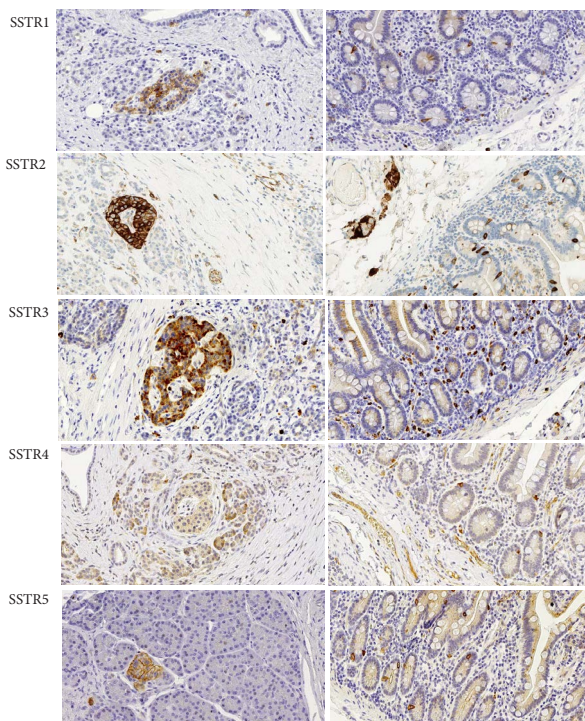
**Figure 18.** Proprotein convertase subtilisin/kexin type 2 expression in the normal A) adrenal medulla, B) small intestine, C) pancreas, and D) rectum. Objective: 40x.

**Table 11.** Immunohistochemical expression of neuropeptide S receptor 1 (NPSR1) and proprotein convertase subtilisin/kexin type 2 (PCSK2) in NENs of different origins.

TUMOR LOCATION	NPSR1	PCSK2
LUNG	POS (+)	+
THYMUS	+	NEG (-)
GASTRIC MUCOSA	+	-
PANCREAS	+	-
APPENDIX	+	+
SMALL INTESTINE	+	+
RECTUM	+	-
THYROID	+	-
PARATHYROID	+	-
ADRENAL MEDULLA	-	+
PARAGANGLIA	+	+
SKIN	+	-

### 5.3 DESCRIPTION OF SOMATOSTATIN RECEPTOR CLONES AND THEIR EXPRESSION IN DIFFERENT NEUROENDOCRINE TUMORS (STUDY III)

In study III, SSTR1 clones sstr1 and UMB7, SSTR2 clone UMB1, SSTR3 clone UMB5, SSTR4 clone sstr4, and SSTR5 clones sstr5 and UMB4 demonstrated the expected staining patterns (membranous and cytoplasmic) and tissue locations (small intestine NE cells and the islet of Langerhans) using standard protocol settings (Figure 19). However, the polyclonal SSTR3 primary antibody and clone sstr3 did not yield the appropriate staining pattern or localization in the positive and negative control tissues. The UMB clones (UMB7, UMB1, UMB5, and UMB4) showed clear membrane positivity and localization in the positive control tissues. The clones sstr1, sstr4, and sstr5 exhibited the expected staining in the correct cell types, but at a weaker intensity than the corresponding rabbit monoclonal. The polyclonal SSTR3 antibody and the clone sstr3 yielded an overall nonspecific staining in the control tissues. The UMB clones were considered preferable clones for the SSTR staining.



**Figure 19.** Somatostatin receptor (SSTR) clone validation for positive normal tissue controls, where the pancreas (left column) and the small intestine (right column) indicated the correct tissue localization of SSTRs in normal tissue.

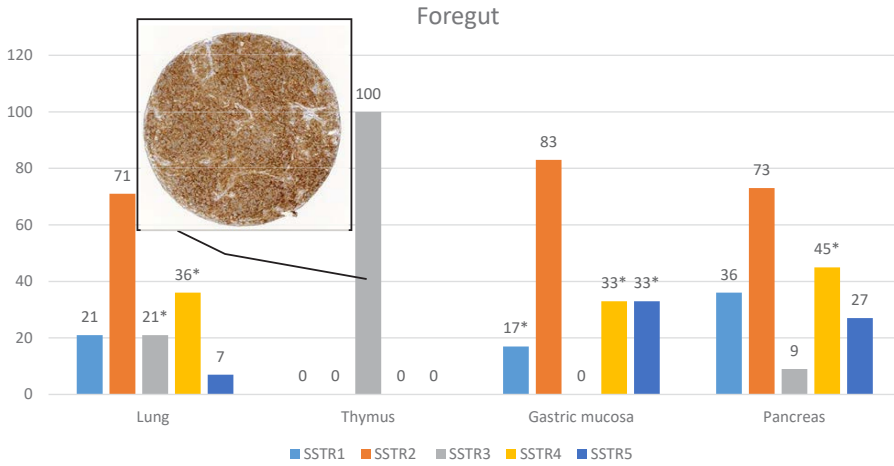
Table 12 shows the overall SSTR positivity (including membranous and cytoplasmic positivity) in NENs using the UMB clones and sstr4.

**Table 12.** Immunohistochemical expression of somatostatin receptor (SSTR) subtypes in neuroendocrine neoplasms (NENs) of different origins. Results are shown as a percentage of overall positivity.

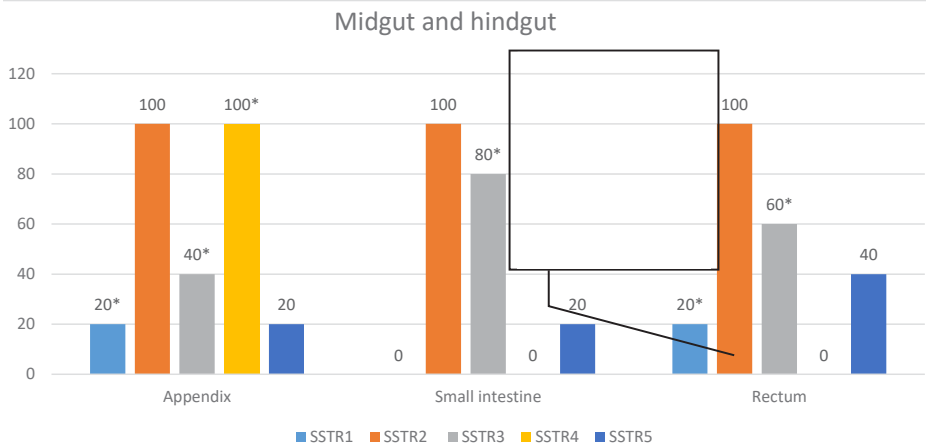
NEN	SSTR1 (UMB7) %		SSTR2 (UMB1) %		SSTR3 (UMB5) %		SSTR4 (sstr4) %		SSTR5 (UMB4) %	
	Membrane	Cytoplasmic	Membrane	Cytoplasmic	Membrane	Cytoplasmic	Membrane	Cytoplasmic	Membrane	Cytoplasmic
Pulmonary NENs (n = 14)	21.4	21.4	71.4	57.1	0	21.4	0	35.7	7.1	0
Thymic NEN (n = 1)	0	0	0	0	100	100	0	0	0	0
Gastric mucosal NEN (n = 6)	0	16.6	83.3	83.3	0	0	0	33.3	0	33.3
Pancreatic NENs (n = 11)	36.6	63.6	72.7	72.7	9	45.4	0	45.4	27.2	18.2
Appendicular NENs (n = 5)	0	20	100	100	0	40	0	100	20	20
Small intestine NENs (n = 5)	0	0	100	100	0	80	0	0	20	0
Rectal NENs (n = 5)	0	20	100	100	0	60	0	0	40	60
Medullary carcinomas (n = 5)	20	60	20	20	0	60	0	0	20	40
Parathyroid adenomas and carcinomas (n = 5)	0	0	0	0	0	0	0	20	0	0
PHEOs (n = 5)	0	0	60	40	20	100	0	0	0	20
PGLs (n = 5)	20	20	80	80	20	100	0	0	0	0
Merkel cell carcinoma (n = 4)	0	0	100	50	0	0	0	25	0	0

Figures 20 through 22 summarize the SSTR staining in different NENs, with the results shown as the highest percentage of membranous positivity. If membranous positivity was not detected, the corresponding percentage of cytoplasmic is shown in Figures 20, 21, and 22. In NENs, SSTR2 was the most commonly detected receptor followed by SSTR5, SSTR1, SSTR3, and SSTR4.

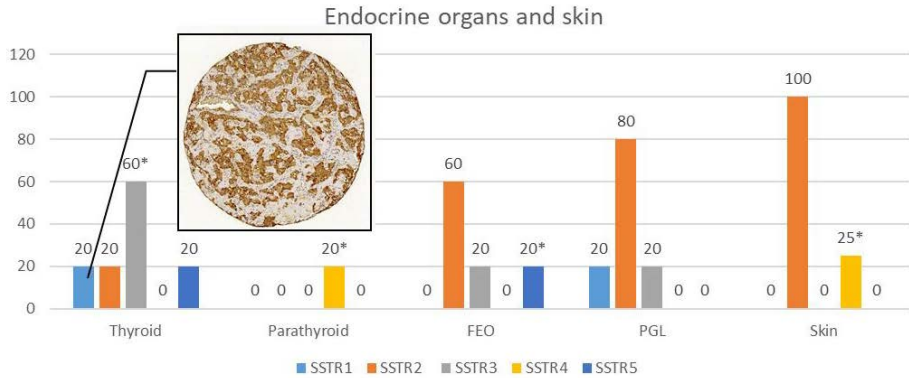
5 RESULTS



**Figure 20.** Percentage of highest somatostatin receptor (SSTR) positivity in foregut NENs. The insert shows an image of SSTR3 staining. \*Indicates cytoplasmic positivity.



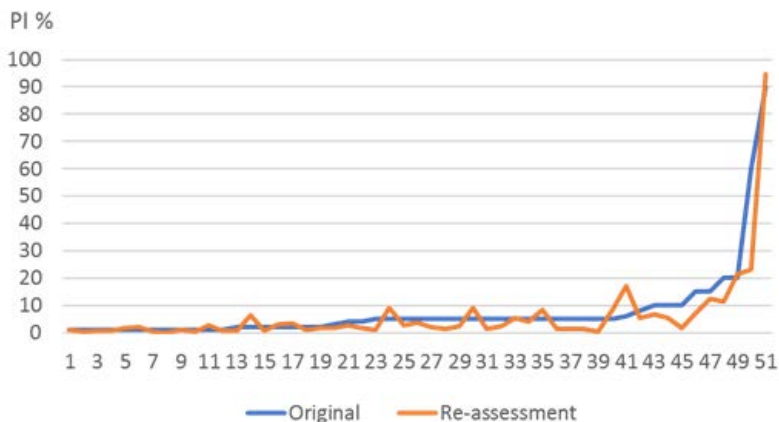
**Figure 21.** Percentage of the highest somatostatin receptor (SSTR) positivity in midgut and hindgut NENs. The insert shows an image of SSTR2 staining. \*Indicates cytoplasmic positivity.



**Figure 22.** Percentage of the highest somatostatin receptor (SSTR) positivity in NENs from endocrine organs and skin. The insert shows an image of SSTR1 staining. \*Indicates cytoplasmic positivity.

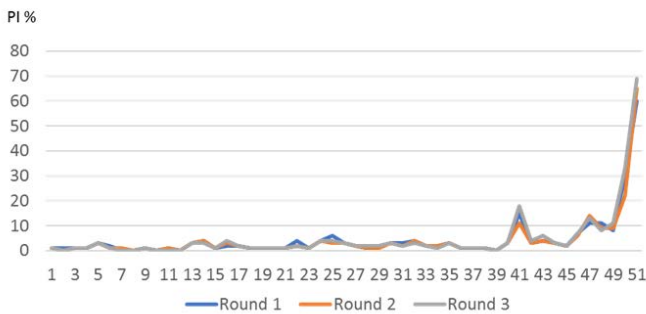
#### 5.4 ASSESSMENT OF THE PROLIFERATION INDEX (STUDY IV)

In study IV, the conventional assessment of PI by eyeballing for the same tumor varied between the different pathologists, the PI values taken from the original pathology reports, and the reassessment by one observer. The PI values were significantly different yielding moderate coherence in the tumor grading ( $\kappa = 0.373$ ;  $p = 0.000$ ; Figure 23). When two observers blinded to one another assessed the same tumors ( $n = 20$ ), the variation in PI was smaller compared to the differences detected in the re-evaluation of the original PI, demonstrating a good correlation between observers ( $p < 0.001$ ) with a high agreement in grading ( $\kappa = 0.662$ ;  $p = 0.000$ ; data not shown).

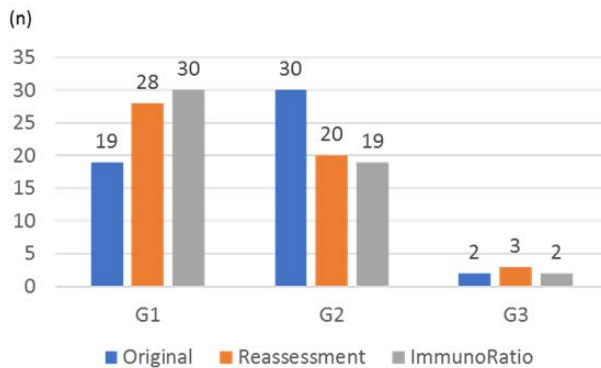


**Figure 23.** Variation of proliferation index (PI) between conventional assessments of Ki-67 in 51 neuroendocrine neoplasias. Original values are from pathology reports. The reassessment was completed by one observer.

The PI assessment using ImmunoRatio was highly reproducible in the three repeated assessments, with the standard PI values correlating ( $r = 0.985$ ,  $r = 0.987$ , and  $r = 0.995$ ;  $p < 0.001$ ) and the coefficients of variation (CV = 2.08, 2.26, and 2.27) in repeated series (Figure 24). Tumor gradings using ImmunoRatio were also quite similar ( $\kappa = 0.886$ ,  $\kappa = 0.886$ , and  $\kappa = 1.000$ ;  $p = 0.000$ ). The differences in grades were mainly between G1 and G2 rather than between G2 and G3 for all assessment methods. The ImmunoRatio PI values were close to those analyzed by a qualified observer in a conventional manner. Conventional and ImmunoRatio assessments (mean PI value of three independent assessment rounds) conducted by the same person were in good agreement ( $r = 0.969$ ;  $p < 0.001$ ; Figure 25).



**Figure 24.** Reproducibility of the proliferation index (PI) in repeated assessment of Ki-67 in ImmunoRatio for 51 neuroendocrine neoplasias.



**Figure 25.** Grading across different assessments for 51 neuroendocrine tumors.

## 6 DISCUSSION

### 6.1 TISSUE MICROARRAY IN STUDY OF NEUROENDOCRINE NEOPLASIAS

#### *(Studies I-IV)*

Tumors of an NE origin appear in various organs due to the disseminated NE cell system (Rekhtman 2008), yet NENs are considered a rare tumor entity. The study of rare tumors is challenging. Constructing a TMA using technology, including automated tissue microarraying and digitalization, carries multiple advantages when studying these rare tumors and novel markers (Zlobec et al. 2014). Therefore, this thesis includes studies using TMA material constructed from a broad spectrum (n = 91) of well-documented NENs from 12 different primary tumor origins including metastatic pairs. Typically, NEN studies have included only a few NEN locations (Qian et al. 2016, Zhao et al. 2019) or a moderate number of tissue cores in a TMA (Schmid et al. 2012, Qian et al. 2016, Bellizzi 2020). Our study setting enabled the simultaneous and comparative analysis of NENs arising from different primary sites in order to examine their expression of potential biomarkers. Although TMAs are efficient for large-scale screening research, a problem persists in the representativeness of the antigen expression in TMA spots. In this NEN cohort, six to seven parallel tissue cores were analyzed from the same NEN to improve the representativeness of the samples (Elfving et al. 2019). In addition, interesting findings were re-evaluated with larger tumor cohorts.

### 6.2 VALIDATION OF IMMUNOHISTOCHEMICAL MARKERS

#### *(Studies I-III)*

In modern surgical pathology, the use of IHC remains crucial. IHC is used for tumor typing, and the classification of tumor subtypes and malignancies of an unknown primary origin (Conner and Hornick 2015), as well as demonstrating prognostic and predictive markers (Wolff et al. 2018). When new IHC markers are studied, the verification and validation of the primary antibodies and detection reagents used remain important (Matos et al. 2010). A lack of technical standardization represents an observable challenge in diagnostic pathology (Howat et al. 2014, Cheung et al. 2016).

Ideally, validation analyses should include tissue known to express the target antigen as well as tissue devoid of the antigen in question (Burry 2011, Torlakovic et al. 2014, Torlakovic et al. 2015). In our studies, we used normal tissues from the organs from whence the tumor cohort NENs originated. In study I, control specimens from the small intestine and pancreas showed NPSR1 receptor positivity in NE cells as previously stated (Sundman et al. 2010). Our results regarding NPSR1 expression confirm that receptors are also expressed in non-inflamed human NE tissues. In study II, PCSK2 positivity localized to the cytoplasm of NE cells similar to previous descriptions by Portela-Gomes et al. (2008) and Scopsi et al. (1995). This indicates that the polymer-based detection of the protein localizes the enzyme correctly according to its biological nature (Portela-Gomes et al. 2004). In the normal tissue material, consisting of the bronchus, gastric mucosa, pancreas, small intestine, colorectum, thyroid C cells, and adrenal medulla, the intensities of the PCSK2 expression varied between different NE cells. Perhaps the staining intensity of PCSK2 relates to the presence of the enzyme in these cells. As Portela-Gomes et al. (2008) showed, PCSK2 expression varies in the islet of Langerhans; PCSK2 is present in insulin cells, glucagon cells, and somatostatin cells, but absent in pancreatic polypeptide cells (Portela-Gomes et al. 2008).

### ***Primary antibody validation of somatostatin receptor clones (Study III)***

NEN patients with proper SSTR expression profiles benefit from SSA therapy (Gatto et al. 2013, Pokuri et al. 2016) and radio-labeled SSA imaging (Pauwels et al. 2018, Vitale et al. 2018). The therapy of NEN patients using SSA relies on the membrane expression of SSTRs (Theodoropoulou and Stalla 2013, Kanakis et al. 2015). Many studies have found a correlation between IHC and autoradiography (Körner et al. 2005, Körner et al. 2012), scintigraphy (Diakatou et al. 2015), and PET/CT (Kaemmerer et al. 2011). The evaluation of SSTRs using IHC compares favorably to PET/CT (Miederer et al. 2009, Kaemmerer et al. 2011).

Study III aimed to validate the staining protocols for commercially available SSTR clones and to identify the most favorable protocol settings for each clone. SSTRs are transmembrane protein receptors pointing to a membranous staining pattern in IHC (Reubi 2014). Our validation of the SSTR primary antibodies indicated a specific and correct location in the small intestine NE cells, the islet of Langerhans, and the nerves, similar to findings from earlier studies (Reubi et al. 2001, Fischer et al. 2008, Lupp et al. 2011, Lupp et al. 2012, Lupp et al. 2013). SSTR antibodies showed both membranous and cytoplasmic staining as previously described (Reubi et al. 2001, Fischer et al. 2008, Lupp et al. 2011, Lupp



et al. 2012, Schmid et al. 2012, Lupp et al. 2013, Elston et al. 2015, Kaemmerer et al. 2015). However, the membranous staining pattern depended upon the clone used. We found that UMB clones were more likely to detect membrane positivity in SSTRs. Polyclonal antibodies were suboptimal due to the background staining. The differences between clones could be explained through antibody production methods. The monoclonal antibodies have a higher specificity because of the hybridoma production method (Spieker-Polet et al. 1995, Saper 2009, Buchwalow and Böcker 2010). Polyclonal antibodies, on the other hand, are produced by the immunization of the production animal (Saper 2009, Buchwalow and Böcker 2010). In addition, according to our study, mouse monoclonal antibodies showed membranous but less intense staining compared to rabbit monoclonal antibodies. Rabbit monoclonal antibodies have a demonstrably higher affinity than the mouse monoclonal (Huang et al. 2006, La Rosa et al. 2010, Weber et al. 2017), possibly explaining the visible correct but less intense membranous staining pattern for SSTRs.

SSTRs are internalized after the ligand binds to the receptor (Jacobs and Schulz 2008, Waser et al. 2009, Csaba et al. 2012). The cytoplasmic staining observed in SSTRs (Schmid et al. 2012, Elston et al. 2015, Kaemmerer et al. 2015) may result from the ligand-induced internalization of the receptors (Reubi et al. 2010). In addition, given the ability of antibodies to crossreact between different epitopes (Saper 2009), hypothetically different SSTR clones (Fischer et al. 2008, Righi et al. 2010, Lupp et al. 2011, Körner et al. 2012, Lupp et al. 2012, Schmid et al. 2012, Lupp et al. 2013) may react differently to internalized receptors or differentially recognize epitope-like structures in the cytoplasm, thereby explaining the cytoplasmic reactions of SSTR antibodies.

NENs originating from different organs feature varying SSTR subtype profiles. SSTR2 is the most universally expressed subtype, followed by SSTR5, SSTR1, SSTR3, and SSTR4 (Reubi et al. 2001, Hankus and Tomaszewska 2016) as demonstrated in our work as well. The evidence for IHC's suitability to evaluate the SSTR profile in NENs (Körner et al. 2005, Miederer et al. 2009, Kaemmerer et al. 2011, Körner et al. 2012, Diakatou et al. 2015) underscores the need for the verification and validation of the SSTR primary antibodies (Matos et al. 2010, Howat et al. 2014, Cheung et al. 2016). Thus, the IHC analysis of SSTRs to predict patients' suitability for SSA therapy is possible, however, only if the technical requirements for IHC are prioritized (Torlakovic et al. 2017).

### **6.3. NEUROPEPTIDE S RECEPTOR 1 AND NEUROPEPTIDE S IN NEUROENDOCRINE NEOPLASIAS (STUDY I)**

Not all NETs express conventional NE markers, despite the histopathology presenting NE-type features (Gut et al. 2016, Perren et al. 2017). The differential diagnosis of NEN may be difficult, particularly for poorly differentiated NECs, small biopsies, or cytological samples (Schmitt et al. 2016, Fujino et al. 2017). In this thesis, we aimed to identify NE-specific markers. Previously, the G-protein coupled receptor NPSR1 was found to express in the NE cells of the GI tract (Sundman et al. 2010). In study I, the majority of NENs widely expressed NPSR1 and its ligand NPS, with only PHEOs emerging as an exception. Both the N-terminal and C-terminal antibodies of NPSR1 yield the same staining result. Furthermore, the staining of the receptor and ligand NPS recognized the same NENs. This observation supports Sundman et al. (2010), who showed that the NPS expression pattern mirrored NPSR1. According to our tumor cohort, widely expressed NPSR1 or NPS could serve as a general NE marker, excluding tumors with a PHEO origin.

Earlier studies found that NPS stimulated the growth of Colo205 human colon cancer cells (Reinscheid et al. 2005). In our work, we sought to study the role of NPS in tumorigenesis. NPSR1-transfected SH-SY5Y neuroblastoma cells were stimulated with NPS, revealing the expression of many genes in different signaling pathways, especially genes of the MAPK pathway. We detected an abundant IHC expression of NPSR1 in most NENs, except in PHEOs. Thus, the potential activation of intracellular signaling pathways may be relevant to malignant behavior in NENs. PHEOs are potentially malignant tumors and histological indicators of their metastatic behavior remain limited (Tischler et al. 2017). The lack of NPSR1 expression in PHEOs may be partly related to the benign behavior of these tumors, since they may not link to NPS stimulation with gene activation, which is relevant to tumorigenesis.

### **6.4 PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 2 EXPRESSION INDICATES A NEUROENDOCRINE TUMOR ORIGIN (STUDY II)**

Tumor markers and organ-specific markers represent transcription factors (Goto et al. 1992, Koo et al. 2012, Li et al. 2015, Schmitt et al. 2016, Zhao et al. 2019), naturally occurring proteins (Perren et al. 2017), or structural components (Gerdes et al. 1991) of a given cell type. PCSK2 is part of the NE secretory granules (Portela-Gomes et al. 2004, Seidah et al. 2011). A few earlier studies

have speculated the role of PCSK2 as a marker for NENs (Scopsi et al. 1995, Kajiwara et al. 1999, Kimura et al. 2000, Tomita 2001). In our NEN material, we found a strong cytoplasmic PCSK2 positivity in midgut NENs, PHEOs, and PGLs as well as in half of the typical and atypical pulmonary carcinoids. NENs from other organs such as the thymus, gastric mucosa, pancreas, and colorectum did not express PCSK2. These findings agreed with previous studies (Scopsi et al. 1995, Kajiwara et al. 1999, Kimura et al. 2000, Tomita 2001). According to our results, however, thyroid medullary carcinomas were PCSK2 negative unlike previous reports, although the expression in parathyroid adenomas and carcinomas was comparable (Scopsi et al. 1995, Kajiwara et al. 1999).

Technical factors may explain these differences in the staining results. The antigen morphology changes during tissue fixation (Hladik and White 2008, Buchwalow and Böcker 2010, Meyer and Hornickel 2010). Part of the tumor material used in Scopsi's (1995) study was fixed in a Bouin fixative carrying both coagulating and cross-linking effects on proteins (Grizzle et al. 2008), unlike our formalin-fixed tumor material. The streptavidin-biotin technique (Hsu et al. 1981) was widely used before the introduction of polymer techniques (Kammerer et al. 2001). Diverging from Scopsi et al. (1995) and Kajiwara et al. (1999), we employed a polymer-based detection system (Sabattini et al. 1998), eliminating the characteristic problems of biotin (Buchwalow and Böcker 2010). Finally, all PCSK2 studies including ours used a polyclonal antibody. Repeated production of a polyclonal primary antibody against the same antigen will provide unique combinations of antibody clones in the serum, leading to an antibody content that may differ (Saper 2009), albeit polyclonal antibodies are good in detecting a low expression level or heterogeneous antigens (Acharya et al. 2017).

The primary tumor location of the NEN influences patient management (Alexandraki et al. 2017, Chan et al. 2017). Tissue-specific markers for the detection of NENs of an unknown origin remain valuable (Schmitt et al. 2016). PCSK2 is an endogenous proteolytic enzyme of NE cells, activating and cleaving prohormones arising in a number of biologically active peptides (Doblinger et al. 2003, Portela-Gomes et al. 2004, Portela-Gomes et al. 2008). We found that the primary tumor exhibited similar PCSK2 staining profiles as the corresponding metastatic tumor. Thus, PCSK2 positivity indicates a NEN tumor arising in the small intestine, appendix, lungs, or adrenal medulla, and paraganglions. Furthermore, the expression of PCSK2 did not associate with the NEN grade. Other studies have identified similar correlations between Ki-67 and PCSK2 (Iino et al. 2010). These may stem from the stability of PCSK2 as an antigen sustaining its expression in tumor differentiation. Yet, PCSK2 is an integral part of dense-core granules (Portela-Gomes et al. 2004). Because the staining

intensity of CGA depends on the amount of granules in the tumor cells (Gut et al. 2016), PCSK2 expression may vary also depending upon the number of granules.

## 6.5 ASSESSMENT OF THE PROLIFERATION INDEX (STUDY IV)

In the most recent WHO guidelines for endocrine organs published in 2017 and digestive system tumors released in 2019, Ki-67 is used as the key determinant for NEN grading (Klöppel et al. 2017b, Klimstra et al. 2019). NENs are divided into two groups according to their morphology: 1) well-differentiated NENs, grades G1 through G3 depending on their Ki-67 PI and/or the number of mitosis; and 2) poorly differentiated NENs, namely, NECs, which are high grade by definition (Cavalcanti et al. 2016). A well-known challenge in Ki-67-based PI assessment is the subjective interpretation that causes inter- and intraobserver variation (Klimstra et al. 2010). We also illustrated the pitfalls of the conventional assessment of proliferation via eyeballing. Variations in conventional PI assessment can be explained in several ways. The most important factors consist of the experience and competence of the pathologist, the choice of hot spots, and the quality of IHC along with the interpretation of the staining outcome.

The assessment of Ki-67 should be based on a more accurate and reliable method than subjective visual estimation (Reid et al. 2015). Different image analysis software (Roge et al. 2016, Bankhead et al. 2017, Koopman et al. 2018, Acs et al. 2019) and supervised machine learning (Luo et al. 2017, Valkonen et al. 2020) can assist in quantitative pathology (Niazi et al. 2019). Digitalized slides together with image analysis are suitable for diagnostics (Snead et al. 2016, Mukhopadhyay et al. 2018). To demonstrate this, we used a cohort of GEP-NETs and online image analysis software, ImmunoRatio. ImmunoRatio and eyeballing assessments of PIs yielded comparable PI values, supporting the suitability of image analysis for clinical use. The strengths of such image analysis tools include their user-friendliness, speed, and objectivity (Aeffner et al. 2019). In repeated rounds of assessment, ImmunoRatio yielded comparable grades. The low PI values determined between G1 and G2 were the most prone to errors. If correctly used, image analysis is better than conventional human assessment for determining the proliferation activity of NETs.

## 6.6 STRENGTH AND LIMITATIONS OF THE STUDY

In this thesis, we constructed a broad-spectrum TMA platform of well-characterized NE tumors including NENs from 12 different primary locations with various grades together with primary tumor–metastases pairs. During a metastatic event, tumor cell populations may differ from those of the primary tumor. Having tumor material from both the primary and metastatic tumor cell populations makes it possible to study both the differences and similarities between these populations. Using NENs from different anatomical sites and grades provided a solid overview of the expression of markers and their possible expression patterns among NENs.

The proper validation of the markers studied given current knowledge renders the assessment of expression profiles more reproducible. Combining these technical aspects to image analysis and their standardization increases the objectivity and reproducibility of NEN diagnostics.

Given these strengths, this study also carries limitations, including the use of TMAs compared to whole slides, which possibly excluded some tumor areas. However, using many parallel multiple tissue cores from the same tumor area limits the sampling error. In addition, the low number of G3 tumors may have biased the grade variation analysis. However, recognizing the rarity and infrequent operations involving NEC tumors, the option to use these tumors for research remains limited. The availability of the offered antibody clones of SSTR4 was restricted, whereby only one clone could be tested. Similarly, the imaging and SSA therapy data were not available for a comparison of SSTR IHC expression profiles. Finally, variation in the preclinical handling of the tumor material, including its sampling and processing, cannot be completely avoided.

## 7 FUTURE PROSPECTS

As our understanding of the nature of NENs expands, ideally future studies should further investigate the role of NPSR1 and its ligand in NENs. NPSR1 expression may indicate metastatic potential. NPS can influence tumor cell growth through the phosphorylation of the MAPK kinase pathways (Reinscheid et al. 2005). This association should be studied using a larger tumor material that includes more metastatic and nonmetastatic NENs. The role of NPS should also be examined more deeply to understand the mechanism behind the stimulation of tumor cell growth.

In addition, the predictive role of the SSTR profile and Ki-67 requires further study. Image analysis and digital pathology offer the needed objectivity and accuracy for assessing these important prognostic and predictive markers. In addition, the prerequisite development of image analysis will change the pathology laboratory workflow towards digitalization. Virtual double staining of prognostic and predictive markers using common NE markers could improve the specificity and reproducibility of NEN diagnostics in future. Utilizing AI and ANNs could also provide the needed accuracy in classifying and categorizing this heterogeneous tumor group.

## 8 CONCLUSIONS

To conclude, NPSR1 and PCSK2 can be used as a part of the NE antibody panel. Different antibody clones should be tested in a standardized setting in order to obtain a validated clone optimal for diagnostic purposes. The accuracy of grading NENs can be further improved by using image analysis tools.

The specific conclusions are:

1. The majority of NENs express NPSR1 and its ligand NSP, while the PHEO expression level is low. Thus, a strong expression of NPSR1 points towards an NE nature of a tumor.
2. The strong PCSK2 expression in midgut NENs, lung carcinoids, PHEOs, and PGLs allows for the use of this marker, directing pathologists towards the location of unknown primary tumors.
3. NENs with different tumor locations exhibited distinctive SSTR profiles, and UMB clones indicating that validated staining protocols should be used.
4. The conventional assessment of the PI in NENs is subject to inter- and intraobserver variation. Image analysis provides a more objective and reproducible NEN grading.

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To the boys in my life – without you I would be rootless.



Helsinki, July 2020

*Satu Maria Remes*

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