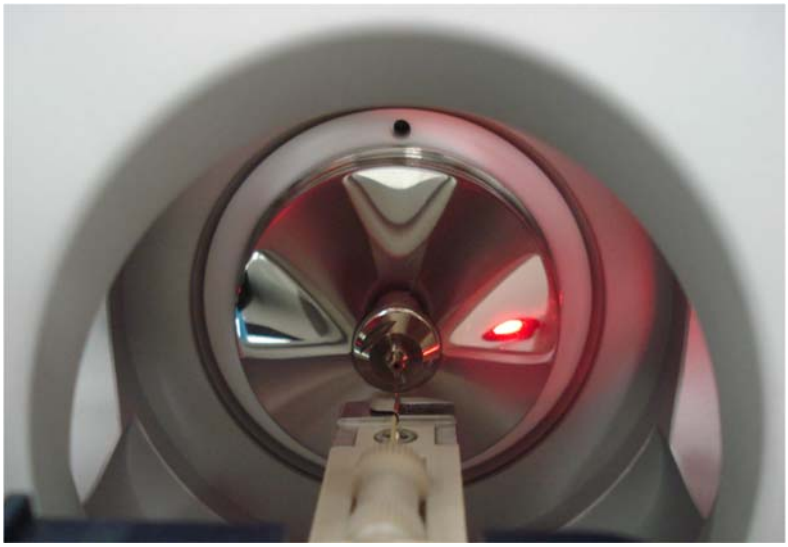
Annual report 2015

Interfaculty Mass Spectrometry Center



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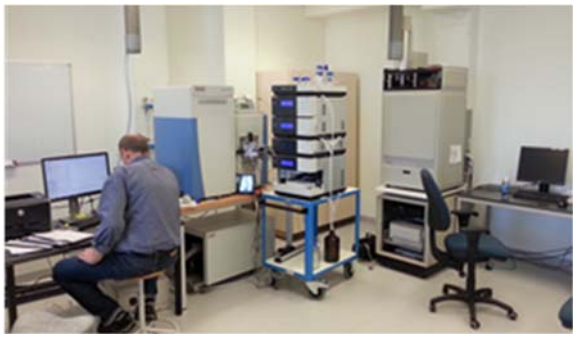
1. Introduction

The annual report of the Interfaculty Mass Spectrometry Center gives an overview of the activities, and new developments in 2015, and the current status of the IMSC. The second year of operation of the facility in the ERIBA building was marked by the implementation of new methods as well as routine workflows making full use of the new mass spectrometry equipment. Several new high-end MS instruments were installed in the Center at the end of 2014 and are now available for service. The Q Exactive Plus instrument has become a workhorse for high-throughput proteomics measurements and finds use by numerous groups in RUG and UMCG for both discovery-based and quantitative proteomics.

The IMSC at its current size is capable of providing a wide variety and complexity of MS services which is reflected in the variety of research groups and sample types which are detailed in section 4. Papers with direct contributions from IMSC staff that have been published in 2015 are listed in section 5. This includes publications related to service projects as well as scientific collaborations.

For education and dissemination of mass spectrometry knowledge we participate in several student and PhD courses. The annual two-day MS course of the IMSC itself was attended by about 45 people this year, from a variety of RuG and UMCG groups and a few industry participants.



2. Equipment & facilities

The equipment in the IMSC comprises 15 fully functional (LC)-MS systems, listed in detail below. One instrument, an Agilent QToF has been retired in 2015. Extensive repairs which were necessary for this instrument were deemed not financially justified. The role of this instrument has been superseded by the new MaXis plus QToF which was installed late 2014. In addition to the listed 15 systems, the IMSC since mid-2015 temporarily houses two LC-MS instruments from the UMCG Pharmacy, a Q Exactive Orbitrap and a TSQ Quantum triple quadrupole. This 'outplacement' was made possible and attractive due to the available infrastructure and scientific environment of the IMSC, and has already led to collaboration with UMCG Pharmacy researchers on antibody characterization.
A notable investment in equipment was the acquisition of the new IonKey interface of Waters. This LC chip-based low-flow rate electrospray ionization interface was tested in 2014-2015 with excellent results for the sensitive quantification of biopharmaceutical peptides and proteins, on the Waters TQ-S triple quadrupole instrument. The IMSC has therefore decided to purchase the IonKey interface in 2015, and the IonKey chip LC-MS system installed on the Xevo TQ-S is now the state-of-the-art system for quantitative biopharmaceutical analysis.
Smaller investments were made for expansion of data storage and analysis, and for noise-reduction measures in the MS labs.

2.1 Mass spectrometry equipment

All equipment housed and supported by the IMSC is intended to be accessible to researchers from RuG and UMCG, as well as for external customers. Instrument use is charged based on an hourly fee or on lump sum payments for larger projects (see section 3).
The list of MS equipment below is organized by instrument type and for each instrument information on the most commonly associated HPLC systems and ion sources is shown. HPLCs are often interchangeable, ion sources less commonly so. Triple quadrupole MS systems are mostly used for targeted quantification, while high-resolution MS systems and ion traps are most useful for identification and characterization of compounds. High-resolution MS systems are becoming increasingly important for quantification purposes as well. Different ionization methods are used for specific compound classes but the bulk of the analyses are performed with electrospray ionization (ESI). NanoLC and nanoESI are used for small sample amounts, primarily for proteomics applications. MALDI-TOF is suitable for fast analysis of single compounds and simple mixtures, particularly of large molecules (intact biomacromolecules and polymers). The instruments are all available for versatile use, but in order to streamline the analysis of samples, some instruments are used primarily or exclusively for specific applications. For example, the new Q Exactive Plus instrument, installed in late 2014, is ideally suited for shotgun as well as quantitative proteomics, and as such is used as a high-availability, high-throughput proteomics instrument. Another example is the API365 triple quadrupole used for targeted, quantitative analysis of polar metabolites. The LC mobile phase composition is optimized for polar metabolite separation, but the additives strongly interfere with analysis of most other analytes. The availability of a number of triple quadrupole systems makes it possible to reserve an instrument for such specific applications, and laborious cleaning and reoptimizing procedures for switching between applications can be avoided.

Table 1a. High resolution MS equipment

	MS instrument	MS Manufac-turer	MS type	Ionization source	LC instrument	LC Manufacturer
1	**LTQ-Orbitrap XL**	Thermo	linear trap-orbitrap	ESI, nanoESI	Ultimate 3000 nanoHPLC Prominence UFLC	Dionex Shimadzu
2	**Synapt G2-Si**	Waters	quadrupole-time of flight	ESI	Acquity UPLC	Waters
3	**MaXis plus**	Bruker	quadrupole-time of flight	ESI, nanoESI	Ultimate 3000 nanoHPLC	Dionex/Thermo
4	**Q Exactive Plus**	Thermo	quadrupole-orbitrap	ESI, nanoESI	Ultimate 3000 nanoHPLC	Dionex/Thermo

Table 1b. Triple quadrupole MS equipment

	MS instrument	MS Manufacturer	Ionization source	LC instrument	LC Manufacturer
5	**Xevo TQ-S**	Waters	ESI, IonKey chip-based ESI	Acquity UPLC nanoAcquity	Waters Waters
6	**TSQ Vantage**	Thermo	ESI, nanoESI	Ultimate 3000 nanoHPLC	Dionex/Thermo
7	**TSQ Vantage**	Thermo	ESI, nanoESI, APCI	Accela UPLC Ultimate 3000 nanoHPLC	Thermo Dionex/Thermo
8	**TSQ Quantum AM**	Thermo	ESI, APCI, APPI	Surveyor HPLC LC Packings Ultimate nanoLC	Thermo Dionex
9	**API 3000**	PE Sciex	ESI, nanoESI, APCI, APPI	Prominence UFLC	Shimadzu
10	**API 365, upgraded EP10+**	PE Sciex, Ionics	ESI	Ultimate 3000 HPLC	Dionex
11	**API 365, upgraded EP10+**	PE Sciex, Ionics	ESI	LC Packings Ultimate nanoLC	Dionex
12	**6410**	Agilent	ESI, nanoChipCubeESI	1200 series nanoHPLC	Agilent

Table 1c. Ion trap MS equipment

	MS instrument	MS Manufacturer	Ionization source	LC instrument	LC Manufacturer
13	**HCTultra ETDII**	Bruker	nanoChipCubeESI	1100/1200 series HPLC	Agilent

Table 1d. MALDI-TOF MS equipment

	MS instrument	MS Manufacturer	MS type
14	**Voyager DE-Pro**	Applied Biosystems	MALDI-TOF
15	**UltrafleXtreme**	Bruker	MALDI-TOF/TOF

Figure 2. Mass spectrometry setups installed at the IMSC, at the end of 2015. The numbers refer to table 1 above.

3. Personnel & organization

3.1 Personnel

The core IMSC staff members are Hjalmar Permentier, head of the IMSC, and the technicians Margot Jeronimus-Stratingh and Annie van Dam. The head of the scientific board of the IMSC is Prof. Rainer Bischoff (Analytical Biochemistry). Marcel de Vries is seconded to the IMSC as an MS technician from Paediatrics, UMCG. MS technician Jos Hermans of Analytical Biochemistry is responsible for several LC-MS instruments which are used both for AB projects and within the IMSC. Further technical support is provided by technician Natalia Govorukhina of Analytical Biochemistry, in particular for sample preparation related to proteomics. Data analysis and bioinformatics support is also provided as part of the IMSC, with support of Prof. Peter Horvatovich (Computational Mass Spectrometry).

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Group photo of IMSC and Analytical Biochemistry department, January 2016
From left to right and back to front: Larry Zhang, Tao Yuan, Nico van de Merbel (PRAHS), Daan Pouwels (UMCG), Wenxuan Zhang (UMCG), Marcel de Vries (UMCG), Hjalmar Permentier, Jos Hermans, Andres Gil, Natalia Govorukhina, Peter Bults (PRAHS), Annie van Dam, Jan Willem Meints, Turan Gül, Frank Klont, Karin Wolters (UMCG), Mireille Wessels (UMCG), Vikthor Nijenhuis, Rainer Bischoff, Jolanda Meindertsma, Alienke van Pijkeren; Not on photo: Margot Jeronimus-Stratingh, Peter Horvatovich, Jiaying Han.

3.2 Organization and policy

All MS instruments and associated equipment listed in the previous section are operated, supported and supervised by one or more IMSC technicians. The technicians all have broad MS experience and often have in-depth knowledge on specific subjects or methods. The general policy of the IMSC is to provide high-level service to every scientist and research group from the RuG and UMCG to the best of our abilities. However, since many research groups make use of the facilities, and resources are sometimes limited, access to the IMSC has to be granted and regulated. The Facility manager together with its Director are responsible for making optimal use of equipment and personnel. There are different levels of users depending on their initial commitment to the Center, their involvement in acquisition of instrumentation and in providing personnel:

1. Regular customers: scientists that wish to have samples analyzed on an occasional basis, with questions that do not require extensive methods development, will usually interact directly with the technical staff of the IMSC and have their analyses done for the hourly user fee, which is currently 30 euros irrespective of the MS instrument. Long analyses which run for more than a day consecutively and require limited or no extra work from the technicians are charged at half the hourly rate for the hours in excess of a day. These high-throughput measurements pose a smaller burden on the IMSC resources, and for even larger projects a lump sum may be negotiated as discussed in the next category.
2. Project customers: scientists that have research questions which require extensive method development discuss first with the IMSC manager and, if necessary, the scientific head, to define the approach and workload. Users will have to contribute financially to the methods development work at least on a partial basis, by paying the regular hourly user fee. In the case of long-term developments (e.g. 3 months or more), which will also enhance the overall competence of the IMSC, an agreement can be made for a fixed fee (lump sum) according to agreed-upon criteria which will be lower than just adding the hourly user fee. Users foreseeing such a use of the IMSC are encouraged to apply for funding to include the significant MS costs in their regular project budget. Lump sums of 5000 euros per year per project/group are deemed reasonable to cover in the order of 300-400 MS hours.
3. Collaborators: scientists that have research questions, where the use of cutting-edge biological mass spectrometry and related techniques is required on a structural basis (e.g. biomarker discovery projects, systems biology projects) collaborate with the IMSC on a scientific level. This implies, in general, that the IMSC is already involved at the stage of the grant application and that cost for the use of instrumentation, personnel and consumables are part of the project budget. Such projects may also request dedicated instrumentation in their grants, which will be housed in the IMSC and reserved with priority for these users.
4. External customers: scientists and commercial parties from outside the University of Groningen or the UMCG will be classified in the same way as internal academic users, but the user fees include salary cost and instrument depreciation or agreed-upon contract criteria as mentioned above.

The services of the IMSC are discussed and reviewed on an annual basis with a committee composed of committed users and other stakeholders. The general structure of the IMSC is shown in the figure below. The role of the Scientific Board, the composition of which needs to be defined, is to help define long-term strategies for embedding the IMSC in the major national and local research themes and networks.

4. Overview of projects

The main task of the IMSC is to perform MS service and this overview lists the service work categorized by research institute and department with a brief description of the type of analyses and techniques. For project background information please refer to the respective research groups or their websites. The size of the service projects varies greatly, from a few hours to hundreds of hours a year, but the list gives a good indication of the variety of samples and techniques that the IMSC handles. The work is performed primarily by the IMSC technicians, in most cases not only the MS analysis itself but also a significant amount of sample preparation and data analysis. Most of the listed work involving the MALDI-TOF is performed by the researchers independently, after initial training on the instrument, but is continuously supported by the IMSC.
In section 4.2 our scientific collaborations are listed, which are defined as those where a researcher is working for extended periods, or permanently, in the IMSC, and in the case of PhD students and postdocs usually supervised by our staff. The distinction between service work and collaboration is sometimes small, and we support proposals to upgrade service work into collaborative projects.

4.1 Service work and projects

University of Groningen

GBB

- **Enzymology**
  LC-MS of proteins
- **Microbial Physiology**
  LC-MS/MS proteomics of bacteria
- **Molecular Cell Biology**
  LC-MS/MS proteomics of yeast
- **Molecular Genetics**
  MALDI-TOF and LC-MS, of peptides and proteins
- **Molecular Microbiology**
  LC-MS/MS of proteins
- **Molecular Systems Biology**
  quantitative LC-MS/MS metabolomics, energy metabolites
- **X-ray Crystallography**
  LC-MS and MALDI-TOF of proteins and peptides

GIELS

- **Behavioural Biology**
  LC-MS/MS quantification of steroids from eggs
- **Microbial Ecology**
  LC-MS/MS proteomics & metabolomics of sponges and fungal cultures

GRIP

- **Analytical Biochemistry**
  MALDI-TOF and LC-MS of protein reagents and oxidation products
- **Pharmaceutical Analysis**
  (LC)-MS of reagents

- **Drug Design**
  (LC)-MS of organic synthesis products
- **Pharmaceutical Biology**
  (LC-)MS of enzyme substrates, metabolomics of bacteria
  MALDI-TOF and (LC-)MS of proteins and peptides
- **Pharmaceutical Gene Modulation**
  (LC-)MS and MALDI-TOF of proteins and protein reagents
- **Pharmacokinetics, Toxicology and Targeting**
  LC-MS/MS quantification of drugs and metabolites

Stratingh

- **Chemistry of (Bio)organic Materials and Devices**
  MALDI-TOF and LC-MS of synthetic organic compounds
- **Synthetic Organic Chemistry**
  MALDI-TOF and (LC)-MS of synthetic organic compounds,
  MALDI-TOF and LC-MS of modified peptides & proteins
- **Molecular Inorganic Chemistry**
  ESI-MS of organometallic complexes

ZIAM

- **Molecular Biophysics**
  LC-MS
- **Macromolecular Chemistry & New Polymeric Materials**
  MALDI-TOF
- **Polymer Chemistry and Bioengineering**
  MALDI-TOF of polymers, modified peptides and proteins, and nucleic acids,
  LC-MS modified peptides and proteins, and synthetic organic compounds

University Medical Center Groningen

- **Aging Biology (ERIBA)**
  LC-MS/MS proteomics: nematodes, human
- **Biomedical Engineering**
  MALDI-TOF and LC-MS/MS proteomics, serum and nanoparticles
- **Nano-biomaterials and interfaces**
  MALDI-TOF
- **Cell Biology-Autophagy**
  LC-MS/MS proteomics
- **Cell Biology-Radiation and Stress Cell Biology**
  LC-MS/MS proteomics
- **Nuclear Medicine & Molecular Imaging**
  LC-MS
- **Medical Oncology**
  LC-MS of proteomics

- **Pathology & Medical Biology**
  LC-MS/MS proteomics of human cell cultures
- **Clinical Pharmacy & Pharmacology**
  LC-MS/MS proteomics
- **Paediatrics**
  LC-MS/MS quantitative metabolomics and proteomics
- **Paediatrics-Hematology**
  LC-MS/MS quantitative metabolomics
- **Medical Microbiology-Molecular Virology**
  LC-MS/MS proteomics

External

- **Lanthio Pharma, Groningen**
  MALDI-TOF and LC-MS of peptides
- **Respiratory Medicine, UMC, Utrecht**
  LC-MS proteomics
- **IQ products, Groningen**
  LC-MS proteomics of serum & plasma
- **Greenmove, Groningen**
  LC-MS proteomics of fungal cultures
- **BasidioFactory, Milsbeek**
  LC-MS proteomics of fungal cultures
- **AMC Pharmaceuticals, Zeewolde**
  LC-MS identification of drug impurity
- **Guests reseacher, University of Bologna**
  LC-MS quantitation of proteins

4.2 Scientific projects and collaborations

The IMSC is closely involved in several larger scientific projects, where equipment and/or PhDs and postdocs are placed in the IMSC and make use of our infrastructure, expertise and scientific input.

Electrochemistry-mass spectrometry
A research project that has been running in the IMSC for more than 15 years involves the coupling of electrochemistry (EC) with mass spectrometry, for drug and protein oxidation research. A new STW-project started in 2012 with two PhD students, and a third PhD student started at the same time with a Chinese Scholarship grant, all co-supervised by Hjalmar Permentier and Rainer Bischoff. The projects make extensive use of our older triple quadrupole LC-MS systems (nr 9 and 12), as well as dedicated EC equipment acquired as part of the project. The current research focuses on (1) the specific synthesis by EC of drug metabolites and their analysis by LC-MS and (2) the specific digestion of proteins by EC followed by enrichment and analysis of resulting peptides by LC-MS. The methods are potentially interesting for drug development, metabolism research and proteomics, and the STW project encompasses both instrumental and pharmaceutical industry partners.

In parallel with the STW project, an NWO-CW-ECHO project on electrochemically-assisted redox enzyme reactors by cofactor immobilization was granted with one PhD student, which is supervised by Prof Marco Fraaije (Biotechnology, RuG), and co-supervised by Hjalmar Permentier and Rainer Bischoff. In collaboration with the PhD students of the STW EC-MS project, experiments are regularly performed in the IMSC.

Targeted proteomics and metabolomics of ageing

The Systems Biology Centre for Energy Metabolism and Ageing (SBC-EMA) has 1 dedicated LC-MS instrument (nr 7) and two postdocs working on quantitative proteomics (Karin Wolters) and metabolomics (David Siegel) projects, working in collaboration and with supervision of IMSC staff. New LC-MS/MS methods based on SRM analysis are developed for large-scale high-throughput quantitative analyses of complex proteome and metabolome samples of yeast and mouse model systems. The expertise and methods developed in this project are also very useful for many other groups outside SBC-EMA and these types of analyses can now also be offered to other research groups. Karin Wolters is employed by UMCG as of end 2014 and continues to develop and perform targeted proteomics analyses for several UMCG and ERIBA research groups. Her methods employ isotopically labeled peptide standards or synthetic proteins (QConCAT technology) in order to do absolute quantification of dozens of proteins in a single experiment. David Siegel left in summer 2014, and the quantitative energy metabolite LC-MS/MS methods were taken over by the IMSC technicians. There are plans to extend the metabolite analyses to enable flux measurements using ^{13}C labeling experiments.

Metabolomics in metabolic disease

Since 2013 the IMSC houses a high-resolution Q-TOF LC-MS instrument with ion mobility capability acquired by the Laboratory Medicine department (Prof Dirk-Jan Reijngoud, UMCG). In 2014 this instrument has been operated by a PhD student of Analytical Biochemistry for the study of the stability of energy metabolites during metabolomics sample preparation. At the end of 2015 this PhD and a PhD student of Prof Reijngoud starting with implementing high-resolution screening of lipids in complex samples, using methods developed in close collaboration with the IMSC.

Ionization methods for mass spectrometry

The Pharmaceutical Analysis group (Prof Sabeth Verpoorte, RuG) has placed a triple quadrupole mass spectrometer (API2000 QQQ, not listed above) in the IMSC for the development of new ionization methods, notably paper spray ionization interfaces. The IMSC assists with the technical and instrumental aspects of this research project.

New approaches for MALDI imaging of proteins

A new collaboration project was started in 2014 with the groups of Angela Casini (Pharmacokinetics, Toxicology and Targeting, RuG) and Peter Horvatovich, with a Chinese Scholarship PhD student, aiming at the synthesis of photocleavable linkers which can be employed in MALDI imaging of proteins. The analyses will be performed on the IMSC MALDI-TOF (non-imaging method development), and on a new MALDI-TOF/TOF (with imaging option) which was acquired as part of STW-Perspectief grant on Biomarker validation of the Analytical Biochemistry department.

Analysis of biopharmaceuticals

There is a growing interest in accurate and validated analytical methods for therapeutic peptide and proteins, both from industry and the clinical side. We collaborate with PRA Health Sciences, and the group of Nico van de Merbel (RuG) in developing the methods using improved sample preparation and sensitive SRM approaches. These methods are now already being applied to the protein IGF-1, in collaboration with Laboratory Medicine (UMCG). Currently, new methods for the characterization of therapeutic antibodies are being developed.

5. Publications, presentations, teaching

In this section papers and activities are included of IMSC-employed personnel (Hjalmar Permentier, Annie van Dam, and Margot Jeronimus-Stratingh), as well as Marcel de Vries (seconded to IMSC from UMCG. Papers with explicit mention of IMSC personnel in the acknowledgements are separately listed. For other (unpublished) contributions refer to section 4. Teaching comprises both lectures and practical work. The two-day mass spectrometry course is organized yearly to inform, educate, and interest students and researchers on the practical and theoretical aspects of MS and how they can make use of the IMSC.

5.1 Peer-reviewed papers

Published in 2015

1. Baas, B-J., Poddar, H., Geertsema, E. M., Rozeboom, H. J., de Vries, M. P., Permentier, H. P., Thunnisen, A.-M., Poelarends, G. J. Functional and structural characterization of an unusual cofactor-independent oxygenase. *Biochemistry* 54 (2015) 1219-1232. doi:10.1021/bi501200j
2. Bischoff, R., Permentier, H., Guryev, V., Horvatovich, P. Genomic variability and protein species - improving sequence coverage for proteogenomics. *Journal of Proteomics* (2015) in press. doi:10.1016/j.jprot.2015.09.021
3. Gil, A., Siegel, D., Permentier, H., Reijngoud, D-J., Dekker, F., Bischoff, R. Stability of energy metabolites - An often overlooked issue in metabolomics studies: A review. *Electrophoresis* 36 (2015) 2156-2169. doi:10.1002/elps.201500031
4. Gul, T., Bischoff, R., Permentier, H. P. Optimization of reaction parameters for the electrochemical oxidation of lidocaine with a Design of Experiments approach. *Electrochimica Acta* 171 (2015). 23-28. doi:10.1016/j.electacta.2015.04.160
5. Gul, T., Bischoff, R., Permentier, H. P. Electrosynthesis methods and approaches for the preparative production of metabolites from parent drugs. *TrAC-Trends in Analytical Chemistry* 70 (2015) 58-66. doi:10.1016/j.trac.2015.01.016
6. Yuan, T., Le Thi Ngoc, L., van Nieuwkasteele, J., Odijk, M., van den Berg, A., Permentier, H., Bischoff, R., Carlen, E. T. In situ surface-enhanced Raman spectroelectrochemical analysis system with a hemin modified nanostructured gold surface. *Analytical Chemistry* 87 (2015) 2588-2592. doi:10.1021/ac504136j
7. Yuan, T., Permentier, H., Bischoff, R. Surface-modified electrodes in the mimicry of oxidative drug metabolism. *TrAC-Trends in Analytical Chemistry* 70 (2015) 50-57. doi:10.1016/j.trac.2015.01.017
8. Sakulkhu, U., Mahmoudi, M., Maurizi, L., Coullerez, G., Hofmann-Amtenbrink, M., de Vries, M., Motazacker, M., Rezaee, F., Hofmann, H. Significance of surface charge and shell material of superparamagnetic iron oxide nanoparticle (SPION) based core/shell nanoparticles on the composition of the protein corona. *Biomaterials Science* 3 (2015) 265-278. doi:10.1039/c4bm00264d

In press and accepted

1. Krzek, M., van Beek, H. L., Permentier, H. P., Bischoff, R., Fraaije, M. W. Covalent immobilization of a flavoprotein monooxygenase via its flavin cofactor. *Enzyme and Microbial Technology* 82 (2016) 138–143. doi:10.1016/j.enzmictec.2015.09.006

2. Ruokolainen, M., Gul, T., Permentier, H., Sikanen, T., Kostiainen, R., Kotiaho, T. Comparison of TiO_2 photocatalysis, electrochemically assisted Fenton reaction and direct electrochemistry for simulation of phase I metabolism reactions of drugs. *European Journal of Pharmaceutical Sciences* 83 (2016) 36–44. doi:10.1016/j.ejps.2015.12.012

Publications in 2015 with IMSC acknowledgement

1. Thomas, A.S., Krikken, A.M., van der Klei, I.J., Williams, C.P. Phosphorylation of Pex11p does not regulate peroxisomal fission in the yeast *Hansenula polymorpha*. *Scientific Reports* 5 (2015) 11493. doi:10.1038/srep11493
2. Mu, D., Montalbán-López, M., Deng, J., Kuipers, O.P. Lantibiotic reductase LtnJ substrate selectivity assessed with a collection of nisin derivatives as substrates. *Applied and Environmental Microbiology* 81 (2015) 3679-3687. doi:10.1128/AEM.00475-15
3. Lammerts van Bueren, A., Saraf, A., Martens, E.C., Dijkhuizen, L. Differential metabolism of exopolysaccharides from probiotic lactobacilli by the human gut symbiont *Bacteroides thetaiotaomicron*. *Applied and Environmental Microbiology* 81 (2015) 3973-3983. doi:10.1128/AEM.00149-15
4. Jiménez, D.J., Maruthamuthu, M., van Elsas, J.D. Metasecretome analysis of a lignocellulolytic microbial consortium grown on wheat straw, xylan and xylose. *Biotechnology for Biofuels* 8 (2015) 199. doi:10.1186/s13068-015-0387-8

5.2 Teaching, (under)graduate courses

21 February 2015	COAST biomarker day
6 February 2015:	Quantitative Bioanalysis course (lecture)
March 2015:	Proteomics / Genomics course WLB07041
May 2015:	Medical Genomics & Proteomics course WLB07090
29 May 2015:	practicum day MALDI-TOF Hanze University of Applied Sciences
November 2015:	2-day course on Mass Spectrometry (10 & 11 November)
November 2015:	Topmasters MPDI, 3-day lab introduction