**Project Description – Project Proposals**

**[First name last name, city of all applicants]**

**[Research position (e.g. research assistant, professor)]**

**[Term of contract (fixed-term, permanent)]**

**Project Description**

# State of the art and preliminary work

Omic sciences (omics), also referred to as high-dimensional biology, are a relatively new field of research in life sciences aiming at the study of structure, functions and dynamics of living organisms. Information technology is an integral part of this research, given the analysis of colossal amount of data spawning by the research instruments is vital. Mass spectrometer, for instance, being one of the most multipurpose analytical instrument has been extensively used in proteomics (also metabolomics) for the identification of analytes. In a state of the art proteomics lab with several Mass spectrometer instruments, hundreds of data files are produced and analyzed daily, whereas, the amount of data carried out by each single file is of several GBs. According to some recent statistics, the data store size of one of the world’s largest Bioinformatics lab, European Bioinformatics Institute (EBI) in UK, reaches to 20 petabytes.

The vendor lock-in applications and data formats is a known issue in mass spectrometry based proteomics research. There is a broad range of mass spectrometer vendors (about 24) available in the market competing with each other in terms of technology, design and performance. Typically, each vendor supports one or more native data formats of its own and keeps on extending them with new features as required by emerging instrumentation. The native data format of each vendor instrument differs from others and, therefore, non-interchangeable too. Consequently, only the vendor proprietary applications can be primarily used to read and analyze the vendor specific data, impeding the pace of collaborative work of various research labs running different types of mass spectrometers in terms of exchanging and comparing of results of different biological experiments. Nevertheless, efforts have been made in past to deal with this issue and a variety of vendor-neutral formats (also called open formats) and open-source analysis tools have been developed by various research groups working in the domain to enhance the sharing of results and data analytics among the researchers in the community. HUPO Proteomics Standard Initiative (HUPO-PSI), for instance, is one of the most active community in Proteomics working for the development of standardized data representations for data exchange and verification based on vendor APIs.

Reproducibility is another known issue in proteomics that researchers have to deal with. The data analysis studies in mass spectrometery is a complex multistep operation, which involves collecting the raw data from instruments, extraction of spectral data to one or more open data-formats, submitting the data into shared repositories, and analysis of data with some available software tools. The lack of automation of this high-throughput workflow, therefore, questions the accuracy, speed, consistency, and transparency of data processing outcome. Therefore, in a well-equipped research facility that operates a range of mass spectrometery instruments and multiple data analysis programs, it becomes extremely challenging to maintain reproducibility without automating the highly sophisticated SOPs (standard operating procedures) of data analysis.

Essentially, as mentioned earlier, mass spectometery is a key multidisciplinary analytical technique commonly used under the domain of omics. To setup a centralized research infrastructure for various local and distributed mass spectometery labs is therefore vital. It should offer:

* Secure and highly scalable network of the researcher instruments.
* Storage of data into a common data repository.
* Compliance to the departmental SOPs for data processing and analytics.
* Centralized policy management and control to help enforce disciplinary regulations and policies in order to gain proper control and prevent uncontrolled distribution.

## Current practices and challenges at Göttingen Proteomics Forum (GPF)

The Göttingen Proteomics Forum (GPF) is a local network of scientists and researchers of the Georg-August-University, the University Medical Center Göttingen (UMG), the Max-Planck Institutes (MPI) of Experimental Medicine and Biophysical Chemistry, and the local corporate data processing facility of the University and Max-Planck-Society (GWDG) with the common interest in the analysis of proteins by mass spectrometry. The ambition of the forum is the pooling of local proteomics expertise and tools to generate synergism and provide mutual support for the proteomics community in Göttingen.

At present, different working groups under GPF are running their mass spectometery labs. Table 1 lists down a range of mass spectometery instrumentations and software these state-of-the-art labs possess for experimentation. Based on its vendor lock-in technology and solutions, each lab follows a set of operations (i.e., SOP) for raw data collection, data conversions to meaningful formats, analysis and storage of data for research purposes. Whereas, GWDG being a common data processing center for GPF, supports the proteomics labs in the data analysis part. For this, GWDG hosts a proteomics analysis software, MASCOT server, which has become a standard for protein identification using mass spectometery data for many big vendors.

Apart from the above mentioned high-tech research facilities at GPF, all the processes and operations at proteomics labs and data processing cooperation currently following a strict manual routine, hence prone to reproducibility, productivity and transparency issues. Also in its current setup, the existing infrastructure supports no common and public research data repositories for an open exchange of data across different research settings. Furthermore, the lack of common workflow practices among the labs and non-adherence to open data standards may also hinder a systematic and spontaneous sharing of results among the settings.

|  |  |  |
| --- | --- | --- |
| **Institute** | **Vendor MS Devices** | **MS Software** |
| UMG  (Institute of Clinical Chemistry ) | * Thermo Scientific Q Exactive * Q-TOF Ultima Global mass spectrometer (Micromass) * MALDI MicroMX mass spectrometer (Micromass) | * Mascot (Matrixscience) * Scaffold (Proteome Software) * MaxQuant with Perseus. |
| MPI of  Experimental Medicine (Proteomics Group) | * Ultraflex I (Bruker) * Synapt GS 2(Water) * Acquity-QDa(Waters) | Details to be added |
| MPI Biophysical Chemistry | Orbitrap instrumentation   * LTQ Orbitrap XL * Q Exactive Plus * Q Exactive HF * Tribrid Fusion * Tribrid Lumos   Triple quadrupole instrumentation   * TSQ Vantage * TSQ Quantiva | Details to be added |

Table 1: A list of Mass Spectometery instruments available at GPF

## Available Tools and Technologies for the development of ArCare

ArCare proposes a secure, robust and automated research platform for proteomics labs, which offers:

* The automation of different mass spectometery operations (from data collection till data storage and analysis) currently followed in proteomics labs.
* The support and automation of standardized workflows (defined by HUPO-PSI and other active communities) based on open data formats and open source tools and software.
* Integration of data into existing transregional repositories, such as NFDI (Nationalen Forschungsdateninfrastruktur), for a sustainable and open exchange of data across different research settings.

Figure 1 depicts a high level design of ArCare solution based on the existing off-the-shelf tools and technological testbeds developed at the Göttingen campus. The heart of the solution is the SDN (Software Defined networking) capabilities to improvise a sophisticated control and management plane to increase efficiency of big data applications, such as proteomics in this case. In a given automation scenario proposed by ArCare, the vendor specific raw data will be captured from the MS devices through device specific agents, which is transformed into some open data format (such as OpenMS) with the help of some data adapter applications locally. This data is later sent to the ArCare controller, where it is stored in a shared data repository among different proteomics labs. Finally, for data analysis and reporting, the ArCare controller further transforms the OpenMS data into other application specific formats if required by different data analysis application.

Following is a short description of the available testbed, tools and technologies that will be used in the realization of ArCare ecosystem:

**OpenNets:**

OpenNets is the implementation of GWDG’s SDN testbed based on the OpenDaylight controller, Lithium version, extended with additional domain specific SDN applications. OpenNets exposes the REST API of the Application Affinity service component of OpenDaylight controller, which allows the automation of provisioning and deletion requests of network connections at the switching/forwarding plane. The capabilities of OpenNets also include the advanced network management of legacy network infrastructure using SDN agents. The SDN agent is a novel concept to bridge the communication gap between SDN control plane and non-SDN data plane. For instance, as depicted in Figure 1, in order to provision a centralized control and automation of mass spectometery big data labs, at first level we need to utilize the strength of SDN agents to facilitate the communication between the ArCare controller and the network switches. At the second level, we need to introduce device agents to collect and transfer the mass spectometery data from the vendor devices.

**MS Proteowizard:**

In biological experiments, after receiving raw data by using mass spectrometers and in order to manipulate by other software, it is mandatory to convert these data from vendor-specific binary files to open-format files. In order to unify access to mass spectrometry data file and enforce standard chemistry analysis and computation on LCMS data set, MS Proteowizard project provides a modular and extensible collection of cross-platform and open-source tools and libraries for proteomics data analyses. MS Proteowizard provide a framework which can be used specially to read different vendor-specific and dedicated format and transform the data to open-format.

**MS Applications:**

During the last two decade Mass spectrometry has developed extremely quickly. Novel high throughput mass spectrometry devices were produced for confronting with the request of the proteomic, metabolomic and other ‘omics’. This progress has conducted to invention of fully new instruments which direct developer to create and develop new applications. A list of all available MS applications in different classification can be seen here [7].

**OpenMS:**

OpenMS is a skillful open-source library for data analysis of data captured from mass spectrometer devices. For developing mass spectrometry data analysis tools, it provides a framework for data structure from basic format capture from input/output file and visualisation to experienced and mature algorithms. Hence, OpenMS lets developers can turn their attention to novel algorithmic approaches instead of focusing on implementation of infrastructure.

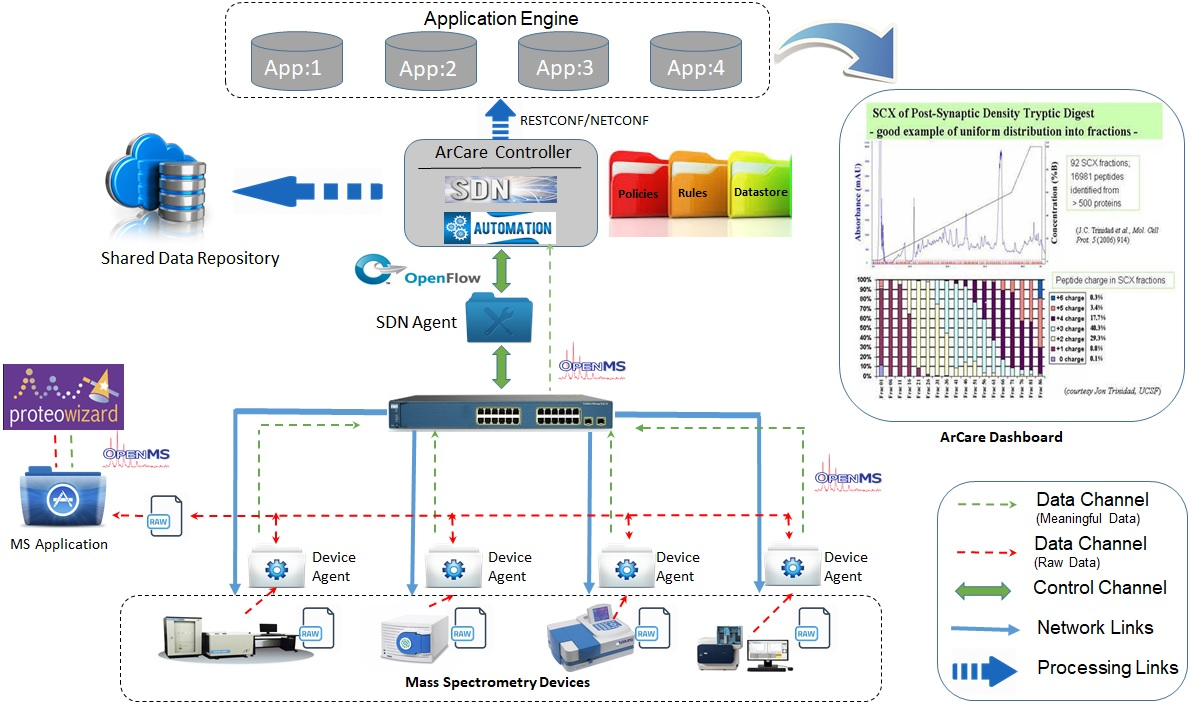


Figure 1: Overview of ArCare solution

## Comparison to already available alternative solutions

Scientific research is extremely data driven. Tremendous collected data was produced by plenty scientific research. Moreover, part of scientific big data cannot be processed and analyzed at the identical spot where they are formed and developed, regarding political and technical point of view. Since the big data is considered by the scientists or researcher for analyzing tasks in their research, the data should be sent and stored in different data centers or at different universities or institutes. On the other hand, currently it is not possible to manage such a massive volume of data in campus networks. As the amount of data increases, there is a greater need for unsophisticated, scalable end-to-end network architectures and implementations that enable applications to use the network most efficiently.

In the area of Healthcare data, as one of the straight example of big data, is increasing to an impressive rate— over 40% yearly. By 2020, Electronic Healthcare Record (EHR) is anticipated to need over 2000 exabytes—that’s two billion terrabytes. [2].

In the domain of Biological data , the European Bioinformatics Institute (EBI) , as a part of the European Molecular Biology Laboratory and one of the world's largest biology-data repositories, currently stores 20 petabytes of data and back-ups about genes, proteins and small molecules. Genomic data account for 2 petabytes of that, a number that more than doubles every year [3].

Unfortunately, healthcare IT spending is not only unsuccessful to preserve with this rate of growth, but is awaited to fall. And today’s data center infrastructures situation and architecture add to the difficulty, since they are frequently based on branded storage and network technologies which are challenging and expensive to manage and scale. Healthcare IT decision makers requires new opportunities to scale quicker and more cost effectively [4].

Healthcare organizations are using virtualization to integrate health IT infrastructure solutions to achieve more easily manage processes and overcome the pressure on network hardware. As a novel technology, recently organizations are using software-defined networking (SDN) solutions as well to form IT systems more easy and flexible. Research and Markets analysts anticipate that the SDN market is awaited to increase at a CAGR of 48 percent through 2025 because of the requirement of making IT systems smaller and simpler to control [5].

Study shows healthcare and Bioinformatics are one of the best context to deploy SDN technology. As healthcare organizations reconcile to electronic health records (EHRs) and cloud computing, networks require to be capable of manage the increased amount of traffic [6]. A Software-Defined Infrastructure can assist healthcare facilities remove challenges and recognize fresh possibilities by reorganizing legacy networks, as shown above, into a more flexible SDN. As an outcome, IT can provide application-aware network, gain agility and flexibility for applications and services, and optimize cycle management [4].

## Project-related publications

### Articles published by outlets with scientific quality assurance, book publications, and works accepted for publication but not yet published

Partners should include their publications here

1. Aziz M, Fazely H A, Landi, Gallico D, Christodoulopoulos K, Wieder P (2016) SDN-enabled application-aware networking for data center networks, DOI: 10.1109/ICECS.2016.7841210
2. Landi G, Patronas I, Kontodimas K, Aziz M, Christodoulopoulos K, Kyriakos A, Capitani M, Fazely H A, Reisis D, Varvarigos E, Bakopoulos P, Avramopoulos H (2017) SDN Control Framework with Dynamic Resource Assignment for Slotted Optical Datacenter Networks. DOI: 10.1364/OFC.2017.Tu3L.1

### Other publications

1. M Sturm, A Bertsch, C Gröpl, A Hildebrandt,R Hussong, E Lange, N Pfeifer, O Schulz ,A Zerck , K Reinert and O Kohlbacher(2008) OpenMS – An open-source software framework for mass spectrometry.BMC Bioinformatics 2008, 9:163, doi:10.1186/1471-2105-9-163
3. J D. Holman,D Tabb, and P Mallick, Employing ProteoWizard to Convert Raw Mass Spectrometry Data (2015),Department of Radiology, Stanford School of Medicine Curr Protoc Bioinformatics. ; 46: 13.24.1–13.24.9. doi:10.1002/0471250953.bi1324s46.

### Patents

None.

# Objectives and work programme

## Anticipated total duration of the project

The total duration of the project is anticipated as 36 months (01.09.2018 – 01.08.2021), depending on the length of the review process.

## Objectives

The consortium has defined a set of general objectives for the project, which serve as guidelines and lead questions for the overall development:

Objective 1: Integration and Broad Usability

Objective 2: Sustainable software and Service Operation

Objective 3: maximize outreach into the life sciences communities

**2.2.1 Objective 1: Integration and Broad Usability**

The first main objective is the integration of existing MS massive data with the focus on an extensive usability for research scope, especially for the life sciences. During the proposed project, GWDG with UMG and with kindly support of GPF will integrate selection of prototype MS data in to sustainable, portable, standard data format based on MIAPE guidelines and sharing the data in the central repository in order to serve general requirements of most life science consortia. Moreover to metadata handling, work flow design and operation of ArCare implicate to consider ethical, data protection and data consistency issues. Therefore these issues will be monitored and mapped into usage principles and design intension of our services.

**2.2.2 Objective 2: Sustainable Software and Service Operation**

The second main objective is to define and implement sustainable standard and methodologies to develop the integrated platform for massive MS proteomics data and to provide the service for the global mass spectrometry scope. Regarding sustainability, this objective is not only achieved during the project life time, but also further. Moreover, it is necessary to plan potential operation scenarios and provide the platform suit (DevOps) in the way that makes future operation possible and easy. To fulfil this goal, the project will consider the use of state-of-the-art DevOps methodologies and tools to achieve the entire chain of development and operation.

**2.2.3 Objective 3: Outreach**

The third main objective focuses on the engagement of (potential) users, i.e. researchers and infrastructure. Outreach encompasses a service and platform of ArCare, the documentation, best practice, face-to-face workshop/training sessions, but also deals with feedback by the users and providing a platform for connecting users. Feedback can be input for quality assurance and further development of ArCare (cf., objectives 1 and 2). The experience and figures collected regarding technical and personnel efforts in providing and operating ArCare will be documented and provided via platform and can serve as a point of references for establishing and integrating this project at other research site.

## Work programme incl. proposed research methods

* + 1. **WP1 -** **Data collection from MS devices**

1. Proteomics partners should review this and provide some details about data collection procedures, if necessary.
2. A systematic chain of proteomics experiments and the collection of Mass spectrometry data are the most crucial phases and is a prerequisite for the seamless functioning of the overall ArCare system. However, this must be achieved together with the efforts in WP2 for providing a network infrastructure to collect the experimentation data from all the devices in the Lab. Here, the target is to collect the experimentation data from different proteomics labs of Gottingen Proteomics Forum (GPF), who have kindly extended their active support for this. The types and number of experiments required to be performed is kept open for later discussions among the labs.

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| **Work Package 1 Overview** | | | |
| WP Lead |  | | |
| Partner |  |  |  |
| PM pro Partner |  |  |  |
| PM Gesamt |  |  |  |

**2.3.2 WP2 - Formation of SDN Infrastructure and Integration with Proteomics Lab**

Within work package 2, we will provide and implement common network infrastructure among different types of Mass spectrometry devices available in the premises of every proteomics Lab (from partners), in order to collect the Mass spectrometry data from proteomics devices and transfer them to the common repository, then select and implement SDN controller which is appropriate for ArCare project. Since SDN controllers have more prominent role in Software-Defined-Networking and functions as a strategic control point in order to provide intelligent network and there are a variety of Open Source Controller under development, from NOX to OpenDaylight and ONOS, selecting the appropriate controller is a significant part of for this project. By considering our expertise and the fact that OpenDaylight and ONOS can be deployed in diversity of production network environment, we consider OpenDaylight and ONOS as potential candidates for this project. As an outcome of this work package, we set up a SDN testbed for the project which will provide network service operation and support beyond the project life time. To achieve this, GWDG as the Göttingen campus service provider and Göttingen eResearch Alliance will provide modest sample data center and equip essential SDN-Based hardware (Router/Switch) with convenient network infrastructure.

Milestones

* MS 2.1 – Selection of appropriate ArCare Controller.
* MS 2.2 – Implement physical networking among different proteomics Labs
* MS 2.3 – Setting up SDN testbed for ArCare

Deliverables

* D 2.1 - Preliminary report on SDN Infrastructure for ArCare
* D 2.2 - Functional architecture of ArCare automation ecosystem

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| **Work Package 2 Overview** | | | |
| WP Lead | GWDG | | |
| Partner | GWDG |  |  |
| PM pro Partner |  |  |  |
| PM Gesamt |  |  |  |

**2.3.3 WP3 - Automation of different SOPs for Mass Spectrometry Analysis in Proteomics Labs**

Proteomics partners should update and provide (if necessary) a short description of their SOP for MS Analysis and how automation (either partially or fully) would benefit using ArCare infrastructure in figure 1.

This work package is designated for the implementation procedures related to the automation of Mass spectrometry analysis for each proteomics lab. As we know, currently each proteomics lab have their own set of instructions and procedures (e.g., SOPs) to follow in their daily routine for the analysis of experimentation data. This needs to be changed from manual to automated procedures to minimize the overall inaccuracy and imprecision of health-sensitive data as well as to achieve reproducibility. Thus, in this work package, the ArCare automation setup proposed in figure 1, will be modified and accommodated according to the needs of required procedures for each proteomics lab.

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| **Work Package 3 Overview** | | | |
| WP Lead |  | | |
| Partner |  |  |  |
| PM pro Partner |  |  |  |
| PM Gesamt |  |  |  |

**2.3.4 WP4 - Definition of standardized output format for Reporting and Publications**

Proteomics partners should review this section and update if necessary. Also, please specify if there are other related standards else than MIAPE.

A clear and standardized reporting of Mass spectrometry results is very crucial and of high importance in proteomics. This is certainly required when a data set acquired by the MS experiments needs to be stored in a common database for later research and analysis, as well as to be submitted as a supplementary information to a journal. Due to wide-scale heterogeneity of vendor specific instrumentations, data types, and data analysis software available in market, it is quite challenging and also desirable to follow a set of common guidelines for the reporting of MS data. Thus, in this work package, the MIAPE (The Minimum Information about a Proteomics Experiment) guidelines will be extensively studied and analyzed for the purpose of reporting of MS experimentations. MIAPE provides a set of recommendations for experimentation and analysis that have been developed by the HUPO-PSI community together with the input from a broad spectrum of stakeholders in proteomics. For instance, the MIAPE Quant is a module which presents a common set of the most important data types and metadata required for a quantitative experiment to be analyzed and, or a data analysis pipeline to be reproduced [8]. Therefore, the outcome of this work package will be the proposal and implementation of a standardized workflow definition of MS proteomics data reporting and publication in Journals.

Milestones

* M 4.1 – Implementation of an automated submission of publication results to Journals

Deliverables

* D 4.1 – Study and analysis of different modules of MIAPE required for standardized reporting

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| --- | --- | --- | --- |
| **Work Package 4 Overview** | | | |
| WP Lead |  | | |
| Partner |  |  |  |
| PM pro Partner |  |  |  |
| PM Gesamt |  |  |  |

**2.3.5 WP5 - Implementation of a shared data repository and integration with HiGHmed**

HiGHmed partner should review this section and update if necessary. Also, please provide some more details about HiGHmed and why proteomics data is important for it.

This work package is dedicated for the implementation efforts envisaged to set up a data sharing mechanism among different proteomics labs. The effort certainly requires the creation of data models, NoSQL (open-source) database design repository and configurations, and an automated mechanism of sending and storage of MS experimentation data (raw and processed data) from the proteomics labs. Furthermore, this work package also aims to provide an integration mechanism of proteomics data (based on MIAPE guidelines) with HiGHmed ecosystem for a sustainable and open exchange of data across different nation-wide research settings. HiGHmed is an ongoing project funded by BMBF, which aims to develop and use innovative information infrastructures to increase the efficiency of clinical research and to swiftly translate research results into validated improvements of patient care [http://www.highmed.org].

Milestones

* MS 5.1 – Design and implementation of ArCare data repository
* MS 5.2 – Integration of ArCare repository with HiGhmed

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| **Work Package 5 Overview** | | | |
| WP Lead | [Medizinische Informatik](https://ecampus.uni-goettingen.de/sb/rds;jsessionid=20DF7A7C3B3DC74119311208F31FB0CB.s46?state=verpublish&status=init&vmfile=no&moduleCall=webInfo&publishConfFile=webInfoEinrichtung&publishSubDir=einrichtung&keep=y&einrichtung.eid=494) (UMG) | | |
| Partner |  |  |  |
| PM pro Partner |  |  |  |
| PM Gesamt |  |  |  |

**2.3.6 WP6 - Project Coordination**

Project coordination mainly consists of the following tasks:

Milestones

* MS 6.1 – Detailed elaboration of the project plan
* MS 6.2 – Monitoring of project workflow including the status of milestones and deliverables.
* MS 6.3 – Coordination of surveys to evaluate software components and their documentation
* MS 6.4 – Management of the project-specific infrastructures
* MS 6.5 – Financial, resource planning: budgeting, proof of the use of funds
* MS 6.6 – Preparation of regular reporting to project partners and the DFG
* MS 6.7 – Establishing and maintenance of communication networks of internal and external project partners
* MS 6.8 – Summarizing annual reports of the project results are finalized (Months 12, 24 and 30)

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| **Work Package 6 Overview** | | | |
| WP Lead | GWDG | | |
| Partner |  |  |  |
| PM pro Partner |  |  |  |
| PM Gesamt |  |  |  |



## Data handling

[Text]

## Other information

*Please use this section for any additional information you feel is relevant which has not been provided elsewhere.*

[Text]

## Descriptions of proposed investigations involving experiments on humans, human materials or animals

[Text]

## Information on scientific and financial involvement of international cooperation partners

[Text]

# Bibliography

* 1. Laizhong Cui, F. Richard Yu, and Qiao Yan, “When Big Data Meets Software-Defined Networking: SDN for Big Data and Big Data for SDN ”, IEEE Network, January/February 2016
  2. 2. EMC Digital Universe, “Driving data growth in HealthCare”,

[http://www.emc.com/analystreport/digital-universe-healthcare-vertical-report-ar.pd](http://www.emc.com/analyst         report/digital-universe-healthcare-vertical-report-ar.pd)f

3. Marx, Vivien, “The big challenges of big data”, Nature 2013/06/12/online, Nature Publishing Group, a division of Macmillan Publishers Limited. <http://dx.doi.org/10.1038/498255a10>,<https://www.nature.com/articles/498255a>

4. Intel, “[Transforming Healthcare IT Through Software-Defined Infrastructure”, printed in USA, 334041-001US](file://D:\\Work\\GWDG\\Proteomics\\DFG Proposal\\Transforming Healthcare IT Through Software-Defined Infrastructure\”, printed in USA, 334041-001US, https:\\www.intel.com\\content\\dam\\www\\public\\us\\en\\documents\\casestudies\\transforming-       healthcare-it-through-software-define-infrastructure.pdf)

5. Research and Markets, “[Global $432.2 Billion Software Defined Networking Market Analysis & Trends 2013-2017 & Industry Forecast to 2025 - Emergence of Hyper- Scale Cloud Networking”, Dublin, Feb23, 2017/PRNewswire,](file://D:\\Work\\GWDG\\Proteomics\\DFG Proposal\\Global $432.2 Billion Software Defined Networking Market Analysis & Trends 2013-2017 & Industry Forecast to 2025 - Emergence of Hyper-Scale Cloud Networking\”, Dublin, Feb23, 2017\\PRNewswire,  https:\\www.prnewswire.com\\news-releases\\global-4322-billion-software-defined-networking-Market-analysis--trends-2013-2017--industry-forecast-to-2025---emergence-of-hyper-scale-cloud-networking---research-and-markets-300412458.html)

[https://www.prnewswire.com/news-releases/global-4322-billion-software-defined- networking-Market-analysis--trends-2013-2017--industry-forecast-to-2025--- emergence-of-hyper-scale-cloud-networking---research-and-markets- 300412458.html](file://D:\\Work\\GWDG\\Proteomics\\DFG Proposal\\Global $432.2 Billion Software Defined Networking Market Analysis & Trends 2013-2017 & Industry Forecast to 2025 - Emergence of Hyper-Scale Cloud Networking\”, Dublin, Feb23, 2017\\PRNewswire,  https:\\www.prnewswire.com\\news-releases\\global-4322-billion-software-defined-networking-Market-analysis--trends-2013-2017--industry-forecast-to-2025---emergence-of-hyper-scale-cloud-networking---research-and-markets-300412458.html)

# 6. HIT Infrastructure, “Software-Defined Networking Advances Health IT Connectivity”,

[https://hitinfrastructure.com/news/software-defined-networking-advances-health-it- connectivity](https://hitinfrastructure.com/news/software-defined-networking-advances-health-it-%09%09connectivity)

7. <https://en.wikipedia.org/wiki/List_of_mass_spectrometry_software>

8. Salvador Martínez-Bartolomé, Eric W. Deutsch, Pierre-Alain Binz et al.,”Guidelines for reporting quantitative mass spectrometry based experiments in proteomics”, Journal of Proteomics, Volume 95,2013, Pages 84-88,ISSN 1874-3919, https://doi.org/10.1016/j.jprot.2013.02.026.

# Requested modules/funds

*Explain each item for each applicant (stating last name, first name). Follow the outline given in the relevant programme and module guidelines.*

[Text]

# Project requirements

## Employment status information

*For each applicant, state the last name, first name, and employment status (including duration of contract and funding body, if on a fixed-term contract).*

[Text]

## First-time proposal data

*Only if applicable: Last name, first name of first-time applicant.*

[Text]

## Composition of the project group

*List only those individuals who will work on the project but will not be paid out of the project funds. State each person’s name, academic title, employment status, and type of funding.*

[Text]

## Cooperation with other researchers

### Researchers with whom you have agreed to cooperate on this project

[Text]

### Researchers with whom you have collaborated scientifically within the past three years

[Text]

## Scientific equipment

*List larger instruments that will be available to you for the project. These may include large computer facilities if computing capacity will be needed.*

[Text]

## Project-relevant cooperation with commercial enterprises

*If applicable, please note the EU guidelines on state aid or contact your research institution in this regard.*

[Text]

## Project-relevant participation in commercial enterprises

*Information on connections between the project and the production branch of the enterprise.*

[Text]

# Additional information

*If applicable, please list proposals requesting major instrumentation and/or those previously submitted to a third party here.*

[Text]