Global Engage are pleased to announce the Global Pharma R&D Informatics Congress. The meeting will be held in Lisbon, Portugal and will take place on 30th November-1st December 2017.

Data is constantly being generated in the pharmaceutical industry from a wide number of sources creating opportunities to extract new insights into how diseases work and how drugs can be developed to provide targeted and effective treatments. This is only possible, though, if pharma and biotech companies can structure, integrate, and analyse large volumes of data to derive useful knowledge from it.

This congress looks at new methods and new technologies that get the best out of the information available and strategies to integrate internal and external systems so that all teams get the information they need to accelerate the drug development pipeline. Attracting experts working in all areas of pharmaceutical R&D IT and discovery informatics, the event will focus on innovations and strategies in these 4 key topic areas:

- Complex Data Analytics
- System Integration
- AI and Machine Learning
- Data Storage and Management

The conference will provide an interactive networking forum to both further develop and answer your queries through a vibrant exhibition room full of solution providers showcasing their technologies and software, poster presentation sessions, roundtable discussions, a dynamic panel discussion, and interactive Q&A sessions from a 40-strong speaker faculty examining the latest developments in the field.

EXPERT SPEAKERS Include:

- **MARGRET ASSFALG**
  Global Head, Research Informatics and Discovery Workflows, Roche

- **TUDOR OPREA**
  Professor and Chief of Translational Informatics, University of New Mexico, USA

- **JOHN BALDONI**
  SVP, InSilico Drug Discovery Unit, GSK

- **DEREK MARREN**
  Director of IT, Eli Lilly and Company
DAY 1 & 2 - TRACK 1 COMPLEX DATA ANALYTICS & METHOD DEVELOPMENT

- Big data management systems for research and clinical trials
- Knowledge representation and visualisation
- Improving data usability for different teams
- ELN and LIMS development
- Data mining methods
- In silico modelling
- Statistical significance analysis
- Data searching and algorithms
- Utilising real-world evidence and clinical trial feedback to improve the drug development process
- Sensitive data collection
- Maintaining high quality data
- Publication pooling and automated text mining
- Repurposing archived data
- Improving user interfaces

DAY 1, TRACK 2 - SYSTEM INTEGRATION AND WORKFLOW OPTIMISATION

- SDMS implementation and optimisation
- Automating workflow streamlining
- Integrating heterogeneous data sets
- Integrating different software and hardware systems
- Knowledge management
- Managing system changes and discontinued packages
- Using publication data to improve your own research
- Software for distributed computing
- Internal and External data sharing and collaboration
- Cross-discipline collaboration strategies
- Internal workflow management

DAY 2, TRACK 2

A) AI AND MACHINE LEARNING

- Deep learning
- Automation
- Intelligent workflow systems
- Implementing machine learning systems for improved target and biomarker discovery and validation
- Next steps for AI
- Virtual compound modelling and virtual screening
- Computer aided drug design

B) DATA STORAGE AND MANAGEMENT

- Data storage and maintenance methods
- Cloud storage
- Data Archiving methods
- Centralised data integration and accessibility for research and clinical trials
- Panel Discussion - The Current Challenges of Data Security and Regulation for the Pharmaceutical Industry

ROUNDTABLE DISCUSSIONS

1. Data standardisation within smart lab systems
2. Virtual compound modelling
3. Integrating systems to improve user interfaces
4. Leveraging IoT in the Lab
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CONFIRMED SPEAKERS

VASANT HONAVAR
Professor and Edward Frymoyer Chair of Information Sciences and Technology, Director of the Artificial Intelligence Research Laboratory and the Center for Big Data Analytics and Discovery Informatics, Pennsylvania State University, USA

JOHN DAVIS
Lead Scientist, Operational Technology and Informatics, Lonza Biologics

PETER SCHMIDTKE
Scientific Project Manager, Discngine

CONOR SCULLY
(Track Chair)
Senior Scientist, Heptares Therapeutics

GUY DESMARQUETS
Director of Strategy and Business Development, Software Solutions and Informatics Services, Bruker

IRINA EFIMENKO
Founder and CEO, Semantic Hub
KEYNOTE ADDRESS: 
VAIBHAV NARAYAN 
Vice President, Research and Therapeutic Area IT, Janssen Pharmaceuticals LLC 
Informatics of Early Disease Interception

• Therapeutic interventions have traditionally been developed for patients with established pathologies and overt clinical symptoms. However, many diseases are not tractable in later stages and therefore therapies will need developed that intervene earlier in the disease continuum.

• While earlier disease interception can be of considerable value to patients and the health care system, many barriers exist in the successful discovery and development of early stage therapeutics. These range from early science challenges, e.g. understanding of causative biological processes that lead to full blown pathology, to more downstream challenges such as demonstrating therapeutic benefit in patients with minimal symptoms or clinical deficits. This talk explores how Informatics and ‘Big Data’ can help address these challenges and enable discovery and development of ‘disease intercepting’ therapeutics.

KEYNOTE ADDRESS: 
JOHN BALDONI 
SVP, InSilico Drug Discovery Unit, GSK 
ATOM – Accelerating Therapeutics for Opportunities in Medicine

The success of the pharmaceutical industry has as its foundation a richness of failed programs. Those failed programs contain much more information than those that have succeeded. In a world of high performance computing these failed data have great value as the drug discovery process is modernized. ATOM was created to integrate high performance computing, scientific expertise in cancer, cutting edge technology and deep data sources that have historically not been available to researchers. ATOM is a precompetitive, public/private partnership established to create a place for like-minded organizations to come together to create new workflows for drug discovery, using cancer as the exemplar disease.

SOLUTION PROVIDER PRESENTATION: 
ERIC LITTLE 
Chief Data Officer, OSTHUS GmbH 
Allotrope Framework: How Semantics Can Help Transform R&D Data Across the Pharma Enterprise

Semantic technologies provide a powerful means for knowledge management, including data dictionaries, reference master data, taxonomies, and ontology models. These allow better understanding of patterns in data and provide significant value to Life Sciences organizations. The Allotrope Framework utilizes semantic metadata for R&D lab instruments, inside of a revolutionary file structure – The Allotrope Data Format (.ADF). The talk will discuss the Allotrope Data Framework and highlight how this framework is rapidly transforming the pharma R&D space. It will also show how Allotrope’s semantic framework can be extended into other areas such as Regulatory Affairs, Precision Medicine and Translational Medicine, as well as how other technologies such as Data Science, Cloud Computing, Data Lakes, Data Warehouses, and Archiving can all benefit from it.

SOLUTION PROVIDER PRESENTATION: 
EDDY VANDE WATER 
Senior Director, BIOVIA Field Applications 
Connecting Data and People to Drive Scientific Decision Making

• Pharma R&D Innovation is not hindered by the lack of scientific data. The challenge is the capture, access and analysis of large amounts of data generated throughout the product lifecycle (big data) and the disrupted decision workflow.

• Organizations need to make sure to capture and store data and their context for advanced analytics and machine learning for faster and better insights. And they need to enable collaboration by connecting data and people so the data flow provides decision makers with relevant information.

• This presentation covers scientific decision process challenges, possible workflow improvements, examples of advanced analytics and how a platform-based strategy can deliver data, information and knowledge to the right people at the right time and provide R&D organizations with a competitive advantage.
TUDOR OPREA
Professor and Chief of Translational Informatics, University of New Mexico, USA
Illuminating the Druggable Genome and the Quest for new Drug Targets
The Illuminating the Druggable Genome Knowledge Management Center (IDG KMC) evaluates, organizes and distills more than 80 protein-centric and over 20 gene-centric resources for over 20,000 curated human proteins. KMC knowledge graphs (ontologies) are focused on five major branches of the target knowledge tree (tkt): Genotype, Phenotype, Expression, Structure and Function, and Interactions and Pathways, each with appropriate sub-branches (normal vs. disease, gender, etc.). Complex data integration shows that only 3% of the proteome are drug targets associated with mechanism of action (“Tclin”), while 2 out of 5 human proteins lack functional information and disease relevance (“Tdark”). Using advanced analytics and machine learning, tkt knowledge graphs utilize biological systems networks linked predictions (meta-paths) to articulate knowledge via computational assertions, with focus on phenotype/disease associations for target and drug repurposing. More information about IDG KMC is available at http://targetcentral.ws/ (IDG Consortium), https://pharos.nih.gov/idg/index (Targets) and http://drugcentral.org/ (Medicines). Our interactive target-disease explorer is available at http://newdrugtargets.org/.

JONNY WRAY
Head of Discovery Informatics, e-Therapeutics
Network Driven Drug Discovery: Development of a computational network biology based approach to early drug discovery
• Conceptual foundations of an approach to early drug discovery that explicitly addresses the complex system level aspects of cellular disease mechanisms.
• The application of the concepts, based on network biology and analytics, to the development of a practical discovery process.
• Details of the implementation of an in silico drug discovery engine, consisting of our proprietary data libraries and computational platform, based on the described conceptual foundations.
• Validation of the approach via phenotypic screening results from a number of internal of projects across a range of biological mechanisms.

ALEXANDER KRUPP
Head of Computational Life Science IT, Pharmaceuticals R&D, Bayer
How to eat the elephant – getting information integration to work
• How to make information architecture a priority in corporate environments and deliver immediate impact?
• Insights into a structured approach to overcome the core challenges of large enterprises to build key data assets
• Best practices in applying this framework to a pharmaceutical R&D business

SOLUTION PROVIDER PRESENTATION:
HANS DE BIE
Senior Director Solution Delivery, ACD/Labs
Addressing the challenges of Analytical Data Management in R&D
Analytical data is at the heart of pharmaceutical research and development efforts and often required in response to critical questions raised in regulatory filings, or when there is an irregularity in manufacturing. Many organizations, however, continue to struggle with the variety of different formats, instrument vendors, and search and retrieval of analytical data. Cloud computing, automation, data integrity, and externalization are key topics for organizations looking for new ways to integrate analytical systems into their core informatics stack. In this presentation we will discuss the fundamental underpinnings of automated data capture, data exchange formats, data integrity, and next generation analytical data management systems.
FRIEDRICH RIPPmann
Director of Computational Chemistry and Biology, Merck KGaA
Boosting discovery research productivity by generating novel digital components, and integrating them into coherent workflows

With recent methodological and technological progress, and the increase of relevant electronically accessible data, drug discovery is now on the verge of becoming a truly predictive and, in aspects, even quantitative science. We will highlight the areas of progress, e.g. cryo-Electron Microscopy, large-scale virtual compound libraries, Deep Learning-based predictive models, quantitative estimation of binding constants, and will touch on the infrastructure requirements, where large-scale GPU and Cloud Computing play a central role. Towards the goal of Digital Drug Discovery, other areas show great promise as well, ranging from comprehensive Artificial Intelligence-supported workflows, to the computer-assisted "connected" lab. Altogether, a paradigm change towards "leading by design" is under way in the pharma industry. Consequences of this will be discussed, including resources, people attitudes, collaboration, and more.

ASIM SIDDQUI
CTO, Numedii
Tackling rare diseases with big data
There are an estimated 30,000 diseases and typically only the most common have treatments. To develop therapeutics for all these conditions, the cost of drug development must be substantially reduced. This can be done by increasing the chances of a drug passing human trials and through the use of drugs for which safety in humans is already known or can be deduced. At NuMedii, we are addressing these points by applying, big data methods that integrate biological knowledge built on trillions of data points. We use AI and machine learning to interpret that information and create drug-disease linkages. Using this approach, we have developed a pipeline in inflammatory disease and oncology with one candidate ready for testing in humans.

BIN CHEN
Assistant Professor, University of California San Francisco, USA
Can data scientists lead the discovery of therapeutic in cancer?
Rapidly decreasing costs of molecular measurement technologies not only enable profiling of disease sample molecular features at different levels (e.g., transcriptome, proteome, metabolome) but also enable measuring of cellular signatures of individual drugs in clinically relevant models. Exploring systematic approaches to find drugs for diseases through various molecular features is important in the discovery of new therapeutics. We propose a systems-approach to identifying drugs that reverse the molecular state of a disease. We used this approach to discover drug candidates for hepatocellular carcinoma and Ewing's sarcoma. In this talk, I will talk about this systems-approach and share how a data scientist led the discovery of new therapeutic candidates for liver cancer.

MARIE HELENE ANDERSSON
Senior Manager, IT Strategy and Knowledge Management, Global Pharmaceutical R&D, Ferring Pharmaceuticals
Sharing knowledge internally
• 'Data as an asset' principles
• Search, share and access

SOLUTION PROVIDER PRESENTATION:
PETER SCHMIDTKE
Scientific Project Manager, Discgine
3decision®: Bringing structural data analytics to the masses
Rational structure based drug design techniques are still used in >50% of all drug discovery projects. They strongly rely on structural data for proteins and protein:ligand complexes. Unfortunately, a more widespread adoption of these techniques is hindered by the inconsistent data persistence and the mere complexity of analysing structural data. 3decision® is a structural analytics platform aiming to facilitate and speed up the use of structural data for Molecular Modelers and Medicinal Chemists. It transforms the massive amount of data coming from 3D structures, sequence and other meta data into structural knowledge that you can exploit in your day-to-day work. You no longer need to be an expert to exploit the full potential of the structural interactome and pocketome.

SOLUTION PROVIDER PRESENTATION:
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SOLUTION PROVIDER PRESENTATION:
PAUL DENNY-GOULDSON
VP of Strategic Solutions, IDBS
Title TBC
**Chair’s Closing Remarks / End of Day One**

**Networking Drinks Reception**

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**ROUNDTABLE DISCUSSIONS:**

1. **Data standardisation within smart lab systems**
   - **Daniel Juchli**
   - CTO, Standardization in Lab Automation (SiLA)

2. **Virtual compound modelling**
   - **Friedrich Rippmann**
   - Director of Computational Chemistry and Biology, Merck KGaA

3. **Integrating systems to improve user interfaces**
   - **Dimitar Hristozov**
   - Team Leader, Research Informatics, Evotec

4. **Leveraging IoT in the Lab**
   - **Daniela Jansen**
   - Director of Solution Marketing, Dassault Systèmes BIOVIA

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**DEREK MARREN**

Director of IT, Eli Lilly and Company

*What you are never told about Public - Private Consortia and Pre-competitive Engagements: so just how do they work and why should you care*

There are many philanthropic reasons for collaborations and we hear many statements from those who say that pre-competitive collaborations are a way of providing value to the members with the combined focus of vision and common goals, spreading the risk and getting more for the monetary investment. With examples of real success stories and those which leave us with nightmares, why do we continue to do it, and what have we learned from the various forms of these pre-competitive ventures… Is there real gold at the end of this pre-competitive rainbow, in this presentation I will share my experiences in this arena.

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**JAY BERGERON**

Director of Translational and Bioinformatics, Pfizer

*eTRIKS: Successes, Surprises and Lessons on the Verge of Completing the Largest General Translational Informatics Public Private Partnership to Date*

- eTRIKS is a 5 year IMI project to provide a translational informatics products and services to other IMI programs and Eu PPPs
- eTRIKS served over 60 projects during its tenure
- eTRIKS created a tranSMART-based platform that is fully open source

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**JEREMY EDMUNDS**

Director of Immunology Chemistry, AbbVie

*Measuring project success and Shannon’s maxim: the enemy knows the system*

Discovery projects often require long periods of time and large amount of resources to proceed from an exploratory phase to clinical candidate generation. It is common for hundreds or thousands of compounds to be generated over the course of several years by project teams pursuing multiple lead series, often while facing many roadblocks along the way. Frequently one is left to wonder whether projects should continue or whether additional optimisation efforts are futile. This talk will illustrate an objective tractability approach retrospectively applied within Abbvie Immunology for projects achieving clinical candidates and those curtailed in the lead optimization phase.

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17:30 Chair’s Closing Remarks / End of Day One

17:30-18:30 Networking Drinks Reception
KEYNOTE ADDRESS: MARGRET ASSFALG  
Global Head, Research Informatics and Discovery Workflows, Roche, Switzerland  
*Introduction of a knowledge system in Discovery spanning processes and data analysis across several therapeutic modalities*

The talk will describe the design, implementation, and introduction of a process and knowledge management system in Discovery research at Roche. The described system spans across 3 therapeutic modalities; small molecules, protein therapeutics, and RNA therapeutics.

KEYNOTE ADDRESS: BRANDON ALLGOOD  
CTO and Co-Founder, Numerate Inc  
*AI in drug discovery: Current state and opportunities*

- Review the state of AI currently being applied to drug discovery through case studies: both biology forward and clinic backward
- Examine some of the challenges with AI, such as, explainability vs predictability and handling noise and bias
- Explore the future of AI in drug discovery

SOLUTION PROVIDER PRESENTATION: ARIE BAAK  
Co-founder, Euretos  
*In-silico identification & validation of targets and biomarkers for the casual IT user*

Life sciences research is increasingly relying on big data analytics to drive scientific discovery. The majority of researchers are, however, casual users of IT and need the support of highly skilled data experts and bioinformaticians to benefit from these technologies. The Euretos platform bridges this divide and puts the power of bioinformatics and big data analytics directly in the hands of biologists and researchers. Achieving this requires an approach that fundamentally matches the needs, interests and abilities of this type of user.

The presentation will cover the following themes:
- The life sciences researcher as casual user of IT
- Integrating in-silico with in-vitro and in-vivo research
- Organising knowledge for life sciences research
- Artificial Intelligence and NLP
- Case studies

SONALI QUANTIUS  
Director of Computational Biology, GSK  
*Advanced computational analysis methods for big data – Title TBC*

PATRICK KEOHANE  
Chief Medical Officer, Benevolent Bio  
*A CMO’s view of disruptive technology*

- 14,000 identified human diseases. 5,000 of these diseases are ‘treated diseases’, 9,000 diseases ineffectively treated
- A life science paper is published every 30 seconds, there are 10,000 updates to PubMed every day. Scientists cannot keep up.
- AI can offer a solution to this problem, and machine learning technology is radically changing how new medicines are discovered and developed. AI is augmenting not bypassing human intelligence and is essential to disrupt the legacy processes of medicines discovery and development.
OLIVER KOCH
Group Leader, Medicinal Chemistry, Technical University of Dortmund, Germany
A medicinal chemistry guide to binding site comparison
The growing number of published protein structures and the vast amount of software to detect binding site similarities allow a fast and user-friendly comparison of thousands of protein pockets. The identification of binding site similarities can have an impact on binding site identification, function annotation, polypharmacology, off-target prediction, and drug repurposing [1]. Nevertheless, the choice of a suitable tool, for example, to compare a binding site of interest to various known binding sites is still a difficult task. Based on an exhaustive evaluation it becomes obvious that the choice highly depends on the aim of the study. This presentation will focus on different applications and present a detailed guide to binding site comparison.

WILLEM VAN HOORN
Head of ChemoInformatics, Exscientia
Scaling de novo design, from single target to disease portfolio
An overview is given of the technology that Exscientia applies to automatically design patentable compounds and how this technology has been successfully used in collaborations designing compounds for single protein targets as well as target combinations. Finally it is shown how scaling the technology enabled designing compounds against a matrix of disease-related targets.

JENNIFER RUSSO WORTMAN
Senior Director, Bioinformatics, Seres Therapeutics, USA
Unravelling microbiome signatures for drug design
Seres Therapeutics is a clinical-stage company with the mission to transform the lives of patients worldwide with revolutionary microbiome therapeutics. Our proprietary reverse translation discovery and design platform enables us to identify key alterations in the microbiome that are associated with or lead to specific diseases, and to rationally design tailored therapies that disrupt the disease state and may establish a healthy microbiome. There are myriad technical challenges to be overcome transitioning a microbiome therapeutic through the drug discovery pipeline. Seres is well positioned to tackle these challenges leveraging our discovery informatics capabilities, extensive strain library and demonstrated ability to translate microbiome candidates into clinical trials.

MICHAL FOJTAK
Research Consultant, Biology Results & Neuroscience IT, Eli Lilly and Company
Animal behavior detection from experiment videos
A tale of how we implemented Deep Learning approach for detection and classification of spatio-temporal activities in video signals.
- Evaluation of supervised learning models
- Neural Network Training and inference at scale – findings and observations on our way towards GPU cluster

SOLUTION PROVIDER PRESENTATION:
IRINA EFIMENKO
Founder and CEO, Semantic Hub
Automated identification and qualification of promising drug candidates based on semantic analysis of "big text data"
Semantic Hub helps the Experts of R&D departments in pharmaceutical companies to significantly accelerate the identification of promising developments (e.g. new targets, molecules, combinations, delivery systems) based on the semantic analysis of "big text data". We provide knowledge extraction on drug candidates from a variety of information sources (papers, posters, patents, clinical trial results, news, etc.) according to our customers' criteria, and the automated qualification and evaluation of candidates based on success and risk factors.
GLOBAL PHARMA R&D INFORMATICS CONGRESS 2017

SOLUTION PROVIDER PRESENTATION:
GUY DESMARQUETS
Director of Strategy and Business Development, Software Solutions and Informatics Services, Bruker

Improving NMR data quality, consistency and standardization for better decision-making support and improved mining of stored analytical information.

Summary: The quantitative nature of NMR makes it a very efficient choice over other analytical techniques such as LC-MS, but for decades the technology has been perceived as complex and a tool for experts. Today’s NMR is easier to use and to further expand its accessibility. Bruker has developed an informatics environment which includes automated performance validation and experiment optimization at the spectrometer level. Additional enhancements include expert-systems providing results in full automation, integration of the applications into third parties software such as ELN or LIMS, conversion into universal format for efficient mining, tools and SOPs for GxP, 21CFRp11, QbD compliance and more.

COMPANY SHOWCASE

For sponsorship opportunities please contact
Faizel Ismail at faizel@globalengage.co.uk

DATA STORAGE AND MANAGEMENT

TRACK CHAIR: JOHN DAVIS, Lead Scientist, Operational Technology and Informatics, Lonza Biologics

PANEL DISCUSSION:
The Current Challenges of Data Security and Regulation for the Pharmaceutical Industry

BRANDON ALLGOOD
CTO and Co-Founder, Numerate Inc

SARION BOWERS
Research Policy Lead, Sanger Institute

JAMES WILLANS
Chief Technology Officer, Lhasa Limited

MARGRET ASSFALG
Global Head, Research Informatics and Discovery Workflows, Roche

JAY BERGERON
Director of Translational and Bioinformatics, Pfizer
## ROUNDTABLE DISCUSSIONS:

### TABLE 1: Data Standardisation Within Smart Labs

**DANIEL JUCHLI**  
CTO, Standardization in Lab Automation (SiLA), Switzerland

**BURKHARD SCHAEFER**  
President, BSSN Software GmbH

- Introduction to SiLA – Standards in Laboratory Automation – The New SiLA 2 Framework For Lab Automation and AnIML – Analytical Information Markup Language
- How to employ Internet of Things (IoT) and Industry 4.0 Concepts in Smart Labs
- SiLA compared to other standards and organizations like Pistoia, OPC Foundation, Allotrope Foundation

### TABLE 2: Virtual Compound Modelling

**FRIEDRICH RIPPMANN**  
Director of Computational Chemistry and Biology, Merck KGaA, Germany

- Large-scale virtual libraries: how to generate and use them?
- How to assess impact?
- Integrated IT from compound idea to synthesised and tested compound

### TABLE 3: Integrating Systems to Improve User Interfaces

**DIMITAR HRISTOZOV**  
Team Leader, Research Informatics, Evotec, UK

- Bringing computational tools to the scientist’s work bench – is the web browser the operating system of the 21st century?
- Workflow management suites as a software integration platform
- Drug discovery on the go - should computational tools go mobile?
- Interfacing open source software - approaches to and challenges with leveraging the work of the community

### TABLE 4: Leveraging IoT in the Lab

**DANIELA JANSEN**  
Director of Solution Marketing, Dassault Systèmes BIOVIA

New technologies allow the industry to connect a plethora of different new devices and go beyond simple integration of lab equipment. The Internet of Things (IoT) can have a deep impact on data collection, data integration and collaboration in the lab in research, development and quality. In this round table we will discuss the requirement for IoT in the lab, (potential) value and outcomes, experiences and lessons learned as well as the impact it can have on the lab and on the larger organization.
MAKING A POSTER PRESENTATION

Poster presentation sessions will take place in breaks and alongside the other breakout sessions of the conference. Your presentation will be displayed in a dedicated area, with the other accepted posters from industry and academic presenters. We also issue a poster eBook to all attendees with your full abstract in and can share your poster as a PDF after the meeting if you desire (optional). Whether looking for funding, employment opportunities or simply wanting to share your work with a like-minded and focused group, these are an excellent way to join the heart of this congress.

In order to present a poster at the congress you need to be registered as a delegate. Please note that there is limited space available and poster space is assigned on a first come first served basis (subject to checks and successful registration). We charge an admin fee of €100 to industry delegates to present, that goes towards the shared cost of providing the poster presentation area and display boards, guides etc. This fee is waived for those representing academic institutions and not for profit organisations.
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For more information, please contact Scott Taylor at: scott@globalengage.co.uk
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Hotel accommodation will be available at a group rate.

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For updates on the Global Pharma R&D Informatics Congress 2017, plus free resources and reports, as and when our speakers authorise their release dates, check for updates at:
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