

CAIMAN project



Making most of our data with D360

The CAIMAN project

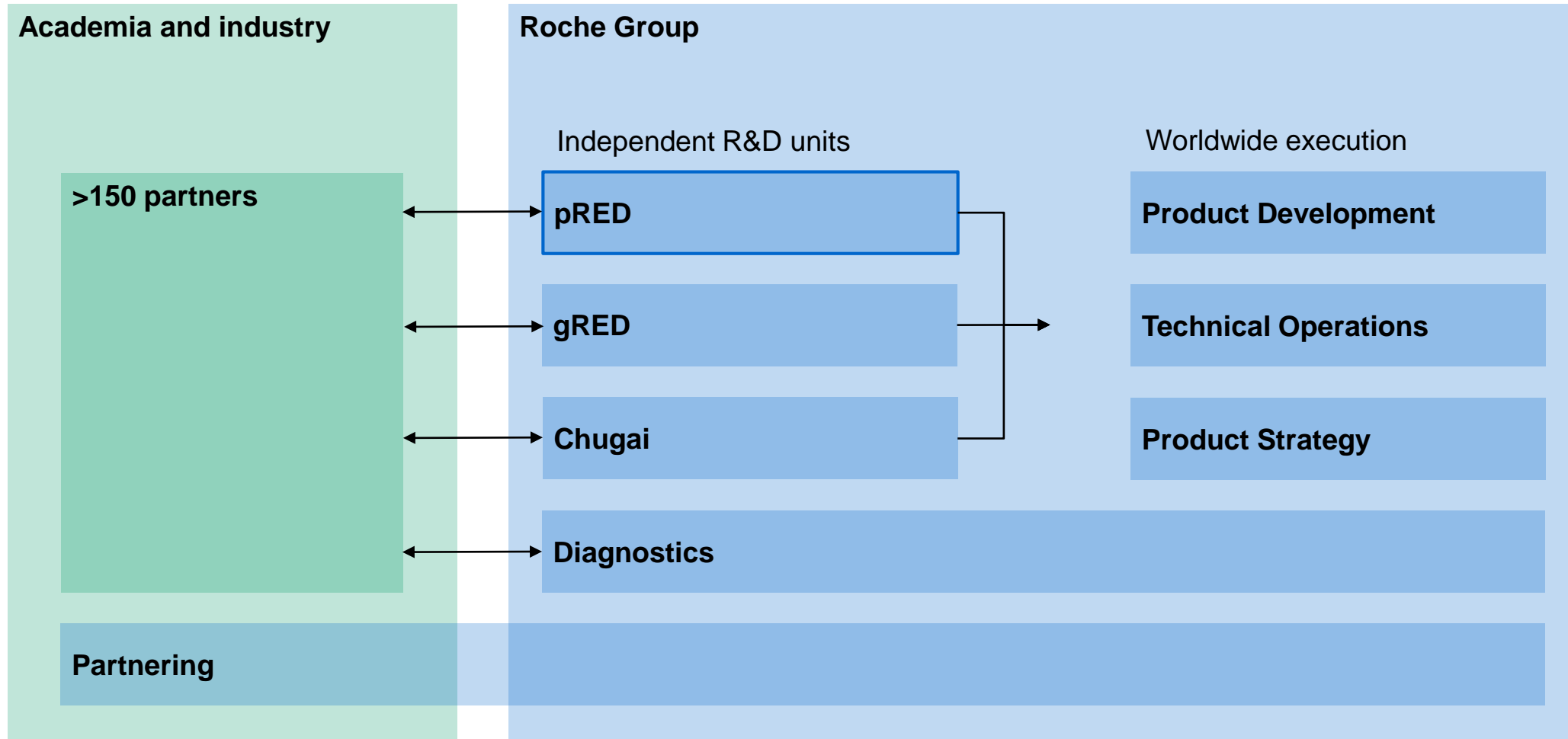
Making most of our data with D360

***Marc Pompiati, LMR, Roche Innovation Center
Munich***

Roche *pRED*

The Roche Group organisational structure

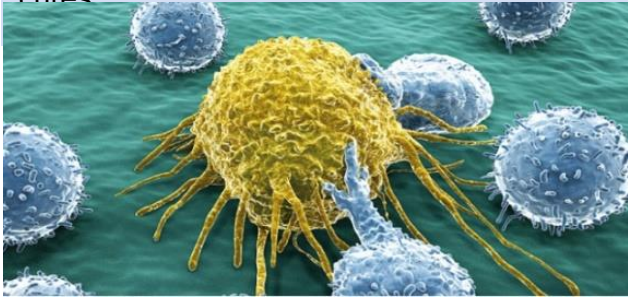
Roche pRED is one of three independent research & development units



The Roche pRED disease areas

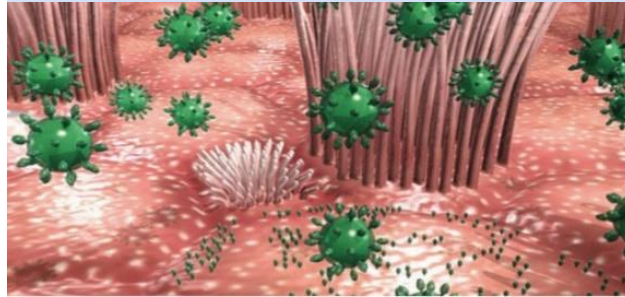
Oncology

Combining cancer immunotherapy and tumour targeted therapy approaches to seek cures



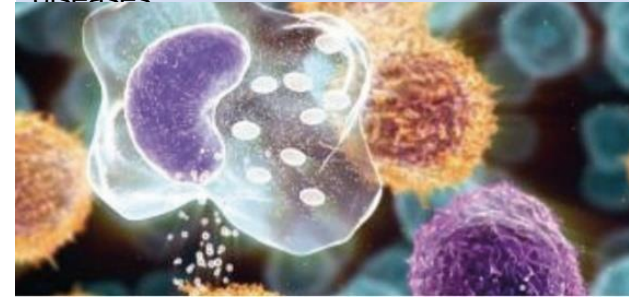
Infectious diseases

Developing targeted treatments for life-threatening infectious diseases



Immunology & inflammation

Developing differentiated medicines for people with immune and inflammatory diseases



Ophthalmology

Restoring sight



Neuroscience

Developing medicines for serious neurological diseases



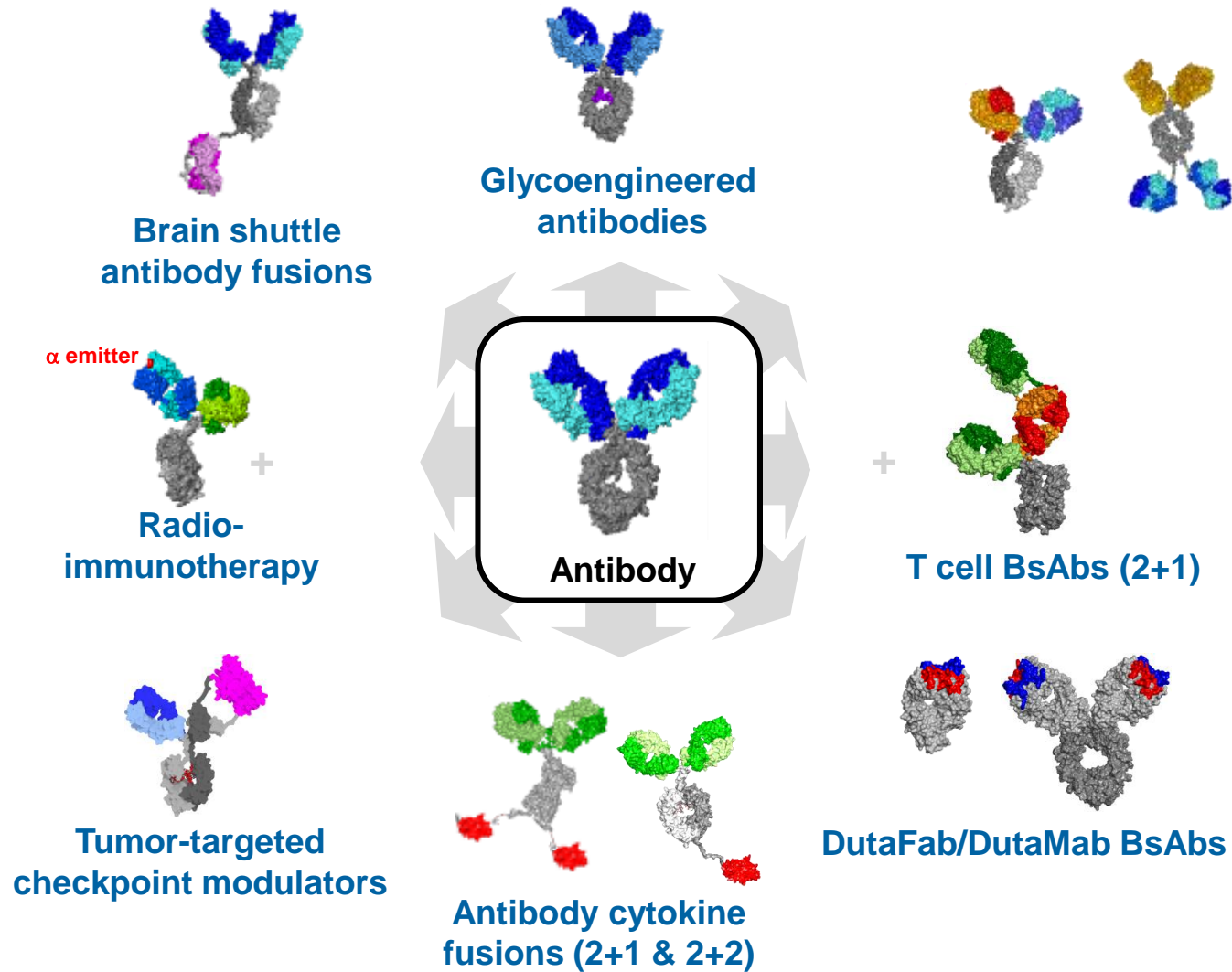
Monogenic rare diseases

Tackling inherited genetic disorders



Roche pRED's modular biologics

Advancing therapeutic antibody sciences






Roche business opportunities and digitalization



- Digitalization is creating exciting new opportunities .
- To be equally successful in this new environment, Roche pRED depends on making better use of our research data, which continue to increase exponentially.
- The **CAIMAN project** is part of the Lab of the future initiative that addresses digitalization and supports the overall pRED digitalization goals.

LMR: Lab of the future

Embrace digital and automated solutions to aid discover and develop superior biologics

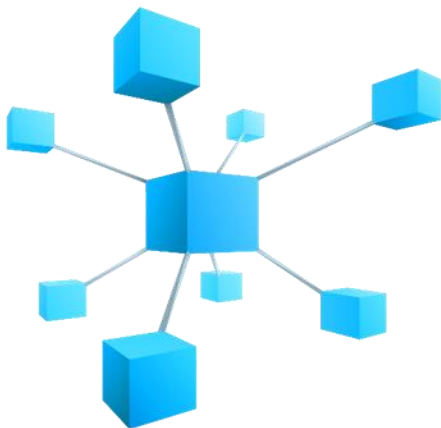
Landscape	Data&learning	People
<p>We are developing ONE landscape from registration, data capture, visualisation to interpretation and learning.</p> 	<p>Value will increasingly be generated by digital and automated solutions. Data are a central asset.</p> 	<p>Skills in biology, biotechnology, data science and automation is needed.</p> 

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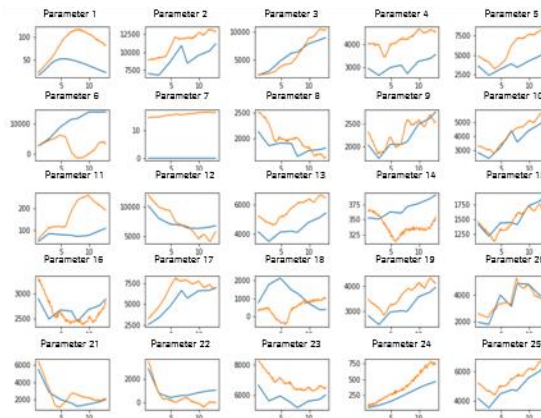
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People

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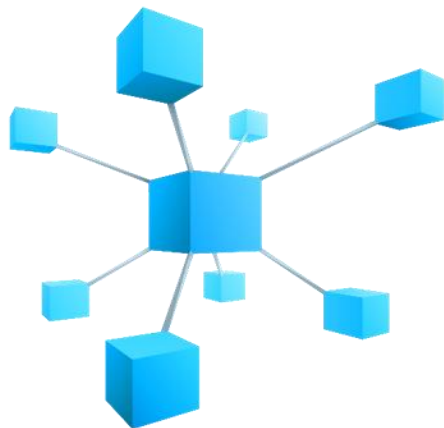


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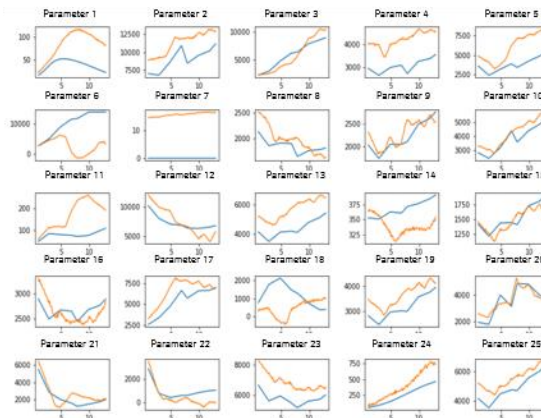
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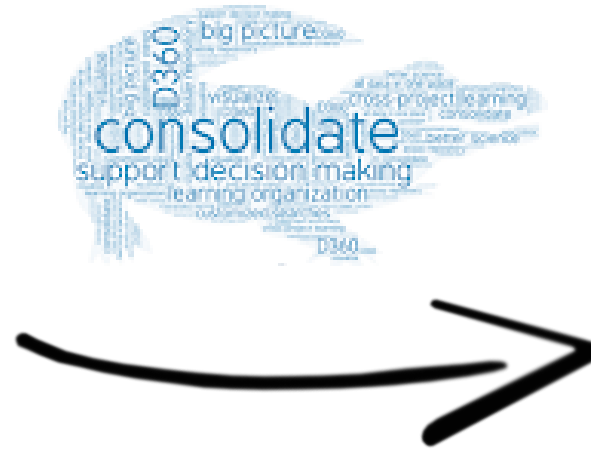
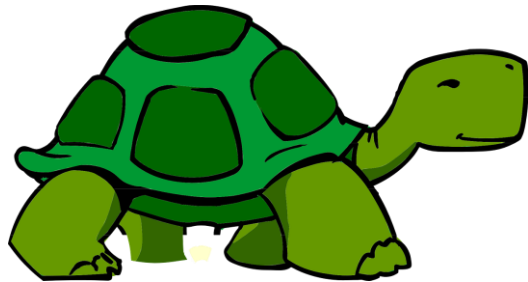
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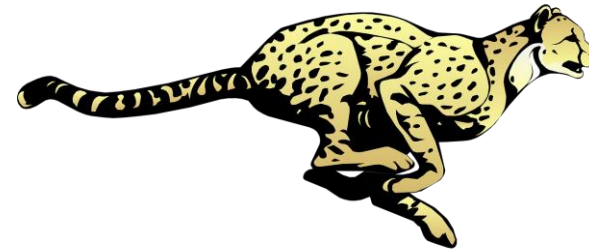
The CAIMAN project

CAIMAN = Consolidated Platform for **A**ssay, **I**nventory, **M**olecule and **A**nalytics Data

Before CAIMAN

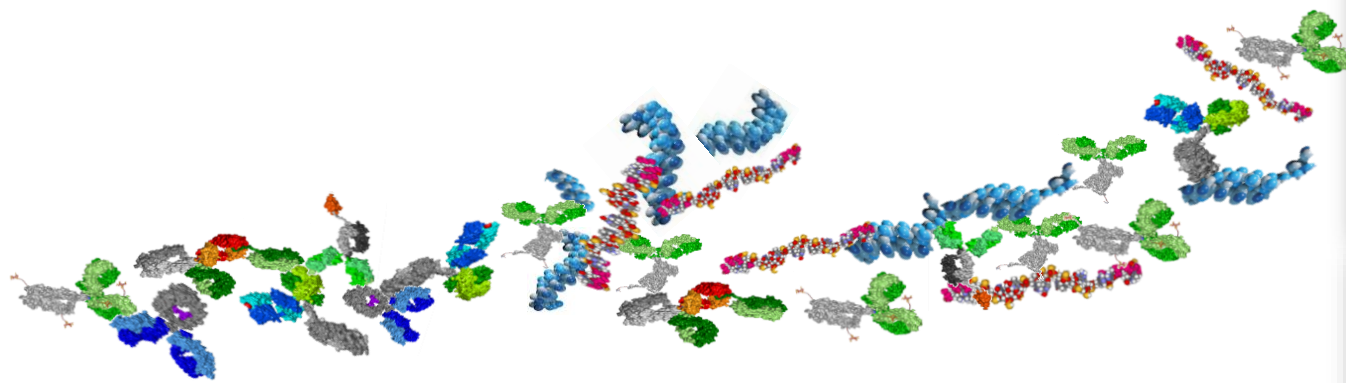


After CAIMAN



CAIMAN Vision

A single interface for accessing and analyzing data across modalities and achieving quality data mining for project teams to increase efficiency and reduce effort for advancing portfolio projects



The goals of the CAIMAN project

- Make access, integration and analysis of relevant and understandable data less cumbersome and time-consuming and more reliable.
- Help shift the focus from data collection and capture to data analysis by establishing automated data workflows that use existing assay data-capturing tools like BioBook and registration systems like TaPIR, and merging them with other existing project metadata into scientifically meaningful records.
- Guarantee that high-quality data are available in pRED for informed decisions by establishing a review process for assay description and data structure.

LMR: Lab of the future

The Project



TaPIR

▶ Therapeutic Protein Identifier and Registration

SaLaManDeR

▶ Sample Management

CAIMAN

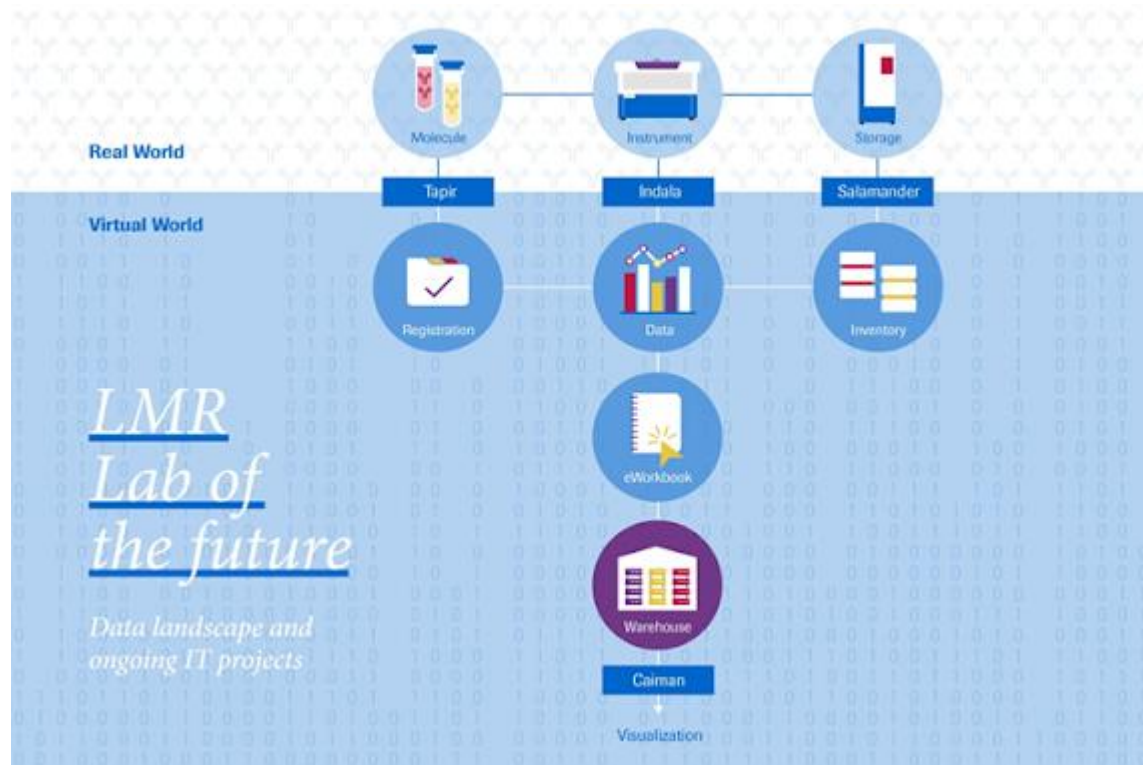
▶ Consolidated Platform for Assay, Inventory, Molecule and Analytics Data

INDALA

▶ Integrated Data Analysis for LMR Automation

LMR: Lab of the future

The Project



TaPIR

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CAIMAN Definition Phase

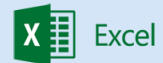
In a Nutshell – User Stories and Data define the Project



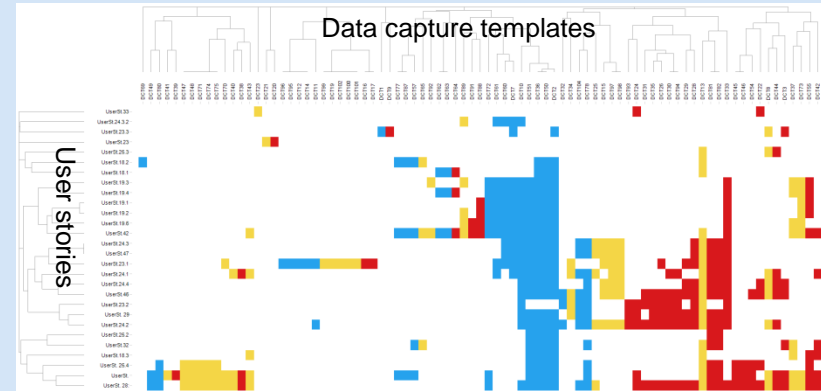
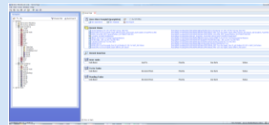
As a <project leader> I want <goal> so that <reason>.



PowerPoint



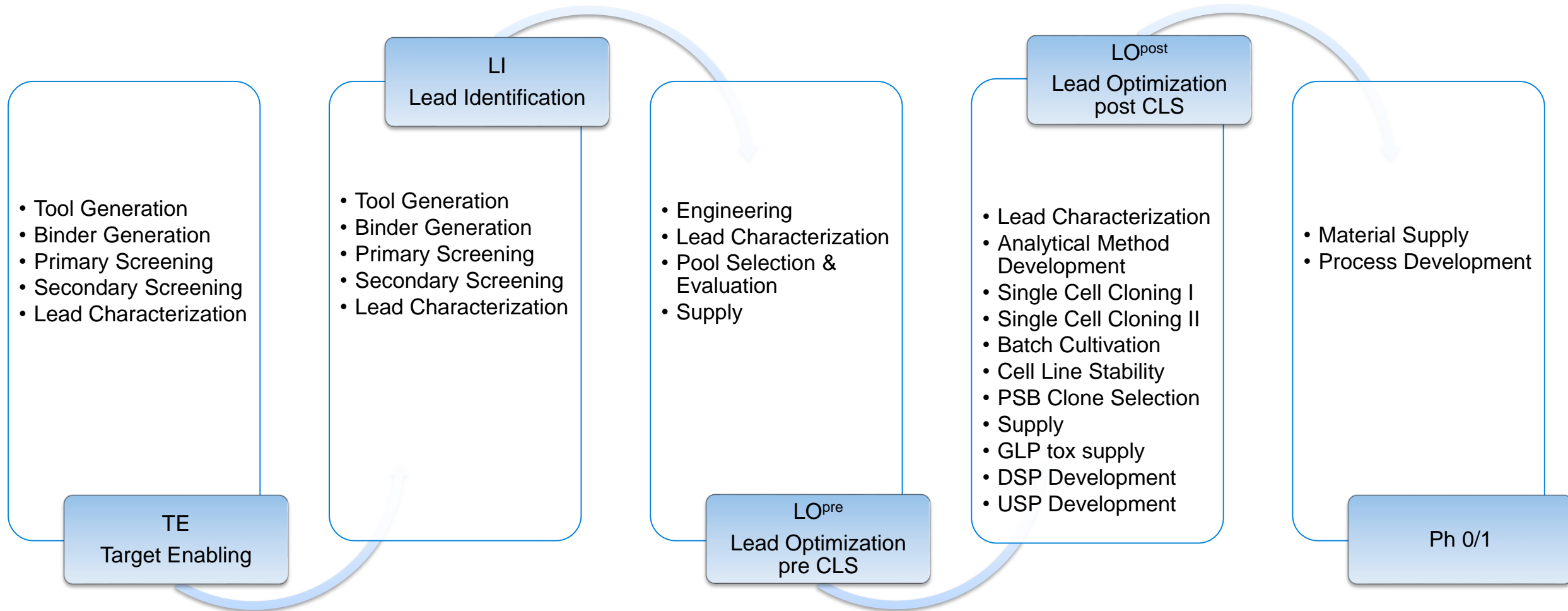
Excel



- Minor effort
- Medium effort
- Major effort

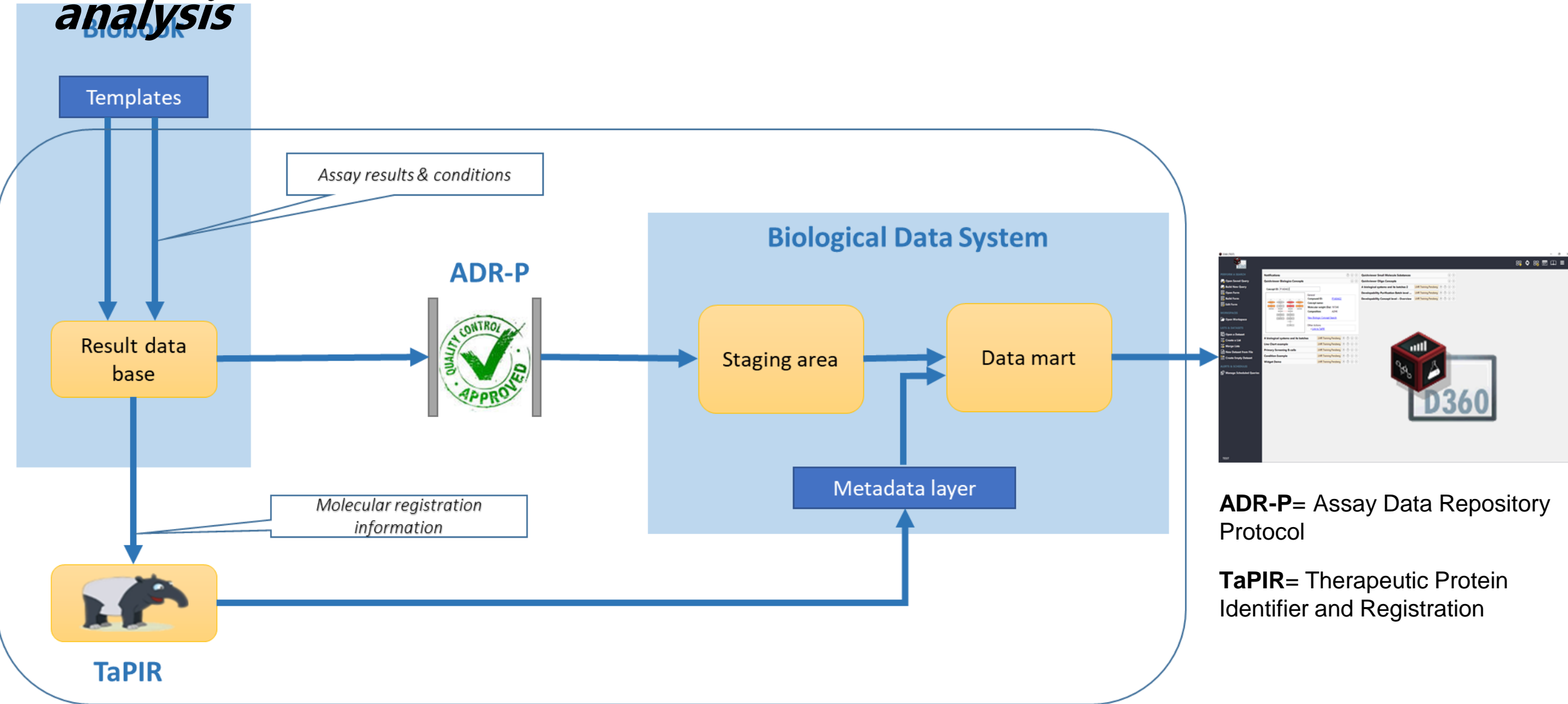
User Stories evolved into **23** Decision Points in **5** major phases

The CAIMAN phases



The CAIMAN solution

A modular landscape and foundation for advanced data analysis



ADR-P= Assay Data Repository Protocol

TaPIR= Therapeutic Protein Identifier and Registration

Implementation of quality controlled assay information



Assay data upload: IDBS BioBook templates

Quality control: [Roche ADR-P System](#)

Assay Data warehouse: Roche BDS System

From detailed assay description

to template

Title: Purification of antibodies and antibody like constructs on a liquid handling platform using OPUS robocolumns

LIMS protocol name: |

Assay owner: |

Date/Site: 27.03.2018

ASSAY PURPOSE & PRINCIPLE

Protein samples are purified from cell culture supernatants before being tested in assays, because cell culture medium can disturb assay results. Another reason is that proteins are concentrated for further analysis, in order to improve signal-to-noise ratio in the assay.

A common technique is affinity chromatography. It is based on specific interaction between antibodies (or antibody like constructs, Fabs ...) and chromatography material (see Figure 1). The antibodies bind to the column and are separated from the undesired material that does not interact. Washing the stationary phase with washing buffer, undesired molecules are eluted first while the desired proteins are eluted using an acidic buffer.

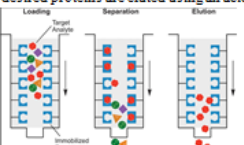


Figure 1: Principle of affinity chromatography

For the fully automated purification of antibodies in parallel, the liquid handling robot Freedom EVO from Tecan in combination with OPUS robocolumns (Repligen) (see Figure 2) is used

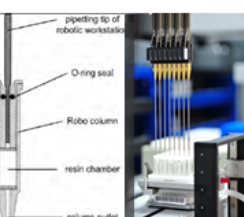
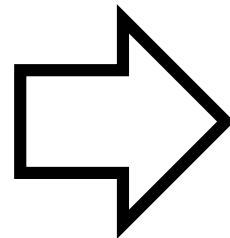


Figure 2: OPUS Robocolumn

The robocolumns can be filled with any commercial available chromatography material. Loading of the robocolumn is performed using an 8 channel liquid handling arm (LiHa) with steel needles.

Protein concentration is determined by UV measurement at 280 nm. Sample volume is determined by measurement at 998 nm and 900 nm.



Results: PRODUCT_CONCENTRATION, PRODUCT_VOLUME, PRODUCT_AMOUNT	
Conditions: LMR_PROJECT_PHASE, CHROMATOGRAPHIC_COLUMN, PROJECT, BUFFER, BUFFER_PH, TAPIR_BATCH	
LIMS protocol reference: IgG_Micropurification_Tecan/v1	
Annotation scheme: general	Protocol comment:
Owner: werneru	Editors: avinashn,werneru (-> RUD)
Last modified by: rocheo	Detailed assay protocol: Micropurification (-> Template)
Creation site: PENZBERG	Data producer group: PhysChem
NMP Project short name: PHYSICOCHEMICAL_STUDIES [-> details]	Used for multiple projects: No
Biosample & Target	
Biological system: in-vitro	Species: ~NotApplicable
	Strain:
Tissue type: ~NotApplicable	Cell line: (-> RNCB)
Subcellular fraction: ~NotApplicable	Assay target: (-> IDM)

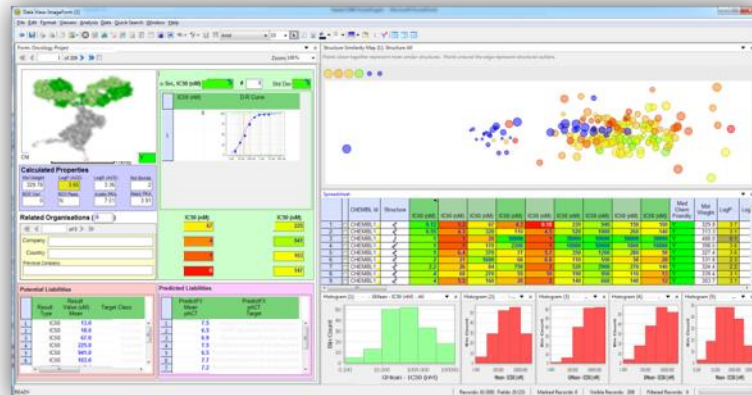
Technical & data query template coverage

23 data query templates (decision points) in total, **13** decision points ready

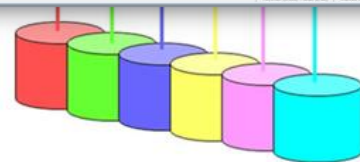
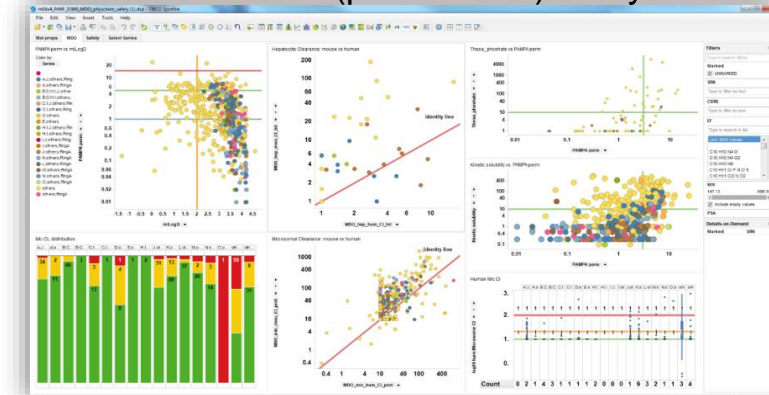
55 Spotfire visualizations supporting **8** decision points, **22** D360 visualizations supporting, **3** decision points

7 special data categories based on TaPIR data packages, **4** additional data sources integrated, **1** data source left

Data access, project layouts and analyses



Advanced (pre-defined) analyses



Multiple data sources
(internal and external)

Technical & data query template coverage

631 experiments loaded to BDS/D360 PROD (**128** Assay protocols, **117** LIMS protocols , **207.539** TaPIR batches, **1.184.545** data points, **16** TaPIR projects)

In total: **1085** Assay protocols created, **42** assay protocol owner

65 BioBook templates overall productive or close to productive

Title: Purification of antibodies and antibody like constructs on a liquid handling platform using OPUS robocolumns

LIMS protocol name: |

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Date/Site: | 27.03.2018

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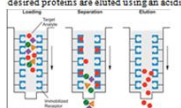


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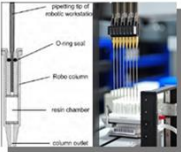


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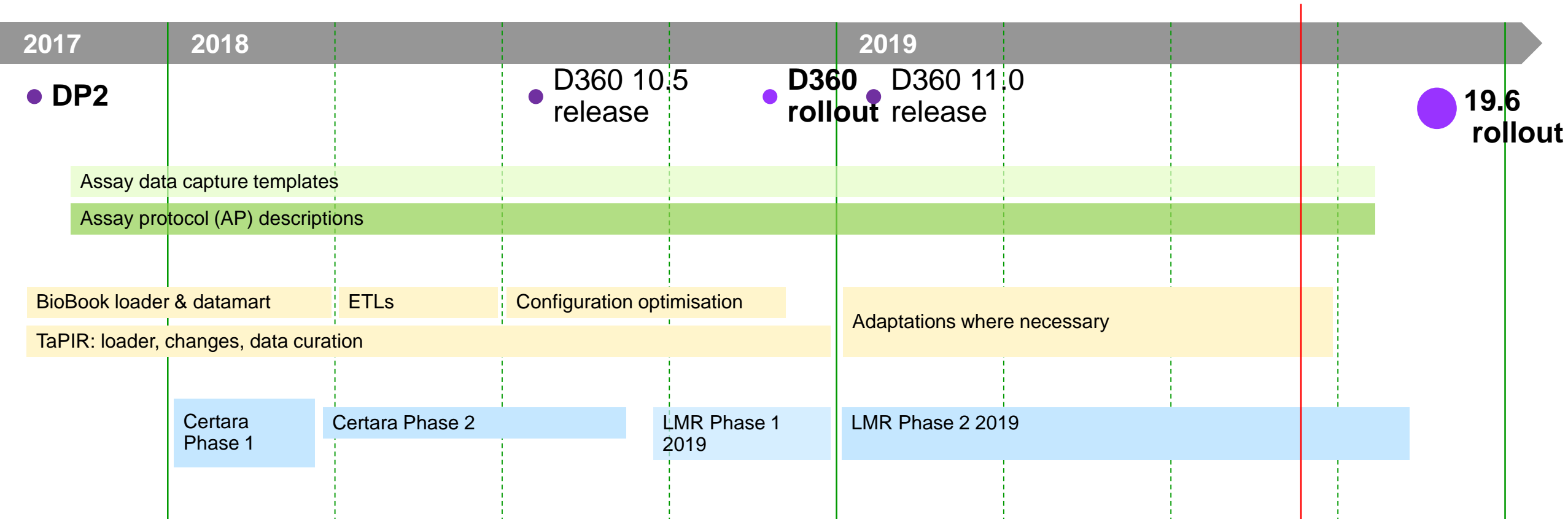
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LIMS protocol reference:	IgG_Micropurification_Tecan/v1	Protocol comment:
Annotation scheme:	general	Editors:
Owner:	werneru	(-> RUD)
Last modified by:	rocheo	Detailed assay protocol:
Creation site:	PENZBERG	(-> Template)
NMP Project short name:	PHYSICOCHEMICAL_STUDIES [-> details]	Data producer group:
		PhysChem
		Used for multiple projects: No
Biosample & Target		
Biological system:	in-vitro	Species:
		Strain:
		~NotApplicable
Tissue type:	~NotApplicable	Cell line:
		(-> RNCB)
Subcellular fraction:	~NotApplicable	Assay target:
		(-> IDM)

Timelines

CAIMAN delivery – high level activities



The CAIMAN project

Value

The CAIMAN project helps to ...	By ...
<p>shift focus from data collection to data analysis</p>	<ul style="list-style-type: none"> • establishing an industry-leading project-data-analysis platform • enabling comprehensive data access, tracking, comparison and visualization
<p>support collaboration and faster decision-making</p>	<ul style="list-style-type: none"> • streamlining and simplifying the compilation of project reports • reducing elapse time to complete a particular stage of research
<p>promote improved quality decisions</p>	<ul style="list-style-type: none"> • ensuring provisioning of all project-relevant information • providing multifaceted analysis capabilities tailored to project needs
<p>enable a learning organization</p>	<ul style="list-style-type: none"> • supporting rapid hypothesis testing (across projects) for knowledge generation • facilitating cross-project learning • using a sustainable platform to ensure data quality and

Acknowledgements

Business Team

Annette Vogt

Xenia Wezler

Lydia Jasmin Dürner

Christine Küttel

Hubert Kettenberger

Wolfgang Paul

Project Organization

Jan Wörner, Project Lead

Petra Harr-Dehn, Project Coordination

Christian Blumenröhr, Technical Team

Oliver Roche, Data Quality

Marc Pompiati, Business Project Manager

Business Analysis

Monika Bug

Cathrin Pautsch, Quattro

Research

Anke Eisenmann

Noan Rajamani, Zifo

Niveda Avinashilingam, Zifo

Christophe Chabbert

D360 Support

Shijun Yu

***Doing now what patients
need next***