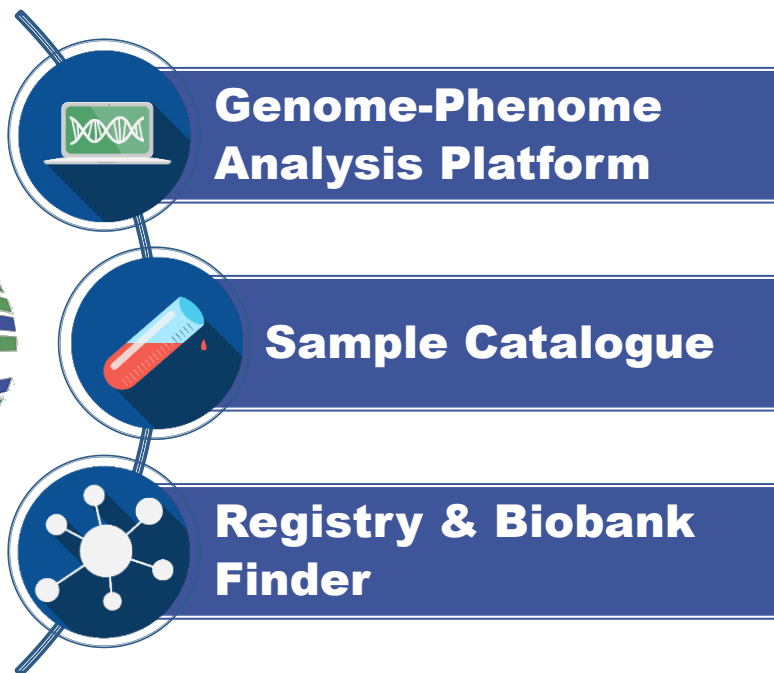


RD-CONNECT AND THE GENOME-PHENOME ANALYSIS PLATFORM (GPAP)

4th Conference on European Reference Networks
Parallel Session 3, Brussels November 21st

I have no actual or potential conflict of interest in relation to this program/presentation



**Genome-Phenome
Analysis Platform**

4,160 GENOME-PHENOME
DATASETS

Sample Catalogue

24,857 BIOSAMPLES
COVERING **112** RD

**Registry & Biobank
Finder**

382 PATIENT REGISTRIES AND
BIOBANKS COVERING **1500** RD



Data linkage
across
resources



Standardized
phenotypic data
collection



Ethical, legal &
social issues



Bioinformatics and
Omics data analysis



Patient
engagement

The BBMRI-LPC Whole Exome Sequencing Call as an example

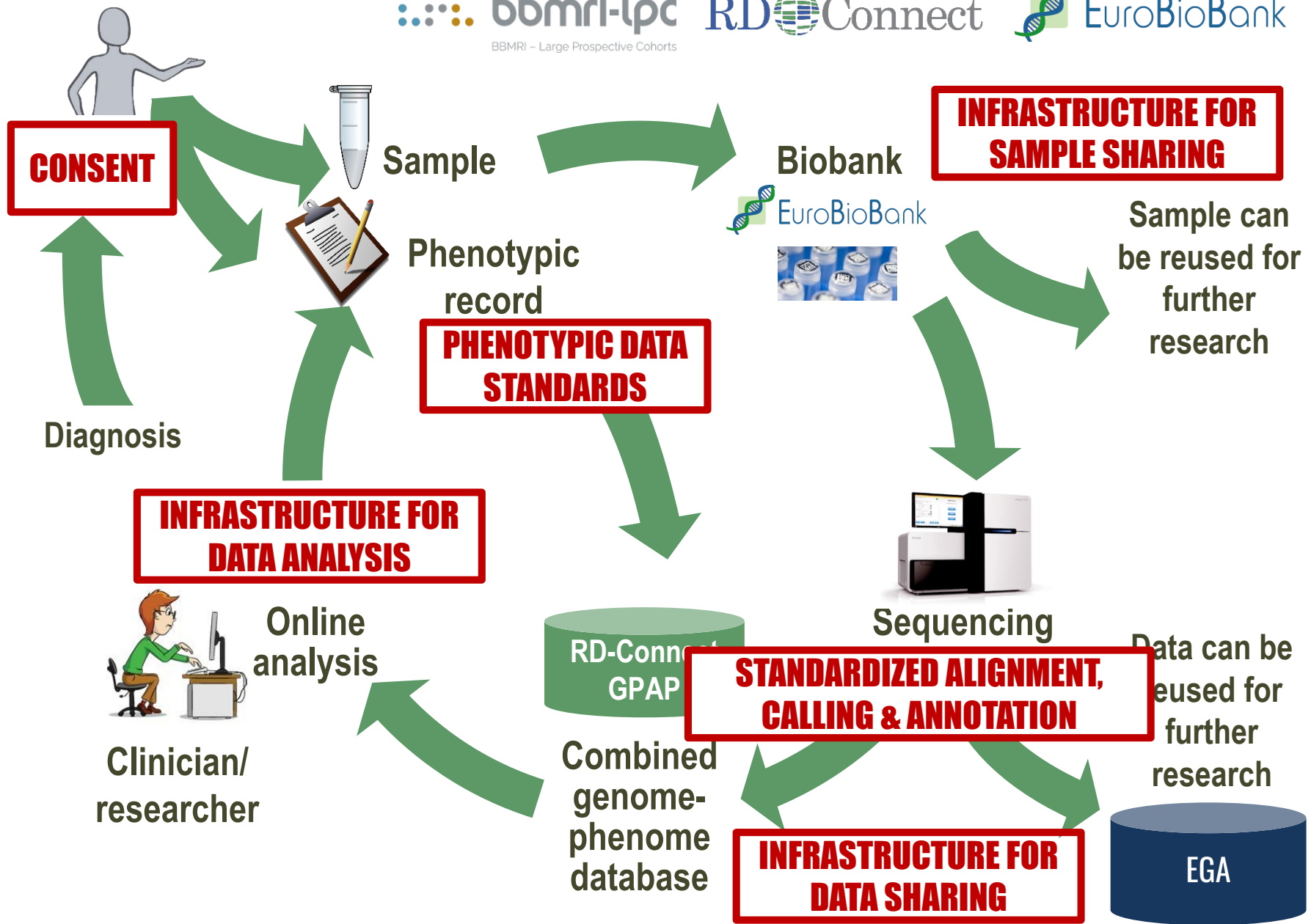
>800 exomes from 17 RD transnational projects
in collaboration with EuroBioBank and RD-Connect

Objectives

- ✓ to promote the usage of biobanks for rare diseases
 - samples deposited in the EuroBioBank network
- ✓ to promote the utilization of cutting-edge next-generation sequencing technology for the identification of novel causative variants and genes
 - free-of-charge sequencing of 900 exomes
- ✓ to molecularly diagnose rare disease patients
 - analysis through the RD-Connect platform
- ✓ to promote data sharing for rare disease research to enable future discovery
 - data sharing through the EGA and RD-Connect and phenotyping with HPO

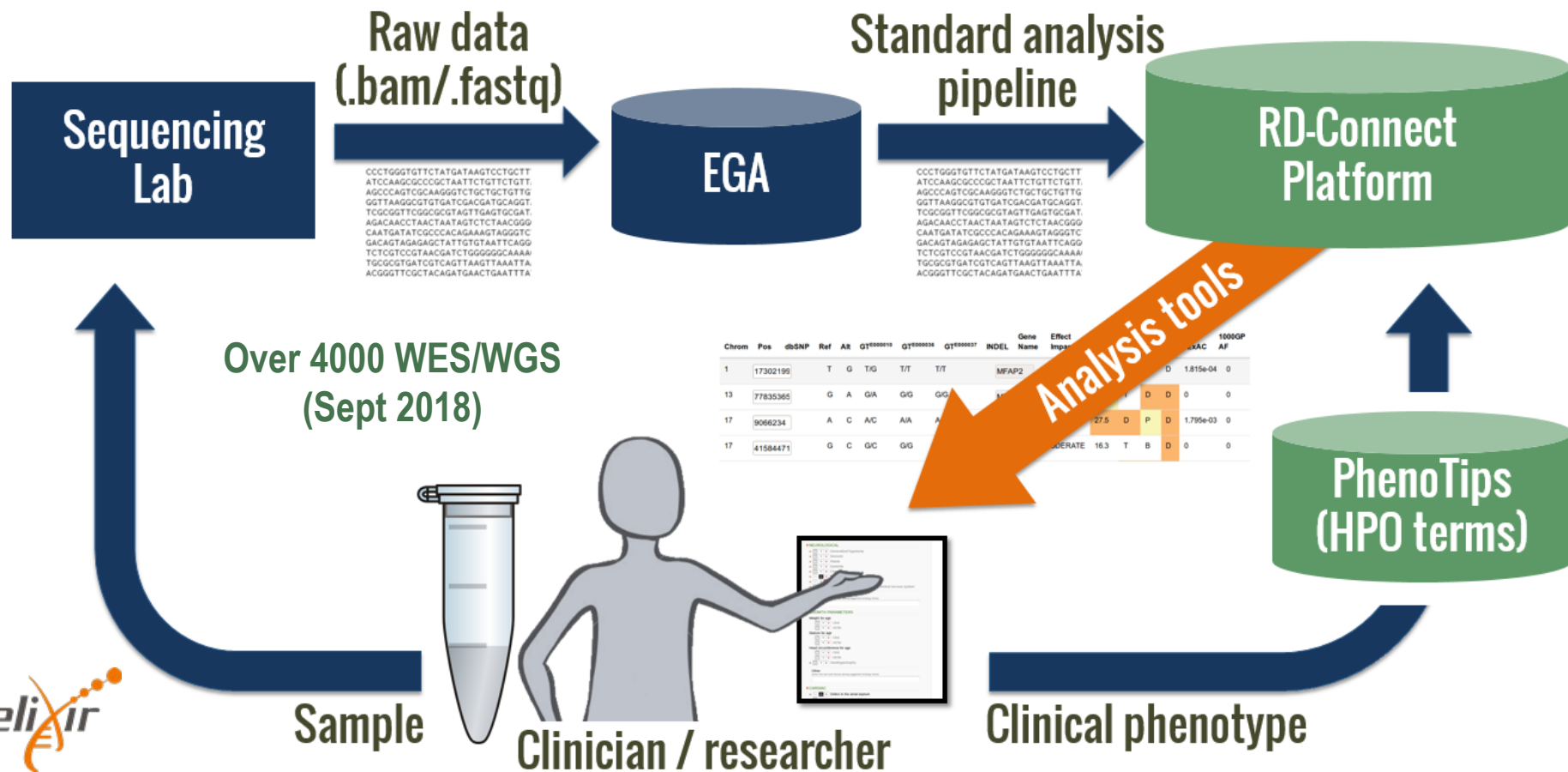


A paradigm for best practice in data sharing in genomic studies?





RD-Connect Genome-Phenome Analysis Platform (GPAP)



Ethics Committee Approval, GDPR Compliance, Code of Conduct, Data Access Committee, Security audited, User Activity logged



RD-Connect GPAP interface

https://platform.rd-connect.eu

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GENOMICS

ABOUT

WELCOME S.BELTRAN

{PLATFORM V0.13.0, DATASET 20170426 }

FAQ

LOGOUT

Filters ▼

PRESET FILTERS

RESET

SHARE

▶ RUN QUERY

Variant Type: coding high moderate Population: exac SNV->MT: A D SNV->SIFT: D SNV->PP2: D P

Samples	Functional	Predictive	Population	Diseasecard	Candidate	Links	ALFA				
Gene Name	Transcript ID	Effect Impact	Consequence	Feature Type	HGVS coding	Amino Acid change	Amino Acid length	Genotype Number	Exon Rank	CDS Position	Transcript BioType
MFAP2	ENST0000037553	MODERATE	missense_variant	transcript	c.313A>C	p.Thr105Pro	183	1	7/9	313/552	protein_coding
MFAP2	ENST0000037553	MODERATE	missense_variant	transcript	c.310A>C	p.Thr104Pro	182	1	6/8	310/549	protein_coding
MFAP2	ENST0000043854	MODERATE	missense_variant	transcript	c.310A>C	p.Thr104Pro	182	1	7/9	310/549	protein_coding

Variants (11)

Exomiser

First

Previous

1

Next

Last

EXPORT ALL

Chr	Pos	dbSNP	Ref	Alt	Candidate	GT ^{E000010}	GT ^{E000036}	GT ^{E000037}	INDEL	Gene Name	Effect Impact	ClinVar	CADD	SIFT	PP2	MT	ExAC	1000GP AF
1	17302199	.	T	G	ADD	T/G	T/T	T/T		MFAP2	MODERATE		26.9	D	D	D	NA	0
11	93535027	.	C	A	ADD	C/A	C/C	C/C		MED17	MODERATE		34	D	D	D	NA	0
13	77835365	.	G	A	ADD	G/A	G/G	G/G		MYCBP2	MODERATE		25.6	T	D	D	NA	0
13	110437802	.	A	C	ADD	A/C	A/A	A/A		IRS2	MODERATE		24.6	D	D	D	NA	0



RD-Connect GPAP functionalities

<https://platform.rd-connect.eu>

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- ✓ **Standard filters and annotations** (variant impact on protein, frequency in control populations, frequency within database, *in silico* predictors, gene, genomic position, etc.)
- ✓ **Filter by genes of interest** (predefined/custom lists, associated to OMIM disease, HPO symptoms or Reactome)
- ✓ Filter by variants annotated in **ClinVar database**
- ✓ Filter to regions with observed long **Runs of homozygosity** (RoH)
- ✓ Direct link to **multiple external resources** (Ensembl, UCSC, gnomAD, HGMD, Human Splicing Finder, DiseaseCards, ALFA, etc.)
- ✓ **Phenotype driven strategy for variant prioritization** (Exomiser)
- ✓ **TAG and share candidate variants** using ACMG guidelines
- ✓ **Collaborative environment:** share data and queries
- ✓ **Anonymized data discovery** through Beacon and Matchmaker exchange

BBMRI-LPC RD WES Call: Preliminary analysis results (Oct 2018)



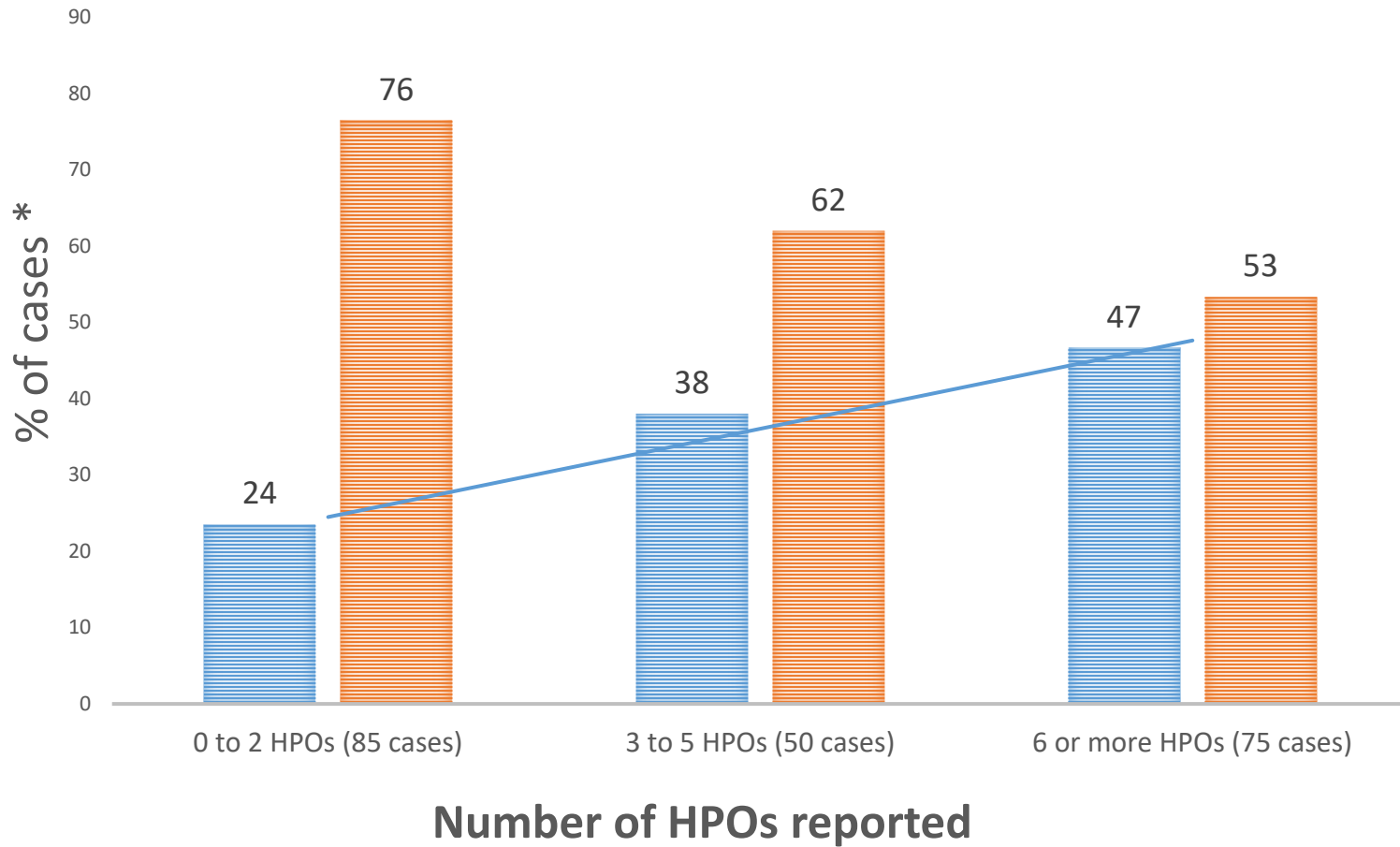
PROJECT	CLINICAL REFERRAL	TOTAL SAMPLES	TOTAL FAMILIES	CANDIDATES PROPOSED (%)	CONFIRMED SOLVED CASES (%)
1	Ophthalmogenetic Diseases	41	10	40	40
2	Congenital Myasthenic Syndrome	87	47	68	30
3	Mitochondrial Disorders	50	41	61	43
4	Intellectual disability	60	26	54	46
5	Epileptic Encephalopathies	50	32	59	27
6	Neuropathic pain	15	1	0	awaiting feedback
7	Neuromuscular diseases	81	52	46	awaiting feedback
8	Ataxia	50	28	57	19
9	Pyruvate Kinase Deficiency	31	15	100	awaiting feedback
10	Sudden Cardiac Death	83	33	ongoing analysis	-
11	Familial hyperinsulism	57	Not released	-	-
12	Neuropathies*	45	45	85	awaiting feedback
13	Metabolic acidurias	31	15	67	40
14	Albinism	47	27	ongoing analysis	-
15	Gastric neuroendocrine tumors	7	5	80	awaiting feedback
16	Rett Syndrome	46	21	67	awaiting feedback
17	Gastrointestinal disorders	30	Not released	-	-

Total	811	383	40-100%	19-46%
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*27 samples released only - 7 families

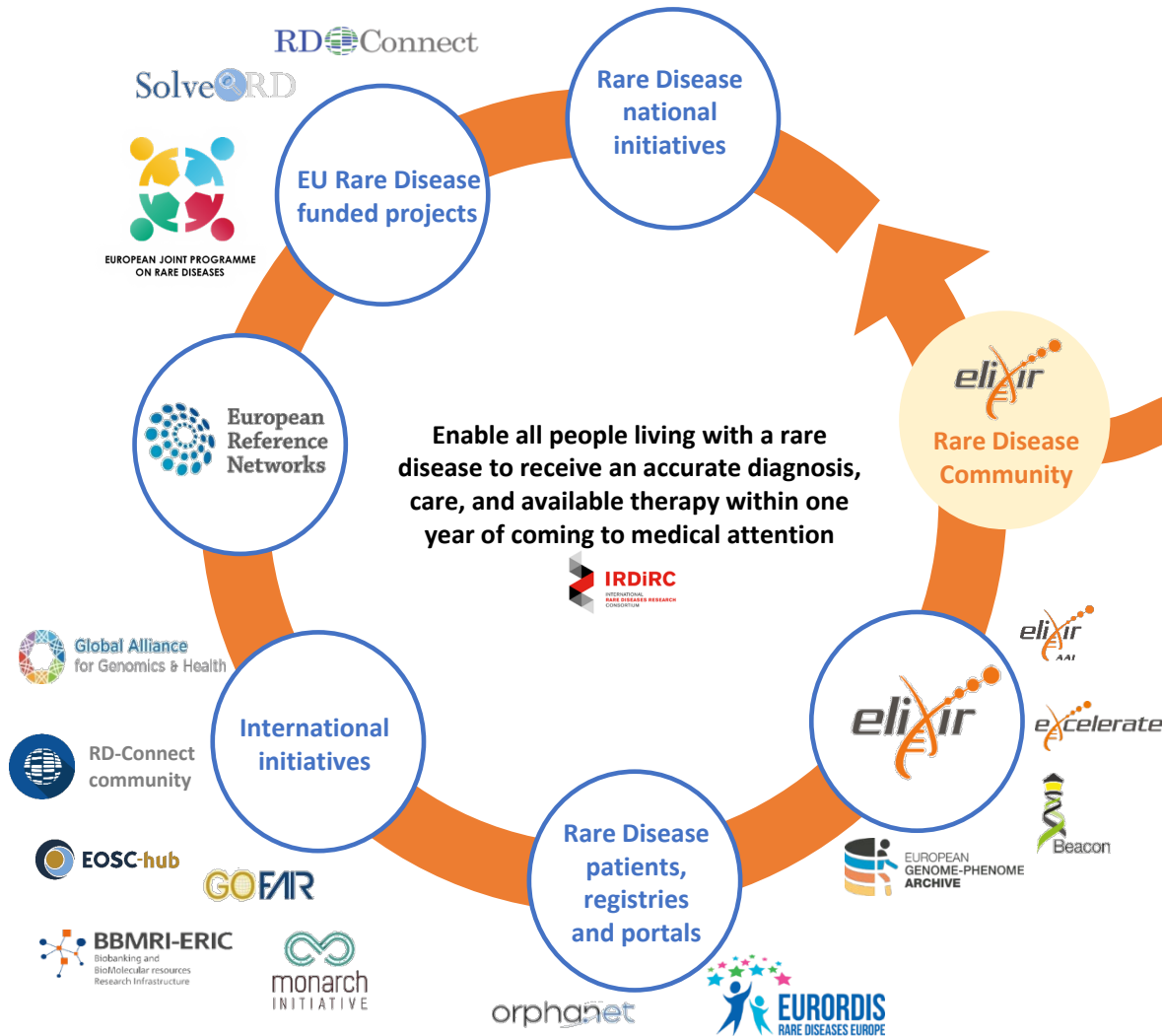
BBMRI-LPC WES DIAGNOSTIC YIELD*

■ solved ■ unsolved — Linear (solved)



*N=210; Only cases with strong candidates have been taken into account

ELIXIR Rare Disease community



- **Global Infrastructure for Rare Disease research:**
 - Registry of Rare Disease data resources and analysis tools (<https://rare-diseases.bio.tools>)
 - Interconnection of secure data repositories and resources
 - Data sharing and data discovery
 - Benchmarking resources and activities
- **Interoperability of Rare Disease resources:**
 - Quality in terms of FAIR principles
 - Standards and ontologies
 - FAIR data services
- **Training:**
 - BYOD workshops
 - Rare Disease researchers focused trainings



Thank you!

<https://rd-connect.eu>

<https://platform.rd-connect.eu/>

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SolveRD



NeurOmics



EURenOmics



cnag

centre nacional d'anàlisi genòmica
centro nacional de análisis genómico



RD  Connect