

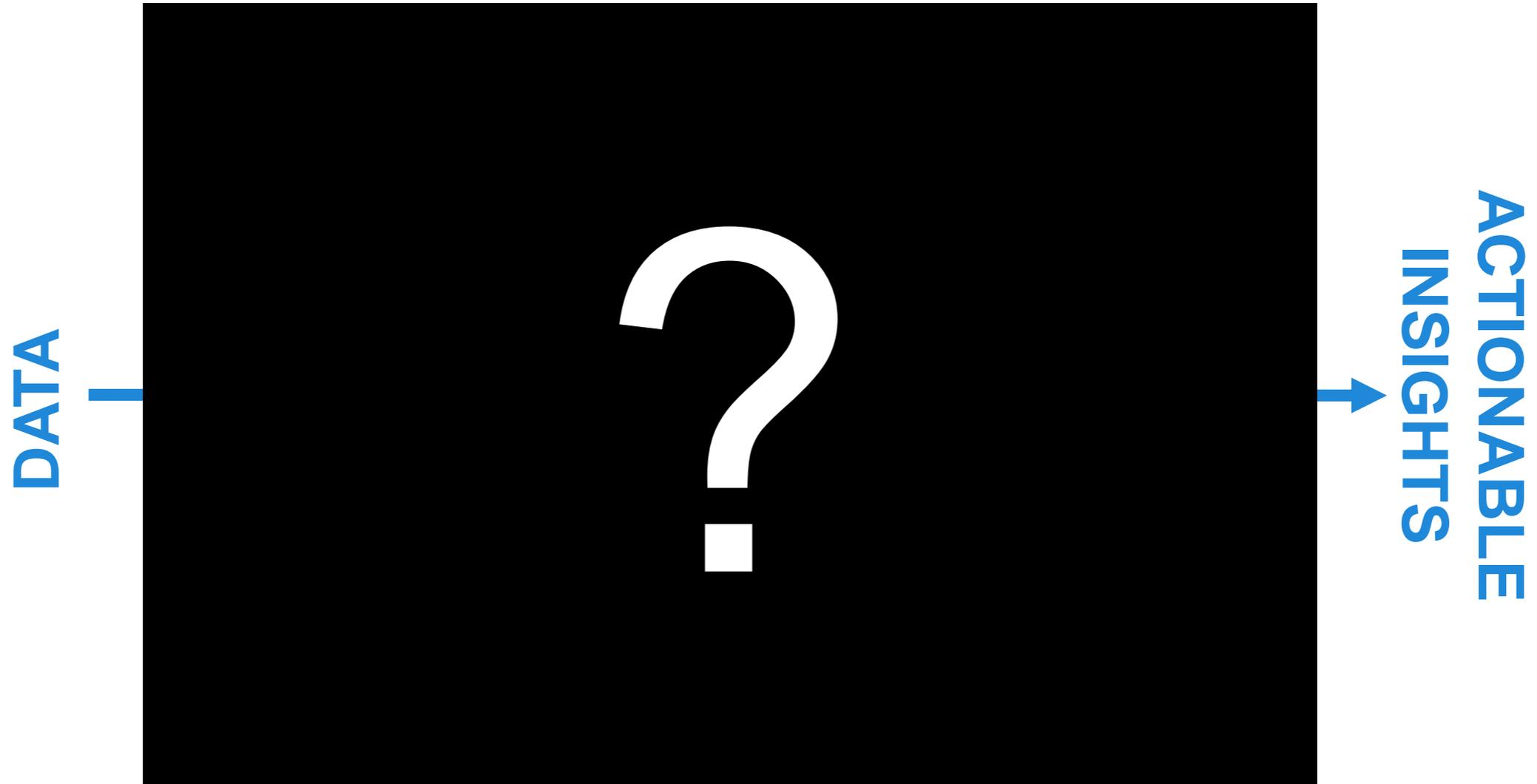
ares genetics

Artificial Intelligence in AMR Diagnostics

**Advancing Data Technologies to corner AMR | Amsterdam | June 5th 2019
Dr. Andreas Posch | Managing Director & CEO | Ares Genetics**

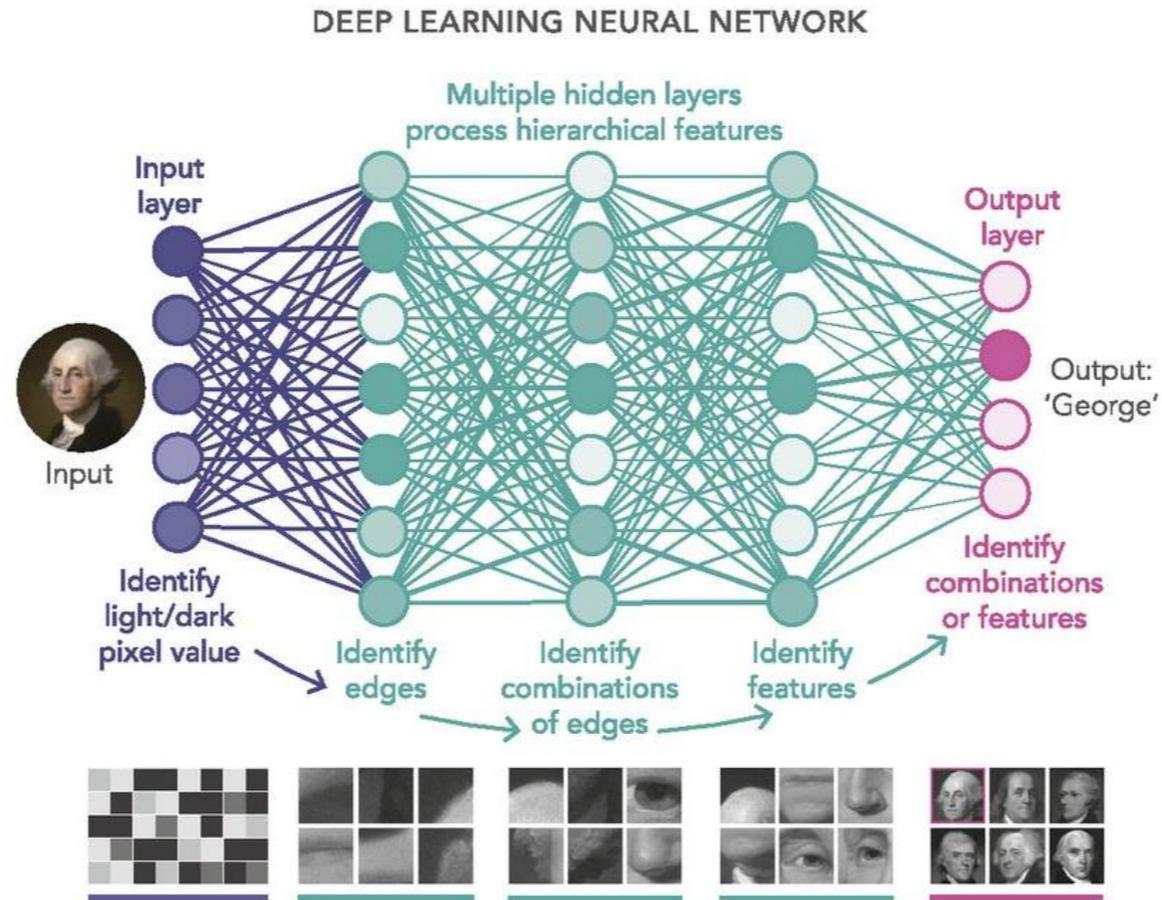
WHAT WE ARE TALKING ABOUT WHEN WE TALK ABOUT AI

WHAT WE ARE TALKING ABOUT WHEN WE TALK ABOUT AI



WHAT WE ARE TALKING ABOUT WHEN WE TALK ABOUT AI

DATA



INSIGHTS

ACTIONABLE

M. Mitchell Waldrop PNAS 2019;116:4:1074-1077

WHAT WE ARE TALKING ABOUT WHEN WE TALK ABOUT AI

DATA

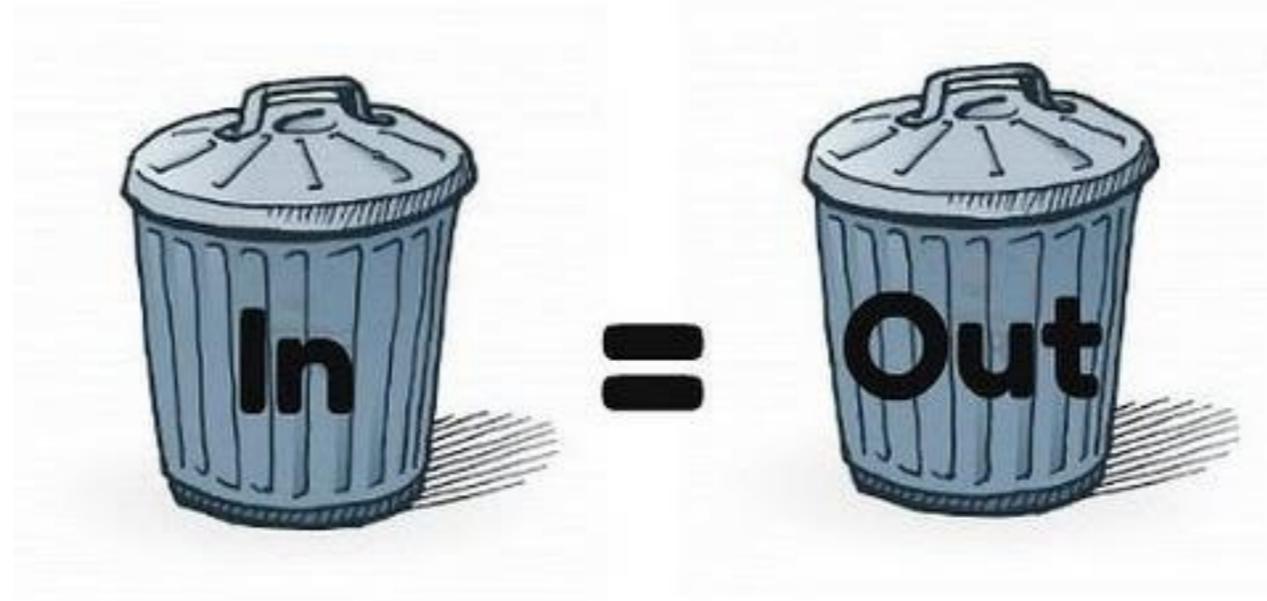


ACTIONABLE
INSIGHTS

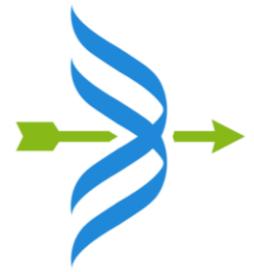
WHAT WE ARE TALKING ABOUT WHEN WE TALK ABOUT AI

DATA

|



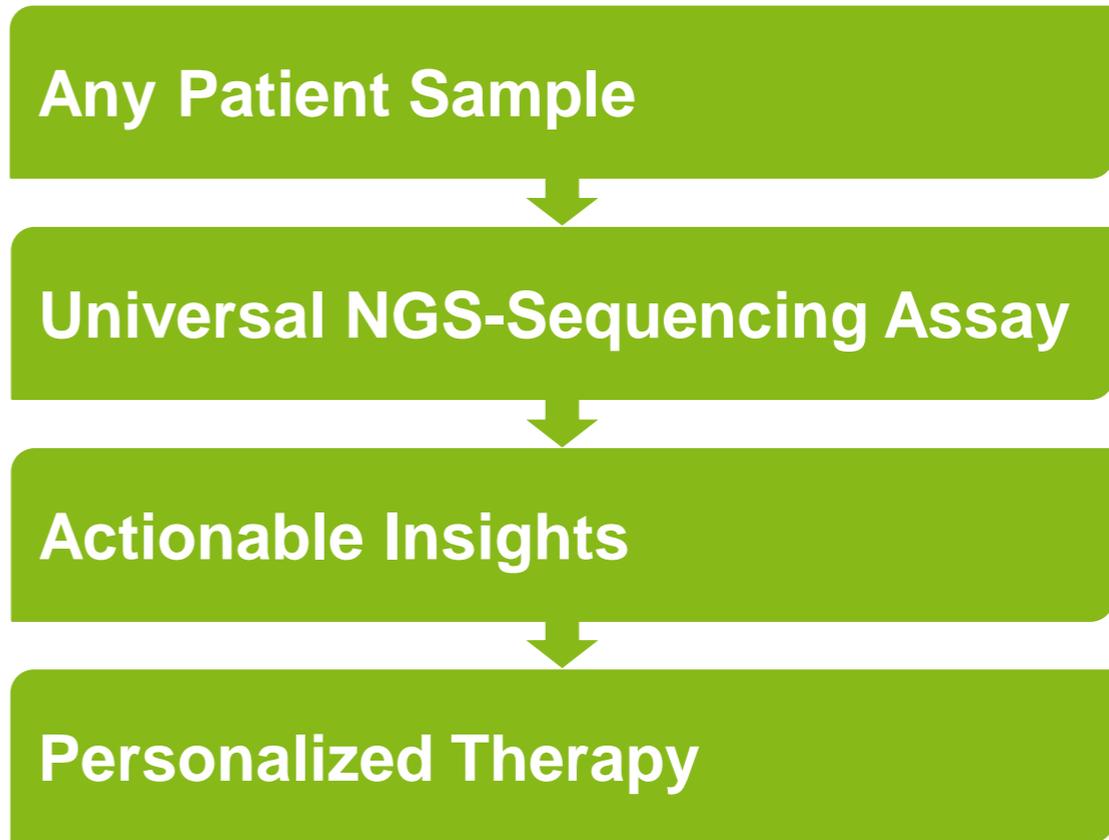
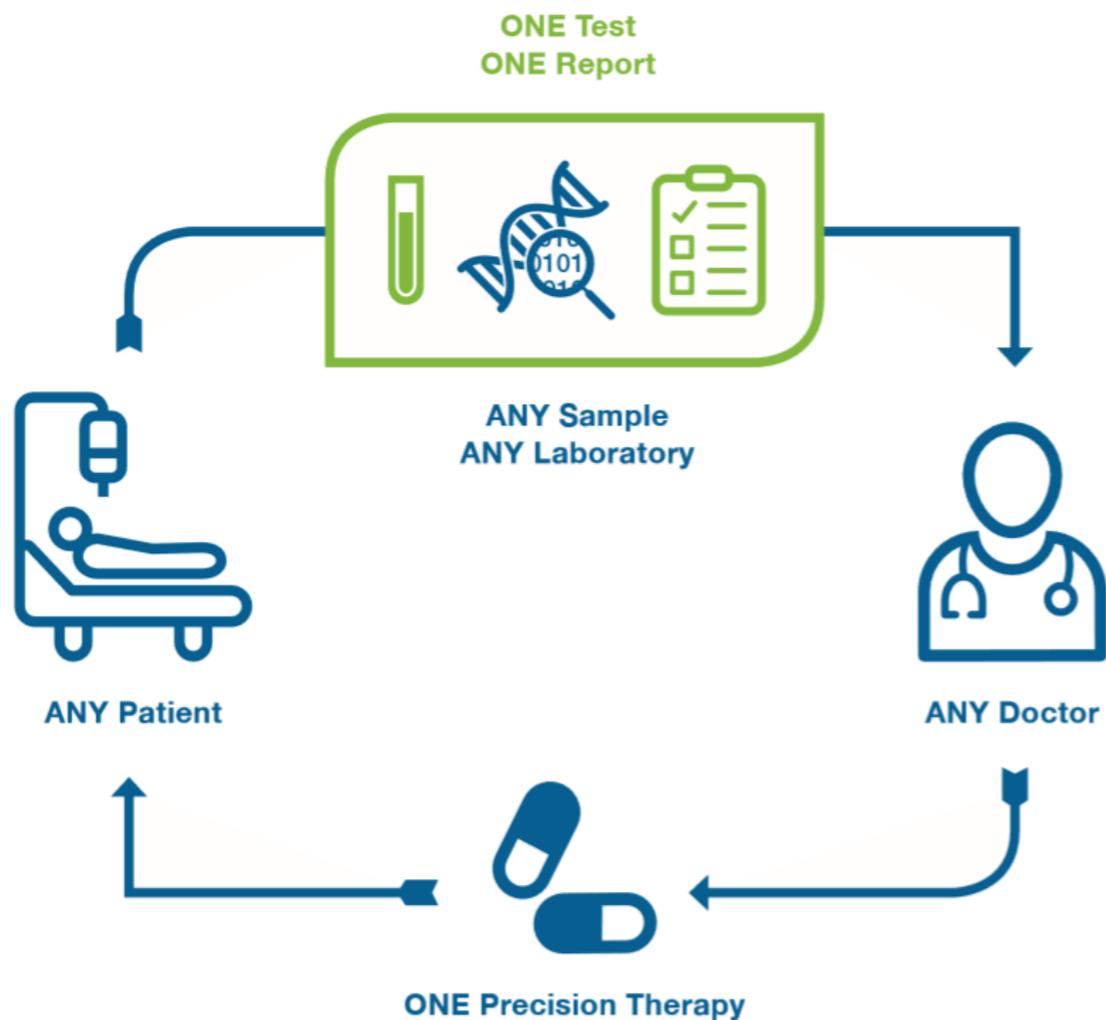
ACTIONABLE
INSIGHTS



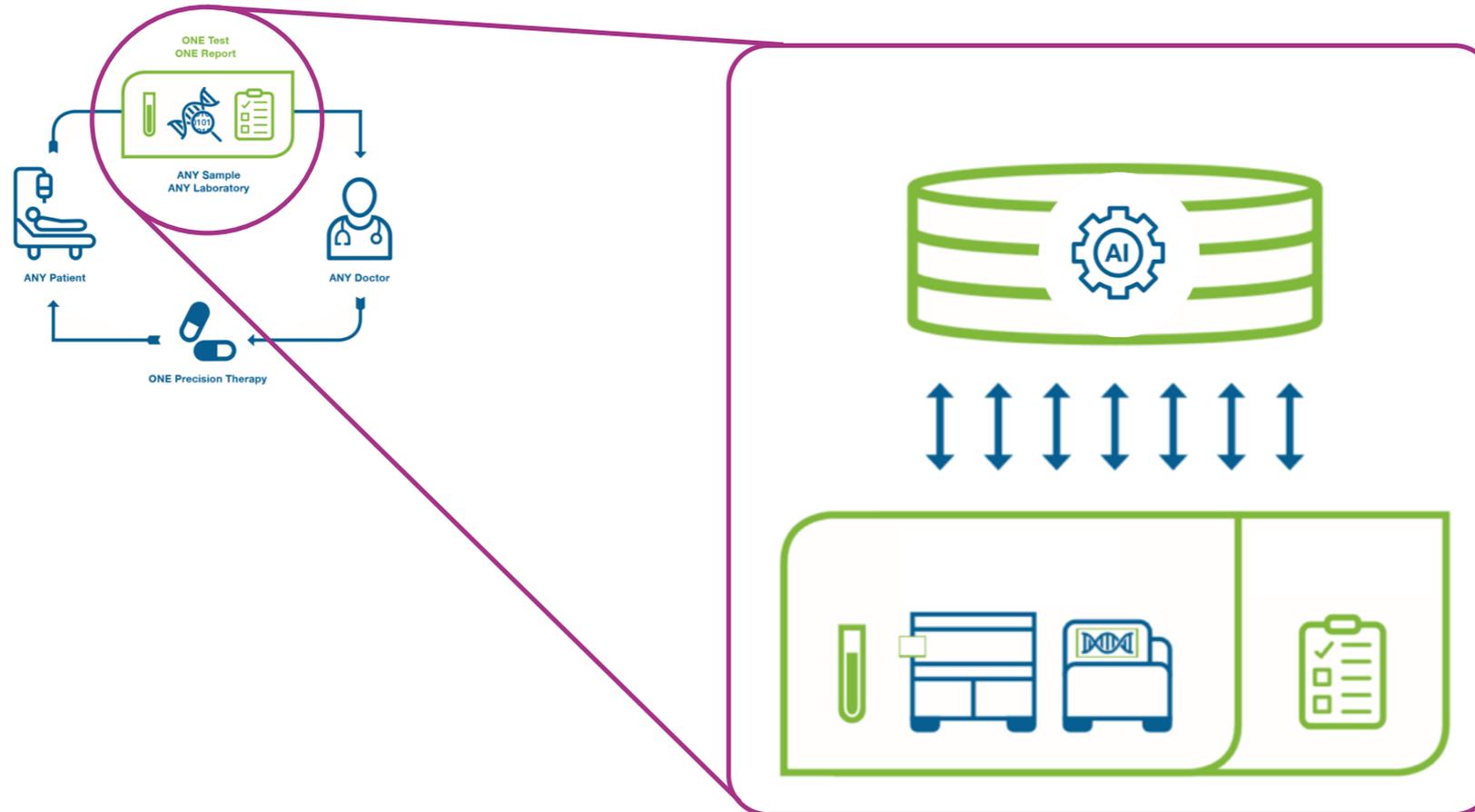
ares genetics

Actionable Insights in AMR Diagnostics

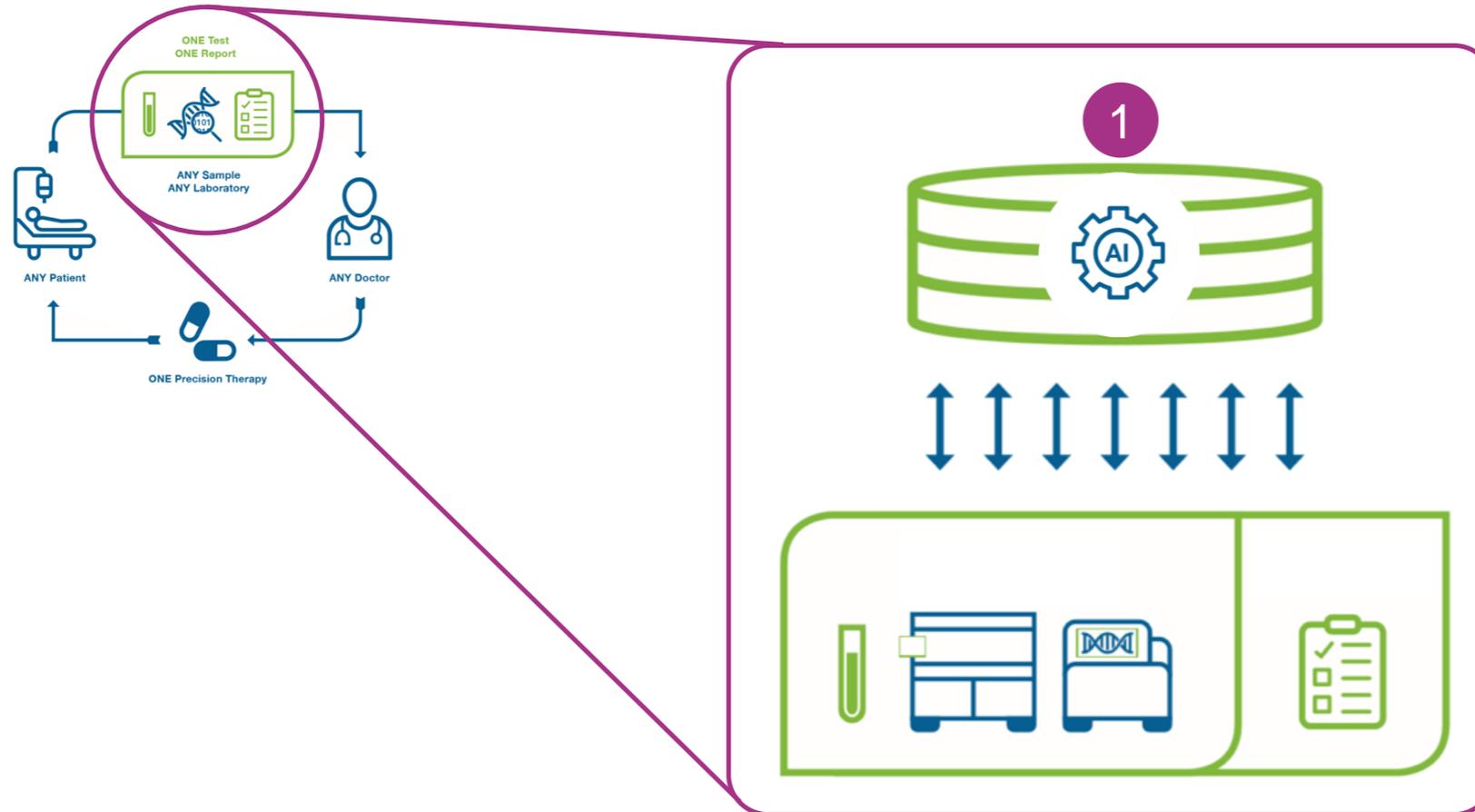
OUR VISION: ONE RAPID UNIVERSAL ASSAY FOR PATHOGEN ID AND PRECISE DRUG RESPONSE



OUR UNIVERSAL PATHOGENOME ASSAY: KEY ELEMENTS

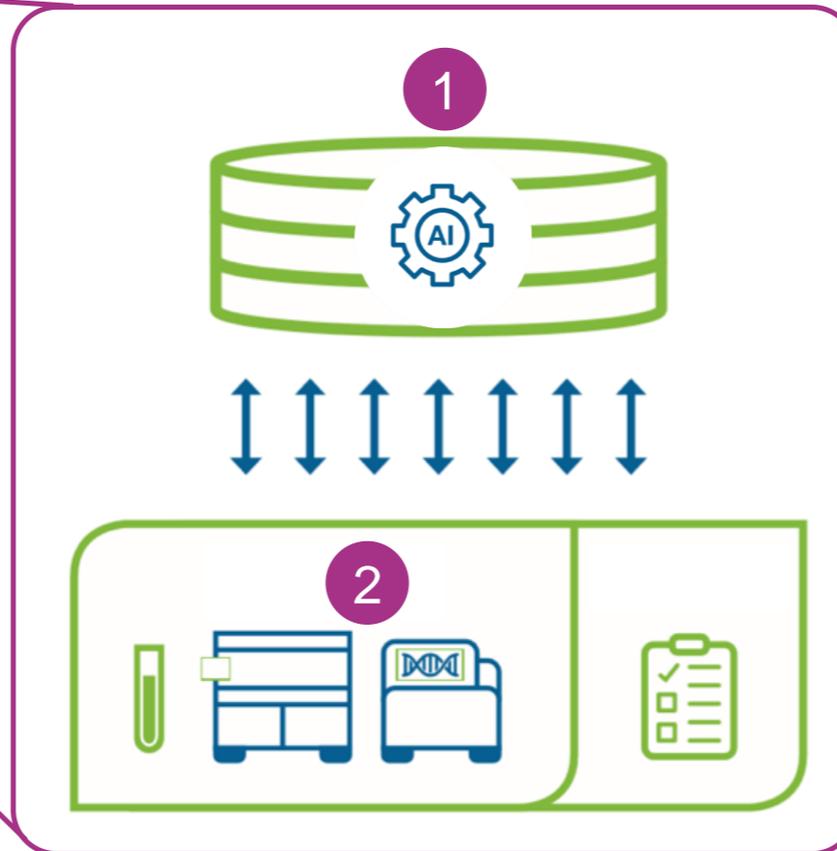
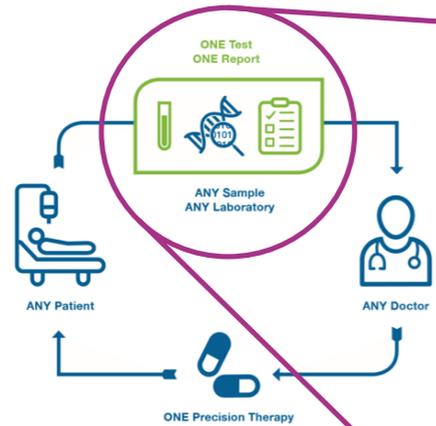


OUR UNIVERSAL PATHOGENOME ASSAY: KEY ELEMENTS



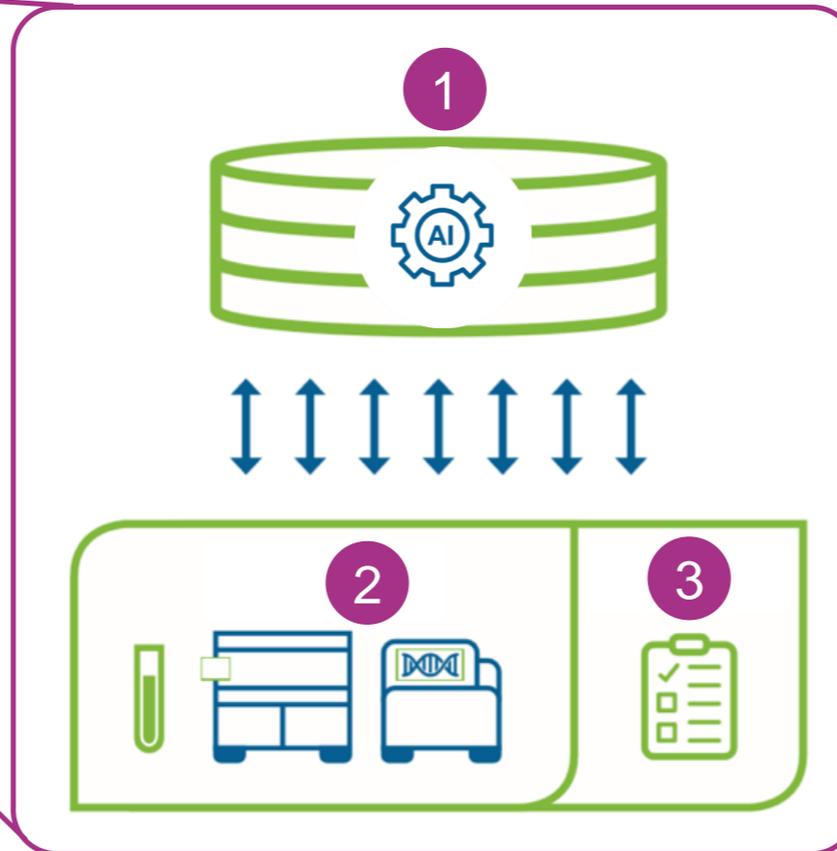
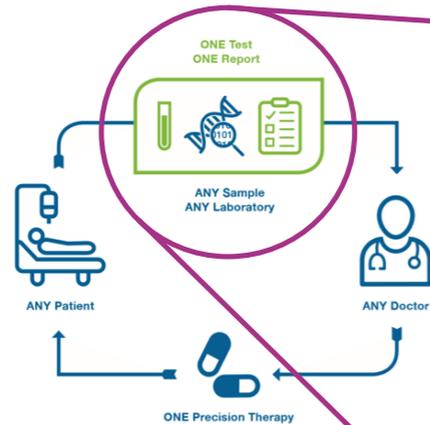
- 1 A curated & validated, global reference database that is sustainably up-to-date with AMR evolution and epidemiology.

OUR UNIVERSAL PATHOGENOME ASSAY: KEY ELEMENTS



- 1 A curated & validated, global reference database that is sustainably up-to-date with AMR evolution and epidemiology.
- 2 A universal, fully automated NGS lab workflow for generic local data generation.

OUR UNIVERSAL PATHOGENOME ASSAY: KEY ELEMENTS



- 1 A curated & validated, global reference database that is sustainably up-to-date with AMR evolution and epidemiology.
- 2 A universal, fully automated NGS lab workflow for generic local data generation.
- 3 A HIPAA compliant, cloud-based data interpretation & clinical decision support system translating NGS data into actionable insights.

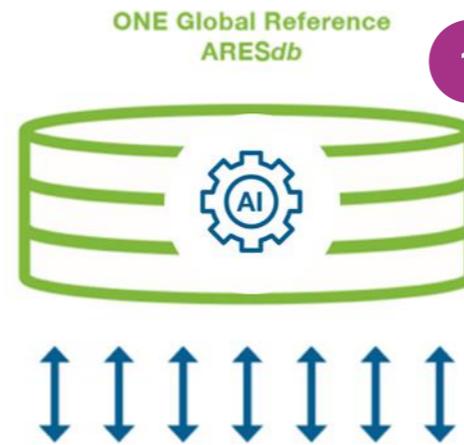
OUR UNIVERSAL PATHOGENOME ASSAY: IMPLEMENTATION

ARESupa

Sample-to-Answer NGS Workflow



- Collaboration with BGI
- Feasibility demonstrated
- Data presented at ASM NGS 2018 | USA and ICG-13 2018 | China



AREScdb

Expert Curated & AI-Powered Reference Database

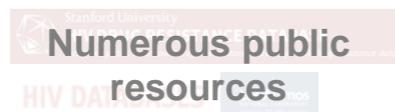


AREScds

Clinical Decision Support Platform



TURNING NGS INTO ACTIONABLE INSIGHTS: A CHALLENGE THAT CAN BUILD ON LEARNINGS IN HIV & CANCER

	 HIV	 Cancer	 AMR
Annual Casualties	~1 Mio ¹	8,8 Mio ¹	> 10 Mio ²
BioIT Complexity	~ 10 kb genome (low)	~ 3 Gb genome (high)	~ 5Mb genome 1000s of strains genetic plasticity
Reference Databases	 Numerous public resources	 Numerous public resources	Few public resources, but not suitable as diagnostic reference
Competitive Landscape	 Saturated (established Laboratory Diagnostics)	 Growing but Crowded (Molecular Pathology & BioIT companies)	Untapped Potential: Next-Gen Molecular Microbiology

1000s of Strains
X
100s of Drugs
X
100s of MoRs

¹ WHO Factsheets, 2017 ² projected by 2050, The Review on Antimicrobial Resistance, 2014

TURNING NGS INTO ACTIONABLE INSIGHTS IN AMR: A DATA INTEGRATION & CURATION CHALLENGE

TURNING NGS INTO ACTIONABLE INSIGHTS IN AMR: A DATA INTEGRATION & CURATION CHALLENGE

!!! Fragmented public AMR databases

TURNING NGS INTO ACTIONABLE INSIGHTS IN AMR: A DATA INTEGRATION & CURATION CHALLENGE

- !!! Fragmented public AMR databases
- !!! Lack of diagnostic performance parameters for AMR genes (i.e. PPV, NPV, etc.)

TURNING NGS INTO ACTIONABLE INSIGHTS IN AMR: A DATA INTEGRATION & CURATION CHALLENGE

- !!! Fragmented public AMR databases
- !!! Lack of diagnostic performance parameters for AMR genes (i.e. PPV, NPV, etc.)
- !!! Limited phenotypic information

TURNING NGS INTO ACTIONABLE INSIGHTS IN AMR: A DATA INTEGRATION & CURATION CHALLENGE

- !!! Fragmented public AMR databases
- !!! Lack of diagnostic performance parameters for AMR genes (i.e. PPV, NPV, etc.)
- !!! Limited phenotypic information
- !!! Lack of standardization

TURNING NGS INTO ACTIONABLE INSIGHTS IN AMR: A DATA INTEGRATION & CURATION CHALLENGE

- !!! Fragmented public AMR databases
- !!! Lack of diagnostic performance parameters for AMR genes (i.e. PPV, NPV, etc.)
- !!! Limited phenotypic information
- !!! Lack of standardization
- !!! Lack of defined quality criteria

TURNING NGS INTO ACTIONABLE INSIGHTS IN AMR: A DATA INTEGRATION & CURATION CHALLENGE

- !!! Fragmented public AMR databases
- !!! Lack of diagnostic performance parameters for AMR genes (i.e. PPV, NPV, etc.)
- !!! Limited phenotypic information
- !!! Lack of standardization
- !!! Lack of defined quality criteria
- !!! Lack of meta data

TURNING NGS INTO ACTIONABLE INSIGHTS IN AMR: A DATA INTEGRATION & CURATION CHALLENGE

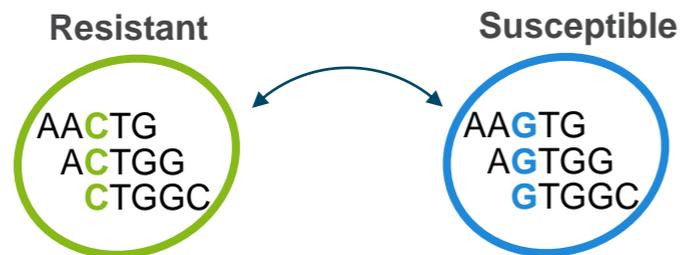
- !!! Fragmented public AMR databases
- !!! Lack of diagnostic performance parameters for AMR genes (i.e. PPV, NPV, etc.)
- !!! Limited phenotypic information
- !!! Lack of standardization
- !!! Lack of defined quality criteria
- !!! Lack of meta data
- !!! Genomic & phenotypic data not always from identical & pure clones

TURNING NGS INTO ACTIONABLE INSIGHTS IN AMR: A DATA INTEGRATION & CURATION CHALLENGE

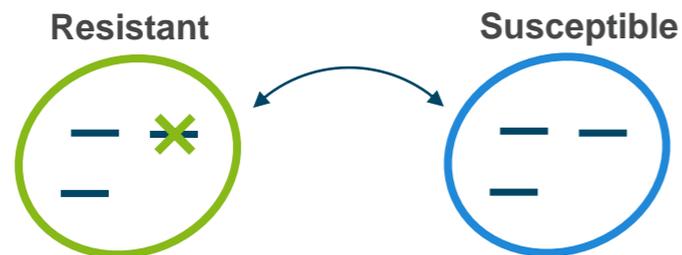
- !!! Fragmented public AMR databases
- !!! Lack of diagnostic performance parameters for AMR genes (i.e. PPV, NPV, etc.)
- !!! Limited phenotypic information
- !!! Lack of standardization
- !!! Lack of defined quality criteria
- !!! Lack of meta data
- !!! Genomic & phenotypic data not always from identical & pure clones
- !!! Limited information on AMR conferring mutations
- !!! ...

AREScdb: EXPERT CURATED REFERENCE DATABASE CATALOGUING AMR RESISTANCE GENES AND MUTATIONS

Gene **mutation** determines resistance



Gene **presence / absence** determines resistance



AREScdb. A highly **standardized, quality controlled** resource of **pathogen genomes, AMR phenotypes & AMR marker** building on **CLSI guidelines**

ONE Global Reference
AREScdb



ARESDb: GLOBALLY LEADING, CONTINUOUSLY UPDATED AMR KNOWLEDGEBASE ESTABLISHED BY SIEMENS



~ 40,000 whole-genome sequenced bacterial strains collected globally from over 200 clinical centers.

Quantitative antibiotic susceptibility data for **more than 100 antibiotics**.

Originally established based on the **SIEMENS** Microbiology strain collection.



- Home
- Lab Services
- My Orders
- My Reports
- My Cloud
- ARESDb
 - Dashboard
 - AMR Panels
 - AMR Search
 - AMR Statistics
- AMR Cards

ARESDb Dashboard

Antibiotics

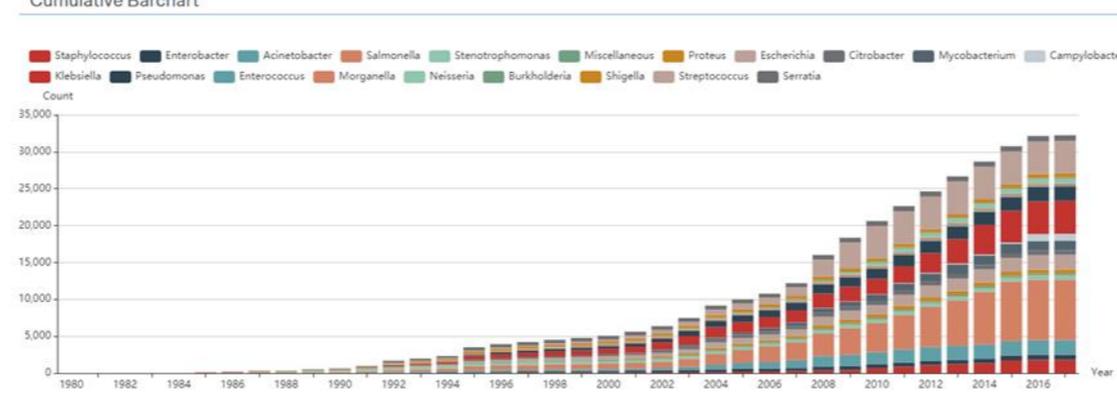
Show 10 entries Search:

No.	Antibiotic Name	Abbreviation	Antibiotic Class
1	Amikacin	AMI	Aminoglycoside
2	Amoxicillin	AMO	Penicillin
3	Amoxicillin-clavulanic acid	AMC	Penicillin
4	Ampicillin	AMP	Penicillin
5	Ampicillin-sulbactam	AMP-SLB	Penicillin
6	Azithromycin	AZI	Macrolide
7	Aztreonam	AZT	Monobactam
8	Bacitracin	BCT	Peptide
9	Bedaquiline	BDQ	Diarylquinolines
10	Benzyloxyphenylpenicillin	PCG	Penicillin

Showing 1 to 10 of 142 entries Previous 1 2 3 4 5 ... 15 Next

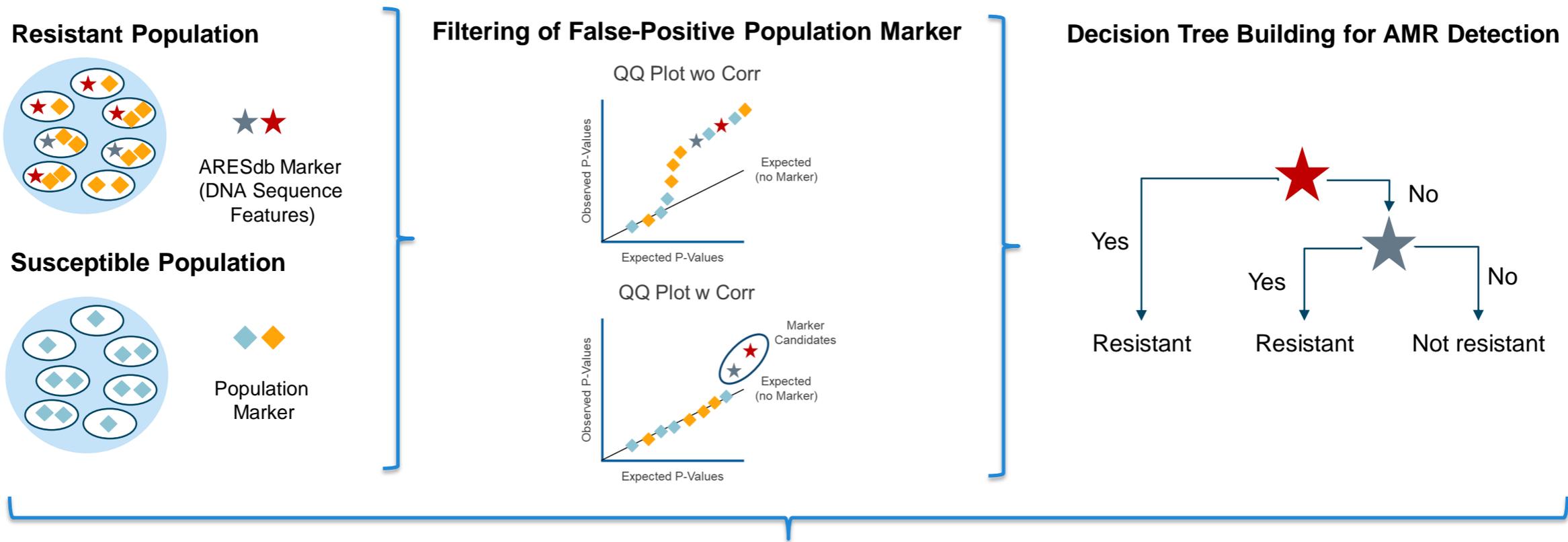
Sample Distribution Per Annum

Chart Type: Cumulative Barchart



AREScdb: ACTIONABLE GENETIC RESISTANCE MARKERS FOR AMR DIAGNOSTICS

Adv. & Robust Biostatistics | Population Structure Correction | Decision Trees | Gradient Boosting



Combining weak learners in ensemble model for optimal accuracy by gradient tree boosting (up to >98%)

AREScdb: BUILDS ON CURATION PRACTICE IN ONCOLOGY

New marker are systematically classified based on predefined criteria and rules

- Public Resources, Clinical studies & Scientific papers all provide a wealth of unstructured AMR data
- There is a need for interpretative categories for clinical utilization of AMR markers
- A similar problem was faced (and solved) in the field of oncology via consensus guidelines for marker classification
- AREScdb is automating the process of AMR marker classification reducing manual curation needs

HHS Public Access
 Author manuscript
 Genet Med. Author manuscript; available in PMC 2015 November 01.
 Published in final edited form as:
 Genet Med. 2015 May; 17(5): 405–424. doi:10.1038/gim.2015.30.

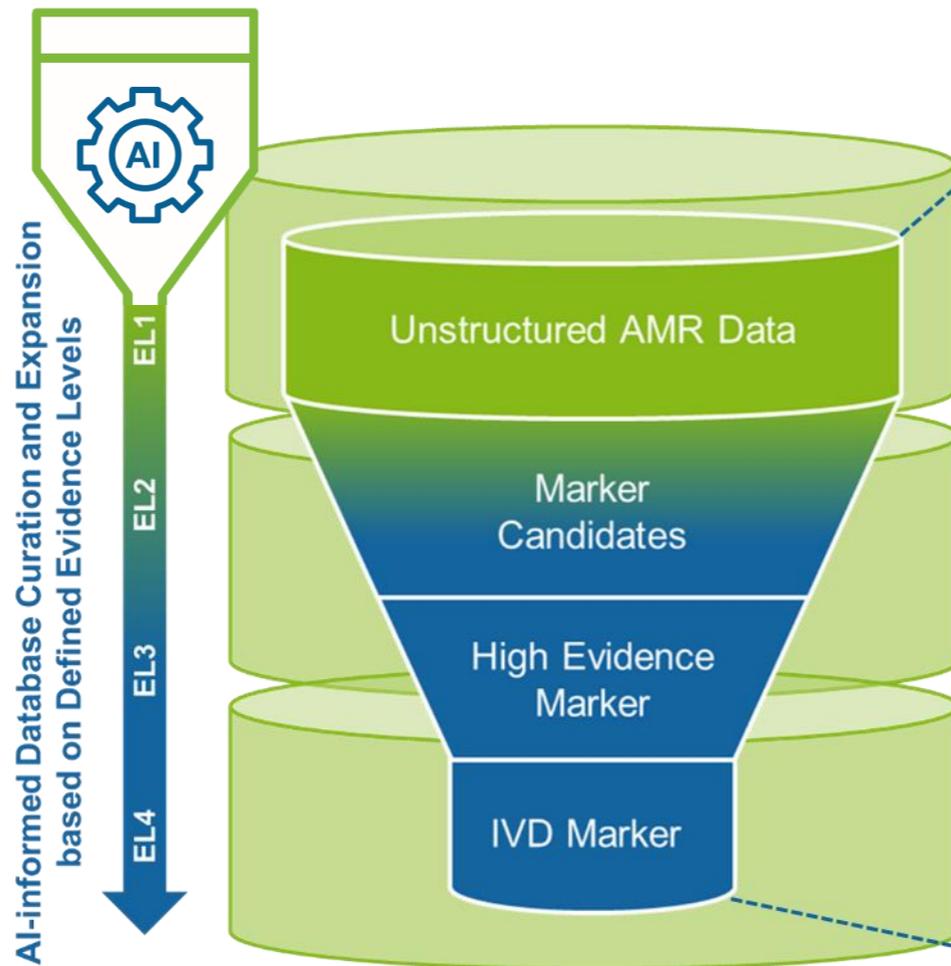
Standards and Guidelines for the Interpretation of Sequence Variants: A Joint Consensus Recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology

Sue Richards [Chair, ACMG],
 Knight Diagnostic Laboratories, Department of Molecular and Medical Genetics, Oregon Health & Science University, Portland, OR, USA

Nazneen Aziz [CAP],
 College of American Pathologists, Chicago, IL, USA

	Benign		Pathogenic			
	Strong	Supporting	Supporting	Moderate	Strong	Very Strong
Population Data	MAF is too high for disorder BA1/BE1 OR observation in controls inconsistent with disease penetrance BS2			Absent in population databases PM2	Prevalence in affecteds statistically increased over controls PS4	
Computational And Predictive Data		Multiple lines of computational evidence suggest no impact on gene /gene product BP4 Missense in gene where only truncating cause disease BP1 Silent variant with non predicted splice impact BP7	Multiple lines of computational evidence support a deleterious effect on the gene /gene product PP3	Novel missense change at an amino acid residue where a different pathogenic missense change has been seen before PM5 Protein length changing variant PM4	Same amino acid change as an established pathogenic variant PS1	Predicted null variant in a gene where LOF is a known mechanism of disease PVS1
Functional Data	Well-established functional studies show no deleterious effect BS3		Missense in gene with low rate of benign missense variants and path. missenses common PP2	Mutational hot spot or well-studied functional domain without benign variation PM1	Well-established functional studies show a deleterious effect PS3	
Segregation Data	Non-segregation with disease BS4		Co-segregation with disease in multiple affected family members PP1	Increased segregation data →		
De novo Data				De novo (without paternity & maternity confirmed) PM6	De novo (paternity & maternity confirmed) PS2	
Allelic Data		Observed in trans with a dominant variant BP2 Observed in cis with a pathogenic variant BP2		For recessive disorders, detected in trans with a pathogenic variant PM3		
Other Database		Reputable source w/out shared data = benign BP5	Reputable source = pathogenic PP5			
Other Data		Found in case with an alternate cause BP5	Patient's phenotype or FH highly specific for gene PP4			

AREScdb: AI-POWERED AMR MARKER DISCOVERY, CLASSIFICATION, VALIDATION AND CURATION



AMR Marker Details

AMR Sequence: AMR Marker
 Sequence ID: AR000594
 Sequence Name: TEM-1
 Creator: TEM-1
 Creation Date: 2018-12-28
 Resource: ARES family
 Comment: MSQPHALDPIFAPFLPAPFVETLWVHDAEQLSARVQVLELNGSLSPFRRPHTVLLGSLRVCAGQQLGKQVHFNQDLETGPTVTKLTDGTFVGLLSAATHTDITAAALLTTGGNELTAVHMDZHTLVLDVDFEAPKDKDPTMRAAATLTKGLTLARQQLDTHMREDDVHAPLGGALHAGDFPAGQAGRQSGCALVDFQVDFVDTTQVQVDFRPFQAGLALDHE

Source ID	Source Name	Pathogen	Resource
1	C3839-193_04729	TEM-1	Escherichia coli
2	C3839-221_05212	TEM-1	Klebsiella pneumoniae
3	C3833-470_05050	TEM-1	Klebsiella oxytoca
4	C3839-220_04644	TEM-1	Klebsiella pneumoniae
5	C4448-917_00014	TEM-1	Shigella boydii
6	C4447-782_04382	TEM-1	Shigella flexneri
7	C4447-795_04638	TEM-1	Shigella sonnei
8	C4447-778_04075	TEM-1	Serratia marcescens

Evidence Criteria

- A well-established functional study proving no link to AMR
- Prevalence in susceptible isolates is statistically significant over controls
- Multiple lines of evidence showing a variant in a conserved region or having
- Multiple lines of evidence showing a variant in a conserved region or having a deleterious effect on gene function of a well-known variant
- A sequence motif of a variant in a mutational hotspot or a domain integral to the function of a gene
- SCS
- Scientific literature supporting link to AMR
- Reputable sources showing link to AMR
- A sequence motif of a variant in a mutational hotspot or a domain integral to the function of a gene of a well-known variant
- A well-established functional study proving link to AMR

Compounds

Compound	Compound Class	Pathogen
1	Ciprofloxacin	Fluoroquinolone
2	Ciprofloxacin	Fluoroquinolone
3	Levofloxacin	Fluoroquinolone
4	Levofloxacin	Fluoroquinolone
5	Ampicillin-sulbactam	Penicillin
6	Ampicillin-sulbactam	Penicillin
7	Ampicillin	Penicillin
8	Ampicillin	Penicillin

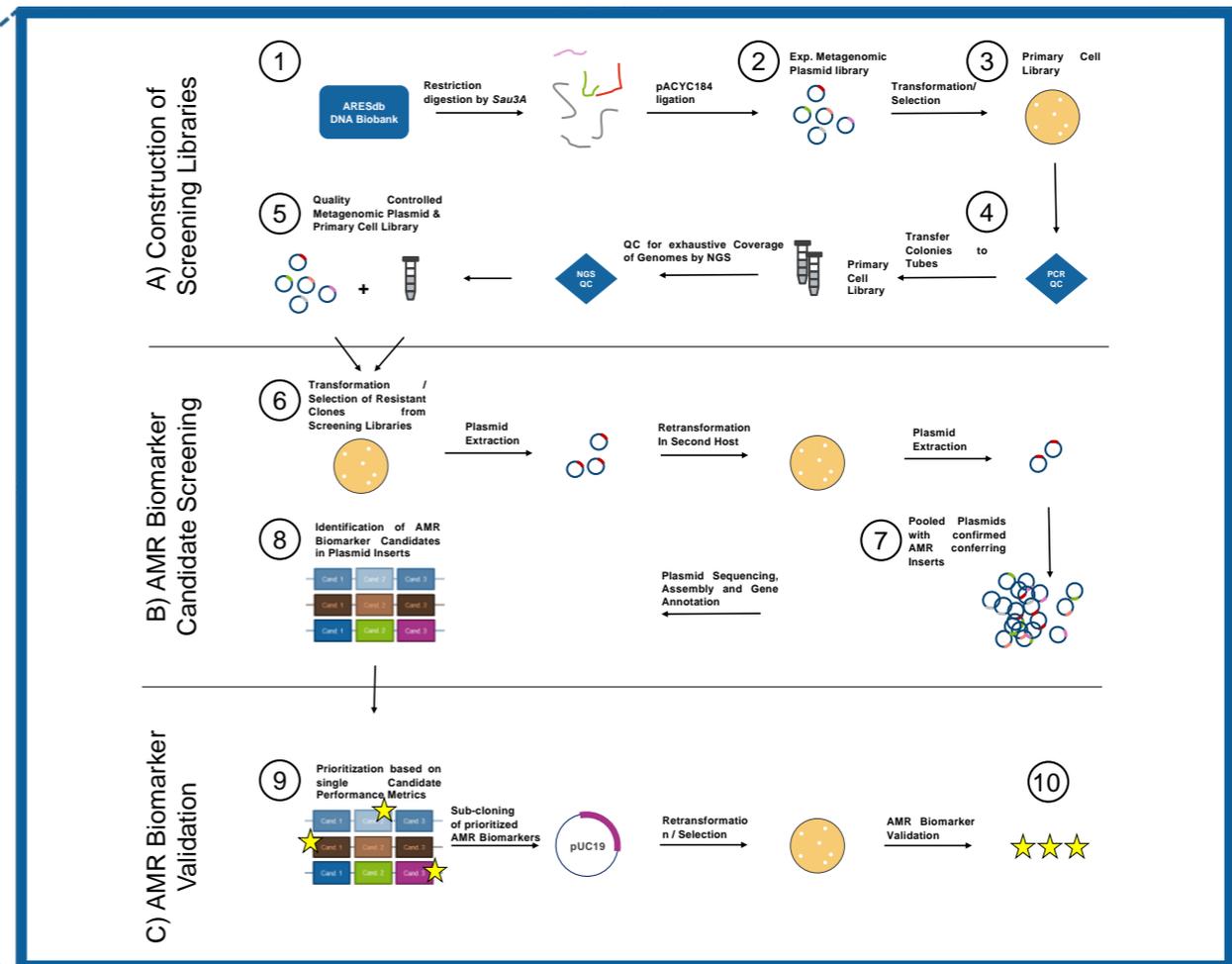
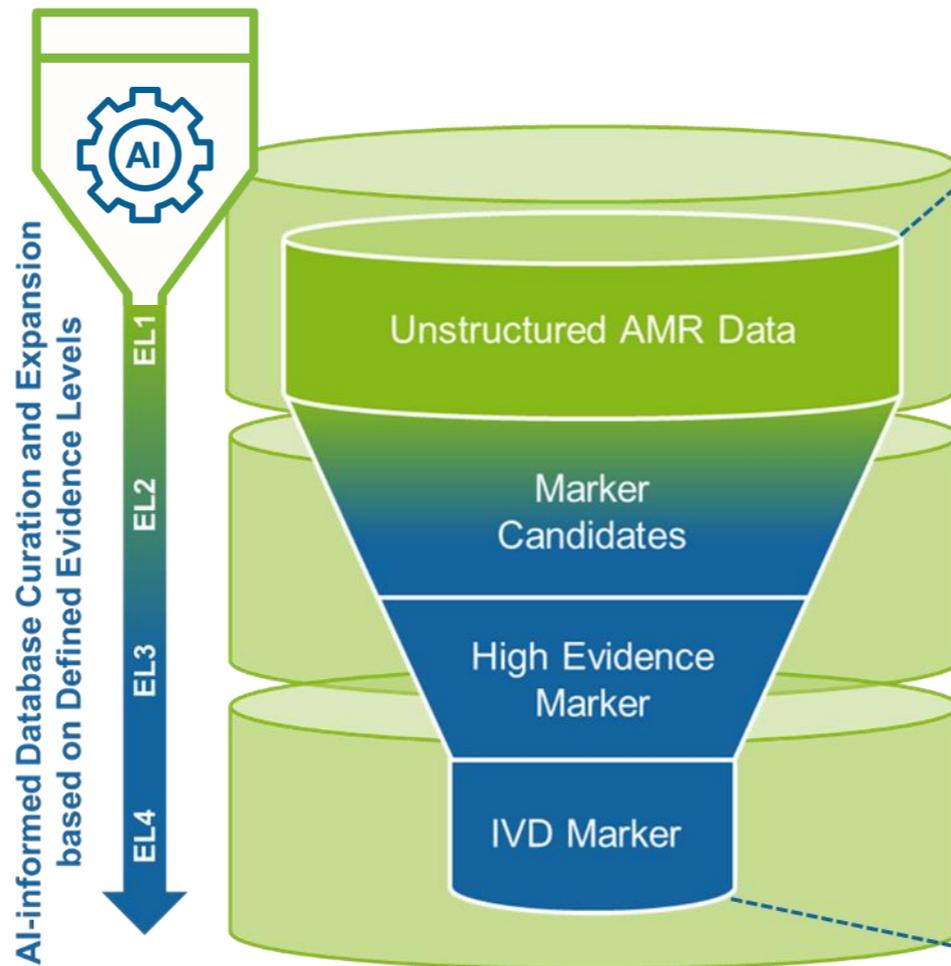
Marker Curation

Curator ID	Compound	Compound Class	Pathogen
1	302930	Ciprofloxacin	Fluoroquinolone
2	389408	Ciprofloxacin	Fluoroquinolone
3	303811	Levofloxacin	Fluoroquinolone
4	389408	Levofloxacin	Fluoroquinolone
5	389751	Ampicillin-sulbactam	Penicillin
6	654227	Ampicillin-sulbactam	Penicillin
7	351754	Ampicillin	Penicillin
8	683731	Ampicillin	Penicillin

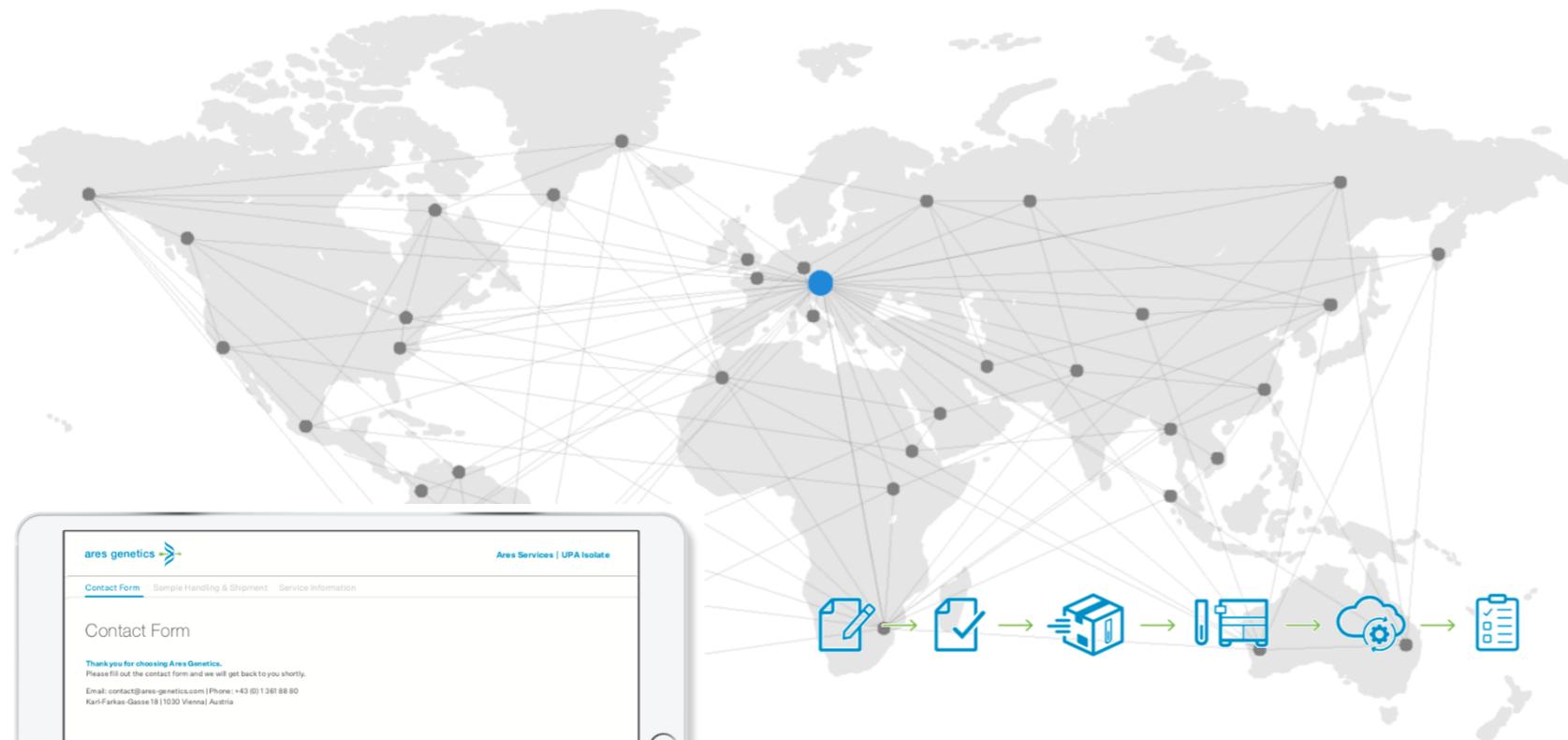
Evidence Criteria (continued)

- rrC31
- rrC32
- rrC33
- rrC34
- rrC35
- rrC36
- rrC37
- rrC38
- rrC39
- rrC40
- rrC41
- rrC42
- rrC43
- rrC44
- rrC45
- rrC46
- rrC47
- rrC48
- rrC49
- rrC50
- rrC51
- rrC52
- rrC53
- rrC54
- rrC55
- rrC56
- rrC57
- rrC58
- rrC59
- rrC60
- rrC61
- rrC62
- rrC63
- rrC64
- rrC65
- rrC66
- rrC67
- rrC68
- rrC69
- rrC70
- rrC71
- rrC72
- rrC73
- rrC74
- rrC75
- rrC76
- rrC77
- rrC78
- rrC79
- rrC80
- rrC81
- rrC82
- rrC83
- rrC84
- rrC85
- rrC86
- rrC87
- rrC88
- rrC89
- rrC90
- rrC91
- rrC92
- rrC93
- rrC94
- rrC95
- rrC96
- rrC97
- rrC98
- rrC99
- rrC100

ARESDb: PATENTED HIGH-THROUGHPUT FUNCTIONAL VALIDATION FOR HIGH-QUALITY IVD MARKER



AREScds: CLOUD-BASED DECISION SUPPORT SYSTEM TURNING NGS DATA INTO ACTIONABLE INSIGHTS



ares genetics  Ares Services | UPA Isolate

Contact Form Sample Handling & Shipment Service Information

Contact Form

Thank you for choosing Ares Genetics. Please fill out the contact form and we will get back to you shortly.
Email: contact@ares-genetics.com | Phone: +43 (0) 1 361 88 80
Kurt-Frank-Gasse 18 | 1030 Vienna | Austria

Full Name: Jane Doe Date: 2019-04-13

Organisation: John Doe Dx Number of Isolates: 96

Email: jane@johndoe.com Additional Notes:

Submit

1. Register online at ares-genetics.com
2. Request a quote or order a test
3. Submit your isolates
4. Isolate profiling by next-generation sequencing via **ARESupa**
5. Strain identification and drug resistance detection by **ARESdb**
6. Interpret results, access and download reports via **AREScds**

Actionable Findings

Klebsiella pneumoniae ST14 detected by next-generation sequencing.
Genetic antibiotic resistance marker(s) indicate resistance against:

Level of Evidence (EL)
EL4 - IVD Markers

Show 10 entries Search:

Antibiotic	Antibiotic Class	Evidence Level
Amoxicillin-clavulanic acid	Penicillin	4
Ampicillin	Penicillin	4
Ampicillin-sulbactam	Penicillin	4
Aztreonam	Monobactam	4
Cefazolin	Cephalosporin (1st)	4
Cefepime	Cephalosporin (4th)	4
Cefotaxime	Cephalosporin (3rd)	4
Ciprofloxacin	Fluoroquinolone	4
Tetracycline	Tetracycline	4
Trimethoprim-sulfamethoxazole	Folate pathway inhibitors	4

Genetic Antibiotic Resistance Markers
Diagnostic marker performance parameters for *Klebsiella pneumoniae* and Trimethoprim-sulfamethoxazole.

Antibiotic	Marker	PPV	NPV	Accuracy	Sensitivity	Specificity
Trimethoprim-sulfamethoxazole	Sul	0.78	0.96	0.88	0.94	0.84

Legend: PPV (Green), NPV (Blue), Accuracy (Orange), Sensitivity (Red), Specificity (Dark Blue)

OUR SOLUTIONS: FROM PUBLIC HEALTH AND PHARMA SERVICES TO DIAGNOSTIC SERVICES AND IVD PRODUCTS

	Offer	Customer	Need	Timeline
	IVD & SaaS Products	Healthcare Provider	Early informed treatment by rapid near-patient testing for Hospital Acquired Infections	tbd Under development
	Diagnostic Testing Services	Healthcare Provider	Informed treatment in situations where current culture methods often fail and/or take > 3 days	2020 (est.) Under development
	Public Health & Pharma Services	Healthcare Provider Public Health Labs	Infection control & Outbreak monitoring	Launched 2018
		Pharma Companies	Accelerated drug development & Improved drug positioning	

AREScds: ISOLATE SEQUENCING POWERED BY ARESdb

[Contact](#)
[Service Information](#)
[Sample Handling & Shipment](#)

Contact Form

Thank you for visiting Ares Genetics.

Please fill out the form below and we will get back to you shortly.
We appreciate your interest and we look forward to working with you soon.

Service*

Clinical Isolate Sequencing

Full Name*

Stephan Beisken

Organisation*

Organisation 

Email*

stephan.beisken@ares-genetics.com

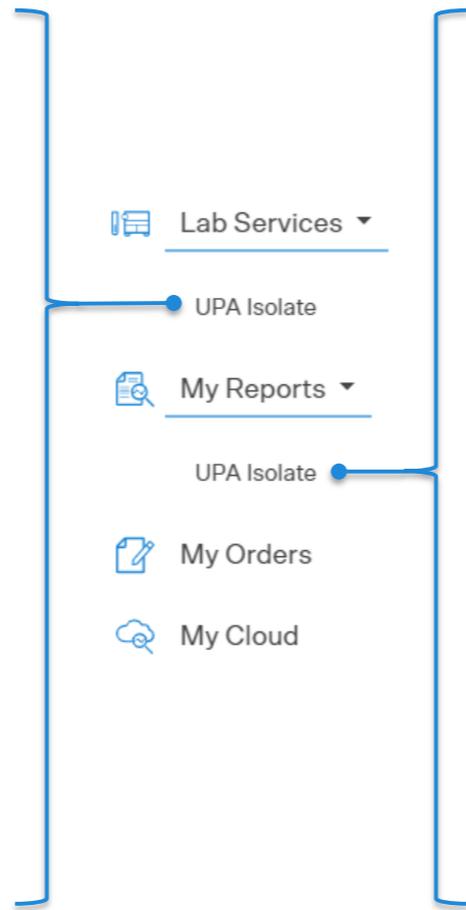
Date*

2019-04-08

Number of Isolates*

96

Contact Details
 contact@ares-genetics.com
 +43 (0) 1 361 8880
 Karl-Farkas-Gasse 18
 1030 Vienna
 Austria



Isolate Listing

Isolates sequenced with the UPA Isolate service are listed by their tracking ID and isolate names.

For further information on a single isolate, please click on the isolate's row. This will bring up information on multiple locus sequence typing, antimicrobial resistance testing, assembly statistics and taxonomy identification.

Show entries

Search:

Isolate Name	Organism	ST	Origin	Date	Tracking ID	Report
AS012926 (DESF)	<i>Escherichia coli</i>	ST69				
AS012925 (R2746)	<i>Escherichia coli</i>	ST354				
AS012924 (R2745)	<i>Escherichia coli</i>	ST226				
AS012923 (R619)	<i>Serratia marcescens</i>	-				
AS012922 (R208)	<i>Serratia marcescens</i>	-				
AS012921 (R186)	<i>Pseudomonas aeruginosa</i>	ST1560				
AS012920 (R38)	<i>Providencia stuartii</i>	-				
AS012919 (R494)	<i>Klebsiella pneumoniae</i>	ST70				
AS012918 (R179)	<i>Klebsiella pneumoniae</i>	ST14				
AS012917 (R24)	<i>Klebsiella pneumoniae</i>	ST14				
AS012239 (14C3)	<i>Klebsiella pneumoniae</i>	ST147				
AS012238 (13G2)	<i>Klebsiella pneumoniae</i>	ST307				
AS012237 (LANN)	<i>Escherichia coli</i>	ST12				
AS012236 (DESF)	<i>Escherichia coli</i>	ST69				
AS012235 (R2757)	<i>Escherichia coli</i>	ST5409				
AS012234 (R2752)	<i>Escherichia coli</i>	ST410				
AS012233 (R2746)	<i>Escherichia coli</i>	ST354				



Isolate Name	Organism	ST	Origin	Date	Tracking ID	Report
AS012238 (13G2)	<i>Klebsiella pneumoniae</i>	ST307				



AREScds: ISOLATE SEQUENCING POWERED BY ARESdb

AS012238 (13G2)

Klebsiella pneumoniae



Actionable Findings

Genetic species identification detected *Klebsiella pneumoniae*. Antibiotic resistance marker(s) indicate resistance against:

Level of Evidence (EL)

= EL4 - IVD Markers

Show 25 entries

Search:

Antibiotic	Antibiotic Class	Evidence Level
Amoxicillin-clavulanic acid	Penicillin	4
Ampicillin	Penicillin	4
Ampicillin-sulbactam	Penicillin	4
Aztreonam	Monobactam	4
Cefazolin	Cephalosporin (1st)	4
Cefepime	Cephalosporin (4th)	4
Cefotaxime	Cephalosporin (3rd)	4
Ciprofloxacin	Fluoroquinolone	4
Gentamicin	Aminoglycoside	4
Tetracycline	Tetracycline	4
Tobramycin	Aminoglycoside	4
Trimethoprim-sulfamethoxazole	Folate pathway inhibitors	4

Resistance Markers

Show 10 entries

Search: sul2

Antibiotic	Marker	Marker Family	PPV	NPV	Sensitivity	Specificity
Trimethoprim-sulfamethoxazole	Sul2		0.81	0.80	0.38	0.97

Metadata

Isolate Name	Organism	Taxonomy ID
AS012238	<i>Klebsiella pneumoniae</i>	573
Country	Date	Tracking ID
	-	

Multilocus Sequence Typing

Sequence Type	MLST Scheme
ST307	kpneumoniae

gapA	infB	mdh	pgi	phoE	rpoB	tonB
4	1	2	52	1	1	7

Assembly Statistics

Assembly	Quality Tier	GC Content
13G2	Tier 1	56.72%
Size	N50	L50
5.9 Mbp	104516	16
Coding Sequences	tRNA Anticodons	rRNA Anticodons
5491	19	3

Isolate Name	Organism	ST	Origin	Date	Tracking ID	Report
AS012238 (13G2)	<i>Klebsiella pneumoniae</i>	ST307				

AREScds: ISOLATE SEQUENCING POWERED BY ARESdb

Resistance Markers

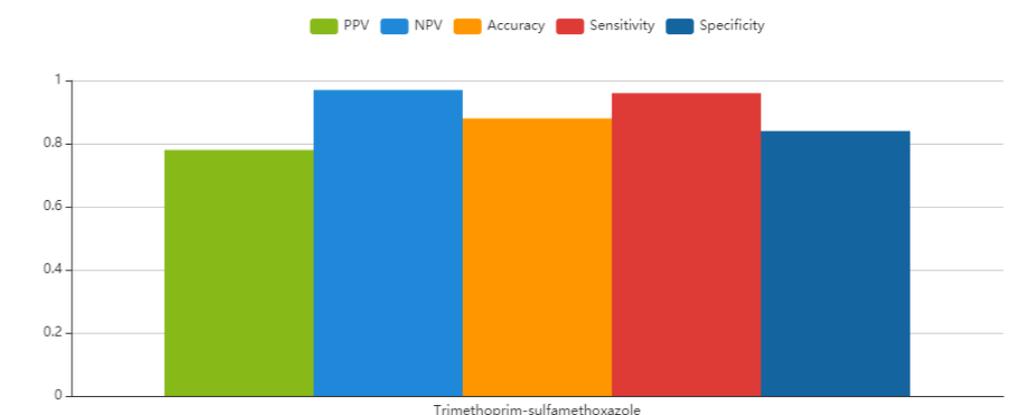
Show entries Search:

Antibiotic	Marker	Marker Family	PPV	NPV	Sensitivity	Specificity
Trimethoprim-sulfamethoxazole	Sul2	 Sul	0.81	0.80	0.38	0.97

Diagnostic Performance for family "Sul" (based on ARESdb)

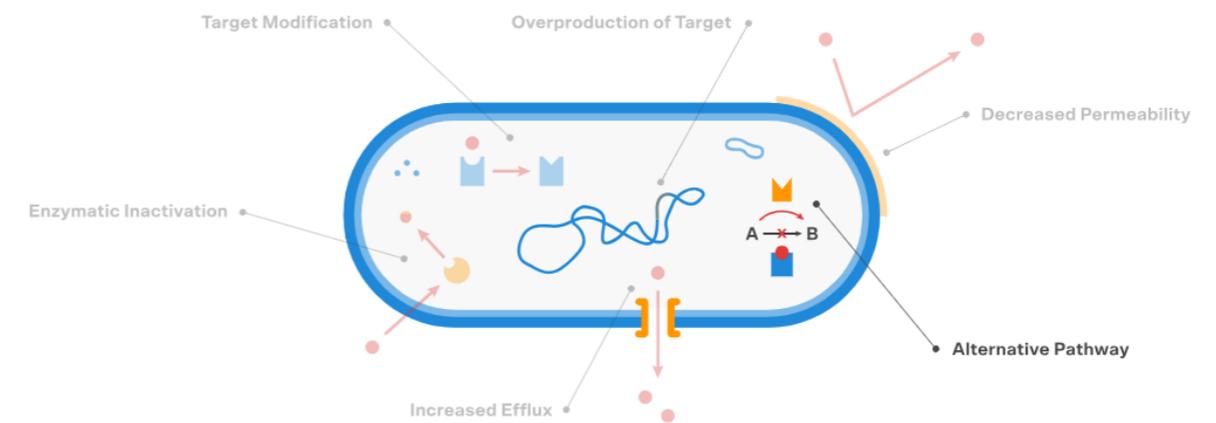
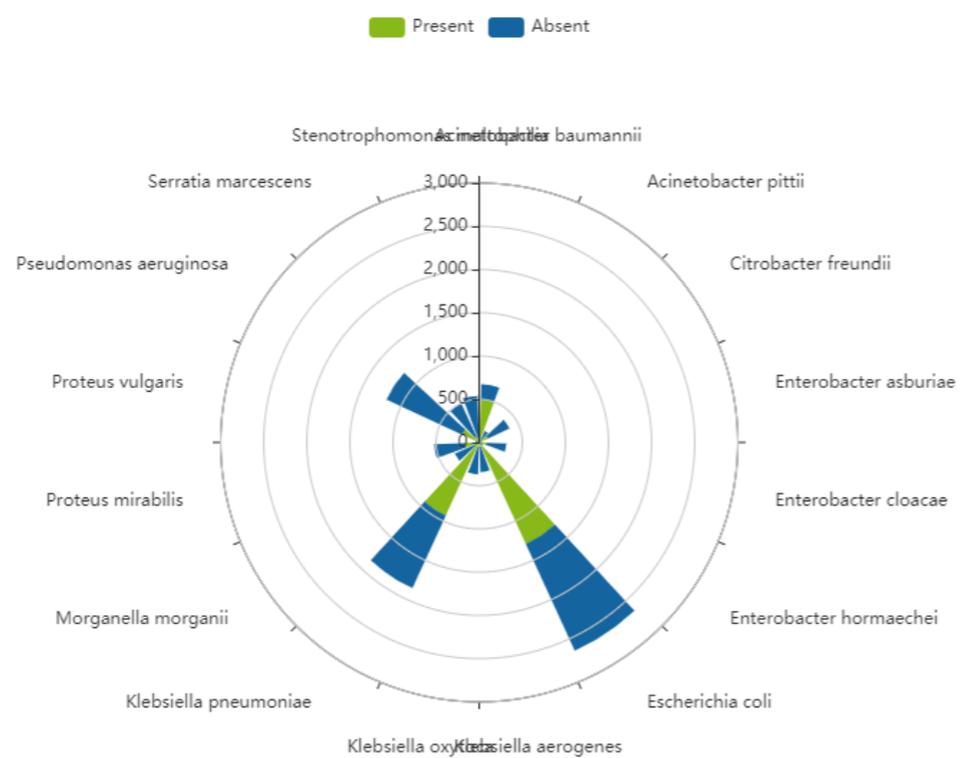
Query Pathogen: *Klebsiella pneumoniae* Query Antibiotic: Trimethoprim-sulfamethoxazole

Diagnostic marker performance parameters for *Klebsiella pneumoniae* and Trimethoprim-sulfamethoxazole



Diagnostic Relevance

Prevalence Among Affected Pathogens for family "Sul" (based on ARESdb)



AREScds: DETAILED INTERACTIVE REPORTS PER STUDY & SAMPLE | MCR-1 CASE STUDY

AS012230 (R2739)
Escherichia coli

Sample Information

Sample ID	Species	Taxonomy ID
AS012230	Escherichia coli	# 562
Source	Date	Project ID
	2015-08-01	

Multilocus Sequence Typing

Sequence Type: ST10
MLST Scheme: # ecoli

adk	fumC	gyrB	icd	mdh	purA	recA
10	11	4	8	8	8	2

Assembly Statistics

Assembly	Quality Tier	GC Content
R2739	Tier 1	50.61%
Size	NSI	LSI
4.9 Mbp	88409	18
Coding Sequences	tRNA Anticodons	rRNA Anticodons
4586	21	3

My Reports My Analyses

UPA Isolate Reports

Detailed information on strain and multiple locus sequence typing, antimicrobial resistance testing as well as UPA test report can be accessed for each sample.

Show 25 entries Search: Escherichia coli

Sample ID	Species	Sequence Type	Source	Date	UPA Report
AS012230	Escherichia coli	ST10		2015-08-01	
AS012237	Escherichia coli	ST12		-	
AS012144	Escherichia coli	ST131		-	
AS012232	Escherichia coli	ST226		2015-08-01	
AS012924	Escherichia coli	ST226		2015-08-01	
AS012233	Escherichia coli	ST354		2016-01-01	
AS012925	Escherichia coli	ST354		2016-01-01	
AS012234	Escherichia coli	ST410		2015-11-01	
AS012235	Escherichia coli	ST5409		2016-05-01	
AS012231	Escherichia coli	ST57		2015-08-01	
AS012236	Escherichia coli	ST69		-	
AS012926	Escherichia coli	ST69		-	

Showing 1 to 12 of 12 entries (filtered from 109 total entries)

UPA Report: AS012230

Ares Genetics GmbH
Karl-Farkas-Gasse 18
A-1030 Vienna
Austria
+43 (0)1361888020
services@ares-genetics.com
www.ares-genetics.com



Summary

Actionable Findings

Level of Evidence (EL)

Show 10 entries Search: Colistin

Antibiotic	Antibiotic Class	Evidence Level
Colistin	Lipopeptide	4

Showing 1 to 1 of 1 entries (filtered from 11 total entries)

Resistance Markers

Isolate AMR Graph

Investigate antibiotic resistance and clonal outbreaks.

Select Species / Compound

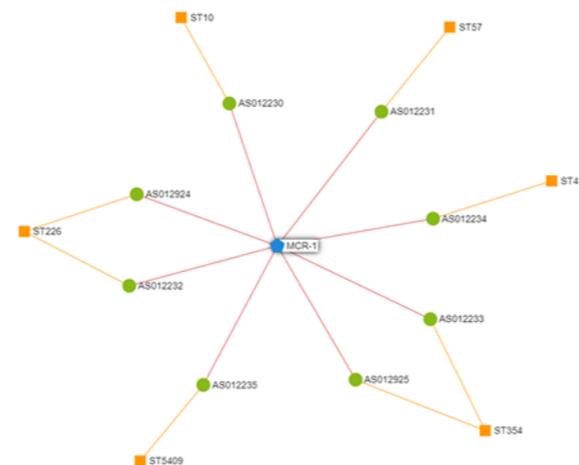
Escherichia coli - Colistin

Min. Clonal Cluster Size

1

Min. AMR Gene Cluster Size

1



Get in Contact for
Early Access!

AREScds | DIAGNOSTIC PERFORMANCE: VERIFIED PANELS FOR >150 BUG / DRUG COMBINATIONS – GROWING FAST

Home

Lab Services

My Orders

My Reports

My Cloud

AREScdb

Dashboard

AMR Panels

AMR Search

AMR Statistics

AMR Cards

AREScdb AMR Marker Panels

Summary

AREScdb enables molecular detection of antibiotic resistance for > 150 pathogen / drug combinations with up to 98% accuracy. More than 50 AREScdb AMR Marker Panels have already been optimized for *research use only* as part of ARESupa Universal Pathogenome Assay.

Pathogen/Compound Panels

Select Pathogen

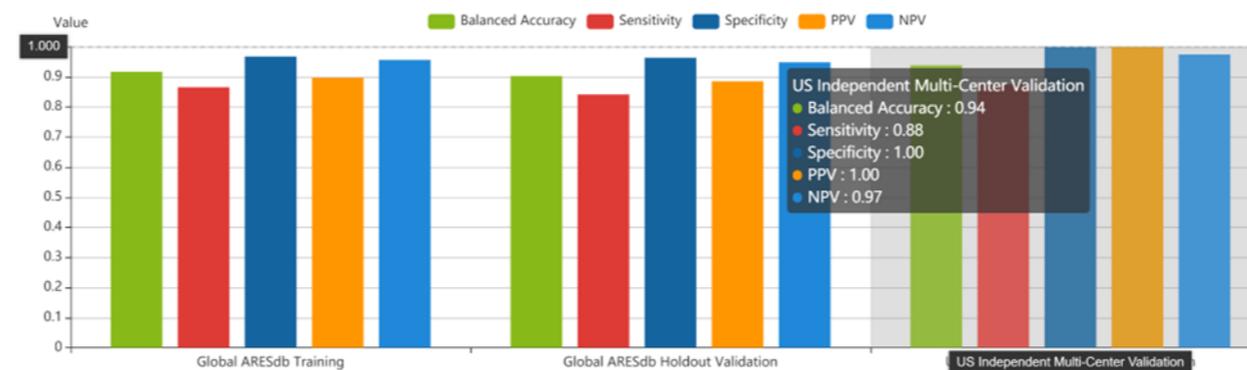
Select Antibiotic

Klebsiella pneumoniae

Gentamicin

Query

Panel Performance



ARES GENETICS: ACTIONABLE INSIGHTS FOR AMR DIAGNOSTICS AND DRUG DEVELOPMENT



FEB 18 2019

QIAGEN partners with Ares Genetics to advance global fight against antibiotic-resistant pathogens

Developing Sample to Insight solutions to accelerate research on growing public health threat

Hilden, Germany, Holzgerlingen, Germany, ar 2019 - QIAGEN N.V. (NYSE: QGEN; Frankfurt Pri a broad agreement with Ares Genetics, a subsidiary develop innovative bioinformatics and assay solution growing global health challenges posed by antibioti QIAGEN has acquired an exclusive license to levera antimicrobial resistance database, ARESdb, as well c from the ARES Technology Platform, ARESstools, in Q services for researchers. QIAGEN also obtained a n develop and commercialize molecular research assa QIAGEN next-generation sequencing (NGS) and pc solutions. Powered by artificial intelligence, ARESdb and continuously updated proprietary knowledge bc markers and their diagnostic relevance.



Sandoz teams up to drive cutting-edge digital solutions in global fight against antimicrobial resistance (AMR)

Dec 18, 2018

- Strategic collaboration agreement with Curetis subsidiary Ares Genetics to develop digital platform for development and life-cycle management of antibiotics
- Program will combine established microbiology laboratory techniques with advanced bioinformatics and AI methods
- Short-term focus on repurposing existing antibiotics to treat infections involving multi-drug-resistant pathogens

Holzkirchen, December 18, 2018 – Sandoz today announces the signature of a strategic collaboration agreement with Ares Genetics GmbH, to jointly develop a digital platform for development and life-cycle management of antibiotics.

QIAGEN and ARES to develop BioIT AMR Community Platform. Preferred access to Ares Genetics' partners contributing to ARESdb.

SANDOZ and ARES build on ARESdb for development of combination therapies & optimal drug positioning.

BGI and ARES develop integrated NGS-based workflows for infectious disease diagnostics.

ARES listed by **Forbes** as **leading AI start-up**

...

**JOIN THE FIGHT!
TALK TO US!**

LET'S TAKE INFECTIOUS DISEASE TESTING TO THE NEXT LEVEL. **TOGETHER.**

ACKNOWLEDGEMENTS



Andreas Keller
Valentina Galata
Christina Backes
Cédric Christian Laczny



Yong Chen
Chunyang Zhang
Jing Zou
Jinjing Wang
Yongping Li
Roy Tan et al.

SIEMENS



Susanne Schmolke
Howard Li
Laura Smoot
Patrick Froese
Holger Quast
Cord Stähler

Helmholtz-Institut für Pharmazeutische Forschung Saarland

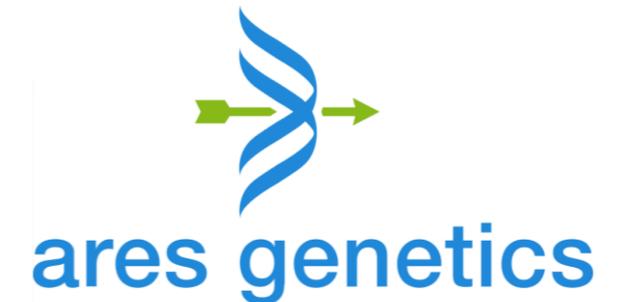


Rolf Müller
Carsten Volz

CONTACT



Dr. Andreas Posch
Managing Director & CEO
Ares Genetics GmbH
Karl-Farkas-Gasse 18
1030 Vienna
Austria
andreas.posch@ares-genetics.com
+43 664 4377 196



www.ares-genetics.com