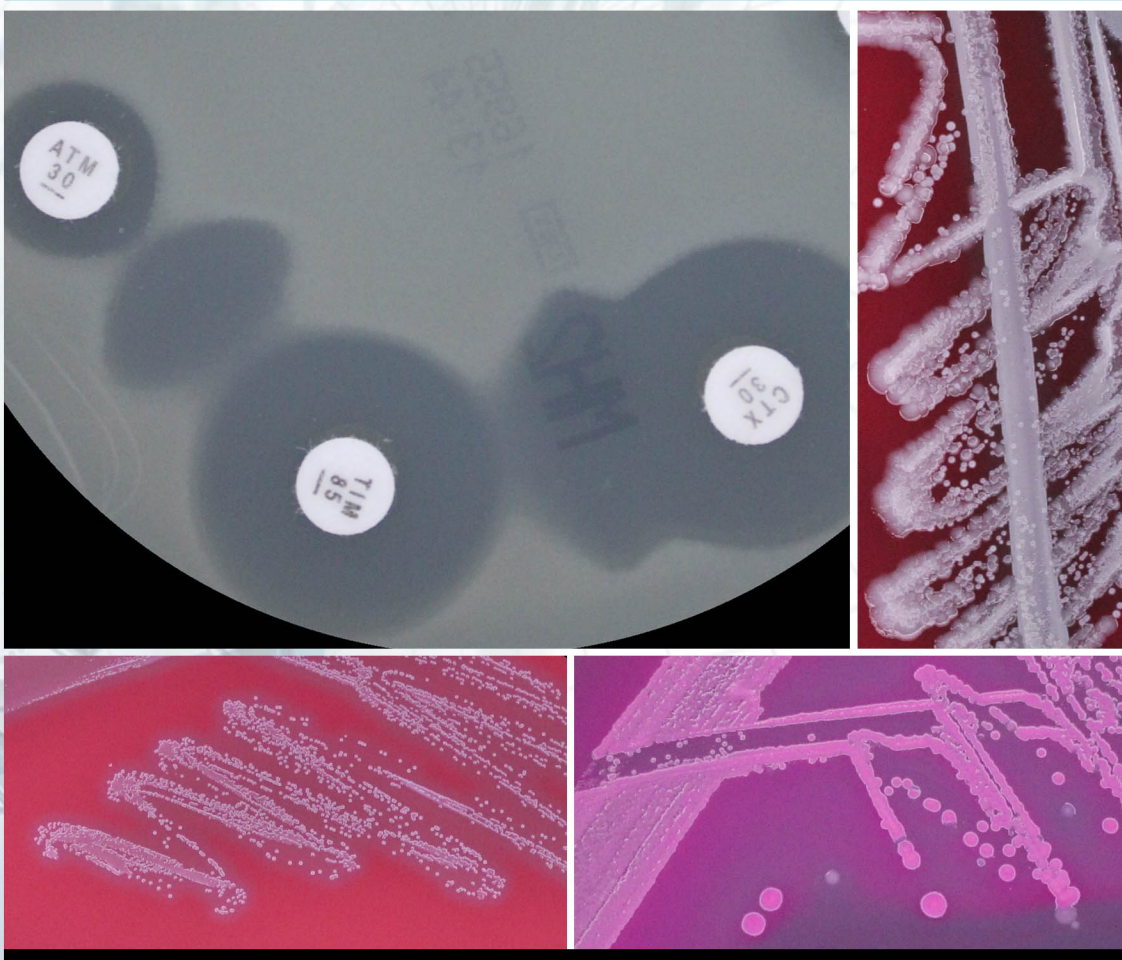


ASPIAG

INNOVATION INTELLIGENCE IMPLEMENTATION



PRODUCT LIST

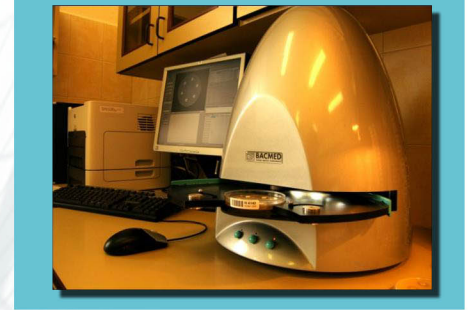
BACMED[®] 6iG2



Automated AST reader and analyser

- Quick and precise measuring of inhibitive zones

Integrated 18 Megapixel APS-C CMOS sensor, 2D barcode reader (Data Matrix), LED - field illumination, 0.05 mm precision vector analyse in below 50 milliseconds.

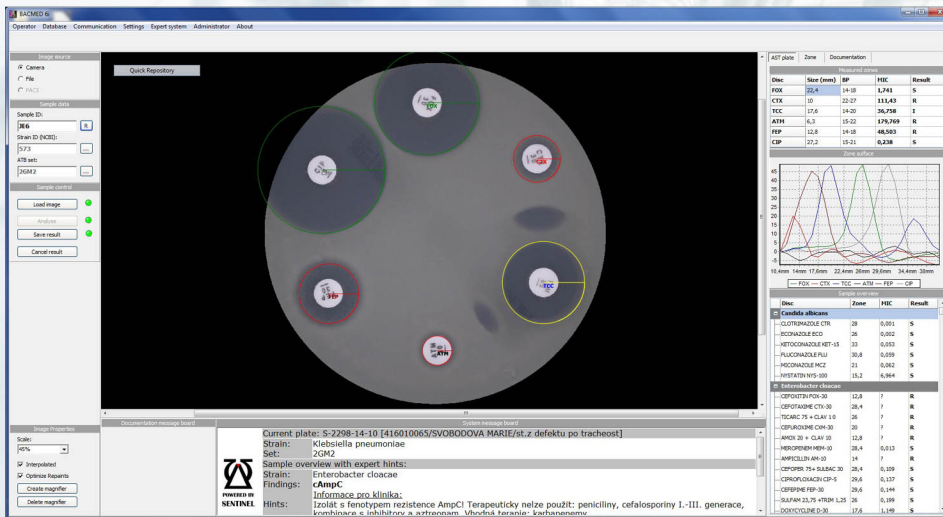


- Interpretation based on EUCAST, CLSI or any other custom breakpoint set

System supports definition of multiple breakpoint sets with assigned priority. Local science advisor can create own breakpoint library with data specific for a laboratory, missing breakpoints will be taken from library with lower priority, e.g. CLSI standard.

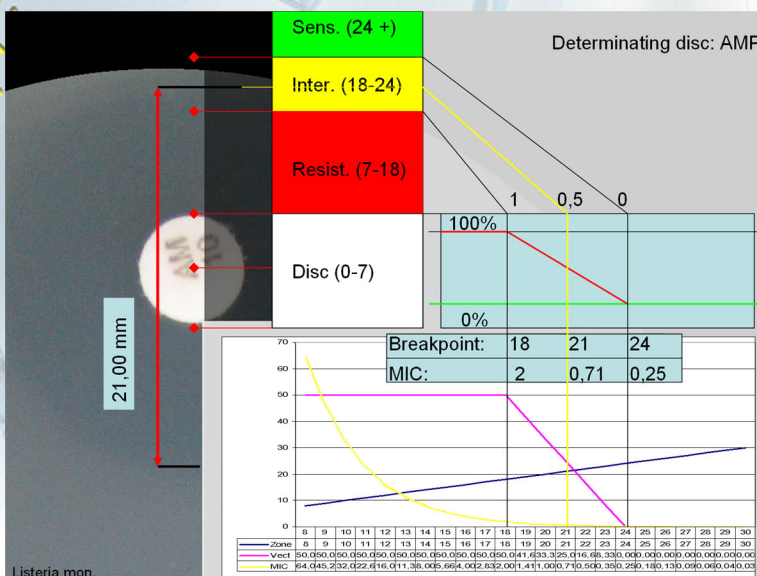
- One-click control

Entire measuring procedure is reduced to loading sample and "read" button click. Barcode assigned to AST test will manage data required for rest of the analysis; Usual length of this procedure is 6-8 seconds.



- Orientational MIC calculation

Automatic calculation of MIC value offers additional resources for further therapy decision. Used calculation method was approved by US-FDA 510(k) and British BSAC control procedures.



- Image documentation for scientific and forensic purposes

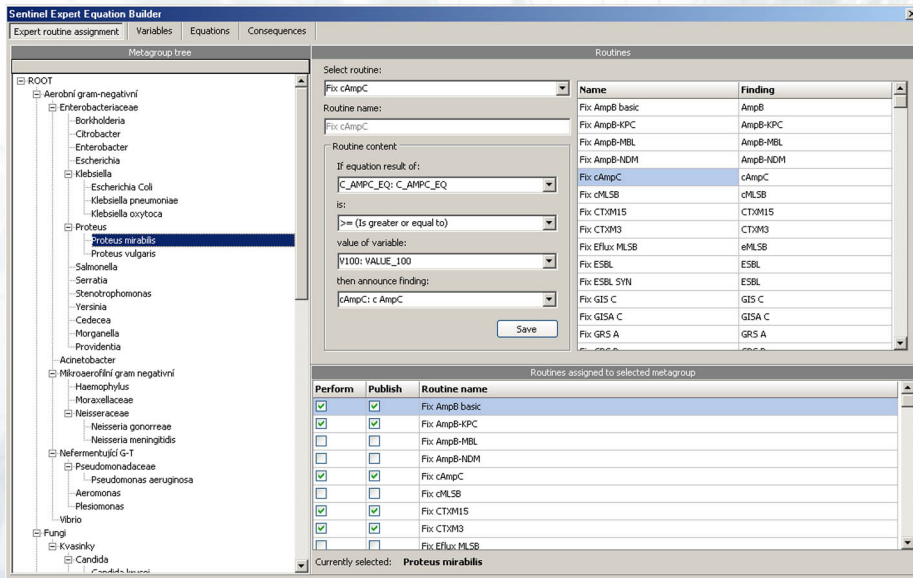
All tests are now stored both in PACS system and database, offering fast and easy to use review of past samples. Documentation doesn't extend time required for analysis.

Besides automated measuring mode, system also offers possibility of manual "any sample" documentation.



Equation builder based expert system

- **Solid tool for phenotypes detection, allowing to perform “on the fly” analysis.** Already during BACMED® 6i measuring and data-gathering procedure, expert system can evaluate circumstances referring to specific phenotypes (such as zone synergies or specific SIR combinations).



- **Advance in technology.**

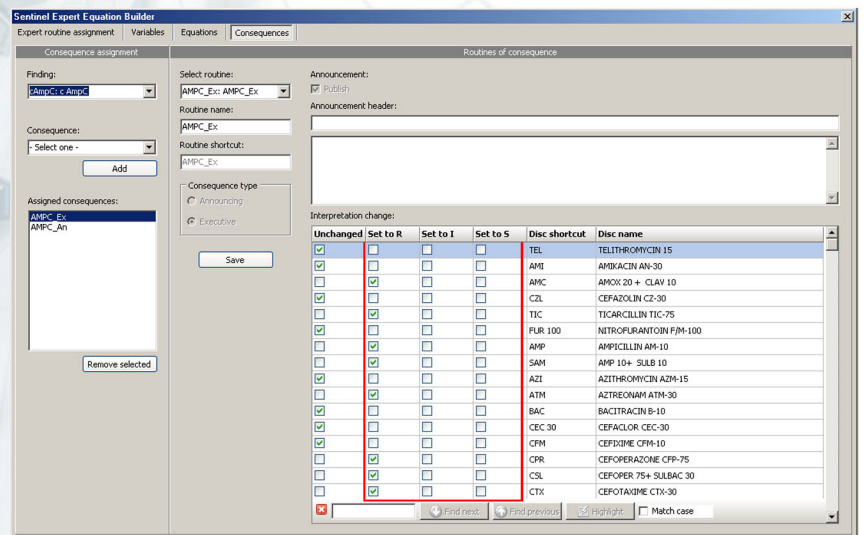
There are many findings, however some of them require further confirmation, are very valuable for treatment decision.

Sentinel Expert System performs thousands of calculations in no time, far away from what any human can do.

- **Re-interpretation: Fixing irrelevant results regarding to phenotype findings.**

Optional functionality, which may change interpretation of test results. Once set, in a full-automatic mode the system can prevent potential treatment failure.

Entire system can be customized to fulfill any local directives and recommendations.



- **Example: Result list corrected by expert system.**

Phenotype-based interpretation “cutback” for sample with cAmpC CTXM15 ESBL Qnr SHV 1-10 and TEM-1. (Just part of result is showed on image)

In this particular example, few discs were marked as resistant by expert system, in order to avoid using them in treatment (in our case Cefoxitin, Cefoperazon - Sulbactam and few others).



List of results

Results for sample 5269 (ZOLUBKOVA HILDEGARD, 2.12.2011)

Disc	Zone size	MIC	Result
Test O2Q (Klebsiella pneumoniae, CIGM1)			
AMPC	6,3	1,385 (e)	R (r)
AMOX 20 + CLAV 10	12,8	22,825 (e)	R (r)
CEFUROXIME CXM-30	6,3	256 (e)	R (r)
SULFAM 23,75 + TRIM 1,25	17,6	1,385	S
DOXYCYCLINE D-30	10,76	12,295	I
TIGECYCLINE 15	16	18,379	I



Disc	Zone size	MIC	Result
Test O2R (Klebsiella pneumoniae, CIGM2)			
CEFOXITIN FOX-30	19,62	4,563 (e)	R (s)
CEFOTAXIME CTX-30	11,6	74,506 (e)	R (r)
TICARC 75 + CLAV 1 0	14	±28 (e)	R (l)
AZTREONAM ATM-30	11,6	62,683 (e)	R (r)
CEFEPIME FEP-30	12,8	46,563 (e)	R (r)
CIPROFLOXACIN CIP-5	12,8	6,635	R



Disc	Zone size	MIC	Result
Test O2S (Klebsiella pneumoniae, CIGM3)			
IMPENEM IPM-10	23,6	0,119	S
AMP 10+ SULB 10	11,6	25,992 (e)	R (l)
CEFOPERAZONE CFP-75	11,6	140,07 (e)	R (r)
COLISTIN COL-25	12,8	1,149	S
CEFTAZIDIME CAZ-30	11,6	8,456 (e)	R (r)
EDTA 930 + IPM 10	21,2	0,109	S

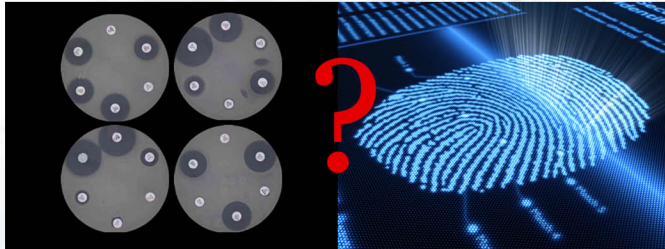




Epidemiology expert system

- Unique tool for samples match marking, based on AST susceptibility fingerprints.

Using basic assumption, that each strain, in certain amount of generations, keeps same or very similar characteristics in AST discs interactions, allows system to create fingerprints for each strain – and so enables its tracking across various samples, patients or even departments.



We can never be 100% sure of a transfer, as mutations may occur randomly and anytime. But even after considering such an option, this tool gives lots of points for further investigation...

- Tracking incidence of similar strains, warning in case of possible transfer between patients.

Let the numbers talk first. Even after we admit that part of the conclusion is a dead end, recent studies confirm over 85% patient-to-patient transfers on over 3.000 samples. Considering massive amount of data to be analyzed, yet again, system was designed to create reports “on the fly”. In numbers – match marking of 1.000 samples requires below 1 minute of analysis, including side statistics.

System also creates strains and Phenotypes overview report for departments – stand alone or grouped by any custom key.

In-Depth Expert Analysis (IDEA) is meant to be an additional service that laboratories offer primarily to hospitals, or any other bigger health care facilities. As it doesn't require additional expensive tests and related expenses, it's also considered as very effective competitive advantage among microbiology laboratories.

Of course other common statistics, such as antibacterial resistance reports and trend analysis are included as part of the system.

In-Depth Expert Analysis
 Report by department (>> Circular-reference)
 01.12.2011 - 01.01.2012

Analyse resources:
 1273 patients with 1595 samples in 196 departments with 96% match trashold.

Prchal Radovan	VLACH chi	550926
DG: S623	SID: 2905	stěr z op.rány
30.12.2011		

Staphylococcus aureus

WARNING: Same department! Prchal Radovan probably gained infection from Vratil Dusan

96%/96%/96%	Vratil Dusan	80060	
2743	redon	VLACH chi	L059 7.12.2011

Prchal Radovan shares infection with HRUBES LADISLAV

96%/96%/96%	HRUBES LADISLAV	54030	
2895	stěr z rány	VLACH cha	L030 30.12.2011

ZOUBKOVA HILDEGARD	ETTL ARO	40520
DG: I64	SID: 2518	aspirát z trachostomie
10.12.2011		

Klebsiella pneumoniae
cAmpC CTXM15 ESBL SHV 1-10 TEM-1

WARNING: Same department! ZOUBKOVA HILDEGARD probably infected HLUBINKOVA MARIE

96%/96%/96%	HLUBINKOVA MARIE	26570	
6083	mot	ETTL ARO	R509 20.12.2011

Pseudomonas aeruginosa
Achromobacter xylosoxidans

AmpB AmpB-KPC CTXM15 Qnr
cAmpC CTXM15 ESBL Qnr SHV 1-10 TEM-1
