







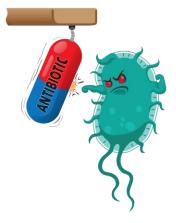
De novo L-cysteine biosynthesis as a target for antibiotic development: identification of
Pseudomonas aeruginosa
CysH inhibitors via a
multidisciplinary approach











Antimicrobial resistance



More than 35000 deaths

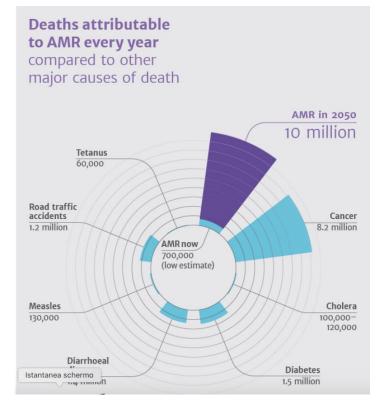
Each year, more than 35 000 people die from antibiotic-resistant infections in the European Union, Iceland and Norway. This is equivalent to the number of passengers on 13 cruise ships.

Antibiotic resistance is a silent pandemic and a growing threat to



Over 70% of the health impact of antibiotic-resistant infections is directly linked to healthcare-associated infections. This could be minimized through adequate infection prevention and control measures, as well as antibiotic stewardship in healthcare settings.





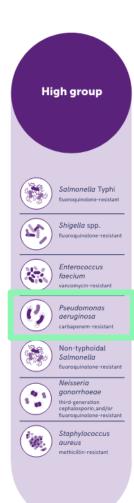














Antimicrobial resistance IDSA REPORT Bad Bugs, No Drugs: No ESKAPE! An Update from the Infectious Diseases Society of America Helen W. Boucher, George H. Talbot, John S. Bradley, 4 John E. Edwards, Jr, 5,6,7 David Gilbert, Louis B. Rice, 9,10 Michael Scheld,11 Brad Spellberg,5,6,7 and John Bartlett12

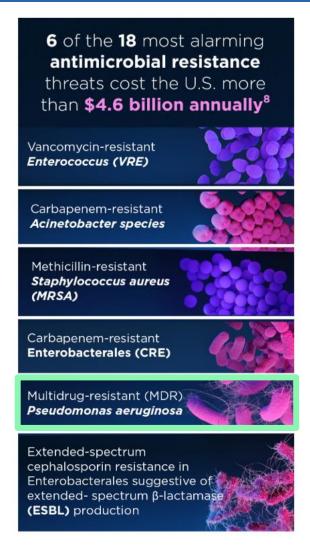
aeruginosa

Klebsiella

pneumoniae

Staphylococcus

faecium/faecalis

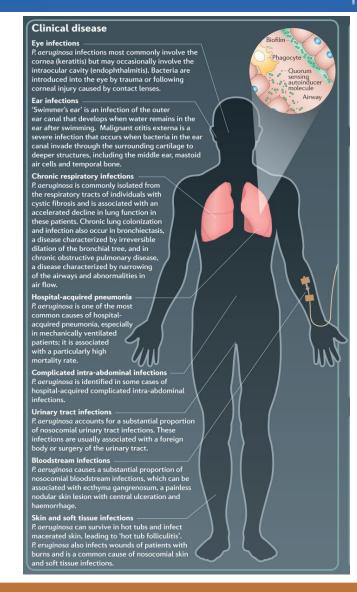


Escherichia









Pseudomonas aeruginosa

- Ranked # 1 in lung infection of cystic fibrosis (CF) patients (1:2,500 newborns)
- Ranked # 1 in intensive care unit (ICU) infections
- Ranked # 3 in non-ICU hospital-acquired (HA) infections
- Ranked # 2 in HA bacterial pneumonia
- Severity of infection
- Intrinsic antibiotic resistance
- Acquired antibiotic resistance (HGT)
- Pan-resistance in nosocomial and CF strains



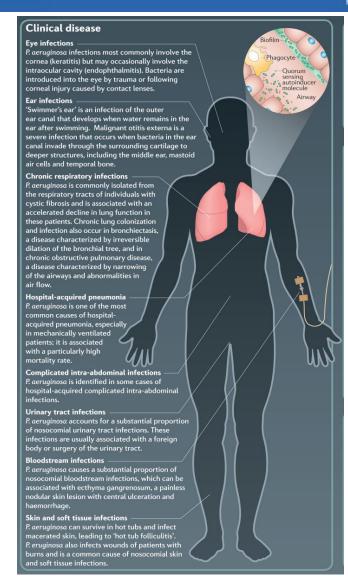


Extended-spectrum
cephalosporin resistance in
Enterobacterales suggestive of
extended- spectrum β-lactamase
(ESBL) production







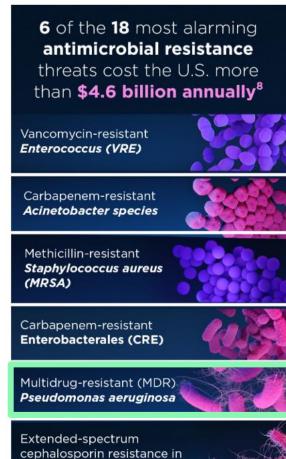


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Need for new therapeutic options



Enterobacterales suggestive of

(ESBL) production

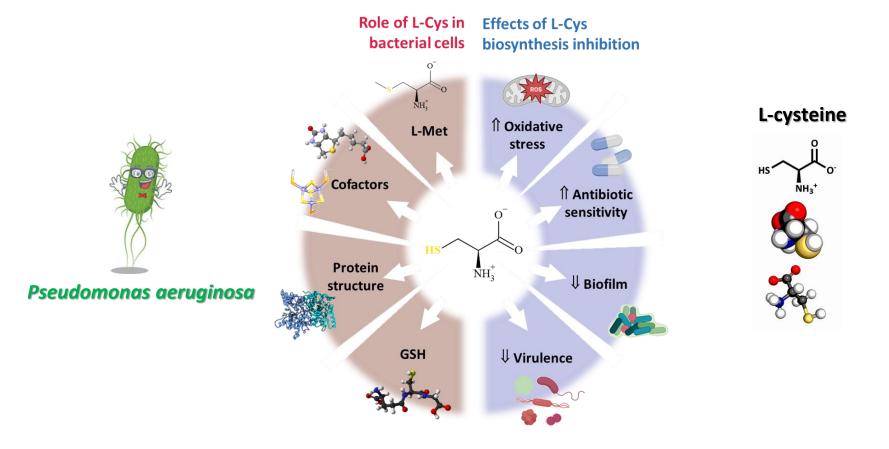
extended- spectrum β-lactamase







L-cysteine is fundamental for many biological processes

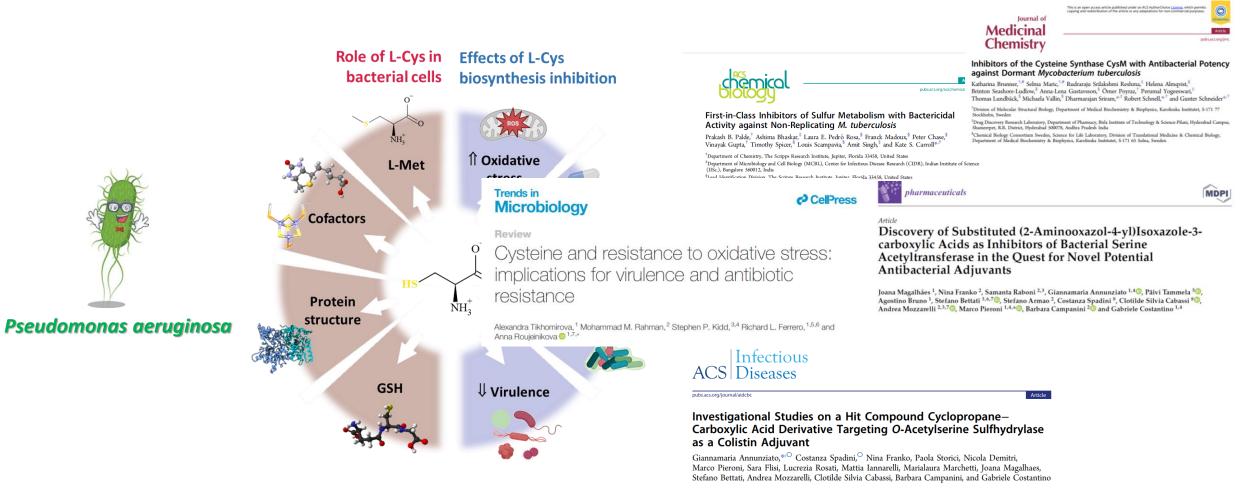








L-cysteine is fundamental for many biological processes









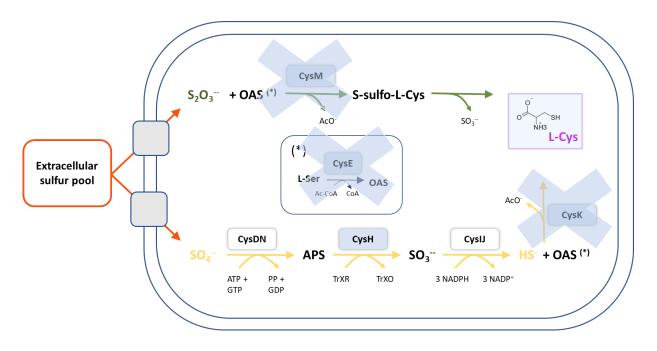
L-cysteine metabolism as target for antibiotic development

Bacteria, <u>differently from humans</u>, are able to synthesise aminoacids, including L-Cys, from inorganic salts.

The pathway has been characterized in Mycobacteria and some gram-negative bacteria...

...but it has been overlooked in *Pseudomonas aeruginosa*







Martedì R., D'Angelo J., Sassi G., Marchetti M., Hijazi S., Percudani R., Bettati S., Campanini B., Frangipani E. *De novo* cysteine biosynthesis in *Pseudomonas aeruginosa*: characterization of the two main cysteine synthase isoforms. *Under review in iScience*.







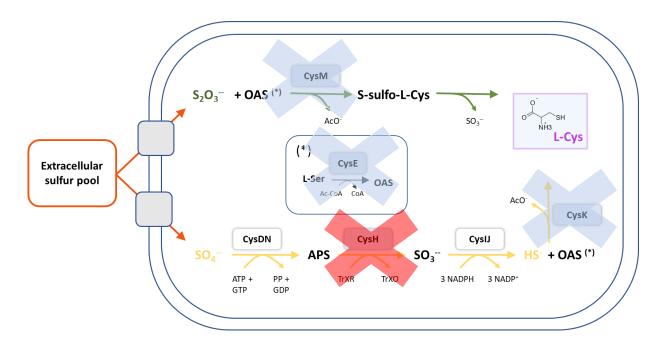
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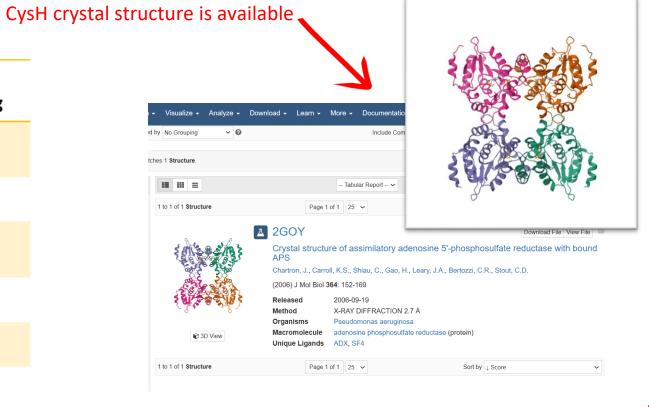






L-cysteine metabolism as target for antibiotic development

Gene	PAdb ID	Identity with E. coli ortholog
cysD cysN	PA4443 PA4442	78 % 56 %
cysH	PA1756	27 %
cysI cysJ	PA1838 PA4513	22 % 32 %
cysE	PA3816	40 %
cysK	PA2709	71 %
cysM	PA0932	69 %



How could we assay inhibitor activity ?







CysH virtual screening

ACTIVITY

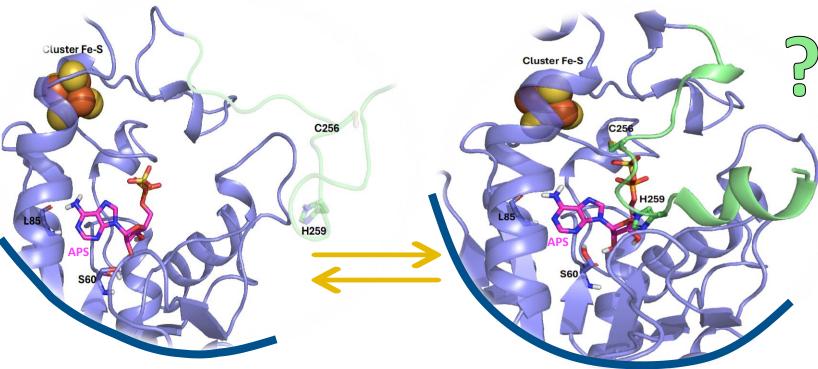
Enzyme in the open/inactive conformation

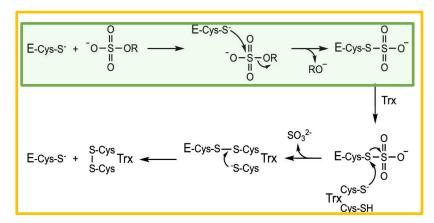
☐ Lack the *C*-terminal region in X-ray structures

☐ Missing catalytic C256

Enzyme in the closed/active conformation

☐ Prediction of the *C*-terminal region through AlphaFold2.



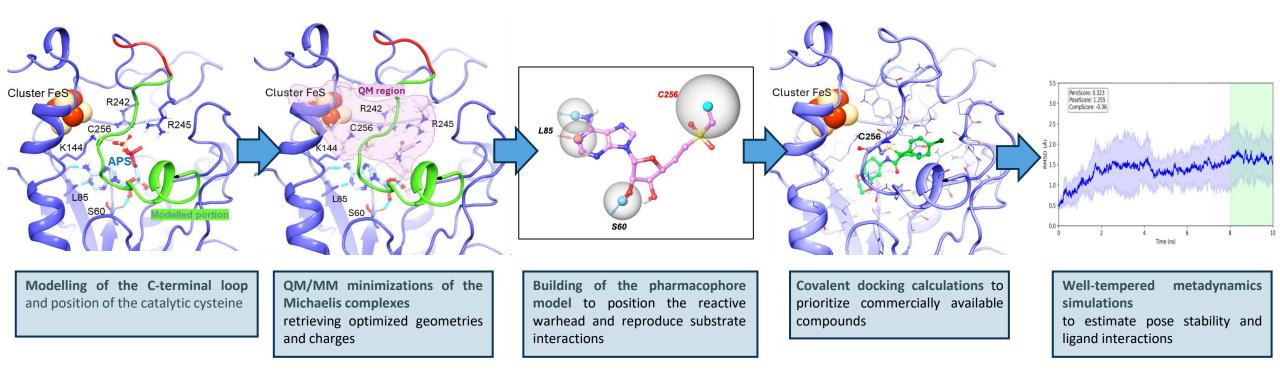








Computational workflow retrieving APSR covalent inhibitors



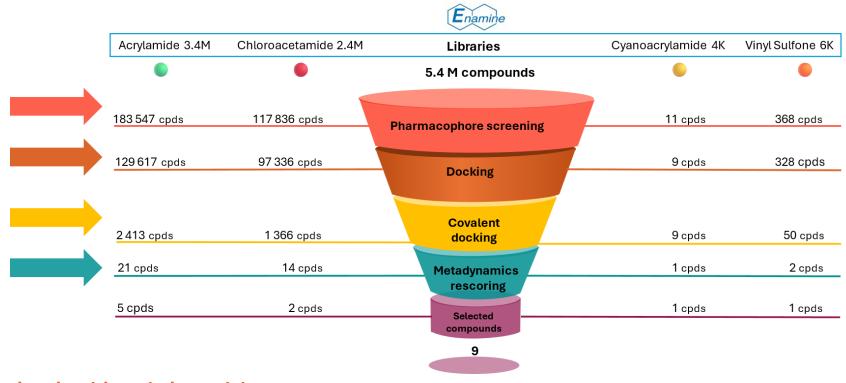


Strategies





Results of virtual screening protocol



- Retrieval of warheads with varied reactivity
- Acceleration of covalent docking via starting reactive docking poses
- ☐ Prioritization of compounds with Binding-Pose Metadynamics, prioritizing stable binding modes (RMSD<2Å)





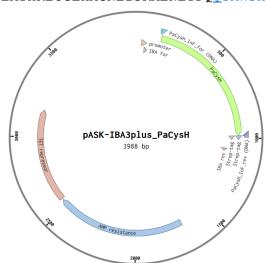


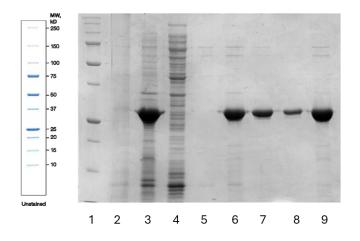
$CysH_{Pa}$ activity (and inhibition) can be investigated through different in vitro assays

Protein recombinant production in E. coli (C-terminal Strep-tag). Purification under aerobic conditions, good yields (30 mg/L)

005927 · CYSH PSEAE

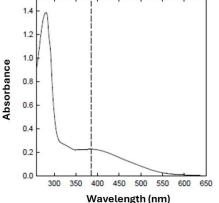
https://www.uniprot.org/uniprotkb/005927/entry MLPFATIPATERNSAAOHODPSPMSOPFDLPALASSLADKSPODILKA AFEHFGDELWISFSGAEDVVLVDMAWKLNRNVKVFSLDTGRLHPETYR FIDOVREHYGIAIDVLSPDPRLLEPLVKEKGLFSFYRDGHGECCGIRK IEPLKRKLAGVRAWATGQRRDQSPGTRSQVAVLEIDGAFSTPEKPLYK FNPLSSMTSEEVWGYIRMLELPYNSLHERGYISIGCEPCTRPVLPNOH EREGRWWWEEATHKECGLHAGNLISKAENLYFQ_SAWSHPQFEK





1- marker 2- insoluble fraction 3- soluble fraction 4- flow through 5- wash 6- elution 1 7- elution 2

8- elution 3 9- final preparation



AMP detection:

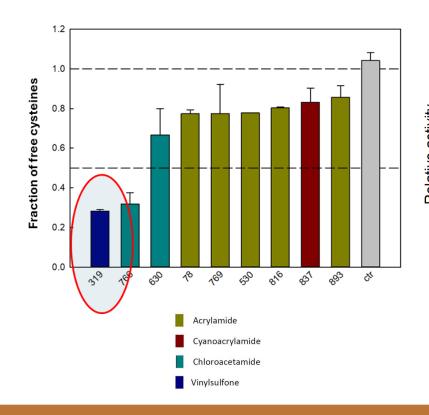
AK/PK/LDH coupled assay – 340 nm

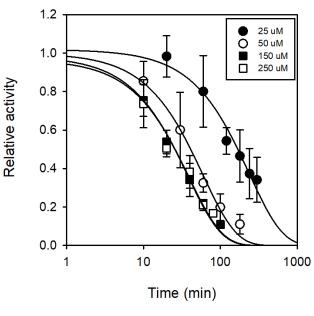




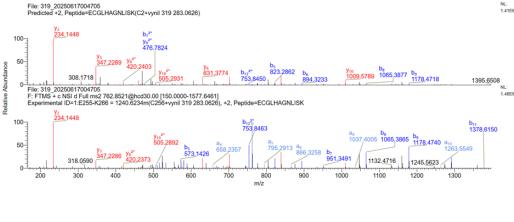


CysH is catalytically active and forms a covalent adduct with 319 that involves the catalytic cysteine





MS studies confirm selective vinylation of C256 through fragmentation patterns of peptide E[C-vinyl]GLHAGNLISK





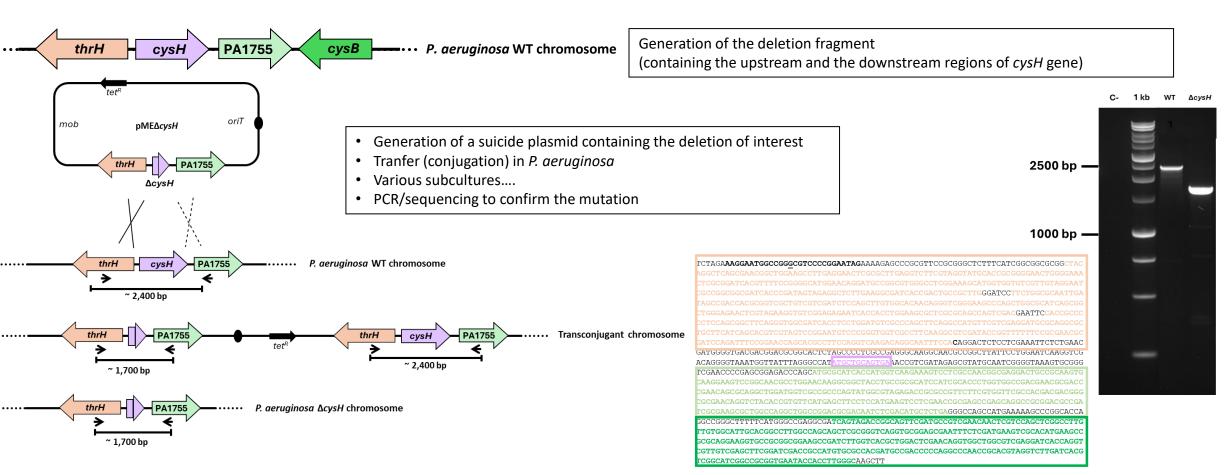




What we have done about **CysH** in *Pseudomonas aeruginosa*...



We have successfully generated a *cysH* in-frame deletion mutant and characterized its phenotype





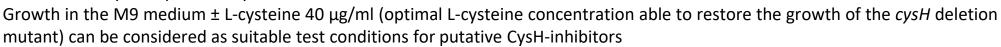




What we have done about **CysH** in *Pseudomonas aeruginosa*...

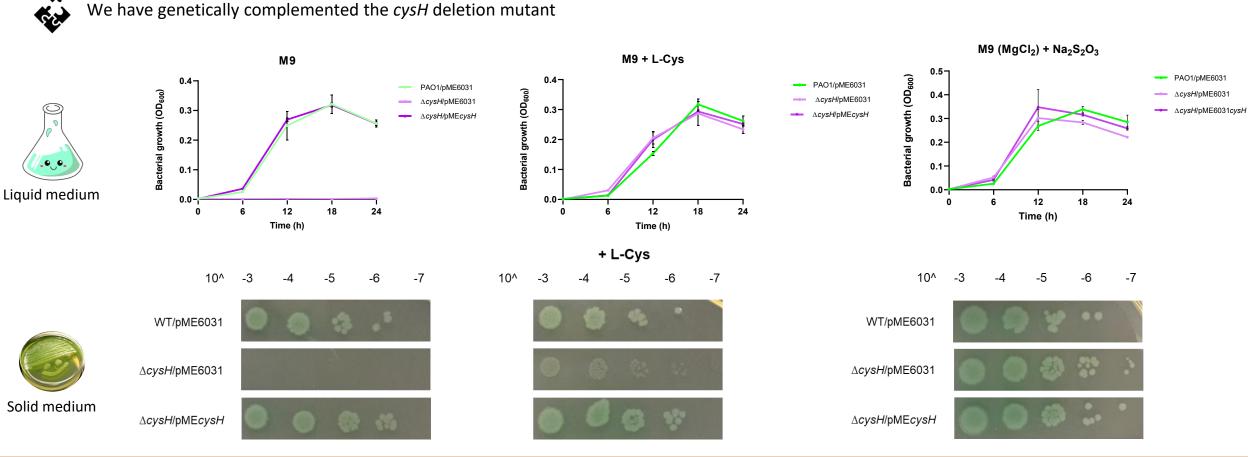


We successfully set-up the assay conditions









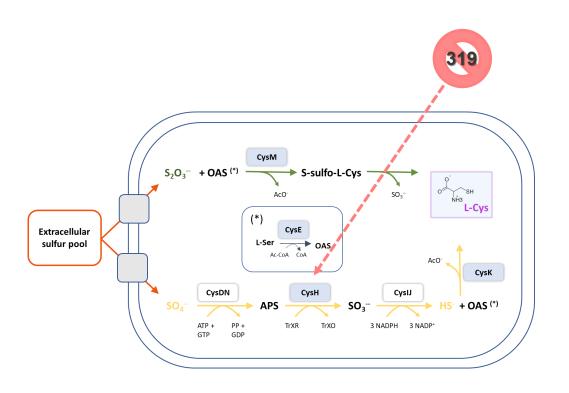




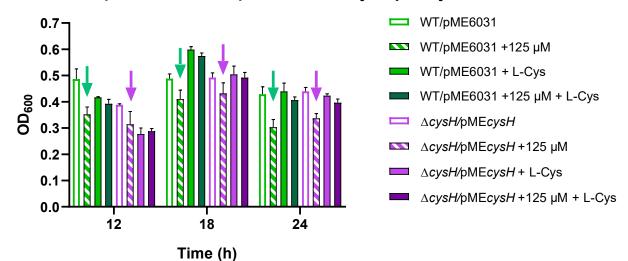








compound 319 on WT/pME6031 and ∆cysH/pMEcysH









Conclusions and future perspectives



• We have successfully identified a lead compound targeting *P. aeruginosa* CysH with good activity *in vitro* and in bacterial cells, in line with the primary aim of WP1 (*Development of a third party-accessible, enabling platform for efficient preclinical drug discovery*)



• We plan to solve CysH crystal structure in complex with 319 to gain insights on the functional and catalytic properties of the C-terminal region (in collaboration with Yvain Nicolet, IBS, Grenoble) and guide further med chem efforts



• Further validate the microbiological data on 319 by increasing the number of experimental replicates



• Assay 319 derivatives that possess the same warhead to investigate a putative increase in efficacy







Acknowledgements

Molecular modeling

Giovanni Bottegoni Gian Marco Elisi Matilda Ymeraj

Microbiology

Emanuela Frangipani Sarah Hijazi Rebecca Martedì

Organic synthesis
Michele Mari

MS studies
Michele Menotta



Biochemistry

Barbara Campanini Stefano Bettati Marialaura Marchetti Francesco Guggino























Grazie per l'attenzione





MODELING OF THE CATALYTIC PORTION OF APSR

- The **folding of the C-terminal tail** was predicted from its amino acid sequence using AlphaFold2.
- The catalytic cysteine is close to the sulfur atom of APS and to basic residues, such as K144 and arginine residues, that may increase cysteine nucleophilic proprieties.
- Comparison with PAPS reductase:
 - Conserved residues (ECG(I/L)H motif) are similarly positioned
 - Given the absence of the cluster Fe-S in the PAPS structure, its role may not be relevant for APSR mechanism.

