

Resource Summary Report

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Pasteur Institute

RRID:SCR_011485

Type: Tool

Proper Citation

Pasteur Institute (RRID:SCR_011485)

Resource Information

URL: <http://www.pasteur.fr/fr>

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Description: Institute that contributes to the prevention and treatment of infectious diseases through research, teaching and public health initiatives. The Institut Pasteur enjoys an independent status and has numerous other assets, with its research laboratories, technological platforms, teaching center and medical center all located on one campus in the heart of Paris. It also has an international network which currently counts 30 members spread over the five continents. With its unique setup and prestigious history, the Institut Pasteur has always stood at the forefront of innovation, adapting to the rapidly developing world of biological research and its applications, in particular in the field of biotechnology. Nowadays, the Institut Pasteur has four priorities to carry out its activities successfully : * to target its scientific strategy towards infectious diseases, microbiology, virology and immunology; * to adopt an outward-looking attitude, both within France, through agreements and collaborations with its partners : CNRS (French National Scientific Research Centre), Inserm (French National Institute for Health and Medical Research), universities, hospitals, industrial partners, etc., and at international level with the development of the Réseau International des Instituts Pasteur (International Network of the Institut Pasteur or RIIP), which counts 30 institutes; * to implement transversal research programs on ambitious themes and led by young researchers; * to preserve the foundation's independence, in particular through increased resources from sponsorship and donations. These priorities, upholding the traditional tasks and values of the Institut Pasteur, place it at the cutting edge of the 21st century's scientific and human challenges.

Synonyms: Pasteur Institute; Paris; France, Institut Pasteur; Paris; France, Institut Pasteur

Resource Type: institution

Resource Name: Pasteur Institute

Resource ID: SCR_011485

Alternate IDs: nlx_52301

Record Creation Time: 20220129T080305+0000

Record Last Update: 20260815T182431+0000

Ratings and Alerts

No rating or validation information has been found for Pasteur Institute.

No alerts have been found for Pasteur Institute.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 95 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Asencio Egea MA, et al. (2018) [Monoclonal spread of multi-drug resistant CTX-M-15-producing *Klebsiella pneumoniae*. Impact of measures to control the outbreak]. *Revista espanola de quimioterapia : publicacion oficial de la Sociedad Espanola de Quimioterapia*, 31(3), 237.

Muslin C, et al. (2015) Evolution and Emergence of Enteroviruses through Intra- and Inter-species Recombination: Plasticity and Phenotypic Impact of Modular Genetic Exchanges in the 5' Untranslated Region. *PLoS pathogens*, 11(11), e1005266.

Souverein D, et al. (2014) Polyclonal spread and outbreaks with ESBL positive gentamicin resistant *Klebsiella* spp. in the region Kennemerland, The Netherlands. *PloS one*, 9(6), e101212.

Almendros C, et al. (2014) CRISPR-Cas functional module exchange in *Escherichia coli*. *mBio*, 5(1), e00767.

Mora A, et al. (2014) Virulence patterns in a murine sepsis model of ST131 *Escherichia coli* clinical isolates belonging to serotypes O25b:H4 and O16:H5 are associated to specific virotypes. *PloS one*, 9(1), e87025.

Donati V, et al. (2014) Extended-spectrum-beta-lactamases, AmpC beta-lactamases and plasmid mediated quinolone resistance in *klebsiella* spp. from companion animals in Italy. *PloS one*, 9(3), e90564.

Laksanalamai P, et al. (2014) Genomic characterization of novel *Listeria monocytogenes* serotype 4b variant strains. *PloS one*, 9(2), e89024.

- Ramos PI, et al. (2014) Comparative analysis of the complete genome of KPC-2-producing *Klebsiella pneumoniae* Kp13 reveals remarkable genome plasticity and a wide repertoire of virulence and resistance mechanisms. *BMC genomics*, 15, 54.
- Sung JY, et al. (2014) Epidemiological characterizations of class 1 integrons from multidrug-resistant *Acinetobacter* isolates in Daejeon, Korea. *Annals of laboratory medicine*, 34(4), 293.
- Mavroidi A, et al. (2014) Successful control of a neonatal outbreak caused mainly by ST20 multidrug-resistant SHV-5-producing *Klebsiella pneumoniae*, Greece. *BMC pediatrics*, 14, 105.
- Cao X, et al. (2014) Molecular characterization of clinical multidrug-resistant *Klebsiella pneumoniae* isolates. *Annals of clinical microbiology and antimicrobials*, 13, 16.
- Smith D, et al. (2014) Investment into the future of microbial resources: culture collection funding models and BRC business plans for biological resource centres. *SpringerPlus*, 3, 81.
- Hamidian M, et al. (2014) A GC1 *Acinetobacter baumannii* isolate carrying AbaR3 and the aminoglycoside resistance transposon TnaphA6 in a conjugative plasmid. *The Journal of antimicrobial chemotherapy*, 69(4), 955.
- Hudson CM, et al. (2014) Resistance determinants and mobile genetic elements of an NDM-1-encoding *Klebsiella pneumoniae* strain. *PloS one*, 9(6), e99209.
- Laurens C, et al. (2014) Sacroiliitis secondary to catheter-related bacteremia due to *Mycobacterium abscessus* (sensu stricto). *Annals of clinical microbiology and antimicrobials*, 13, 9.
- Faye O, et al. (2014) Molecular evolution of Zika virus during its emergence in the 20(th) century. *PLoS neglected tropical diseases*, 8(1), e2636.
- Wang X, et al. (2013) Clonal diversity of *Acinetobacter baumannii* clinical isolates revealed by a snapshot study. *BMC microbiology*, 13, 234.
- Mshana SE, et al. (2013) Predominance of *Klebsiella pneumoniae* ST14 carrying CTX-M-15 causing neonatal sepsis in Tanzania. *BMC infectious diseases*, 13, 466.
- Travier L, et al. (2013) ActA promotes *Listeria monocytogenes* aggregation, intestinal colonization and carriage. *PLoS pathogens*, 9(1), e1003131.
- Da Re S, et al. (2013) Identification of commensal *Escherichia coli* genes involved in biofilm resistance to pathogen colonization. *PloS one*, 8(5), e61628.