Dr. Mohamed Belhocine – دكتور محمد بلحسين

Ph.D. Genomics & Bioinformatics
M.Sc. Genomics, Bioinformatics & Structural Biochemistry
B.Sc. Cell and Molecular Biology
D.E.S. Microbiology

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Mohamed Belhocine, Assistant Professor at Molecular Medicine Department of the Jawhara Center, and Arabian Gulf University of Bahrain. Mohamed holds an MSc in Microbiology from the University of Blida (Algeria), a bachelor's degree in cell and molecular biology and an MSc in bioinformatics, genomics and structural biochemistry and a PhD. of Bioinformatics and Genomics from Luminy university (France).
His research focuses on the application large-scale genomic approaches to understand epigenetic mechanisms associated with development of normal and leukemic lymphoid cells. Through his experience in laboratories as the Center of Immunology Marseille Luminy (CIML) and the Technological Advances for Genomics and Clinics Laboratory (TAGC), Mohamed has acquired extensive knowledge in experimental and computational biology, specifically in transcriptome analysis and chromatin immuno-precipitation coupled with deep sequencing (CHIP-Seq) and RNA-sequencing analysis. Mohamed is proficient in R, python, and JAVA. Mohamed is currently a Senior Bioinformatician at Jawhara center, where he supervises a clinical NGS analysis. Additionally, Mohamed develops and oversees research training programs in a few Algerian Universities.

Education:

- 2012 - 2016 - Ph.D. Bioinformatics and Genomics from **Aix-Marseille University (France)**
- 2010 - 2012 - M.Sc. Bioinformatics, genomics and structural biochemistry from **Aix-Marseille University (France)**
- 2007 - 2010 - B.Sc. Cell and Molecular Biology from **Aix-Marseille University (France)**
- 2001 - 2005 - D.E.S. Microbiology from the **University of Blida (Algeria)**

Certificates:

- 2021 - Graphical Design Certificate from **Shaw Academy – Online program**
- 2020 - Web Development Certificate from **Paris University – Online program**
- 2005 - Control of the microbiological quality of food Certificate from **Pasteur Institute of 'Algiers -Algeria**

Funding and Grants:

- PhD fellowship from The French Cancer Research Association to complete PhD project (2015-2016; 40 k€)
- Collaborative grant "Hubert Curien – Tassili" (2014-2017; ~80 k€)
- Research Project ARC (2012-2014; 50 k€)
- Research Project GEFLUC (2015-2016; 30 k€)
- Rising Star - A*MIDEX. Aix-Marseille University (2013-2016; 350 k€)
- INCA – National Cancer plan "Epigenetic and Cancer" (2015-2018; 180 k€)

Language Skills:

- **Arabic**: Native.
- **English**: Fluent.
- **French**: Native.

Professional Experiences:

- **2024 – Present** - Assistant Professor at Molecular Medicine Department of the Jawhara Center, and Arabian Gulf University of Bahrain.
- **Jan 2024 – June 2024 - Prepaire Labs Masdar Abu Dahbi, UAE: Senior Bioinformatician.**
  R&D and Bioinformatics pipelines development for scRNA-Seq and scATAC-Seq data.
- **2016 - 2024 - Molecular Biology and Genomics Center Dubai, UAE: Senior Bioinformatician.**
  Bioinformatics pipelines development and Genomics data analysis for Whole genome, Whole Exome and Targeted sequencing data, and also Metagenomics data.
- **2014 – 2016 – TAGC Marseille – France, Blueprint Epigenome Consortium: Bioinformatician.**
  Bioinformatics pipelines development and Genomics data analysis for ChIP-Seq and RNA-Seq data. (With Dr. Salvatore Spicuglia Team)
- **2012 – Present – Blida, Tlemcen, Chlef, Oran and Algiers Universities : Bioinformatics Lectures. (Part times)**
  Bioinformatics and Genomics lectures and training to B.Sc., M.Sc. and Ph.D. Students
- **2012-2014 – Necker Hospital of Paris, Hematology Department - France: Bioinformatician**
  Bioinformatics/Genomics analysis (with Pr. Vahid Asnafi Team.).
- **2011-2012 Center of Immunology Luminy (CIML) Marseille -France : Bioinformatician**
  Bioinformatics pipelines development for transcriptome analysis with microarray data (with Pr. Pierre Ferrier Team.).
- **2008-2011 Carrefour Platform Marseille -France: Food Quality Control - Microbiologist (Part times)**
  Assess the quality of the products before distribution to all carrefour of south of France.
- **2007 (4 months) Marseille Timone Hospital -France: Research assistant**
  Study of the genome evolution of Archaea (with Pr. Didier Raoult Team.)
- **2006 (8 months) Center of Immunology Marseille Luminy – CIML, France: Research assistant**
  Study the fundamental transcriptional processes to better understand the inner workings of the genome in terms of mechanistic expression of genes (With Dr. Salvatore Spicuglia at Pierre Ferrier's team)
- **2003-2005 Pasteur Institute of 'Algiers -Algeria: Research assistant**
  Study of the Probiotics effect on the immunity (with Pr. Labress Team.)

Other Professional Experiences:

- 2024: Member of the Algerian National Committee of Biobank and Genome Database.
- 2023: Algerian Genome Project: My proposal was approved by the Presidency and currently in implementation.
- 2023: Education Committee member - Arab Society of Genetic Counselors (ASGC).
- 2022: Founder member of Algerian Sci-Tech Scholars and Competences Abroad (https://algeriansca-dz.org/)
- 2012: Funder and Director of the BHK group, Bioinformatics Freelancer (https://groupe-bhk.fr/facilities/index.php).
- 2008: Creation of the E-gene Project – Bioinformatics eLearning Platform (https://groupe-bhk.fr/egeneIII/).

Professional Skills:

Computer Science:

- Computer administration: Linux (mainly Ubuntu), Windows, Docker, Conda.
- Computer programming: Bash, Python, R, Git, Perl.
- Office: Inkscape, GIMP, LibreOffice, Microsoft Office.
- Web development: HTML5, CSS3, Javascript, Bootstrap, PHP, MySQL.

Bioinformatics:

- Workflow management: Snakemake.
- Read alignment: STAR, Bowtie2, BWA, TopHat, Blast.
- Quality trim: cutadap, trimmomatic.
- Quality control: FastQC, Qualimap, FastQ Screen, MultiQC.
- Alignment processing: Samtools, Bcftools, Bedtools, Picard.
- Variant calling: GATK, Platypus, Freebayes, Deepvariant.
- De novo assembly: Spades, Edena.
- Peak calling: MACS, SICER, Danpos.
- Differential expression: DESeq2, EdgeR, Kallisto, GFOLD.
- Functional enrichment: Kegg DAVID,gProfiler, rGREAT, clusterProfiler, GOSemSim, RSAT.
- Data integration: ChromHMM, mixOmics.
- Statistics: R/Bioconductor.
- Visualization: R/ggplot2, IGV, DeepTools, JavaTreeView.
- **and many more tools and software…**

Cheminformatics:

- Molecular Modeling: Maestro, VMD,Rasmol, Jmol, Pymol, MOE, SYBYL-X.
- Molecular Dynamics: CHARMM, NAMD, GROMACS, ACEMD, Desmond.
- Drug Design: Schrodinger suite.

Engineering skills:

- Protocols and reports writing: R Markdown, LaTeX.
- Project and Team Management: Jira, figma, Agile, Kanban.

References:

Dr. Salvatore Spicuglia
Theories and Approaches of Genomic Complexity (TAGC) – Marseille, France
Salvatore.spicuglia@inserm.fr

Pr. Vahid Asnafi
Necker Hospital, Hematology Department – Paris, France
Vahid.asnafi@aphp.fr

Dr. Denis Puthier
Aix-Marseille University – Marseille, France
Denis.puthier@univ-amu.fr

Publications (Full List): i10-Index :21 / H-index: 15

- **RUNX3 is a Potential Marker for Vaso-Occlusive Crises by a Whole Blood Transcriptomic Analysis in Sickle Cell Disease.**
  (06 November 2024 - Research Square - Impact factor: Peer Review in Progress)
  Safa Taha, Hawra Abdulwahab, Ameera Sultan, Moiz Bakheit, **Mohamed Belhocine.**

- **Development of an Optimization Software for Bioremediation of Hydrocarbon-Contaminated Soils mechanisms.**
  (October 2024 - International Journal of Current Science Research and Review- Impact factor: **7.943**)
  Meriem BENBERNOU, Hadja Fatima TBAHRITI, **Mohamed Belhocine***
  * Corresponding Author.

- **DNA methylation analysis as a new tool for the differential diagnosis between T-LBL and lymphocyte-rich thymoma.**
  (September 2024 - The Journal of Pathology - Impact factor: **8.000**)
  Mohamed Belhocine*, Mehdi Latiri*, Charlotte Smith, Nathalie Garnier, Estelle Balducci, Antoine Pinton, Guillaume Andrieu, Julie Bruneau, Salvatore Spicuglia, Vincent Thomas de Montpreville, Lara Chalabreysse, Alexander Marx, Nicolas Girard, Benjamin Besse, Christoph Plass, Laure Gibault, Cécile Badoual, Elizabeth Macintyre, Vahid Asnafi, Thierry Jo Molina, Aurore Touzart.
  * Equal contributors.

- **Dynamic of broad H3K4me3 domains uncover an epigenetic switch between cell identity and cancer-related genes.**
  (June 2022 - Genome Research - Impact factor: **9.043**)
  Mohamed Belhocine, Mathieu Simonin, José David Abad Flores, Agata Cieslak, Iris Manosalva, Lydie Pradel, Charlotte Smith, Eve-Lyne Mathieu, Guillaume Charbonnier, Joost H.A. Martens, Hendrik G. Stunnenberg, Muhammad Ahmad Maqbool, Aneta Mikulasova, Lisa J. Russell, Daniel Rico, Denis Puthier, Pierre Ferrier, Vahid Asnafi and Salvatore Spicuglia..

- **Blueprint of human thymopoiesis reveals molecular mechanisms of stage-specific TCR enhancer activation.**
  (07 September 2020 – Journal of Experimental Medicine - Impact factor: 14.307)
  Agata Cieslak, Guillaume Charbonnier, Melania Tesio, Eve-Lyne Mathieu, **Mohamed Belhocine**, Aurore Touzart, Charlotte Smith, Guillaume Hypolite, Guillaume P Andrieu, Joost HA Martens, Eva Janssen-Megens, Marta Gut, Ivo Gut, Nicolas Boissel, Arnaud Petit, Denis Puthier, Elizabeth Macintyre, Hendrik G Stunnenberg, Salvatore Spicuglia, Vahid Asnafi.

- **A transcriptomic continuum of differentiation arrest identifies myeloid interface acute leukemias with poor prognosis.** (13 July 2020 – Leukemia - Impact factor: **11.528**)
  Jonathan Bond, Aleksandra Krzywon, Ludovic Lhermitte, Christophe Roumier, Anne Roggy, **Mohamed Belhocine**, Alexander Abdulkader Kheirallah, Patrick Villarese, Guillaume Hypolite, Francine Garnache-Ottou, Sylvie Castaigne, Nicolas Boissel, Vahid Asnafi, Claude Preudhomme, Hervé Dombret, Elisa Laurenti, Elizabeth Macintyre.

- **Low level CpG island promoter methylation predicts a poor outcome in adult T-cell acute lymphoblastic leukemia.**
  (19 September 2019 – Haematologica - Impact factor: **9.941**)
  Touzart A, Boissel N, **Belhocine M**, Smith C, Graux C, Latiri M, Lhermitte L, Mathieu EL, Huguet F, Lamant L, Ferrier P, Ifrah N, Macintyre E, Dombret H, Asnafi V and Spicuglia S.

- **A critical regulator of Bcl2 revealed by systematic transcript discovery of lncRNAs associated with T-cell differentiation.** (18 March 2019 - Scientific Reports - Impact factor: **4.379**)
  Wiam Saadi, Yasmina Kermezli, Lan T. M. Dao, Evelyne Mathieu, David Santiago-Algarra, Iris Manosalva, Magali Torres, **Mohamed Belhocine**, Lydie Pradel, Beatrice Loriod, Mourad Aribi, Denis Puthier & Salvatore Spicuglia

- **Explore, edit and leverage genomic annotations using Python GTF toolkit.**
  (Feb 2019 - Bioinformatics - Impact factor: **6.937**)
  F. Lopez, G. Charbonnier, Y. Kermezli, **M. Belhocine**, Q. Ferré, N. Zweig, M. Aribi, A. Gonzalez, S. Spicuglia, D. Puthier

- **Epigenetic silencing affects L-asparaginase sensitivity and predicts outcome in T-ALL** (Dec 2018 - Clinical Cancer Research - Impact factor: **12.531**)
  Dr. Aurore Touzart , Dr. Etienne Lengline , Mr. Mehdi Latiri , **Dr. Mohamed Belhocine** , Charlotte Smith , Dr. Xavier Thomas , Dr. Salvatore Spicuglia , Dr. Denis Puthier , Dr. Françoise Pflumio , Dr. Thibaut Leguay , Dr. Carlos Graux , Dr. Yves Chalandon , Dr. Francoise Huguet , Dr. stéphane leprêtre , Dr. Norbert Ifrah , Dr. Hervé Dombret , Dr. Elizabeth Macintyre , Dr. Mathilde Hunault-Berger , Dr. Nicolas Boissel

- **A comprehensive catalog of LncRNAs expressed in T-Cell Acute Lymphoblastic Leukemia.** (Nov 2018 - Leukemia & Lymphoma Journal - Impact factor: **3.280**)

Yasmina Kermezli, Wiam Saadi, **Mohamed Belhocine**, Eve-Lyne Mathieu, Marc-Antoine Garibal, Vahid Asnafi, Mourad Aribi, Salvatore Spicuglia and Denis Puthier.

- **Novel Intergenically-spliced Chimera, NFATC3-PLA2G15, is Associated with Aggressive T-ALL Biology and Outcome.** (Jan 2018 - Molecular Cancer Research - Impact factor: **5.852**)
  Jonathan Bond, Christine Tran Quang, Guillaume Hypolite, **Mohamed Belhocine**, Aurélie Bergon, Gaëlle Cordonnier, Jacques Ghysdael, Elizabeth Macintyre, Nicolas Boissel, Salvatore Spicuglia and Vahid Asnafi.

- **Early response-based therapy stratification improves survival in adult ETP-ALL: a GRAALL study.** (Jun 2017 - Journal of Clinical Oncology - Impact factor: **44.544**)
  Jonathan Bond, Carlos Graux, Ludovic Lhermitte, Diane Lara, Thomas Cluzeau, thibaut leguay, Agata Cieslak, Amélie Trinquand, Cedric Pastoret, **Mohamed Belhocine**, Salvatore Spicuglia, Véronique LHERITIER, Stéphane Leprêtre, Xavier Thomas, RIGAL-HUGUET Françoise, Ifrah Norbert, Herve Dombret, Elizabeth Macintyre, Nicolas Boissel, and Vahid Asnafi.

- **TCR rearrangments identify a subgroup of NKL-deregulated adult T-ALLs associated with favorable outcome.** (Jun 2017 - Leukemia - Impact factor: **11.528**)
  P Villarese, C Lours, A Trinquand, S Le Noir, **M Belhocine**, L Lhermitte, A Cieslak, M Tesio, A Petit, M LeLorch, S Spicuglia, N Ifrah, H Dombret, A W Langerak, N Boissel, E Macintyre & V Asnafi.

- **Homeobox protein TLX3 activates miR-125b expression to promote T-cell acute lymphoblastic leukemia.** (April 2017 - Blood Advances - Impact factor: **22.133**)
  Laurent Renou, Pierre-Yves Boelle, Caroline Deswarte, Salvatore Spicuglia, Aissa Benyucef, Julien Calvo, Benjamin Uzan, **Mohamed Belhocine**, Agata Cieslak, Judith Landman-Parker, Andre Baruchel, Vahid Asnafi, Françoise Pflumio, Paola Ballerini, and Irina Naguibneva.

- **CBFβ-SMMHC regulates ribosomal gene transcription and alters ribosome biogenesis.** (Feb 2017 - Leukemia - Impact factor: **11.528**)
  Cordonnier G, Mandoli A, Radhouane A, Hypolite G, Lhermitte L, **Belhocine M**, Asnafi V, Macintyre E, Martens JH, Fumagalli S, Bond J.

- **Triggering the TCR Developmental Checkpoint Activates a Therapeutically Targetable Tumor Suppressive Pathway in T-cell Leukemia.** (Jun 2016 - Cancer Discovery - Impact factor: **39.397**)
  Amélie Trinquand, Nuno R. dos Santos, Christine Tran Quang, Francesca Rocchetti, Benedetta Zaniboni, **Mohamed Belhocine**, Cindy Da Costa de Jesus, Ludovic Lhermitte, Melania Tesio, Michael Dussiot, François-Loïc Cosset, Els Verhoeyen, Françoise Pflumio, Norbert Ifrah, Hervé Dombret, Salvatore Spicuglia, Lucienne Chatenoud, David-Alexandre Gross, Olivier Hermine, Elizabeth Macintyre, Jacques Ghysdae, and Vahid Asnafi.

- **Transcription dependent generation of a specialized chromatin structure at the Tcrβ locus.**
  (Feb 2015 - Journal of immunology - Impact factor: **5.422**)
  Zacarias-Cabeza J*, **Belhocine M***, Vanhille L, Cauchy P, Koch F, Pekowska A, Fenouil R, Bergon A, Gut M, Gut I, Eick D, Imbert J, Ferrier P, Andrau JC and Spicuglia S.
  * Equal contributors.

- **Functions of lncRNA in development and diseases.**
  (Sep 2014 - Médecine/Sciences - Impact factor: **0.818**)
  Eve-Lyne Mathieu, **Mohamed Belhocine**, Lan T.M. Dao, Denis Puthier, Salvatore Spicuglia.

- **Divergent transcription is associated with promoters of transcriptional regulators.**
  (Dec 2013 - BMC Genomics - Impact factor: **3.969**)
  Lepoivre C*, **Belhocine M***, Bergon A, Griffon A, Yammine M, Vanhille L, Zacarias-Cabeza J, Garibal MA, Koch F, Maqbool MA, Fenouil R, Loriod B, Holota H, Gut M, Gut I, Imbert J, Andrau JC, Puthier D, Spicuglia S.
  * Equal contributors.

- **H3K4 tri-methylation provides an epigenetic signature of active enhancers.**
  (Jul2011 - EMBO Journal - Impact factor: **11.598**)
  Aleksandra Pekowska, Touati Benoukraf, Joaquin Zacarias Cabeza, **Mohamed Belhocine**, Frederic Koch, Hélène Holota, Jean Imbert, Jean-Christophe Andrau, Pierre Ferrier and Salvatore Spicuglia.

Statistics:

Impact Factor	#nb of Articles
0 – 5	4
5-10	8
10-20	5
>30	3

Seminars and Conferences:

- 2024: CAR-T Therapy: The Basics and Promises. (WAST24 webinar)
- 2023: Precision Medicine Exhibition & Summit (Dubai - UAE)
- 2023: 2nd MENA Stem Cells Forum (Dubai - UAE)
- 2023: Mena Hospital Project Forum (Dubai - UAE)
- 2022: Yawm El-ilm meeting (Algerian SCA)
- 2021: The National Day on SARS-CoV-2: Bioinformatics & Biotechnology. (Boumerdes' University)
- 2021: Precision Medicine Conference (Dubai - UAE)
- 2020: Epigenetic Regulation in Leukemias. (WeMed Club)
- 2020: 8th Pan Arab Human Genetics Conference. (Dubai - UAE)
- 2019: 1st International Bioinformatics Day. (Boumerdes University)
- 2018: Next Generation Sequencing: Single Nucleotide Polymorphisms And Copy Number Variation.(Blida University)
- 2018: 7th Pan Arab Human Genetics Conference. (Dubai - UAE)
- 2017: 1st Seminar in Bioinformatics and Genomics - Bioinformatic Study of the Epigenome during the Differentiation of T Lymphocytes and Leukemias. (Blida University)
- 2016: 3rd Workshop of Immunoinformatics - High-throughput Transcriptome Analysis. (BIOMOLIM Laboratory - Tlemcen University)
- 2015: The 1st international congress of immunology and molecular immunopathology. (Tlemcen University)
- 2015: High-throughput (Epi)Genomic Data Analysis of the Immune System (Normal and Leukemic). (Blida University)
- 2015: Chromatin Meets South 2015. (Polytech Marseille)
- 2014: High-throughput Epigenomic Data Analysis of the Immune System (Normal and Leukemic). (Tlemcen University)
- 2014: Chromatin Meets South 2014. (Montpellier University)
- 2014: 2nd Workshop NGS and non-coding RNA data analysis (Plovdiv, Bulgaria)

Theses and Projects Supervision:

➢ PhD Projects:

- A comprehensive catalog of LncRNAs expressed in T-Cell acute lymphoblastic leukemia.
  2014 - 2016 – Yasmine Kermezli.
- A critical reguator of BCL2 revealed by systematic transcript discovery of LncRNAs associated with T-Cell differentiation.
  2014 - 2016 – Wiam Saadi.

➢ MSc. Projects

- Determination of tissue-specific genes through a differential study of the transcriptome (Atlas database).
  2011 - 2012 – Nour Yahiaoui.
- Identification of an epigenetic H3K4me2 footprint associated with gene tissue specificity.
  2011 - 2012 – Yasmine Ait Ouamer.
- Large-scale genomic study of the dynamics of Pseudomonas aeruginosa evolution in a hostile environment.
  2012 - 2013 – Rym Abdous.
- Epigenetic and transcriptional dynamics involved in the differentiation of T lymphocytes.
  2012 - 2013 – Nesrine Dahman.
- Identification of LncRNAs associated with leukemia patients (LBL-T) using RNA-sequencing analysis.
  2012 - 2013 – Meriem Baghdid.
- Identification of bidirectional genes and their intrinsic characteristics in mice.
  2013 - 2014 – Karima Rabehi.
- Recruitment of the oncogene TLX3 to the enhancers of lymphatic-specific genes via the ETS1 and RUNX1 complex.
  2013 - 2014 – Yasmine Kermezli.
- Deciphering the biological mechanisms involved during dengue virus infection in patients with shock syndrome.
  2014 - 2015 – Fatima Damiche.

Newspapers articles:

- 2012 - L'Oranie:
  CHLEF, Le département de biologie voit grand.

- 2019 - El Waten:
  Boumerdès, A quand des formations en bio-informatique ?

- 2020 - El Waten:
  MOHAMED BELHOCINE, Chercheur algérien en bioinformatique à Dubaï «Je peux aider mon pays»

- 2020 - El Waten:
  MOHAMED BELHOCINE, Chercheur en bioinformatique et génomique «Le coronavirus a eu un nouveau souffle»

- 2020 - Al Nassar:
  الباحث في المعلوماتية الحيوية والجينوم الدكتور محمد بلحسين للنصر: ما نزال نعيش الموجة الأولى للجائحة وهذه آلية عمل لقاح فايزر

- 2020 - L'actuel Magazine:
  A 37 ans, il dirige une équipe de chercheurs !

- 2020 - Al Nassar:
  الباحث في المعلوماتية الحيوية والجينوم الدكتور محمد بلحسين للنصر: التطعيم مفيد مع السلالة الجديدة لكورونا

- 2022 - Sheehab Magazine:
  من سارس إلى اوميكرون . كيف تنشأ الطفرات

- 2022 - Al Nassar:
  فيروس تنفسي ينتشر بسبب تبعات الجائحة وهكذا تتم الوقاية

- 2023 - Al Nassar:
  مشاكل إدراكية تهدد المصابين بمتالزمة كوفيد الطويل