Ben Lehner
Head of Generative Genomics, Wellcome Sanger Institute, Cambridge, UK
Senior Group Leader and Associate ICREA Professor, Systems and Synthetic Biology Programme, Centre for Genomic Regulation (CRG), Barcelona, ES.
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Education

2004	PhD, University of Cambridge, UK
2000	BA, Natural Sciences (Biochemistry and Molecular Biology), First Class, University of Cambridge

Positions and employment

2023-	Head of Generative Genomics, Wellcome Sanger Institute
2023-	Founder and Chief Scientific Advisor, ALLOX
2023-	Honorary Professor of Biochemistry, University of Cambridge
2022-23	Senior Group Leader, Human Genetics Programme, Wellcome Sanger Institute
2022-	Co-Founder and Co-Chair, EMBL-CRG Barcelona Collaboratorium for Modelling and Predictive Biology
2017-23	Coordinator of Systems Biology Programme, CRG
2021-23	AXA Chair, CRG
2009-22	Research Professor, Catalan Institute for Advanced Studies (ICREA)
2014-	Senior Group Leader, Systems Biology Programme, CRG
2014-17	AXA Chair in risk prediction in age-related diseases, CRG
2013-17	Professor of Integrative Biology/Associated investigator, MRC-London Institute of Medical Sciences, Imperial College
2007-09	ICREA Junior Researcher
2006-14	Junior Group Leader, EMBL-CRG Systems Biology Research Unit
2004-06	Postdoctoral Fellow, Wellcome Sanger Institute, UK
2000-04	PhD student, MRC-HGMP, University of Cambridge
1999	Visiting researcher, Cold Spring Harbor Laboratory, USA

Awards and Prizes

2025	Alkis Seraphim Lecture, University of Cambridge
2024	Jenkinson Memorial Lecture, University of Oxford
2023	Fellow of the Royal Society
2023	Fellow of the Academy of Medical Sciences
2018	Paper of the Year, Catalan Society of Biology
2017	European Molecular Biology Organisation (EMBO) Member
2016	EMBO Gold Medal
2016	Liliane Bettencourt Prize for Life Sciences
2015	The Genetics Society Balfour Prize
2013	Eppendorf/Nature Award for a Young European Investigator
2012	The National Research Prize of Catalonia for a Young Scientist
2012	Banc Sabadell Prize for Biomedical Research (National Spanish Prize)
2011	The City of Barcelona Prize for Science

2010 The FEBS Anniversary Prize
2010 EMBO Young Investigator
2000 Mellon Scholar, Clare Hall College, University of Cambridge
2000 Hobbes Scholar, St Catharine's College, University of Cambridge
1999 The Biological Sciences Scholarship, St Catharine's College
1998 The Natural Sciences Scholarship, St Catharine's College, ranked first in year (>600 students)

Highlighted publications

(From a total of 122; 95 as last/corresponding author; 11 as first author; h-index = 66)

1. Escobedo A, Voigt G, Faure AJ, Lehner B. Genetics, energetics, and allostery in proteins with randomized cores and surfaces. **Science**. 2025 Jul 24;389(6758):eadq3948
2. Arutyunyan A*, Seuma M*, Faure AJ, Bolognesi B*, Lehner B*. Massively parallel genetic perturbation suggests the energetic structure of an amyloid-β transition state. **Science Advances.** 2025 Jun 13;11(24):eadv1422.
3. Thompson M, Martín M, Olmo TS, Rajesh C, Koo PK, Bolognesi B*, Lehner B*. Massive experimental quantification allows interpretable deep learning of protein aggregation**. Science Advances**. 2025 May 2;11(18):eadt5111.
4. Mighell TL, Lehner B. A small molecule stabilizer rescues the surface expression of nearly all missense variants in a GPCR. **Nature Structural Molecular Biology**. 2025 Sep 22. doi: 10.1038/s41594-025-01659-6.
5. Beltran A, Jiang X, Shen Y, Lehner B. Site-saturation mutagenesis of 500 human protein domains. **Nature**. 2025 Jan;637(8047):885-894.
6. Faure AJ, Martí-Aranda A, Hidalgo-Carcedo C, Beltran A, Schmiedel JM, Lehner B. The genetic architecture of protein stability. **Nature**. 2024 Oct;634(8035):995-1003.
7. Toledano I, Supek F, Lehner B. Genome-scale quantification and prediction of pathogenic stop codon readthrough by small molecules. **Nature Genetics**. 2024 Sep;56(9):1914-1924.
8. Weng C, Faure AJ, Escobedo A, Lehner B. The energetic and allosteric landscape for KRAS inhibition. **Nature**. 2024 Feb;626(7999):643-652.
9. Seuma M, Lehner B*, Bolognesi B*. An atlas of amyloid aggregation: the impact of substitutions, insertions, deletions and truncations on amyloid beta fibril nucleation. **Nature Communications**. 2022 Nov 18;13(1):7084.
10. Faure AJ*, Domingo J*, Schmiedel JM*, Hidalgo-Carcedo C, Diss G, Lehner B. Mapping the energetic and allosteric landscapes of protein binding domains. **Nature**. 2022 Apr;604(7904):175-183.
11. Lindeboom RGH, Vermeulen M, Lehner B*, Supek F*. The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. **Nature Genetics.** 2019 Nov;51(11):1645-1651.
12. Schmiedel J, Lehner B. Determining protein structures using deep mutagenesis. **Nature Genetics**. 2019 Jul 51(7):1177-1186.
13. Baeza-Centurion P, Miñana B, Schmiedel JM, Valcárcel J*, Lehner B*. Combinatorial Genetics Reveals a Scaling Law for the Effects of Mutations on Splicing. **Cell.** 2019 24;176(3):549-563.

14. Domingo J, Diss G, Lehner B. Pairwise and higher-order genetic interactions during the evolution of a tRNA. **Nature**. 2018 Jun;558(7708):117-121.
15. Perez MF, Francesconi M, Hidalgo-Carcedo C, Lehner B. Maternal age generates phenotypic variation in *Caenorhabditis elegans*. **Nature**. 2017 Dec 7;552(7683):106-109.
16. Supek F, Lehner B. Clustered mutation signatures reveal that error-prone DNA repair targets mutations to active genes. **Cell**. 2017 Jul 27;170(3):534-547.
17. Klosin A, Casas E, Hidalgo-Carcedo C, Vavouri T, Lehner B. Transgenerational transmission of environmental information in *C. elegans*. **Science**. 2017 Apr 21;356(6335):320-323
18. Lindeboom RG, Supek F, Lehner B. The rules and impact of nonsense-mediated mRNA decay in human cancers. **Nature Genetics.** 2016 Oct;48(10):1112-8
19. Supek F, Lehner B. Differential DNA mismatch repair underlies mutation rate variation across the human genome. **Nature**. 2015. 521:81-4
20. Francesconi M, Lehner B. The effects of genetic variation on gene expression dynamics during development. **Nature**. 2014. 505:208-11.
21. Supek F, Minana B, Valcarcel J, Gabaldon T, Lehner B. Synonymous mutations frequently act as driver mutations in human cancers. **Cell**. 2014. 156:1324-1335.
22. Schuster-Böckler, Lehner B. Chromatin organisation is a major influence on regional mutation rates in human cancer cells. **Nature**. 2012. 488:504-507.
23. Casanueva MO, Burga A, Lehner B. Fitness trade-offs and environmentally-induced mutation buffering in isogenic *C. elegans*. **Science**. 2012. 335:82-85.
24. Burga A, Casanueva MO, Lehner B. Predicting mutation outcome from early stochastic variation in genetic interaction partners. **Nature**. 2011. 480:250-254.
25. Jelier R, Semple JI, Garcia-Verdugo R, Lehner B. Predicting phenotypic variation in yeast from individual genome sequences. **Nature Genetics**. 2011. 43:1270-4.
26. Vavouri T, Semple JI, Garcia-Verdugo R, Lehner B. Intrinsic protein disorder and interaction promiscuity are widely associated with dosage sensitivity. **Cell**. 2009. 138:198–208.
27. Lee I*, Lehner B*, Crombie C, Wong W, Fraser AG, Marcotte E. A single network comprising the majority of genes accurately predicts the phenotypic effects of gene perturbation in an animal. **Nature Genetics**. 2008. Feb;40(2):181-8.
28. Lehner B, Crombie C, Tischler J, Fortunato A, Fraser AG. Systematic mapping of genetic interactions in *Caenorhabditis elegans* identifies common modifiers of diverse signaling pathways. **Nature Genetics**. 2006 Aug;38(8):896-903.

Institutional Responsibilities

2023- Member of the Senior Leadership Team, Wellcome Sanger Institute
2023- Head of Generative and Synthetic Genomics, Wellcome Sanger Institute
2022- Co-chair, Barcelona Collaboratorium for Modelling and Predictive Biology
2021-23 Member of the Scientific Board, CRG
2021-23 Member of the Direction Board, CRG
2017-21 Member of the Executive Board, CRG
2017-23 Coordinator of Systems Biology Programme, CRG
2006-20 Member of Postdoc, Genomics, Microscopy, and Alumni CRG committees

Scientific advisory boards and review panels

2025- Scientific Advisory Board, MRC Human Genetics Unit, Edinburgh, UK
2024- Scientific Advisory Board, VIB.AI, BE
2020- Eppendorf Award for Young European Investigators Jury Member
2020-24 EMBO Membership Committee
2019- Scientific Advisory Board, Centre for Integrative Genomics, University of Lausanne, CH
2018-22 Medical Research Council (MRC) Molecular and Cellular Medicine Board (MCMB), UK
2018-20 Biochemistry and Molecular Biology Panel, Independent Research Fund, DK
2017- Scientific Advisory Board, LBMC, Ecole Normale Supérieure de Lyon, FR
2017-21 Quantitative Biology Strategy Advisor, MRC-LMS, Imperial College London, UK
2016-22 Steering Committee, Quantitative Biology Programme, MRC-LMS, London, UK
2017 MRC Human Genetics Unit Quinquennial Review Panel, UK
2017,20 EMBL-EBI Review Panel, UK
2017 LBMC group leader recruitment, FR
2016,17 EMBL-EBI group leader recruitment, UK
2016 Italian Institute of Technology (IIT) group leader recruitment, IT
2013 MRC-CSC group leader recruitment, UK

Entrepreneurship

Co-founder and Chief Scientific Advisor, ALLOX

Scientific objectives

My current primary interest is the transformation of molecular biology into a predictive, quantitative, engineering science. I believe that the combination of massively parallel DNA synthesis/selection/sequencing and machine learning is opening up a new era that is allowing us to finally address some of the most fundamental and recalcitrant problems of molecular biology – our basic inability to predict and engineer the sequence-to-activity relationships that underlie biology, (clinical) genetics, medicine, and evolution.

Towards this goal, we have developed simple and fast assays that quantify the stability, binding affinities, allostery, and aggregation of hundreds of thousands of proteins in parallel and the computational methods to infer the underlying causal changes in biophysical parameters (free energy changes and energetic couplings) from the interactions between mutations in these datasets. At the Wellcome Sanger Institute we are now implementing these methods at scale, allowing the comprehensive mapping of the mutational, energetic and allosteric landscapes of proteins. In parallel, we have developed similar approaches to quantitatively understand splicing and gene regulation.

The immediate objective is to be able to understand and predict the effects of individual and combinatorial mutations on the activities of individual macromolecules, building out to pathways and systems. The long-term goal is to make biology 'programmable' and to expand biotechnology into the vast sequence space of possibilities beyond the Earth

Biogenome. I see the challenge of quantitatively understanding, predicting and engineering how sequences encode the biophysical properties of macromolecules as the foundational problem of molecular biology and a practical problem to be solved for clinical genetics and to realise the promises of synthetic biology, synthetic genomics and biological engineering.

My research has always focussed on fundamental questions in genetics, primarily concerned with understanding and predicting phenotypic variation in both genetically diverse and genetically identical individuals. This has included work on incomplete penetrance, inter-generational epigenetic inheritance, noise, genetic interactions (epistasis), mutation rates and processes, and genetic prediction. My strategy has been to pick fundamental questions and then choose tractable model systems and approaches to address them. As a result, we have worked with quite diverse systems and varied experimental, computational, mechanistic, genomic, and quantitative approaches.

Grants and funding - active

- OpenTargets Affinity and Stability (2025-2027)
- OpenTargets Splicing variant effects (2024-2026)
- Google Deepmind (2025-2026)
- ERC Proof of Concept Grant 'DeepHelix' (2025-2027)
- ERC Advanced Grant 'Mutanomics' (2021-2026)
- La Caixa Foundation 'DeepAmyloid' (2022-2025)
- Plan Estatal Grant 'AlloEnzymes' (2025-2029)

Grants and funding - previous

- ERC Consolidator Grant (2014-20)
- ERC Starting Grant (2008-14)
- Bettencourt Foundation (2017-21)
- AXA Research Fund (2021-2023)
- AXA Research Fund Endowed Chair (2014-17)
- EMBO Young Investigator (2010-2013)
- EU Framework 7 '4DCellFate' (partner, 2012-17)
- ERASysBio+ EUI2009-04059 (partner, 2010-13)
- Plan Estatal Grant 'DeepAllostery' (2021-2024)
- Plan Estatal Grant, Spanish Ministry of Economy and Competitiveness (2018-21)
- Plan Estatal Grant, Spanish Ministry of Economy and Competitiveness (2012-14)
- Plan Nacional Grant, Spanish Ministry of Science and Innovation (2009-12)
- AGAUR SGR (2017-21)
- AGAUR SGR (2014-17)
- AGAUR SGR (2009-13)

Grants and funding - fellowships to lab members

EMBO (12), Marie Skłodowska-Curie (6), MC co-fund (6), Juan de la Cierva (5), FEBS (2), HFSP, SNSF, Beatriu de Pinós, Novartis, Ramon Areces, Leonardo da Vinci (2), La Caixa (2), Severo Ochoa (3), FPI (4).

Organisation of scientific meetings & courses

2025,26 AI X BIO, Wellcome Connecting Science, Hinxton, UK
2025 Mutation Scanning Symposium 2025, Barcelona, ES
2025 Ri.MED Symposium Engineering Biology for Next-Gen Medicine
2022 Programmable Life, Barcelona Collaboratorium Opening Symposium
2020 Keystone Skirting Mendel: Non-Classical Mechanisms of Phenotypic Variation, Inheritance and Disease, Whistler, CA (cancelled due to pandemic)
2019 EMBO/EMBL Systems Genetics: From Genomes to Complex Traits, Heidelberg, DE
2019 CSHL Network Biology, NY, USA
2019 CRG Symposium 2019: Single Cell and Single Molecule Biology, Barcelona, ES
2018 EMBO Cell and Developmental Systems, Arolla, CH
2018 Wellcome Evolutionary Systems Biology, Hinxton, UK
2017 CSHL Systems Biology: Networks, NY, USA
2017 *C. elegans* practical course (Courses@CRG), Barcelona
2016 Wellcome Evolutionary Systems Biology, Hinxton, UK
2015 *C. elegans* practical course (Courses@CRG), Barcelona
2015 CSHL Systems Biology: Networks, NY, USA
2014 IMPPC/4DCellFate Computational and Integrative Biology, Barcelona, ES
2012 EMBO YIP Systems Biology, Barcelona, ES
2010 EMBL-CRG Evolution of Genetic Networks, Barcelona, ES
2009 Spanish *C. elegans* Meeting, Barcelona, ES

Local organiser:

2018 EMBO *C. elegans* development, cell biology and gene expression, Barcelona, ES
2013 CIFAR Genetic Networks, Barcelona, ES

Scientific committees: SMBE 2019; International *C. elegans* Meeting 2019, 2017; International Conference on Systems Biology 2016, 2015.

Alumni

19 alumni of my laboratory have become principal investigators:

1. Albert Escobedo, Autonomous University of Barcelona (UAB), Barcelona, Spain
2. Toni Beltran, IBV, Valencia, Spain
3. Xianghua (Cici) Li, King's College London, UK
4. Chenchun Weng, University of Science and Technology, Hefei, China
5. Rick Lindeboom, Netherlands Cancer Institute (NKI), Amsterdam, Netherlands
6. Marcos Perez, Molecular Biology Institute of Barcelona (IBMB), Spain
7. Adam Klosin, Nencki Institute of Experimental Biology, Warsaw, Poland
8. Solip Park, Spanish National Cancer Research Center (CNIO), Madrid, Spain
9. Guillaume Diss, Friedrich Miescher Institute (FMI), Basel, Switzerland
10. Alejandro Burga, Institute of Molecular Biotechnology (IMBA), Vienna, Austria
11. Mirko Francesconi, École Normale Supérieure de Lyon, France

12. Benedetta Bolognesi, Catalan Institute for Bioengineering (IBEC), Barcelona, Spain
13. Riddhiman Dhar, IIT, Kharagpur, India
14. Fran Supek, Institute for Research in Biomedicine (IRB), Barcelona, Spain
15. Rob Jelier, KU Leuven, Belgium
16. Benjamin Schuster-Böckler, Ludwig Institute, Oxford, UK
17. Tobias Warnecke, Biochemistry, Oxford (previously MRC-LMS, London), UK
18. Olivia Casanueva, Babraham Institute, Cambridge, UK
19. Tanya Vavouri, Josep Carreras Leukaemia Research Institute (IJC), Barcelona, Spain

PhD theses supervised: Mirko Francesconi (2010), Alejandro Burga (2012), Angela Krüger (2012), Kiana Toufighi (2014), Adam Klosin (2015), Kadri Reis (2016), Marcos Perez (2017), Pablo Baeza-Centurion (2020), Julia Domingo (2020), Mischan Vali-Pour (2022), Ignasi Toeldano (2025), Magdalena Topolska (2025).

Media and outreach (not a complete list)

- The first 'human domainome' reveals the cause of a multitude of diseases. El Pais 8 Jan 2025
- Hope in battle against deadliest types of cancer after scientists discover new ways to target impenetrable 'Death Star' protein that fuels tumour growth. Daily Mail 18 Dec 2023.
- Researchers discover the weak points of the protein that causes one in 10 cancers. El Pais 19 Dec 2023.
- BBC World Service Newshour: Interview + headline. 6 April 2022.
- Ansede M. Una nueva técnica ilumina el segundo secreto de la vida: el alosterismo. El Pais. 6 April 2022.
- Troytiño I. El CRG desarrolla una técnica que acelerará el descubrimiento de nuevos fármacos. La Vanguardia. 6 April 2022.
- Garrido C. Descubren multitud de 'mandos a distancia' de las proteínas que podrían utilizarse para buscar fármacos más eficaces. ABC. 6 April 2022
- Lucio C. Investigadores españoles desarrollan un método que permite localizar nuevas dianas terapéuticas. El Mundo. 6 April 2022
- Yanai I, Lercher M. Night Science Podcast Interview 'Ben Lehner on how to start your own scientific field'. Sep 02 2021. https://nightscience.buzzsprout.com/
- Service R. Mutant genes could supercharge efforts to decipher protein structures. Science. June 18, 2019
- Chiasson M, Fowler D. Mutagenesis-based protein structure determination. Nature Genetics 51, pages1072–1073. 2019.
- Epigenetic inheritance in nematodes. The Scientist. 2017
- Nature podcast 30/11/2017
- Els factors ambientals provoquen canvas genetics que es trasmeten de generacio en generacio. TV3 16/08/2017.
- Ancestors' Genetic "Memories" Could Be Passed On For 14 Generations. IFLS 2017.
- Katsnelson A. The shape shifting army inside your cells. Scientific American. Jan 26 2017.
- Elvidge S. Inside View: Ben Lehner. Nature. 2016

- How do our genes work? Talk at Royal Institution. 2016.
- Arney K. Herding Hemingway's Cats: Understanding how our genes work (Bloomsbury Publishing). Chapter 17. Opening a Can of Wobbly Worms. 2016.
- Hufton A. Interview with Ben Lehner. Scientific Data Blog. 2016.
- Corbella J. Cuesionario BIG VANG. La Vanguardia. 16 June 2016.
- Esteller M. La investigación tiene future. El Periodico. 7 June 2015.
- Zheng S, Kim, H, Verhaak RGW. Silent mutations make some noise. Cell. 2014. 156:1129-131
- Virginia Gewin. Turning point: Ben Lehner. Nature. 2013. 502:261.
- Nature Podcast Interview – 18 July 2013.
- Cómo nos ven. La Vanguardia 7 July 2013
- Ana Pantaleoni. La ópera-banquete de los Roca. El Pais. 6 May 2013 (amongst others).
- Claudia Schiller. Individuen sind glücklicerweise unterschidlich (interview) Labor&More 2013.
- Lluis Amiguet. La Contra: Vostès aquí fan moltes coses bé en investigació. La Vanguardia 10 April 2012
- Aguilar X. Genetista per casualitat. El Punt Avui, 17 March 2013
- Jones B. Cancer genomics: Chromatin influence on cancer mutation rate. Nature Reviews Genetics. 2012; 13: 596-7.
- Corbella J. Qué hace una cientifico como tú en un país como este? La Vanguardia 13 Jul 2012.
- Baker M. The changes that count. Nature. 2012. 482:257-262.
- Williams R. The trade off of stress. The scientist. Dec 15 2011.
- Deplancke B, Verstrepen KJ. Variable outcome of mutations. Science. 2012; 335:44-5.
- Corbella J, El azar es el motor de la evolución. la Vanguardia 19Feb 2012.
- Casci T. Gene expression: genetic support network to the rescue. Nature Reviews Genetics. 2011. 13:74.
- El-Samad H, Weissman JS. Genetics: Noise rules. Nature. 2011. 480:188-9.
- Myers M. Gene Regulation: Noise versus plasticity. Nature Reviews Genetics. 2011.
- Chamberlin HM. *C. elegans* select. Nature Methods. 2010; 7:693-5.
- Casci T. Research Highlights: A Network of Interactors. Nature Reviews Genetics. 2010.
- Marcotte EM, Tsechansky M. Disorder, promiscuity, and toxic partnerships. Cell. 2009 Jul 10;138(1):16-8.
- Von Stetina SE and Mango S. Wormnet: a crystal ball for *Caenorhabditis elegans*. Genome Biology 2008; 9:226.
- Borgwardt K. Predicting phenotypic effects of gene perturbations in *C. elegans* using integrated network model. Bioessays. 2008. 30:707-710.
- Cristina Sáez. España ya ficha a cracks de la ciencia. la Vanguardia. 2008.
- Research Highlights: Networking an organism. Nature Methods. 2008; 5:217.
- Research Highlights: Genome Evolution. Nature Reviews Genetics. 2007; 8:251.
- Suzuki Y, Roth FP. Systematic genetics swims forward elegantly. Molecular Systems Biology. 2006;2:48.

- Casci T. Research Highlights: Network fundamentals, via hub genes. Nature Reviews Genetics. 2006 Sep;7(9).
- Bussey H, Andrews B, Boone C. From worm genetic networks to complex disease in humans. Nature Genetics. 2006 Aug;38(8):862-3.
- Research highlights: buffering disease. Nature. 2006 July;442(20):226-7.
- Bosch X, Vogel G. Spain aims to lure systems biologists to a place in the sun. Science. 2006 Jun;312(5778):1295.
- Human protein interaction map. Journal of Proteome Research. 2004 3(8):1005.

Members of my lab designed and participated in a weekly hands-on *C. elegans* course for high school students attended by >600 Spanish school students a year and a course for secondary school science teachers. They (and the worms) also participated in 'YoMo' (Youth Mobile Festival, 150 participants), the PRBB open day, and 'girls in STEM' visits to schools.

Invited talks and seminars (not a complete list)

Prizer, 2025; ETH Zurich, 2025; University of Leeds, 2025; Ri.MED Sicily, 2025; AITHYRA Vienna, 2025; Alkis Seraphim Lecture, University of Cambridge, 2025; Benzon Symposium, Copenhagen, 2025; Tsinghua University, Beijing, 2025; USTC, Hefei, 2025; BGI, Shenzhen, 2025; Milner Institute, Cambridge, 2025; JST-BBSRC, Osaka Japan, 2025; Utrecht, NL, 2024; VIB.AI, BE, 2024; Genentech, CA, 2024; UCSF, CA, 2024; EMBO-EMBL AI in life sciences, DE, 2024; Collaboratorium Annual Symposium, Barcelona, 2024; Jenkinson Memorial Lecture, Oxford, 2024; CRG-TAU-Berkeley Symposium, Barcelona 2024; Altos Labs, 2024; Ludwig Cancer Institute, Oxford, 2024; MRC-LMB, Cambridge, 2024; Flatiron Institute, NY, 2023; CSHL Genome Informatics, 2024; UPenn, 2023; CSHL Biology of Genomes, 2023; ZJE University, online, 2023; Wellcome Synthetic Biology, Hinxton, UK, 2023; Festival of Genomics and Biodata, London, UK 2023; Wellcome CRISPR and Beyond, Hinxton, 2022; AlloDD, Barcelona 2022; Weizmann Institute, Israel (online), 2022; FMI, Basel, 2022;CNIO, Madrid, 2022; MSKCC, NY, 2021; Oncode, Amsterdam, 2021; Donnelly Centre, Toronto, 2021; ISMB, 2021; Mutation Scanning Symposium (Keynote), Seattle, 2021; SEBBM, 2021; EMBO Predicting Evolution, 2021; CSHL Network Biology, 2021; Wellcome Evolutionary Systems Biology, 2020; EDGE, Key West 2020; Stanford, 2019; Salk, 2019; BRIC Copenhagen, 2019; Oslo, 2019; Physics of Living Matter Cambridge, 2019; Wellcome CRISPR and beyond, 2019; St Jude's Biomedical Symposium, 2019; Vienna Biocenter, 2019; MRC-LMB, Cambridge, 2018; Gurdon Institute, Cambridge, 2018; Princess Takamatsu Symposium, Tokyo, 2018; NKI, Amsterdam, 2018; Utrecht, 2018; UK *C. elegans* Meeting (keynote), 2018; Swiss *C. elegans* Meeting (keynote), Basel, 2018; CRUK Cambridge, 2018; IHES, Paris, 2018; EMBO Arolla, 2018; QMUL, London, 2018; Wellcome Nematode evolution, 2018; University of Chicago, 2017; IGH, Montpellier, 2017; EMBL Cancer Genomics, Heidelberg, 2017; MRC-HGU Edinburgh, 2017; FMI, Basel, 2017; EPFL, Lausanne, 2017; Systems Biology of Human Disease, Heidelberg, 2017; EMBO: Chromatin and Epigenetics, Heidelberg, 2017; HUGO Meeting, Barcelona, 2017; Human Cell Atlas, Berlin, 2017; MPI Freiburg, 2017; EMBL Rome, 2017; Genetics Society, Royal Society, London 2016; EMBO From Functional Genomics to Systems Biology, Heidelberg 2016;

Harvard MCB, Cambridge, USA, 2016; 2016 Epigenetics in Development, IMB Mainz, 2016; University of Tel Aviv, 2016; Weizmann Institute, 2016; Beyond Cancer genomes, Barcelona 2016; Royal Institution of London, 2016;EMBL Heidelberg, 2016; CNIC, Madrid, 2016; CABIMER, Seville, 2016; ESHG, Barcelona, 2016; CIML, Marseille, 2016; GRC Mutagenesis and Genome Alteration, Spain, 2016; EMBO Meeting, Mannheim, 2016; Intersectional Max Planck Symposium on Biological Networks, Germany, 2015; QBiC Symposium, Osaka, 2015; EMBO Arolla, 2015; University of Lausanne, 2015; Wellcome Functional Genomics and Systems Biology, Hinxton, 2015; Barcelona Supercomputing Center, 2015; CSHL Systems Biology: Networks 2015; Seminar CSHL 2015; Vienna Biocenter, 2014; SEBD, Madrid, 2014; Bioinformatics, Seville, 2014; ISDB, Seattle, 2014; Cambridge epigenetics club, 2014; Complex traits, Nice, 2014; Systems Genetics, Ascona, 2014; Laval University, Quebec, 2014; V IMPPC Annual Conference 2014; Academia Sinica 2014; Biozentrum, Basel, 2013; ENS, Paris, 2013; MDC-CSC Retreat, London, 2013; Cell Cancer Epigenomics, Sitges 2013; ISMB-RegGenSIG, Berlin 2013; Univ. Edinburgh, 2013; Utrecht University 2013; Systems Biology of Human Disease, Heidelberg, 2013; Dept. Biochemistry, Cambridge, 2013; Wellcome Trust Genomic Disorders, 2013; University of Colorado, 2013; FEBS Human Fungal Pathogens, Nice, 2013; University of Salamanca, 2013; Sequence to consequence, Oslo 2012; EMBL PhD Symposium, 2012; IRB Retreat, 2012; ETH Zurich D-BSSE, 2012; ICSB, Toronto (plenary) 2012; Memorial Sloan Kettering Cancer Center, 2012; Networks, University of Minnesota 2012; Physics of Living Matter, London 2012; VIB Symposium, Gent 2012; ECCB, Basel 2012; Max Planck Institute-Tübingen 2012; Network Medicine, Denmark, 2012; Gulbenkian Institute, 2012; CSHL Systems Biology: gene expression, 2012; IBMB Barcelona, 2012; Bioinformatics for evolutionary biology, Leipzig 2012.

Full publications list – articles

1. Zhang X, Jiang X, Wang Y, Chen Q, Jiang H, Zhang H, Beltran A, Yang W, Chen T, Liang C, Cheng N, Huang Y, Ding G, Xie C, Gao N, Liu J, Xu W, Huang J, Cai D, Zhu L, Mo S, Shen M, Zhang W, Lehner B, Ni M, Wang J, Xu X, Shen Y. Scaling DNA synthesis with a microchip-based massively parallel synthesis system. **Nature Biotechnology. 2**025 Oct 1. doi: 10.1038/s41587-025-02844-0.
2. Mighell TL, Lehner B. A small molecule stabilizer rescues the surface expression of nearly all missense variants in a GPCR. **Nature Structural Molecular Biology**. 2025 Sep 22. doi: 10.1038/s41594-025-01659-6.
3. Baeza-Centurión P, Miñana B, Faure AJ, Thompson M, Bonnal S, Quarantani G, Clarke J, Lehner B*, Valcárcel J*. Deep indel mutagenesis reveals the regulatory and modulatory architecture of alternative exon splicing. **Nature Communications.** 2025 Aug 30;16(1):8117.
4. Escobedo A, Voigt G, Faure AJ, Lehner B Genetics, energetics, and allostery in proteins with randomized cores and surfaces. **Science**. 2025 Jul 24;389(6758):eadq3948
5. Arutyunyan A*, Seuma M*, Faure AJ, Bolognesi B*, Lehner B*. Massively parallel genetic perturbation suggests the energetic structure of an amyloid-β transition state. **Science Advances.** 2025 Jun 13;11(24):eadv1422.

6. Thompson M, Martín M, Olmo TS, Rajesh C, Koo PK, Bolognesi B*, Lehner B*. Massive experimental quantification allows interpretable deep learning of protein aggregation**. Science Advances**. 2025 May 2;11(18):eadt5111.
7. Topolska M, Beltran A, Lehner B. Deep indel mutagenesis reveals the impact of amino acid insertions and deletions on protein stability and function. **Nature Communications**. 2025 Mar 17;16(1):2617. doi: 10.1.
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