

Curriculum Vitae

Personal information

Name: Judith B., Zaugg
Nationality: Swiss
Date of birth: 19. June 1983
Children: 3 (2016, 2018, 2018)
ORCID: 0000-0001-8324-4040
Website: <http://www.zaugg.embl.de>



Current position

2018 – Group leader at Molecular Medicine Partnership Unit (MMPU) – joint venture with University Hospital Heidelberg

Our vision: To understand how alterations of the bone marrow niche contribute to Leukemia development, therapy resistance and relapse.

2014 – **Group leader at European Molecular Biology Laboratory, Heidelberg**

Our vision: To understand how the interplay of genetics, epigenetics and cellular signalling converge onto gene regulatory programmes that eventually gives rise to complex phenotypes, including diseases.

Education

2011 PhD degree awarded by **Cambridge University** (UK)
2004-07 Diploma Studies (equivalent to MA) in Biological Chemistry at **ETH Zurich**
2005 Visiting Student at Massachusetts Institute of Technology (MIT) (USA)

Research experience

2012-14 Postdoctoral Fellow at **Stanford University** (CA, USA) with **Prof. Lars Steinmetz** in personalized transcriptomics and epigenetics, using NGS data to understand regulation of gene expression across human individuals and its links to complex traits and diseases
2007-12 PhD/postdoc research at **EMBL-EBI and University of Cambridge** (Cambridge, UK) with **Dr. Nick Luscombe**
2007 Internship at Roland Berger Strategy Consulting (3 months, Germany)

Supervision and teaching

2018/19/21 Main organizer of EMBL course Attacking open chromatin with ATAC-seq (experimental and computational analysis)
2018- Scientific coordinator the EMBL PhD course (2-month course for all PhD students)
2015-2017 Master class lecture at Heidelberg University (Topic: Genetic Variation)
2014- **Main supervisor:** 10 postdoctoral fellows, 11 PhD students (4 graduated), 5 MSc students

Ten selected publications/preprints of the past five years

- Lai MC, Ruiz-Velasco M, Arnold C, Sigalova O, Bunina D, Berest I, Ding X, Hennrich ML, Poisa-Beiro L, Claringbould A, Mathioudaki A, Pabst C, Ho AD, Gavin A-C & **Zaugg JB** (2021) Enhancer-priming in ageing human bone marrow mesenchymal stromal cells contributes to immune traits. *BioRxiv*: <https://doi.org/10.1101/2021.09.03.458728>

- Sigalova OM, Shaeiri A, Forneris M, Furlong EEM+, **Zaugg JB+** (2020). *Predictive features of gene expression variation reveal mechanistic link with differential expression* (2020). *Molecular Systems Biology* 16 (8), e9539 - **selected for cover**
- Bunina D, Abazova N, Diaz N, Noh KM+, Krijgsveld J+, **Zaugg JB+** (2020). *Genomic rewiring of SOX2 chromatin interaction network during differentiation of ESCs to postmitotic neurons*. *Cell Systems* 10, 6, 480-494.e8
- Reyes-Palomares A, Gu M, Grubert F, Berest I, Sa S, Kasowski M, Arnold C, Shuai M, Srivas R, Miao S, Snyder MP+, Rabinovitch M+, **Zaugg JB+** (2020). *Remodeling of active endothelial enhancers is associated with aberrant gene-regulatory networks in pulmonary arterial hypertension*. *Nature Communications* 11 (1), 1-14
- Berest I, Arnold C, Reyes-Palomares A, Palla G, Rasmussen KD, Giles H, Bruch P-M, Huber W, Dietrich S, Helin K & **Zaugg JB** (2019) *Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF*. *Cell Rep.* 29, 3147–3159.e12.
- Ibarra IL, Hollmann NM, Klaus B, Augsten S, Velten B, Hennig J & **Zaugg JB** (2020) *Mechanistic insights into transcription factor cooperativity and its impact on protein-phenotype interactions*. *Nature Communications* 11, 124.
- Rasmussen KD+, Berest I, Keßler S, Nishimura K, Simón-Carrasco L, Vassiliou GS, Pedersen MT, Christensen J, **Zaugg JB+** & Helin K+ (2019) *TET2 binding to enhancers facilitates transcription factor recruitment in hematopoietic cells*. *Genome Res.* 29, 564–575.
- Garg S, Reyes-Palomares A, He L, Bergeron A, Lavallée V-P, Lemieux S, Gendron P, Rohde C, Xia J, Jagdhane P, Müller-Tidow C, Lipka DB, Imren S, Humphries RK, Waskow C, Vick B, Jeremias I, Richard-Carpentier G, Hébert J, Sauvageau G, **Zaugg JB+**, Barabé F+ & Pabst C+ (2019) *Hepatic leukemia factor is a novel leukemic stem cell regulator in DNMT3A, NPM1, and FLT3-ITD triple-mutated AML*. *Blood* 134, 263–276.
- Ranzoni AM, Tangherloni A, Berest I, Riva SG, Myers B, Strzelecka PM, Xu J, Panada E, Mohorianu I, **Zaugg JB** & Cvejic A (2021) *Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Hematopoiesis*. *Cell Stem Cell* 28, 472-487.e7.
- Ibarra IL, Ratnu VS, Gordillo L, Hwang I-Y, Mariani L, Weinand K, Hammaren HM, Bulyk ML, Savitski MM, **Zaugg JB+** & Noh K-M+ (2021) *Comparative chromatin accessibility upon BDNF-induced neuronal activity delineates neuronal regulatory elements*. *BioRxiv*.

Invited talks (selected from past five years)

I've been invited to over 30 international conferences, workshops and summer schools; a selection is listed below. Due maternity leaves (2016/2018) and twin pregnancy (2017/2018) I had to decline several invitations.

- 2021:
- Gene Forum Estonia, (virtual)
 - EMBO workshop: Enhanceropathies, (*Santander, Spain*)
 - International nucleome consortium, (virtual)
 - Genomic Regulation 2020: 'Focus on Cancer', (virtual)
- 2020:
- Keynote at 'Dutch Bioinformatics and Systems Biology conference', (virtual)
 - EMBL conference: 'Expanding the druggable Genome', Heidelberg (DE)
- 2019:
- EMBO|EMBL Symposium: 'From Multiomics to Mechanisms', Heidelberg (DE)
 - EMBO workshop: 'Systems Genetics', Heidelberg (DE)
 - Keynote lecture at Swiss Genomics Forum, Geneva (CH)
- 2017:
- EMBO|EMBL Symposium: 'From Single to Multiomics', Heidelberg (DE)
 - EMBL|Stanford conference: 'Personalized Health', Stanford (US)
 - EMBO | Wellcome Trust conference: 'Big Data in Biology', Hinxton (UK)
 - DKFZ conference: 'Systems Biology in Human Disease', Heidelberg (DE)

- Keynote lecture at ISMB: *'Regulatory Systems track'*, Prague (CZ)
- IMB conference: *'Gene Regulation by the Numbers'*, Mainz (DE)
- 2016: - Cell Symposium: *'Technology. Data. Biology.'*, Berkley (US)
- EMBO|Wellcome Trust: *'Big Data in Biology'*, Heidelberg (DE)
- Keynote at Bioinformatics Symposium, Leiden (NL)

Organization of scientific meetings since 2014

- 2021: - EMBL|EMBO symposium: ***Multimics to Mechanisms*** (Heidelberg)
- Chair of Regulatory Systems Track at ***ISMB*** (virtual)
- 2019: - EMBO workshop: ***Precision Health*** (Heidelberg)
- EMBL|EMBO symposium: ***Multimics to Mechanisms*** (Heidelberg)
- Chair of Regulatory Systems Track at ***ISMB*** (Basel)
- 2017: - EMBL|Stanford conference: ***Personalized Health Stanford*** (Stanford, US)
- EMBL|EMBO symposium: ***From Single- to Multimics*** (Heidelberg)
- 2016: Co-Chair - Genome track at European Conference on Computational Biology
- 2015: EMBL|Stanford conference: ***Personalised Health*** (Heidelberg)

Service to the community and scientific advisory roles

- 2020/21 Member of ATIP-Avenir LS2 grant review panel (French starting grant)
- 2020- **Scientific Advisory Board**: Norwegian Centre of Molecular Medicine (NCMM)
- 2019- Academic Editor: Life Science Alliance (<https://www.life-science-alliance.org>)
- 2019- Steering board: Heidelberg Leukemia Network (<https://www.leukemia-heidelberg.de>)
- 2019- **Scientific Advisory Panel**: Hungarian Centre of Excellence in Molecular Medicine (HCEMM)
- 2018-20 Academic Editor: FEBS Letters
- 2017-18 Editorial Board, Physiological Genomics, UK
- 2015- Member of international search committee for group leaders: EMBL, NCMM (Norway), CRG (Spain), HCEMM (Hungary)
- 2014- Regular reviewing for: Cell, Nature Genetics, eLife, Nature Communications, Cell Reports, NAR, Bioinformatics, Molecular Systems Biology
- 2004-07 Head of SiROP ETH, a student founded association aiming to enhance student education and support scientific research
- 2003-11 Member of Swiss Study Foundation, an institution that supports talented students during their studies, by providing them with interdisciplinary seminars and workshops complementary to their field of study (www.studienstiftung.ch)
- 2004- Board member of Pantok Dialogos, an association promoting interdisciplinary exchange between science and business in Switzerland (www.pantok.ch)

Prizes, awards, funding

- 2013 Award for best Scientific Contribution (ex aequo) CSF foundation (Switzerland)
- 2013 Fellowship awarded by Swiss National Foundation for Advanced Researchers financing postdoctoral study at Stanford University
- 2012 Fellowship awarded by Janggen-Poehn foundation (Switzerland) for postdoctoral research at Stanford University
- 2007 Honorary scholarship received from Cambridge Overseas Trust, Cambridge University (UK)
- 2005 Swiss Study Foundation Fellowship for research at MIT Cambridge (US)
- 2002-11 Member of Swiss Study Foundation – foundation supporting talented students

Funding:

Principal investigator	Funding organisation	Duration
Judith Zaugg	GSK	2.5 years
Judith Zaugg	BW-Stiftung	3.5 years
Judith Zaugg	Marie-Curie Action international training network (MCA-ITN)	4 years
PI: Evangelia Petsalaki; co-PI Judith Zaugg	OpenTargets	3 years
Judith Zaugg	GSK	2 years

Fellowships attracted to the group:

Funding type	Funding organisation	# fellowships
Postdoctoral fellowship	EMBO	1
Postdoctoral fellowship	Swiss National Foundation	1
Postdoctoral fellowship	Marie-Curie co-fund (EiPOD)	3
Postdoctoral fellowship	Finnish medical foundation	1
Postdoctoral fellowship	Sigrid Juselius Foundation	1

Full list of publications

Overall, I've co-authored 34 papers (4 currently in review/revision and published on preprint servers, 3 invited reviews). 24 publications (including reviews and preprints) are from my work as group leader at EMBL, in 15 I'm corresponding author. **Work in which I contributed as first or corresponding author is highlighted in blue.**

Work as group leader**In review / revision published on *bioRxiv***

1. Lai MC, Ruiz-Velasco M, Arnold C, Sigalova O, Bunina D, Berest I, Ding X, Hennrich ML, Poisa-Beiro L, Claringbould A, Mathioudaki A, Pabst C, Ho AD, Gavin A-C & **Zaugg JB** (2021) Enhancer-priming in ageing human bone marrow mesenchymal stromal cells contributes to immune traits. *BioRxiv*.
2. Bunina D+, Germain P-L, Lopez Tobon A, Fernandez-Novel Marx N, Arnold C, Ó hEachteirn A, Claringbould A, Lai MC, Rangasamy S, Narayanan V, Testa G, **Zaugg JB+** & Noh K-M+ (2021) Pathological LSD1 mutations cause HDAC-mediated aberrant gene repression during early cell differentiation. *BioRxiv*.
3. Bruch P-M, Giles H, Kolb C, Herbst SA, Becirovic T, Roeder T, Lu J, Scheinost S, Wagner L, Hüllein J, Berest I, Kriegsmann M, Kriegsmann K, Zgorzelski C, Dreger P, **Zaugg JB**, Müller-Tidow C, Zenz T, Huber W & Dietrich S (2021) Mapping drug-microenvironment-genetic interplay in CLL reveals trisomy 12 as a modulator of microenvironmental signals. *BioRxiv*.
4. Ibarra IL, Ratnu VS, Gordillo L, Hwang I-Y, Mariani L, Weinand K, Hammaren HM, Bulyk ML, Savitski MM, **Zaugg JB+** & Noh K-M+ (2021) Comparative chromatin accessibility upon BDNF-induced neuronal activity delineates neuronal regulatory elements. *BioRxiv*.

Published in peer-reviewed journals:

5. *Invited review*: Claringbould A & **Zaugg JB** (2021) Enhancers in disease: molecular basis and emerging treatment strategies. *Trends Mol Med*. 10.1016/j.molmed.2021.07.012

6. *Invited review*: Weidemüller P, Kholmatov M, Petsalaki E+ & **Zaugg JB+** (2021) Transcription factors: Bridge between cell signaling and gene regulation. *Proteomics*, e2000034.
7. Scheller M, Ludwig AK, Göllner S, Rohde C, Krämer S, Stäble S, Janssen M, Müller J-A, He L, Bäumer N, Arnold C, Gerß J, Schönung M, Thiede C, Niederwieser C, Niederwieser D, Serve H, Berdel WE, Thiem U, Hemmerling I,..., **Zaugg JB**,... & Müller-Tidow C (2021) Hotspot DNMT3A mutations in clonal hematopoiesis and acute myeloid leukemia sensitize cells to azacytidine via viral mimicry response. *Nat Cancer* **2**, 527–544.
8. Ranzoni AM, Tangherloni A, Berest I, Riva SG, Myers B, Strzelecka PM, Xu J, Panada E, Mohorianu I, **Zaugg JB** & Cvejic A (2021) Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Hematopoiesis. *Cell Stem Cell* **28**, 472-487.e7.
9. Kim K-P, Li C, Bunina D, Jeong H-W, Ghelman J, Yoon J, Shin B, Park H, Han DW, **Zaugg JB**, Kim J, Kuhlmann T, Adams RH, Noh K-M, Goldman SA & Schöler HR (2021) Donor cell memory confers a metastable state of directly converted cells. *Cell Stem Cell* **28**, 1291-1306.e10.
10. Sigalova OM, Shaeiri A, Forneris M, Furlong EEM+, **Zaugg JB+** (2020). *Predictive features of gene expression variation reveal mechanistic link with differential expression* (2020). *Molecular Systems Biology* 16 (8), e9539 - **selected for cover**
11. Bunina D, Abazova N, Diaz N, Noh KM+, Krijgsveld J+, **Zaugg JB+** (2020). *Genomic rewiring of SOX2 chromatin interaction network during differentiation of ESCs to postmitotic neurons*. *Cell Systems* 10, 6, 480-494.e8
12. Reyes-Palomares A, Gu M, Grubert F, Berest I, Sa S, Kasowski M, Arnold C, Shuai M, Srivas R, Miao S, Snyder MP+, Rabinovitch M+, **Zaugg JB+** (2020). *Remodeling of active endothelial enhancers is associated with aberrant gene-regulatory networks in pulmonary arterial hypertension*. *Nature Communications* 11 (1), 1-14
13. Grubert F, Srivas R, Spacek D, Kasowski M, Ruiz-Velasco M, Greenside P, Narasimha A, Liu Q, Geller B, Sanghi A, Kulik M, Sa S, Rabinovitch M, Kundaje A, Dalton S, Sinnott-Armstrong N, **Zaugg JB**, Snyder M (2020). *Landscape of Cohesin-Mediated Chromatin Loops in the Human Genome*. *Nature* 583 (7818), 737-743
14. Gehre M, Bunina D, Sidoli S, Luebke M, Diaz N, Trovato M, Benjamin Garcia B, **Zaugg JB**, Noh K-M. (2020) *Lysine 4 of histone H3.3 is required for embryonic stem cell differentiation, histone enrichment at regulatory regions and transcription fidelity*. *Nature Genetics* 52(3), pp. 273–282.
15. Ibarra IL, Hollmann NM, Klaus B, Augsten S, Velten B, Hennig J & **Zaugg JB** (2020) *Mechanistic insights into transcription factor cooperativity and its impact on protein-phenotype interactions*. *Nature Communications* **11**, 124.
16. Berest I, Arnold C, Reyes-Palomares A, Palla G, Rasmussen KD, Giles H, Bruch P-M, Huber W, Dietrich S, Helin K & **Zaugg JB** (2019) *Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF*. *Cell Rep.* 29, 3147–3159.e12.
17. Rasmussen KD+, Berest I, Keßler S, Nishimura K, Simón-Carrasco L, Vassiliou GS, Pedersen MT, Christensen J, **Zaugg JB+** & Helin K+ (2019) *TET2 binding to enhancers facilitates transcription factor recruitment in hematopoietic cells*. *Genome Res.* 29, 564–575.

18. Garg S, Reyes-Palomares A, He L, Bergeron A, Lavallée V-P, Lemieux S, Gendron P, Rohde C, Xia J, Jagdhane P, Müller-Tidow C, Lipka DB, Imren S, Humphries RK, Waskow C, Vick B, Jeremias I, Richard-Carpentier G, Hébert J, Sauvageau G, **Zaugg JB**+, Barabé F+ & Pabst C+ (2019) *Hepatic leukemia factor is a novel leukemic stem cell regulator in DNMT3A, NPM1, and FLT3-ITD triple-mutated AML*. Blood 134, 263–276.
19. Hennrich ML, Romanov N, Horn P, Jaeger S, Eckstein V, Steeples V, Ye F, Ding X, Poisa-Beiro L, Lai MC, Lang B, Boultonwood J, Luft T, **Zaugg JB**, Pellagatti A, Bork P, Aloy P, Gavin A-C & Ho AD (2018) *Cell-specific proteome analyses of human bone marrow reveal molecular features of age-dependent functional decline*. Nature Communications 9, 4004.
20. Ruiz-Velasco M, Kumar M, Lai MC, Bhat P, Solis-Pinson AB, Reyes A, Kleinsorg S, Noh K-M, Gibson TJ & **Zaugg JB** (2017) *CTCF-Mediated Chromatin Loops between Promoter and Gene Body Regulate Alternative Splicing across Individuals*. Cell Systems 5, 628–637.e6.
21. *Invited review*: Ruiz-Velasco M, **Zaugg JB** (2017). *Structure meets function: How chromatin organisation conveys functionality*. Current Opinion in Systems Biology: 1, Feb 2017, 129-136, ISSN 2452-3100
22. Lai MC, Bechy A-L, Denk F, Collins E, Gavriliouk M, **Zaugg JB**, Ryan BJ, Wade-Martins R & Caffrey TM (2017) *Haplotype-specific MAPT exon 3 expression regulated by common intronic polymorphisms associated with Parkinsonian disorders*. Mol. Neurodegener. 12, 79.
23. Ignatiadis N, Klaus B, **Zaugg JB** & Huber W (2016) *Data-driven hypothesis weighting increases detection power in genome-scale multiple testing*. Nature Methods 13, 577–580.
24. Arnold C, Bhat P & **Zaugg JB** (2016) *SNPhood: investigate, quantify and visualise the epigenomic neighbourhood of SNPs using NGS data*. Bioinformatics 32, 2359–2360.

Work from Postdoc (* joint first author)

25. Arnold C, Bhat P & **Zaugg JB** (2016) *SNPhood: investigate, quantify and visualise the epigenomic neighbourhood of SNPs using NGS data*. Bioinformatics 32, 2359–2360.
26. Grubert F*, **Zaugg JB***, Kasowski M*, Ursu O, Spacek DV*, Martin AR, Greenside P, Srivas R, Phanstiel DH, Pekowska A, Heidari N, Euskirchen G, Huber W, Pritchard JK, Bustamante CD, Steinmetz LM, Kundaje A & Snyder M (2015) *Genetic control of chromatin states in humans involves local and distal chromosomal interactions*. Cell 162, 1051–1065.
27. Kasowski M*, Kyriazopoulou-Panagiotopoulou S*, Grubert F*, **Zaugg JB***, Kundaje A, Liu Y, Boyle AP, Zhang QC, Zakharia F, Spacek DV, Li J, Xie D, Olarerin-George A, Steinmetz LM, Hogenesch JB, Kellis M, Batzoglou S & Snyder M (2013) *Extensive variation in chromatin states across humans*. Science 342, 750–752.

Work from PhD (*joint first author, +joint corresponding author)

28. Cakiroglu SA, **Zaugg JB**+ & Luscombe NM+ (2016) *Backmasking in the yeast genome: encoding overlapping information for protein-coding and RNA degradation*. Nucleic Acids Res. 44, 8065–8072.
29. Castelnovo M*, **Zaugg JB***+, Guffanti E, Maffioletti A, Camblong J, Xu Z,

- Clauder-Münster S, Steinmetz LM, Luscombe NM & Stutz F+ (2014) *Role of histone modifications and early termination in pervasive transcription and antisense-mediated gene silencing in yeast*. *Nucleic Acids Res.* 42, 4348–4362.
30. Tan-Wong SM*, **Zaugg JB***, Camblong J, Xu Z, Zhang DW, Mischo HE, Ansari AZ, Luscombe NM, Steinmetz LM+ & Proudfoot NJ+ (2012) *Gene loops enhance transcriptional directionality*. *Science* 338, 671–675.
31. **Zaugg JB** & Luscombe NM (2012) *A genomic model of condition-specific nucleosome behavior explains transcriptional activity in yeast*. *Genome Research* 22, 84–94.

Work from before PhD

32. Kotte O, **Zaugg JB** & Heinemann M (2010) *Bacterial adaptation through distributed sensing of metabolic fluxes*. *Molecular Systems Biology* 6, 355.
33. Hoskins AA, Morar M, Kappock TJ, Mathews II, **Zaugg JB**, Barder TE, Peng P, Okamoto A, Ealick SE & Stubbe J (2007) *N5-CAIR mutase: role of a CO₂ binding site and substrate movement in catalysis*. *Biochemistry* 46, 2842–2855.
34. Gattin Z, **Zaugg J** & van Gunsteren WF (2010) *Structure determination of a flexible cyclic peptide based on NMR and MD simulation 3J-coupling*. *ChemPhysChem* 11, 830–835.