

**Stefan L. Ameres, PhD** (\*Jan. 10, 1978, Munich, DE)

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E-mail: [stefan.ameres@univie.ac.at](mailto:stefan.ameres@univie.ac.at) Tel.: +43 664 1077857Web: <https://www.maxperutzlabs.ac.at/research/research-groups/ameres>Professional Networks: [ResearchGate](#) // [Linkedin](#) // [Loop](#)Social media: [Facebook](#) (@AmeresLab) // [Twitter](#) (@AmeresSL)ORCID ID: [0000-0002-8248-3098](https://orcid.org/0000-0002-8248-3098) ResearcherID: [B-4046-2012](https://pubs.rsos.royalsocietypublishing.org/author/B-4046-2012)**Main Areas of Research**

RNA silencing, RNA metabolism, RNP enzymology, RNA modifications, PTGS, non-coding RNAs

**Professional Employment**

- Since 2020 Univ.-Prof. of RNA Biology, Max Perutz Labs, **University of Vienna**, AT
- 2012–2020 Group Leader (PI), **Institute of Molecular Biotechnology (IMBA)**, Vienna, AT
- 2007–2011 PostDoc (with Phillip D. Zamore), **University of Massachusetts Medical School**, Worcester, MA, USA: *MicroRNA-mediated gene regulation in flies and mammals; Regulation of small RNA biogenesis and turnover; Development of tools for the analytical and therapeutic interference with miRNA function in mammals.*
- 2006–2007 PostDoc (with Renée Schroeder), MFPL, **University of Vienna**, AT: *Rational siRNA design for effective RNA interference in mammals.*

**Education**

- Dec. 21<sup>st</sup>, 2006 Graduation to Ph.D. (Dr. rer. nat.), **University of Vienna**, Vienna, AT
- 2004–2006 Ph.D. Thesis (with Renée Schroeder), RNA Biochemistry, MFPL, **University of Vienna**, AT: *Molecular Basis for Target-RNA recognition and cleavage by human RISC*. Final grade: 1.0 (1=best, 4=bottom), awarded best PhD Thesis in all fields at Viennese Universities.
- Mar. 31<sup>st</sup>, 2003 Graduation to Dipl. Biol. Univ. (M.Sc.), **Friedrich-Alexander University Erlangen-Nuremberg**, Erlangen, DE
- 2002–2003 Diploma Thesis (with Wolfgang Hillen), Microbiology, **Friedrich-Alexander University Erlangen-Nuremberg**, Erlangen, DE: *DNA Topology-dependent regulation of Enhancer-function in human cells*. Final grade: 1.0 (1=best, 4=bottom), awarded best Master Thesis in Biological Sciences at the University Erlangen-Nuremberg.
- 1998–2003 Studies of Biology, **Friedrich-Alexander University Erlangen-Nuremberg**, DE

**Selected Honors, Awards and Fellowships**

- 2019 ERC Consolidator Grant Awardee (European Research Council, ERC)
- 2018 ERC Proof-of-Concept Grant Awardee
- 2018 Houska Award (B&C Privatstiftung)
- 2016 Selected member of the EMBO Young Investigator Program (EMBO YIP)
- 2015 Elected member of the Austrian Academy of Sciences (Young Academy, OEAW)
- 2013 ERC Starting Grant Awardee (European Research Council, ERC)
- 2013 FWF START Grant Awardee (Austrian Research Fund, FWF)
- 2008–2011 Erwin Schrödinger Fellowship (FWF) and EMBO Long-Term Fellowship (EMBO)
- 2008 DOC Award (City of Vienna) to honor outstanding PhD Theses in all fields
- 2007 OEGGGT Research Award for Young Scientists and Vienna Biocenter PhD Award
- 2007 Best Talk Award at the 2<sup>nd</sup> Microsymposium on Small RNAs (Vienna, Austria)
- 2003 Diploma Award for excellence in exams and Diploma Thesis (Univ. Erlangen)

**Funding ID**

Since 2013, I have acquired > **EUR 4.8 MM third-party funding** from European, Austrian, and Viennese funding agencies (ERC, FWF, and WWTF):

- 2013 – 2019 **FWF-START Grant**, “Molecular Characterization of the MicroRNA Life Cycle” (PI, Y-733-B22 START), **EUR 200 K** (EUR 1.200 K declined upon ERC funding)
- 2013 – 2017 Doctorate Program, “**DK-RNA Biology**” (Co-PI, FWF, W-1207-B09), **EUR 144 K**
- 2014 – 2019 **ERC StG**, “Molecular Characterization of the MicroRNA Life Cycle”; miRLIFE (PI, ERC-StG-338252), **EUR 1.500 K**
- 2014 – 2019 **SFB**, “RNA Regulation of the Transcriptome” (PI, FWF, F-4322), **EUR 350 K**
- 2017 – 2020 Doctorate Program, “**DK-RNA Biology**” (Co-PI, FWF, W-1207-B09 ext), **EUR 152 K**
- 2018 – 2022 **WWTF Chemical Biology Grant**, “Elucidating sister chromatid structure by chemical DNA labeling and conformation capture” (Co-PI, WWTF, LS17-003), **EUR 140 K**
- 2019 – 2021 **ERC PoC**, “SLAMseq: Temporal resolution in gene expression profiling across multiple platforms”; SLAMseq (PI, ERC-PoC-825710), **EUR 150 K**
- 2020 – 2025 **ERC CoG**, “Bridging temporal resolution gaps to dissect RNA silencing at the molecular and genomic scale”; RiboTrace (PI, ERC-CoG-866166), **EUR 2.000 K**
- 2020 – 2024 **SFB** “RNA-DECO: Decorating RNA for a purpose” (PI, FWF, G257), **EUR 236 K**

**Patent and licensed Technology**

Ameres, S.L., Reichholf, B., Herzog, V.A., Zuber, J., Muhar, M.; Institute of Molecular Biotechnology GmbH. *Nucleic acid modification and identification method*. Patent application US20190177785A1 / EP3589748. Licensed and commercialized as “*SLAMseq® metabolic RNA sequencing kit*” by Lexogen GmbH. Licensed by QUANTRO Therapeutics GmbH for drug discovery. SLAMseq is a trademark of IMBA GmbH (EU and US).

**Invited Research Seminars and International Conference Presentations**

>60 oral presentations at international conferences and institute seminars. For a complete list of presentation see <https://bit.ly/2qnfjtU>. Selected recent presentations include:

- 2019 **Crossroads in Biology**, Center for Medical Biochemistry (Cologne, DE)  
**NCCR RNA & Disease**, Summer School (Saas-Fee, CH)  
**RNA Transcriptomics**, Wellcome Genome Campus (Hinxton, UK)  
**EMBO YIP Meeting**, A\*STAR (Singapore, SG)  
**Louis-Jeantet Symposium** (Geneva, CH)
- 2018 **FEBS Congress** “Biochemistry forever”, The Epitranscriptome (Prague, CZ)  
**Advances in Genome Biology and Technology**, General Conference (Orlando, US)  
**Gurdon Institute**, Cambridge RNA Club (Cambridge, UK)  
**University of Tokyo**, “Tokyo RNA Club” (Tokyo, JP)  
**Helmholz Center for Radiation Biology** (Munich, DE)  
**RNA-REG: Regulatory Circuits in RNA Biology**, Vienna Biocenter (Vienna, AT)  
**Molecular Biology Society of Japan**, Annual Conference (Yokohama, JP)
- 2017 **EMBO conference** “Eukaryotic RNA turnover” (Oxford, UK)  
**22nd Annual Meeting of the RNA Society** (Prague, CZ)  
**6th International Workshop “NON-CODING GENOME”** (Curie Institute, Paris, FR)  
**Max Delbrück Center**, Berlin Institute for Medical Systems Biology (BIMSB, Berlin, DE)  
**Helmholz Institute for RNA-based Infection Research** (HIRI, Würzburg, DE)  
**CNRS**, Institut de Biologie Moleculaire et Cellulaire (Strasbourg, FR)

**Online Webinars**

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- 2018 **Science** Webinar on “Time-resolved RNA profiling in cancer research and beyond”  
 2017 **Labroots** Webinar on “Thiol-linked alkylation for the metabolic sequencing of RNA”

**Memberships**

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- Since 2017 Member of the European Epitranscriptomics Network (COST Action CA16120)  
 Since 2017 Member of the EMBO Young Investigator Program  
 Since 2015 Member of the Austrian Academy of Sciences (Young Academy)  
 Since 2011 Member of the RNA Society (Membership #1184211)

**Academic and Scientific Community Service**

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- \* Advisory board member of *Review Commons* (<http://reviewcommons.org>)
- \* Referee for (inter-)national funding agencies, incl. *European Research Council* (ERC), *Research Council UK* (RCUK), *Human Frontiers in Science Program* (HFSP), *European Molecular Biology Organization* (EMBO), *Deutsche Forschungsgesellschaft* (DFG), *French National Research Agency* (ARN), *German-Israeli Foundation* (GIF), etc.
- \* Reviewer for *Nature*, *Cell*, *Mol. Cell*, *eLife*, *Cell Rep.*, *Curr Biol.*, *Nat Biotech.*, *NSMB*, *PLoS Genet*, *EMBO J*, *EMBO Rep*, *Mol Sys Biol*, *Genome Res*, *PNAS*, *FEBS J*, *NAR*, *RNA*, etc.
- \* Substitute member of the Gentechnikkommission, an advisory board for the Ministry of Health of the Austrian Government (Molecular Biology Section; 2020–2024)
- \* Member of the Austrian Academic Scholarship selection committee (Österr. Studienstiftung der Österr. Akademie der Wissenschaften; OEAW)
- \* Served as part of HDR Jury (French Habilitation; Univ. de Strasbourg, FR) and external evaluator of Swiss habilitations (University of Basel, CH)

**Outreach and Dissemination Activity**

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- 2020 – Founder and Scientific Advisor of QUANTRO Therapeutics<sup>®</sup>, a research-based biotech company that identifies and develops new chemical entities for the therapeutic intervention with disease-causing transcriptional programs in cancer.
- 2020 Member of the Vienna COVID-19 Diagnostics Initiative (Part of Research and Development Team)
- 2020 Online Interview on “CRISPR/Cas” (with OpenScience and DK RNA Biology)
- 2018 Invited presentation at “Health Pioneers”, an international conference on digital and exponential medical technologies that transform the public health cycle (Vienna, AT)
- 2018 Co-organizer of the 18th EMBO Young Investigator Program Meeting (Vienna, AT)
- 2018 Presentation at IMBA Fundraising event “*Meet the Expert*” on the successful symbiosis of biomedical research and commercial biotech companies at the VBC (Vienna, AT)
- 2018 Co-organizer of the int. conference “RNA-Reg: Regulatory circuits in RNA Biology” of the SFB 43 RNA-Reg (VBC, Vienna, AT)
- 2017 – Member of the *European Epitranscriptomics Network* coordinating research on the emerging function of RNA modifications in Europe (COST Action CA16120)
- 2013 – Co-organizer of the annual “Microsymposium on Small RNAs”, the major European conference on RNA silencing
- 2012 – Co-organizer of the VBC RNA Club (since 2017 supported by the RNA Society)

**Selected recent Public Media Coverage and Press Releases of our Science**\_\_\_\_\_

- 2020, Sep 23 **APA**, “Eine 3D-Landkarte des Erbguts”
- 2020, Sep 7 **OEAW Online**, “An den Achillesfersen von Krebszellen”
- 2020, Jul 21 **APA**, “Krebsforschung: Wiener Start-Up QUANTRO Therapeutics geht völlig neue Wege in der Arzneimittelforschung”
- 2020, May **MAKRO MIKRO OEAW Podcast**, “Coronavirus: Wie funktionieren Tests?”
- 2019, Dec 10 **Chemie Report**, “Dritter ERC Grant für IMBA-Forscher Stefan Ameres”
- 2019, Dec 10 **Der Standard**, “ERC-‘Consolidator Grants’ für sechs [...] Forscher”
- 2019, Nov 5 **Kronen Zeitung**, Krone der Wissenschaft, “Das Genom in Aktion”
- 2019, May **Jahresbericht der OEAW**, “Wie werden unsere Gene ein- und ausgeschaltet?”
- 2019, Jan 21 **Regionalmedien Austria**, “Von Schaf Dolly bis CRISPR”
- 2018, Oct **Metropole**, “From Slaughterhouse to Lighthouse – Biomedical research in Vienna [...]”
- 2018, Sep 14 **Die Presse**, “Österreich holt eine Milliarde Euro EU-Forschungsgelder”
- 2018, Sep 12 **Der Standard**, “Zwei ‘Proof-of-Concept’-Förderungen des ERC gehen nach Österr.”
- 2018, Jul 26 **ScienceDaily**, “Changes to sperm’s small RNA in the epididymis [...]”
- 2018, Jun 17 **Kurier**, “Immunsystem und Krebs: Forschung aus Österreich macht Hoffnung”
- 2018, Jun **Transkript**, “Transkript persönlich: Dr. Stefan Ameres”
- 2018, Jun **LaborJournal**, “Neulich an der Bench: SLAMseq”
- 2018, May 28 **Profil**, “Houska Preis 2018”
- 2018, May 7 **Innovations Report**, “Wissenschaftler entdecken bahnbrechende neue Methode [...]”
- 2018, Apr 27 **Der Standard**, “IMBA Forscher Stefan Ameres erhält Houska Preis”
- 2018, Apr 27 **Die Presse**, “Den Genen auf der Spur”, “Jetzt kommt Dynamik in die Zelle”, “Genexpression ist die Essenz des Lebens” (Houska Award Special Issue)
- 2018, April 13 **Der Standard**, “Krebszellen beim Sterben zusehen”
- 2018, Apr 7 **Die Presse**, “Wie Krebszellen anwachsen”
- 2018, Apr 5 **ScienceDaily**, “Cancer genes characterized using ground-breaking method”
- 2016, Nov 19 **Der Standard**, “Wie unsere Keimzellen springende Gene einbremsen”
- 2016, Nov 16 **ScienceDaily**, “A milestone in small RNA biology – piRNA biogenesis ...”
- 2016, Nov 16 **Wiener Zeitung**, “‘Zucchini’ und ‘Nibbler’ zähmen springende Gene”
- 2013, Jul 19 **Der Standard**, “Acht Forscher in Österreich erhalten ERC ‘Starting Grants’”
- 2013, Jun 22 **Die Presse**, “Herausragende helle Köpfe”
- 2013, Jun 17 **Ö1 Radio**, “Wissen aktuell: Jungforscher”
- 2012, Feb 07 **Der Standard**, “Kleine Teilchen, große Hoffnung”
- 2007, Jul 13 **Der Standard**, “Dem ‘Immunsystem’ der Zelle auf der Spur”

**Publications**\_\_\_\_\_

Our work has been **published in top-tier, multidisciplinary journals** (*Nature*, *Science*, *Cell*, *Mol. Cell*, *Nature Biotech.*, *Nature Methods*, *Curr. Biol.* and *EMBO J*). In sum, those publications were **cited >4,000 times** (Google Scholar 10/2020). For complete list see **Pubmed** (<https://bit.ly/2YBVz0Q>) or **Google Scholar** (<https://bit.ly/2V2PaPb>).

1. Mitter M, Gasser C, Takacs Z., Langer CC, Tang W, Jessberger G, Beales CT, Neuner E, **Ameres SL**, Peters, J-M, Goloborodko A, Micura R, Gerlich DW. 2020. Conformation of siter chromatins in the replicated human genome. **Nature**. 2020 Sep 23. doi: 10.1038/s41586-020-2744-4. Online ahead of print.
2. Herzog VA, Fasching N, **Ameres SL**. 2020. Determining mRNA stability by metabolic RNA labeling and chemical nucleoside conversion. **Methods Mol. Biol.** 2062: 169-189, doi: 10.1007/978-1-4939-9822-7\_9

3. Reichholf B, Herzog VA, Fasching N, Manzenreither RA, Sowemimo I, **Ameres SL**. 2019. Time-resolved small RNA sequencing unravels the molecular principles of microRNA homeostasis. *Mol Cell*. 75(4): 756-768, doi: 10.1016/j.molcel.2019.06.018  
*Cover story*; highlighted in *Mol Cell* and *Nat Rev Mol Cell Biol*
4. Matsushima W, Herzog VA, Neumann T, Gapp K, Zuber J, **Ameres SL**, Miska EA. 2019. Sequencing cell-type-specific transcriptomes with SLAM-ITseq. *Nat Protoc*. Jun 26. doi: 10.1038/s41596-019-0179-x.
5. Neumann T, Herzog VA, Muhar M, von Haeseler A, Zuber J, **Ameres SL**, Rescheneder P. 2019. Quantification of experimentally induced nucleotide conversions in high-throughput sequencing datasets. *BMC Bioinformatics*. 20(1): 258, doi: 10.1186/s12859-019-2849-7
6. Kroupova A, Ivascu A, Reimão-Pinto MM, **Ameres SL**, Jinek M. 2019. Structural basis for acceptor RNA substrate selectivity of the 3' terminal uridylyl transferase Tailor. *Nucleic Acids Res*. Nov 20, 2018, doi: 10.1093/nar/gky1164.
7. Sharma U, Sun F, Conine CC, Reichholf B, Kukreja S, Herzog VA, **Ameres SL**, Rando OJ. 2018. Small RNAs are trafficked from the Epididymis to developing mammalian Sperm. *Dev Cell*. July 26, 2018, doi: 10.1016/j.devcel.2018.06.023.  
Highlighted in *ScienceDaily*, *EurekAlert!* and *Nat Rev Genetics*
8. Reimão-Pinto MM, Rodrigues-Viana AM, **Ameres SL**. 2018. Analysis of 3' End Modifications in microRNAs by High-Throughput Sequencing. *Methods Mol Biol*. 1823: 115-139, doi: 10.1007/978-1-4939-8624-8\_10.
9. Matsushima W, Herzog VA, Neumann T, Gapp K, Zuber J, **Ameres SL**, Miska EA. 2018. SLAM-ITseq: Sequencing cell type-specific transcriptomes without cell sorting. *Development*. 145: dev164640, doi: 10.1242/dev.164640.  
Highlighted in *Development*.
10. **Ameres S**, Zuber J. 2018. Principles of Systems Biology, No. 29. *Cell Syst*. 6(5):533-535. doi: 10.1016/j.cels.2018.05.005.
11. Jantsch MF, Quattrone A, O'Connell M, Helm M, Frye M, Macias-Gonzales M, Ohman M, **Ameres S**, Willems L, Fuks F, Oulas A, Vanacova S, Nielsen H, Bousquet-Antonelli C, Motorin Y, Roignant JY, Balatsos N, Dinnyes A, Baranov P, Kelly V, Lamm A, Rechavi G, Pelizzola M, Liepins J, Holodnuka Kholodnyuk I, Zammit V, Ayers D, Drablos F, Dahl JA, Bujnicki J, Jeronimo C, Almeida R, Neagu M, Costache M, Bankovic J, Banovic B, Kyselovic J, Valor LM, Selbert S, Pir P, Demircan T, Cowling V, Schäfer M, Rossmann W, Lafontaine D, David A, Carre C, Lyko F, Schaffrath R, Schwartz S, Verdell A, Klungland A, Purta E, Timotijevic G, Cardona F, Davalos A, Ballana E, O Carroll D, Ule J, Fray R. 2018. Positioning Europe for the EPITRANSCRIPTOMICS challenge. *RNA Biol*. 2018 May 9:1-3. doi: 10.1080/15476286.2018.1460996.
12. Muhar M, Ebert A, Neumann T, Umkehrer C, Jude J, Wieshofer C, Rescheneder P, Lipp JJ, Herzog VA, Reichholf B, Cisneros DA, Hoffmann T, Schlapansky MF, Bhat P, von Haeseler A, Köcher T, Obenauf AC, Popow J, **Ameres SL\***, Zuber J\*. 2018. SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis. *Science*. 360(6390):800-805, doi: 10.1126/science.aao2793. \* co-corresponding authors  
Highlighted in *Science*, *Nat. Chem. Biol.*, *Nat. Rev. Genet.* and *Cancer Discovery*.
13. Alberti C, Manzenreither RA, Sowemimo I, Burkard TR, Wang J, Mahofsky K, **Ameres SL\***, Cochella L\*. 2018. Cell type-specific sequencing of microRNAs from complex animal tissues. *Nat Methods*. 15(4):283-289, doi: 10.1038/nmeth.4610. \* co-corresponding authors
14. Herzog VA, Reichholf B, Neumann T, Rescheneder P, Bhat P, Burkard TR, Wlotzka W, von Haeseler A, Zuber J, **Ameres SL**. 2017. Thiol-linked alkylation to assess expression dynamics. *Nat Methods*. 14(12):1198-1204. doi: 10.1038/nmeth.4435.  
Highlighted in *Nature Methods*.
15. Hayashi R, Schnabl J, Handler D, Mohn F, **Ameres SL\***, Brennecke J\*. 2016. Genetic and mechanistic diversity of piRNA 3'-end formation. *Nature*. 539(7630):588-592. doi: 10.1038/nature20162. \* co-corresponding authors

16. Reimão-Pinto MM, Manzenreither RA, Burkard TR, Sledz P, Jinek M, Mechtler K, **Ameres SL**. 2016. Molecular basis for cytoplasmic RNA turnover by uridylation-triggered RNA decay in *Drosophila*. *EMBO J*. 35(22):2417-2434. doi: 10.15252/embj.201695164.
17. Reimão-Pinto MM, Ignatova V, Burkard TR, Hung JH, Manzenreither RA, Sowemimo I, Herzog VA, Reichholf B, Fariña-Lopez S, **Ameres SL**. 2015. Uridylation of RNA hairpins by Tailor confines the emergence of microRNAs in *Drosophila*. *Mol Cell*. 59(2):203-16. doi: 10.1016/j.molcel.2015.05.033.  
Highlighted in *Molecular Cell*.
18. Bortolamiol-Becet D, Hu F, Jee D, Wen J, Okamura K, Lin CJ, **Ameres SL**, Lai EC. 2015. Selective suppression of the splicing-mediated microRNA pathway by the terminal uridyltransferase Tailor. *Mol Cell*. 59(2):217-28. doi: 10.1016/j.molcel.2015.05.034.  
Highlighted in *Molecular Cell*.
19. Herzog VA, **Ameres SL**. 2015. Approaching the golden fleece a molecule at a time: Biophysical insights into Argonaute-instructed nucleic acid interactions. *Mol Cell*. 59(1):4-7. doi: 10.1016/j.molcel.2015.06.021.
20. **Ameres SL\***, Zamore PD\*. 2013. Diversifying microRNA sequence and function. *Nat Rev Mol Cell Biol*. 14(8):475-88. doi: 10.1038/nrm3611. \* co-corresponding authors
21. Xie J\*, **Ameres SL\***, Friedline R, Hung JH, Zhang Y, Xie Q, Zhong L, Su Q, He R, Li M, Li H, Mu X, Zhang H, Broderick JA, Kim JK, Weng Z, Flotte TR, Zamore PD, Gao G. 2012. Long-term efficient inhibition of microRNA function in mice using rAAV vectors. *Nat Methods*. 9(4):403-9. doi: 10.1038/nmeth.1903. \* equal contribution
22. Han BW, Hung JH, Weng Z, Zamore PD\*, **Ameres SL\***. 2011. The 3'-to-5' exoribonuclease Nibbler shapes the 3' ends of microRNAs bound to *Drosophila* Argonaute1. *Curr Biol*. 21(22):1878-87. doi: 10.1016/j.cub.2011.09.034. \* co-corresponding authors.  
Highlighted in *Nat Rev Genetics*.
23. Xie J, Xie Q, Zhang H, **Ameres SL**, Hung JH, Su Q, He R, Mu X, Seher Ahmed S, Park S, Kato H, Li C, Mueller C, Mello CC, Weng Z, Flotte TR, Zamore PD, Gao G. 2011. MicroRNA-regulated, systemically delivered rAAV9: a step closer to CNS-restricted transgene expression. *Mol Ther*. 19(3):526-35. doi: 10.1038/mt.2010.279.
24. **Ameres SL**, Hung JH, Xu J, Weng Z, Zamore PD. 2011. Target RNA-directed tailing and trimming purifies the sorting of endo-siRNAs between the two *Drosophila* Argonaute proteins. *RNA*. 17(1):54-63. doi: 10.1261/rna.2498411.
25. **Ameres SL**, Horwich MD, Hung JH, Xu J, Ghildiyal M, Weng Z, Zamore PD. 2010. Target RNA-directed trimming and tailing of small silencing RNAs. *Science*. 328(5985):1534-9. doi: 10.1126/science.  
Highlighted in *Science* and *Cell*.
26. **Ameres SL**, Fukunaga R. 2010. Riding in silence: a little snowboarding, a lot of small RNAs. *Silence*. 1(1):8. doi: 10.1186/1758-907X-1-8.
27. Tafer H\*, **Ameres SL\***, Obernosterer G\*, Gebeshuber CA, Schroeder R, Martinez J, Hofacker IL. 2008. The impact of target site accessibility on the design of effective siRNAs. *Nat Biotechnol*. 26(5):578-83. doi: 10.1038/nbt1404. \* equal contribution
28. **Ameres SL**, Martinez J, Schroeder R. 2007. Molecular basis for target RNA recognition and cleavage by human RISC. *Cell*. 130(1):101-12. doi: 10.1016/j.cell.2007.04.037.
29. **Ameres SL**, Shcherbakov D, Nikonova E, Piendl W, Schroeder R, Semrad K. 2007. RNA chaperone activity of L1 ribosomal proteins: Phylogenetic conservation and splicing inhibition. *Nucleic Acids Res*. 35(11):3752-63. doi: 10.1093/nar/gkm318.
30. Leuschner PJ, **Ameres SL**, Kueng S, Martinez J. 2006. Cleavage of the siRNA passenger strand during RISC assembly in human cells. *EMBO Rep*. 7(3):314-20. doi: 10.1038/sj.embor.7400637.
31. **Ameres SL\***, Druempel L\*, Pfeleiderer K, Schmidt A, Hillen W, Berens C. 2005. Inducible DNA-loop formation blocks transcriptional activation by an SV40 enhancer. *EMBO J*. 24(2):358-67. doi: 10.1038/sj.emboj.7600531. \* equal contribution