

CURRICULUM VITAE

EDUCATION:

Columbia University
Ph.D. (with distinction), *Mentor: Lawrence A. Chasin Ph.D.*
My doctoral thesis title "Effects of context on cis-elements in pre-mRNA splicing".
The title "with distinction" represents the top 10% Ph.D. graduates from Columbia University
New York, NY
February 2011

University of Science and Technology of China
B.S., *Mentor: Haiyan Liu Ph.D.*
Hefei, China
June 2004

POSITIONS AND HONORS:

Positions and Employment

2002-2004 Research Assistant, Computational Biology Lab, University of Science and Technology of China, Mentor: Haiyan Liu (*developed bioinformatics methods to effectively analyze genomic microarray data*)

2005-2012 Graduate Student Researcher, Department of Biological Sciences, Columbia University then stayed briefly as a postdoc with my Ph.D. mentor, Lawrence A. Chasin (William R. Kenan Jr. Professor Columbia University) (*published multiple high quality peer-reviewed research papers, filed two patents pending in genetics/genomics methodology, received several prestigious awards for outstanding research, focused on pre-mRNA splicing, bioinformatics, genetics & genomics*)

2012-2017 Post-doctorate Fellow, Mentor: Robert B. Darnell (Heilbrunn Professor and Senior Physician The Rockefeller University; Investigator, HHMI; Member of NAS; Founding Director of New York Genome Center), **Co-Mentor: James E. Darnell Jr.** (Vincent Astor Professor Emeritus The Rockefeller University; The Lasker Award Laureate; Member of NAS) **Rockefeller University;** (*received several prestigious post-doc fellowships, established m⁶A-CLIP, an important genomics technology that precisely maps m⁶A in single-nucleotide resolution genome-wide; developed bioinformatics algorithm to integrate large-scale genomic and transcriptomic deep sequencing data; discovered key roles of m⁶A mRNA modification in regulating mRNA turnover and alternative polyadenylation; discovered that m⁶A in mRNA is added to exons in nascent pre-mRNA, with fundamental importance: m⁶A addition is part of the synthesis of mammalian pre-mRNA*)

2017-present Assistant Professor, The Jackson Laboratory (The Ke Lab focuses on RNA, a central node of genetic information flow from DNA to protein. Malfunction of RNAs leads to many human diseases, including cancer and neurological diseases.)

Other Experience and Professional Memberships

2006, 2010-present Member, RNA Society
2011-present Full Membership, Sigma XI Society

Grants & Awards

2019 NIH Maximizing Investigators' Research Award (MIRA)(R35GM133711)
2019 American Cancer Society Pilot Award (#IRG-16-191-33)
2019 JAX Cancer Center New Investigator Award (NCI CA034196)
2016 Rockefeller University Post-doc Career Development Travel Award
2013 NIH Ruth L. Kirschstein National Research Service Award---F32 NRSA (declined)
2013 American Cancer Society Postdoctoral Fellowship (declined)
2013 Leukemia & Lymphoma Society Fellow Award (declined)
2012 CRI-Irvington Institute Postdoctoral Fellowship (from Jan. 1st 2013 to Dec. 31th 2015)
2011 *John S. Newberry Prize* (for outstanding graduate research), Columbia University
2011 *The Ph.D. degree with distinction*, Columbia University (the title "with distinction" represents the top 10% Ph.D. graduates from Columbia Univ.)

1. Lawrence Chasin and **Shengdong Ke**, Quantitative Total Definition of Biologically Active Sequence Elements (*US Application No.:* [US 13/818,777](#)) (*International Application No.:* [PCT/US2011/049098](#))
2. Lawrence Chasin and **Shengdong Ke**, Quantitative Total Definition of Biologically Active Sequence Elements and Positions (*US Application No.:* [US 13/776,696](#))

PUBLICATIONS: (list in chronological order)

1. **Ke, S.***, Zhang, X. H.* & Chasin, L.A. Positive selection acting on splicing motifs reflects compensatory evolution. *Genome Research* 2008, 18: 533-543. (* Joint-first author) (PMID: 18204002)
2. Yu, H., Chen, X., Hong, Y.Y., Wang, Y., Xu, P., **Ke, S.D.**, Liu, H.Y., Zhu, J.K., Oliver, D.J., Xiang, C.B. Activated expression of an Arabidopsis HD-START protein confers drought tolerance with improved root system and reduced stomatal density. *Plant Cell* 2008, 20:1134-51. (PMID: 18451323)
3. Zhang, X.H., Arias, M.A., **Ke, S.** & Chasin, L.A. Splicing of designer exons reveals unexpected complexity in pre-mRNA splicing. *RNA* 2009, 15: 367-76. (PMID: 19155327)
4. Arias, M.A., **Ke, S.** & Chasin, L.A. Splicing by cell type. *Nature Biotechnology* 2010, 28:686-687. (PMID: 20622839)
5. **Ke, S.** & Chasin, L.A. Intronic motif pairs cooperate across exons to promote pre-mRNA splicing. *Genome Biology* 2010, 11:R84. [**Highly accessed** at *Genome Biology*][**Recommended by Faculty of 1000**] (PMID: 20704715)
6. **Ke, S.** & Chasin, L.A. Context-dependent splicing regulation: exon definition, co-occurring motif pairs and tissue specificity. *RNA Biology* 2011, 8:384-388. (PMID: 21444999)
7. **Ke, S.**, Shang, S., Kalachikov, S.M., Morozova, I., Yu, L., Russo, J.J., Ju, J. & Chasin, L.A. Quantitative evaluation of all hexamers as exonic splicing elements, *Genome Research* 2011, 21:1360-74. [**Top 10 Most Read Articles** at *Genome Research* for the first 6 months online] (PMID: 21659425)
8. **Ke, S.**, Alemu, E.A., Mertens, C., Gantman, E.C., Fak, J.J., Mele, A., Haripal, B., Zucker-Scharff, I., Moore, M.J., Park, C.Y., Vagbo, C.B., Kussnierczyk, A., Klungland, A., Darnell J.E. Jr. & Darnell R.B. A majority of m⁶A residues are in the last exons, allowing the potential for 3' UTR regulation, *Genes & Development* 2015, 29:2037-53. (PMID: 26404942)
9. **Ke, S.**, Pandya-Jones, A., Saito, Y., Fak, J.J., Vagbo, C.B., Geula, S., Black, D.L., Darnell J.E. Jr. & Darnell R.B. m⁶A mRNA modifications are deposited in nascent pre-mRNA and are not required for splicing but do specify cytoplasmic turnover, *Genes & Development* 2017, 31: 990-1006. (PMID: 28637692)
---*Outlook* by Dr. Joan Steitz and colleagues: [Settling the m⁶A debate: methylation of mature mRNA is not dynamic but accelerates turnover.](#)
10. **Ke, S.***, Anquetil, V.*, Rojas-Zamalloa J.*, Maity, A., Yang, A., Arias, M.A., Kalachikov, S., Ju, J. & Chasin L.A. Saturation mutagenesis reveals manifold determinants of exon definition, *Genome Research* 2018, 28:1-14. (* Joint-first author)(PMID: 29242188)
11. Darnell, R.B., **Ke, S.**, Darnell, J.E. Pre-mRNA processing includes N⁶ methylation of adenosine residues that are retained in mRNA exons and the fallacy of "RNA epigenetics", *RNA* 2018, 24: 262-267. (PMID: 29222117)

TEACHING EXPERIENCE:

Faculty Mentor

- 1) Fall Semester 2018-Spring Semester 2019, Tufts University Department of Genetics Graduate Course GENE-0295-101 *Journal Club Seminar*
- 2) Summer Semester 2019, Tufts University Department of Genetics Graduate Course GENE-0208 *Medical & Experimental Mammalian Genetics*
- 3) Fall Semester 2019-Spring Semester 2020, Tufts University Department of Genetics Graduate Course GENE-0295-101 *Journal Club Seminar*

Teaching Assistant for the course Biotechnology (W3034, W4034) (grading, review seminar, working with professors Lawrence Chasin and Daniel Kalderon), Columbia University, for two fall semesters of 2005 and 2006.

- 1) Bhagwattie Haripal, (co-supervised with Claudia Mertens), Research Assistant, The Rockefeller University, from 2013-2017
- 2) Jorge Rojas-Zamalloa, Computational Biologist, Columbia University, from 2011 till 2016
- 3) Ilana Lefkovitz, Undergraduate Researcher, Columbia University, from 2010 summer till 2012
- 4) Katie Thomas, Undergraduate Researcher, Amgen scholar from MIT, 2009 summer
- 5) David Berman, (co-supervised with Mauricio Arias), Undergraduate Researcher, Columbia University, from 2006 summer till 2007 summer

CONFERENCE PRESENTATIONS:

1. **Ke, S.**, Zhang, X. H. Arias, M. & Chasin, L.A. 2006. Splicing of de novo designer exons depends on ESE content. RNA 2006 Annual Meeting June 20th - June 25th in Seattle, WA.(poster)
2. **Ke, S.**, Zhang, X. H. & Chasin, L.A. 2007. How do exons survive as splicing units under the sculpting of evolutionary force? *Aug 22-26 in Cold Spring Harbor, NY.* (poster)
3. **Ke, S.**, Zhang, X. H. & Chasin, L.A. 2007. Positive selection acting on splicing motifs reflects compensatory evolution. *Eukaryotic mRNA Processing. Department Retreat of Biological Sciences, Columbia University, Sept. 7-9 in Mohonk, NY.* (talk)
4. **Ke, S.** & Chasin, L.A. 2009. Intronic motif pairs cooperate across exons to promote pre-mRNA splicing, *Eukaryotic mRNA processing. Aug 18-22 in Cold Spring Harbor, NY.* (poster)
5. **Ke, S.** & Chasin, L.A. 2009. Intronic motif pairs cooperate across exons to promote pre-mRNA splicing, *Department Retreat of Biological Sciences, Columbia University, Sept 11-13 in Tarrytown, NY.* (talk)
6. **Ke, S.** & Chasin, L.A. 2011. Quantitative evaluation of all hexamers as exonic splicing elements, *RNA symposium 2011, January 21st in New York, NY.* (poster)
7. **Ke, S.** & Chasin, L.A. 2011. Quantitative evaluation of all hexamers as exonic splicing elements, *Eukaryotic mRNA processing. Aug 23-27 in Cold Spring Harbor, NY.* (talk)
8. **Ke, S.**, Darnell J.E. Jr. & Darnell R.B. 2013. RNA epigenetics CLIP: A new approach to understanding leukemia/lymphoma, *21st Annual International Cancer Immunotherapy Symposium. Sep 30-Oct 2 in New York City, NY.* (poster)
9. **Ke, S.**, Darnell J.E. Jr. & Darnell R.B. 2014. RNA epigenetics: A new approach to understanding leukemia/lymphoma, *22nd Annual International Cancer Immunotherapy Symposium. Oct 5-8 in New York City, NY.* (poster)
10. **Ke, S.**, Darnell J.E. Jr. & Darnell R.B. 2015. A majority of m6A residues are in the last exons, allowing the potential for 3' UTR regulation, *23rd Annual International Cancer Immunotherapy Symposium. Sept 16-19 in New York City, NY.* (poster)
11. **Ke, S.**, Darnell J.E. Jr. & Darnell R.B. 2017. m⁶A mRNA modifications are deposited in nascent pre-mRNA and are not required for splicing but do specify cytoplasmic turnover, *Eukaryotic mRNA processing. Aug 22-26 in Cold Spring Harbor, NY.* (poster)
12. **Ke, S.**, Darnell J.E. Jr. & Darnell R.B. 2017. m⁶A mRNA modifications are deposited in nascent pre-mRNA and are not required for splicing but do specify cytoplasmic turnover, *Eukaryotic mRNA processing. Aug 22-26 in Cold Spring Harbor, NY.* (poster)
13. **Ke, S.**, Darnell J.E. Jr. & Darnell R.B. 2017. m⁶A mRNA modifications are deposited in nascent pre-mRNA and are not required for splicing but do specify cytoplasmic turnover, *RNA Modifications & Epitranscriptomics. Nov 13-17 in Cold Spring Harbor Asia, Suzhou* (talk)

REFERENCES:

Robert B. Darnell, M.D. Ph.D. (Post-doc Mentor)
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