**PROGRAM—RNA 2010**

The Fifteenth Annual Meeting of the RNA Society  
Seattle, Washington USA  
June 22 – 26, 2010

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### Tuesday, June 22

- **12 noon – 7:00 p.m.** Registration  
  Meany Lobby
- **5:00 – 6:00 p.m.** Welcome Reception  
  By George Café
- **6:00 – 7:30 p.m.** Dinner  
  By George Café
- **8:00 – 10:00 p.m.** Opening & Plenary Session 1  
  *Tim Nilsen, Chair*  
  Meany Theater
  8:00 – 8:15 p.m. Welcome & Opening remarks
  8:15  
  Joan Steitz
  8:45  
  Jim Manley
  9:15 – 9:45 p.m.  
  Kathy Collins

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### Wednesday, June 23

- **8:00 a.m. – 1:00 p.m.** Registration/Information  
  Meany Lobby
- **9:00 a.m. – 12 noon** Plenary Session 2  
  *Doug Black, Chair*  
  Meany Theater
  9:00  
  Reinhard Luhrmann
  9:30  
  Harry Noller
  10:00 – 10:30 a.m. Break
  10:30  
  Jon Lorsch
  11:00  
  David Tollervey
  11:30 – 12 noon  
  Nahum Sonenberg
- **12:30 – 2:00 p.m.** Lunch  
  By George Café
- **12:30 – 2:00 p.m.** Board of Directors Lunch Meeting  
  HUB - 200BC
- **1:00 – 7:30 p.m.** Poster Installation  
  HUB - Ballroom & 209AB
- **2:00 – 7:30 p.m.** Registration/Information  
  Kane Lobby
- **2:00 – 5:30 p.m.** Concurrent Session 1  
  Kane Hall - 130
  **Part 1: Mechanisms of Pre-mRNA Splicing**  
  *Jean Beggs, Chair*  
  Abstracts 1 – 7
  **Part 2: RNA and Disease**  
  *Lucca Cartegni, Chair*  
  Abstracts 8 – 14
Concurrent Session 2  
**Ribosomes Structure, Function, and Biogenesis**  
*Marina Rodnina, Chair*

Abstracts 15 – 28

5:30 – 7:30 p.m.  
Career Development Workshop  
*Kane Hall - 130*

*Communications Workshop “Putting Your Science to Work”*  
*Peter Fiske*

6:30 – 8:00 p.m.  
Dinner  
*By George Café*

7:30 – 8:30 p.m.  
Junior Scientists Social  
*HUB - Upper Husky Den*

8:00 – 10:30 p.m.  
Poster Session 1 (browsing)  
*HUB - Ballroom & 209AB*

(Scout for your favorite posters tonight.  
**EVEN NUMBERED** posters will be staffed on Thursday,  
**ODD NUMBERED** posters on Friday.)

(abstract)  
(topic)

<table>
<thead>
<tr>
<th>Abstract</th>
<th>Topic</th>
</tr>
</thead>
<tbody>
<tr>
<td>(112 - 129)</td>
<td>3’ End Formation</td>
</tr>
<tr>
<td>(130 - 153, 670)</td>
<td>Bioinformatics</td>
</tr>
<tr>
<td>(154 - 162)</td>
<td>Chemical Biology of RNA</td>
</tr>
<tr>
<td>(163 - 179)</td>
<td>Emerging Methodologies for RNA Science</td>
</tr>
<tr>
<td>(180 - 196)</td>
<td>Interconnections Between Gene Expression Processes</td>
</tr>
<tr>
<td>(197 - 210, 671)</td>
<td>Mechanisms of RNA Interference</td>
</tr>
<tr>
<td>(211 - 244)</td>
<td>Non-coding and Regulatory RNAs</td>
</tr>
<tr>
<td>(245 - 246)</td>
<td>Riboregulation in Development</td>
</tr>
<tr>
<td>(247 - 273)</td>
<td>Ribosomes</td>
</tr>
<tr>
<td>(275 - 278)</td>
<td>RNA and Epigenetics</td>
</tr>
<tr>
<td>(279 - 295)</td>
<td>RNA Catalysis</td>
</tr>
<tr>
<td>(296 - 325)</td>
<td>RNA Editing and Modification</td>
</tr>
<tr>
<td>(326 - 376)</td>
<td>RNA Structure and Folding</td>
</tr>
<tr>
<td>(377 - 389)</td>
<td>RNA Transport and Localization</td>
</tr>
<tr>
<td>(390 - 415, 668)</td>
<td>RNA Turnover</td>
</tr>
<tr>
<td>(416 - 449)</td>
<td>RNA-Protein Interactions</td>
</tr>
<tr>
<td>(450 - 472)</td>
<td>RNAs in Diseases</td>
</tr>
<tr>
<td>(473 - 497, 669)</td>
<td>RNP Structure, Function and Biosynthesis</td>
</tr>
<tr>
<td>(498 - 521)</td>
<td>Small RNAs</td>
</tr>
<tr>
<td>(522 - 547)</td>
<td>Splicing Mechanisms</td>
</tr>
<tr>
<td>(548 - 604)</td>
<td>Splicing Regulation</td>
</tr>
<tr>
<td>(605 - 624)</td>
<td>Translation Regulation</td>
</tr>
<tr>
<td>(625 - 650)</td>
<td>tRNA, snoRNA and rRNA</td>
</tr>
<tr>
<td>(651 - 667)</td>
<td>Viral RNAs</td>
</tr>
</tbody>
</table>

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**Thursday, June 24**

8:00 a.m. – 1:00 p.m.  
Registration/Information  
*Meany Lobby*

9:00 a.m. – 12 noon  
Plenary Session 3  
*Juli Feigon, Chair*

9:00  
Brent Graveley

9.30  
Alan Lambowicz
<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:00 – 10:30</td>
<td>Break</td>
</tr>
<tr>
<td>10:30</td>
<td>Michael Ibba</td>
</tr>
<tr>
<td>11:00</td>
<td>Ronald Breaker</td>
</tr>
<tr>
<td>11:30 – 12 noon</td>
<td>Susan Gottesman</td>
</tr>
<tr>
<td>12:30 – 2:00 p.m.</td>
<td>Lunch</td>
</tr>
<tr>
<td>12:30 – 2:00 p.m.</td>
<td>Mentor-Mentee Lunch</td>
</tr>
<tr>
<td>2:00 – 5:30 p.m.</td>
<td>Registration/Information</td>
</tr>
<tr>
<td>2:00 – 5:30 p.m.</td>
<td>Concurrent Session 3</td>
</tr>
<tr>
<td></td>
<td><strong>Alternative Splicing and Splicing Regulatory Networks</strong></td>
</tr>
<tr>
<td></td>
<td>Don Rio, Chair</td>
</tr>
<tr>
<td></td>
<td>Abstracts 29 – 42</td>
</tr>
<tr>
<td>12:30 – 2:00 p.m.</td>
<td>Mentor-Mentee Lunch</td>
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<tr>
<td>2:00 – 5:30 p.m.</td>
<td>Concurrent Session 3</td>
</tr>
<tr>
<td></td>
<td><strong>Part 1: Transfer RNA Metabolism</strong></td>
</tr>
<tr>
<td></td>
<td>Eric Phizicky, Chair</td>
</tr>
<tr>
<td></td>
<td>Abstracts 43 – 50</td>
</tr>
<tr>
<td>2:00 – 5:30 p.m.</td>
<td>Concurrent Session 4</td>
</tr>
<tr>
<td></td>
<td><strong>Part 2: RNA Modulation of RNA Synthesis</strong></td>
</tr>
<tr>
<td></td>
<td>Torben Jensen, Chair</td>
</tr>
<tr>
<td></td>
<td>Abstracts 51 – 56</td>
</tr>
<tr>
<td>6:30 – 8:00 p.m.</td>
<td>Dinner</td>
</tr>
<tr>
<td>6:30 – 8:30 p.m.</td>
<td>RNA &amp; Society Dinner</td>
</tr>
<tr>
<td>8:00 – 10:30 p.m.</td>
<td>Poster Session 2</td>
</tr>
</tbody>
</table>

**Friday, June 25**

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>8 a.m. – 1:00 p.m.</td>
<td>Registration/Information</td>
</tr>
<tr>
<td>9 a.m. – 12 noon</td>
<td>Plenary Session 4</td>
</tr>
<tr>
<td>9:00</td>
<td>Elena Conti</td>
</tr>
<tr>
<td>9:30</td>
<td>Lynne Maquat</td>
</tr>
<tr>
<td>10:00 – 10:30 a.m.</td>
<td>Break</td>
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<tr>
<td>10:30</td>
<td>Eckard Jankowsky</td>
</tr>
<tr>
<td>11:00</td>
<td>Adrian Ferre-d’Amare</td>
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<tr>
<td>11:30 – 12 noon</td>
<td>Daniel Herschlag</td>
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<td>12:30 – 2:00 p.m.</td>
<td>Lunch</td>
</tr>
<tr>
<td>12:30 – 2:00 p.m.</td>
<td>Meetings Committee Lunch</td>
</tr>
<tr>
<td>2:00 – 7:00 p.m.</td>
<td>Registration/Information</td>
</tr>
</tbody>
</table>

By George Café
Kane Hall - 120
Kane Hall Lobby
Kane Hall - 130
Kane Hall - 200BC
HUB - 106B, 108, 200ABC, 310
HUB - 200BC
2:00 – 5:30 p.m. Concurrent Session 5  
**Post-processing mRNA Metabolism**  
*Jens-Lykke Anderson, Chair*  
Abstracts 57 – 70  
Kane Hall - 130

Concurrent Session 6  
**RNA Structure, Folding, and Catalysis**  
*James Williamson, Chair*  
Abstracts 71 – 84  
Kane Hall - 120

5:30 – 7:00 p.m. Career Development Workshop  
**Grant Writing**  
Kane Hall - 130

6:30 – 8:00 p.m. Dinner  
By George Café

8:00 – 10:30 p.m. Poster Session 3  
(ODD numbered posters staffed)  
HUB - Ballroom & 209AB

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**Saturday, June 26**

8:00 a.m. – 1:00 p.m. Registration/Information  
Meany Lobby

9:00 a.m. – 12:00 noon Plenary Session 5  
*Tim Nilsen, Chair*  
Meany Theater

9:00  
Rob Singer  
9:30  
Christopher Burge  
10:00 – 10:30 a.m. Break

10:30  
David Bartel  
11:00  
Eric Sontheimer  
11:30 – 12 noon  
Phil Zamore  
12:30 – 2:00 p.m. Lunch  
By George Café

2:00 – 5:30 p.m. Registration/Information  
Kane Hall Lobby

2:00 – 5:30 p.m. Concurrent Session 7  
**Regulation of 3’ End Processing and RNA Localization**  
*Ulrike Kutay, Chair*  
Abstracts 85 – 97  
Kane Hall - 120

Concurrent Session 8  
**RNA silencing pathways**  
*James Dahlberg, Chair*  
Abstracts 98 – 111  
Kane Hall - 130

5:30 – 6:30 p.m. Awards Ceremony  
Meany Theater

7:00 – 8:00 p.m. Reception  
HUB - Ballroom

8:00 – 11:00 p.m. Banquet and Dance  
HUB - Ballroom
ABSTRACT LISTING
(Note: Numbers refer to abstract numbers, not page numbers)

WEDNESDAY, JUNE 23, 2010: 2:00 PM – 3:45 P.M.
Concurrent Session 1, Part 1: Kane Hall 130
Part 1: Mechanisms of pre-mRNA Splicing
Jean Beggs, Chair
Abstracts 1 – 7

1 Dynamic and Ordered Assembly of Single Spliceosomes
Aaron Hoskins, Larry Friedman, Sarah Gallagher, Eric Anderson, Richard Wombacher, Virginia Cornish, Jeff Gelles, Melissa Moore

2 Monitoring Pre-mRNA and Spliceosome Dynamics in Real-Time using Single Molecule Fluorescence Microscopy
Ramya Krishnan, Mario Blanco, Christine Guthrie, John Abelson, Nils Walter

3 Dynamics of spliceosome assembly in living cells
Martina Huranova, Ivan Ivani, Ales Benda, Ina Poser, Martin Hof, Yaron Shav-Tal, Karla Neugebauer, David Stanek

4 A Functional Role of Prp16 in the First Catalytic Step in Proofreading the Branchpoint Sequence
Hsueh-Lien Liu, Chi-Kang Tseng, Chang-Hung Lin, Soo-Chen Cheng

5 Genome-wide in vivo RNA binding sites of key spliceosomal protein Prp8 identified using CLIP-seq
Jennie Li, Wenzheng Zhang, Rui Zhao

6 Implications Of The RNA Interactions Of Brr2p
Daniela Hahn, Grzegorz Kudla, Sander Granneman, David Tollervey, Jean Beggs

7 Widespread Recognition of 5’ Splice Sites by Base-Pairing to U1 snRNA Involving Bulged Nucleotides
Xavier Roca, Martin Akerman, Adrian Krainer

WEDNESDAY, JUNE 23, 2010: 3:45– 5:30 P.M.
Concurrent Session 1, Part 2: Kane Hall 130
RNA and Disease
Lucca Cartegni, Chair
Abstracts 8 – 14

8 Disease-Associated Mutations that Lead to Structural Rearrangements in Untranslated Regions of RNA
Matthew Halvorsen, Lauren Neulander, Joshua Martin, Alain Laederach

9 RNA Splicing Changes in Mouse Models of SCA1
Smita Agrawal, Huda Zoghbi, Harry Orr

10 Role of RNA Processing in the Pathogenesis of Amyotrophic Lateral Sclerosis
Magdalini Polymenidou, Clotilde Lagier-Tourenne, Kasey Hutt, Tiffany Liang, Shuo-Chien Ling , Gene W. Yeo, Don W. Cleveland

11 Small Molecule Modulation of HIV-1 RNA Metabolism
Raymond Wong, Alan Cochrane

12 Minor introns are differentially spliced in cells derived from SMA patients
Nawal Boulisfane, Henry Neel, Florence Rage, Johann Soret, Remy Bordonne

13 Antisense Correction of SMN2 Splicing in the Central Nervous System of Mouse Models of Spinal Muscular Atrophy
Yimin Hua, Kentaro Sahashi, Gene Hung, Frank Rigo, Marco Passini, C. Frank Bennett, Adrian Krainer
Induction of antagonistic soluble Receptor Tyrosine Kinases by Intronic PolyA Activation
Sandra Vorlova, Erik Henke, Luca Cartegni

WEDNESDAY, JUNE 23, 2010: 2:00 PM – 5:30 P.M.
Concurrent Session 2: Kane Hall 120
Ribosomes Structure, Function, and Biogenesis
Marina Rodnina, Chair
Abstracts 15 – 28

15 Molecular Model Of Two Eukaryotic 80S Ribosome Based On A 5.5 Å Cryo-EM Map
Alexander Jarasch, Jean-Paul Armache, Elizabeth Villa, Andreas Anger, Thomas Becker, Shashi Bhushan, Fabrice Jossinet, Michael Habeck, Johannes Soeding, Thorsten Mielke, Otto Berninghausen, Eric Westhof, Daniel Wilson, Roland Beckmann

16 The Way to Ribosome GTPase Crystal Structure and The Structure of Elongation Factor G Bound to Ribosome
Yong-Gui Gao, Maria Selmer, Albert Weixlbaumer, Ann Kelley, Venki Ramakrishnan

17 Insights into Translational Termination from Crystal Structures of the 70S Ribosome Bound to Release Factor
Hong Jin, Albert Weixlbaumer, Cajetan Neubauer, Rebecca Voorhees, Sabine Petry, Ann Kelley, David Loakes, Venki Ramakrishnan

18 The Crystal Structure of the Signal Recognition Particle in Complex with its Receptor
Sandro Ataide, Nikolaus Schmitz, Ailong Ke, Jennifer Doudna, Nenad Ban

19 Two Steps for mRNA Selection During Translation Initiation in Bacteria
Pohl Milon, Marina Rodnina

20 Stm1 Promotes Translation Repression By Stalling 80S Ribosomes In Saccharomyces cerevisiae.
Vidya Balagopal, Roy Parker

21 The HCV IRES Pseudoknot Positions the Initiation Codon on the 40S Ribosomal Subunit
Katherine Berry, Shruti Waghray, Jennifer Doudna

22 Translational Enhancement by 5' Untranslated Regions
Wendy Gilbert, Maria Rojas Duran, Mary Thompson

23 A first protein inventory of human ribosome biogenesis reveals an essential function of exportin 5 in 60S subunit export
Thomas Wild, Peter Horvath, Emanuel Wyler, Barbara Widmann, Ivo Zemp, Gabor Csucs, Elsebet Lund, Ulrike Kutay

24 Quantitative Proteomic analysis of Ribosome Assembly and Turnover In Vivo
Zahra Shajani, Michael Sykes, Edit Sperling, James Williamson

25 Cryo-EM Structure of a Small Ribosomal Subunit Assembly Intermediate from Saccharomyces cerevisiae
Bethany Strunk, Cherisse Loucks, Min Su, Justin Schilling, Melody Campbell, Georgios Skiniotis, Katrin Karbstein

26 Evolutionarily Conserved Function of RRP36 in Early Cleavages of the Pre-ribosomal RNA and Production of the 40S Ribosomal Subunit
Marie GERUS, Chrystelle BONNART, Michèle CAIZERGUES-FERRER, Yves HENRY, Anthony HENRAS

27 Defining the Pathway of Cytoplasmic Maturation of the 60S Ribosomal Subunit
Kai-Yin Lo, Zhihua Li, Cyril Bussiere, Stefan Bresson, Edward Marcotte, Arlen Johnson

28 A New U3 snoRNA:pre-rRNA Base-pairing Interaction in Yeast Revealed by in Vivo Chemical Probing
Laura Dutca, Susan Baserga
THURSDAY, JUNE 24, 2010: 2:00 – 5:30 P.M.
Concurrent Session 3: Kane Hall 130
Alternative Splicing and Splicing Regulatory Networks
Don Rio, Chair
Abstracts 29 – 42

29 An alternative large subunit of U2AF regulates tissue-specific alternative splicing events in the Drosophila testes
Jefferson Taliaferro, Nehemiah Alvarez, Marco Blanchette, Donald Rio

30 HnRNP L versus hnRNP L-like: Mutational Analysis of Functional Domain Structure and Identification of Target Genes by RNA-Sequencing and CLIP
Oliver Rossbach, Marco Preussner, Inna Grishina, Silke Schreiner, Monika Heiner, Lee-Hsueh Hung, Albrecht Bindereif

31 NMR Structure Of hnRNP L In Complex With RNA
Markus Blatter, Christophe Maris, Frédéric Allain

32 FOX2 is a Mitogen Responsive Alternative Splicing Factor
Paul Boutz, Mohini Jangi, Scott Carlson, Forest White, Phillip Sharp

33 Genetic Ablation of Fox-1 in the Brain Modifies Alternative Splicing of Neuronal Target Exons and Results in Dentate Gyrus Hyperactivity and Spontaneous Seizures
Lauren Gehman, Peter Stoiol, Jamie Maguire, Lily Shiue, Manuel Ares Jr., Istvan Mody, Douglas Black

34 Ptbp2 Represses Exon Splicing Events In The Mouse Brain And Is Required For Postnatal Survival
Donny Licatalosi, John Fak, Aldo Mele, Chaolin Zhang, Robert Darnell

35 Comprehensive determination of an ESRP-regulated epithelial splicing network that is suppressed during the Epithelial-Mesenchymal Transition
Kimberly Dittmar, Claude Warzecha, Juw Won Park, Shihao Shen, Karine Amirikian, Peng Ziang, Yi Xing, Russ Carstens

36 Using RNAi and RNA-Seq to Identify Alternative Exons Regulated by Individual RNA Binding Proteins and their Associated Regulatory Motifs
Li Yang, Angela Brooks, Michael Duff, Kasper Hansen, Susan Celniker, Sandrine Dudoit, Steven Brenner, Brenton Graveley

37 Reconstruction of Splicing Regulatory Networks from High Throughput Transcriptome Data
Panagiotis Papasaikas, Arvind Rao, Peter Huggins, A. Javier Lopez

38 Systematic analysis of the role of neural-specific alternative exons in the regulation of a protein-protein interaction network
Jonathan Ellis, Miriam Barrios-Rodiles, John Calarco, Qun Pan, Daniel Tong, Jeffrey Wrana, Benjamin Blencowe

39 Functional Interactions Between Splicing Factors and Chromatin Remodelers in S. pombe Revealed by Genome-wide Epistatic Mini-array Profiling
Kristin Patrick, Nevan Krogan, Christine Guthrie

40 A High-Throughput, Reverse Genetic Approach to Identify Global Connections with the Pre-mRNA Splicing Pathway
Laura-Oana Bud, Nevin Sabet, Jeffrey Pleiss

41 Pre-mRNA splicing enhances co-transcriptional H3K36 trimethylation
Sergio de Almeida, Ana Grosso, Jean-Christophe Andrau, Frederic Koch, Pierre Ferrier, Maria Carmo-Fonseca

42 Transcription and Splicing of Large Human Genes
Jarnail Singh, Richard Padgett
THURSDAY, JUNE 24, 2010: 2:00 – 3:45 P.M.
Concurrent Session 4: Kane Hall 120
Part 1: Transfer RNA Metabolism
Eric Phizicky, Chair
Abstracts 43 – 50

43 Structural basis for translational fidelity ensured by transfer RNA lysidine synthetase
Kotaro Nakanishi, Luc Bonnefont, Satoshi Kimura, Tsutomu Suzuki, Ryuichiro Ishitani, Osamu Nureki

44 A Tale of Two Editing Domains: Molecular Basis of Substrate Specificity of Bacterial Prolyl-tRNA Synthetase and YbaK
Sandeep Kumar, Mom Das, Christopher Hadad, Karin Musier-Forsyth

45 Kinetic And Thermodynamic Framework For Gln-tRNA<sup>qn</sup> Synthesis By a Two-Step Pathway in Archaea
Hari Bhaskaran, John Perona

46 A Novel Role for tRNA<sup>guanylyl</sup>transferase (Thg1) Family Enzymes in Mitochondrial 5′-tRNA Editing
Maria Abad, Yicheng Long, Jonatha Gott, Michael Gray, Jane Jackman

47 Box C/D snoRNA-directed rRNA modification is enhanced by additional conserved base-pairing adjacent to the methylation target sites
Rob van Nues, Sander Granneman, Grzegorz Kudla, Kate Sloan, Matthew Chicken, David Tollervey, Nicholas Watkins

48 Bacterial Proteins Pnkp and Hen1 Constitute a Novel RNA Repair and Modification System
Chio Mui Chan, Chun Zhou, Raven Huang

49 The Rapid tRNA Decay Pathway Monitors the Structural Integrity of Mature tRNAs
Joseph Whipple, Elizabeth Lane, Sonia D'Silva, Eric Phizicky

50 Genome-Wide Investigations of Translating mRNAs to Study the Cellular Functions of the tRNA Retrograde Pathway in S. cerevisiae
Hui-Yi Chu, Anita Hopper

THURSDAY, JUNE 24, 2010: 3:45 – 5:00 P.M.
Concurrent Session 4: Kane Hall 120
Part 2: RNA Modulation of RNA Synthesis
Torben Jensen, Chair
Abstracts 51 – 56

51 Molecular Recognition and Transcriptional Regulation by the Lysine Riboswitch
Andrew Garst, Robert Batey

52 The Glycolytic Pathway: a Paradigm to Study Hidden Transcription in Yeast
Helen Neil, Frank Feuerbach, Christophe Malabat, Rajani Gudipatti, Alain Jacquier

53 Differential Role of the Two Bacillus subtilis 6S RNAs
Benedikt Beckmann, Roland Hartmann

54 Controlling the activity of the host P-TEFb by the HIV Tat
Lisa Muniz, Beata Jady, Bettina Ughy, Sylvain Egloff, Tamas Kiss

55 Recruitment and dissociation of Nrd1 CID at RNA Polymerase II C-terminal domain
Karel Kubicek, Hana Cerna, Richard Stefl

56 The 5′-3′ exonuclease Rat1p functions during transcription elongation
Torben Heick Jensen, Silvia Jimeno-González, Francisco Malagon, Line Haaning
57 Genome-wide Exon Junction Complex Occupancy Sites in Human Cells
Guramrit Singh, Alper Kucukural, Zhiping Weng, Melissa Moore

58 Drosophila Exon-Exon Junction Complexes (EJC) assemble only on a subset of spliced mRNAs
Nazmul Haque, Marco Blanchette

59 SMG6 Interacts with the Exon Junction Complex via Two Conserved EJC-binding Motifs (EBMs), which are Required for Nonsense-mediated mRNA Decay
Isao Kashima, Stefanie Jonas, Elisa Izaurralde

60 mRNP Disassembly by the Upf1 ATPase Allows Turnover of mRNPs Targeted for NMD
Tobias Franks, Guramrit Singh, Jens Lykke-Andersen

61 Translational readthrough antagonizes 3’ UTR length-dependent Upf1 recruitment and NMD
J. Robert Hogg, Stephen Goff

62 The Convergence of Two Negative Post-Transcriptional Pathways Elicits Activation of Gene Expression
Rachid Karam, Ivone Bruno, Lulu Huang, Anjana Bhardwaj, Miles Wilkinson

63 Rampant and Regulated Alternative Splicing in S. cerevisiae
Tadashi Kawashima, Stephen Douglass, Matteo Pellegrini, Guillaume Chanfreau

64 Widespread Co-Translational Degradation of Cellular mRNAs by the Herpesviral SOX Protein Involves the Cellular Xrn1 Ribonuclease
Sergio Covarrubias, Marta Gaglia, Gagandeep Kumar, Britt Glaunsinger

65 A Split Active Site Couples Cap Recognition by Dcp2 to Activation
Stephen Floor, Brittnie Jones, Gail Hernandez, John Gross

66 Functional Cross-talk between the Poly(A) Polymerase Trf4p and the RNA Helicase Mtr4p in the TRAMP Complex during Adenylation and Unwinding
Huijue Jia, Xuying Wang, Fei Liu, James Anderson, Eckhard Jankowsky

67 Structure of Mtr4 reveals features of the DExD helicases involved in exosome-mediated RNA degradation
John Weir, Jendrik Hentschel, Elena Conti

68 Analysis of E. coli RNase E and RNase III Activity in vivo Using High-density Tiling Arrays
Mark Stead, Sarah Marshburn, Lourdes Pe a Castillo, Debashish Ray, Harm Van Bakel, Tim Hughes, Sidney Kushner

69 The La Domain of La-Related Protein-4 (LARP4) Binds Poly(A) and its Variant PAM2 Motif Interacts With PABP to Promote mRNA Stability
Ruiqing Yang, Sergei Gaidamakov, Amanda Crawford, Richard Maraia

70 Stacking Interactions in PUF–RNA Complexes
Yvonne Koh, Laura Opperman, Yeming Wang, Chen Qiu, Leah Gross, Traci Hall, Marvin Wickens

71 High-Throughput Mapping of RNA-RNA Interactions in Living Yeast
Grzegorz Kudla, Sander Granneman, Daniela Hahn, Jean Beggs, David Tollervey
Femtoscale RNA Structure Analysis by SHAPE and Ultra-Sensitive Capillary Electrophoresis
Jacob Grohman, Sumith Kottegoda, Nancy Allbritton and Kevin M. Weeks

Structural and Functional Studies of Cooperative Ligand Binding by the Glycine Riboswitch
Alexander Sereganov, Lili Huang, Dinshaw Patel

Kinetics of Metabolite-activated glmS Riboswitch Self-cleavage in Yeast
Peter Watson, Martha Fedor

A trans-Acting Riboswitch Controls Expression of the Virulence Regulator PrfA in Listeria monocytogenes
Edmund Loh, Olivier Dussurget, Jonas Gripenland, Karolis Vaitkevicius, Teresa Tiensuu, Pierre Mandin, Francis Repoila, Carmen Buchrieser, Pascale Cossart, Jörgen Johansson

Self-cleaving ribozymes in retrotransposition
Dana Ruminski, Chiu-Ho Webb, Nathan Riccitelli, Andrej Luptak

The Structural Basis of RNA-Catalyzed RNA Polymerization
David Shechner, David Bartel

Single-Molecule Analysis of Mss116-Mediated Group II Intron Folding
Krishanthi Karunatilaka, Amanda Solem, Anna Pyle, David Rueda

ATP Utilization by the DEAD-Box Protein CYT-19 During Refolding of a Misfolded Group I Intron Ribozyme
Inga Jarmoskaite, Rick Russell

Recognition of Oligo(A) RNA by a Viral RNA Clamp
Rachel Mitton-Fry, Jimin Wang, Suzanne DeGregorio, Thomas Steitz, Joan Steitz

Structural Basis For Substrate Placement By An Archaeal Box C/D Ribonucleoprotein Particle
Ruizing Wang, Song Xue, Rebecca Terns, Michael Terns, E. Stuart Maxwell, Hong Li

A New Trick by RNA: Quaternary Self-assembly in Prohead RNA of Bacteriophage ø29
Fand Ding, Changrui Lu, Anderson Dwight, Paul Jardine, Shelley Grimes, Ailong Ke

Structure of a bacterial ribonuclease P holoenzyme in complex with tRNA
Nicholas Reiter, Amy Osterman, Alfredo Torres-Larios, Kerren Swinger, Tao Pan, Alfonso Mondragon

Structural Organization of P3 Domains of Eukaryotic RNases P/MRP
Anna Perederina, Olga Esakova, Chao Quan, Elena Khanova, Andrey Krasilnikov

SATURDAY, JUNE 26, 2010: 2:00 – 5:00 P.M.
Concurrent Session 7: Kane Hall 120
Regulation of 3’ End Processing and RNA Localization
Ulrike Kutay, Chair
Abstracts 85 – 97

Live Cell Imaging of Cell Cycle Dependent Telomerase RNA Dynamics.
Franck Gallardo, Laterreur Nancy, Emmanuelle Querido, Pascal Chartrand, Raymund Wellinger

Yeast Telomerase: Towards a New Model for Ku Heterodimer - TLC1 RNA Interaction
Jennifer Pfingsten, Andrew Dalby, Thomas Cech

Histone locus bodies: Novel components involved in histone pre-mRNA processing and cell cycle regulation
William Marzluff, Brandon Burch, Anne White, Deirdre Tatomer, Ashley Godfrey, Pam Gasdaska, Zbigniew Dominski, Robert Duronio

Structure of the Homodimerization Domain of CstF-50
María Moreno-Morcillo, Cameron Mackereth, Lionel Minvielle-Sebastia, Sébastien Fribourg

Structural Basis of UGUA Recognition by the Human Cleavage Factor I_m (CFIm) and Implications for a Regulatory Role in mRNA 3’ Processing
Qin Yang, Gregory Gilmartin, Sylvie Doublé
A Non-splicing Function For U1 snRNP Required For Producing Full-length Transcript  
Daisuke Kaida, Michael Berg, Gideon Dreyfuss

HnRNPC1/C2 Tetramer Measures RNA Length prior to RNA Export from the Nucleus  
Asako McCloskey, Mutsuhito Ohno

Structural and functional analysis of the mRNA export factors Dbp5 and Gle1  
Ben Montpetit, Nathan Thomsen, Kara Helmke, Markus Seeliger, James Berger, Karsten Weis

Gle1 is a Versatile Regulator of DEAD-Box Proteins in mRNA Export and Translation  
Timothy Bolger, Susan Wente

Role of the ESCRT II complex in microtubule-dependent mRNA localization in Xenopus  
Michael Blower, Joshua Plant

Identification of Localized mRNAs by Purification of Motor Proteins and Microarrays  
Jason Casolari, Patrick Brown

ZBP1 Recognition Of The β-actin Zipcode Induces RNA Looping  
Jeffrey Chao, Vivek Patel, Yury Patskovsky, Matthew Levy, Steven Almo, Robert Singer

The “G-quartet” RNA binding site of the Fragile X Mental Retardation Protein is a novel zipcode for dendritic mRNA transport  
Murugan SUBRAMANIAN, Florence RAGE, Ricardos TABET, Eric FLATTER, Jean-Louis MANDEL, Hervé MOINE

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SATURDAY, JUNE 26, 2010: 2:00 – 5:00 P.M.
Concurrent Session 8: Kane Hall 130
RNA Silencing Pathways  
James Dahlberg, Chair  
Abstracts 98 – 111

Self vs. non-self discrimination during CRISPR immunity against horizontal gene transfer  
Luciano Marraffini, Erik Sontheimer

Competition among small RNAs in Escherichia coli  
Kyung Moon, Susan Gottesman

Active RNA Cycling on Hfq  
Aurelie Fender, Johan Elf, E. Gerhart Wagner

Comparative RNA-seq Reveals Small RNA Diversity within the Hyperthermophilic Genus Pyrobaculum  
David Bernick, Patrick Dennis, Aaron Cozen, Andrew Uzilov, Lauren Lui, Todd Lowe

Dicer’s Helicase Domain Mediates Processive Cleavage of dsRNA in Response to Specific Duplex Termini  
Noah Welker, Tuinh Maity, Xuecheng Ye, Joseph Aruscavage, Ammie Krauchuk, Qinghua Liu, Brenda Bass

The Inside-Out Mechanism of Dicers from Budding Yeasts  
David Weinberg, Kotaro Nakanishi, Dinshaw Patel, David Bartel

The double stranded RNA-dependent ATPase DRH-3: Insight into its Role in RNA silencing in Caenorhabditis elegans  
Christian Matranga, Anna Pyle

RDE-8 is a Novel Protein with a Conserved RNase Domain Required for RNAi-related Pathways in Caenorhabditis elegans  
Hsin-Yue Tsai, Chun-Chieh Chen, James Moresco, Weifeng Gu, John Yates III, Craig Mello

Structural Basis For 5’-Nucleotide Base-Specific Recognition Of Guide RNA By hAGO2  
Filipp Frank, Nahum Sonenberg, Bhushan Nagar

Target RNA-directed Destruction of Small Silencing RNAs  
Stefan Ameres, Michael Horwich, Jui-Hung Hung, Jia Xu, Zhiping Weng, Phillip Zamore
Lack of RNAi in X. laevis oocytes and early embryos due to a deficiency of Ago proteins
Elsebet Lund, Michael Sheets, Suzanne Imboden, James Dahlberg

Mouse oocyte growth is accompanied by reduction of microRNA activity and P-body disassembly
Matyas Flemr, Jun Ma, Radek Malik, Paula Stein, Philipp Berninger, Mihaela Zavolan, Richard Schultz, Petr Svoboda

DROSHA/DGCR8 sequestration by expanded CGG repeats leads to global micro-RNA processing alteration in FXTAS patients
Chantal Sellier, Rob Willemsen, Nicolas Charlet Berguerand

Viral MicroRNAs: Non-Canonical from Transcription to Processing
Kevin Diebel, Linda van Dyk

POSTERS
3’ End Formation
Abstracts 112 – 129

Multiple Factors Determine tRNA 3’ Maturation by RNase R of Mycoplasma genitalium
Ravi Kumar Alluri, Zhongwei Li

NMR Study of Nrd1 CID in Complex with Ser5-phosphorylated CTD of RNA Polymerase II
Hana Cerna, Karel Kubicek, Richard Stefl

The Polyadenylation Inhibitor Cordycepin Targets Unstable mRNAs and Blocks the Inflammatory Response
Hedda Meijer, Alexander Kondrashov, Asma Khurshid, Adeline Barhet-Barateig, Linhua Pang, Cornelia de Moor

hnRNP H/F bind to a G-quadruplex of the p53 pre-mRNA to regulate its 3’ end processing during DNA damage
Adrien Decorsiere, Anne Cayrel, Stéphan Vagner, Stefania Millevoi

Integrator 4 is a Critical Component of the Integrator Complex Required for snRNA 3’ End Formation and Development
Nader Ezzeddine, Jiandong Chen, Todd Albrecht, and Eric Wagner

The Structural Characterization of Cleavage factor I
James Gordon, Sergei Shikov, Mike Rigney, Nikolaus Grigorieff, Claire Moore, Andrew Bohm

Analysis of Polyadenylation Regulation in Rous Sarcoma Virus
Stephen Hudson, Mark McNally

Nuclear Deadenylation/Polyadenylation/Tumor Suppressor Factors Regulate 3’ Processing in Response to DNA Damage
Xioakan Zhang, Murat Cevher, Anders Virtanen, Frida Kleiman

The Impact of Cis-acting Polyadenylation Elements and RNA Structure on Alternative Polyadenylation
Sarah Darmon, Ashley Cornett, Lisa Hague-Canto, Wencheng Li, Ju Youn Lee, Bin Tian, Carol Lutz

Structure of a Minimal Rna14/Rna15 Heterodimer From the Yeast CF IA Complex
Maria Moreno Morcillo, Lionel Minvielle-Sébastia, Sébastien Fribourg, Cameron Mackereth

Dual Function for the Yeast Clp1 Protein
Frédérique Maurice, Raphaël Haddad, Céline Douat-Casassus, Nicolas Viphakone, Sébastien Fribourg, Lionel Minvielle-Sébastia

Functional analysis of conserved cis-acting elements within the antisense overlap between two nuclear receptor genes
Stephen Munroe, Corey Nemec, Tessa Hoff, Michael Brown, Brandon Rindfleisch, Chao Zhang

The Role of the Putative RNase III Mrpl3 and the Mitochondrial Degradosome in Mitochondrial RNA Processing
Kevin Roy, Guillaume Chanfreau

Interactions of Symplekin, CstF-64, and CstF-77. Implications for Localisation, Stability and Function
Marc-David Ruepp, Christoph Schweinruber, Nicole Kleinschmidt, Daniel Schümperli
126 Structural and Enzymatic Properties of a Novel RNR Family Nuclease from Deinococcus Radiodurans
Brad Schmier, Murray Deutscher, Arun Malhotra

127 Transcriptome-wide Quantitative Analyses Of RNA Polyadenylation In Mouse Embryonic Stem Cells And Differentiated Cells Using Poly(A) Site Deep Sequencing (PAS-Seq)
Peter Shepard, Eun-A Choi, Jente Lu, Lisa Flanagan, Klemens Hertel, Yongsheng Shi

128 The Poly(rc)-Binding Protein αCP2 is a Noncanonical Mediator of Cytoplasmic Polyadenylation in the Xenopus laevis Embryo
Melanie Vishnu, Marina Sumaroka, Peter Klein, Stephen Liebhaber

129 Integrator 12 is a Phosphoprotein Involved in snRNA Biosynthesis
Jiandong Chen, Nader Ezzeddine, Todd Albrecht, Eric Wagner

POSTERS
Bioinformatics
Abstracts 130 – 153

130 Structural Analysis of RNA Base Triples: Classification, Prediction, and Effects of Mutations
Amal S. Abu Almakarem, Anton Petrov, Craig Zirbel, Neocles Leontis

131 Modular Evolution and Increase of Functional Complexity in RNA
Carlos Briones, Michael Stich, Susanna Manrubia

132 Bioinformatic approaches to finding cis-acting mRNA elements
Chris Brown, Tracy Wilkinson, Joshua Gagnon, Hao Yang, Stewart Stevens, Cushla McKinney, Sylvia Chen, Augustine Chen

133 A Statistical Model for Comparing Transcriptomes at the Individual Transcript Isoform Level
Sika Zheng, Liang Chen

134 Large-scale Transposition of tRNA Introns in the Archaeal Order Thermoproteales
Kosuke Fujishima, Junichi Sugahara, Masaru Tomita, Akio Kanai

135 Information Statistical Analysis to Uncover trm10 Modification Determinants in tRNAs in Yeast
Katherine Harris, Jane Jackman, David Ardell

136 Identification and Analysis of Fungal tRNase Z Genes, Homologs of the Human Putative Prostate-Cancer Susceptibility Gene ELAC2 Encoding tRNA 3'-end Processing Enzyme
Wei Zhao, Jing Yang, Yingying Yu, Ying Huang

137 Standardization and Classification of Single Nucleotide Resolution Nucleic Acid Structure Mapping (SNRNASM) Experiments.
Alain Laederach, Stanislav Bellaousov, Amanda Birmingham, Lauren Davis-Neulander, Neocles Leontis, David Mathews, Philippe Rocca-Serra, Jesse Stombaugh, Kevin Weeks, Craig Zirbel, Rob Knight

138 Identifying Splicing Elements by Genomic Word Distributions
Kian Lim, Ben Raphael, William Fairbrother

139 A Statistical Analysis of the Folded Ensemble of Human UTRs
Joshua Martin, Matt Halvorsen, Alain Laederach

140 RNAcontext: A New Motif Method for Learning the Sequence and Structure Binding Preferences of RNA-binding Proteins
Hilal Kazan, Debashish Ray, Esther Chan, Timothy Hughes, Quaid Morris

141 RiceRBP: A Database Of Experimentally Identified RNA-binding Proteins in Oryza sativa
Robert Morris, Kelly Doroshenk, Andrew Crofts, Nicholas Lewis, Thomas Okita, John Wyrick

142 RNA09: Non-Redundant Dataset for Conformation Analysis
Laura Murray, Gary Kapral, Swati Jain, Jane Richardson

143 Constructing a Library of RNA 3D Motifs
Anton Petrov, Craig Zirbel, Neocles Leontis
144 Characterization of DGCR8 binding sites using CLIP-Seq data
Mireya Plass, Sara Macías, Javier Cáceres, Eduardo Eyras

145 New Software for Designing Modified Oligonucleotides and Eliminating siRNA Off-Target Effects
Norman Watkins, Marc Korn, William Kennelly, Kelly Damm-Ganamet, Astrid Tuin, Mike Tsay, John SantaLucia, Jr.

146 An RNA kink-turn database
Kersten Schroeder, Scott McPhee, Jonathan Ouellet, David Lilley

147 PETcofold: Prediction of Conserved RNA-RNA Cofolding and RNA-RNA Interaction Sites
Stefan Seemann, Andreas Richter, Tanja Gesell, Rolf Backofen, Jan Gorodkin

148 NA-CAD Software for Analysis and 3D Structure Prediction of RNA
Fredrick Sijenyi, Kelly Damm-Ganamet, Pirro Saro, Zheng Ouyang, John SantaLucia, Jr.

149 Abstract Withdrawn

150 Towards Computational Prediction of MicroRNA Function and Activity
Igor Ulitsky, Louise Laurent, Ron Shamir

151 Evolution of G-rich Intronic Splicing Enhancers
Rodger Voelker, Andy Berglund

152 RNA World - A distributed supercomputer to advance RNA research
Michael Weber, Uwe Beckert, Nico Mittenzwey, Volker Hatzenberger, Martin Bertheau

153 Using the RNA Ontology for Data Annotation and Queries
Michel Dumontier, Neocles Leontis, Craig Zirbel

POSTERS
Chemical Biology of RNA
Abstracts 154 – 162

154 Platinum Complexes as Drugs and Tools in RNA Chemical Biology
Erich Chapman, Victoria DeRose

155 Quantification of Cisplatin-RNA Binding in Saccharomyces cerevisiae by ICP-MS
Alethia Hostetter, Victoria DeRose

156 Substituent-substituent interactions in RNA base stacking and DNA/RNA intercalator binding
Charles Johnson, Laura Hardebeck, Michael Lewis, Brent Znosko

157 Effects of RNA-Binding Peptoid Display Modules On Uptake, Localization and Toxicity in Mammalian Cells
Melissa Lee, Matthew Disney

158 Amelioration of Oxidative Damage in RNA by Pseudouridine
Meredith Newby Spano, Robert Hampton Andrews, Jessica Graham, Kristine Bryson Schaeffer, Hsiao Sabina Wang, Julia Brumaghim

159 Ribosomal RNA targeting by the antitumor drug, cisplatin
Maire Osborn, Victoria DeRose

160 Click chemistry with RNA: Labeling and Ligations
Eduardo Paredes, Subha Das

161 Modified Phospho-amino Sugars and the Activation of the GlmS Ribozyme; Investigation of the Mechanism and Hydrogen Bond Interactions
Jeff Posakony, Adrian Ferre-D’Amare

162 Structural Behavior of the Bacterial Ribosomal A-site RNA using SHAPE Chemistry and NMR
Chandar Thakur, Kwaku Dayie

xxii
163 **Quantification of Pseudouridine in RNA**  
Balasubrahmanyam Addepalli, Patrick Limbach

164 **Optimizing siRNA by Chemical Engineering**  
Jesper Bramsen, Jyoti Chattopadhyaya, Marino Zerial, Joachim Engels, Piet Herdwijn, Jesper Wengel, Jørgen Kjems

165 **Engineering a Novel class of Enzymes: Artificial Site-specific RNA Endonucleases**  
Rajarshi Choudhury, Zefeng Wang

166 **Selection of Archaeal Endoribonucleases Optimized for Expression in Mammalian Cells**  
Giancarlo Deidda, Sabrina Putti, Nicoletta Rossi, Glauco Tocchini-Valentini

167 **Probing Secondary Structures of Spin-Labeled RNA by Pulsed EPR Spectroscopy**  
Giuseppe Sicoli, Falk Wachowius, Marina Bennati, Claudia Hoebartner

168 **Expressing RNA Aptamers to Increase Drug Efficacy**  
Muslum Ilgu, Khalid Boushaba, Howard Levine, Marit Nilsen-Hamilton

169 **A Novel RNA-based Method for Real-time Imaging of Gene Activity via IMAGEtags (Intracellular Multiaptamer Genetic tags)**  
Muslum Ilgu, Ilchung Shin, Eirik Haarberg, Vinayak Gupta, George Kraus, Marit Nilsen-Hamilton

170 **Selection of RNA Aptamers Targeting Mouse Embryonic Stem Cells**  
Toshiro Iwagawa, Shoji Ohuchi, Sumiko Watanabe, Yoshikazu Nakamura

171 **A Novel Tool For Capture and Investigation Of Nascent Transcriptome**  
Kapil Kumar, Brian Agnew

172 **An Experimentally Generated Fitness Landscape of a Small RNA Ligase Ribozyme**  
Jason Pitt, Adrian Ferré-D’Amaré

173 **Genome-Wide Intron Discovery via High Throughput Sequencing of Enriched Lariat RNAs**  
Ali Awan, Amanda Manfredo, Jeffrey Pleiss

174 **Evaluation of the Agilent Bioanalyzer 2100 for Quality Determination of IVT RNA**  
Jacoba Slagter-Jäger, Charles Nicolette, Irina Tcherepanova

175 **Making the Most of Cryogenic Electron Microscopy as a Tool to Analyze the Structure of Spliceosomes**  
M. Elizabeth Stroupe, Nikolaus Grigorieff

176 **A High-Throughput Experimental Approach to RNA Secondary Structure Prediction**  
Jason Underwood, Andrew Uzilov, Sol Katzman, Courtney Onodera, Jacob Mainzer, David Mathews, Sofie Salama, Todd Lowe, David Haussler

177 **FragSeq: High-Throughput Experimental Screen for Structured RNAs in a Complex Transcriptome.**  
Andrew Uzilov, Jason Underwood, Sol Katzman, Courtney Onodera, Jacob Mainzer, David Mathews, Sofie Salama, David Haussler, Todd Lowe

178 **Towards high resolution structure determination of large RNAs in solution**  
Jinbu Wang, Xiaobing Zuo, Yun-Xing Wang

179 **RIPseq and CLIPseq analysis of SLBP RNA Ligands**  
Lionel Brooks, Michael Whitfield
180 Evidence for a Splicing-Dependent Transcriptional Checkpoint in Yeast
Ross Alexander, Steven Innocente, David Barrass, Jean Beggs

181 Identification and Characterization of a Mutually Exclusive Alternative Splicing Event that Promotes Embryonic Stem Cell Self-renewal and Somatic Cell Reprogramming
Mathieu Gabut, Payman Tehrani, Dave O’Hanlon, Valentina Slobodeniuc, Knut Woltjen, Raheem Peerani, Timothy Hughes, Andras Nagy, Peter Zandstra, Jeff Wrana, Benjamin Blencowe

182 Elucidating the Role of the *Saccharomyces cerevisiae* Cap Binding Complex (yCBC) at the Interface of Transcription and RNA Processing
Julia Claggett, Tracy Johnson

183 Characterization of Conditional prp43 Alleles: Searching for Substrate Specificity
Jennifer Hennigan, Scott Stevens

184 Meiotically-Induced Coupling of Transcript Architecture with uORF Control in *S. cerevisiae*
Sara Hurtado, Karen Kim Guisbert, Erik Sontheimer

185 The “SAGA” of Co-transcriptional Spliceosome Assembly: A Novel Role for Dynamic Histone Acetylation in U2 snRNP Recruitment and Spliceosome Dynamics
Felizza Gunderson, Tracy Johnson

186 MicroRNAs Coordinate An Alternative Splicing Network During Postnatal Heart Development
Auinash Kalsotra, Kun Wang, Pei-feng Li, Thomas Cooper

187 Exploring the Transcription-Splicing Co-Regulatory Network
Idit Kosti, Yael Mandel-Gutfreund

188 A Role for Npl3 in the Coordination of Transcription and mRNA Splicing
Erica Moehle, Kinisha Gala, Ian London, Christine Guthrie, Tracy Kress

189 AtCPSF30, a Polyadenylation Factor Involved in Multi-developmental Processes, is Functionally Associated with Calmodulin
Man Liu, Ruqiang Xu, Arthur Hunt, Qingshun Li

190 Regulation of OXT6 Gene, Encoding a Polyadenylation Factor and a Potential Splicing-related Protein, through Alternative Splicing and Polyadenylation
Zhaoyang Liu, Qingshun Li

191 A role for DEAD Box RNA helicases in the mammalian circadian clock
Kiran Padmanabhan, Maria Robles, Charles Weitz

192 nSR100 regulates an alternative splicing event in REST/NRSF to control neural-specific gene expression at the transcriptional level
Bushra Raj, John Calarco, Qun Pan, Dave O’Hanlon, Benjamin Blencowe

193 Alternative Splicing and NMD in Arabidopsis
Craig Simpson, Maria Kalyna, Dominika Lewandowska, Branislav Kusenda, John Fuller, Linda Milne, Jim McNicol, Gillian Clark, Andrea Barta, John Brown

194 Genome-Wide Analysis of Gene Expression Processes Using a Sensitive Fluorescent Reporter in Yeast
Matthew Sorenson, Scott Stevens

195 Deciphering the Role of the DEAD-box Protein Dbp2 in Regulation of Gene Expression
Sara Ess, Elizabeth Tran

196 Transcriptional and Post-transcriptional Regulation of the Musashi1 RNA-binding Protein
Dat Vo, Mei Qiao, Uthra Suresh, Derek Murphy, Tarea Burton, Suzanne Burns, Myriam Gorospe, Raymond Stallings, Luiz Penalva
197 Structural Basis for the RNA- and DNA-Dependent Activities of a Multifunctional RNA polymerase
   Antti Aalto, Minna Poranen, Jonathan Grimes, David Stuart, Dennis Bamford

198 Identification of MicroRNA Targets Using MicroRNA Modulation Techniques and High-throughput Gene Expression Detection
   Allison St. Amand, Maren Mayer, Emily Anderson, Kevin Sullivan, Barbara Robertson, Matthew Brenton, Anja Smith, Devin Leake, Annaleen Vermeulen

199 Synergism between RNA interference and U1 inhibition and its application for HBV infection
   Lorea Blazquez, Amaya Abad, Xabier Abad, Nerea Razquin, Puri Fortes

200 Structural analysis of an eukaryotic Argonaute protein
   Andreas Boland, Felix Tritschler, Oliver Weichenrieder, Elisa Izaurralde

201 Effect of Platinum Modification of siRNAs
   Hanna Hedman, Sofi Elmroth

202 Identification of protein factors associated with uridylated pre-let-7
   Minju Ha, Inha Heo, Chirlmin Joo and V. Narry Kim

203 GW182 Proteins Promote miRNA-mediated Gene Silencing by Interfering with PABPC1 Function
   Eric Huntzinger, Susanne Heimstädt, Joerg Braun, Elisa Izaurralde

204 miR-8 is a molecular link between steroid signaling and insulin signaling in Drosophila
   Hua Jin, Seogang Hyun, Minju Ha, and V. Narry Kim

205 Catch and Release: Viral RNA Silencing Suppressor Competes with Human Dicer and Impairs RISC Assembly by Reversibly Binding siRNA
   Vishalakshi Krishnan, Renata Afi Rawlings, Nils Walter

206 The Tetrahymena Argonaute-binding protein Giw1p directs a mature Argonaute-siRNA complex to the nucleus
   Henriette Kurth, Tomoko Noto, Kensuke Kataoka, Lucia Aronica, Leroi DeSouza, Michael Siu, Ronald Pearlman, Martin Gorovsky, Kazufumi Mochizuki

207 Understanding the Interaction Between Human Argonaute2 and the 5’-Phosphate of the Antisense Strand of siRNA Using Modified 5’-Phosphate Analogs
   Cheryl Li, Walt Lima, Thazha Prakash, Heather Murray, Wenyu Li, Punit Seth, Garth Kinberger, Eric Swayze, Stanley Crooke

208 Molecular characterization of siRNA interactions with endogenous Argonaute1-4 proteins
   Sebastian Petri, Gunter Meister

209 Staircase to RNA Interference: Analysis by Single Molecule Fluorescence - Stepwise Photobleaching to deduce the number of miRNAs bound per mRNA target molecule
   Sethuramasundaram Pitchiaya, Rachel Leslie, Nils Walter

210 The terminal loop region regulates microRNA processing by Drosha and Dicer
   Xiaoxiao Zhang, Yan Zeng

211 3D Modeling and Docking of Pro-apoptotic RNA Aptamer: A new class of RNA Therapeutics causing cell death of Human Breast Cancer cell lines MCF-7
   Jyoti Bala
212 Quantitative Analyses of Multiple Small Non-coding RNAs that Regulate Virulence in the Bacterial Pathogen, *Vibrio cholerae*
J. Patrick Bardill, Brian Hammer

213 The ON conformation of the SAM I Riboswitch and Design of Novel Riboswitch Binding Small Molecules
Aboul-Ela Fareed, Vamsi Boyapati, Wei Huang, Sunayana Mitra

214 *In vivo* study of the lysine riboswitch mechanism in *Escherichia coli*
Marie-Pier Caron, Eric Massé, Daniel Lafontaine

215 Functionally Characterizing a Riboswitch
Pablo Ceres, Robert Batey

216 microRNA/Argonaute2 Regulates Nonsense-mediated mRNA Decay
Junho Choe, Hana Cho, Kyoung Mi Kim, Yoon Ki Kim

217 Gene order conservation to predict RNA and protein transcriptional control
Marcela Davila, Tore Samuelsson

218 Molecular Insights into the Switching Mechanism of the preQ1 Riboswitch Aptamer Domain
Jun Feng, Katie Eichhorn, Hashim Al-Hashimi, Charles Brooks III

219 Characterization of A Novel Blood Induced ncRNA In The Human Pathogen *Listeria monocytogenes*
Jonas Gripenland, Alejandro Toledo-Arana, Karolis Vaitekivicius, Olivier Dusserut, Pascale Cossart, Jörgen Johansson

220 MicroRNA-671 Mediates CDR1 mRNA Suppression by Destabilisation of a Circularised Antisense Transcript
Thomas Hansen, Erik Wiklund, Jesper Bramsen, Sune Villadsen, Aaron Statham, Susan Clark, Jørgen Kjems

221 MicroRNA Processing and Polycystic Kidney Disease
Mallory Havens, Stephane Burtey, Michelle Hastings

222 Discovery of a Hammerhead Ribozyme in the 3'UTR of a Natural Killer Cell Inhibitory Ligand
Lucas Horan, Monika Martick, Jason Fine, James Carlyle, David Raulet

223 Characterization of mRNA-like Non-coding RNA Candidates in *Drosophila*
Sachi Inagaki, Yuji Fukuda, Yuji Kageyama

224 Identification of noncoding and regulatory RNAs in *Bacillus subtilis*
Irnov Irnov, Cynthia Sharma, Jörg Vogel, Wade Winkler

225 MicroRNA-155 functions as an oncomiR in breast cancer by targeting the suppressor of cytokine signaling-1 gene
Shuai Jiang, Ming-Hua Lu, Xiao-Hong He, En-Duo Wang, Mo-Fang Liu

226 Temporal and spatial expression patterns of the Sm Y-10 snRNA in *Caenorhabditis elegans.*
Arata Kato, Kiyoaki Sato, Junichi Amakawa, Chisato Ushida

227 Human Splicing Factor SF1 is a New Component of Paraspeckles and Interacts with MEN-ε/β
Maria Cheole, Goranka Tanackovic, Angela Kramer

228 Scalable Control of Gene Expression Networks with Homogeneous RNA Transcription Attenuators
Julius Lucks, Lei Qi, Vivek Mutalik, Adam Arkin

229 Transcriptome Analysis Revealed Novel sRNAs Related to Catabolite Repression in *Escherichia coli*
Motomu Matsui, Atsuko Shinbara, Kiriko Hiraoka, Kenji Nakahigashi, Masaru Tomita, Akio Kanai

230 Alternative 3’ end processing of long noncoding RNAs is the underlying regulatory mechanism of nuclear paraspeckle organization
Takao Naganuma, Shinichi Nakagawa, Naoki Goshima, Yasnory Sasaki, Tetsuro Hirose

231 MiR-200b Precursor can Ameliorate Renal Tubulointerstitial Fibrosis
SHIGEYOSHI OBA, SHINTARO KUMANO, ETSU SUZUKI, HIROAKI NISHIMASTU, YASUNOBUVU HIRATA, TOSHIRO FUJITA

232 Folding of E. coli Riboswitches During Transcription by the E. coli RNA Polymerase
George Perdrizet, Terrence Wong, Tobin Sosnick
Characterizing The Interaction Between B2 RNA and RNA Polymerase II

Steven Ponicsan, Jennifer Kugel, James Goodrich

Scalable Gene Regulatory Motifs with Homogeneous RNA-Only Transcription Attenuators

Lei Qi, Julius Lucks, Vivek Mutlik, Adam Arkin

Transcription Regulation By Noncoding RNAs

Jacob Schwartz, Tom Cech

Deep Sequencing of Low Molecular Weight RNA Reveals Over One Hundred Novel sRNAs in Escherichia coli

Atsuko Shinohara, Motomu Matsui, Kiriko Hiraoka, Kenji Nakahigashi, Masaru Tomita, Hirotada Mori, Akio Kanai

Thermodynamic Studies of the PreQ1 Riboswitch

Nakesha Smith, Carla Theimer

A Mouse Model Lacking U50 box C/D-type snRNA Expression

Yuichi Soeno, Kazuya Fujita, Tomoo Kudo, Yuji Taya, Takaaki Aoba

COOLAIR - Cold Induced Long Antisense Intragenic RNA in cold sensing in plants

Szymon Swiezewski, Fuquan Liu, Filomena De Lucia, Andreas Magusin, Caroline Dean

Computational Prediction and Experimental Validation of Evolutionary Conserved microRNA Target Genes in Bilateral Animals

Kahori Takane, Kosuke Fujishima, Yuka Watanabe, Asako Sato, Nobuto Saito, Masaru Tomita, Akio Kanai

Profiling the antisense transcriptome of Schizosaccharomyces pombe

Ting Ni, Kang Tu, Han Wu, Bin Xie, Kristin Scott, Yuan Gao, Jun Zhu, Shiv Grewal

LIN-28 co-transcriptionally binds endogenous primary let-7 microRNA to inhibit early processing steps in let-7 biogenesis

Priscilla Van Wynsberghhe, Zoya Kai, Victoria Burton, Amy Pasquinelli

A Splicing-independent Function Of SF2/ASF In MicroRNA Processing

Han Wu, Shuying Sun, Kang Tu, Yuan Gao, Bin Xie, Adrian Krainer, Jun Zhu

Divergent GW182 Functional Domains in the Regulation of Translational Repression

Bing Yao, Songqing Li, Hyunmin Jung, Shangli Lian, Grant Abadal, Frank Han, Marvin Fritzler, Edward Chan

Detection and Analysis of Extensive Spatio-temporal Regulation of Alternative Splicing During C. elegans Development

John Calarco, Arun Ramani, Qun Pan, Bushra Raj, Sepand Mavandadi, Leo Lee, Quaid Morris, Andrew Fraser, Benjamin Blencowe, Mei Zhen

Analysis of Planarian Stem Cell Regulation by Conserved Cytoplasmic Ribonucleoprotein Granule Components

Labib Rouhana, Norito Shibata, Phillip Newmark, Kiyokazu Agata

The Art Of Aligning Domains: Ribosomal Small Subunit Assembly As Observed By R-Protein S8

Deepika Calidas, Gloria Culver

Investigation of Ribosome Biogenesis Defects Induced by Genetic Manipulation of Ribosome Biogenesis Factors

Keith Connolly, Gloria Culver

Mass Spectrometry-based Characterization of Antibiotic-Induced Ribosome Assembly Intermediates

Romel Dator, Patrick Limbach
250 Structures of the Ribosome in Intermediate States of Ratcheting.
Jack Dunkle, Wen Zhang, Jamie Cate

251 Utp25p, a Novel Nucleolar Saccharomyces cerevisiae Protein, Interacts with U3 snoRNP Subunits and Affects Processing of the 35S pre-rRNA
Mauricio Goldfeder, Carla Oliveira

252 A new insight on the structure of the Transfer-Messenger RNA
Jie Fu, Iwona Wower, Yaser Hashem, Jianlin Lei, Hstau Liao, Christian Zwieb, Jacek Wower, Joachim Frank

253 Nol9, A Novel Polynucleotide Kinase In Human Cells, Is Involved In rRNA Maturation
Katrin Heindl, Alexander Schleiffer, Javier Martinez

254 Modeling Elongation Factor-Dependent Formation of Open 80S Ribosomes, Cognate aa-tRNA Docking and Reestablishment of Closed Ribosomes
Ulf Hornemann

255 Evaluation/Discussion of Benefits and Drawbacks of the New Ribosomal Oscillation Cycle, Its Reconciliation With Previous Ribosome Studies and Thoughts Concerning Future Work
Ulf Hornemann

256 Modeling the Fungal 80S Ribosome as an ATP and GTP-Driven Large Amplitude Oscillator Comprising a Novel Rearranged/Open Subunit Juxtaposition
Ulf Hornemann

257 Differential Expression and Localization of Ribosomal Protein L22e Family Paralogues in Drosophila melanogaster
Michael Kearse, Vassie Ware

258 Biochemical Purification and Characterization of Nonfunctional Mutant Ribosomes from S. cerevisiae
Makoto Kitabatake, Kotaro Fujii, Tomoko Sakata, Mutsuhito Ohno

259 Multistep RNA Degradation Mechanism in the Nonfunctional 25S rRNA Decay
Fujii Kotaro, Ohno Mutsuhito, Kitabatake Makoto

260 Recognition of Ribosomal RNA by rProtein S4
Megan Mayerle, Sarah Woodson

261 In Vivo Analysis of Ribosomal RNA Structure and Dynamics
Jennifer McGinnis, Kevin Weeks

262 Nucleotide Dissociation in Elongation Factor Tu: A Molecular Dynamics Study in silico and in vitro.
Evan Mercier, Hans-Joachim Wieden

263 Temperature-Dependent Conformational Rearrangement or Multimerization of Ribosomal Protein S7 Promote RNA binding
Allison Pappas, Gloria Culver, Marit Nilsen-Hamilton

264 Translation inhibitors induce ubiquitination of ribosomal particles.
Tomoko Sakata, Mutsuhito Ohno, Makoto Kitabatake

265 Study of the exosome activity regulation in yeast
Márcia Cristina Santos, Nilson Zanchin, Carla Oliveira

266 Dynamics of the Base of Ribosomal A-site Finger Revealed by Molecular Dynamics Simulations and Cryo-EM
Kamila Reblova, Wen Li, Joachim Frank, Jiri sponer

267 RNA Three-Way Junctions Can Act as Flexible RNA Structural Segments in the Ribosome
Ivana Besseova, Kamila Reblova, Neocles Leontis, Jiri Sponer

268 A bacterial elongation factor G homologue exclusively functions in ribosome recycling in the spirochaete Borrelia burgdorferi
Takuma Suematsu, Shin-ichi Yokobori, Hiroyuki Morita, Shigeo Yoshinari, Takuya Ueda, Kiyoshi Kita, Nono Takeuchi, Yoh-ichi Watanabe
269  Elements of Human Translation Initiation Factor elf3 Important for Pre-initiation Complex Assembly on the 40S Ribosomal Subunit
Aleksandar Todorovic, Jamie Cate

270  Ribosomal Dysfunction and Bone Marrow Failure: Analysis of Zebrafish Model for Diamond-Blackfan Anemia
Tamayo Uechi, Yukari Nakajima, Hidetsugu Torihara, Naoya Kenmochi

271  Effects of Imbalance Between the Large and Small Ribosomal Subunits
Kerri McIntosh, Arpita Bhattacharya, Ian Willis, Jonathan Warner

272  Simulations of tRNA Hybrid-State Formation and accommodation Reveal Multiple Pathways Through the Ribosome
Paul Whitford, Jose' Onuchic, Karissa Sanbonmatsu

273  In vitro Characterization of Rrp5's Binding Sites on Pre-40S and Pre-60S rRNAs
Crystal Young, Katrin Karbstein

POSTERS
RNA and Epigenetics
Abstracts 274 – 278

274  Abstract Withdrawn

275  Histone H3 Lysine-9 Tri-methylation and HP1y Favor Inclusion of Alternative Exons
Violaine Saint-André, Eric Batsché, Christian Muchardt

276  Battles Between the Plant Genome and its Parasites through the Action of Small RNAs
Yutaka Sato, Misuzu Nosaka

277  Noncoding RNAs involved in RNAi-mediated DNA Elimination in Tetrahymena
Ursula Schoeberl, Kazufumi Mochizuki

278  Coordinate Recruitment of ARGONAUTE4 and SPT5L is Needed for RNA-dependent DNA Methylation
Jordan Rowley, Maria Avrutsky, Ligia Pereira, Andrzej Wierzbicki

POSTERS
RNA Catalysis
Abstracts 279 – 295

279  Protonation States of the Key Active Site Residues and the Reaction Mechanism of the glmS Riboswitch Self-Cleavage
Pavel Banas, Nils Walter, Jiri Sponer, Michal Otyepka

280  How to avoid cell death by controlling the folding of a ribozyme located in the ribosomal RNA precursor
Bertrand BECKERT, Mads HEDEGAARD, Benoît MASQUIDA, Henrik NIELSEN

281  A Double-Site Acting Kinase Ribozyme
Elisa Biondi, Donald Burke

282  A Remarkably Stable Loop / Loop Interaction for Substrate Recognition in the Varkud Satellite Ribozyme
Patricia Bouchard, Pascale Legault

283  Cation and coenzyme specificities for very rapid glmS ribozyme catalysis
Krista Brooks-Greco, Ken Hampel

284  Validating Ribosomal Protein L7Ae as a Subunit of Archaeal RNase P
I-Ming Cho, Dwi Susanti, Biswarup Mukhopadhyay, Venkat Gopalan

285  Ubiquitous Presence of the Hammerhead Ribozyme Motif Along the Tree of Life: From Bacterial Genomes to Human Antioncogenes
Marcos De la Peña
286 Processing of tRNA Precursors by RNase BN/ RNase Z
Tanmay Dutta, Murray Deutscher

287 Chemo-genetic Analysis of the Hepatitis Delta Virus Ribozyme Active Site Network
Molly Evans, Xochina El Hilali, Subha Das

288 Cleavage of Mutant Substrates with Different Stem Sizes by the VS Ribozyme
Julie Lacroix-Labonté, Pascale Legault

289 Structural Analysis and Evolution of the glmS Ribozyme
Matthew Lau, Adrian Ferré-D’Amaré

290 Inhibition of the Intrinsic Activity of SOFA-HDV Ribozymes by the SOFA Module.
Michel Levesque, Jean-Pierre Perreault

291 Involvement of canonical G8 and protonated A38H+ forms in structure stabilization and catalysis by hairpin ribozyme
Vojtech Mlynsky, Pavel Banas, Nils Walter, Jiri Sponer, Michal Otyepka

292 Numerous Hammerhead Ribozymes Exist in All Domains of Life
Jonathan Perreault, Zasha Weinberg, Adam Roth, Olivia Popescu, Pascal Chartrand, Gerardo Ferbeyre, Ronald Breaker

293 Functional Analysis of HDV-like Ribozymes
Nathan Riccitelli, Chiu-Ho Webb, Andrej Lupáč

294 The Group I Intron Uses A Catalytic Metal Ion To Bind, Position, And Activate The Nucleophile During Self-Splicing
Raghuvir Sengupta, Aiichiro Yoshida, Daniel Herschlag, Joseph Piccirilli

295 Investigating the Roles of Divalent Metals in the Mechanism of a Native Hammerhead Ribozyme
Luke Ward, Victoria DeRose

POSTERS
RNA Editing and Modification
Abstracts 296 – 325

296 The Mitochondrial RNA Binding Complex 1 (MRB1) Component TbRGG2 Facilitates Kinetoplastid RNA Editing Progression Past Intrinsic Pause Sites
Michelle Ammerman, Hassan Hashimi, Kurtis Downey, Anthony King, Julius Lukes, Laurie Read

297 Abstract Withdrawn

298 Uridylylation Shapes the Mitochondrial Transcriptome in Trypanosoma brucei
Inna Aphasizheva, Ruslan Aphasizhev

299 Dissecting the Role of Box C/D s(no)RNA Conserved Sequences in Di-sRNP Assembly and Function
Franziska Bleichert, Susan Baserga

300 Getting U out of RNA: Editing Exonucleases in Trypanosoma brucei
Jason Carnes, Nancy Ernst, Carey Wickham, Brian Panicucci, Kenneth Stuart

301 Determination of the Relationship Between 2’-O-Methylation and Splicing of an Archaeal pre-tRNA<sup>Tm</sup>
Kunal Chatterjee, Priyatansh Gurha, Sanjay Singh, Ramesh Gupta

302 Probing An RNA Editing Reaction With Small Molecule Inhibitors
Gregory Connell, Shuang Liang

303 Functional consequences of RNA editing on the squid ADAR2 from Loligo opalescens
Rodrigo Correa, Juan Palavicini, Joshua Rosenthal

304 Genome-wide analysis of N'-methyl-adenosine modification in human tRNAs
Mridusmita Saikia, Ye Fu, Mariana Pavon-Eternod, Chuan He, Tao Pan

XXX
The AlkB domain of mammalian ABH8 catalyzes hydroxylation of 5-methoxycarbonylmethyluridine at the anticodon wobble position in tRNA
Ye Fu, Qing Dai, Wen Zhang, Jin Ren, Tao Pan, Chuan He

Functional Analysis of RNA editing proteins unique for distinct editosomes in Trypanosoma brucei
Xuemin Guo, Jason Carnes, Nancy Ernst, Carmen Zelaya-Soares, Matt Winkler and Kenneth Stuart

Functional Analysis of Core Subunits of the Putative Mitochondrial RNA Binding Complex in the Parasitic Protist Trypanosoma brucei
Hassan Hashimi, Michelle Ammerman, Lucie Novotná, Lucie Hanzliková, Laurie Read, Julius Lukes

Differences in tRNA Ψ55- and Ψ54-Synthase Activities of Archaeal Pus10 Proteins
Archi Joardar, Priyatansh Gurha, Elisabeth Fitzek, Mrinmoyee Majumder, Kunal Chatterjee, Matt Geisler, Ramesh Gupta

Biochemical Characterization of a GTP-Dependent RNA 3'-Terminal Phosphate Cyclase from a Hyperthermophilic Archaeon Pyrococcus furiosus
Asako Sato, Masaru Tomita, Akio Kanai

Towards the Kinetic Mechanism of Bacterial Pseudouridine Synthases
Jaden Wright, Selina Dobing, Ute Kothe

Expanding the Editosome Protein Complex: Introducing KREPB9 and KREPB10
Melissa Lerch, Jason Carnes, Achim Schnaufer, Kenneth Stuart

Pseudouridylation of Haloferax volcanii 23S rRNA mediated by a unique H/ACA box guide RNA
Mrinmoyee Majumder, Kunal Chatterjee, Ian Blaby, Valérie de Crécy-Lagard, Ramesh Gupta

Dynamic posttranslational regulation of the RNA editing enzyme ADAR2
Roberto Marcucci, Simona Paro, Anne Leroy, Liam Keegan, Giannino del Sal, Mary O'Connell

The extra dsRNA binding domain of squid ADAR2 compensates for the negative effects of marine ionic strength on RNA editing
Juan Palavicini, Rodrigo Correa, Joshua Rosenthal

Identification of the Enzyme Responsible for m3C Modification at Position 32 of tRNAThr in Budding Yeast
Sonia D'Silva, Steffen Haider, Eric Phizicky

Characterization of Two Human Pseudouridine Synthases Homologous to E. coli TruD
Claudia Recinos, Arun Malhotra

Ribosomal RNA Modification Profiles for Ribosome Assembly Intermediates
Rebecca Rohlf, Patrick Limbach

Isolation of an Invertebrate ADAR1 Homolog
Juan Palavicini, María Montiel, Joshua Rosenthal

High Precision, Quantitative Measurements of Changes in the Modification Status of tRNAs and rRNAs
Susan Russell, Patrick Limbach

Cooperation between Mismatch Repair and RNase H Factors in the Removal of an RNA/DNA Mispair in E. coli and Yeast Cells
Ying Shen, Bernard Weiss, Francesca Storici

dsRNAs containing multiple IU pairs are sufficient to suppress induction of interferon and apoptosis
Patrice Vitali, A.D.J Scadden

Arrangement of mRNAsEncoded by Linear Plasmids of the Yeast Kluyveromyces lactis – These mRNAs Probably doesn't Support Cap-dependent Translation
Vaclav Vopalensky, Martin Pospisek

Editing of MicroRNAs in C. elegans by ADARs
M Bryan Warf, Noah Welker, Brent Shepard, W. Evan Johnson, Brenda Bass
325 Tudor-SN binds inosine-containing dsRNA and is found in cytoplasmic stress granules
Rebekka Weissbach, Deirdre Scadden

POSTERS
RNA Structure and Folding
Abstracts 326 – 376

326 Fluorometric Analysis of S4-rRNA interactions
Sanjaya Abeysirigunawardena, Megan Mayerle, Sarah Woodson

327 Structural Correlates of Cooperativity And Efficiency In the Folding of A Group I Ribozyme
Reza Behrouzi, Joon Ho Roh, John Kilburn, Sarah Woodson

328 Aminoacylation of 3’-[32P] labeled tRNA: A Sensitive Method to Study Kinetics of tRNA Folding
Hari Bhaskaran, John Perona

329 Extending the MC-Fold Statistical Scoring Scheme to Predict Tertiary Interactions
Marc-Frederick Blanchet, Francois Major

330 Characterization of the 'Panhandle' Motif in Infectious Salmon Anemia Virus by High Resolution Nuclear Magnetic Resonance
John Marino, Robert Brinson

331 Understanding the Role of the Initial Conformation on RNA Topological Frustration when Misfolding
Chunxia Chen, Magdalena Jonikas, Somdeb Mitra, Michael Brenowitz, Alain Laederach

Scott Quarrier, Joshua Martin, Lauren Davis-Neulander, Arthur Beauregard, Alain Laederach

333 Crystal structure of the SAH riboswitch aptamer
Andrea Edwards, Francis Reyes, Annie Héroux, Robert Batey

334 Single-Molecule RNA Folding: Kinetic and Thermodynamic Contributions of Tertiary Interactions
Julie Fiore, David Nesbitt

335 Effect of Single Nucleotide Polymorphism (SNP) in the 5′ UTR on the secondary structure of RNA
Chetna Gopinath, Lauren Neulander, Matt Halvorsen, Alain Laederach

336 Fold of the Human U2-U6 SnRNA Complex
Caijie Zhao, Ravichandra Bachu, Matthew Devany, Nancy Greenbaum

337 Single Molecule Studies of Spliceosomal RNAs U2 and U6
Zhuojun Guo, David Rueda

338 RNA Fingerprinting by the Nanochannel of Bacterial Virus phi29 DNA Packaging Motor
Jia Geng, Farzin Haque, Peng Jing, Peixuan Guo

339 NMR Structure of Prohead RNA E-loop Hairpin
Steven Harris, Susan Schroeder

340 Integrating simulation and experiment: Magnesium mediates aptamer response to ligand in the SAM-I riboswitch
Scott Hennelly, Alex Schug, Paul Whitford, Jose Onuchic, Karissa Sanbonmatsu

341 Structure of Glycine-Sensing Riboswitch: Insights into Ligand Recognition and Cooperativity
Lili Huang, Alexander Serganov, Dinshaw Patel

342 Self-dimerizing RNAs as designed templates for a chemical peptide ligation
Yoshiya Ikawa, Kohei Yamashita, Hiroyuki Furuta

343 The Central Role of the Reverse-Hoogsteen Base-pair U54-A58 in the Folding of the DT Region
Tetsu Ishii, Sergey Steinberg
xxxiii

344 SuiteAlign: Alignment Technique for RNA Backbone Conformers for Structural Motif Mining
Swati Jain, Gary Kapral, Paraewe Lekprasert, David Richardson, Jane Richardson

345 The Complete Solution Structure of RNase P RNA
Alexei Kazantsev, Robert Rambo, John Tainer, Norman Pace

346 Semi-automated Model Building for RNA Crystallography Using a Directed Rotameric Approach
Kevin Keating, Anna Marie Pyle

347 Robust and Generic RNA Modeling Using Inferred Constraints: A Structure for the Hepatitis C Virus IRES Pseudoknot Domain
Christopher Lavender, Feng Ding, Nikolay Dokholyan, Kevin Weeks

348 Predicting the Secondary Structures of Long RNA Sequences: MC-Fold Overlapping Small-Window Assemblies versus Thermodynamics Long-Sequence-At-Once
Veronique Lisi, Francois Major

349 Conformational equilibrium in the yeast telomerase RNA pseudoknot domain
Fei Liu, Yoora Kim, Charmion Cruickshank, Carla Theimer

350 NMR Solution Structures of the 970 hairpin of E.coli 16S rRNA: the Effects of Modifications on Thermodynamics, Structure, and Function
Yu Liu, Nuwan Abeydeera, Tek Lamichhane, Christine Chow, Philip Cunningham, John SantaLucia

351 Effect of Mutations on Fitness: The Case of RNA Secondary Structure
Susanna Manrubia, Michael Stich, Ester Lázaro, Rafael Sanjuán

352 Time-Resolved Folding Studies of the GAAA Tetraloop-Receptor Interaction by NMR
Lauren Michael, Kirk Vander Meulen, Roger Chylla, Marco Tonelli, Samuel Butcher

353 Exploring the Interactions of Pt(II) Anticancer Drugs with RNA Loop Motifs
Amanda Miller, Victoria DeRose

354 Identification and Characterization of a Thiamine Pyrophosphate Riboswitch in Mycobacterium tuberculosis: A New Drug Target in Tuberculosis Drug Design
Sunayana Mitra, Diana Williams, Thomas Gillis, Tana Pittman, Fareed Aboul-ela

355 Cooperative Self-Assembly of H-Shaped TectoRNA to Form Closed Complexes of Variable Stoichiometry
Irina Novikova, Neocles Leontis

356 Recognition of the 5' Splice Site of a Group II Intron by a Stem Loop of Domain 1
Milena Popović, Nancy L. Greenbaum

357 Site-Directed Spin Labeling Studies of RNA Structure and Dynamics
Peter Qin

358 Improving Small-Angle X-ray Scattering Data for Accurate Structural Analyses in the RNA World
Robert Rambo, John Tainer

359 The structure solution of the S-adenosyl-(L)-homocysteine riboswitch
Francis Reyes, Andrea Edwards, Annie Héroux, Robert Batey

360 Probing Loop and Stem Dynamics of RNA Hairpin Folding by T-jump and Molecular Dynamics
Krishnarjun Sarkar, Duc Nguyen, Martin Gruebele

361 Ion-induced folding of non-standard kink turn RNA sequences
Kersten Schroeder, David Lilley

362 Computing RNA Folding Funnels
Susan Schroeder, Jonathan Stone, Sean Lavelle, Theodore Gibbons, Montana Rowe, Xiaobo Gu

363 Sequence-Structure Relationships in RNA Loops: Establishing the Basis for Loop Homology Modeling
Christian Schudoma, Patrick May, Dirk Walther

364 Automated All-Atom RNA Tertiary Structure Prediction
Matthew Seetin, David Mathews

xxxiii
### POSTERS

**RNA Transport and Localization**

Abstracts 377 – 389

<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>365</td>
<td>The SHAPE of Human Telomerase</td>
<td>Vijay Sekaran, Michael Jarstfer</td>
</tr>
<tr>
<td>366</td>
<td>Sequence Dependence of Stability for Group II Single Nucleotide Bulge Loops</td>
<td>Martin Serra, Michael McCann, Michelle Manni, Julie Estes, Kelly Klapec, Jessica Gratton, Gregeory Frattini, Robert Knarr, Geoff Lim, Ryan Hanson</td>
</tr>
<tr>
<td>367</td>
<td>RNA Structure Prediction with Step-Wise Assembly (SWA)</td>
<td>Parin Sripakdeevong, Rhiju Das</td>
</tr>
<tr>
<td>368</td>
<td>Selective 2'-Hydroxyl Acylation Analyzed by Protection from Exoribonuclease</td>
<td>Kady-Ann Steen, Arun Malhotra, Kevin Weeks</td>
</tr>
<tr>
<td>369</td>
<td>Elucidating the Three Dimensional Structure of the HIV-1 5' Untranslated Region RNA by Single Molecule FRET</td>
<td>James Stephenson, Julia Kenyon, Haitao Li, David Klenerman, Andrew Lever</td>
</tr>
<tr>
<td>370</td>
<td>Multiscale Structural Dynamics of the preQ1 Riboswitch from Single-Molecule Fluorescence Microscopy, NMR Spectroscopy and Molecular Dynamics Simulations Reveal Ligand-Dependent Conformational Docking</td>
<td>Krishna Suddala, Catherine Eichhorn, Jun Feng, Hashim Al-Hashimi, Charles Brooks III, George Garcia, Nils Walter</td>
</tr>
<tr>
<td>371</td>
<td>Molecular Mechanics Analysis of Minimal Energy RNA Conformational Change Pathways</td>
<td>Keith Van Nostrand, Scott Kennedy, Douglas Turner, David Mathews</td>
</tr>
<tr>
<td>372</td>
<td>RNA Tapestries: Two Dimensional Structure Probing</td>
<td>Christopher VanLang, Wipapat Kladwang, Rhiju Das</td>
</tr>
<tr>
<td>373</td>
<td>The Identification of Tertiary Interactions Important for Cooperative Ligand Binding in the Glycine Riboswitch</td>
<td>Thanh Vu, Scott Strobel</td>
</tr>
<tr>
<td>374</td>
<td>Enhanced Specificity Against Misfolding in a Thermostable Mutant of the Tetrahymena Ribozyme</td>
<td>Yaqi Wan, Rick Russell</td>
</tr>
<tr>
<td>375</td>
<td>Positional and Neighboring Base Pair Effects on the Thermodynamic Stability of RNA Single Mismatches</td>
<td>Amber Davis, Brent Znosko</td>
</tr>
<tr>
<td>376</td>
<td>The Translational Enhancer and Ribosome Binding Structural Element in 3' UTR of Turnip Crinkle Virus RNA Folds into a tRNA-like Shape in Solution</td>
<td>Xiaobing Zuo, Jinbu Wang, Ping Yu, Dan Eyler, Anne Simon, Charles Schwieters, Bruce Shapiro, Yun-Xing Wang</td>
</tr>
</tbody>
</table>

---

## POSTERS

**RNA Transport and Localization**

Abstracts 377 – 389

<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>377</td>
<td>The Role of Pur-alpha in RNA Transport during Drosophila Oogenesis</td>
<td>Verena Aumiller, Klaus Förstemann</td>
</tr>
<tr>
<td>378</td>
<td>Characterization of SMN and hnRNP Q1 granules</td>
<td>Hung-Hsi Chen, Hsin-I Yu, Wen-Cheng Chiang, Woan-Yuh Tarn</td>
</tr>
<tr>
<td>379</td>
<td>HnRNP D/AUF1 Isoforms Regulate HIV-1 Replication</td>
<td>Nicole Lund, Tharmila Sammugananthanam, Kathryn Woolaway, Raymond Wong, Benoit Chabot, Sherif Abou Elela, Alan Cochrane</td>
</tr>
<tr>
<td>380</td>
<td>Structures of the tRNA export factor in the nuclear and cytosolic states</td>
<td>Atlanta Cook, Noemi Fukuhara, Martin Jinek, Elena Conti</td>
</tr>
<tr>
<td>381</td>
<td>Resolution of the ER Stress Response During Host-Temperature Adaptation Requires Ccr4 in Cryptococcus neoformans</td>
<td>Virginia Havel, Nathan Wool, David Ayad, John Panepinto</td>
</tr>
<tr>
<td>382</td>
<td>Structural Analysis of the RNA Export Element of the MusD Murine LTR Retrotransposon Reveals Tertiary Interactions Essential for Function</td>
<td>Michal Legiewicz, Guy Pilskington, Andrei Zolotukhin, Hiroaki Uranishi, Jennifer Bear, George Pavlakis, Stuart Le Grice, Barbara Felber</td>
</tr>
</tbody>
</table>
POSTERS
RNA Turnover
Abstracts 390 – 415, 668

390  Nonsense-mediated mRNA Decapping Occurs on Polyribosomes in Saccharomyces cerevisiae
Wenqian Hu, Christine Petzold, Jeff Coller, Kristian Baker

391  The C-terminal α-α superhelix of Pat1 is required for the assembly of decapping complexes and for mRNA
decapping in metazoa
Joerg Braun, Felix Tritschler, Gabrielle Haas, Cátia Igreja, Vincent Truffault, Oliver Weichenrieder, Elisa Izaurralde

392  Tight Posttranscriptional Regulation of Nucleophosmin is Required for Muscle Fiber Formation
Anne Cammas, Kate van der Giessen, Virginie Dormoy-Raclet, Imed-Eddine Gallouzi

393  AU-rich Motifs Are Enriched In mRNAs Stabilized During Meiosis: A Role For ELAVL2?
Katerina Chalupnikova, Hynek Strnad, Matyas Flemr, Alain Sewer, Petr Svoboda

394  The human core exosome utilizes differentially localized processive ribonucleases: hDIS3 and hDIS3L
Rafal Tomecki, Maiken Kristiansen, Søren Søren Lykke-Andersen, Aleksander Chlebowski, Katja Larsen, Roman Szczesny, Karolina Drazkowska, Agnieszka Pastula, Jens Andersen, Piotr Stepien, Andrzej Dziembowski, Torben Jensen

395  The Physiological Role of the 5’-Sensor Domain of RNase E
Stephen Garrey, George Mackie

396  Structure and Preliminary Functional Analysis of Yeast Ski2
Felix Halbach, Elena Conti

397  Detailed Analysis of Functional Domains Within the TRAMP4 Complex
Peter Holub, Marie Sárazová, Jana Laláková, Štěpánka Vařová

398  mRNP Rearrangements During the Pioneer Round of Translation and Nonsense-Mediated mRNA Decay
Jungwook Hwang, Hanae Sato, Yalan Tang, Daiki Matsuda, Lynne Maquat

399  Regulation of CTR2 expression by the Saccharomyces cerevisiae Nonsense-Mediated mRNA Decay pathway
Bessie Kebaara, Audrey Atkin

400  UPF1 Modulates Translation Termination Efficiency
Kathrin Kerschgens, Gaby Neu-Yilik, Matthias Hentze, Tatyana Pestova, Andreas Kulozik

401  Biochemical Identification and Functional Annotation of Glucose-dependent RNA Decay Signals
Mathieu Lavoie, Dongling Ge, Jules Gagnon, Sherif Abou Elela
402 Systematic Analysis of cis-elements in Unstable mRNAs Demonstrates that CUGBP1 is a Key Regulator of mRNA Decay in Muscle Cells
Jerome Lee, Ju Youn Lee, Carolina Lopez, Jeffrey Wilusz, Bin Tian, Carol Wilusz

403 The Physiological Role of NMD during Cellular Stress
Jana Loeber, Matthias Hentze, Andreas Kulozik, Gabriele Neu-Yilik

404 The ability to promote reinitiation after premature termination is the major determinant of the NMD insensitivity of exon 1 PTCs in the human beta-globin gene
Gabriele Neu-Yilik, Beate Amthor, Jana Loeber, Niels Gehring, Matthias Hentze, Andreas Kulozik

405 STAT3 is a novel promoter of cytokine-induced muscle wasting
Jennifer Ma, Sergio Di Marco, Imed-Eddine Gallouzi

406 Most mRNAs Encoding Human NMD Factors Are NMD Substrates: Evidence for Auto-Regulation
Hasmik Yepiskoposyan, Florian Aeschimann, Oliver Mühlemann

407 Effects of Long Double-stranded RNA in Mammals
Jana Nejepinska, Radek Malik, Jody Filkowski, Witold Filipowicz, Petr Svoboda

408 The poly(A)-tail as a battlefield for quality control
Mathias Poulsen, Manfred Schmid, Claire Moore, Torben Jensen

409 The Drosophila EJC loaded on specific exon-exon junctions is involved in NMD of particular transcripts
Jerome Sauliere, Nazmul Haque, Scot Harms, Isabelle Barbosa, Marco Blanchette, Herve Le Hir

410 Split CRAC Distinguishes Substrates for the Endonuclease and Exonuclease Activities of the Exosome
Claudia Schneider, Sander Granneman, David Tollervey

411 Dis3-like 1: A Novel Exoribonuclease Associated With The Human Exosome
Raymond Staals, Alfred Bronkhorst, Geurt Schilders, Shimyn Slomovic, Gadi Schuster, Albert Heck, Reinout Raijmakers, Ger Pruijn

412 Analysis of the C-Terminal Domain of Yeast Lsm1
Ashis Chowdhury, Sundaresan Tharun

413 RNA-Protein Cross-linking and Deep Sequencing Reveal Numerous mRNA Targets for the Nuclear RNA Surveillance Machinery
Wiebke Wlotzka, Grzegorz Kudla, David Tollervey

414 Dcp2 phosphorylation by Ste20 modulates stress granule and mRNA decay in Saccharomyces cerevisiae
Je-Hyun Yoon, Eui-Ju Choi, Roy Parker

415 Mechanistic analysis of selective inhibition during RNA processing
Li Zhou, George Georgiou

POSTERS
RNA-Protein Interaction
Abstracts 416 – 449

416 Mechanism of antitermination by NusG-like proteins
Anastasia Sevostianova, Robert Landick, Rachel Mooney, Georgiy Belogurov, Irina Artsimovitch

417 The pre-snRNA 3’-extra sequences function as enhancers in snRNP biogenesis
Jennifer Bachorik, Jeongsik Yong, Mumtaz Kasim, Tina Glisovic, Lili Wan, Gideon Dreyfuss

418 The yeast exosome functions as a macromolecular cage to channel RNA substrates for degradation
Jer@me Basquin, Fabien Bonneau, Judith Ebert, Esben Lorentzen, Elena Conti

419 A comparison of the binding specificity of human versus drosophila Muscleblind
Danielle Cass, Rachel Hotchko, J. Andrew Berglund

420 Large-scale Purification and RNA-Seq Analysis of Endogenous S. pombe Splicing Complexes
Weijun Chen, Hennady Shulha, Ami Ashar, Jing Yan, Charles Query, Nick Rhind, Zhiping Weng, Melissa Moore
421 Molecular basis of purine-rich recognition by the SR-like protein Tra2-β1
Antoine CLERY, Natalya BENDERSKA, Sandrine JAYNE, Cyril DOMINGUEZ, Stefan STAMM, Frederic ALLAIN

422 HIV-1 Bypasses Cellular Stress Responses Through Unique Properties of the Viral mRNP
Kim Marsh, Alper Yilmaz, Kathleen Boris-Lawrie, Alan Cochrane

423 Intracellular Localization and FRET-based Detection of Interactions of RNA Binding Proteins
Pamela David Gerecht, J. David Port

424 Determinants of recognition between the pluripotency factor Lin28 and let-7 precursor miRNA
Nabanita De, Kristi Kass, Ian MacRae

425 Binding Interfaces of HIV Reverse Transcriptase-Aptamer Complexes with Implications for Broad-Spectrum Inhibition of HIV
Mark Ditzler, Nikolozi Shkriabai, Bruno Marchand, Elisa Biondi, Stefan Sarafianos, Mamuka Kvaratskhelia, Donald Burke

426 RGNEF, a Novel RNA Binding Protein that Binds NFL mRNA, forms Aggregates and is Differentially Expressed in the Spinal Cord of ALS Patients.
Cristian Droppelmann, Brian Keller, Kathryn Volkening, Michael Strong

427 Identification and Characterization of RNA Binding Proteins that Bind to Human IL-3 ARE in Jurkat Leukemic T cells
José González-Feliciano, Armando López-Mercado, Luis Estrella, Marimar Hernández, Marina Martínez, Carlos González

428 Genome-wide Identification of Cellular RNA Substrates of the DEAD-box Helicase Ded1p
Ulf-Peter Guenther, Mark Adams, Eckhard Jankowsky

429 Drosophila SNF protein and its RNA binding preferences
Sandra Williams, Kathleen Hall

430 Recognition of dsRNA by the dsRBD of S. cerevisiae RNase III (Rnt1p)
Elon Hartman, Qi Zhang, Zhonghua Wang, Juli Feigon

431 Genome-wide Identification of Lin28 mRNA Targets in Human Embryonic Stem Cells
Shuping Peng, Li Yang, Yingqun Huang

432 Interaction of the HIV-1 Nucleocapsid Protein with RNA Ligands
Abhijit Jadhav, Hua Shi, Rabi Musah

433 Functional and Molecular Analysis of Eschericia coli Strains lacking Multiple DEAD-box Helicases
Kevin Jagessar, Chaitanya Jain

434 Modulation of Cellular IL-6 Gene Expression and mRNA Stability by Kaposi's Sarcoma-Associated Herpesvirus
Yeon Lee, Britt Glaunsinger

435 Structure-function analysis of the fission yeast nuclear poly(A)-binding protein
Caroline Lemieux, Jennifer Lafontaine, François Bachand

436 Predicting in vivo Binding Sites of RNA-Binding Proteins Using mRNA Secondary Structure
Xiao Li, Gerald Quon, Howard Lipshitz, Quaid Morris

437 FOX2 RNA binding protein regulates 3’UTR of genes in addition to splicing regulation
Katlin Massirer, Stephanie Huelga, Thomas Stark, Gene Yeo

438 Cryptococcus neoformans Ccr4-target transcripts encoding ribosomal proteins share a 3’UTR cis element with protein binding activity
Amanda Misener, John Panepinto

439 A Non-Radioactive Labeling Method for the Isolation of RNA:Protein Interactions
Kay Opperman, Chris Etienne, Jean-Samuel Schultz, Barbara Kaboord

440 Exploring the Biological Role of Tudor Staphylococcal Nuclease (TSN) in C. elegans
Marissa Perez, Nicole Lambert, Dayle Juliano, Alan Zahler
A Comprehensive Kinetic Framework for Duplex Unwinding by the DEAD-box RNA Helicase Ded1p
Andrea Putnam, Quansheng Yang, Eckhard Jankowsky

The sRNA chaperone Hfq is a Pleiotropic Regulator required for Virulence of Bacteria of the Burkholderia cepacia complex
Christian Ramos, Sílvia Sousa, Leonilde Moreira, Jorge Leitão

The Evolutionarily Conserved Protein Cwc2/RBM22 Assists In Stabilization Of The Spliceosomal RNA Network Before And During Catalysis
Nicolas Rasche, Olexandr Dybkov, Jana Schmitzova, Berktan Akyildiz, Patrizia Fabrizio, Reinhard Lührmann

Systematic Analysis of RNA-binding Proteins Using RNAcompete
Debashish Ray, Hilal Kazan, Sarah Votruba, Quaid Morris, Timothy Hughes

Hotspots for RNA-dependent amino acid binding in a tRNA:aminoacyl-tRNA synthetase complex
Annia Rodriguez-Hernandez, John Perona

Exploring leucyl-tRNA synthetase as a target of a novel group of benzoaborole based antimicrobials
Jaya Sarkar, Susan Martinis

HIV-1 Rev is Highly Mutable with Partner RNAs and R35G Allows Substitution of N40 without Loss of RRE Binding
Elite Possik, Ingrid Ghattas, Colin Smith

A Role for Nucleolin in Post-transcriptional Regulation of Beta-globin mRNA
Sebastiaan van Zalen, J. Eric Russell

Apoptotic-Induced Cleavage Shifts HuR From Being a Promoter of Survival to an Activator of Death
Christopher von Roretz, Xian Jin Lian, Eveline Clair, Nahid Punjani, Olivier Drouin, Virginie Dormoy-Raclet, Imed-Ed-dine Gallouzi

POSTERS
RNAs in Diseases
Abstracts 450 – 472

Development of a Mouse Model to Study SMN Splicing and Replacement Therapy
Thomas Bebee, Jordan Gladman, Dawn Chandler

Tune-able microRNAs with anti-viral functions
Amy Buck, Nouf Laqtom, Diwakar Kumar

Yanbo Chen, Kazuo Fushimi, Xiaohong Zhou, Xiaoping Chen, David Zhang, Yan Li, Jane Wu

The C-terminus of Utp4, Mutated in Childhood Cirrhosis, is Essential for Ribosome Biogenesis
Emily Freed, Susan Baserga

TDP-43 Target Genes and TDP-43 Proteinopathy
Kazuo Fushimi, Yanbo Chen, Zhou Xiaohong, Xiaoping Chen, David Zhang, Jane Wu

Identification of Modulators of RNA-dependent Toxicity in Myotonic Dystrophy
Susana Garcia, Gary Ruvkun

NMD inhibition as a therapeutic approach for genetic diseases caused by nonsense mutation
Sara Gonzalez-Hilarion, Terence Beghyn, Wéronika Fic, Benoit Deprez, Fabrice Lejeune

A Novel Mouse and Embryonic Stem Cell Model for Studying the Biological Role of Neurofibromatosis Type 1 Exon 23a Alternative Splicing
Melissa Hinman, Victoria Barron, Guangbin Luo, Hua Lou

An SMN Feedback Loop Regulates Splicing of the Spinal Muscular Atrophy-Modifying Gene, SMN2
Francine Jodelka, Allison Ebert, Michelle Hastings
459 The Splicing Factor hnRNP A2/B1 Regulates Splicing of the RON Proto-Oncogene and is A Driving Oncogene in Glioblastoma
Regina Golan-Gerstl, Michal Cohen, Asaf Shilo, Shulamit Sebban, Ben Davidson, Reuven Reich, Rotem Karni

460 RNA Vaccination As a Therapeutic Tool Against Cancer: Increased Immunostimulatory Capacity By A Phosphorothioate Cap Analog
Andreas Kuhn, Mustafa Diken, Sebastian Kreiter, Selmi Abderraouf, Joanna Kowsalska, Jacek Jemielity, Edward Darzynkiewicz, Christoph Huber, Özlem Türeci, Ugur Sahin

461 Splicing Factor HnRNP H Drives an Oncogenic Splicing Switch in Gliomas
Clare LeFave, Ying-Xian Pan, Cameron Brennan, Eric Holland, Luca Cartegni

462 A Conserved Polyadenosine RNA Binding, ZC3H14, is Required for Proper Brain Function: A Novel Link to Mental Retardation/Intellectual Disability
Sara Leung, Masoud Garshasbi, Christina Gross, Luciano Apponi, Gary Bassell, Andreas Kuss, Anita Corbett

463 Expression Profile of eIF4E Variants in Human ALL Leukaemia Model
Katerina Mocova, Zuzana Feketova, Jan Trka, Martin Pospisek

464 Specific Alteration of micro-RNA Processing is associated with Heart Defects in Myotonic Dystrophy type 1
Frédérique RAU, Fernande FREYERMUTH, Natacha DREUMONT, Charlotte FUGIER, Marie-Christine FISCHER, Masanori TAKAHASHI, Denis FURLING, Nicolas CHARLET-BERGUERAND

465 Characterization of Alternative Splicing Events of AML1-ETO Fusion Protein in Leukemia
Gina Rocco, Luca Cartegni

466 The Role of SMN in Co-Transcriptional Alternative Splicing
Gabriel Sanchez, Jocelyn C@té

467 Regulation of alternative splicing by psnoRNAs, new small nuclear RNAs that are derived from snoRNAs
Amit Khanna, Manli Shen, Mihaela Zavolan, Stefan Stamm

468 ALS-associated RNA Binding Proteins TDP-43 and FUS/TLS Function in a Common Biochemical Complex to Coregulate HDAC6 mRNA Expression
Randal Tibbetts, Sang Hwa Kim, Naval Shanware, Michael Bowler

469 Developing Small Molecules to Target the CUG Repeats of Myotonic Dystrophy
Leslie VanOs, Cameron Hilton, Amy Mahady, Jamie Purcell, Andy Berglund

Zhongping He, Kathryn Volkening, Michael Strong

471 Amyotrophic Lateral Sclerosis Associated Mutations in FUS/TLS and TDP-43 Proteins can alter their interaction with the Low Molecular Weight Neurofilament mRNA
Kathryn Volkening, Cheryl Leystra-Lantz, Michael Strong

472 Modulation of STAT3 alternative splicing as a tool to dissect its anti-tumorigenic potential
Francesca Zammarchi, Luca Cartegni

POSTERS
RNP Structure, Function and Biosynthesis
Abstracts 473 – 497

473 The RNA helicase Prp43 interacts with pre-rRNA and fulfills diverse functions at different sites
Roman Martin, Fabian Mück, Maike Ruprecht, Enrico Schleiff, Markus Bohnsack

474 Hundreds of New Protein-Protein Interactions in the SSU Processome Identified by High-Throughput Yeast Two-Hybrid
J. Michael Charette, Kathleen McCann, Young Lim, Susan Baserga

475 The DEAD-Box RNA Helicase-Like Utp25 is an SSU Processome Component
J. Michael Charette, Susan Baserga
Mercury (HgCl₂) Influence in Expression of Fibrillarin in Bean Embryos
Josefina Huerta, Francisco Cabral, Edgar Esparza, Lucia Delgadillo, Jesus Cortes

Microtubule association of a neuronal RNA-binding protein HuD through its binding to the light chain of MAP1B
Miho Fukuda, Akira Fukao, Yumi Sasano, Akihiko Kondo, Kunio Inoue, Hiroshi Sakamoto, Toshinobu Fujiwara

Structural Studies of Signal Sequence Binding of the Signal Recognition Particle
Tobias Hainzl, Shenhua Huang, Elisabeth Sauer-Eriksson

Engineerability of the Bacteriophage Lambda N Antitermination Complex
Kazuo Harada, Satoru Horiya, Mitsuhiro Inaba, Maki Sugaya, Chang-Song Koh, Hitoshi Suzuki, Misa Mizuguchi, Midori Ohtsuki, Yoshimasu Takeda, Hiroaki Uehara, Naomi Masui, Senya Matsufuji

Identification of Kinases and Phosphorylation Sites Involved in MicroRNA Biogenesis
Erica Jacobs, Brian Chait

New Pucker-specific Parameters for Crystallographic Refinement of RNA
Gary Kapral, Jeff Headd, Ralf Gross-kunstleve, Laura Murray, Jane Richardson

hU3-55K levels regulate U3 snoRNP production whilst hU3-55K phosphorylation is important for rRNA processing
Andrew Knox, Kenneth McKeegan, Charles Debieux, Hannah Richardson, Nicholas Watkins

Ribonucleases P and MRP: Similar Enzymes for Distinct Substrates
Olga Esakova, Anna Perederina, Chao Quan, Elena Khanova, Andrey Krasilnikov

Structure of Human Dicer Determined by High Throughput Single Particle Electron Microscopy
Pick-Wei Lau, Clinton Potter, Bridget Carragher, Ian MacRae

Structure and Function of the Box H/ACA Small Nucleolar Ribonucleoprotein Assembly Factor Shq1.
Hélène Walbott, Rosario Machado-Pinilla, Michael Szmyga, Kate Godin, Dominique Liger, Herman van Tilbeurgh, Thomas Meier, Gabriele Varani, Nicolas Leulliot

Assembling an Interactome Map of the SSU Processome from Existing Protein-Protein Interaction Datasets
Young Lim, Michael Charette, Susan Baserga

Functional Relationship Between the RNA Binding Protein Npl3p and the THO Complex-associated Helicase Sub2p
Mette Lund, Francisco Malagan, Cyril Saguez, Fernando Gonzales, Torben Jensen

Human NOP56 and fibrillarin are present in non-snoRNP complexes
Kenneth McKeegan, Andrew Knox, Charles Debieux, Nicholas Watkins

Structural Studies of Archaeal Box C/D sRNPs
Kathleen Phipps, Susan Baserga

Essential nuclear role of the SMN protein in snRNA-specific Sm core assembly in trypanosomes
Christian Preußer, Nicolas Jaé, Albrecht Bindereif

The Largest Telomerase RNA From The Non-Yeast Fungus, Neurospora crassa
Xiaodong Qi, Yang Li, Shinji Honda, Manja Marz, Steve Hoffmann, Peter Stadler, Eric Selker, Julian Chen

HIV-1 assembly proceeds through body-like complexes and is facilitated by the P body factor DDX6
Jonathan Reed, Kevin Klein, Samina Giri, Jaishi Lingappa

RNA chaperone activates a U3 snoRNA switch - implications for Ribosome Biogenesis
Binal Shah, Timea Gérczei, Carl Correll

NMR Studies of the YTH-domain in Complex with RNA
Dominik Theler, Cyril Dominguez, Zhaiyi Zhang, Stefan Stamm, Frederic Allain

NMR Structure Study of theSpecifier Loop Domain and K-turn Motif from the Bacillus subtilis tyrS T Box Leader RNA
Jiachen Wang, Tina Henkin, Edward Nikonowicz
POSTERS
Small RNAs
Abstracts 498 – 521

Conserved Function of a Ribosomal Protein RACK1 in the microRNA pathway
Sarah Bajan, Guillaume Jannot, Nellie Giguere, Isabelle Banville, Sandra Piquet, Martin Simard, Gyorgy Hutzvagner

In-depth sequencing of small RNAs associated with peach latent mosaic viroid infection
Francois Bolduc, Jean-Pierre Perreault

Widespread Regulation of microRNAs by Reticuloendotheliosis Virus and its Oncogene v-Rel in B-cell lymphomas.
Mohan Bolisetty, Karen Beemon

Digital Genome-Wide ncRNA Expression, Including snoRNAs, Across 11 Human Tissues Using PolyA-Neutral Amplification
John Castle, Chris Armour, David Haynor, Matt Biery, Heather Bouzek, Ron Chen, Jason Johnson, Carol Rohl, Chris Raymond

Downregulation of a host microRNA by a Herpesvirus saimiri noncoding RNA
Demian Cazalla, Therese Yario, Joan Steitz

PIR-1 Is a Conserved, Essential RNA Phosphatase that Interacts with ERI/Dicer Complexes in C. elegans
Daniel Chaves, James Moresco, Weifeng Gu, Shohei Mitani, Craig Mello

Changes in Topological Isomeric Space Correlate with microRNA Maturation Efficiency
Paul Dallaire, Marc Parisien, Karine St-Onge, Huiping Tan, Keith Szulwach, Christopher Ma, Peng Jin, Francois Major

MI RNA Gene Evolution in Arabidopsis lyrata and Arabidopsis thaliana
Noah Fahlgren, Sanjuro Jogdeo, Kristin Kasschau, Christopher Sullivan, Elisabeth Chapman, Sascha Laubinger, Lisa Smith, Mark Dasenko, Scott Givan, Detlef Weigel, James Carrington

Structural and Functional Investigations of the MiR-23~24-2 Micro RNA Cluster.
H. Ebhardt, Steven Chaulk, Richard Fahlman

Mouse oocyte growth is accompanied by reduction of microRNA activity and P-body disassembly
Matyas Flemr, Jun Ma, Radek Malik, Paula Stein, Philipp Berninger, Mihaela Zavolan, Richard Schultz, Petr Svoboda

Small RNA-Aminoglycoside Interactions Re-evaluated
Muslum Ilgu, Ichung Shin, Marit Nilsen-Hamilton

Structural insights into the human GW182-PABC interaction in miRNA-mediated deadenylation
Martin Jinek, Marc Fabian, Nahum Sonenberg, Jennifer Doudna

Cloning of Double stranded RNAs using modified oligos
Amit Khanna, Stefan Stamm

Argonaute-Containing Complexes Pre-Organize microRNA Seed Regions
Nicole Lambert, Sam Gu, Ian MacRae, Alan Zahler

R2D2 Organizes Small Regulatory RNA Pathways in Drosophila
Katsutomo Okamura, Nicolas Robine, Ying Liu, Na Liu, Qinghua Liu, Eric Lai

Interplay Between microRNAs and the Cell Cycle
Olivia Rissland, Sue-Jean Hong, David Bartel

Characterization of Squash Activity Reveals a Potential Role in piRNA Length Determination
Dipali Sashital, Jennifer Doudna
515  Recognition of Prokaryotic Small RNAs by the Hfq Protein  
Evelyn Sauer, Oliver Weichenrieder, Jörg Vogel

516  Filtering Of Deep Sequencing Data Reveals The Existence Of Abundant Dicer-Dependent Small RNAs Derived From tRNAs  
Andrew Sobala, Christian Cole, Cheng Lu, Shawn Thatcher, Andrew Bowman, John Brown, Pamela Green, Geoffrey Barton, Gyorgy Hutvagner

517  Small RNAs processed from Arabidopsis thaliana pri-miRNAs  
Łukasz Sobkowiak, Bogna Szarzynska, Wojciech Karłowski, Hanna Marciszek, Ewa Sobiesczuk, Artur Jarmolowski, Zofia Szewykowska-Kulinska

518  Increased Specificity of RNA Interference with siRNAs Incorporating Unlocked Nucleobase Analogs  
Narendra Vaish, Feng Chen, Shaguna Seth, Kathy Fosnaugh, Roger Adami, Yan Liu, Yan Chen, Pierrot Harvie, Rachel Johns, Tod Brown, Gregory Severson, Susan Bell, Brian Granger, Tianying Zhu, Yoshiyuki Matsui, Pat Charmley, Alan So, Mike Houston, Michael Templin, Barry Polisky

519  Development of Lentiviral-based miRNA Overexpression Particles  
Melissa Kelley, Jamie Cearley, Allison St. Amand, Katie Spayd, Jon Karpilow, Annaleen Vermeulen, Devin Leake

520  Abstract Withdrawn

521  Small RNA with 5’-Polyphosphate Termini Regulate Gene Expression in the Deep Branching Eukaryote Entamoeba histolytica  
Hanbang Zhang, Neil Hall, Upinder Singh

POSTERS
Splicing Mechanisms
Abstracts 522 – 547

522  In vitro and in vivo approaches to study chromatin, transcription and splicing coupling  
Eric Allemand, Michael Myers, Adrian Krainer, Christian Muchardt

523  Direct observation of the DEAH-box ATPase Prp22 during splicing using single molecule fluorescence microscopy  
Eric Anderson, Aaron Hoskins, Larry Friedman, Jeff Gelles, Melissa Moore

524  Mechanism Of CD45 Exon 4 ESS1 In Repressing The Spliceosome Assembly  
Ni-ting Chiou, Kristen Lynch

525  Breaking down the spliceosome: searching for the core  
Patricia Coltri, Kerstin Effenberger, Robert Chalkley, Al Burlingame, Melissa Jurica

526  A novel class of intron requires an intron-spanning stem loop for correct processing  
Eric Lim, Will Fairbrother

527  The effects of genome reduction on splicing and transcription in microsporidia  
Renny Lee, Cameron Grisdale, Naomi Fast

528  A Residue in the RNaseH-like Domain of Prp8 is Important During the Catalytic Stage of pre-mRNA Splicing  
Sebastian Fica, Joseph Piccirilli, Jonathan Staley

529  Pre-mRNA Micro-Introns in the Human Genome: Are They Spliced by the Massive Spliceosome?  
Noriko Haraguchi, Makoto Shimada, Akila Mayeda

530  Screening For Factors Involved In The 'Unconventional Splicing' Of Xbp1 mRNA  
Katrin Heindl, DRSC Consortium, Toshikatsu Hanada, Javier Martinez

531  Genome-Wide Analyses of prp8 Alleles Implicated in the Two-State Model for Spliceosome Activity  
Maki Inada, Jeffrey Pleiss

532  Displacement of SF3 From the Intron Branchpoint Initiates the First Step of pre-mRNA Splicing  
Rea Lardelli, Scott Stevens
Using smFRET to Probe the Mechanism of U4/U6 Unwinding by the Brr2 Helicase and its Prp8 Regulator
Sarah Ledoux, John Abelson, Haralambos Hadjivassiliou, Corina Maeder, Christine Guthrie

The Role of hPRP2/DHX16 and hSPP2/GPKOW in Human Spliceosome Function
Ting-Yu Lin, Shengbing Zang, Shwu-Bin Lin, Aimin Huang, Ren-Jang Lin

Getting Close to Splice Sites: The Proximity Rule Revisited
William Mueller, Peter Shepard, Eun-A Choi, Martin Hicks, Klemens Hertel

Unusual and unexpected spliced leader RNAs in basal nematodes shed new light on the evolution of trans-splicing in nematodes
Jonathan Pettitt, Neale Harrison, Andreas Kalbfleisch, Bernadette Connolly, Berndt Muller

Interactions between a novel motif in the DEAD-box Prp5 protein and U2 RNA
R. Otero, S. Ruby

Characterization of Prp24’s U4/U6 Matchmaking Activity in a Minimal Fluorescent System
Ashley Richie, David Brow, Samuel Butcher

The Role of 3’ splice site Recognition During Human Spliceosome Assembly
Gabriel Roybal, Janine Ilagan, Melissa Jurica

A Novel Motif in the DEAD-box Prp5 Protein Required for RNA-dependent ATPase Activity and for Splicing Fidelity
S. Ruby, A. Hermes, R. Otero, E. Vaughn

RNA Binding by the Spliceosomal Protein p14
Matthew Schellenberg, Erin Dul, Andrew MacMillan

Role of Transcript Identity in Yeast Spliceosome Assembly
Inna Shcherbakova, Aaron Hoskins, Larry Friedman, Jeff Gelles, Melissa Moore

Analysis of XBP1mRNA splicing reaction in unfolded protein response.
Sayoko Shinya, Yusuke Imagawa, Hiroshi Kadokura, Kenji Kohno

Characterization of a Novel Role for the Bur Cyclin Dependent Kinase Complex in pre-mRNA Splicing
Hervé Tiriac, Tracy Johnson

Dynamics In The Catalytic Center Of The Spliceosome
Chi-Kang Tseng, Hsin-Chou Chen, Soo-Chen Cheng

Deciphering 3’ Splice Site Selection In The Saccaromyces cerevisiae Genome
Markus Meyer, Mireya Plass, Eyra Eduard, Josep Vilardell

The Role of the DEAH box ATPase Prp2 in snRNA Rearrangements and Spliceosome Activation
Alissa Wlodaver, Yong Zhang, Jonathan Staley

POSTERS
Splicing Regulation
Abstracts 548 – 604

hnRNP M and MyEF2 are Novel Fox-binding Proteins and Regulators of Fox-dependent Splicing
Andrey Damianov, Lori Kohlstaedt, Douglas Black

Functional characterization of the RNA binding properties of Epithelial Splicing Regulatory Protein 1 (ESRP1)
Karine Amirikian, Claude Warzecha, Kimberly Dittmar, Russ Carstens

Genome-Wide Analysis of Alternative Splicing by Drosophila Polypyrmidine Tract Binding Protein, dPTB/hephaestus
Julie Aspden, Marco Blanchette, Don Rio

Characterization of Alternative Splicing Events Co-regulated by Drosophila hrp48 and PSI
Julie Aspden, Angela Brooks, Steven Brenner, Marco Blanchette, Don Rio
RNA Targets of Plant-Specific SR-Proteins and Their Role in Stress Response
Maria Kalyna, Olga Bannikova, Monika Maronova, Craig Simpson, John Brown, Andrea Barta

DNA Damage Induces Exon Skipping Independently of Transcriptional Coupling to Alternative Splicing
Ravi Singh, Thomas Bebee, Aishwarya Jacob, Dawn Chandler

Analyzing the Global Splicing Regulatory Networks of the SR Family of Proteins
Todd Bradley, Marco Blanchette

Mutational Analysis of an SR Protein in the Fission Yeast Schizosaccharomyces pombe
James Broughton, Jeffrey Pleiss

Mechanism of a U1snRNA-dependent Silencing Module
Michael Chen, Panagiotis Papasaikas, Stephanie Hughes, A. Javier Lopez

The ASF/SF2 RS Domain Phosphorylation and Dephosphorylation Act as a Regulatory Switch in Pre-mRNA Splicing
Suhyung Cho, Rahul Sinha, Adrian Krainer, Gourisankar Ghosh

Efficient Manipulation of Alternative Splicing Events Using Antisense Morpholinos Allows In Vivo Testing of Splicing Regulation Models in Mice
Marilyn Parra, Thomas Gallagher, Sharon Amacher, Narla Mohandas, John Conboy

Deep Intron Fox2-dependent Enhancers Regulate Breast Cancer Subtype-Specific Alternative Splicing Events In Vitro and In Vivo
Henry Marr, Marilyn Parra, Sherry Gee, Joe Gray, John Conboy

Alternative Polyadenylation Affects Alternative Splicing
Tara Crabb, Peter Shepard, Klemens Hertel

Alternate binding of SRp20 and hnRNPs K and L regulate pre-mRNA splicing in response to changing nutrient availability
Travis Cyphert, Callee Walsh, Lisa Salati

Splicosomal Cyclophilins: From Structure to Function and Back Again
Tara Davis, John Walker, Patrick Finerty, Jr., Elan Eisenmesser, Sirano Dhe-Paganon, Melissa Jurica

Modulation of VEGF-A alternative splicing as new anti-angiogenic therapeutics
Daniel Dominguez, Zefeng Wang

The Mechanism of Muscleblind-like 1 (MBNL1)- Mediated Splicing Activation
Gloria Echeverria, Thomas Cooper

Identification of a putative G-quadruplex Structure Regulating BACE1 Alternative Splicing
Jean-Francois Fisette, Michael Wolfe

Elucidating the Functions of Splicing Regulatory Proteins through the Use of High-throughput Proteomics.
Oliver Fregoso, Adrian Krainer

Fox1 and Fox4 regulate muscle-specific splicing during zebrafish embryogenesis and are required for proper cardiac and skeletal muscle function
Thomas Gallagher, Joshua Arriberre, Henry Marr, Kariena Dill, Shaunak Adkar, Sharon Amacher, John Conboy

Auto-regulation of pre-mRNA Splicing by MBNL1
Devika Gates, Amy Mahady, Andy Berglund

Elucidating the Complex pre-mRNA Splicing Regulation of the SMN Genes using Evolutionarily Conserved Sequence Comparison
Jordan Gladman, Thomas Bebee, Dawn Chandler

Defining Determinants of Splicing Regulation by hnRNP L and hnRNP LL
Sarah Glenn, Ni-ting Chiou, Kristen Lynch

The Conserved Splicing Factor Cwc21p Stabilises The Spliceosome's Catalytic Centre Under Episodes Of Thermal Stress
Richard Grainger, David Barrass, Daniela Hahn, Jean Beggs
572 Regulation of Ribosomal Protein Gene Splicing by an Intron-Independent, Promoter-Dependent Mechanism in Budding Yeast
Megan Bergkessel, Jaclyn Greimann, Christine Guthrie

573 Identifying the Molecular Basis for Transcript-Specific Splicing Defects in prp8-101
Mohanram Gudipati, Laura-Oana Bud, Nevin Sabet, Jeffrey Pleiss

574 Splicing Regulation and Human Cell Aging
Houda Hallay, Ana Rita Grosso, Joana Cardoso, Noélia Custódio, Birgit Weissenböck, Teresa Pacheco, João Ferreira, Maria Carmo-Fonseca

575 Exporting a Natural Cassette Exon for Engineered Gene Regulation in Plants
Scott Hickey, Alexander Westermann, Ming Hammond

576 Regulation of Hypoxic Cell Death by RNA-binding Protein hnRNP A1
Kyoung Ha Han, Won-Ki Kim, Hyo-Jin Kim, Byung Kwan Jin, Yong-Keun Jung

577 Understanding the Structural and Functional Differences between PTB and Neuronal PTB
Niroshika Keppetipola, Douglas Black

578 A Change in the Splicing Pattern as a Function of Time
Hadas Keren, Gil Ast

579 New actors in regulation of HIV-1tat mRNA production
Georges Khoury, Lilia Ayadi, Jean Michel Saliou, Sarah Sanglier, Delphine Ropers, Christiane Branlant

580 RBM38 is a Mammalian Spicing Factor
Yi Li, Behnam Nabet, Debashish Ray, Timothy Hughes, Russ Carstens

581 Coordinated control of alternative splicing during muscle cell differentiation
Jung-Chun Lin, Woan-Yuh Tarn

582 A Role for Cell Type-Specific snRNP Profiles in the Regulation of Alternative Splicing.
Francesco Lotti, Luciano Saieva, Michael Briese, Jernej Ule, Livio Pellizzoni

583 A Zebrafish Model for the in vivo Study of the Biological Role of U12-type Introns in Development
Francesco Lotti, Luciano Saieva, Michael Briese, Jernej Ule

584 The Circadian Clock regulates Alternative Splicing in the Mouse.
Nicholas McGlincy, Amandine Valomon, Johanna Chesham, Elizabeth Maywood, Michael Hastings, Jernej Ule

585 Analysis of Factors That Bind the Retroviral SSS Splicing Repressor
Lisa McNally, Mark McNally

586 EJC components moonlight as splicing regulators of Bcl-x and other apoptotic genes
Laetitia Michelle, Prinos Panagiotis, Philippe Thibault, Roscoe Klinck, Sherif Abou Elela, Benoit Chabot

587 A Functional Genomic Screen Defines An Alternative Splicing Network Linking Cell Cycle Control to Apoptosis
Michael Moore, Pamela Silver

588 Polyphenols as splicing inhibitors
Andrea Pawellek, Ursula Ryder, Angus Lamond

589 Investigating the Mechanism Through Which MBNL1 Functions as a Splicing Enhancer
Jamie Purcell, Benjamin Armstrong, Andy Berglund

590 Antisense Oligonucleotides Can Be Chemically Modified to Manipulate Splicing in the Desired Direction
Frank Rigo, Frank Bennett, Yimin Hua, Adrian Krainer

591 A role for the core snRNP protein SmB/B' in the regulation of alternative splicing
Arneet Saltzman, Qun Pan, Benjamin Blencowe

592 Functionally Swappable RNA Domains in Human U12 and U6atac snRNAs
Kavleen Sikand, Tupa Basu-Roy, Girish Shukla
Arginine Methylation Controls the Subcellular Localization and Functions of the Oncoprotein Splicing Factor SF2/ASF
Rahul Sinha, Eric Allemand, Zuo Zhang, Rotem Karni, Michael Myers, Adrian Krainer

Adaptive Significance of Unproductive Alternative Splicing in Longevity and Aging
Adonis Skandalis, Emma Bondy-Chorney

Histone acetylation regulates alternative splicing
Jarmila Hnilicova, Eva Duskova, Tereza Tomankova, David Stanek

A role for Drosophila Argonaute 2 in the regulation of alternative splicing
Jefferson Taliaferro, Angela Brooks, Marco Blanchette, Donald Rio

PTB/nPTB Regulation of ROD1 Isoforms and their Functional Consequences
Lit Yeen Tan, Miriam Llorian, Chris Smith

The U11 snRNP-binding Splicing Enhancer Activates Upstream 3' Splice Sites by Promoting the Assembly of the U2-type Spliceosomal Complex E
Janne Turunen, Mikko Frilander

The Splicing of the REST/NRSF Exon N is Activated by hnRNP H and U2AF65 Over-expression in Small Cell Lung Cancer (SCLC) H69 Cells
Carlos Ortuño Pineda, Jesús Valdés

Activation of Pyruvate Kinase-M Exon 10 in proliferating cells
Zhenxun Wang, Deblina Chatterjee, Martin Akerman, Cynthia Clower, Matthew Vander Heiden, Lewis Cantley, Adrian Krainer

Identification of a Depolarization-Dependent Mechanism Regulating Alternative Splicing of Synaptic Receptor Neurexin
Harald Witte, Takatoshi Iijima, Karen Wu, Peter Scheiffele

Discovery of alternative splicing modulators and general splicing inhibitors by multiplex high throughput screening with rapid response reporters
Ihab Younis, Gideon Dreyfuss

Is The Functional Difference Between Two Alternatively Spliced SR45 Isoforms In Arabidopsis Preserved In Two Rice SR45 Orthologs During Evolution?
Jason Chien, Kevin Cilano, Stephen Mount, Xiao-Ning Zhang

Regulation of Co-Transcriptional Splicing by Hu Proteins
Hualin Zhou, Hua Lou

POSTERS
Translation Regulation
Abstracts 605 – 624

The AtLARP1 protein is a new component of A.thaliana stress granules that interacts with AtPAB2 and AtXRN4
Cécile Bousquet-Antonelli, Julie Descombin, Jean-Marc Deragon

Functional Overlap of eIF4G Isoforms in Saccharomyces cerevisiae
Bryan Clarkson, Wendy Gilbert, Jennifer Doudna

Interactions Between Adjacent CGA Codons Affect Translation Efficiency in Saccharomyces cerevisiae
Kimberly Dean, Daniel Letzring, Elizabeth Grayhack

Ambiguous Decoding of the CUG Codon Alters Functionality of the Candida albicans Translation Initiation Factor 4E
Zuzana Feketova, Tomas Masek, Vaclav Vopalensky, Martin Pospisek

Running Red Lights: A Search for Stop Codon Readthrough in Drosophila and Human Genomes
Eli Fine, William Fairbrother
The RNA binding protein HuD interacts with active Akt1 to trigger neurite outgrowth
Akira Fukao, Yumi Sasano, Kunio Inoue, Hiroshi Sakamoto, Nahum Sonenberg, Thoma Christian, Toshinobu Fujiwara

Viral and Cellular IRESs utilize a common mechanism to initiate translation
Marla Hertz, Dori Landry, Anne Willis, Guangxiang Luo, Sunnie Thompson

Loss of PDCD4 Derepresses Translation of Antiapoptotic Genes in Glioblastoma
Lindsay Jordan, Stephen Lewis, Olivier Pardo, Michael Seckl, Martin Holcik

The Shuttling Protein Npl3 Promotes Translation Termination Accuracy in Saccharomyces cerevisiae
Clarivel Lasalde, Luis Estrella, Maria Correa, Miles Wilkinson, Carlos Gonzalez

Wobble decoding of CGA codons reduces translation but not mRNA stability
Daniel Letzring, Kimberly Dean, Elizabeth Grayhack

m7G cap-assisted internal initiation of translation
Franck Martin, Sharief Barends, Laure Schaeffer, Lydia Prongidi-Fix, Gilbert Eriani

The Chemotherapeutic Bortezomib Agent Induces Stress Granules Formation
Cristina Gareau, Marie-Josée Fournier, Rachid Mazroui

The Role of Structured Elements Within Human 3' UTRs in MicroRNA-Mediated Regulation
Stefanie Mortimer, Jennifer Doudna

Biochemical characterization of yeast translation initiation factor (eIF) 4A
Vaishnavi Rajagopal, Jon Lorsch

A novel type of IRES recruits up to three initiation complexes on HIV Genomic RNA
Nathalie Chamond, Nicolas Locker, Nathalie Ulryck, Bruno Sargueil

Two Distinct Complexes Containing RBG GTPases Collaborate with a new Factor and Are Required for Efficient Translation
Marie-Claire Daugeron, Manoël Prouteau, François Lacroute, Bertrand Séraphin

Analysis of the 5’ Splice Site of a MicroRNA Coding Intron
Neha Aggarwal, Jagjit Singh, Kavleen Sikand, Girish Shukla

Determining the Role of mRNA Structure in Translational Bypassing of Bacteriophage T4 Gene 60
Gabrielle Todd, Nils Walter

Unraveling the role of starvation-induced Translation Machinery Associated proteins
Pavanapuresan Vaidyanathan, Wendy Gilbert

Role of mRNA Circularization in Eukaryotic Translation Initiation
Sarah Walker, Jon Lorsch

POSTERS

tRNA, snoRNA and rRNA
Abstracts 625 – 650

Bioinformatics of tRNA Identity Elements across the Tree of Life
David Ardell

Structural Changes in Box C/D sRNPs during Catalysis of 2'-O-ribose methylation
Franziska Bleichert, Susan Baserga

Discovery of Permut ed tRNAs and Widely Distributed Split tRNAs in Crenarchaea
Patricia Chan, Aaron Cozen, Lauren Lui, Todd Lowe

The Adenylation Reaction in Valyl-tRNA Synthetase
Mark Cunningham

Structural and Stability Effects of Base Modifications on the Tyrosyl-Anticodon Stem-Loop from Bacillus subtilis
Andria Denmon, Edward Nikonowicz
An RNA ligase and kinase/cyclic phosphodiesterase resemble the yeast-type RNA ligation pathway in an animal model organism
Markus Englert, Sarath Gundlupalli, Hildburg Beier, Dieter Söll

An RNA ligase and kinase/cyclic-phosphodiesterase resemble the yeast-type RNA ligation pathway in an animal model organism
Markus Englert, Sarath Gundlupalli, Hildburg Beier, Dieter Söll

Comprehensive Prediction of Eukaryotic tRNAs with Introns Located at Non-Canonical Positions
Kiyofumi Hamashima, Junichi Sugahara, Kosuke Fujishima, Masaru Tomita, Akio Kanai

snOPY: A Small Nucleolar RNA Orthological Gene Database
Jun-ichi Iwakiri, Maki Yoshihama, Hiroki Tateishi, Akihiro Nakao, Naoya Kenmochi

Revisiting the Role of RNase P in tRNA Processing in *Escherichia coli*
Sidney Kushner, Ankit Agarwal, Bijoy Mohanty

Characterization of *S. pombe* tRNA Isopentenyltransferase and Discovery of tRNA<sup>Trp</sup> as a Previously Unknown Substrate
Tek Lamichhane, Nathan Blewett, Vera Cherkasova, Amanda Crawford, Thomas Begley, Richard Maraia

The Nuclear Poly(A)-binding Protein Interacts with the Exosome to Promote Synthesis of Noncoding Small Nucleolar RNAs
Jean-François Lemay, Annie D’Amours, Caroline Lemieux, Daniel Lackner, Valérie St-Sauveur, Jürg Bähler, François Bachand

Depletion of Key Protein Components of the RISC Pathway Impairs Pre-ribosomal RNA Processing
Xuehai Liang, Stanley Crooke

Identification of C/D Box Small RNAs in Archaea via RNA-Seq and Computational Screens
Lauren Lui, Andrew Uzilov, David Bernick, Todd Lowe

A Novel Role of hClp1 in pre-tRNA Processing
Barbara Mair, Stefan Weitzer, Johannes Popow, Toshikatsu Hanada, Sabrina Bandini, Tilmann Bürckstümmer, Christopher Trotta, Javier Martinez

The NIP7 protein is required for accurate pre-rRNA processing in human cells
Luis Morello, Cedric Hesling, Patricia Coltri, Beatriz Castilho, Nilson Zanchin

Metagenomic Analysis of Small RNA Fraction Obtained from Uncultured Microbes in Yunohama Hot Spring
Shinnosuke Murakami, Kosuke Fujishima, Junichi Sugahara, Motomu Matsui, Masaru Tomita, Akio Kanai

Crystal Structure of a Splicing Endonuclease from the Crenarchaeon *Aeropyrum pernix*
Maho Okuda, Tsubasa Kitajima, Tomoo Shiba, Akira Hirata, Daniel Inaoka, Kiyoshi Kita, Genji Kurisu, Shigeharu Harada, Hiroyuki Hori, Yoh-ichi Watanabe, Shigeo Yoshinari

Wanted and Probably Found: the Human tRNA Ligase Revealed?
Johannes Popow, Markus Englert, Stefan Weitzer, Alexander Schleiffer, Thomas Biederer, Beata Mierzwa, Karl Mechtler, Simon Trowitzsch, Cindy Will, Reinhard Lührmann, Dieter Söll, Javier Martinez

Saccharomyces cerevisiae tRNA<sup>His</sup> undergoes Modification Changes Under Different Conditions
Melanie Preston, Kady Krivos, Patrick Limbach, Eric Phizicky

Novel 5’-tRNA repair-like activity of bacterial and archael tRNA<sup>His</sup> guanylyltransferase (Thg1) homologs
Bhalchandra Rao, Emily Maris, Jane Jackman

AtNUFIP is required for *Arabidopsis* development and its role on snoRNP assembly is linked to snoRNA genomic structure

The role of the human exosome in pre-rRNA turnover
Katherine Sloan, Nicholas Watkins
Mechanistic insight into novel 3'--5' nucleotide addition activity catalyzed by eukaryotic tRNA\textsuperscript{His} guanylyltransferase (Thg1)
Brian Smith, Samantha Hyde, Brian Eckenroth, Sylvie Doublié, Jane Jackman

The mutation of the C. elegans genomic locus encoding a snoRNA has a defect in the pre-rRNA processing.
Chisato Ushida, Yusuke Hokii, Yumi Sasano, Mayu Sato, Hiroshi Sakamoto, Hyouta Himeno, Akira Muto, Toshinobu Fujiwara

The 3' maturation of human 18S rRNA
Andrew Knox, Nicholas Watkins

POSTERS
Viral RNAs
Abstracts 651 – 667

Splicing in High and Low Pathogenic Influenza A Viruses
Ellenor Backström, Susanne Tingsborg, Samir Abdurahman, Sofia Lindström, Anna Tranell, Stefan Schwartz

RNA Processing Factors Interact with the Assembly Pathway of the Oncogenic Retrovirus MMTV
Darrin Bann, Andrea Beyer, Leslie Parent

An EJC-Independent Mechanism of Nonsense-Mediated RNA Decay Requires an RNA Stabilizing Sequence in the 3’ UTR
Karen Beemon, Johanna Withers, Jason Weil

Studies on the Mechanism of the Upstream RNA Element that Down-Regulates the -1 PRF Efficiency of SARS CoV
Ming-Yuan Chou, Kung-Yao Chang

Thermodynamics of Aminoglycoside Binding to the HIV-1 Genomic RNA Dimerization Initiation Site and Structure-guided Discovery of a Novel Aminoglycoside Mimetic Targeting the Viral Genome
Eric Ennifar, Severine Freisz, Serena Bernacchi, Waqar Aslam, Floris van Delft, Philippe Dumas

Kinetic Analysis for the Interaction of Initiation Factors (eIFs) with Tobacco Etch Virus Internal Ribosome Entry Site RNA
Mateen Khan, Dixie Goss

Modular domains of the dicistrovirus intergenic internal ribosome entry site
Christopher Jang, Eric Jan

High-throughput SHAPE analysis of FIV packaging and genome dimerisation signals
Julia Kenyon, Sian Tanner, Michal Legiewicz, Pretty Phillip, Tahir Rizvi, Stuart Le Grice, Andrew Lever

Engineering Aptamers to HIV-1 RT for Improved Antiviral Bioactivity
Margaret Lange, Angela Whately, Donald Burke

HTLV-1 Tax Inhibits Stress Granules Formation by Interacting with the Histone Deacetylase 6 (HDAC6)
Sebastien Legros, Mathieu Boxus, Jean-Claude Twizere, Richard Kettmann, Franck Dequiedt

In silico interrogation of the complete rotavirus genome database, and selective biochemical probing, reveal highly conserved RNA structures with potential cis-acting functions
Emily Manktelow, Wilson Li, Johann von Kirchbach, Julia Gog, Ulrich Desselberger, Andrew Lever

Thermodynamic characterization of an unusual pseudoknot from influenza A virus RNAs
Fei Liu, Carla Theimer

The Distribution and Function of the Adenovirus L4-33K Protein
Heidi Persson, Sara Östberg, Ellenor Backström, Göran Akusjärvi

An Analysis of the RNA Transport Element of the MusD Murine LTR Retrotransposon Reveals Functionally Necessary Structural Interactions
Guy Pilkington, Michal Legiewicz, Andrei Zolotukhin, Hiroaki Uranishi, Jenifer Bear, George Pavlakis, Stuart Le Grice, Barbara Felber
<table>
<thead>
<tr>
<th>Number</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>665</td>
<td>Investigating New Structural Motifs in HIV-1 and SIV&lt;sub&gt;mac239&lt;/sub&gt; Genomic RNA</td>
<td>Elizabeth Pollom, Joseph Watts, Robert Gorelick, Kevin Weeks, Ronald Swanstrom</td>
</tr>
<tr>
<td>666</td>
<td>Identification and Functional Conservation of gamma-Herpesviral microRNAs</td>
<td>Kasandra Riley, Gabrielle Rabinowitz, Joan Stetiz</td>
</tr>
<tr>
<td>667</td>
<td>Packaging of Ro RNP RNAs by Murine Leukemia Virus is Highly Selective and May Occur Early During Y RNA Biogenesis</td>
<td>Eric Garcia, Adewunmi Onafuwa-Nuga, Soyeong Sim, Sandra Wolin, Alice Telesnitsky</td>
</tr>
</tbody>
</table>

**POSTER**

**RNA Turnover**

Abstract 668

**POSTER**

**RNP Structure, Function and Biosynthesis**

Abstract 669

**POSTER**

**Bioinformatics**

Abstract 670

**POSTER**

**RNAi**

Abstract 671

<table>
<thead>
<tr>
<th>Number</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>668</td>
<td>Understanding the Role of Phosphorylation of Upf1 in the NMD Pathway</td>
<td>Clarivel Lasalde, Andrea Rivera, Eva Rodriguez-Cruz, Alfredo Leon, Irving Vega, Miles Wilkinson, Carlos Gonzalez</td>
</tr>
<tr>
<td>669</td>
<td>Structural basis for double-stranded RNA processing and insights into the catalytic mechanism and evolution of a non-canonical Dicer</td>
<td>Kotaro Nakanishi, David Weinberg, David Bartel, Dinshaw Patel</td>
</tr>
<tr>
<td>670</td>
<td>SwS (2.0): A Structural and Solvation web Service for Nucleic Acids – Link between Solvation and Amino Acid Binding Sites</td>
<td>Pascal Auffinger, Ludovic Roy, Yaser Hashem</td>
</tr>
<tr>
<td>671</td>
<td>Diverse endonucleolytic cleavage sites in the mammalian transcriptome depend upon microRNAs, Drosha, and additional nucleases</td>
<td>Fedor V. Karginov, Sihem Cheloufi, Alexander Stark, Andrew D. Smith, and Gregory J. Hannon</td>
</tr>
</tbody>
</table>