

Eukaryotic mRNA Processing

Session 1 SYSTEMS-LEVEL APPROACHES TO REGULATION OF mRNA

WEDNESDAY 8/24/2005, 7:30 PM

M. Ares

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
1	Ares	Tissue-regulated alternative exons identified by splicing microarrays are enriched for adjacent blocks of extreme intron sequence conservation	6
2	Conboy	Analysis of conserved sequences flanking tissue-specific exons discovered by genome-wide exon expression	6
3	Fu	Splicing arrays revealed cell type specific alternative splicing, extensive coupling between transcription and splicing, and cancer specific mRNA isoform markers	12
4	Corioni	Isolation of in vivo RNA targets of human splicing factor SF1	12
5	Gama-Carvalho	The polypyrimidine-binding splicing factors U2AF ⁶⁵ and PTB associate with functionally distinct subsets of mRNA molecules post-splicing	12
6	Spellman	Global survey of PTB function by RNAi and quantitative proteomics reveals functional redundancy between PTB and nPTB	12
7	Damianov	Zebrafish mutant in U4/U6 snRNP recycling factor p110 reveals network of coregulated spliceosomal components	12
8	Blanchette	Distinct transcript and protein composition of individual <i>Drosophila</i> hnRNP A/B family members	12
9	Yeakley	Large-scale identification of alternative splicing regulators and their regulated targets in <i>Drosophila</i> using high-throughput microarrays	12
10	Rehwinkel	Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets	12
11	Pleiss	Genome-wide profiling reveals complex splicing regulation in yeast	12
12	Foat	Profiling condition-specific, genome-wide regulation of mRNA stability in yeast	12

Session 2 ALTERNATIVE AND REGULATED SPLICING I

THURSDAY 8/25/2005, 9:00 AM

D. Black

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
13	Shi	Multiple factors regulate SRp38 phosphorylation	12
14	Srebrow	Concerted regulation of alternative splicing and translation by extracellular cues through SR proteins	12
15	Karni	Oncogenic activity of alternative splicing factors	12
16	Cheng	A positive feedback loop of CD44 alternative splicing and its regulation by SRm160	12
17	Lynch	hnRNP-L binds to a regulated exonic splicing silencer and blocks exon usage at a step past U1 and U2 snRNP binding	12
18	Lin	Delinearizing SR protein functions in RNA metabolism by somatic complementation in mouse embryo fibroblasts	12
19	Baralle	Heterogeneity of the G run RNA-protein complexes and definitions of 5' and 3' splice	12
20	Zhu	Hu proteins regulate the neuron-specific processing of the human calcitonin/CGRP pre-mRNA by blocking activity of TIA-1/TIAR proteins	12
21	An	Roles of RNA sequence motifs in depolarization induced alternative splicing in primary neurons	12
22	Ule	Position of YCAY clusters predicts Nova-dependent splicing regulation	12
23	Wise	Meiosis-specific splicing in fission yeast—Intron retention in vegetative cells is enforced by novel regulatory mechanisms	12

Session 3 RNA TRAFFICKING AND LOCALIZATION

THURSDAY 8/25/2005, 2:00 PM

U. Kutay

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
24	Corbett	Nuclear pore-associated Mlp proteins assure both rapid and accurate export of mRNA transcripts	10
25	Palancade	A new protein of the nuclear periphery required for nuclear retention of improper mRNPs in <i>S. cerevisiae</i>	10
26	Weis	The local activation of the DExD/H-box protein Dbp5 at the nuclear pore is essential for mRNA export in yeast	10
27	Prasanth	Regulating gene expression through RNA nuclear retention	10
28	Kedersha	TTP promotes dynamic interactions between stress granules and mRNA processing bodies	10
29	Andrei	eIF4E-T interacts with the cap-binding protein eIF4E inside the processing bodies and is required for their assembly	10
30	Caceres	Signaling mechanisms regulate the localization and activity of hnRNP A1—A role in the stress response	10
31	Wagner	Identification of a nuclear deadenylase complex associated with cajal bodies	10
32	Tretyakova	Mouse NXF7 is part of mRNA transport intermediates in the cytoplasm	10
33	Jambhekar	A seven base motif mediates bud localization of mRNA in <i>S. cerevisiae</i>	10

#	Iname	Title	Talk Length
34	Abdelmohsen	SIRT1-mRNA is a target of RNA-binding protein HuR	
35	Addepalli	A random combinatorial approach identifies novel protein-protein interactions involving <i>Arabidopsis</i> polyadenylation factors	
36	Allemand	Regulation of alternative splicing by a functional interaction between phosphatase PP2C γ and YB-1	
37	Armisen	Mer1p recruits U1 and U2 snRNPs to pre-mRNA containing Mer1p enhancer sequence but lacking a branchpoint sequence	
38	Araujo	Regulation of alternative splicing of the MIA gene	
39	Ayala	Exon splicing—Sophisticated regulation or struggle for survival?	
40	Kaufmann	A novel protein kinase involved in RNA Pol II transcriptional termination in <i>S.</i>	
41	Sperling	Reconstitution of supraspliceosomes from native spliceosomes	
42	Berg	High level mRNA and protein production from transgenes in the adenoviral MLTU	
43	Bergkessel	Regulation of mRNA splicing in response to amino acid starvation	
44	Moraes	LSM proteins bind the 5' poly(A) tract of poxvirus mRNA and inhibit its decay	
45	Bhalla	Premature termination codons elicit a nuclear-to-cytoplasmic partitioning shift	
46	Wieslander	Ct-RSF represses SR protein function locally on pre-mRNA exons and is displaced at correct splice sites	
47	Blechingberg	Mechanisms of alternative polyadenylation and splicing events in the GFAP gene	
48	Zheng	HPV-16 E2 and E6 are promiscuous RNA-binding proteins that interact with cellular splicing factors and inhibit in vitro splicing of a subset of pre-mRNAs	
49	Bor	The Wilms' tumor 1 (WT1) gene (+KTS isoform) functions with a CTE to enhance expression from an unspliced RNA with a retained intron	
50	Boulanger	Charting the surface of the human spliceosome	
51	Bourgeois	What does make SC35 a powerful sequence-specific splicing transactivator?—Searching for SC35 cofactors	
52	Bruno	Analysis of the effects of depleting the NMD factors BTZ and eIF4A3 by inducible	
53	Gunderson	In vitro studies to reconstitute caffeine induced alternative splicing	
54	Barabino	Multiple domains control subnuclear localization and nucleocytoplasmic shuttling of the heterodimeric pre-mRNA 3' end processing factor CF I _m	
55	Cass	SF3b155: A scaffold for A complex	
56	Castorino	Functional dissection of the <i>c-myc</i> coding region determinant	
57	Kleiman	Role of the DNA damage-induced inhibition of polyadenylation in transcription-coupled repair (TCR)	
58	Chakrabarti	Non-coding RNA genes in malaria parasites	
59	Chan	TCR nonsense-mediated decay is insensitive to Upf3b depletion	

60	Chang	A transcriptionally competent nuclear substructure induced by transcription inhibition
61	Chang	T-cell receptor nonsense-associated altered splicing
62	Chawla	Studies on the interaction of polypyrimidine tract binding protein and Sam68
63	She	Crystal structure and functional analysis of DEAD-box protein Dhh1p
64	Chu	Apoptosis is induced in mammalian cells by siRNA knock-down of mRNA capping enzymes
65	Clark	Genome-wide analysis of alternative splicing using high-density human exon
66	Clement	MK2 induced phosphorylation of tristetraprolin inhibits ARE-mediated mRNA decay downstream of mRNA binding
67	Cogan	Improved mutation detection in clinical samples using RT-PCR and direct
68	Crawford	Activation of α -tropomyosin exon 2 is regulated by the SR protein 9G8 and heterogeneous nuclear ribonucleoproteins H and F
69	Horowitz	The Prp18 protein stabilizes the interaction of both exons with loop 1 of U5 during the second transesterification reaction of pre-mRNA splicing
70	Custodio	The carboxy-terminal domain of the large subunit of RNA polymerase II is important for the release of mRNA from the site of transcription
71	Dassah	Tales from the cryptic splice junction—Suppressing +1 mutations at 5' splice sites
72	Datta	Functional dissection of the AU-rich sequence in KC mRNA
73	Davis	A genome-wide screen for increased expression upon loss of Rrp6 allows accumulation of a set of heterogeneous Trf4p polyadenylated promoter-associated transcripts in <i>S. cerevisiae</i>
74	DeCervo	Evidence for the association of p54 ^{nrb} with edited <i>Alu</i> elements in human cells
75	Del Rosario	A role for the essential mRNA export factor, Yra1, in Nap1 function
76	Dery	Suppressor study of U2:U6 snRNA helix 1a mutations in <i>S. cerevisiae</i>
77	Hertel	Genome-wide analysis of cryptic splice site activation
78	Fasken	Analysis of Mlp1 protein function in mRNA quality control
79	Feng	Sequence-specific activation of splicing by the general splicing repressor SRp38
80	Fox-Walsh	The architecture of pre-mRNAs affect mechanisms of splice site pairing
81	Frato	Characterization of DNA and RNA binding of site-directed mutants of U2AF ⁶⁵
82	Hagiwara	Prevention of HIV-1 propagation by synthetic SRPK inhibitor
83	Fukumura	Regulation of alternative splicing by Fox-1 via binding to GCAUG sequence upstream of alternative exon
84	Furic	Identification of the Staufen1-binding motif in mRNAs
85	Garbarino Pico	The deadenylase Nocturnin is acutely induced by different extracellular stimuli

86	Glaunsinger	Accelerated cellular mRNA turnover during lytic herpesvirus infection is mediated by a viral protein that interacts with mammalian exosome components
87	Glover-Cutter	Integration of capping with transcriptional elongation—The roles of transcriptional activators, capping enzyme, and P-TEFb
88	Gooding	A simple algorithm based on AG exclusion zone predicts a number of exons with distant branchpoints
89	Neugebauer	Co-transcriptional spliceosome assembly occurs in a stepwise fashion and requires the cap-binding complex
90	Blanchette	Global analysis of the impact of NMD on the expression of the alternatively spliced mRNA isoforms in <i>Drosophila</i>
91	Lareau	Conserved unproductive splicing of SR proteins
92	Salati	Identification and characterization of a splicing regulatory element involved in insulin and fatty acid regulation of mRNA accumulation
93	Lima	Structural insights into cap-dependent mRNA processing and decay
94	Halasz	A novel method for detecting transcripts using genome-wide tiling arrays
95	Hastings	PUF60 and U2AF ⁶⁵ have similar functions but different effects on alternative
96	Hausmann	Mechanism of RNA cap specific guanine-N2 methyltransferases
97	Henras	Regulation and surveillance of normal and 3'-extended forms of the yeast Aci-reductone dioxygenase mRNA by rnae III cleavage and exonucleolytic degradation
98	Hims	Investigating the mechanism of kinetin induced improvement of <i>1KBKAP</i> exon inclusion in the neurodegenerative disease Familial Dysautonomia
99	Hirose	The ATPase-like spliceosomal protein, X160, is a general intron-binding protein that recruits factors involved in late stages of splicing and post-splicing events
100	Hilleren	The decay fate of splice-defective RNA intermediates
101	Hoopes	Functional analysis of alternative 3'-end formation in the <i>S. cerevisiae</i> <i>SUA7-SRP54</i> intergenic region
102	Olivas	Yeast Puf3 mutants demonstrate the complexity of Puf-RNA binding and identify a region required for regulation of mRNA decay
103	Hua	Correction of exon 7 skipping in <i>SMN2</i> pre-mRNA splicing
104	Huang	Affinity purification and characterization of pre-spliceosome from <i>S. pombe</i>
105	Imam	Nonsense codons upregulate precursor RNA in a frame-dependent manner
106	Iyer	Protein synthesis with self-similar RNAs
107	Jiao	Identification a novel regulator of decapping
108	Kabat	Using evolutionary conservation to identify alternative splicing regulators in <i>C. elegans</i>
109	Sperling	Stop codon-mediated suppression of splicing in vivo and in vitro

110	Kashima	Association between hUPF1 and hUPF2 is required for hSMG-1-mediated phosphorylation of hUPF1 and NMD
111	Kashima	SMN2 exon 7 exclusion involves cooperation between exonic and intronic hnRNP A1 binding sites
112	Kataoka	Analysis of hDBR1 protein that is involved in the post-splicing intron turnover
113	Bedwell	Pst21p is a novel protein that influences poly(A) length, mRNA turnover, and multiple steps of translation in <i>S. cerevisiae</i>
114	Kelly	Interaction between the N-terminal domain of the yeast RNA binding protein, Nab2, and Mlp proteins at the nuclear pore complex regulates export of mature mRNA
115	Ruby	Mapping the interactions of the DEAD-box protein Prp5 with RNA
116	Khandelia	Genetic analysis of fission yeast second step pre-mRNA splicing factors
117	Zieve	Sm core particles assemble from three RNA-free precursors and snRNA in the
118	Gaur	An artificial riboswitch for controlling pre-mRNA splicing
119	Kim	Mechanism behind kinetic coupling between transcription and pre-mRNA processing
120	Takahashi	Association of stress-induced mRNA stabilization with translational repression of upstream open reading frames in ATF5 mRNA
121	Klein	Stimulus specific expression of CREB-induced microRNAs
122	Kozlov	Structural studies of the C-terminal domain of poly(A)-binding protein
123	Kreader	RNase activity in cultured mammalian cells
124	Kupsco	Characterization of <i>Drosophila</i> sniper, a DEDD family exonuclease, homologous to 3'hEXO/ERI-1, in replication dependent histone mRNA expression and RNAi
125	Lal	Post-transcriptional regulation of gadd45 α mRNA by RNA binding proteins AUF1 and TIAR
126	Laneve	Functional and structural characterization of XendoU, the <i>X. laevis</i> endoribonuclease involved in snoRNA biosynthesis, representing the cellular
127	Ohman	Coordination of editing and splicing by the transcription machinery
128	MEREAU	Tissue-specific inclusion of a 3' terminal exon is controlled in vivo by PTB acting on both processing, splicing, and polyadenylation
129	Lee	Characterization of iron homeostasis regulation by RNA surveillance and Rnase III in <i>S. cerevisiae</i>
130	LEE	Multiple RNA elements mediate depolarization-induced alternative splicing of NMDA r1 exon 21
131	Lynch	An enhanced-sensitivity cell based screen to identify modifiers of alternative splicing
132	Li	Expression of the splicing regulatory proteins, PTB and nPTB, is tissue-specific and developmentally regulated

- 133 Li Tap/NXT1 promotes the function of constitutive transport elements isolated from cellular genes
- 134 Lindtner RNA binding motif protein 15 (RBM15), a novel factor participating in mRNA export
- 135 Lopez Leban Analysis of condition-specific regulation of Puf protein-mediated mRNA decay in
- 136 Lund MicroRNA metabolism during *Xenopus* development
- 137 Luo Coupling of transcription termination by Rat1 to yeast pre-mRNA 3' end processing
- 138 Akusjarvi Substrate dependent differences in U2AF requirement for splicing in adenovirus-infected nuclear extracts

Session 5 MECHANISM AND REGULATION OF 3' END FORMATION

FRIDAY 8/26/2005, 9:00 AM

J. Manley

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
139	He	Regulation of yeast mRNA 3' end processing by phosphorylation	12
140	Tong	Crystal structure of CPSF-100 and direct evidence for CPSF-73 ribonuclease activity	12
141	Gilmartin	Analysis of the function of the human mRNA 3' processing factor CFI _m	8
142	Cheng	Genetic dissection of mRNA 3'-end processing mechanisms	12
143	Lou	Hu proteins block in vitro polyadenylation at sites containing U-rich sequences	12
144	McMahon	Polyadenylation of male germ cell mRNAs	12
145	Blumenthal	An operon pre-mRNA processing protein interacts with the 3' end formation factor, CstF-50, and the novel snRNA, Sm Y	12
146	Kaneko	The mammalian RNA polymerase II C-terminal domain interacts with RNA to suppress transcription-coupled 3' end formation	12
147	Bucheli	Npl3 antagonizes Hrp1 and Rna15 in mRNA 3' end formation	8
148	Gu	Evidence for poly(A) site editing as a new form of gene regulation	12
149	Burch	A genome-wide RNAi screen for factors involved in <i>Drosophila</i> histone pre-mRNA processing	12
150	Kolev	RNA determinants for in vivo assembly of functional U7 snRNPs	8

Session 6 SPLICEOSOME—MECHANISM ASSEMBLY AND FACTORS

FRIDAY 8/26/2005, 2:00 PM

C. Guthrie

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
151	Staley	The DEAH-box ATPase Prp22 enforces 3' splice site fidelity	12
152	Xu	Prp5 SAT mutants alter substrate selectivity of spliceosome assembly	12
153	Perriman	Regulating U2 snRNP assembly with pre-mRNA	12
154	Hilliker	snRNA structures that promote exon ligation	12
155	Kress	A role for the SR protein Npl3 in pre-mRNA splicing in <i>S. cerevisiae</i>	12
156	Cheng	Functional association of Ntr1 and Ntr2 with Prp43 in mediating disassembly of the spliceosome	12
157	Bellare	Functional evidence that ubiquitin controls spliceosome assembly in budding yeast	12
158	Kielkopf	Structural basis of pyrimidine-tract recognition by the essential pre-mRNA splicing factor U2AF ⁶⁵	12
159	Karaduman	Structure probing and EM analyses of the yeast U6 snRNP reveal new insights into the structure of the U6 snRNA and its interaction with Prp24p and LSm 2p-8p	12
160	Lau	Crystal structure of Gemin6 and Gemin7 from the survival of motor neurons complex—Novel Sm-like proteins	12
161	Battle	The SMN complex decodes snRNAs and assembles them into snRNPs	12

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
162	Ma	Changing U1A levels during B cell differentiation may regulate IgM secretory poly(A) site expression	
163	MacDonald	Mice lacking τ CstF-64 are infertile due to a failure of spermatogenesis	
164	Macias	Regulation of spliceosome assembly by <i>Saccharomyces</i> L30	
165	McNally	A RSV RNA processing element promotes viral polyadenylation	
166	Maita	A novel tool to detect a discard pathway in pre-mRNA splicing	
167	Mancino	Identification of mRNA molecules interacting with EBP1, a novel RNA binding protein	
168	Michaeli	<i>Trans</i> -splicing in trypanosomes—The spliced leader RNP-C—A novel intermediate in SL RNA biogenesis and discovery of snRNA-specific Sm proteins	
169	Hernandez-Sanchez	Developmental regulation of a proinsulin mRNA generated by intron retention	
170	Marinescu	PTB regulation of FosB splicing	
171	Mcglincy	A proteomics based approach to identify genes regulated by alternative splicing resulting in nonsense mediated mRNA decay	
172	McNally	Splicing of a subclass of U12-dependent introns is promoted by hnRNP H	
173	Meldgaard	Exogenous reference RNA as an alternative to internal control genes in RT real-time	
174	Melton	Investigation of signal-induced changes controlling CD45 exon 4 repression	
175	Menon	Interaction of CSN1 (COP9 signalosomesubunit 1) and components of transcription / RNA processing complexes SAP130/SF3b3, Ddx15 and CFIm68	

176	Misawa	Further analysis of the role of Sam68 in CTE and Rev/RRE mediated expression of RNA with retained introns
177	Mizuki	RNA export and rRNA processing are affected by a mutation of the gene encoding a component of TFIIF in fission yeast
178	Valadkhan	A U2/U6 "minimal spliceosome" can catalyze a splicing-like reaction to a 5' exon and 5' splice site in <i>trans</i>
179	Graham	SR proteins are regulated by HPV-16 infection of epithelial cells in a differentiation stage-specific manner
180	Moraes	CUG-BP and 3'-UTR sequences influence deadenylation by PARN
181	Munchel	The regulation of mRNA stability by the DEAD box protein Dhh1p in <i>S. cerevisiae</i>
182	Murray	Investigating the role of non-canonical motifs in splicing of introns lacking well-defined U2AF65 binding sites
183	Nair	Translational repression of luteinizing hormone receptor, a member of GPCR family, by a hormonally regulated mRNA binding protein in the ovary
184	Nandakumar	Mechanistic insights into RNA repair by an RNA ligase
185	Newnham	Examining the role of MeCP2 3'-UTR in Rett Syndrome
186	Nilsson	Overlapping cap- and RNA binding sites in poly(A)-specific ribonuclease (PARN)
187	Nojima	Development of a coupled in vitro transcription-splicing system from HeLa cell nuclear extract
188	Oberstrass	Solution structure of the PTB RRM 1 & 2 in complex with RNA
189	O'Brien	Small molecular inhibitors of pre-mRNA splicing
190	Mendell	<i>MYC</i> -regulated microRNAs modulate E2F1 expression
191	Ohi	Structural analysis of an <i>S. pombe</i> spliceosomal complex by electron microscopy
192	Ohn	Identification of functional regions of yeast CAF1 indicates it functions in mRNA deadenylation and post-deadenylation processes separate from its contact to CCR4
193	Okochi	Activity-dependent splicing and stabilization of trkB mRNA regulate the supply of local RNA-pool for plastic responsiveness
194	Valdes	The recognition of a strong 3' splice site by U2AF and SR proteins is synergistically enhanced
195	Palakodeti	Identification of planarian microRNAs required for regeneration
196	Palaniswamy	Nucleophosmin is selectively deposited on mRNA during polyadenylation
197	Park	The KH domain proteins PS and MUB function to regulate alternative splicing of the <i>Drosophila Dscam</i> pre-mRNA
198	Hawkins	SR proteins repress GH1 exon 3 splicing through their interactions with ESS
199	Peterson	Afr1 post-transcriptionally regulates Afp mRNA through sequences within the Afp

200	Phillips	The abundance of the polyadenylation inhibitory factor, U1A protein, is regulated by translational repression during B cell differentiation
201	Pinto	Polo's alternative polyadenylation is required for normal <i>Drosophila</i> development
202	Placek	Splicing and translation are coordinately modulated by a unique 5' terminal structured retroviral post-transcriptional control element
203	Prasad	Analysis of the CCR2 mRNA instability
204	Sontheimer	Double-stranded RNA processing does not alter siRNA strand selection during RNAi in <i>Drosophila</i> lysates
205	Qian	A novel and necessary role for RNA helicase a in translation of unspliced retrovirus
206	Rajyaguru	Dynamic nature of RNA degradosome in the antarctic bacterium <i>P. syringae</i> —Analogy to eukaryotic exosome
207	Rissland	A structural-functional analysis of Cid1, a novel poly(A) polymerase in <i>S. pombe</i>
208	Roca	5' splice sites exhibit different requirements for the 5' end of the U1 snRNA
209	Sachidanandam	Catalog and analyses of U2 and U12-dependent splice sites from model
210	Rondon	Role of 3'-end formation machinery in gene loops
211	Rossi	Identification of SL trans-spliced genes in the planarian <i>S. mediterranea</i>
212	Ruiz-Luis	SRp20 is involved in the 3' splice site recognition of the alternative α exon of the ZO-1 pre-mRNA
213	Sakashita	CUG-BP represses the splicing of the intron downstream across an exon
214	Graber	Comparative analysis of metazoan 3'-processing downstream elements and CstF-64 RNA binding domains
215	Sanchez	Connections of the transcription elongation regulator CA150 with the elongation and splicing machineries
216	Schaal	Analysis of the intrinsic strength of human 5' ss of constitutively and alternatively spliced exons
217	Scherrer	Mer1p requires components of RES complex to activate splicing of <i>AMA1</i> pre-
218	Schluepen	Investigation of proteins interacting with the splicing regulator Fox-2
219	Seidl	The imprinted <i>Air</i> noncoding RNA is an atypical Pol II transcript that shows reduced splicing potential and escapes nuclear export
220	SHANKARLING	An evolutionarily conserved splice variant of CstF-64 from mouse brain
221	She	Crystal structure and functional analysis of <i>S. pombe</i> decapping enzyme Dcp2p
222	Shi	Caffeine regulates alternative splicing of a subset of genes
223	Shi	PPP family phosphatases are essential for the second step of pre-mRNA splicing
224	Padgett	A motif at the 3' end of U6atac snRNA can direct U6 snRNA to the minor spliceosome

225	Skrisovska	Solution structure of the potential splicing factor RBMY in complex with an RNA
226	Small	The guanosine state of the GTPase Snu114 regulates Brr2-mediated spliceosome deactivation
227	Smirnova	New splice variants of lymphotoxin α —Relation to lymphocyte activation and allelic deviation
228	Smith	Distribution of SR protein exonic splicing enhancer motifs in human protein-coding
229	Spiller	Localization of the Lsm proteins and the U6 snRNA
230	Stevenson	Cid1, a cytoplasmic poly(A) polymerase in <i>S. Pombe</i>
231	Suzuki	Evidence that supports nested splicing, introns in a large intron
232	Tan	Evolutionarily conserved coupling of transcription and alternative splicing in the protein 4.1R, and 4.1B genes
233	Tanzhaus	Identification of factors involved in human pre-snRNA processing
234	Trevino	Uncovering the meiotic gene expression program through pre-mRNA splicing in <i>S. cerevisiae</i>
235	Tseng	Novel binding of HuR, poly \cap -binding protein, hnRNP-K, and hnRNP-I to a UC-rich motif within the 3'-untranslated region of the thrombomodulin messenger RNA
236	Ulbricht	Identification of new mRNA targets of Puf-mediated decay in yeast
237	Vanacova	A new yeast poly(A) polymerase complex involved in RNA quality control
238	Vasilieva	Nrd1 interacts with the nuclear exosome for processing of diverse RNA polymerase II transcripts
239	Maas	Novel recoding targets for A-to-I RNA editing
240	Vertegaal	Spliceosome components are targets for SUMO-2
241	Vethantham	An emerging role for SUMO modification in the regulation of polyadenylation
242	Wallace	Activation of regulated 5' splice sites
243	Wan	The SMN complex determines the capacity for snRNP assembly—A biochemical deficiency in spinal muscular atrophy
244	Wang	PLP1 alternative splicing in differentiating oligodendrocytes—Characterization of an exonic splicing enhancer
245	wang	Essential and unexpected interactions of the yeast SF3b splicing factors
246	Weil	3' UTR sequence stabilizes termination codons in the unspliced RNA of RSV
247	Weischenfeldt	Novel interaction partners in nonsense-mediated mRNA decay
248	West	Coupling between transcriptional termination and RNA turnover
249	Whitworth	A genomic approach to profiling splicing in yeast

250	Dawson	Isolation of mRNA and qRT-PCR from "finger-stick" whole blood archived on absorbent matrix
251	Yamanegi	Regulation by exon definition of alternative splicing of KSHV K8 pre-mRNA
252	Yamashita	A concerted action of PAN2 and CCR4 poly(A) nucleases and DCP2 decapping enzyme is involved in cytoplasmic decay of stable and nonsense mRNAs in
253	Yamashita	New approaches to study the in vivo enzymatic pathways for mRNA turnover in mammalian cells
254	Yang	Human p100 protein interacts with U5 snRNP specific proteins
255	Zekri	Control of fetal growth and neonatal survival by the RasGAP associated endoribonuclease G3BP
256	Zhang	Cellview—A program defining exons according to the cell
257	Zhang	Exon inclusion is dependent on predictable exonic splicing enhancers in natural

Session 8 MECHANISMS OF mRNA DECAY AND SURVEILLANCE

SATURDAY 8/27/2005, 9:00 AM

A.-B. Shyu

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
258	Davis	Dcp2 decaps m ^{2, 2, 7} Gppn-capped RNA and its activity is sequence and context dependent	12
259	Liu	The scavenger decapping activity can influence overall mRNA decay	8
260	Chang	Regulation of CCR4/CAF1 poly(A) nuclease complex-mediated deadenylation by the anti-proliferative factor, TOB	12
261	Moore	Functional proofreading of eukaryotic ribosomes	12
262	Behm-Ansmant	PABP1 provides positional information to discriminate premature from natural stop codons in <i>Drosophila</i>	12
263	Longman	A systematic analysis of nonsense mediated decay in <i>C. elegans</i>	8
264	Gudikote	Efficient RNA splicing promotes translation and RNA surveillance	12
265	Ohno	Mechanism of SMG-1 mediated phosphorylation of UPF1	12
266	Le Hir	The exon junction core complex is locked onto RNA by inhibition of eIF4A3 ATPase	10
267	Stroupe	Imaging the exon junction complex core with negative-stain electron microscopy	8
268	Mishler	RNA elements essential for stable exon junction complex deposition	8
269	Lee	Protein eIF4A3 links spliceosomal proteins to the translation initiation machinery	10

A. Krainer

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
270	Graveley	A mechanism for the mutually exclusive splicing of the insect <i>Dscam</i> gene	12
271	Allain	Structural insight into splicing regulation with the solution structure of PTB and Fox-1 in complex with RNA	12
272	Thickman	Sequential protein interactions at the 3' splice site—Implications for constitutive and alternative splicing	12
273	Sharma	Polypyrimidine tract binding protein blocks the 5' splice site dependent assembly of U2AF and the prespliceosomal E complex	12
274	Raker	Regulation of Fas alternative splicing and autoimmune lymphoproliferative syndrome	12
275	SAULIERE	PTB-mediated repression of the β -tropomyosin muscle-specific exon prevents U2 snRNA interaction of the branchpoint but does not impair the binding of the large U2AF ⁶⁵ subunit	12
276	Heyd	U2AF26 and Gfi1 modulate T-cell activation by regulating CD45 alternative splicing	12
277	Tam	Regulation of alternative splicing factor RBM4 by cellular signaling	12
278	Yu	Regulation of pre-mRNA splicing in mammalian cells—Identification and characterization of intronic and exonic silencers	12
279	Zhang	Splicing of de novo designer exons depends on ESE and ESS content	12
280	Kornblihtt	A polar mechanism coordinates different regions of alternative splicing within a	12

M. Rosbash

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
281	Abruzzi	Co-transcriptional dot formation and recruitment of export and 3'-end processing factors to a ribozyme-terminated mRNA	12
282	Listerman	Co-transcriptional accumulation of pre-mRNA splicing factors on human genes in vivo requires the presence of introns	12
283	Visa	The nascent pre-mRNA recruits actin and chromatin-remodeling factors to transcriptionally active genes	12
284	Gromak	Role of RNA polymerase II pausing in transcriptional termination of human genes	12
285	Kim	The Rat1 exonuclease promotes transcription termination by RNA polymerase II	12
286	Kyburz	CPSF and U2 snRNP mediate coupling of pre-mRNA 3' end processing and	12
287	Merz	Recruitment of the TREX complex to mRNPs spliced in vitro is dependent on the exon junction complex	12
288	Natalizio	An efficient in vitro coupled transcription/splicing system to study constitutively and alternatively spliced transcripts	12
289	Price	Functional coupling of cleavage and polyadenylation with transcription of mRNA	12
290	Li	Inactivation of the SR protein ASF/SF2 results in genomic instability	12
291	Chandler	DNA damage induces coordinated regulation of the p53 modulators MDM2 and MDMX by differential splicing	8
292	Batsche	The Swi/Snf complex regulates alternative splicing	8