# Elisa Izaurralde

## List of Publications by Year in Descending Order

**Source:** https://exaly.com/author-pdf/1132253/elisa-izaurralde-publications-by-year.pdf
**Version:** 2024-04-20



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|---|---|---|---|
| 151<br>papers | 24,909<br>citations | 84<br>h-index | 157<br>g-index |
| 159<br>ext. papers | 27,155<br>ext. citations | 14.9<br>avg, IF | 7.2<br>L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 151 | Rapid Gene evolution in an ancient post-transcriptional and translational regulatory system compensates for meiotic X chromosomal inactivation. *Molecular Biology and Evolution*, **2021**, | 8.3 | 1 |
| 150 | Crystal structure and functional properties of the human CCR4-CAF1 deadenylase complex. *Nucleic Acids Research*, **2021**, 49, 6489-6510 | 20.1 | 3 |
| 149 | 4E-T-bound mRNAs are stored in a silenced and deadenylated form. *Genes and Development*, **2020**, 34, 847-860 | 12.6 | 17 |
| 148 | 4EHP and GIGYF1/2 Mediate Translation-Coupled Messenger RNA Decay. *Cell Reports*, **2020**, 33, 108262 | 10.6 | 15 |
| 147 | Molecular basis for GIGYF-Me31B complex assembly in 4EHP-mediated translational repression. *Genes and Development*, **2019**, 33, 1355-1360 | 12.6 | 7 |
| 146 | A conserved CAF40-binding motif in metazoan NOT4 mediates association with the CCR4-NOT complex. *Genes and Development*, **2019**, 33, 236-252 | 12.6 | 12 |
| 145 | Direct role for the Drosophila GIGYF protein in 4EHP-mediated mRNA repression. *Nucleic Acids Research*, **2019**, 47, 7035-7048 | 20.1 | 12 |
| 144 | A low-complexity region in human XRN1 directly recruits deadenylation and decapping factors in 5Ʉ3Ʉmessenger RNA decay. *Nucleic Acids Research*, **2019**, 47, 9282-9295 | 20.1 | 12 |
| 143 | Bag-of-marbles directly interacts with the CAF40 subunit of the CCR4-NOT complex to elicit repression of mRNA targets. *Rna*, **2018**, 24, 381-395 | 5.8 | 20 |
| 142 | Structural motifs in eIF4G and 4E-BPs modulate their binding to eIF4E to regulate translation initiation in yeast. *Nucleic Acids Research*, **2018**, 46, 6893-6908 | 20.1 | 17 |
| 141 | Structural and biochemical analysis of a NOT1 MIF4G-like domain of the CCR4-NOT complex. *Journal of Structural Biology*, **2018**, 204, 388-395 | 3.4 | 7 |
| 140 | A CAF40-binding motif facilitates recruitment of the CCR4-NOT complex to mRNAs targeted by Drosophila Roquin. *Nature Communications*, **2017**, 8, 14307 | 17.4 | 40 |
| 139 | GIGYF1/2 proteins use auxiliary sequences to selectively bind to 4EHP and repress target mRNA expression. *Genes and Development*, **2017**, 31, 1147-1161 | 12.6 | 41 |
| 138 | The Structures of eIF4E-eIF4G Complexes Reveal an Extended Interface to Regulate Translation Initiation. *Molecular Cell*, **2016**, 64, 467-479 | 17.6 | 60 |
| 137 | Distinct modes of recruitment of the CCR4-NOT complex by Drosophila and vertebrate Nanos. *EMBO Journal*, **2016**, 35, 974-90 | 13 | 31 |
| 136 | miRISC and the CCR4-NOT complex silence mRNA targets independently of 43S ribosomal scanning. *EMBO Journal*, **2016**, 35, 1186-203 | 13 | 51 |
| 135 | Structure of the Dcp2-Dcp1 mRNA-decapping complex in the activated conformation. *Nature Structural and Molecular Biology*, **2016**, 23, 574-9 | 17.6 | 33 |

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| 134 | Molecular architecture of 4E-BP translational inhibitors bound to eIF4E. *Molecular Cell*, **2015**, 57, 1074-1087 | 17.6 | 88 |
| 133 | Towards a molecular understanding of microRNA-mediated gene silencing. *Nature Reviews Genetics* , **2015**, 16, 421-33 | 30.1 | 1098 |
| 132 | GENE REGULATION. Breakers and blockers□miRNAs at work. *Science*, **2015**, 349, 380-2 | 33.3 | 47 |
| 131 | Mextli proteins use both canonical bipartite and novel tripartite binding modes to form eIF4E complexes that display differential sensitivity to 4E-BP regulation. *Genes and Development*, **2015**, 29, 1835-49 | 12.6 | 15 |
| 130 | A DDX6-CNOT1 complex and W-binding pockets in CNOT9 reveal direct links between miRNA target recognition and silencing. *Molecular Cell*, **2014**, 54, 737-50 | 17.6 | 187 |
| 129 | An asymmetric PAN3 dimer recruits a single PAN2 exonuclease to mediate mRNA deadenylation and decay. *Nature Structural and Molecular Biology*, **2014**, 21, 599-608 | 17.6 | 33 |
| 128 | 4E-BPs require non-canonical 4E-binding motifs and a lateral surface of eIF4E to repress translation. *Nature Communications*, **2014**, 5, 4790 | 17.4 | 46 |
| 127 | Structural basis for the Nanos-mediated recruitment of the CCR4-NOT complex and translational repression. *Genes and Development*, **2014**, 28, 888-901 | 12.6 | 65 |
| 126 | The activation of the decapping enzyme DCP2 by DCP1 occurs on the EDC4 scaffold and involves a conserved loop in DCP1. *Nucleic Acids Research*, **2014**, 42, 5217-33 | 20.1 | 64 |
| 125 | The role of GW182 proteins in miRNA-mediated gene silencing. *Advances in Experimental Medicine and Biology*, **2013**, 768, 147-63 | 3.6 | 81 |
| 124 | Structure of the PAN3 pseudokinase reveals the basis for interactions with the PAN2 deadenylase and the GW182 proteins. *Molecular Cell*, **2013**, 51, 360-73 | 17.6 | 79 |
| 123 | GW182 proteins cause PABP dissociation from silenced miRNA targets in the absence of deadenylation. *EMBO Journal*, **2013**, 32, 1052-65 | 13 | 87 |
| 122 | Structure and assembly of the NOT module of the human CCR4-NOT complex. *Nature Structural and Molecular Biology*, **2013**, 20, 1289-97 | 17.6 | 74 |
| 121 | An unusual arrangement of two 14-3-3-like domains in the SMG5-SMG7 heterodimer is required for efficient nonsense-mediated mRNA decay. *Genes and Development*, **2013**, 27, 211-25 | 12.6 | 58 |
| 120 | The SMG5-SMG7 heterodimer directly recruits the CCR4-NOT deadenylase complex to mRNAs containing nonsense codons via interaction with POP2. *Genes and Development*, **2013**, 27, 2125-38 | 12.6 | 125 |
| 119 | The role of disordered protein regions in the assembly of decapping complexes and RNP granules. *Genes and Development*, **2013**, 27, 2628-41 | 12.6 | 136 |
| 118 | The interactions of GW182 proteins with PABP and deadenylases are required for both translational repression and degradation of miRNA targets. *Nucleic Acids Research*, **2013**, 41, 978-94 | 20.1 | 87 |
| 117 | miRISC recruits decapping factors to miRNA targets to enhance their degradation. *Nucleic Acids Research*, **2013**, 41, 8692-705 | 20.1 | 54 |

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| 116 | NOT10 and C2orf29/NOT11 form a conserved module of the CCR4-NOT complex that docks onto the NOT1 N-terminal domain. *RNA Biology*, **2013**, 10, 228-44 | 4.8 | 69 |
| 115 | A direct interaction between DCP1 and XRN1 couples mRNA decapping to 5Uexonucleolytic degradation. *Nature Structural and Molecular Biology*, **2012**, 19, 1324-31 | 17.6 | 111 |
| 114 | A molecular link between miRISCs and deadenylases provides new insight into the mechanism of gene silencing by microRNAs. *Cold Spring Harbor Perspectives in Biology*, **2012**, 4, | 10.2 | 43 |
| 113 | The structural basis of Edc3- and Scd6-mediated activation of the Dcp1:Dcp2 mRNA decapping complex. *EMBO Journal*, **2012**, 31, 279-90 | 13 | 84 |
| 112 | Elucidating the temporal order of silencing. *EMBO Reports*, **2012**, 13, 662-3 | 6.5 | 40 |
| 111 | The structural basis for the interaction between the CAF1 nuclease and the NOT1 scaffold of the human CCR4-NOT deadenylase complex. *Nucleic Acids Research*, **2012**, 40, 11058-72 | 20.1 | 93 |
| 110 | The Caenorhabditis elegans GW182 protein AIN-1 interacts with PAB-1 and subunits of the PAN2-PAN3 and CCR4-NOT deadenylase complexes. *Nucleic Acids Research*, **2012**, 40, 5651-65 | 20.1 | 44 |
| 109 | GW182 proteins directly recruit cytoplasmic deadenylase complexes to miRNA targets. *Molecular Cell*, **2011**, 44, 120-33 | 17.6 | 266 |
| 108 | Gene silencing by microRNAs: contributions of translational repression and mRNA decay. *Nature Reviews Genetics*, **2011**, 12, 99-110 | 30.1 | 1686 |
| 107 | CUP promotes deadenylation and inhibits decapping of mRNA targets. *Genes and Development*, **2011**, 25, 1955-67 | 12.6 | 70 |
| 106 | Crystal structure of the MID-PIWI lobe of a eukaryotic Argonaute protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 10466-71 | 11.5 | 88 |
| 105 | Structure-function studies of nucleocytoplasmic transport of retroviral genomic RNA by mRNA export factor TAP. *Nature Structural and Molecular Biology*, **2011**, 18, 990-8 | 17.6 | 41 |
| 104 | The C-terminal alpha-alpha superhelix of Pat is required for mRNA decapping in metazoa. *EMBO Journal*, **2010**, 29, 2368-80 | 13 | 41 |
| 103 | Two PABPC1-binding sites in GW182 proteins promote miRNA-mediated gene silencing. *EMBO Journal*, **2010**, 29, 4146-60 | 13 | 82 |
| 102 | Crystal structure and ligand binding of the MID domain of a eukaryotic Argonaute protein. *EMBO Reports*, **2010**, 11, 522-7 | 6.5 | 68 |
| 101 | Role of GW182 proteins and PABPC1 in the miRNA pathway: a sense of dJ▯vu. *Nature Reviews Molecular Cell Biology*, **2010**, 11, 379-84 | 48.7 | 63 |
| 100 | HPat provides a link between deadenylation and decapping in metazoa. *Journal of Cell Biology*, **2010**, 189, 289-302 | 7.3 | 61 |
| 99 | SMG6 interacts with the exon junction complex via two conserved EJC-binding motifs (EBMs) required for nonsense-mediated mRNA decay. *Genes and Development*, **2010**, 24, 2440-50 | 12.6 | 53 |

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| 98 | The RRM domain in GW182 proteins contributes to miRNA-mediated gene silencing. *Nucleic Acids Research*, **2009**, 37, 2974-83 | 20.1 | 43 |
| 97 | The silencing domain of GW182 interacts with PABPC1 to promote translational repression and degradation of microRNA targets and is required for target release. *Molecular and Cellular Biology*, **2009**, 29, 6220-31 | 4.8 | 134 |
| 96 | DCP1 forms asymmetric trimers to assemble into active mRNA decapping complexes in metazoa. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 21591-6 | 11.5 | 47 |
| 95 | A C-terminal silencing domain in GW182 is essential for miRNA function. *Rna*, **2009**, 15, 1067-77 | 5.8 | 91 |
| 94 | The C-terminal domains of human TNRC6A, TNRC6B, and TNRC6C silence bound transcripts independently of Argonaute proteins. *Rna*, **2009**, 15, 1059-66 | 5.8 | 112 |
| 93 | The GW182 protein family in animal cells: new insights into domains required for miRNA-mediated gene silencing. *Rna*, **2009**, 15, 1433-42 | 5.8 | 152 |
| 92 | Genome-wide identification of alternative splice forms down-regulated by nonsense-mediated mRNA decay in Drosophila. *PLoS Genetics*, **2009**, 5, e1000525 | 6 | 68 |
| 91 | Nonsense-mediated mRNA decay effectors are essential for zebrafish embryonic development and survival. *Molecular and Cellular Biology*, **2009**, 29, 3517-28 | 4.8 | 135 |
| 90 | Freedom versus constraint in protein function. *Nature Reviews Molecular Cell Biology*, **2009**, 10, 372 | 48.7 | 2 |
| 89 | Structural basis for the mutually exclusive anchoring of P body components EDC3 and Tral to the DEAD box protein DDX6/Me31B. *Molecular Cell*, **2009**, 33, 661-8 | 17.6 | 93 |
| 88 | Deadenylation is a widespread effect of miRNA regulation. *Rna*, **2009**, 15, 21-32 | 5.8 | 311 |
| 87 | GW182 interaction with Argonaute is essential for miRNA-mediated translational repression and mRNA decay. *Nature Structural and Molecular Biology*, **2008**, 15, 346-53 | 17.6 | 314 |
| 86 | Getting to the root of miRNA-mediated gene silencing. *Cell*, **2008**, 132, 9-14 | 56.2 | 811 |
| 85 | The C-terminal region of Ge-1 presents conserved structural features required for P-body localization. *Rna*, **2008**, 14, 1991-8 | 5.8 | 23 |
| 84 | Similar modes of interaction enable Trailer Hitch and EDC3 to associate with DCP1 and Me31B in distinct protein complexes. *Molecular and Cellular Biology*, **2008**, 28, 6695-708 | 4.8 | 60 |
| 83 | SMG6 is the catalytic endonuclease that cleaves mRNAs containing nonsense codons in metazoan. *Rna*, **2008**, 14, 2609-17 | 5.8 | 228 |
| 82 | P-body formation is a consequence, not the cause, of RNA-mediated gene silencing. *Molecular and Cellular Biology*, **2007**, 27, 3970-81 | 4.8 | 511 |
| 81 | P bodies: at the crossroads of post-transcriptional pathways. *Nature Reviews Molecular Cell Biology*, **2007**, 8, 9-22 | 48.7 | 751 |

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|---|---|---|---|
| 80 | A conserved role for cytoplasmic poly(A)-binding protein 1 (PABPC1) in nonsense-mediated mRNA decay. *EMBO Journal*, **2007**, 26, 1591-601 | 13 | 171 |
| 79 | Target-specific requirements for enhancers of decapping in miRNA-mediated gene silencing. *Genes and Development*, **2007**, 21, 2558-70 | 12.6 | 230 |
| 78 | A divergent Sm fold in EDC3 proteins mediates DCP1 binding and P-body targeting. *Molecular and Cellular Biology*, **2007**, 27, 8600-11 | 4.8 | 55 |
| 77 | mRNA quality control: an ancient machinery recognizes and degrades mRNAs with nonsense codons. *FEBS Letters*, **2007**, 581, 2845-53 | 3.8 | 150 |
| 76 | Nonsense-mediated mRNA decay: Target genes and functional diversification of effectors. *Trends in Biochemical Sciences*, **2006**, 31, 639-46 | 10.3 | 113 |
| 75 | Genome-wide analysis of mRNAs regulated by Drosha and Argonaute proteins in Drosophila melanogaster. *Molecular and Cellular Biology*, **2006**, 26, 2965-75 | 4.8 | 119 |
| 74 | Quality control of gene expression: a stepwise assembly pathway for the surveillance complex that triggers nonsense-mediated mRNA decay. *Genes and Development*, **2006**, 20, 391-8 | 12.6 | 74 |
| 73 | mRNA degradation by miRNAs and GW182 requires both CCR4:NOT deadenylase and DCP1:DCP2 decapping complexes. *Genes and Development*, **2006**, 20, 1885-98 | 12.6 | 720 |
| 72 | A tiny helper lightens the maternal load. *Cell*, **2006**, 124, 1117-8 | 56.2 | 3 |
| 71 | MicroRNAs silence gene expression by repressing protein expression and/or by promoting mRNA decay. *Cold Spring Harbor Symposia on Quantitative Biology*, **2006**, 71, 523-30 | 3.9 | 189 |
| 70 | Structures of the PIN domains of SMG6 and SMG5 reveal a nuclease within the mRNA surveillance complex. *EMBO Journal*, **2006**, 25, 5117-25 | 13 | 147 |
| 69 | Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets. *Rna*, **2005**, 11, 1530-44 | 5.8 | 206 |
| 68 | SMG7 is a 14-3-3-like adaptor in the nonsense-mediated mRNA decay pathway. *Molecular Cell*, **2005**, 17, 537-47 | 17.6 | 185 |
| 67 | Decay of mRNAs targeted by RISC requires XRN1, the Ski complex, and the exosome. *Rna*, **2005**, 11, 459-68 | 5.8 | 239 |
| 66 | The structure of the flock house virus B2 protein, a viral suppressor of RNA interference, shows a novel mode of double-stranded RNA recognition. *EMBO Reports*, **2005**, 6, 1149-55 | 6.5 | 107 |
| 65 | Generation and annotation of the DNA sequences of human chromosomes 2 and 4. *Nature*, **2005**, 434, 724-31 | 50.4 | 61 |
| 64 | Nonsense-mediated mRNA decay: molecular insights and mechanistic variations across species. *Current Opinion in Cell Biology*, **2005**, 17, 316-25 | 9 | 366 |
| 63 | A crucial role for GW182 and the DCP1:DCP2 decapping complex in miRNA-mediated gene silencing. *Rna*, **2005**, 11, 1640-7 | 5.8 | 350 |

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|---|---|---|---|
| 62 | Complex genomic rearrangements lead to novel primate gene function. *Genome Research*, **2005**, 15, 343-51 | 9.7 | 82 |
| 61 | RNAi: finding the elusive endonuclease. *Rna*, **2004**, 10, 1675-9 | 5.8 | 27 |
| 60 | RanBP2/Nup358 provides a major binding site for NXF1-p15 dimers at the nuclear pore complex and functions in nuclear mRNA export. *Molecular and Cellular Biology*, **2004**, 24, 1155-67 | 4.8 | 79 |
| 59 | Molecular insights into the interaction of PYM with the Mago-Y14 core of the exon junction complex. *EMBO Reports*, **2004**, 5, 304-10 | 6.5 | 74 |
| 58 | The structural basis for the interaction between nonsense-mediated mRNA decay factors UPF2 and UPF3. *Nature Structural and Molecular Biology*, **2004**, 11, 330-7 | 17.6 | 145 |
| 57 | Genome-wide analysis of mRNAs regulated by the THO complex in Drosophila melanogaster. *Nature Structural and Molecular Biology*, **2004**, 11, 558-66 | 17.6 | 172 |
| 56 | Nucleic acid 3Ʉend recognition by the Argonaute2 PAZ domain. *Nature Structural and Molecular Biology*, **2004**, 11, 576-7 | 17.6 | 259 |
| 55 | The superhelical TPR-repeat domain of O-linked GlcNAc transferase exhibits structural similarities to importin alpha. *Nature Structural and Molecular Biology*, **2004**, 11, 1001-7 | 17.6 | 219 |
| 54 | An eIF4AIII-containing complex required for mRNA localization and nonsense-mediated mRNA decay. *Nature*, **2004**, 427, 753-7 | 50.4 | 299 |
| 53 | Nonsense-mediated messenger RNA decay is initiated by endonucleolytic cleavage in Drosophila. *Nature*, **2004**, 429, 575-8 | 50.4 | 190 |
| 52 | NMR assignment of the Drosophila Argonaute2 PAZ domain. *Journal of Biomolecular NMR*, **2004**, 29, 421-2 | 3 | 3 |
| 51 | SMG7 acts as a molecular link between mRNA surveillance and mRNA decay. *Molecular Cell*, **2004**, 16, 587-96 | 17.6 | 222 |
| 50 | Genome-wide analysis of nuclear mRNA export pathways in Drosophila. *EMBO Journal*, **2003**, 22, 2472-83 | 13 | 126 |
| 49 | Nonsense-mediated mRNA decay in Drosophila: at the intersection of the yeast and mammalian pathways. *EMBO Journal*, **2003**, 22, 3960-70 | 13 | 216 |
| 48 | The interplay of nuclear mRNP assembly, mRNA surveillance and export. *Trends in Cell Biology*, **2003**, 13, 319-27 | 18.3 | 171 |
| 47 | The PAM domain, a multi-protein complex-associated module with an all-alpha-helix fold. *BMC Bioinformatics*, **2003**, 4, 64 | 3.6 | 15 |
| 46 | A novel mode of RBD-protein recognition in the Y14-Mago complex. *Nature Structural and Molecular Biology*, **2003**, 10, 433-9 | 17.6 | 134 |
| 45 | Structure and nucleic-acid binding of the Drosophila Argonaute 2 PAZ domain. *Nature*, **2003**, 426, 465-9 | 50.4 | 347 |

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| 44 | An efficient protein complex purification method for functional proteomics in higher eukaryotes. *Nature Biotechnology*, **2003**, 21, 89-92 | 44.5 | 173 |
| 43 | A novel family of nuclear transport receptors mediates the export of messenger RNA to the cytoplasm. *European Journal of Cell Biology*, **2002**, 81, 577-84 | 6.1 | 45 |
| 42 | REF1/Aly and the additional exon junction complex proteins are dispensable for nuclear mRNA export. *Journal of Cell Biology*, **2002**, 159, 579-88 | 7.3 | 177 |
| 41 | Nuclear export of mRNA by TAP/NXF1 requires two nucleoporin-binding sites but not p15. *Molecular and Cellular Biology*, **2002**, 22, 5405-18 | 4.8 | 83 |
| 40 | Nuclear export of messenger RNA. *Results and Problems in Cell Differentiation*, **2002**, 35, 133-50 | 1.4 | 21 |
| 39 | The protein Mago provides a link between splicing and mRNA localization. *EMBO Reports*, **2001**, 2, 1119-24 | 6.5 | 140 |
| 38 | The exon-exon junction complex provides a binding platform for factors involved in mRNA export and nonsense-mediated mRNA decay. *EMBO Journal*, **2001**, 20, 4987-97 | 13 | 591 |
| 37 | Herpes simplex virus ICP27 protein provides viral mRNAs with access to the cellular mRNA export pathway. *EMBO Journal*, **2001**, 20, 5769-78 | 13 | 133 |
| 36 | NXF5, a novel member of the nuclear RNA export factor family, is lost in a male patient with a syndromic form of mental retardation. *Current Biology*, **2001**, 11, 1381-91 | 6.3 | 58 |
| 35 | The DExH/D box protein HEL/UAP56 is essential for mRNA nuclear export in Drosophila. *Current Biology*, **2001**, 11, 1716-21 | 6.3 | 196 |
| 34 | Nucleocytoplasmic transport enters the atomic age. *Current Opinion in Cell Biology*, **2001**, 13, 310-9 | 9 | 228 |
| 33 | Overexpression of TAP/p15 heterodimers bypasses nuclear retention and stimulates nuclear mRNA export. *Journal of Biological Chemistry*, **2001**, 276, 20536-43 | 5.4 | 107 |
| 32 | Structural basis for the recognition of a nucleoporin FG repeat by the NTF2-like domain of the TAP/p15 mRNA nuclear export factor. *Molecular Cell*, **2001**, 8, 645-56 | 17.6 | 193 |
| 31 | REF proteins mediate the export of spliced and unspliced mRNAs from the nucleus. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 1030-5 | 11.5 | 154 |
| 30 | Prediction of structural domains of TAP reveals details of its interaction with p15 and nucleoporins. *EMBO Reports*, **2000**, 1, 53-8 | 6.5 | 72 |
| 29 | The spliceosome deposits multiple proteins 20-24 nucleotides upstream of mRNA exon-exon junctions. *EMBO Journal*, **2000**, 19, 6860-9 | 13 | 695 |
| 28 | The C-terminal domain of TAP interacts with the nuclear pore complex and promotes export of specific CTE-bearing RNA substrates. *Rna*, **2000**, 6, 136-58 | 5.8 | 268 |
| 27 | REF, an evolutionary conserved family of hnRNP-like proteins, interacts with TAP/Mex67p and participates in mRNA nuclear export. *Rna*, **2000**, 6, 638-50 | 5.8 | 296 |

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|---|---|---|---|
| 26 | Rous sarcoma virus DR posttranscriptional elements use a novel RNA export pathway. *Journal of Virology*, **2000**, 74, 9507-14 | 6.6 | 56 |
| 25 | TAP (NXF1) belongs to a multigene family of putative RNA export factors with a conserved modular architecture. *Molecular and Cellular Biology*, **2000**, 20, 8996-9008 | 4.8 | 189 |
| 24 | Vesicular stomatitis virus matrix protein inhibits host cell gene expression by targeting the nucleoporin Nup98. *Molecular Cell*, **2000**, 6, 1243-52 | 17.6 | 208 |
| 23 | Coordination of tRNA nuclear export with processing of tRNA. *Rna*, **1999**, 5, 539-49 | 5.8 | 105 |
| 22 | CRM1-mediated recycling of snurportin 1 to the cytoplasm. *Journal of Cell Biology*, **1999**, 145, 255-64 | 7.3 | 150 |
| 21 | Dbp5, a DEAD-box protein required for mRNA export, is recruited to the cytoplasmic fibrils of nuclear pore complex via a conserved interaction with CAN/Nup159p. *EMBO Journal*, **1999**, 18, 4332-47 | 13 | 213 |
| 20 | Identification of a tRNA-specific nuclear export receptor. *Molecular Cell*, **1998**, 1, 359-69 | 17.6 | 324 |
| 19 | TAP, the human homolog of Mex67p, mediates CTE-dependent RNA export from the nucleus. *Molecular Cell*, **1998**, 1, 649-59 | 17.6 | 490 |
| 18 | A novel class of RanGTP binding proteins. *Journal of Cell Biology*, **1997**, 138, 65-80 | 7.3 | 374 |
| 17 | A role for the M9 transport signal of hnRNP A1 in mRNA nuclear export. *Journal of Cell Biology*, **1997**, 137, 27-35 | 7.3 | 217 |
| 16 | Participation of the nuclear cap binding complex in pre-mRNA 3Uprocessing. *Proceedings of the National Academy of Sciences of the United States of America*, **1997**, 94, 11893-8 | 11.5 | 184 |
| 15 | The simian retrovirus-1 constitutive transport element, unlike the HIV-1 RRE, uses factors required for cellular mRNA export. *Current Biology*, **1997**, 7, 619-28 | 6.3 | 157 |
| 14 | An immersion in nucleocytoplasmic transport at the Garda lake. *Trends in Cell Biology*, **1997**, 7, 81-3 | 18.3 | 3 |
| 13 | The asymmetric distribution of the constituents of the Ran system is essential for transport into and out of the nucleus. *EMBO Journal*, **1997**, 16, 6535-47 | 13 | 503 |
| 12 | Dominant-negative mutants of importin-beta block multiple pathways of import and export through the nuclear pore complex. *EMBO Journal*, **1997**, 16, 1153-63 | 13 | 310 |
| 11 | A nuclear cap-binding complex binds Balbiani ring pre-mRNA cotranscriptionally and accompanies the ribonucleoprotein particle during nuclear export. *Journal of Cell Biology*, **1996**, 133, 5-14 | 7.3 | 205 |
| 10 | Importin provides a link between nuclear protein import and U snRNA export. *Cell*, **1996**, 87, 21-32 | 56.2 | 178 |
| 9 | ROLES OF IMPORTIN IN NUCLEOCYTOPLASMIC TRANSPORT. *Biochemical Society Transactions*, **1996**, 24, 627S-627S | 5.1 | |

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|---|---|---|---|
| 8 | A cap-binding protein complex mediating U snRNA export. *Nature*, **1995**, 376, 709-12 | 50.4 | 286 |
| 7 | RNA export. *Cell*, **1995**, 81, 153-9 | 56.2 | 188 |
| 6 | Nuclear transport of uracil-rich small nuclear ribonucleoprotein particles. *Membrane Protein Transport*, **1995**, 2, 123-159 | | |
| 5 | A nuclear cap binding protein complex involved in pre-mRNA splicing. *Cell*, **1994**, 78, 657-68 | 56.2 | 439 |
| 4 | Transport of RNA between nucleus and cytoplasm. *Seminars in Cell Biology*, **1992**, 3, 279-88 | | 77 |
| 3 | Highly preferential nucleation of histone H1 assembly on scaffold-associated regions. *Journal of Molecular Biology*, **1989**, 210, 573-85 | 6.5 | 158 |
| 2 | Specific inhibition of DNA binding to nuclear scaffolds and histone H1 by distamycin. The role of oligo(dA).oligo(dT) tracts. *Journal of Molecular Biology*, **1989**, 210, 587-99 | 6.5 | 138 |
| 1 | Interaction of DNA with nuclear scaffolds in vitro. *Journal of Molecular Biology*, **1988**, 200, 111-25 | 6.5 | 126 |