Andreas E Kulozik

List of Publications by Year
in descending order

139	16,159	44069	17105
papers	citations	48 h-index	122 g-index

143	143	143	21569
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic modifiers of fetal hemoglobin affect the course of sickle cell disease in patients treated with hydroxyurea. Haematologica, 2022, 107, 1577-1588.	3.5	6
2	Differential Analysis of the Nuclear and the Cytoplasmic RNA Interactomes in Living Cells. Methods in Molecular Biology, 2022, 2428, 291-304.	0.9	2
3	Constitutional PIGA mutations cause a novel subtype of hemochromatosis in patients with neurologic dysfunction. Blood, 2022, 139, 1418-1422.	1.4	8
4	Combining daratumumab with CD47 blockade prolongs survival in preclinical models of pediatric T-ALL. Blood, 2022, 140, 45-57.	1.4	22
5	Pediatric T-ALL type-1 and type-2 relapses develop along distinct pathways of clonal evolution. Leukemia, 2022, 36, 1759-1768.	7.2	4
6	Germline RET variants underlie a subset of paediatric osteosarcoma. Journal of Medical Genetics, 2021, 58, 20-24.	3.2	7
7	Introduction of Universal Newborn Screening for Sickle Cell Disease in Germanyâ€"A Brief Narrative Review. International Journal of Neonatal Screening, 2021, 7, 7.	3.2	4
8	NMD inhibition by 5-azacytidine augments presentation of immunogenic frameshift-derived neoepitopes. IScience, 2021, 24, 102389.	4.1	22
9	The role of combined ion-beam radiotherapy (CIBRT) with protons and carbon ions in a multimodal treatment strategy of inoperable osteosarcoma. Radiotherapy and Oncology, 2021, 159, 8-16.	0.6	21
10	Blasticidin S inhibits mammalian translation and enhances production of protein encoded by nonsense mRNA. Nucleic Acids Research, 2021, 49, 7665-7679.	14.5	13
11	The Pediatric Precision Oncology INFORM Registry: Clinical Outcome and Benefit for Patients with Very High-Evidence Targets. Cancer Discovery, 2021, 11, 2764-2779.	9.4	110
12	Benefits of a Disease Management Program for Sickle Cell Disease in Germany 2011â€"2019: The Increased Use of Hydroxyurea Correlates with a Reduced Frequency of Acute Chest Syndrome. Journal of Clinical Medicine, 2021, 10, 4543.	2.4	3
13	Recommendations for diagnosis and treatment of methemoglobinemia. American Journal of Hematology, 2021, 96, 1666-1678.	4.1	56
14	Sarcoma classification by DNA methylation profiling. Nature Communications, 2021, 12, 498.	12.8	237
15	Odisha Revisited: A Personal Account. Frontiers in Medicine, 2021, 8, 745337.	2.6	1
16	Does the world need germline editing for ÃŸ-thalassemia?. Haematologica, 2021, , .	3.5	0
17	TP53 and KRAS Variants at Initial Diagnosis Identify an Ultra-High Risk Group of Pediatric T-Lymphoblastic Leukemia (T-ALL). Blood, 2021, 138, 1315-1315.	1.4	0
18	Summary of Joint European Hematology Association (EHA) and EuroBloodNet Recommendations on Diagnosis and Treatment of Methemoglobinemia. HemaSphere, 2021, 5, e660.	2.7	1

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19	Genotyping circulating tumor DNA of pediatric Hodgkin lymphoma. Leukemia, 2020, 34, 151-166.	7.2	53
20	Sickle cell disease in Germany: Results from a national registry. Pediatric Blood and Cancer, 2020, 67, e28130.	1.5	20
21	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	17.5	59
22	Prexasertib (LY2606368) reduces clonogenic survival by inducing apoptosis in primary patientâ€derived osteosarcoma cells and synergizes with cisplatin and talazoparib. International Journal of Cancer, 2020, 147, 1059-1070.	5.1	17
23	Gene Therapy of the Hemoglobinopathies. HemaSphere, 2020, 4, e479.	2.7	18
24	Chromatin accessibility landscape of pediatric Tâ€lymphoblastic leukemia and human Tâ€cell precursors. EMBO Molecular Medicine, 2020, 12, e12104.	6.9	13
25	(Phospho)proteomic Profiling of Microsatellite Unstable CRC Cells Reveals Alterations in Nuclear Signaling and Cholesterol Metabolism Caused by Frameshift Mutation of NMD Regulator UPF3A. International Journal of Molecular Sciences, 2020, 21, 5234.	4.1	6
26	Low-frequency variation near common germline susceptibility loci are associated with risk of Ewing sarcoma. PLoS ONE, 2020, 15, e0237792.	2.5	6
27	2,6-Diaminopurine as a highly potent corrector of UGA nonsense mutations. Nature Communications, 2020, 11, 1509.	12.8	46
28	Plasticity of nuclear and cytoplasmic stress responses of RNA-binding proteins. Nucleic Acids Research, 2020, 48, 4725-4740.	14.5	40
29	Aging of Preleukemic Thymocytes Drives CpG Island Hypermethylation in T-cell Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 274-289.	5.0	21
30	Co-Targeting of CD38 and CD47 in T Cell Acute Lymphoblastic Leukemia. Blood, 2020, 136, 39-40.	1.4	0
31	Title is missing!. , 2020, 15, e0237792.		0
32	Title is missing!. , 2020, 15, e0237792.		0
33	Title is missing!. , 2020, 15, e0237792.		0
34	Title is missing!. , 2020, 15, e0237792.		0
35	The German National Registry of Primary Immunodeficiencies (2012â€“2017). Frontiers in Immunology, 2019, 10, 1272.	4.8	71
36	Daratumumab eradicates minimal residual disease in a preclinical model of pediatric T-cell acute lymphoblastic leukemia. Blood, 2019, 134, 713-716.	1.4	42

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37	Treatment of patients with relapsed or refractory CD19+ lymphoid disease with T lymphocytes transduced by RV-SFG.CD19.CD28.4-1BBzeta retroviral vector: a unicentre phase I/II clinical trial protocol. BMJ Open, 2019, 9, e026644.	1.9	27
38	Intracardiac Extension of Wilms Tumor: A Case of a 2.5-Year-Old Girl Presenting with Upper Venous Congestion Caused by Tumor Growth into the Right Cardiac Ventricle. Case Reports in Oncology, 2019, 12, 33-38.	0.7	3
39	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. Cancer Cell, 2019, 35, 95-110.e8.	16.8	65
40	PTEN abnormalities predict poor outcome in children with Tâ€cell acute lymphoblastic leukemia treated according to ALL ICâ€BFM protocols. American Journal of Hematology, 2019, 94, E93-E96.	4.1	36
41	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
42	DNA methylation-based classification of central nervous system tumours. Nature, 2018, 555, 469-474.	27.8	1,872
43	<scp>PDX</scp> models recapitulate the genetic and epigenetic landscape of pediatric Tâ€cell leukemia. EMBO Molecular Medicine, 2018, 10, .	6.9	38
44	Î²-Thalassemia Mutations in Jamaica: Geographic Variation in Small Communities. Hemoglobin, 2018, 42, 294-296.	0.8	3
45	Expression of CD56 defines a distinct subgroup in childhood Tâ€ALL with inferior outcome. Results of the ALLâ€BFM 2000 trial. British Journal of Haematology, 2018, 183, 96-103.	2.5	16
46	MAP3K7 is recurrently deleted in pediatric T-lymphoblastic leukemia and affects cell proliferation independently of NF-ÎºB. BMC Cancer, 2018, 18, 663.	2.6	11
47	Genome-wide association study identifies multiple new loci associated with Ewing sarcoma susceptibility. Nature Communications, 2018, 9, 3184.	12.8	50
48	Cooperative Enhancer Activation by TLX1 and STAT5 Drives Development of NUP214-ABL1/TLX1-Positive T Cell Acute Lymphoblastic Leukemia. Cancer Cell, 2018, 34, 271-285.e7.	16.8	48
49	Front-line imatinib treatment in children and adolescents with chronic myeloid leukemia: results from a phase III trial. Leukemia, 2018, 32, 1657-1669.	7.2	86
50	Ex vivo drug response profiling detects recurrent sensitivity patterns in drug-resistant acute lymphoblastic leukemia. Blood, 2017, 129, e26-e37.	1.4	195
51	Childhood cancer predisposition syndromesâ€"A concise review and recommendations by the Cancer Predisposition Working Group of the Society for Pediatric Oncology and Hematology. American Journal of Medical Genetics, Part A, 2017, 173, 1017-1037.	1.2	200
52	The epidemiology of sickle cell disease in Germany following recent large-scale immigration. Pediatric Blood and Cancer, 2017, 64, e26550.	1.5	28
53	Haematological malignancies following temozolomide treatment for paediatric high-grade glioma. European Journal of Cancer, 2017, 81, 1-8.	2.8	4
54	Bone marrow failure unresponsive to bone marrow transplant is caused by mutations in thrombopoietin. Blood, 2017, 130, 875-880.	1.4	42

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55	NOTCH1 mutation, TP53 alteration and myeloid antigen expression predict outcome heterogeneity in children with first relapse of T-cell acute lymphoblastic leukemia. Haematologica, 2017, 102, e249-e252.	3.5	6
56	Newborn screening for severe combined immunodeficiency using a novel and simplified method to measure T-cell excision circles (TREC). Clinical Immunology, 2017, 175, 51-55.	3.2	20
57	Dual function of UPF3B in early and late translation termination. EMBO Journal, 2017, 36, 2968-2986.	7.8	89
58	Protocol II vs protocol III given twice during reinduction therapy in children with medium-risk ALL. Blood, 2017, 130, 2146-2149.	1.4	7
59	Histone 3.3 hotspot mutations in conventional osteosarcomas: a comprehensive clinical and molecular characterization of six H3F3A mutated cases. Clinical Sarcoma Research, 2017, 7, 9.	2.3	51
60	The INFORM personalized medicine study for high-risk pediatric cancer patients.. Journal of Clinical Oncology, 2017, 35, 10509-10509.	1.6	1
61	High expression of miR-125b-2 and SNORD116 noncoding RNA clusters characterize ERG-related B cell precursor acute lymphoblastic leukemia. Oncotarget, 2017, 8, 42398-42413.	1.8	19
62	Pediatric Targeted Therapy: Clinical Feasibility of Personalized Diagnostics in Children with Relapsed and Progressive Tumors. Brain Pathology, 2016, 26, 506-516.	4.1	14
63	Dexamethasone vs prednisone in induction treatment of pediatric ALL: results of the randomized trial AIEOP-BFM ALL 2000. Blood, 2016, 127, 2101-2112.	1.4	208
64	The differential expression of alternatively polyadenylated transcripts is a common stress-induced response mechanism that modulates mammalian mRNA expression in a quantitative and qualitative fashion. Rna, 2016, 22, 1441-1453.	3.5	36
65	Exon Junction Complexes Show a Distributional Bias toward Alternatively Spliced mRNAs and against mRNAs Coding for Ribosomal Proteins. Cell Reports, 2016, 16, 1588-1603.	6.4	65
66	Next-generation personalised medicine for high-risk paediatric cancer patients â€“ The INFORM pilot study. European Journal of Cancer, 2016, 65, 91-101.	2.8	262
67	Haemoglobin Variant Screening in Jamaica: Meeting Student's Request. British Journal of Haematology, 2016, 172, 634-636.	2.5	10
68	Mutating heme oxygenase-1 into a peroxidase causes a defect in bilirubin synthesis associated with microcytic anemia and severe hyperinflammation. Haematologica, 2016, 101, e436-e439.	3.5	18
69	Therapy with lowâ€dose azacitidine for <scp>MDS</scp> in children and young adults: a retrospective analysis of the <scp>EWOG</scp>â€<scp>MDS</scp> study group. British Journal of Haematology, 2016, 172, 930-936.	2.5	31
70	Proteomic Analysis Reveals Branch-specific Regulation of the Unfolded Protein Response by Nonsense-mediated mRNA Decay. Molecular and Cellular Proteomics, 2016, 15, 1584-1597.	3.8	28
71	Significant prevalence of sickle cell disease in Southwest Germany: results from a birth cohort study indicate the necessity for newborn screening. Annals of Hematology, 2016, 95, 397-402.	1.8	29
72	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	16.8	438

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73	CRLF2 over-expression is a poor prognostic marker in children with high risk T-cell acute lymphoblastic leukemia. Oncotarget, 2016, 7, 59260-59272.	1.8	24
74	Low-dose Actinomycin-D treatment re-establishes the tumoursuppressive function of P53 in RELA-positive ependymoma. Oncotarget, 2016, 7, 61860-61873.	1.8	27
75	MYCN and HDAC5 transcriptionally repress CD9 to trigger invasion and metastasis in neuroblastoma. Oncotarget, 2016, 7, 66344-66359.	1.8	30
76	The thrombopoietin receptor P106L mutation functionally separates receptor signaling activity from thrombopoietin homeostasis. Blood, 2015, 125, 1159-1169.	1.4	18
77	Bridging to transplant with azacitidine in juvenile myelomonocytic leukemia: a retrospective analysis of the EWOG-MDS study group. Blood, 2015, 125, 2311-2313.	1.4	60
78	Histone deacetylase inhibition sensitizes osteosarcoma to heavy ion radiotherapy. Radiation Oncology, 2015, 10, 146.	2.7	14
79	HIV-1 Recruits UPF1 but Excludes UPF2 to Promote Nucleocytoplasmic Export of the Genomic RNA. Biomolecules, 2015, 5, 2808-2839.	4.0	52
80	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. Cancer Cell, 2015, 27, 728-743.	16.8	933
81	Establishment of a patient-derived orthotopic osteosarcoma mouse model. Journal of Translational Medicine, 2015, 13, 136.	4.4	35
82	Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency. Nature Communications, 2015, 6, 8940.	12.8	242
83	The best of 25 years: mRNA 3â€²end processing. Rna, 2015, 21, 640-641.	3.5	0
84	Improved binding site assignment by high-resolution mapping of RNAâ€“protein interactions using iCLIP. Nature Communications, 2015, 6, 7921.	12.8	32
85	A network of SMG-8, SMG-9 and SMG-1 C-terminal insertion domain regulates UPF1 substrate recruitment and phosphorylation. Nucleic Acids Research, 2015, 43, 7600-7611.	14.5	51
86	Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. Haematologica, 2015, 100, 1442-1450.	3.5	65
87	Mpl Gain-of-Function Mutations Can be Classified By Differential Subcellular Processing, Molecular Mechanisms, Mode of Inheritance and Clinical Impact. Blood, 2015, 126, 1634-1634.	1.4	1
88	Gene Panel Sequencing of Primary and Relapsed Pediatric T-ALL Shows That Relapse-Specific Mutations Are Diverse and Mostly Non-Recurrent. Blood, 2015, 126, 1428-1428.	1.4	0
89	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627
90	Comparison of different IRT-PAP protocols to screen newborns for cystic fibrosis in three central European populations. Journal of Cystic Fibrosis, 2014, 13, 15-23.	0.7	39

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91	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
92	5â€azacytidine inhibits nonsenseâ€mediated decay in a <scp>MYC</scp>â€dependent fashion. EMBO Molecular Medicine, 2014, 6, 1593-1609.	6.9	51
93	Novel activating mutations lacking cysteine in type I cytokine receptors in acute lymphoblastic leukemia. Blood, 2014, 124, 106-110.	1.4	50
94	The activating STAT5B N642H mutation is a common abnormality in pediatric T-cell acute lymphoblastic leukemia and confers a higher risk of relapse. Haematologica, 2014, 99, e188-e192.	3.5	114
95	NOTCH1 activation clinically antagonizes the unfavorable effect of PTEN inactivation in BFM-treated children with precursor T-cell acute lymphoblastic leukemia. Haematologica, 2013, 98, 928-936.	3.5	81
96	Whole Exome Sequencing Identifies Novel Lyst-Missense Mutations In Incomplete Childhood Chediak-Higashi-Syndrome Presenting As Hemphagocytic Lymphohistiocytosis (HLH). Blood, 2013, 122, 3479-3479.	1.4	0
97	Hotspot Mutations in H3F3A and IDH1 Define Distinct Epigenetic and Biological Subgroups of Glioblastoma. Cancer Cell, 2012, 22, 425-437.	16.8	1,551
98	In vivo efficacy of the histone deacetylase inhibitor suberoylanilide hydroxamic acid in combination with radiotherapy in a malignant rhabdoid tumor mouse model. Radiation Oncology, 2012, 7, 52.	2.7	27
99	Treatment of pediatric patients and young adults with particle therapy at the Heidelberg Ion Therapy Center (HIT): establishment of workflow and initial clinical data. Radiation Oncology, 2012, 7, 170.	2.7	44
100	Hereditary thrombocythemia caused by a thrombopoietin (THPO) gain-of-function mutation associated with multiple myeloma and congenital limb defects. Annals of Hematology, 2012, 91, 1129-1133.	1.8	11
101	A 15q24 microdeletion in transient myeloproliferative disease (<scp>TMD</scp>) and acute megakaryoblastic leukaemia (<scp>AMKL</scp>) implicates <scp>PML</scp> and <scp>SUMO</scp>3 in the leukaemogenesis of <scp>TMD</scp>/<scp>AMKL</scp>. British Journal of Haematology, 2012, 157, 180-187.	2.5	9
102	Gain-of-function mutations in interleukin-7 receptor-Î± (IL7R) in childhood acute lymphoblastic leukemias. Journal of Experimental Medicine, 2011, 208, 901-908.	8.5	307
103	p38 MAPK Controls Prothrombin Expression by Regulated RNA 3â€² End Processing. Molecular Cell, 2011, 41, 298-310.	9.7	70
104	Stay Tuned: miRNA Expression and Nonsense-Mediated Decay in Brain Development. Molecular Cell, 2011, 42, 407-408.	9.7	9
105	Oncogenic FAM131Bâ€“BRAF fusion resulting from 7q34 deletion comprises an alternative mechanism of MAPK pathway activation in pilocytic astrocytoma. Acta Neuropathologica, 2011, 121, 763-774.	7.7	211
106	Combination of suberoylanilide hydroxamic acid with heavy ion therapy shows promising effects in infantile sarcoma cell lines. Radiation Oncology, 2011, 6, 119.	2.7	14
107	Reply to J.C. Lindsey et al. Journal of Clinical Oncology, 2011, 29, e348-e349.	1.6	2
108	Mechanism of escape from nonsense-mediated mRNA decay of human Î²-globin transcripts with nonsense mutations in the first exon. Rna, 2011, 17, 843-854.	3.5	120

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109	Non-randomized therapy trial to determine the safety and efficacy of heavy ion radiotherapy in patients with non-resectable osteosarcoma. BMC Cancer, 2010, 10, 96.	2.6	56
110	Enhancement of Radiation Response in Osteosarcoma and Rhabomyosarcoma Cell Lines by Histone Deacetylase Inhibition. International Journal of Radiation Oncology Biology Physics, 2010, 78, 237-245.	0.8	87
111	NMD: RNA biology meets human genetic medicine. Biochemical Journal, 2010, 430, 365-377.	3.7	192
112	Outcome Prediction in Pediatric Medulloblastoma Based on DNA Copy-Number Aberrations of Chromosomes 6q and 17q and the MYC and MYCN Loci. Journal of Clinical Oncology, 2009, 27, 1627-1636.	1.6	274
113	The Hierarchy of Exon-Junction Complex Assembly by the Spliceosome Explains Key Features of Mammalian Nonsense-Mediated mRNA Decay. PLoS Biology, 2009, 7, e1000120.	5.6	114
114	Downregulation of Notch signaling by Î³-secretase inhibition can abrogate chemotherapy-induced apoptosis in T-ALL cell lines. Annals of Hematology, 2009, 88, 613-621.	1.8	27
115	Unusual bipartite mode of interaction between the nonsense-mediated decay factors, UPF1 and UPF2. EMBO Journal, 2009, 28, 2293-2306.	7.8	126
116	Long-term outcome after polychemotherapy and intensive local radiation therapy of high-grade osteosarcoma. European Journal of Cancer, 2009, 45, 2447-2451.	2.8	34
117	Disassembly of Exon Junction Complexes by PYM. Cell, 2009, 137, 536-548.	28.9	162
118	High-resolution genomic profiling of childhood T-ALL reveals frequent copy-number alterations affecting the TGF-Î² and PI3K-AKT pathways and deletions at 6q15-16.1 as a genomic marker for unfavorable early treatment response. Blood, 2009, 114, 1053-1062.	1.4	105
119	Long-term remission of children with relapsed and secondary anaplastic large cell non-Hodgkin lymphoma (ALCL) following treatment with pulsed dexamethasone and low dose etoposide. Pediatric Blood and Cancer, 2008, 50, 126-129.	1.5	10
120	Treatment of neuroblastoma-related opsoclonusâ€“myoclonusâ€“ataxia syndrome with high-dose dexamethasone pulses. Pediatric Blood and Cancer, 2008, 50, 683-687.	1.5	34
121	Interactions between UPF1, eRFs, PABP and the exon junction complex suggest an integrated model for mammalian NMD pathways. EMBO Journal, 2008, 27, 736-747.	7.8	269
122	Unexpected roles for UPF1 in HIV-1 RNA metabolism and translation. Rna, 2008, 14, 914-927.	3.5	83
123	The abundance of RNPS1, a protein component of the exon junction complex, can determine the variability in efficiency of the Nonsense Mediated Decay pathway. Nucleic Acids Research, 2007, 35, 4542-4551.	14.5	107
124	Nonsense-mediated mRNA decay affects nonsense transcript levels and governs response of cystic fibrosis patients to gentamicin. Journal of Clinical Investigation, 2007, 117, 683-692.	8.2	252
125	The efficiency of nonsense-mediated mRNA decay is an inherent character and varies among different cells. European Journal of Human Genetics, 2007, 15, 1156-1162.	2.8	102
126	The Early Treatment Response of the Clinically Challenging Group of Childhood T-ALL without NOTCH1 Mutations Is Signified by a Specific mRNA Gene Profile.. Blood, 2007, 110, 2789-2789.	1.4	0

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127	A chemiluminescence-based reporter system to monitor nonsense-mediated mRNA decay. Biochemical and Biophysical Research Communications, 2006, 349, 186-191.	2.1	55
128	Activating NOTCH1 mutations predict favorable early treatment response and long-term outcome in childhood precursor T-cell lymphoblastic leukemia. Blood, 2006, 108, 1151-1157.	1.4	262
129	Internal ribosome entry sequenceâ€mediated translation initiation triggers nonsenseâ€mediated decay. EMBO Reports, 2006, 7, 722-726.	4.5	19
130	The uORF-containing thrombopoietin mRNA escapes nonsense-mediated decay (NMD). Nucleic Acids Research, 2006, 34, 2355-2363.	14.5	41
131	Functions of hUpf3a and hUpf3b in nonsense-mediated mRNA decay and translation. Rna, 2006, 12, 1015-1022.	3.5	112
132	The role of nonsense-mediated decay in physiological and pathological processes. , 2005, , .		0
133	Exon-Junction Complex Components Specify Distinct Routes of Nonsense-Mediated mRNA Decay with Differential Cofactor Requirements. Molecular Cell, 2005, 20, 65-75.	9.7	277
134	The Prothrombin C>T Mutation at Position 20209 (F2 20209*T) Promotes 3â€²end mRNA Processing and Thus Contributes to Thrombophilia through Gain-of-Function.. Blood, 2005, 106, 2145-2145.	1.4	0
135	Nonsense-mediated decay approaches the clinic. Nature Genetics, 2004, 36, 801-808.	21.4	546
136	Y14 and hUpf3b Form an NMD-Activating Complex. Molecular Cell, 2003, 11, 939-949.	9.7	258
137	Increased efficiency of mRNA 3â€² end formation: a new genetic mechanism contributing to hereditary thrombophilia. Nature Genetics, 2001, 28, 389-392.	21.4	247
138	Reversible central pontine and extrapontine myelinolysis in a 16-year-old girl. Child's Nervous System, 2001, 17, 294-296.	1.1	23
139	A Perfect Message. Cell, 1999, 96, 307-310.	28.9	789