

Torsten Klengel

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

57
papers

6,011
citations

35
h-index

74
g-index

74
ext. papers

7,269
ext. citations

6.9
avg, IF

5.58
L-index

#	Paper	IF	Citations
57	Molecular signature of extracellular matrix pathology in schizophrenia. <i>European Journal of Neuroscience</i> , 2021 , 53, 3960-3987	3.5	10
56	Mineralocorticoid receptors dampen glucocorticoid receptor sensitivity to stress via regulation of FKBP5. <i>Cell Reports</i> , 2021 , 35, 109185	10.6	6
55	Multioomic biological approaches to the study of child abuse and neglect. <i>Pharmacology Biochemistry and Behavior</i> , 2021 , 210, 173271	3.9	0
54	The PedBE clock accurately estimates DNA methylation age in pediatric buccal cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 23329-23335	11.5	53
53	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. <i>Cell Reports</i> , 2020 , 31, 107716	10.6	21
52	MicroRNA regulation of persistent stress-enhanced memory. <i>Molecular Psychiatry</i> , 2020 , 25, 965-976	15.1	16
51	Glucocorticoid exposure during hippocampal neurogenesis primes future stress response by inducing changes in DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 23280-23285	11.5	69
50	Intergenerational Effects of Maternal Holocaust Exposure on Methylation. <i>American Journal of Psychiatry</i> , 2020 , 177, 744-753	11.9	24
49	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. <i>Nature Communications</i> , 2019 , 10, 4558	17.4	151
48	Sensitive Periods for the Effect of Childhood Adversity on DNA Methylation: Results From a Prospective, Longitudinal Study. <i>Biological Psychiatry</i> , 2019 , 85, 838-849	7.9	115
47	An integrated -omics analysis of the epigenetic landscape of gene expression in human blood cells. <i>BMC Genomics</i> , 2018 , 19, 476	4.5	20
46	Novel Bioinformatics Approach Identifies Transcriptional Profiles of Lineage-Specific Transposable Elements at Distinct Loci in the Human Dorsolateral Prefrontal Cortex. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2435-2453	8.3	23
45	A Potential Role for the Noncoding Transcriptome in Psychiatric Disorders. <i>Harvard Review of Psychiatry</i> , 2018 , 26, 364-373	4.1	1
44	Exposure to Violence Accelerates Epigenetic Aging in Children. <i>Scientific Reports</i> , 2017 , 7, 8962	4.9	85
43	Does sleep disruption mediate the effects of childhood maltreatment on brain structure?. <i>Högre Utbildning</i> , 2017 , 8, 1450594	5	11
42	Models of Intergenerational and Transgenerational Transmission of Risk for Psychopathology in Mice. <i>Neuropsychopharmacology</i> , 2016 , 41, 219-31	8.7	65
41	Holocaust Exposure Induced Intergenerational Effects on FKBP5 Methylation. <i>Biological Psychiatry</i> , 2016 , 80, 372-80	7.9	389

40	Dexamethasone Treatment Leads to Enhanced Fear Extinction and Dynamic Fkbp5 Regulation in Amygdala. <i>Neuropsychopharmacology</i> , 2016 , 41, 832-46	8.7	65
39	FKBP5 Epialleles. <i>Epigenetics and Human Health</i> , 2016 , 3-21		
38	LINE1 insertions as a genomic risk factor for schizophrenia: Preliminary evidence from an affected family. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016 , 171, 534-45	3.5	26
37	Epigenetics of Stress-Related Psychiatric Disorders and Gene Environment Interactions. <i>Neuron</i> , 2015 , 86, 1343-57	13.9	203
36	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
35	RNA expression profiling in depressed patients suggests retinoid-related orphan receptor alpha as a biomarker for antidepressant response. <i>Translational Psychiatry</i> , 2015 , 5, e538	8.6	29
34	DNA extracted from saliva for methylation studies of psychiatric traits: evidence tissue specificity and relatedness to brain. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015 , 168B, 36-44	3.5	218
33	DICER1 and microRNA regulation in post-traumatic stress disorder with comorbid depression. <i>Nature Communications</i> , 2015 , 6, 10106	17.4	69
32	Epigenetic and genetic variation at SKA2 predict suicidal behavior and post-traumatic stress disorder. <i>Translational Psychiatry</i> , 2015 , 5, e627	8.6	75
31	Genetic Differences in the Immediate Transcriptome Response to Stress Predict Risk-Related Brain Function and Psychiatric Disorders. <i>Neuron</i> , 2015 , 86, 1189-202	13.9	79
30	FKBP5 allele-specific epigenetic modification in gene by environment interaction. <i>Neuropsychopharmacology</i> , 2015 , 40, 244-6	8.7	53
29	Epigenetic mechanisms underlying learning and the inheritance of learned behaviors. <i>Trends in Neurosciences</i> , 2015 , 38, 96-107	13.3	81
28	The role of DNA methylation in stress-related psychiatric disorders. <i>Neuropharmacology</i> , 2014 , 80, 115-33	3.5	207
27	Hypothalamic-pituitary-adrenocortical axis activity as a potential predictor for withdrawal symptoms in addiction to flupirtine, a nonopioid analgesic. <i>Journal of Clinical Psychopharmacology</i> , 2014 , 34, e6-8	1.7	1
26	Age-associated epigenetic upregulation of the FKBP5 gene selectively impairs stress resiliency. <i>PLoS ONE</i> , 2014 , 9, e107241	3.7	57
25	Accounting for population stratification in DNA methylation studies. <i>Genetic Epidemiology</i> , 2014 , 38, 231-41	2.6	146
24	Epigenomic association analysis identifies smoking-related DNA methylation sites in African Americans. <i>Human Genetics</i> , 2013 , 132, 1027-37	6.3	119
23	Traumata im Kindesalter führen zu epigenetischen Veränderungen bei Risikogruppen. <i>Biologie in Unserer Zeit</i> , 2013 , 43, 13-14	0.1	

22	Allele-specific FKBP5 DNA demethylation mediates gene-childhood trauma interactions. <i>Nature Neuroscience</i> , 2013 , 16, 33-41	25.5	1008
21	Genetic variation in FKBP5 associated with the extent of stress hormone dysregulation in major depression. <i>Genes, Brain and Behavior</i> , 2013 , 12, 289-96	3.6	113
20	Resistance to antidepressant treatment is associated with polymorphisms in the leptin gene, decreased leptin mRNA expression, and decreased leptin serum levels. <i>European Neuropsychopharmacology</i> , 2013 , 23, 653-62	1.2	29
19	Gene Environment interactions in the prediction of response to antidepressant treatment. <i>International Journal of Neuropsychopharmacology</i> , 2013 , 16, 701-11	5.8	20
18	Childhood maltreatment is associated with distinct genomic and epigenetic profiles in posttraumatic stress disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 8302-7	11.5	408
17	Gene-environment interactions in major depressive disorder. <i>Canadian Journal of Psychiatry</i> , 2013 , 58, 76-83	4.8	81
16	Accelerated neurodegeneration through chaperone-mediated oligomerization of tau. <i>Journal of Clinical Investigation</i> , 2013 , 123, 4158-69	15.9	169
15	Possible associations of NTRK2 polymorphisms with antidepressant treatment outcome: findings from an extended tag SNP approach. <i>PLoS ONE</i> , 2013 , 8, e64947	3.7	16
14	Differential Genetic and Epigenetic Regulation of catechol-O-methyltransferase is Associated with Impaired Fear Inhibition in Posttraumatic Stress Disorder. <i>Frontiers in Behavioral Neuroscience</i> , 2013 , 7, 30	3.5	82
13	Peripheral blood gene expression: it all boils down to the RNA collection tubes. <i>BMC Research Notes</i> , 2012 , 5, 1	2.3	213
12	Dexamethasone stimulated gene expression in peripheral blood is a sensitive marker for glucocorticoid receptor resistance in depressed patients. <i>Neuropsychopharmacology</i> , 2012 , 37, 1455-64	8.7	125
11	Epigenetics, depression and antidepressant treatment. <i>Current Pharmaceutical Design</i> , 2012 , 18, 5879-89	3.3	53
10	Genome-wide association study of antidepressant treatment-emergent suicidal ideation. <i>Neuropsychopharmacology</i> , 2012 , 37, 797-807	8.7	62
9	Using gene-environment interactions to target personalized treatment in mood disorder. <i>Personalized Medicine</i> , 2011 , 8, 23-34	2.2	9
8	Somatization in major depression--clinical features and genetic associations. <i>Acta Psychiatrica Scandinavica</i> , 2011 , 124, 317-28	6.5	17
7	Using polymorphisms in FKBP5 to define biologically distinct subtypes of posttraumatic stress disorder: evidence from endocrine and gene expression studies. <i>Archives of General Psychiatry</i> , 2011 , 68, 901-10		167
6	Cryptococcus neoformans senses CO ₂ through the carbonic anhydrase Can2 and the adenylyl cyclase Cac1. <i>Eukaryotic Cell</i> , 2006 , 5, 103-11		148
5	Fungal adenylyl cyclase integrates CO ₂ sensing with cAMP signaling and virulence. <i>Current Biology</i> , 2005 , 15, 2021-6	6.3	338

4	Fungal Adenylyl Cyclase Integrates CO ₂ Sensing with cAMP Signaling and Virulence. <i>Current Biology</i> , 2005 , 15, 2177	6.3	3
3	Sensitive periods for the effect of childhood adversity on DNA methylation: Results from a prospective, longitudinal study		1
2	Largest genome-wide association study for PTSD identifies genetic risk loci in European and African ancestries and implicates novel biological pathways		6
1	Analysis of Genetically Regulated Gene Expression identifies a trauma type specific PTSD gene, SNRNP35		1