

Bernhard Horsthemke

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6510396/publications.pdf>

Version: 2024-02-01

74
papers

5,840
citations

117619

34
h-index

82542

72
g-index

83
all docs

83
docs citations

83
times ranked

5288
citing authors

#	ARTICLE	IF	CITATIONS
1	Inherited microdeletions in the Angelman and Prader-Willi syndromes define an imprinting centre on human chromosome 15. <i>Nature Genetics</i> , 1995, 9, 395-400.	21.4	589
2	Epigenetic changes may contribute to the formation and spontaneous regression of retinoblastoma. <i>Human Genetics</i> , 1989, 83, 155-158.	3.8	488
3	Cloning defined regions of the human genome by microdissection of banded chromosomes and enzymatic amplification. <i>Nature</i> , 1989, 338, 348-350.	27.8	351
4	Epimutations in Prader-Willi and Angelman Syndromes: A Molecular Study of 136 Patients with an Imprinting Defect. <i>American Journal of Human Genetics</i> , 2003, 72, 571-577.	6.2	280
5	Angelman syndrome – insights into a rare neurogenetic disorder. <i>Nature Reviews Neurology</i> , 2016, 12, 584-593.	10.1	256
6	Imprint switching on human chromosome 15 may involve alternative transcripts of the SNRPN gene. <i>Nature Genetics</i> , 1996, 14, 163-170.	21.4	250
7	Mechanisms of imprinting of the Prader-Willi/Angelman region. <i>American Journal of Medical Genetics, Part A</i> , 2008, 146A, 2041-2052.	1.2	246
8	Assisted reproduction: the epigenetic perspective. <i>Human Reproduction Update</i> , 2005, 11, 473-482.	10.8	207
9	A critical view on transgenerational epigenetic inheritance in humans. <i>Nature Communications</i> , 2018, 9, 2973.	12.8	203
10	Molecular diagnosis of the Prader-Willi and Angelman syndromes by detection of parent-of-origin specific DNA methylation in 15q11-13. <i>Human Genetics</i> , 1992, 90, 313-5.	3.8	195
11	Maternal methylation imprints on human chromosome 15 are established during or after fertilization. <i>Nature Genetics</i> , 2001, 27, 341-344.	21.4	193
12	Modification of 15q11 – q13 DNA methylation imprints in unique Angelman and Prader-Willi patients. <i>Human Molecular Genetics</i> , 1993, 2, 1377-1382.	2.9	144
13	Sporadic Imprinting Defects in Prader-Willi Syndrome and Angelman Syndrome: Implications for Imprint-Switch Models, Genetic Counseling, and Prenatal Diagnosis. <i>American Journal of Human Genetics</i> , 1998, 63, 170-180.	6.2	142
14	De novo deletions of SNRPN exon 1 in early human and mouse embryos result in a paternal to maternal imprint switch. <i>Nature Genetics</i> , 2000, 25, 74-78.	21.4	142
15	A Single-Tube PCR Test for the Diagnosis of Angelman and Prader-Willi Syndrome Based on Allelic Methylation Differences at the SNRPN Locus. <i>European Journal of Human Genetics</i> , 1997, 5, 94-98.	2.8	139
16	N6-Adenosine Methylation in MiRNAs. <i>PLoS ONE</i> , 2015, 10, e0118438.	2.5	115
17	A paternal deletion of MKRN3, MAGEL2 and NDN does not result in Prader-Willi syndrome. <i>European Journal of Human Genetics</i> , 2009, 17, 582-590.	2.8	112
18	Unstable TTTTA/TTTCA expansions in MARCH6 are associated with Familial Adult Myoclonic Epilepsy type 3. <i>Nature Communications</i> , 2019, 10, 4919.	12.8	111

#	ARTICLE	IF	CITATIONS
19	The Human Retinoblastoma Gene Is Imprinted. <i>PLoS Genetics</i> , 2009, 5, e1000790.	3.5	110
20	A previously unrecognised phenotype characterised by obesity, muscular hypotonia, and ability to speak in patients with Angelman syndrome caused by an imprinting defect. <i>European Journal of Human Genetics</i> , 1999, 7, 638-644.	2.8	88
21	Mechanisms of imprint dysregulation. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2010, 154C, 321-328.	1.6	82
22	The molecular function and clinical phenotype of partial deletions of the IGF2/H19 imprinting control region depends on the spatial arrangement of the remaining CTCF-binding sites. <i>Human Molecular Genetics</i> , 2013, 22, 544-557.	2.9	78
23	Somatic mosaicism in patients with Angelman syndrome and an imprinting defect. <i>Human Molecular Genetics</i> , 2004, 13, 2547-2555.	2.9	74
24	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016, 9, 33.	3.9	73
25	Microdissection of the Prader-Willi syndrome chromosome region and identification of potential gene sequences. <i>Genomics</i> , 1990, 6, 521-527.	2.9	72
26	Clinical features of maternal uniparental disomy 14 in patients with an epimutation and a deletion of the imprinted <i>DLK1/GTL2</i> gene cluster. <i>Human Mutation</i> , 2008, 29, 1141-1146.	2.5	68
27	Disruption of the Bipartite Imprinting Center in a Family with Angelman Syndrome. <i>American Journal of Human Genetics</i> , 2001, 68, 1290-1294.	6.2	62
28	Epigenetic germline mosaicism in infertile men. <i>Human Molecular Genetics</i> , 2015, 24, 1295-1304.	2.9	58
29	C15orf2 and a novel noncoding transcript from the Prader-Willi/Angelman syndrome region show monoallelic expression in fetal brain. <i>Genomics</i> , 2007, 89, 588-595.	2.9	52
30	FTO levels affect RNA modification and the transcriptome. <i>European Journal of Human Genetics</i> , 2013, 21, 317-323.	2.8	52
31	In Brief: Genomic imprinting and imprinting diseases. <i>Journal of Pathology</i> , 2014, 232, 485-487.	4.5	44
32	Identification of a Testis-Specific Gene (C15orf2) in the Prader-Willi Syndrome Region on Chromosome 15. <i>Genomics</i> , 2000, 65, 174-183.	2.9	42
33	Heritable germline epimutations in humans. <i>Nature Genetics</i> , 2007, 39, 573-574.	21.4	41
34	Identification of cis- and trans-acting factors possibly modifying the risk of epimutations on chromosome 15. <i>European Journal of Human Genetics</i> , 2006, 14, 752-758.	2.8	37
35	New insights into the imprinted MEG8-DMR in 14q32 and clinical and molecular description of novel patients with Temple syndrome. <i>European Journal of Human Genetics</i> , 2017, 25, 935-945.	2.8	35
36	Expression of SNURF-SNRPN upstream transcripts and epigenetic regulatory genes during human spermatogenesis. <i>European Journal of Human Genetics</i> , 2009, 17, 1463-1470.	2.8	33

#	ARTICLE	IF	CITATIONS
37	Clinical utility gene card for: Angelman Syndrome. <i>European Journal of Human Genetics</i> , 2015, 23, 3-3.	2.8	32
38	Pre- and Postovulatory Aging of Murine Oocytes Affect the Transcript Level and Poly(A) Tail Length of Maternal Effect Genes. <i>PLoS ONE</i> , 2014, 9, e108907.	2.5	30
39	Clinical phenotypes of MAGEL2 mutations and deletions. <i>Orphanet Journal of Rare Diseases</i> , 2014, 9, 40.	2.7	28
40	Locus-Specific DNA Methylation Analysis by Targeted Deep Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1767, 351-366.	0.9	28
41	Novel microdeletions on chromosome 14q32.2 suggest a potential role for non-coding RNAs in Kagami-Ogata syndrome. <i>European Journal of Human Genetics</i> , 2016, 24, 1724-1729.	2.8	27
42	A germ cell-specific ageing pattern in otherwise healthy men. <i>Aging Cell</i> , 2020, 19, e13242.	6.7	27
43	Deep Bisulfite Sequencing of Aberrantly Methylated Loci in a Patient with Multiple Methylation Defects. <i>PLoS ONE</i> , 2013, 8, e76953.	2.5	26
44	wg-blimp: an end-to-end analysis pipeline for whole genome bisulfite sequencing data. <i>BMC Bioinformatics</i> , 2020, 21, 169.	2.6	26
45	The imprinted NPAP1/C15orf2 gene in the Prader-Willi syndrome region encodes a nuclear pore complex associated protein. <i>Human Molecular Genetics</i> , 2012, 21, 4038-4048.	2.9	25
46	Preovulatory Aging In Vivo and In Vitro Affects Maturation Rates, Abundance of Selected Proteins, Histone Methylation Pattern and Spindle Integrity in Murine Oocytes. <i>PLoS ONE</i> , 2016, 11, e0162722.	2.5	23
47	The sperm epigenome does not display recurrent epimutations in patients with severely impaired spermatogenesis. <i>Clinical Epigenetics</i> , 2020, 12, 61.	4.1	23
48	The C15orf2 gene in the Prader-Willi syndrome region is subject to genomic imprinting and positive selection. <i>Neurogenetics</i> , 2010, 11, 153-161.	1.4	22
49	The Origin of the RB1 Imprint. <i>PLoS ONE</i> , 2013, 8, e81502.	2.5	21
50	A maternal deletion upstream of the imprint control region 2 in 11p15 causes loss of methylation and familial Beckwith-Wiedemann syndrome. <i>European Journal of Human Genetics</i> , 2016, 24, 1280-1286.	2.8	20
51	Regions of common inter-individual DNA methylation differences in human monocytes: genetic basis and potential function. <i>Epigenetics and Chromatin</i> , 2017, 10, 37.	3.9	20
52	Clinical utility gene card for: Prader-Willi Syndrome. <i>European Journal of Human Genetics</i> , 2014, 22, 1153-1153.	2.8	18
53	Altering TET dioxygenase levels within physiological range affects DNA methylation dynamics of HEK293 cells. <i>Epigenetics</i> , 2015, 10, 819-833.	2.7	18
54	Hormone-induced delayed ovulation affects early embryonic development. <i>Fertility and Sterility</i> , 2011, 95, 2390-2394.	1.0	17

#	ARTICLE	IF	CITATIONS
55	Evolutionary Origin and Methylation Status of Human Intronic CpG Islands that Are Not Present in Mouse. <i>Genome Biology and Evolution</i> , 2014, 6, 1579-1588.	2.5	16
56	Lasp1 regulates adherens junction dynamics and fibroblast transformation in destructive arthritis. <i>Nature Communications</i> , 2021, 12, 3624.	12.8	16
57	The adult phenotype of Schaaf-Yang syndrome. <i>Orphanet Journal of Rare Diseases</i> , 2020, 15, 294.	2.7	14
58	Whole-genome methylation analysis of testicular germ cells from cryptozoospermic men points to recurrent and functionally relevant DNA methylation changes. <i>Clinical Epigenetics</i> , 2021, 13, 160.	4.1	12
59	The Imprinted NPAP1 Gene in the Prader-Willi Syndrome Region Belongs to a POM121-Related Family of Retrogenes. <i>Genome Biology and Evolution</i> , 2014, 6, 344-351.	2.5	11
60	Common genetic variation in the Angelman syndrome imprinting centre affects the imprinting of chromosome 15. <i>European Journal of Human Genetics</i> , 2020, 28, 835-839.	2.8	10
61	Methylation analysis of SST and SSTR4 promoters in the neocortex of Alzheimer's disease patients. <i>Neuroscience Letters</i> , 2014, 566, 241-246.	2.1	9
62	Parental origin and functional relevance of a de novo UBE3A variant. <i>European Journal of Medical Genetics</i> , 2011, 54, 19-24.	1.3	8
63	Waddington's epigenetic landscape and post-Darwinian biology. <i>BioEssays</i> , 2012, 34, 711-712.	2.5	7
64	Genome-wide methylation analysis of retrocopy-associated CpG islands and their genomic environment. <i>Epigenetics</i> , 2016, 11, 216-226.	2.7	7
65	In vitro postovulatory oocyte aging affects H3K9 trimethylation in two-cell embryos after IVF. <i>Annals of Anatomy</i> , 2020, 227, 151424.	1.9	7
66	Genome-Wide Analysis of the Nucleosome Landscape in Individuals with Coffin-Siris Syndrome. <i>Cytogenetic and Genome Research</i> , 2019, 159, 1-11.	1.1	5
67	The Diagnostic Journey of a Patient with Prader-Willi-Like Syndrome and a Unique Homozygous SNURF-SNRPN Variant; Bio-Molecular Analysis and Review of the Literature. <i>Genes</i> , 2021, 12, 875.	2.4	4
68	Human PPP1R26P1 Functions as cis-Repressive Element in Mouse Rb1. <i>PLoS ONE</i> , 2013, 8, e74159.	2.5	4
69	Rhythm is not enough. <i>Nature Genetics</i> , 2007, 39, 1190-1191.	21.4	3
70	GC-rich repeat expansions: associated disorders and mechanisms. <i>Medizinische Genetik</i> , 2022, 33, 325-335.	0.2	2
71	Next-Generation-Sequencing in der Epigenetik. <i>Medizinische Genetik</i> , 2019, 31, 205-211.	0.2	1
72	A human somatic cell culture system for modelling gene silencing by transcriptional interference. <i>Heliyon</i> , 2020, 6, e03261.	3.2	1

#	ARTICLE	IF	CITATIONS
73	Novel strategies to cure imprinting disorders. <i>Medizinische Genetik</i> , 2020, 32, 335-340.	0.2	1
74	Of wolves and men: the role of paternal child care in the evolution of genomic imprinting. <i>European Journal of Human Genetics</i> , 2009, 17, 273-274.	2.8	0