Christine R Beck

List of Publications by Year
in descending order

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Version: 2024-02-01

33 papers	3,123 citations	279798 23 h-index	395702 33 g-index
36 all docs	36 docs citations	36 times ranked	5721 citing authors

#	Article	IF	Citations
1	LINE-1 Retrotransposition Activity in Human Genomes. Cell, 2010, 141, 1159-1170.	28.9	531
2	LINE-1 Elements in Structural Variation and Disease. Annual Review of Genomics and Human Genetics, 2011, 12, 187-215.	6.2	471
3	Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. Nature Genetics, 2020, 52, 891-897.	21.4	273
4	Primary immunodeficiency diseases: Genomic approaches delineate heterogeneous Mendelian disorders. Journal of Allergy and Clinical Immunology, 2017, 139, 232-245.	2.9	261
5	Mus81 and converging forks limit the mutagenicity of replication fork breakage. Science, 2015, 349, 742-747.	12.6	162
6	Assessing structural variation in a personal genomeâ€"towards a human reference diploid genome. BMC Genomics, 2015, 16, 286.	2.8	153
7	PGM3 Mutations Cause a Congenital Disorder of Glycosylation with Severe Immunodeficiency and Skeletal Dysplasia. American Journal of Human Genetics, 2014, 95, 96-107.	6.2	148
8	Global transcriptional disturbances underlie Cornelia de Lange syndrome and related phenotypes. Journal of Clinical Investigation, 2015, 125, 636-651.	8.2	136
9	The Alu-Rich Genomic Architecture of SPAST Predisposes to Diverse and Functionally Distinct Disease-Associated CNV Alleles. American Journal of Human Genetics, 2014, 95, 143-161.	6.2	87
10	Alu-mediated diverse and complex pathogenic copy-number variants within human chromosome 17 at p13.3. Human Molecular Genetics, 2015, 24, 4061-4077.	2.9	83
11	Predicting human genes susceptible to genomic instability associated with Alu/Alu-mediated rearrangements. Genome Research, 2018, 28, 1228-1242.	5.5	74
12	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. Cell, 2019, 176, 1310-1324.e10.	28.9	73
13	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
14	PacBio-LITS: a large-insert targeted sequencing method for characterization of human disease-associated chromosomal structural variations. BMC Genomics, 2015, 16, 214.	2.8	63
15	Hotspots of Human Mutation. Trends in Genetics, 2021, 37, 717-729.	6.7	62
16	Complex Genomic Rearrangements at the PLP1 Locus Include Triplication and Quadruplication. PLoS Genetics, 2015, 11, e1005050.	3.5	57
17	Curcumin facilitates a transitory cellular stress response in Trembler-J mice. Human Molecular Genetics, 2013, 22, 4698-4705.	2.9	43
18	Recurrent HERV-H-Mediated 3q13.2-q13.31 Deletions Cause a Syndrome of Hypotonia and Motor, Language, and Cognitive Delays. Human Mutation, 2013, 34, 1415-1423.	2.5	40

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19	Transduction-Specific ATLAS Reveals a Cohort of Highly Active L1 Retrotransposons in Human Populations. Human Mutation, 2013, 34, 974-985.	2.5	38
20	Nonrecurrent 17p11.2p12 Rearrangement Events that Result in Two Concomitant Genomic Disorders: The PMP22-RAI1 Contiguous Gene Duplication Syndrome. American Journal of Human Genetics, 2015, 97, 691-707.	6.2	33
21	Exonic duplication CNV of NDRG1 associated with autosomal-recessive HMSN-Lom/CMT4D. Genetics in Medicine, 2014, 16, 386-394.	2.4	30
22	A comprehensive long-read isoform analysis platform and sequencing resource for breast cancer. Science Advances, 2022, 8, eabg6711.	10.3	30
23	Optimization of Feline Immunodeficiency Virus Vectors for RNA Interference. Journal of Virology, 2006, 80, 9371-9380.	3.4	29
24	Mutation screening of the IL-1 receptor antagonist gene in chronic non-bacterial osteomyelitis of childhood and adolescence. Clinical and Experimental Rheumatology, 2011, 29, 1040-3.	0.8	26
25	Distinct patterns of complex rearrangements and a mutational signature of microhomeology are frequently observed in PLP1 copy number gain structural variants. Genome Medicine, 2019, 11, 80.	8.2	24
26	Comparative Genomic Analyses of the Human NPHP1 Locus Reveal Complex Genomic Architecture and Its Regional Evolution in Primates. PLoS Genetics, 2015, 11, e1005686.	3.5	21
27	Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. Genome Medicine, 2016, 8, 105.	8.2	20
28	Whole-exome sequencing links TMCO1 defect syndrome with cerebro-facio-thoracic dysplasia. European Journal of Human Genetics, 2014, 22, 1145-1148.	2.8	19
29	The role of combined SNV and CNV burden in patients with distal symmetric polyneuropathy. Genetics in Medicine, 2016, 18, 443-451.	2.4	18
30	Structural variant identification and characterization. Chromosome Research, 2020, 28, 31-47.	2.2	13
31	Spliced integrated retrotransposed element (SpIRE) formation in the human genome. PLoS Biology, 2018, 16, e2003067.	5.6	11
32	Inter-Strain Epigenomic Profiling Reveals a Candidate IAP Master Copy in C3H Mice. Viruses, 2020, 12, 783.	3.3	9
33	SvAnna: efficient and accurate pathogenicity prediction of coding and regulatory structural variants in long-read genome sequencing. Genome Medicine, 2022, 14, 44.	8.2	7