

# Thomas Besnard

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

1,245  
citations

471509

17  
h-index

501196

28  
g-index

31  
all docs

31  
docs citations

31  
times ranked

3296  
citing authors

#	ARTICLE	IF	CITATIONS
1	Stankiewicz-Isidor syndrome: expanding the clinical and molecular phenotype. <i>Genetics in Medicine</i> , 2022, 24, 179-191.	2.4	9
2	Rare germline heterozygous missense variants in BRCA1-associated protein 1, BAP1, cause a syndromic neurodevelopmental disorder. <i>American Journal of Human Genetics</i> , 2022, 109, 361-372.	6.2	6
3	Loss of function variants in ARHGEF9 are associated with an X-linked intellectual disability dominant disorder. <i>Human Mutation</i> , 2021, 42, 498-505.	2.5	1
4	Haploinsufficiency of the Sin3/HDAC corepressor complex member SIN3B causes a syndromic intellectual disability/autism spectrum disorder. <i>American Journal of Human Genetics</i> , 2021, 108, 929-941.	6.2	15
5	Biallelic pathogenic variants in the lanosterol synthase gene LSS involved in the cholesterol biosynthesis cause alopecia with intellectual disability, a rare recessive neuroectodermal syndrome. <i>Genetics in Medicine</i> , 2019, 21, 2025-2035.	2.4	40
6	Complex Compound Inheritance of Lethal Lung Developmental Disorders Due to Disruption of the TBX-FGF Pathway. <i>American Journal of Human Genetics</i> , 2019, 104, 213-228.	6.2	90
7	Dual Molecular Effects of Dominant RORA Mutations Cause Two Variants of Syndromic Intellectual Disability with Either Autism or Cerebellar Ataxia. <i>American Journal of Human Genetics</i> , 2018, 102, 744-759.	6.2	51
8	A new mutation of <i>ANO6</i> in two familial cases of Scott syndrome. <i>British Journal of Haematology</i> , 2018, 180, 750-752.	2.5	15
9	New splicing pathogenic variant in EBP causing extreme familial variability of Conradi-Hallermann-Rieger Syndrome. <i>European Journal of Human Genetics</i> , 2018, 26, 1784-1790.	2.8	7
10	Identification of a new VHL exon and complex splicing alterations in familial erythrocytosis or von Hippel-Lindau disease. <i>Blood</i> , 2018, 132, 469-483.	1.4	70
11	De Novo Disruption of the Proteasome Regulatory Subunit PSMD12 Causes a Syndromic Neurodevelopmental Disorder. <i>American Journal of Human Genetics</i> , 2017, 100, 352-363.	6.2	86
12	Haploinsufficiency of the E3 ubiquitin-protein ligase gene TRIP12 causes intellectual disability with or without autism spectrum disorders, speech delay, and dysmorphic features. <i>Human Genetics</i> , 2017, 136, 377-386.	3.8	36
13	Biallelic Variants in OTUD6B Cause an Intellectual Disability Syndrome Associated with Seizures and Dysmorphic Features. <i>American Journal of Human Genetics</i> , 2017, 100, 676-688.	6.2	54
14	De Novo Missense Mutations in DHX30 Impair Global Translation and Cause a Neurodevelopmental Disorder. <i>American Journal of Human Genetics</i> , 2017, 101, 716-724.	6.2	66
15	De Novo Mutations in Protein Kinase Genes CAMK2A and CAMK2B Cause Intellectual Disability. <i>American Journal of Human Genetics</i> , 2017, 101, 768-788.	6.2	136
16	Germline De Novo Mutations in GNB1 Cause Severe Neurodevelopmental Disability, Hypotonia, and Seizures. <i>American Journal of Human Genetics</i> , 2016, 98, 1001-1010.	6.2	102
17	De Novo Truncating Variants in SON Cause Intellectual Disability, Congenital Malformations, and Failure to Thrive. <i>American Journal of Human Genetics</i> , 2016, 99, 720-727.	6.2	45
18	CUGC for hereditary fibrosing poikiloderma with tendon contractures, myopathy, and pulmonary fibrosis (POIKTMP). <i>European Journal of Human Genetics</i> , 2016, 24, 779-779.	2.8	8

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19	De Novo Truncating Mutations in the Kinetochores-Microtubules Attachment Gene <i>CHAMP1</i> Cause Syndromic Intellectual Disability. <i>Human Mutation</i> , 2016, 37, 354-358.	2.5	40
20	Expanding the clinical spectrum of hereditary fibrosing poikiloderma with tendon contractures, myopathy and pulmonary fibrosis due to <i>FAM111B</i> mutations. <i>Orphanet Journal of Rare Diseases</i> , 2015, 10, 135.	2.7	42
21	Experience of targeted Usher exome sequencing as a clinical test. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2014, 2, 30-43.	1.2	53
22	The contribution of <i>GPR98</i> and <i>DFNB31</i> genes to a Spanish Usher syndrome type 2 cohort. <i>Molecular Vision</i> , 2013, 19, 367-73.	1.1	13
23	Usher syndrome type 2 caused by activation of an <i>USH2A</i> pseudoexon: Implications for diagnosis and therapy. <i>Human Mutation</i> , 2012, 33, 104-108.	2.5	102
24	Non- <i>USH2A</i> mutations in <i>USH2</i> patients. <i>Human Mutation</i> , 2012, 33, 504-510.	2.5	57
25	Four-Year Follow-up of Diagnostic Service in <i>USH1</i> Patients. , 2011, 52, 4063.		47
26	Nasal epithelial cells are a reliable source to study splicing variants in Usher syndrome. <i>Human Mutation</i> , 2010, 31, 734-741.	2.5	29