Juan Botas

List of Publications by Year in descending order

35 papers	4,341 citations	304701 22 h-index	434170 31 g-index
37 all docs	37 docs citations	37 times ranked	6743 citing authors

#	Article	IF	Citations
1	Guidelines for the use and interpretation of assays for monitoring autophagy (4th) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 742 Td	9.1	1,430
2	Identification of genes that modify ataxin-1-induced neurodegeneration. Nature, 2000, 408, 101-106.	27.8	648
3	Huntingtin Interacting Proteins Are Genetic Modifiers of Neurodegeneration. PLoS Genetics, 2007, 3, e82.	3.5	368
4	Integrated genomics and proteomics define huntingtin CAG lengthâ€“dependent networks in mice. Nature Neuroscience, 2016, 19, 623-633.	14.8	342
5	Matrix Metalloproteinases Are Modifiers of Huntingtin Proteolysis and Toxicity in Huntington's Disease. Neuron, 2010, 67, 199-212.	8.1	152
6	Suppression of Neurodegeneration and Increased Neurotransmission Caused by Expanded Full-Length Huntingtin Accumulating in the Cytoplasm. Neuron, 2008, 57, 27-40.	8.1	143
7	Reduction of Nuak1 Decreases Tau and Reverses Phenotypes in a Tauopathy Mouse Model. Neuron, 2016, 92, 407-418.	8.1	120
8	RASâ€“MAPKâ€“MSK1 pathway modulates ataxin 1 protein levels and toxicity in SCA1. Nature, 2013, 498, 325-331.	27.8	119
9	Targeting ATM ameliorates mutant Huntingtin toxicity in cell and animal models of Huntingtonâ€™s disease. Science Translational Medicine, 2014, 6, 268ra178.	12.4	103
10	TRIM28 regulates the nuclear accumulation and toxicity of both alpha-synuclein and tau. ELife, 2016, 5, .	6.0	97
11	DrosophilaMitf regulates the V-ATPase and the lysosomal-autophagic pathway. Autophagy, 2016, 12, 484-498.	9.1	87
12	dAtaxin-2 Mediates Expanded Ataxin-1-Induced Neurodegeneration in a Drosophila Model of SCA1. PLoS Genetics, 2007, 3, e234.	3.5	83
13	Huntingtin proteolysis releases nonâ€polyQ fragments that cause toxicity through dynamin 1 dysregulation. EMBO Journal, 2015, 34, 2255-2271.	7.8	79
14	Uncoupling neuronal death and dysfunction in Drosophila models of neurodegenerative disease. Acta Neuropathologica Communications, 2016, 4, 62.	5.2	77
15	Comparative analysis of genetic modifiers in Drosophila points to common and distinct mechanisms of pathogenesis among polyglutamine diseases. Human Molecular Genetics, 2008, 17, 376-390.	2.9	75
16	A striatal-enriched intronic GPCR modulates huntingtin levels and toxicity. ELife, 2015, 4, .	6.0	60
17	TORC1 Inhibition by Rapamycin Promotes Antioxidant Defences in a Drosophila Model of Friedreichâ€™s Ataxia. PLoS ONE, 2015, 10, e0132376.	2.5	51
18	A Druggable Genome Screen Identifies Modifiers of Î±-Synuclein Levels via a Tiered Cross-Species Validation Approach. Journal of Neuroscience, 2018, 38, 9286-9301.	3.6	49

#	Article	IF	Citations
19	Inhibition of PIP4KÎ³ ameliorates the pathological effects of mutant huntingtin protein. ELife, 2017, 6, .	6.0	49
20	A Genome-Scale RNAâ€“Interference Screen Identifies RRAS Signaling as a Pathologic Feature of Huntington's Disease. PLoS Genetics, 2012, 8, e1003042.	3.5	41
21	High-Throughput Functional Analysis Distinguishes Pathogenic, Nonpathogenic, and Compensatory Transcriptional Changes in Neurodegeneration. Cell Systems, 2018, 7, 28-40.e4.	6.2	32
22	Drosophila researchers focus on human disease. Nature Genetics, 2007, 39, 589-589.	21.4	27
23	Metal Homeostasis Regulators Suppress FRDA Phenotypes in a Drosophila Model of the Disease. PLoS ONE, 2016, 11, e0159209.	2.5	23
24	Downregulation of glial genes involved in synaptic function mitigates Huntington's disease pathogenesis. ELife, 2021, 10, .	6.0	20
25	PAK1 regulates ATXN1 levels providing an opportunity to modify its toxicity in spinocerebellar ataxia type 1. Human Molecular Genetics, 2018, 27, 2863-2873.	2.9	16
26	Dynamics of huntingtin protein interactions in the striatum identifies candidate modifiers of Huntington disease. Cell Systems, 2022, 13, 304-320.e5.	6.2	15
27	Dual targeting of brain regionâ€specific kinases potentiates neurological rescue in Spinocerebellar ataxia type 1. EMBO Journal, 2021, 40, e106106.	7.8	11
28	The developmental roots of neurodegeneration. Neuron, 2022, 110, 1-3.	8.1	11
29	Cross-species genetic screens identify transglutaminase 5 as a regulator of polyglutamine-expanded ataxin-1. Journal of Clinical Investigation, 2022, 132, .	8.2	6
30	Suppression of toxicity of the mutant huntingtin protein by its interacting compound, desonide. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2114303119.	7.1	5
31	Inhibition of HIPK3 by AST487 Ameliorates Mutant HTT-Induced Neurotoxicity and Apoptosis via Enhanced Autophagy. Neuroscience Bulletin, 2022, 38, 99-103.	2.9	2
32	P4â€493: IDENTIFYING GENETIC MODIFIERS OF APOE VIA IMPUTATION OF DEVIATION IN EVOLUTIONARY ACTION LOAD IN ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2019, 15, P1502.	0.8	0
33	Identifying genetic modifiers of APOE in Alzheimerâ€™s disease using evolutionary information and regression analyses. Alzheimer's and Dementia, 2020, 16, e043497.	0.8	0
34	PIP4KÎ³ as a potential target for Huntington's disease. FASEB Journal, 2017, 31, 946.8.	0.5	0
35	Systems genetic dissection of Alzheimerâ€™s disease brain gene expression networks. Alzheimer's and Dementia, 2021, 17, e058716.	0.8	0