Xose S Puente

List of Publications by Year
in descending order

132 papers	32,180 citations	20817 60 h-index	16183 124 g-index
139 all docs	139 docs citations	139 times ranked	46766 citing authors

#	Article	IF	Citations
1	PanCancer analysis of somatic mutations in repetitive regions reveals recurrent mutations in snRNA U2. Npj Genomic Medicine, 2022, 7, 19.	3.8	2
2	ATM germline variants in a young adult with chronic lymphocytic leukemia: 8â€‰years of genomic evolution. Blood Cancer Journal, 2022, 12, .	6.2	2
3	IGLV3-21R110 identifies an aggressive biological subtype of chronic lymphocytic leukemia with intermediate epigenetics. Blood, 2021, 137, 2935-2946.	1.4	49
4	mmsig: a fitting approach to accurately identify somatic mutational signatures in hematological malignancies. Communications Biology, 2021, 4, 424.	4.4	21
5	Altered regulation of BRCA1 exon 11 splicing is associated with breast cancer risk in carriers of BRCA1 pathogenic variants. Human Mutation, 2021, 42, 1488-1502.	2.5	7
6	Specific NOTCH1 antibody targets DLL4-induced proliferation, migration, and angiogenesis in NOTCH1-mutated CLL cells. Oncogene, 2020, 39, 1185-1197.	5.9	22
7	Cryptic insertions of the immunoglobulin light chain enhancer region near CCND1 in t(11;14)-negative mantle cell lymphoma. Haematologica, 2020, 105, e408-e411.	3.5	13
8	The proliferative history shapes the DNA methylome of B-cell tumors and predicts clinical outcome. Nature Cancer, 2020, 1, 1066-1081.	13.2	51
9	Circulating tumour DNA from the cerebrospinal fluid allows the characterisation and monitoring of medulloblastoma. Nature Communications, 2020, 11, 5376.	12.8	67
10	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. Nature Communications, 2020, 11, 3390.	12.8	24
11	Genomic and epigenomic insights into the origin, pathogenesis, and clinical behavior of mantle cell lymphoma subtypes. Blood, 2020, 136, 1419-1432.	1.4	131
12	Genomic and Epigenomic Alterations in Chronic Lymphocytic Leukemia. Annual Review of Pathology: Mechanisms of Disease, 2020, 15, 149-177.	22.4	17
13	Minimal spatial heterogeneity in chronic lymphocytic leukemia at diagnosis. Leukemia, 2020, 34, 1929-1933.	7.2	2
14	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
15	Timing the initiation of multiple myeloma. Nature Communications, 2020, 11, 1917.	12.8	99
16	The IGLV3-21R110 Defines a Subset of Chronic Lymphocytic Leukemia with Intermediate Epigenetic Subtype and Poor Outcome. Blood, 2020, 136, 43-44.	1.4	1
17	Abstract 169: Discovery of clinically distinct CLL subgroups by integrative mapping of large-scale genetic, epigenetic, expression and clinical data. , 2020, , .		0
18	The CLL-1100 Project: Towards Complete Genomic Characterization and Improved Prognostics for CLL. Blood, 2020, 136, 3-4.	1.4	2

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19	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics. Nature Communications, 2019, 10, 3615.	12.8	32
20	A practical guide for mutational signature analysis in hematological malignancies. Nature Communications, 2019, 10, 2969.	12.8	145
21	The U1 spliceosomal RNA is recurrently mutated in multiple cancers. Nature, 2019, 574, 712-716.	27.8	128
22	Chromosome 12p Amplification in Triple-Negative/BRCA1-Mutated Breast Cancer Associates with Emergence of Docetaxel Resistance and Carboplatin Sensitivity. Cancer Research, 2019, 79, 4258-4270.	0.9	17
23	Timing the initiation of multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e6-e7.	0.4	1
24	Recurrent noncoding U1ÂsnRNA mutations drive cryptic splicing in SHH medulloblastoma. Nature, 2019, 574, 707-711.	27.8	129
25	CCND2 and CCND3 hijack immunoglobulin light-chain enhancers in cyclin D1â^' mantle cell lymphoma. Blood, 2019, 133, 940-951.	1.4	77
26	Mutations in the RAS-BRAF-MAPK-ERK pathway define a specific subgroup of patients with adverse clinical features and provide new therapeutic options in chronic lymphocytic leukemia. Haematologica, 2019, 104, 576-586.	3.5	40
27	Igcaller: Reconstructing the Rearranged Immunoglobulin Gene in Lymphoid Neoplasms from Whole-Genome Sequencing Data. Blood, 2019, 134, 3023-3023.	1.4	0
28	The U1 Spliceosomal RNA: A Novel Non-Coding Hotspot Driver Mutation Independently Associated with Clinical Outcome in Chronic Lymphocytic Leukemia. Blood, 2019, 134, 847-847.	1.4	0
29	Timing the Initiation of Multiple Myeloma. Blood, 2019, 134, 573-573.	1.4	0
30	Decapping protein EDC4 regulates DNA repair and phenocopies BRCA1. Nature Communications, 2018, 9, 967.	12.8	33
31	Chronic lymphocytic leukemia and mantle cell lymphoma: crossroads of genetic and microenvironment interactions. Blood, 2018, 131, 2283-2296.	1.4	106
32	Tumor xenograft modeling identifies TCF4/ITF2 loss associated with breast cancer chemoresistance. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	15
33	Dissecting Degradomes: Analysis of Protease-Coding Genes. Methods in Molecular Biology, 2018, 1731, 1-13.	0.9	1
34	Clinical impact of the subclonal architecture and mutational complexity in chronic lymphocytic leukemia. Leukemia, 2018, 32, 645-653.	7.2	91
35	Association Between Germline Mutations in BRF1, a Subunit of the RNA Polymerase III Transcription Complex, and Hereditary Colorectal Cancer. Gastroenterology, 2018, 154, 181-194.e20.	1.3	32
36	The mutational landscape of small lymphocytic lymphoma compared to non-early stage chronic lymphocytic leukemia. Leukemia and Lymphoma, 2018, 59, 2318-2326.	1.3	5

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37	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	30.7	157
38	Germline mutations in the spindle assembly checkpoint genes BUB1 and BUB3 are infrequent in familial colorectal cancer and polyposis. Molecular Cancer, 2018, 17, 23.	19.2	19
39	Germline variation in the oxidative DNA repair genes NUDT1 and OGG1 is not associated with hereditary colorectal cancer or polyposis. Human Mutation, 2018, 39, 1214-1225.	2.5	10
40	An Epigenetic Mitotic Score Tracks the Proliferative History and Capacity of CLL Samples at Diagnosis and Is Associated with Clinical Outcome. Blood, 2018, 132, 1842-1842.	1.4	2
41	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. Oncogene, 2017, 36, 2737-2749.	5.9	34
42	A t(1;9) translocation involving CSF3R as a novel mechanism in unclassifiable chronic myeloproliferative neoplasm. Haematologica, 2017, 102, e510-e513.	3.5	0
43	Overview of transcriptomic analysis of all human proteases, non-proteolytic homologs and inhibitors: Organ, tissue and ovarian cancer cell line expression profiling of the human protease degradome by the CLIP-CHIPâ„¢ DNA microarray. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 2210-2219.	4.1	34
44	Impact of the functional CD5 polymorphism A471V on the response of chronic lymphocytic leukaemia to conventional chemotherapy regimens. British Journal of Haematology, 2017, 177, 147-150.	2.5	8
45	Non-coding recurrent mutations in chronic lymphocytic leukaemia. Nature, 2016, 534, S11-S12.	27.8	519
46	Congenital dilated cardiomyopathy caused by biallelic mutations in Filamin C. European Journal of Human Genetics, 2016, 24, 1792-1796.	2.8	36
47	Clinical impact of clonal and subclonal TP53, SF3B1, BIRC3, NOTCH1, and ATM mutations in chronic lymphocytic leukemia. Blood, 2016, 127, 2122-2130.	1.4	260
48	Transplacental transfer of essential thrombocythemia in monozygotic twins. Blood, 2016, 128, 1894-1896.	1.4	2
49	Genetic Predisposition to Chronic Lymphocytic Leukemia Is Mediated by a BMF Super-Enhancer Polymorphism. Cell Reports, 2016, 16, 2061-2067.	6.4	58
50	Scarce evidence of the causal role of germline mutations in UNC5C in hereditary colorectal cancer and polyposis. Scientific Reports, 2016, 6, 20697.	3.3	9
51	Chronic lymphocytic leukemia: looking into the dark side of the genome. Cell Death and Differentiation, 2016, 23, 7-9.	11.2	4
52	POLE and POLD1 mutations in 529 kindred with familial colorectal cancer and/or polyposis: review of reported cases and recommendations for genetic testing and surveillance. Genetics in Medicine, 2016, 18, 325-332.	2.4	209
53	Clinical Impact of the Quantitative Subclonal Architecture in Chronic Lymphocytic Leukemia. Blood, 2016, 128, 2024-2024.	1.4	0
54	Comprehensive establishment and characterization of orthoxenograft mouse models of malignant peripheral nerve sheath tumors for personalized medicine. EMBO Molecular Medicine, 2015, 7, 608-627.	6.9	36

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55	Loss of <scp>MT</scp> 1â€•<scp>MMP</scp> causes cell senescence and nuclear defects which can be reversed by retinoic acid. EMBO Journal, 2015, 34, 1875-1888.	7.8	78
56	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
57	Human organic cation transporter 1 (hOCT1) as a mediator of bendamustine uptake and cytotoxicity in chronic lymphocytic leukemia (CLL) cells. Pharmacogenomics Journal, 2015, 15, 363-371.	2.0	18
58	Non-coding recurrent mutations in chronic lymphocytic leukaemia. Nature, 2015, 526, 519-524.	27.8	749
59	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. Gastroenterology, 2015, 149, 563-566.	1.3	94
60	Common and rare variants of microRNA genes in autism spectrum disorders. World Journal of Biological Psychiatry, 2015, 16, 376-386.	2.6	27
61	Mutations in the Toll-like receptor/MYD88 pathway in young (â‰50 years) CLL patients. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, S203.	0.4	0
62	Exome sequencing identifiesMUTYHmutations in a family with colorectal cancer and an atypical phenotype. Gut, 2015, 64, 355-356.	12.1	14
63	A B-cell epigenetic signature defines three biologic subgroups of chronic lymphocytic leukemia with clinical impact. Leukemia, 2015, 29, 598-605.	7.2	129
64	Clinical Impact of Clonal and Subclonal TP53, SF3B1, BIRC3, and ATM Mutations in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 4138-4138.	1.4	1
65	The prognostic impact of minimal residual disease in patients with chronic lymphocytic leukemia requiring first-line therapy. Haematologica, 2014, 99, 873-880.	3.5	32
66	Exome sequencing in multiplex autism families suggests a major role for heterozygous truncating mutations. Molecular Psychiatry, 2014, 19, 784-790.	7.9	110
67	Mutations in filamin C cause a new form of familial hypertrophic cardiomyopathy. Nature Communications, 2014, 5, 5326.	12.8	154
68	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	5.5	175
69	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. Nature Biotechnology, 2014, 32, 1106-1112.	17.5	74
70	Mutations in TLR/MYD88 pathway identify a subset of young chronic lymphocytic leukemia patients with favorable outcome. Blood, 2014, 123, 3790-3796.	1.4	97
71	The common marmoset genome provides insight into primate biology and evolution. Nature Genetics, 2014, 46, 850-857.	21.4	225
72	Frequent somatic mutations in components of the RNA processing machinery in chronic lymphocytic leukemia. Leukemia, 2013, 27, 1600-1603.	7.2	28

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73	The genomic landscape of chronic lymphocytic leukemia: clinical implications. BMC Medicine, 2013, 11, 124.	5.5	35
74	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
75	Recurrent Gene Mutations in CLL. Advances in Experimental Medicine and Biology, 2013, 792, 87-107.	1.6	8
76	POT1 mutations cause telomere dysfunction in chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 526-530.	21.4	236
77	The evolutionary biography of chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 229-231.	21.4	40
78	NOTCH1 mutations identify a genetic subgroup of chronic lymphocytic leukemia patients with high risk of transformation and poor outcome. Leukemia, 2013, 27, 1100-1106.	7.2	167
79	Landscape of somatic mutations and clonal evolution in mantle cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18250-18255.	7.1	488
80	Clinical Response to a Lapatinib-Based Therapy for a Li-Fraumeni Syndrome Patient with a Novel HER2V659E Mutation. Cancer Discovery, 2013, 3, 1238-1244.	9.4	43
81	Identification of novel tumor suppressor proteases by degradome profiling of colorectal carcinomas. Oncotarget, 2013, 4, 1919-1932.	1.8	12
82	Abstract C114: Clinical response to a lapatinib-based therapy of a Li-Fraumeni Syndrome patient with a novel HER2-V659E mutation.. , 2013, , .		0
83	Identification of novel tumor suppressor proteases by degradome profiling of colorectal carcinomas. Oncotarget, 2013, 4, 1919-1932.	1.8	1
84	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	21.4	525
85	Estimation of Copy Number Alterations from Exome Sequencing Data. PLoS ONE, 2012, 7, e51422.	2.5	18
86	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 47-52.	21.4	893
87	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	27.8	1,364
88	Cell autonomous and systemic factors in progeria development. Biochemical Society Transactions, 2011, 39, 1710-1714.	3.4	20
89	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
90	Exome Sequencing and Functional Analysis Identifies BANF1 Mutation as the Cause of a Hereditary Progeroid Syndrome. American Journal of Human Genetics, 2011, 88, 650-656.	6.2	189

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91	Comparative genomic analysis of the zebra finch degradome provides new insights into evolution of proteases in birds and mammals. BMC Genomics, 2010, 11, 220.	2.8	26
92	Nuclear envelope alterations generate an agingâ€like epigenetic pattern in mice deficient in Zmpste24 metalloprotease. Aging Cell, 2010, 9, 947-957.	6.7	50
93	The genome of a songbird. Nature, 2010, 464, 757-762.	27.8	770
94	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
95	Absence or Inhibition of Matrix Metalloproteinaseâ€“8 Decreases Ventilator-Induced Lung Injury. American Journal of Respiratory Cell and Molecular Biology, 2010, 43, 555-563.	2.9	57
96	Metalloproteases and the Degradome. Methods in Molecular Biology, 2010, 622, 3-29.	0.9	37
97	Resistance to Bleomycin-Induced Lung Fibrosis in MMP-8 Deficient Mice Is Mediated by Interleukin-10. PLoS ONE, 2010, 5, e13242.	2.5	88
98	The Degradome database: mammalian proteases and diseases of proteolysis. Nucleic Acids Research, 2009, 37, D239-D243.	14.5	146
99	Proteolytic Systems: Constructing Degradomes. Methods in Molecular Biology, 2009, 539, 33-47.	0.9	15
100	Degradome expression profiling in human articular cartilage. Arthritis Research and Therapy, 2009, 11, R96.	3.5	63
101	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
102	Polymorphism +17 C/G in Matrix Metalloprotease MMP8 decreases lung cancer risk. BMC Cancer, 2008, 8, 378.	2.6	49
103	Matrix metalloproteinase-8 is a regulator of the clinical aggressiveness of mammary tumours. Breast Cancer Research, 2008, 10, .	5.0	0
104	Loss of genes implicated in gastric function during platypus evolution. Genome Biology, 2008, 9, R81.	9.6	44
105	Matrix Metalloproteinase-8 Functions as a Metastasis Suppressor through Modulation of Tumor Cell Adhesion and Invasion. Cancer Research, 2008, 68, 2755-2763.	0.9	172
106	Protease Genomics and the Cancer Degradome. , 2008, , 3-15.		6
107	Increased inflammation delays wound healing in mice deficient in collagenaseâ€2 (MMPâ€8). FASEB Journal, 2007, 21, 2580-2591.	0.5	241
108	Polymorphisms in XPC, XPD, XRCC1, and XRCC3 DNA repair genes and lung cancer risk in a population of Northern Spain. BMC Cancer, 2007, 7, 162.	2.6	129

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109	LPS Responsiveness and Neutrophil Chemotaxis In Vivo Require PMN MMP-8 Activity. PLoS ONE, 2007, 2, e312.	2.5	181
110	Comparative analysis of cancer genes in the human and chimpanzee genomes. BMC Genomics, 2006, 7, 15.	2.8	94
111	Initial sequence of the chimpanzee genome and comparison with the human genome. Nature, 2005, 437, 69-87.	27.8	2,222
112	Comparative genomic analysis of human and chimpanzee proteases. Genomics, 2005, 86, 638-647.	2.9	78
113	A genomic view of the complexity of mammalian proteolytic systems. Biochemical Society Transactions, 2005, 33, 331-334.	3.4	124
114	Protease degradomics: mass spectrometry discovery of protease substrates and the CLIP-CHIP, a dedicated DNA microarray of all human proteases and inhibitors. Biological Chemistry, 2004, 385, 493-504.	2.5	110
115	A Genomic Analysis of Rat Proteases and Protease Inhibitors. Genome Research, 2004, 14, 609-622.	5.5	167
116	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
117	Human and mouse proteases: a comparative genomic approach. Nature Reviews Genetics, 2003, 4, 544-558.	16.3	846
118	Human Autophagins, a Family of Cysteine Proteinases Potentially Implicated in Cell Degradation by Autophagy. Journal of Biological Chemistry, 2003, 278, 3671-3678.	3.4	189
119	Matrix Metalloproteinases and Tumor Progression. Advances in Experimental Medicine and Biology, 2003, 532, 91-107.	1.6	134
120	Src-mediated coupling of focal adhesion kinase to integrin Î±vÎ²5 in vascular endothelial growth factor signaling. Journal of Cell Biology, 2002, 157, 149-160.	5.2	323
121	FRNK blocks v-Src-stimulated invasion and experimental metastases without effects on cell motility or growth. EMBO Journal, 2002, 21, 6289-6302.	7.8	154
122	Apoptosis of adherent cells by recruitment of caspase-8 to unligated integrins. Journal of Cell Biology, 2001, 155, 459-470.	5.2	513
123	Integrin Î±vÎ²1 Is an Adenovirus Coreceptor. Journal of Virology, 2001, 75, 5405-5409.	3.4	198
124	Assignment of the disulfide bonds of Ole e 1, a major allergen of olive tree pollen involved in fertilization. Chemical Biology and Drug Design, 2000, 55, 18-23.	1.1	7
125	Membrane Type 4 Matrix Metalloproteinase (MMP17) Has Tumor Necrosis Factor-Î± Convertase Activity but Does Not Activate Pro-MMP2. Journal of Biological Chemistry, 2000, 275, 14046-14055.	3.4	195
126	Structural Characterization and Chromosomal Localization of the Gene Encoding Human Biphenyl Hydrolase-Related Protein (BPHL). Genomics, 1998, 51, 459-462.	2.9	7

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127	Localization of the Human Membrane Type 4-Matrix Metalloproteinase Gene (MMP17) to Chromosome 12q24. Genomics, 1998, 54, 578-579.	2.9	7
128	Identification and Characterization of a Novel Human Matrix Metalloproteinase with Unique Structural Characteristics, Chromosomal Location, and Tissue Distribution. Journal of Biological Chemistry, 1997, 272, 4281-4286.	3.4	207
129	The PLEES proteins: a family of structurally related enzymes widely distributed from bacteria to humans. Biochemical Journal, 1997, 322, 947-949.	3.7	16
130	Ole e 3, An Oliveâ€Tree Allergen, Belongs to a Widespread Family of Pollen Proteins. FEBS Journal, 1996, 241, 772-778.	0.2	94
131	Divergence in properties of two closely related alpha-amylase inhibitors of barley. Physiologia Plantarum, 1996, 98, 523-528.	5.2	7
132	Cloning and Expression Analysis of a Novel Human Serine Hydrolase with Sequence Similarity to Prokaryotic Enzymes Involved in the Degradation of Aromatic Compounds. Journal of Biological Chemistry, 1995, 270, 12926-12932.	3.4	28