

# Xose S Puente

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2167211/publications.pdf>

Version: 2024-02-01

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	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013, 500, 415-421.	27.8	8,060
2	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005, 437, 69-87.	27.8	2,222
3	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
4	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
5	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
6	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2011, 475, 101-105.	27.8	1,364
7	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 47-52.	21.4	893
8	Human and mouse proteases: a comparative genomic approach. <i>Nature Reviews Genetics</i> , 2003, 4, 544-558.	16.3	846
9	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	27.8	770
10	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2015, 526, 519-524.	27.8	749
11	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	27.8	657
12	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
13	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 1236-1242.	21.4	525
14	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2016, 534, S11-S12.	27.8	519
15	Apoptosis of adherent cells by recruitment of caspase-8 to unligated integrins. <i>Journal of Cell Biology</i> , 2001, 155, 459-470.	5.2	513
16	Landscape of somatic mutations and clonal evolution in mantle cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18250-18255.	7.1	488
17	Src-mediated coupling of focal adhesion kinase to integrin $\alpha 5 \beta 1$ in vascular endothelial growth factor signaling. <i>Journal of Cell Biology</i> , 2002, 157, 149-160.	5.2	323
18	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	12.8	266

#	ARTICLE	IF	CITATIONS
19	Clinical impact of clonal and subclonal TP53, SF3B1, BIRC3, NOTCH1, and ATM mutations in chronic lymphocytic leukemia. <i>Blood</i> , 2016, 127, 2122-2130.	1.4	260
20	Increased inflammation delays wound healing in mice deficient in collagenase-2 (MMP-8). <i>FASEB Journal</i> , 2007, 21, 2580-2591.	0.5	241
21	POT1 mutations cause telomere dysfunction in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2013, 45, 526-530.	21.4	236
22	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.	21.4	225
23	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. <i>Genetics in Medicine</i> , 2016, 18, 325-332.	2.4	209
24	Identification and Characterization of a Novel Human Matrix Metalloproteinase with Unique Structural Characteristics, Chromosomal Location, and Tissue Distribution. <i>Journal of Biological Chemistry</i> , 1997, 272, 4281-4286.	3.4	207
25	Integrin $\alpha v \beta 1$ Is an Adenovirus Coreceptor. <i>Journal of Virology</i> , 2001, 75, 5405-5409.	3.4	198
26	Membrane Type 4 Matrix Metalloproteinase (MMP17) Has Tumor Necrosis Factor- $\alpha$ Convertase Activity but Does Not Activate Pro-MMP2. <i>Journal of Biological Chemistry</i> , 2000, 275, 14046-14055.	3.4	195
27	Human Autophagins, a Family of Cysteine Proteinases Potentially Implicated in Cell Degradation by Autophagy. <i>Journal of Biological Chemistry</i> , 2003, 278, 3671-3678.	3.4	189
28	Exome Sequencing and Functional Analysis Identifies BANF1 Mutation as the Cause of a Hereditary Progeroid Syndrome. <i>American Journal of Human Genetics</i> , 2011, 88, 650-656.	6.2	189
29	LPS Responsiveness and Neutrophil Chemotaxis In Vivo Require PMN MMP-8 Activity. <i>PLoS ONE</i> , 2007, 2, e312.	2.5	181
30	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	5.5	175
31	Matrix Metalloproteinase-8 Functions as a Metastasis Suppressor through Modulation of Tumor Cell Adhesion and Invasion. <i>Cancer Research</i> , 2008, 68, 2755-2763.	0.9	172
32	A Genomic Analysis of Rat Proteases and Protease Inhibitors. <i>Genome Research</i> , 2004, 14, 609-622.	5.5	167
33	NOTCH1 mutations identify a genetic subgroup of chronic lymphocytic leukemia patients with high risk of transformation and poor outcome. <i>Leukemia</i> , 2013, 27, 1100-1106.	7.2	167
34	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	30.7	157
35	FRNK blocks v-Src-stimulated invasion and experimental metastases without effects on cell motility or growth. <i>EMBO Journal</i> , 2002, 21, 6289-6302.	7.8	154
36	Mutations in filamin C cause a new form of familial hypertrophic cardiomyopathy. <i>Nature Communications</i> , 2014, 5, 5326.	12.8	154

#	ARTICLE	IF	CITATIONS
37	The Degradome database: mammalian proteases and diseases of proteolysis. <i>Nucleic Acids Research</i> , 2009, 37, D239-D243.	14.5	146
38	A practical guide for mutational signature analysis in hematological malignancies. <i>Nature Communications</i> , 2019, 10, 2969.	12.8	145
39	Matrix Metalloproteinases and Tumor Progression. <i>Advances in Experimental Medicine and Biology</i> , 2003, 532, 91-107.	1.6	134
40	Genomic and epigenomic insights into the origin, pathogenesis, and clinical behavior of mantle cell lymphoma subtypes. <i>Blood</i> , 2020, 136, 1419-1432.	1.4	131
41	Polymorphisms in XPC, XPD, XRCC1, and XRCC3 DNA repair genes and lung cancer risk in a population of Northern Spain. <i>BMC Cancer</i> , 2007, 7, 162.	2.6	129
42	A B-cell epigenetic signature defines three biologic subgroups of chronic lymphocytic leukemia with clinical impact. <i>Leukemia</i> , 2015, 29, 598-605.	7.2	129
43	Recurrent noncoding U1 snRNA mutations drive cryptic splicing in SHH medulloblastoma. <i>Nature</i> , 2019, 574, 707-711.	27.8	129
44	The U1 spliceosomal RNA is recurrently mutated in multiple cancers. <i>Nature</i> , 2019, 574, 712-716.	27.8	128
45	A genomic view of the complexity of mammalian proteolytic systems. <i>Biochemical Society Transactions</i> , 2005, 33, 331-334.	3.4	124
46	Protease degradomics: mass spectrometry discovery of protease substrates and the CLIP-CHIP, a dedicated DNA microarray of all human proteases and inhibitors. <i>Biological Chemistry</i> , 2004, 385, 493-504.	2.5	110
47	Exome sequencing in multiplex autism families suggests a major role for heterozygous truncating mutations. <i>Molecular Psychiatry</i> , 2014, 19, 784-790.	7.9	110
48	Chronic lymphocytic leukemia and mantle cell lymphoma: crossroads of genetic and microenvironment interactions. <i>Blood</i> , 2018, 131, 2283-2296.	1.4	106
49	Timing the initiation of multiple myeloma. <i>Nature Communications</i> , 2020, 11, 1917.	12.8	99
50	Mutations in TLR/MYD88 pathway identify a subset of young chronic lymphocytic leukemia patients with favorable outcome. <i>Blood</i> , 2014, 123, 3790-3796.	1.4	97
51	Ole e 3, An Olive Tree Allergen, Belongs to a Widespread Family of Pollen Proteins. <i>FEBS Journal</i> , 1996, 241, 772-778.	0.2	94
52	Comparative analysis of cancer genes in the human and chimpanzee genomes. <i>BMC Genomics</i> , 2006, 7, 15.	2.8	94
53	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. <i>Gastroenterology</i> , 2015, 149, 563-566.	1.3	94
54	Clinical impact of the subclonal architecture and mutational complexity in chronic lymphocytic leukemia. <i>Leukemia</i> , 2018, 32, 645-653.	7.2	91

#	ARTICLE	IF	CITATIONS
55	Resistance to Bleomycin-Induced Lung Fibrosis in MMP-8 Deficient Mice Is Mediated by Interleukin-10. PLoS ONE, 2010, 5, e13242.	2.5	88
56	Comparative genomic analysis of human and chimpanzee proteases. Genomics, 2005, 86, 638-647.	2.9	78
57	Loss of <i>MT</i> $\cdot$ <i>MMP</i> causes cell senescence and nuclear defects which can be reversed by retinoic acid. EMBO Journal, 2015, 34, 1875-1888.	7.8	78
58	CCND2 and CCND3 hijack immunoglobulin light-chain enhancers in cyclin D1 <sup>hi</sup> mantle cell lymphoma. Blood, 2019, 133, 940-951.	1.4	77
59	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. Nature Biotechnology, 2014, 32, 1106-1112.	17.5	74
60	Circulating tumour DNA from the cerebrospinal fluid allows the characterisation and monitoring of medulloblastoma. Nature Communications, 2020, 11, 5376.	12.8	67
61	Degradome expression profiling in human articular cartilage. Arthritis Research and Therapy, 2009, 11, R96.	3.5	63
62	Genetic Predisposition to Chronic Lymphocytic Leukemia Is Mediated by a BMF Super-Enhancer Polymorphism. Cell Reports, 2016, 16, 2061-2067.	6.4	58
63	Absence or Inhibition of Matrix Metalloproteinase <sup>8</sup> Decreases Ventilator-Induced Lung Injury. American Journal of Respiratory Cell and Molecular Biology, 2010, 43, 555-563.	2.9	57
64	The proliferative history shapes the DNA methylome of B-cell tumors and predicts clinical outcome. Nature Cancer, 2020, 1, 1066-1081.	13.2	51
65	Nuclear envelope alterations generate an aging-like epigenetic pattern in mice deficient in Zmpste24 metalloprotease. Aging Cell, 2010, 9, 947-957.	6.7	50
66	Polymorphism +17 C/G in Matrix Metalloprotease MMP8 decreases lung cancer risk. BMC Cancer, 2008, 8, 378.	2.6	49
67	IGLV3-21R110 identifies an aggressive biological subtype of chronic lymphocytic leukemia with intermediate epigenetics. Blood, 2021, 137, 2935-2946.	1.4	49
68	Loss of genes implicated in gastric function during platypus evolution. Genome Biology, 2008, 9, R81.	9.6	44
69	Clinical Response to a Lapatinib-Based Therapy for a Li-Fraumeni Syndrome Patient with a Novel <i>HER2</i> V659E Mutation. Cancer Discovery, 2013, 3, 1238-1244.	9.4	43
70	The evolutionary biography of chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 229-231.	21.4	40
71	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
72	Metalloproteases and the Degradome. Methods in Molecular Biology, 2010, 622, 3-29.	0.9	37

#	ARTICLE	IF	CITATIONS
73	Comprehensive establishment and characterization of orthoxenograft mouse models of malignant peripheral nerve sheath tumors for personalized medicine. <i>EMBO Molecular Medicine</i> , 2015, 7, 608-627.	6.9	36
74	Congenital dilated cardiomyopathy caused by biallelic mutations in Filamin C. <i>European Journal of Human Genetics</i> , 2016, 24, 1792-1796.	2.8	36
75	The genomic landscape of chronic lymphocytic leukemia: clinical implications. <i>BMC Medicine</i> , 2013, 11, 124.	5.5	35
76	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. <i>Oncogene</i> , 2017, 36, 2737-2749.	5.9	34
77	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-CHIP <sup>+</sup> , <sup>+</sup> DNA microarray. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 2210-2219.	4.1	34
78	Decapping protein EDC4 regulates DNA repair and phenocopies BRCA1. <i>Nature Communications</i> , 2018, 9, 967.	12.8	33
79	The prognostic impact of minimal residual disease in patients with chronic lymphocytic leukemia requiring first-line therapy. <i>Haematologica</i> , 2014, 99, 873-880.	3.5	32
80	Association Between Germline Mutations in BRF1, a Subunit of the RNA Polymerase III Transcription Complex, and Hereditary Colorectal Cancer. <i>Gastroenterology</i> , 2018, 154, 181-194.e20.	1.3	32
81	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics. <i>Nature Communications</i> , 2019, 10, 3615.	12.8	32
82	Cloning and Expression Analysis of a Novel Human Serine Hydrolase with Sequence Similarity to Prokaryotic Enzymes Involved in the Degradation of Aromatic Compounds. <i>Journal of Biological Chemistry</i> , 1995, 270, 12926-12932.	3.4	28
83	Frequent somatic mutations in components of the RNA processing machinery in chronic lymphocytic leukemia. <i>Leukemia</i> , 2013, 27, 1600-1603.	7.2	28
84	Common and rare variants of microRNA genes in autism spectrum disorders. <i>World Journal of Biological Psychiatry</i> , 2015, 16, 376-386.	2.6	27
85	Comparative genomic analysis of the zebra finch degradome provides new insights into evolution of proteases in birds and mammals. <i>BMC Genomics</i> , 2010, 11, 220.	2.8	26
86	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. <i>Nature Communications</i> , 2020, 11, 3390.	12.8	24
87	Specific NOTCH1 antibody targets DLL4-induced proliferation, migration, and angiogenesis in NOTCH1-mutated CLL cells. <i>Oncogene</i> , 2020, 39, 1185-1197.	5.9	22
88	mmsig: a fitting approach to accurately identify somatic mutational signatures in hematological malignancies. <i>Communications Biology</i> , 2021, 4, 424.	4.4	21
89	Cell autonomous and systemic factors in progeria development. <i>Biochemical Society Transactions</i> , 2011, 39, 1710-1714.	3.4	20
90	Germline mutations in the spindle assembly checkpoint genes BUB1 and BUB3 are infrequent in familial colorectal cancer and polyposis. <i>Molecular Cancer</i> , 2018, 17, 23.	19.2	19

#	ARTICLE	IF	CITATIONS
91	Estimation of Copy Number Alterations from Exome Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e51422.	2.5	18
92	Human organic cation transporter 1 (hOCT1) as a mediator of bendamustine uptake and cytotoxicity in chronic lymphocytic leukemia (CLL) cells. <i>Pharmacogenomics Journal</i> , 2015, 15, 363-371.	2.0	18
93	Chromosome 12p Amplification in Triple-Negative/ <i>BRCA1</i> -Mutated Breast Cancer Associates with Emergence of Docetaxel Resistance and Carboplatin Sensitivity. <i>Cancer Research</i> , 2019, 79, 4258-4270.	0.9	17
94	Genomic and Epigenomic Alterations in Chronic Lymphocytic Leukemia. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2020, 15, 149-177.	22.4	17
95	The PLEES proteins: a family of structurally related enzymes widely distributed from bacteria to humans. <i>Biochemical Journal</i> , 1997, 322, 947-949.	3.7	16
96	Proteolytic Systems: Constructing Degradomes. <i>Methods in Molecular Biology</i> , 2009, 539, 33-47.	0.9	15
97	Tumor xenograft modeling identifies <i>TCF4/ITF2</i> loss associated with breast cancer chemoresistance. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	2.4	15
98	Exome sequencing identifies <i>MUTYH</i> mutations in a family with colorectal cancer and an atypical phenotype. <i>Gut</i> , 2015, 64, 355-356.	12.1	14
99	Cryptic insertions of the immunoglobulin light chain enhancer region near <i>CCND1</i> in t(11;14)-negative mantle cell lymphoma. <i>Haematologica</i> , 2020, 105, e408-e411.	3.5	13
100	Identification of novel tumor suppressor proteases by degradome profiling of colorectal carcinomas. <i>Oncotarget</i> , 2013, 4, 1919-1932.	1.8	12
101	Germline variation in the oxidative DNA repair genes <i>NUDT1</i> and <i>OGG1</i> is not associated with hereditary colorectal cancer or polyposis. <i>Human Mutation</i> , 2018, 39, 1214-1225.	2.5	10
102	Scarce evidence of the causal role of germline mutations in <i>UNC5C</i> in hereditary colorectal cancer and polyposis. <i>Scientific Reports</i> , 2016, 6, 20697.	3.3	9
103	Recurrent Gene Mutations in CLL. <i>Advances in Experimental Medicine and Biology</i> , 2013, 792, 87-107.	1.6	8
104	Impact of the functional CD5 polymorphism A471V on the response of chronic lymphocytic leukaemia to conventional chemotherapy regimens. <i>British Journal of Haematology</i> , 2017, 177, 147-150.	2.5	8
105	Divergence in properties of two closely related alpha-amylase inhibitors of barley. <i>Physiologia Plantarum</i> , 1996, 98, 523-528.	5.2	7
106	Structural Characterization and Chromosomal Localization of the Gene Encoding Human Biphenyl Hydrolase-Related Protein (BPHL). <i>Genomics</i> , 1998, 51, 459-462.	2.9	7
107	Localization of the Human Membrane Type 4-Matrix Metalloproteinase Gene ( <i>MMP17</i> ) to Chromosome 12q24. <i>Genomics</i> , 1998, 54, 578-579.	2.9	7
108	Assignment of the disulfide bonds of Ole e 1, a major allergen of olive tree pollen involved in fertilization. <i>Chemical Biology and Drug Design</i> , 2000, 55, 18-23.	1.1	7

#	ARTICLE	IF	CITATIONS
109	Altered regulation of <i>BRCA1</i> exon 11 splicing is associated with breast cancer risk in carriers of <i>BRCA1</i> pathogenic variants. <i>Human Mutation</i> , 2021, 42, 1488-1502.	2.5	7
110	Protease Genomics and the Cancer Degradome. , 2008, , 3-15.		6
111	The mutational landscape of small lymphocytic lymphoma compared to non-early stage chronic lymphocytic leukemia. <i>Leukemia and Lymphoma</i> , 2018, 59, 2318-2326.	1.3	5
112	Chronic lymphocytic leukemia: looking into the dark side of the genome. <i>Cell Death and Differentiation</i> , 2016, 23, 7-9.	11.2	4
113	Transplacental transfer of essential thrombocythemia in monozygotic twins. <i>Blood</i> , 2016, 128, 1894-1896.	1.4	2
114	Minimal spatial heterogeneity in chronic lymphocytic leukemia at diagnosis. <i>Leukemia</i> , 2020, 34, 1929-1933.	7.2	2
115	An Epigenetic Mitotic Score Tracks the Proliferative History and Capacity of CLL Samples at Diagnosis and Is Associated with Clinical Outcome. <i>Blood</i> , 2018, 132, 1842-1842.	1.4	2
116	The CLL-1100 Project: Towards Complete Genomic Characterization and Improved Prognostics for CLL. <i>Blood</i> , 2020, 136, 3-4.	1.4	2
117	PanCancer analysis of somatic mutations in repetitive regions reveals recurrent mutations in snRNA U2. <i>Npj Genomic Medicine</i> , 2022, 7, 19.	3.8	2
118	ATM germline variants in a young adult with chronic lymphocytic leukemia: 8 years of genomic evolution. <i>Blood Cancer Journal</i> , 2022, 12, .	6.2	2
119	Dissecting Degradomes: Analysis of Protease-Coding Genes. <i>Methods in Molecular Biology</i> , 2018, 1731, 1-13.	0.9	1
120	Timing the initiation of multiple myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e6-e7.	0.4	1
121	The IGLV3-21R110 Defines a Subset of Chronic Lymphocytic Leukemia with Intermediate Epigenetic Subtype and Poor Outcome. <i>Blood</i> , 2020, 136, 43-44.	1.4	1
122	Clinical Impact of Clonal and Subclonal TP53, SF3B1, BIRC3, and ATM Mutations in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 4138-4138.	1.4	1
123	Identification of novel tumor suppressor proteases by degradome profiling of colorectal carcinomas. <i>Oncotarget</i> , 2013, 4, 1919-1932.	1.8	1
124	Matrix metalloproteinase-8 is a regulator of the clinical aggressiveness of mammary tumours. <i>Breast Cancer Research</i> , 2008, 10, .	5.0	0
125	Mutations in the Toll-like receptor/MYD88 pathway in young (<math>\leq 50</math> years) CLL patients. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2015, 15, S203.	0.4	0
126	A t(1;9) translocation involving <i>CSF3R</i> as a novel mechanism in unclassifiable chronic myeloproliferative neoplasm. <i>Haematologica</i> , 2017, 102, e510-e513.	3.5	0

#	ARTICLE	IF	CITATIONS
127	Abstract C114: Clinical response to a lapatinib-based therapy of a Li-Fraumeni Syndrome patient with a novel HER2-V659E mutation.. , 2013, , .		0
128	Clinical Impact of the Quantitative Subclonal Architecture in Chronic Lymphocytic Leukemia. Blood, 2016, 128, 2024-2024.	1.4	0
129	Igcaller: Reconstructing the Rearranged Immunoglobulin Gene in Lymphoid Neoplasms from Whole-Genome Sequencing Data. Blood, 2019, 134, 3023-3023.	1.4	0
130	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
131	Timing the Initiation of Multiple Myeloma. Blood, 2019, 134, 573-573.	1.4	0
132	Abstract 169: Discovery of clinically distinct CLL subgroups by integrative mapping of large-scale genetic, epigenetic, expression and clinical data. , 2020, , .		0