

# Tirso Pons

## List of Publications by Year in descending order

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76  
papers

5,115  
citations

236833

25  
h-index

106281

65  
g-index

84  
all docs

84  
docs citations

84  
times ranked

10028  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
2	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
3	Homology modeling, model and software evaluation: three related resources. <i>Bioinformatics</i> , 1998, 14, 523-528.	1.8	297
4	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.	1.1	209
5	Ten years of CAZypedia: a living encyclopedia of carbohydrate-active enzymes. <i>Glycobiology</i> , 2018, 28, 3-8.	1.3	175
6	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. <i>Communications Biology</i> , 2020, 3, 56.	2.0	140
7	Crystal structure of levansucrase from the Gram-negative bacterium <i>Gluconacetobacter diazotrophicus</i> . <i>Biochemical Journal</i> , 2005, 390, 19-27.	1.7	135
8	Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , 2020, 11, 735.	5.8	125
9	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. <i>Gastroenterology</i> , 2015, 149, 563-566.	0.6	94
10	Physico-chemical studies of molecular interactions between non-ionic surfactants and bovine serum albumin. <i>Colloids and Surfaces B: Biointerfaces</i> , 2010, 75, 282-289.	2.5	93
11	Towards a detailed atlas of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 929-940.	2.6	92
12	Three acidic residues are at the active site of a $\beta^2$ -propeller architecture in glycoside hydrolase families 32, 43, 62, and 68. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 424-432.	1.5	87
13	Role of POLE and POLD1 in familial cancer. <i>Genetics in Medicine</i> , 2020, 22, 2089-2100.	1.1	76
14	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	5.8	73
15	Comparison of algorithms for the detection of cancer drivers at subgene resolution. <i>Nature Methods</i> , 2017, 14, 782-788.	9.0	72
16	Beta-propellers: Associated Functions and their Role in Human Diseases. <i>Current Medicinal Chemistry</i> , 2003, 10, 505-524.	1.2	67
17	Structural model for family 32 of glycosyl-hydrolase enzymes. , 1998, 33, 383-395.		59
18	A novel sea anemone peptide that inhibits acid-sensing ion channels. <i>Peptides</i> , 2014, 53, 3-12.	1.2	54

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19	Substitution of Asp-309 by Asn in the Arg-Asp-Pro (RDP) motif of <i>Acetobacter diazotrophicus</i> levansucrase affects sucrose hydrolysis, but not enzyme specificity. <i>Biochemical Journal</i> , 1999, 337, 503-506.	1.7	51
20	Role of MDH2 pathogenic variant in pheochromocytoma and paraganglioma patients. <i>Genetics in Medicine</i> , 2018, 20, 1652-1662.	1.1	45
21	Combined burden and functional impact tests for cancer driver discovery using DriverPower. <i>Nature Communications</i> , 2020, 11, 734.	5.8	39
22	Structure-PPI: a module for the annotation of cancer-related single-nucleotide variants at protein-protein interfaces. <i>Bioinformatics</i> , 2015, 31, 2397-2399.	1.8	38
23	The Kunitz-Type Protein ShPI-1 Inhibits Serine Proteases and Voltage-Gated Potassium Channels. <i>Toxins</i> , 2016, 8, 110.	1.5	38
24	Prediction of a common propeller catalytic domain for fructosyltransferases of different origin and substrate specificity. <i>Protein Science</i> , 2000, 9, 2285-2291.	3.1	34
25	Cloning of the <i>Penicillium minioluteum</i> gene encoding dextranase and its expression in <i>Pichia pastoris</i> . <i>Biotechnology Letters</i> , 1996, 12, 1187-1200.		33
26	Exome Sequencing of Plasma DNA Portrays the Mutation Landscape of Colorectal Cancer and Discovers Mutated VEGFR2 Receptors as Modulators of Antiangiogenic Therapies. <i>Clinical Cancer Research</i> , 2018, 24, 3550-3559.	3.2	32
27	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.	0.6	32
28	Elucidating the molecular basis of MSH2-deficient tumors by combined germline and somatic analysis. <i>International Journal of Cancer</i> , 2017, 141, 1365-1380.	2.3	26
29	Cloning and sequence analysis of the gene encoding invertase (INV1) from the yeast <i>Candida utilis</i> . <i>Yeast</i> , 1998, 14, 1223-1232.	0.8	25
30	Validation of a mutant of the pore-forming toxin sticholysin-I for the construction of proteinase-activated immunotoxins. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 485-493.	1.0	24
31	Characterization and comparative 3D modeling of CmPI-II, a novel non-classical Kazal-type inhibitor from the marine snail <i>Cenchritis muricatus</i> (Mollusca). <i>Biological Chemistry</i> , 2007, 388, 1183-94.	1.2	23
32	Unraveling the binding mechanism of polyoxyethylene sorbitan esters with bovine serum albumin: A novel theoretical model based on molecular dynamic simulations. <i>Colloids and Surfaces B: Biointerfaces</i> , 2014, 116, 720-726.	2.5	22
33	Predicting functional residues in <i>Plasmodium falciparum</i> plasmepsins by combining sequence and structural analysis with molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 440-457.	1.5	19
34	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.	7.9	19
35	Structural insights into serine protease inhibition by a marine invertebrate BPTI Kunitz-type inhibitor. <i>Journal of Structural Biology</i> , 2012, 180, 271-279.	1.3	18
36	Substitution of Asp-309 by Asn in the Arg-Asp-Pro (RDP) motif of <i>Acetobacter diazotrophicus</i> levansucrase affects sucrose hydrolysis, but not enzyme specificity. <i>Biochemical Journal</i> , 1999, 337, 503.	1.7	17

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37	Somatic Embryonic FGFR2 Mutations in Keratinocytic Epidermal Nevi. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1718-1721.	0.3	17
38	Evidence for antimicrobial and anticancer activity of pituitary adenylate cyclase-activating polypeptide (PACAP) from North African catfish ( <i>Clarias gariepinus</i> ): Its potential use as novel therapeutic agent in fish and humans. <i>Fish and Shellfish Immunology</i> , 2019, 86, 559-570.	1.6	17
39	New parameterization approaches of the LIE method to improve free energy calculations of Protein-Ligand complexes. <i>Journal of Computational Chemistry</i> , 2010, 31, 2723-2734.	1.5	15
40	In silico studies of potential phosphoresidues in the human nucleophosmin/B23: Its kinases and related biological processes. <i>Journal of Cellular Biochemistry</i> , 2012, 113, 2364-2374.	1.2	15
41	Akirins in sea lice: First steps towards a deeper understanding. <i>Experimental Parasitology</i> , 2013, 135, 188-199.	0.5	15
42	Two aspartate residues at the putative p10 subunit of a type II metacaspase from <i>Nicotiana tabacum</i> L. may contribute to the substrate-binding pocket. <i>Planta</i> , 2014, 239, 147-160.	1.6	15
43	FlgM anti-sigma factors: identification of novel members of the family, evolutionary analysis, homology modeling, and analysis of sequence-structure-function relationships. <i>Journal of Molecular Modeling</i> , 2006, 12, 973-983.	0.8	14
44	New members of the brachyurins family in lobster include a trypsin-like enzyme with amino acid substitutions in the substrate-binding pocket. <i>FEBS Journal</i> , 2010, 277, 3489-3501.	2.2	14
45	New aspects concerning to the characterization and the relationship with the immune response in vivo of the spiny lobster <i>Panulirus argus</i> nitric oxide synthase. <i>Nitric Oxide - Biology and Chemistry</i> , 2011, 25, 396-406.	1.2	14
46	Germline variation in O6-methylguanine-DNA methyltransferase (MGMT) as cause of hereditary colorectal cancer. <i>Cancer Letters</i> , 2019, 447, 86-92.	3.2	12
47	KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. <i>BMC Genomics</i> , 2016, 17, 396.	1.2	11
48	Functional analysis of archaeal MBF1 by complementation studies in yeast. <i>Biology Direct</i> , 2011, 6, 18.	1.9	10
49	Structure of the recombinant BPTI/Kunitz-type inhibitor ShPI-1A from the marine invertebrate <i>Stichodactyla helianthus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1289-1293.	0.7	10
50	wKinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. <i>Human Mutation</i> , 2016, 37, 36-42.	1.1	10
51	Germline variation in the oxidative DNA repair genes NUDT1 and OGG1 is not associated with hereditary colorectal cancer or polyposis. <i>Human Mutation</i> , 2018, 39, 1214-1225.	1.1	10
52	Geleophysic dysplasia: novel missense variants and insights into ADAMTSL2 intracellular trafficking. <i>Molecular Genetics and Metabolism Reports</i> , 2019, 21, 100504.	0.4	10
53	KSR induces RAS-independent MAPK pathway activation and modulates the efficacy of KRAS inhibitors. <i>Molecular Oncology</i> , 2022, 16, 3066-3081.	2.1	10
54	The cattle tick antigen, Bm95, expressed in <i>Pichia pastoris</i> contains short chains of N- and O-glycans. <i>Archives of Biochemistry and Biophysics</i> , 2004, 432, 205-211.	1.4	9

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55	Computational Biology in Cuba: An Opportunity to Promote Science in a Developing Country. <i>PLoS Computational Biology</i> , 2007, 3, e227.	1.5	9
56	Computational Perspectives into Plasmepsins Structure-Function Relationship: Implications to Inhibitors Design. <i>Journal of Tropical Medicine</i> , 2011, 2011, 1-15.	0.6	8
57	Impaired stem cell differentiation and somatic cell reprogramming in DIDO3 mutants with altered RNA processing and increased R-loop levels. <i>Cell Death and Disease</i> , 2021, 12, 637.	2.7	8
58	Molecular Cloning of an $\alpha$ -Glucosidase-like Gene from <i>Penicillium minioluteum</i> and Structure Prediction of Its Gene Product. <i>Biochemical and Biophysical Research Communications</i> , 2001, 281, 151-158.	1.0	7
59	Enzymic, spectroscopic and calorimetric studies of a recombinant dextranase expressed in <i>Pichia pastoris</i> . <i>Biotechnology and Applied Biochemistry</i> , 2003, 38, 211.	1.4	7
60	Effect of divalent cations on the porcine kidney cortex membrane-bound form of dipeptidyl peptidase IV. <i>International Journal of Biochemistry and Cell Biology</i> , 2011, 43, 363-371.	1.2	7
61	MIB2 variants altering NOTCH signalling result in left ventricle hypertrabeculation/non-compaction and are associated with MÃ©Ã©trier-like gastropathy. <i>Human Molecular Genetics</i> , 2016, 26, ddw365.	1.4	7
62	PhcrTx2, a New Crab-Paralyzing Peptide Toxin from the Sea Anemone <i>Phymanthus crucifer</i> . <i>Toxins</i> , 2018, 10, 72.	1.5	7
63	Systematic Analysis of FASTK Gene Family Alterations in Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11337.	1.8	7
64	Structural model of Dex protein from <i>Penicillium minioluteum</i> and its implications in the mechanism of catalysis. , 1998, 31, 345-354.		6
65	Structures of a bi-functional Kunitz-type STI family inhibitor of serine and aspartic proteases: Could the aspartic protease inhibition have evolved from a canonical serine protease-binding loop?. <i>Journal of Structural Biology</i> , 2016, 195, 259-271.	1.3	6
66	Effect of zinc and calcium ions on the rat kidney membrane-bound form of dipeptidyl peptidase IV. <i>Journal of Biosciences</i> , 2013, 38, 461-469.	0.5	5
67	A computational and structural analysis of germline and somatic variants affecting the DDR mechanism, and their impact on human diseases. <i>Scientific Reports</i> , 2021, 11, 14268.	1.6	4
68	Predicting functional residues of the <i>Solanum lycopersicum</i> aspartic protease inhibitor (SLAPI) by combining sequence and structural analysis with molecular docking. <i>Journal of Molecular Modeling</i> , 2012, 18, 2673-2687.	0.8	3
69	Predicting Protein Relationships to Human Pathways through a Relational Learning Approach Based on Simple Sequence Features. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 753-765.	1.9	3
70	A common structural scaffold in CTD phosphatases that supports distinct catalytic mechanisms. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 103-118.	1.5	3
71	Poorly Conserved P15 Proteins of Cileviruses Retain Elements of Common Ancestry and Putative Functionality: A Theoretical Assessment on the Evolution of Cilevirus Genomes. <i>Frontiers in Plant Science</i> , 2021, 12, 771983.	1.7	3
72	NMR structure and dynamics of Q4D059, a kinetoplastid-specific and conserved protein from <i>Trypanosoma cruzi</i> . <i>Journal of Structural Biology</i> , 2015, 190, 11-20.	1.3	2

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73	Solving the enigma of POLD1 p.V295M as a potential cause of increased cancer risk. European Journal of Human Genetics, 2022, 30, 485-489.	1.4	2
74	Cloning and sequence analysis of the gene encoding invertase (INV1) from the yeast Candida utilis. Yeast, 1998, 14, 1223-1232.	0.8	1
75	DIDO3 Regulates Microtubule Stability at Transcriptional and Posttranslational Levels and is Needed for Fibroblast Adhesion and Movement. SSRN Electronic Journal, 0, , .	0.4	1
76	Whole-exome sequencing of matched germline and plasma cell-free DNA portrays the somatic mutation landscape of refractory metastatic colorectal cancer and identifies mutated KDR/VEGFR2 as new cause of therapy resistance. Annals of Oncology, 2017, 28, v192.	0.6	0