

# Tirso Pons

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

74  
papers

3,090  
citations

25  
h-index

55  
g-index

84  
ext. papers

4,288  
ext. citations

7.1  
avg. IF

7.13  
L-index

#	Paper	IF	Citations
74	Annotating Cancer-Related Variants at ProteinProtein Interface with Structure-PPi. <i>Methods in Molecular Biology</i> , <b>2022</b> , 315-330	1.4	
73	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> , <b>2021</b> , 12, 771983	6.2	1
72	Systematic Analysis of FASTK Gene Family Alterations in Cancer. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	3
71	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> , <b>2021</b> , 12, 637	9.8	1
70	A computational and structural analysis of germline and somatic variants affecting the DDR mechanism, and their impact on human diseases. <i>Scientific Reports</i> , <b>2021</b> , 11, 14268	4.9	2
69	Combined burden and functional impact tests for cancer driver discovery using DriverPower. <i>Nature Communications</i> , <b>2020</b> , 11, 734	17.4	16
68	Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , <b>2020</b> , 11, 735	17.4	53
67	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , <b>2020</b> , 11, 729	17.4	38
66	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , <b>2020</b> , 578, 102-111	50.4	220
65	Pan-cancer analysis of whole genomes. <i>Nature</i> , <b>2020</b> , 578, 82-93	50.4	840
64	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. <i>Communications Biology</i> , <b>2020</b> , 3, 56	6.7	77
63	Role of POLE and POLD1 in familial cancer. <i>Genetics in Medicine</i> , <b>2020</b> , 22, 2089-2100	8.1	23
62	Geleophysic dysplasia: novel missense variants and insights into ADAMTSL2 intracellular trafficking. <i>Molecular Genetics and Metabolism Reports</i> , <b>2019</b> , 21, 100504	1.8	5
61	Germline variation in O-methylguanine-DNA methyltransferase (MGMT) as cause of hereditary colorectal cancer. <i>Cancer Letters</i> , <b>2019</b> , 447, 86-92	9.9	12
60	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> , <b>2019</b> , 86, 559-570	4.3	12
59	Ten years of CAZypedia: a living encyclopedia of carbohydrate-active enzymes. <i>Glycobiology</i> , <b>2018</b> , 28, 3-8	5.8	104
58	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> , <b>2018</b> , 24, 3550-3559	12.9	26

57	Association Between Germline Mutations in BRF1, a Subunit of the RNA Polymerase III Transcription Complex, and Hereditary Colorectal Cancer. <i>Gastroenterology</i> , <b>2018</b> , 154, 181-194.e20	13.3	25
56	PhcrTx2, a New Crab-Paralyzing Peptide Toxin from the Sea Anemone <i>Phymanthus crucifer</i> . <i>Toxins</i> , <b>2018</b> , 10,	4.9	5
55	Role of MDH2 pathogenic variant in pheochromocytoma and paraganglioma patients. <i>Genetics in Medicine</i> , <b>2018</b> , 20, 1652-1662	8.1	33
54	Germline mutations in the spindle assembly checkpoint genes BUB1 and BUB3 are infrequent in familial colorectal cancer and polyposis. <i>Molecular Cancer</i> , <b>2018</b> , 17, 23	42.1	15
53	Germline variation in the oxidative DNA repair genes NUDT1 and OGG1 is not associated with hereditary colorectal cancer or polyposis. <i>Human Mutation</i> , <b>2018</b> , 39, 1214-1225	4.7	6
52	Elucidating the molecular basis of MSH2-deficient tumors by combined germline and somatic analysis. <i>International Journal of Cancer</i> , <b>2017</b> , 141, 1365-1380	7.5	18
51	Comparison of algorithms for the detection of cancer drivers at subgene resolution. <i>Nature Methods</i> , <b>2017</b> , 14, 782-788	21.6	51
50	MIB2 variants altering NOTCH signalling result in left ventricle hypertrabeculation/non-compaction and are associated with MBI-like gastropathy. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 33-43	5.6	7
49	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> , <b>2016</b> , 18, 325-32	8.1	153
48	KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. <i>BMC Genomics</i> , <b>2016</b> , 17 Suppl 2, 396	4.5	7
47	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> , <b>2016</b> , 195, 259-271	3.4	4
46	wKinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. <i>Human Mutation</i> , <b>2016</b> , 37, 36-42	4.7	7
45	The Kunitz-Type Protein ShPI-1 Inhibits Serine Proteases and Voltage-Gated Potassium Channels. <i>Toxins</i> , <b>2016</b> , 8, 110	4.9	26
44	Somatic Embryonic FGFR2 Mutations in Keratinocytic Epidermal Nevi. <i>Journal of Investigative Dermatology</i> , <b>2016</b> , 136, 1718-1721	4.3	15
43	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. <i>Gastroenterology</i> , <b>2015</b> , 149, 563-6	13.3	75
42	NMR structure and dynamics of Q4D059, a kinetoplastid-specific and conserved protein from <i>Trypanosoma cruzi</i> . <i>Journal of Structural Biology</i> , <b>2015</b> , 190, 11-20	3.4	2
41	The 29(th) Annual Symposium of the Protein Society, Barcelona, Spain, July 22-25, 2015. <i>Protein Science</i> , <b>2015</b> , 24 Suppl 1, 1-313	6.3	4
40	Structure-PPI: a module for the annotation of cancer-related single-nucleotide variants at protein-protein interfaces. <i>Bioinformatics</i> , <b>2015</b> , 31, 2397-9	7.2	31

39	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> , <b>2014</b> , 239, 147-60	4.7	12
38	A novel sea anemone peptide that inhibits acid-sensing ion channels. <i>Peptides</i> , <b>2014</b> , 53, 3-12	3.8	41
37	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> , <b>2014</b> , 11, 753-65	3	2
36	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> , <b>2014</b> , 116, 720-6	6	19
35	A common structural scaffold in CTD phosphatases that supports distinct catalytic mechanisms. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82, 103-18	4.2	2
34	Effect of zinc and calcium ions on the rat kidney membrane-bound form of dipeptidyl peptidase IV. <i>Journal of Biosciences</i> , <b>2013</b> , 38, 461-9	2.3	3
33	Akirins in sea lice: first steps towards a deeper understanding. <i>Experimental Parasitology</i> , <b>2013</b> , 135, 188-99	2.9	9
32	Towards a detailed atlas of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , <b>2013</b> , 23, 929-40	8.1	80
31	Structural insights into serine protease inhibition by a marine invertebrate BPTI Kunitz-type inhibitor. <i>Journal of Structural Biology</i> , <b>2012</b> , 180, 271-9	3.4	15
30	Structure of the recombinant BPTI/Kunitz-type inhibitor rShPI-1A from the marine invertebrate <i>Stichodactyla helianthus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2012</b> , 68, 1289-93		7
29	In silico studies of potential phosphoresidues in the human nucleophosmin/B23: its kinases and related biological processes. <i>Journal of Cellular Biochemistry</i> , <b>2012</b> , 113, 2364-74	4.7	12
28	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> , <b>2012</b> , 18, 2673-87	2	2
27	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> , <b>2011</b> , 43, 363-71	5.6	6
26	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> , <b>2011</b> , 25, 396-406	5	13
25	Computational perspectives into plasmepsins structure-function relationship: implications to inhibitors design. <i>Journal of Tropical Medicine</i> , <b>2011</b> , 2011, 657483	2.4	6
24	Functional analysis of archaeal MBF1 by complementation studies in yeast. <i>Biology Direct</i> , <b>2011</b> , 6, 18	7.2	10
23	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> , <b>2011</b> , 24, 485-93	1.9	19
22	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> , <b>2010</b> , 277, 3489-501	5.7	14

21	New parameterization approaches of the LIE method to improve free energy calculations of PlmII-Inhibitors complexes. <i>Journal of Computational Chemistry</i> , <b>2010</b> , 31, 2723-34	3.5	14
20	Physico-chemical studies of molecular interactions between non-ionic surfactants and bovine serum albumin. <i>Colloids and Surfaces B: Biointerfaces</i> , <b>2010</b> , 75, 282-9	6	77
19	Predicting functional residues in Plasmodium falciparum plasmepsins by combining sequence and structural analysis with molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 73, 440-57	4.2	18
18	Computational biology in Cuba: an opportunity to promote science in a developing country. <i>PLoS Computational Biology</i> , <b>2007</b> , 3, e227	5	6
17	Characterization and comparative 3D modeling of CmPI-II, a novel non-classical Kazal-type inhibitor from the marine snail Cenchritis muricatus (Mollusca). <i>Biological Chemistry</i> , <b>2007</b> , 388, 1183-94	4.5	21
16	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> , <b>2006</b> , 12, 973-83	2	13
15	Crystal structure of levansucrase from the Gram-negative bacterium Gluconacetobacter diazotrophicus. <i>Biochemical Journal</i> , <b>2005</b> , 390, 19-27	3.8	121
14	Three acidic residues are at the active site of a beta-propeller architecture in glycoside hydrolase families 32, 43, 62, and 68. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 54, 424-32	4.2	79
13	The cattle tick antigen, Bm95, expressed in Pichia pastoris contains short chains of N- and O-glycans. <i>Archives of Biochemistry and Biophysics</i> , <b>2004</b> , 432, 205-11	4.1	7
12	Beta-propellers: associated functions and their role in human diseases. <i>Current Medicinal Chemistry</i> , <b>2003</b> , 10, 505-24	4.3	52
11	Enzymic, spectroscopic and calorimetric studies of a recombinant dextranase expressed in Pichia pastoris. <i>Biotechnology and Applied Biochemistry</i> , <b>2003</b> , 38, 211-21	2.8	5
10	Molecular cloning of an alpha-glucosidase-like gene from Penicillium minioluteum and structure prediction of its gene product. <i>Biochemical and Biophysical Research Communications</i> , <b>2001</b> , 281, 151-8	3.4	6
9	Prediction of a common beta-propeller catalytic domain for fructosyltransferases of different origin and substrate specificity. <i>Protein Science</i> , <b>2000</b> , 9, 2285-91	6.3	33
8	Substitution of Asp-309 by Asn in the Arg-Asp-Pro (RDP) motif of Acetobacter diazotrophicus levansucrase affects sucrose hydrolysis, but not enzyme specificity. <i>Biochemical Journal</i> , <b>1999</b> , 337, 503-506	3.8	46
7	Substitution of Asp-309 by Asn in the Arg-Asp-Pro (RDP) motif of Acetobacter diazotrophicus levansucrase affects sucrose hydrolysis, but not enzyme specificity. <i>Biochemical Journal</i> , <b>1999</b> , 337, 503	3.8	13
6	Cloning and sequence analysis of the gene encoding invertase (INV1) from the yeast Candida utilis. <i>Yeast</i> , <b>1998</b> , 14, 1223-32	3.4	23
5	Structural model of Dex protein from Penicillium minioluteum and its implications in the mechanism of catalysis. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1998</b> , 31, 345-54	4.2	5
4	Structural model for family 32 of glycosyl-hydrolase enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1998</b> , 33, 383-95	4.2	51

3	Homology modeling, model and software evaluation: three related resources. <i>Bioinformatics</i> , <b>1998</b> , 14, 523-8	7.2	277
2	Cloning and sequence analysis of the gene encoding invertase (INV1) from the yeast <i>Candida utilis</i> <b>1998</b> , 14, 1223		1
1	Cloning of the <i>Penicillium minioluteum</i> gene encoding dextranase and its expression in <i>Pichia pastoris</i> <b>1996</b> , 12, 1187-1200		29