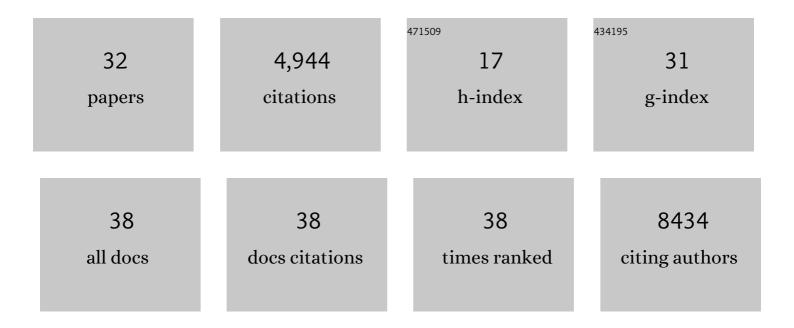
## Janet Piñero

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	DisGeNET: a comprehensive platform integrating information on human disease-associated genes and variants. Nucleic Acids Research, 2017, 45, D833-D839.	14.5	1,865
2	The DisGeNET knowledge platform for disease genomics: 2019 update. Nucleic Acids Research, 2020, 48, D845-D855.	14.5	1,083
3	DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav028-bav028.	3.0	847
4	The DisGeNET cytoscape app: Exploring and visualizing disease genomics data. Computational and Structural Biotechnology Journal, 2021, 19, 2960-2967.	4.1	221
5	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. Nature Communications, 2019, 10, 10.	12.8	193
6	Extraction of relations between genes and diseases from text and large-scale data analysis: implications for translational research. BMC Bioinformatics, 2015, 16, 55.	2.6	170
7	PsyGeNET: a knowledge platform on psychiatric disorders and their genes. Bioinformatics, 2015, 31, 3075-3077.	4.1	79
8	DisGeNET-RDF: harnessing the innovative power of the Semantic Web to explore the genetic basis of diseases. Bioinformatics, 2016, 32, 2236-2238.	4.1	52
9	Network medicine analysis of COPD multimorbidities. Respiratory Research, 2014, 15, 111.	3.6	48
10	Automatic Filtering and Substantiation of Drug Safety Signals. PLoS Computational Biology, 2012, 8, e1002457.	3.2	34
11	Proximal Pathway Enrichment Analysis for Targeting Comorbid Diseases via Network Endopharmacology. Pharmaceuticals, 2018, 11, 61.	3.8	32
12	GUILDify v2.0: A Tool to Identify Molecular Networks Underlying Human Diseases, Their Comorbidities and Their Druggable Targets. Journal of Molecular Biology, 2019, 431, 2477-2484.	4.2	32
13	In silico models in drug development: where we are. Current Opinion in Pharmacology, 2018, 42, 111-121.	3.5	30
14	Uncovering disease mechanisms through network biology in the era of Next Generation Sequencing. Scientific Reports, 2016, 6, 24570.	3.3	29
15	Genetic and functional characterization of disease associations explains comorbidity. Scientific Reports, 2017, 7, 6207.	3.3	28
16	Conservation of key members in the course of the evolution of the insulin signaling pathway. BioSystems, 2009, 95, 7-16.	2.0	20
17	A systems approach identifies time-dependent associations of multimorbidities with pancreatic cancer risk. Annals of Oncology, 2017, 28, 1618-1624.	1.2	20
18	Network, Transcriptomic and Genomic Features Differentiate Genes Relevant for Drug Response. Frontiers in Genetics, 2018, 9, 412.	2.3	18

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19	Comorbidity between Alzheimer's disease and major depression: a behavioural and transcriptomic characterization study in mice. Alzheimer's Research and Therapy, 2021, 13, 73.	6.2	18
20	The eTRANSAFE Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. Pharmaceuticals, 2021, 14, 237.	3.8	17
21	The human hepatocyte TXG-MAPr: gene co-expression network modules to support mechanism-based risk assessment. Archives of Toxicology, 2021, 95, 3745-3775.	4.2	16
22	Pancreatic cancer and autoimmune diseases: An association sustained by computational and epidemiological case–control approaches. International Journal of Cancer, 2019, 144, 1540-1549.	5.1	11
23	An ensemble learning approach for modeling the systems biology of drug-induced injury. Biology Direct, 2021, 16, 5.	4.6	11
24	SARSâ€CoVâ€2 sculpts the immune system to induce sustained virusâ€specific naÃ⁻veâ€like and memory Bâ€cell responses. Clinical and Translational Immunology, 2021, 10, e1339.	3.8	11
25	Nerve growth factor and striatal glutathione metabolism in a rat model of Huntington's disease. Restorative Neurology and Neuroscience, 2000, 17, 217-221.	0.7	11
26	The Ubiquity of the Insulin Superfamily Across the Eukaryotes Detected Using a Bioinformatics Approach. OMICS A Journal of Integrative Biology, 2011, 15, 439-447.	2.0	10
27	ResMarkerDB: a database of biomarkers of response to antibody therapy in breast and colorectal cancer. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	10
28	Mining the Modular Structure of Protein Interaction Networks. PLoS ONE, 2015, 10, e0122477.	2.5	7
29	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5
30	The effects of microencapsulated bovine insulin given to Litopenaeus vannamei juveniles as a feed additive on growth, metabolism, and digestive enzyme activities. Aquaculture, 2010, 306, 252-258.	3.5	3
31	Functional Genomics Analysis to Disentangle the Role of Genetic Variants in Major Depression. Genes, 2022, 13, 1259.	2.4	1
32	Embracing the Dark Side: Computational Approaches to Unveil the Functionality of Genes Lacking Biological Annotation in Drug-Induced Liver Injury. Frontiers in Genetics, 2018, 9, 527.	2.3	0