

# Aniel Sanchez

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

626  
citations

687363

13  
h-index

642732

23  
g-index

40  
all docs

40  
docs citations

40  
times ranked

1319  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic Alterations in Follicular Fluid of Human Small Antral Follicles Collected from Polycystic Ovariesâ€”A Pilot Study. <i>Life</i> , 2022, 12, 391.	2.4	0
2	Novel protein markers of androgen activity in humans: proteomic study of plasma from young chemically castrated men. <i>ELife</i> , 2022, 11, .	6.0	3
3	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1566-1574.	3.7	2
4	Mass spectrometric and kinetics characterization of modified species of Growth Hormone Releasing Hexapeptide generated under thermal stress in different pH and buffers. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 194, 113776.	2.8	1
5	The human melanoma proteome atlasâ€”Defining the molecular pathology. <i>Clinical and Translational Medicine</i> , 2021, 11, e473.	4.0	14
6	The Human Melanoma Proteome Atlasâ€”Complementing the melanoma transcriptome. <i>Clinical and Translational Medicine</i> , 2021, 11, e451.	4.0	20
7	A biobanking turningâ€”point in the use of formalinâ€”fixed, paraffin tumor blocks to unveil kinase signaling in melanoma. <i>Clinical and Translational Medicine</i> , 2021, 11, e466.	4.0	6
8	Proteome of fluid from human ovarian small antral follicles reveals insights in folliculogenesis and oocyte maturation. <i>Human Reproduction</i> , 2021, 36, 756-770.	0.9	17
9	Short-Term Effect of Induced Alterations in Testosterone Levels on Fasting Plasma Amino Acid Levels in Healthy Young Men. <i>Life</i> , 2021, 11, 1276.	2.4	2
10	Mapping the Melanoma Plasma Proteome (MPP) Using Single-Shot Proteomics Interfaced with the WiMT Database. <i>Cancers</i> , 2021, 13, 6224.	3.7	4
11	Novel functional proteins coded by the human genome discovered in metastases of melanoma patients. <i>Cell Biology and Toxicology</i> , 2020, 36, 261-272.	5.3	9
12	Short-term effect of pharmacologically induced alterations in testosterone levels on common blood biomarkers in a controlled healthy human model. <i>Scandinavian Journal of Clinical and Laboratory Investigation</i> , 2020, 80, 25-31.	1.2	7
13	Targeting the hydrophilic regions of recombinant proteins by MS via in-solution buffer-free trypsin digestion. <i>European Journal of Mass Spectrometry</i> , 2020, 26, 230-237.	1.0	7
14	Mass spectrometry-based analysis of formalin-fixed, paraffin-embedded distal cholangiocarcinoma identifies stromal thrombospondin-2 as a potential prognostic marker. <i>Journal of Translational Medicine</i> , 2020, 18, 343.	4.4	10
15	Proteomic analysis enables distinction of earlyâ€”versus advancedâ€”stage lung adenocarcinomas. <i>Clinical and Translational Medicine</i> , 2020, 10, e106.	4.0	7
16	Protein Expression in Metastatic Melanoma and the Link to Disease Presentation in a Range of Tumor Phenotypes. <i>Cancers</i> , 2020, 12, 767.	3.7	2
17	A pilot proteomic study reveals different protein profiles related to testosterone and gonadotropin changes in a short-term controlled healthy human cohort. <i>Journal of Proteomics</i> , 2020, 220, 103768.	2.4	4
18	Progressive changes in human follicular fluid composition over the course of ovulation: quantitative proteomic analyses. <i>Molecular and Cellular Endocrinology</i> , 2019, 495, 110522.	3.2	29

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19	Sodium dodecyl sulfate free gel electrophoresis/electroelution sorting for peptide fractionation. <i>Journal of Separation Science</i> , 2019, 42, 3712-3717.	2.5	4
20	Clinical protein science in translational medicine targeting malignant melanoma. <i>Cell Biology and Toxicology</i> , 2019, 35, 293-332.	5.3	33
21	The Hidden Story of Heterogeneous B-raf V600E Mutation Quantitative Protein Expression in Metastatic Melanoma—Association with Clinical Outcome and Tumor Phenotypes. <i>Cancers</i> , 2019, 11, 1981.	3.7	16
22	Characterization of low abundance species in the active pharmaceutical ingredient of CIGB-300: A clinical-grade anticancer synthetic peptide. <i>Journal of Peptide Science</i> , 2018, 24, e3081.	1.4	9
23	Quantitative Assessment of Urea In-Solution Lys-C/Trypsin Digestions Reveals Superior Performance at Room Temperature over Traditional Proteolysis at 37 °C. <i>Journal of Proteome Research</i> , 2018, 17, 2556-2561.	3.7	32
24	Mass spectrometry evaluation of a neuroblastoma SH-SY5Y cell culture protocol. <i>Analytical Biochemistry</i> , 2018, 559, 51-54.	2.4	2
25	Quantitative proteomic analysis identifies proteins and pathways related to neuronal development in differentiated SH-SY5Y neuroblastoma cells. <i>EuPA Open Proteomics</i> , 2017, 16, 1-11.	2.5	48
26	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , 2017, 150, 170-182.	2.4	56
27	Comparative proteomic analysis of growth hormone secretagogue A233 treatment of murine macrophage cells J774A.2 indicates it has a role in antiviral innate response. <i>Biochemistry and Biophysics Reports</i> , 2016, 5, 379-387.	1.3	7
28	PRIDE Inspector Toolsuite: Moving Toward a Universal Visualization Tool for Proteomics Data Standard Formats and Quality Assessment of ProteomeXchange Datasets. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 305-317.	3.8	140
29	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. <i>Bioinformatics</i> , 2015, 31, 2903-2905.	4.1	30
30	HI-Bone: A Scoring System for Identifying Phenylisothiocyanate-Derivatized Peptides Based on Precursor Mass and High Intensity Fragment Ions. <i>Analytical Chemistry</i> , 2013, 85, 3515-3520.	6.5	7
31	Effectively addressing complex proteomic search spaces with peptide spectrum matching. <i>Bioinformatics</i> , 2013, 29, 1343-1344.	4.1	20
32	Charge state-selective separation of peptides by reversible modification of amino groups and strong cation-exchange chromatography: Evaluation in proteomic studies using peptide-centric database searches. <i>Journal of Proteomics</i> , 2011, 74, 2210-2213.	2.4	4
33	In silico analysis of accurate proteomics, complemented by selective isolation of peptides. <i>Journal of Proteomics</i> , 2011, 74, 2071-2082.	2.4	30
34	Evaluation of Phenylthiocarbonyl-Derivatized Peptides by Electrospray Ionization Mass Spectrometry: Selective Isolation and Analysis of Modified Multiply Charged Peptides for Liquid Chromatography—Tandem Mass Spectrometry Experiments. <i>Analytical Chemistry</i> , 2010, 82, 8492-8501.	6.5	10
35	Double acylation for identification of amino-terminal peptides of proteins isolated by polyacrylamide gel electrophoresis. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 2237-2244.	1.5	6
36	Selective Isolation of Lysine-Free Tryptic Peptides Delimited by Arginine Residues: A New Tool for Proteome Analysis. <i>Journal of Proteome Research</i> , 2006, 5, 1204-1213.	3.7	10

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37	Selective isolation of multiple positively charged peptides for 2-DE-free quantitative proteomics. <i>Proteomics</i> , 2006, 6, 4444-4455.	2.2	18