Xavier Roucou

List of Publications by Year
in descending order

70 papers	3,310 citations	109321 35 h-index	155660 55 g-index
80 all docs	80 docs citations	80 times ranked	3463 citing authors

#	Article	IF	Citations
1	Mosaic translation hypothesis: chimeric polypeptides produced via multiple ribosomal frameshifting as a basis for adaptability. FEBS Journal, 2023, 290, 370-378.	4.7	3
2	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	17.5	86
3	OpenProt 2021: deeper functional annotation of the coding potential of eukaryotic genomes. Nucleic Acids Research, 2021, 49, D380-D388.	14.5	71
4	Potentiation of B2 receptor signaling by AltB2R, a newly identified alternative protein encoded in the human bradykinin B2 receptor gene. Journal of Biological Chemistry, 2021, 296, 100329.	3.4	9
5	Robust Physiological Metrics From Sparsely Sampled Networks. Frontiers in Physiology, 2021, 12, 624097.	2.8	7
6	The FUS gene is dualâ€coding with both proteins contributing to FUS â€mediated toxicity. EMBO Reports, 2021, 22, e50640.	4.5	31
7	Optimized Sample Preparation Workflow for Improved Identification of Ghost Proteins. Analytical Chemistry, 2020, 92, 1122-1129.	6.5	32
8	How to Illuminate the Dark Proteome Using the Multiâ€omic OpenProt Resource. Current Protocols in Bioinformatics, 2020, 71, e103.	25.8	4
9	Reconsidering proteomic diversity with functional investigation of small ORFs and alternative ORFs. Experimental Cell Research, 2020, 393, 112057.	2.6	37
10	UBB pseudogene 4 encodes functional ubiquitin variants. Nature Communications, 2020, 11, 1306.	12.8	34
11	OpenProt: a more comprehensive guide to explore eukaryotic coding potential and proteomes. Nucleic Acids Research, 2019, 47, D403-D410.	14.5	71
12	Mass Spectrometry-Based Proteomics Analyses Using the OpenProt Database to Unveil Novel Proteins Translated from Non-Canonical Open Reading Frames. Journal of Visualized Experiments, 2019, , .	0.3	8
13	Recognition of the polycistronic nature of human genes is critical to understanding the genotype-phenotype relationship. Genome Research, 2018, 28, 609-624.	5.5	54
14	Small Proteins Encoded by Unannotated ORFs are Rising Stars of the Proteome, Confirming Shortcomings in Genome Annotations and Current Vision of an mRNA. Proteomics, 2018, 18, e1700058.	2.2	59
15	Spatially-Resolved Top-down Proteomics Bridged to MALDI MS Imaging Reveals the Molecular Physiome of Brain Regions. Molecular and Cellular Proteomics, 2018, 17, 357-372.	3.8	36
16	The Protein Coded by a Short Open Reading Frame, Not by the Annotated Coding Sequence, Is the Main Gene Product of the Dual-Coding Gene MIEF1. Molecular and Cellular Proteomics, 2018, 17, 2402-2411.	3.8	44
17	Combined Mass Spectrometry Imaging and Top-down Microproteomics Reveals Evidence of a Hidden Proteome in Ovarian Cancer. EBioMedicine, 2017, 21, 55-64.	6.1	45
18	Deep transcriptome annotation enables the discovery and functional characterization of cryptic small proteins. ELife, 2017, 6, .	6.0	93

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19	Death of a dogma: eukaryotic mRNAs can code for more than one protein. Nucleic Acids Research, 2016, 44, 14-23.	14.5	98
20	Found in translation: functions and evolution of a recently discovered alternative proteome. Current Opinion in Structural Biology, 2015, 32, 74-80.	5.7	51
21	Struggling for breath in Sherbrooke 1st Symposium on â€œOne mitochondrion, many diseasesâ€•in Sherbrooke, QuÃ©bec, Canada, March 11th, 2015. Microbial Cell, 2015, 2, 208-213.	3.2	1
22	Regulation of PrPC signaling and processing by dimerization. Frontiers in Cell and Developmental Biology, 2014, 2, 57.	3.7	15
23	Taking advantage of physiological proteolytic processing of the prion protein for a therapeutic perspective in prion and Alzheimer diseases. Prion, 2014, 8, 106-110.	1.8	11
24	Development of kinomic analyses to identify dysregulated signaling pathways in cells expressing cytoplasmic PrP. Virology Journal, 2014, 11, 175.	3.4	2
25	AÎ² induces its own prion protein N-terminal fragment (PrPN1)â€“mediated neutralization in amorphous aggregates. Neurobiology of Aging, 2014, 35, 1537-1548.	3.1	34
26	p53 Aggregates Penetrate Cells and Induce the Co-Aggregation of Intracellular p53. PLoS ONE, 2013, 8, e69242.	2.5	53
27	An Out-of-frame Overlapping Reading Frame in the Ataxin-1 Coding Sequence Encodes a Novel Ataxin-1 Interacting Protein. Journal of Biological Chemistry, 2013, 288, 21824-21835.	3.4	65
28	Aggregation and neurotoxicity of recombinant Î±-synuclein aggregates initiated by dimerization. Molecular Neurodegeneration, 2013, 8, 5.	10.8	71
29	Homodimerization as a molecular switch between low and high efficiency PrP^Ccell surface delivery and neuroprotective activity. Prion, 2013, 7, 170-174.	1.8	7
30	Direct Detection of Alternative Open Reading Frames Translation Products in Human Significantly Expands the Proteome. PLoS ONE, 2013, 8, e70698.	2.5	192
31	The prion protein unstructured Nâ€terminal region is a broadâ€spectrum molecular sensor with diverse and contrasting potential functions. Journal of Neurochemistry, 2012, 120, 853-868.	3.9	53
32	HAltORF: a database of predicted out-of-frame alternative open reading frames in human. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas025-bas025.	3.0	43
33	PrP^CHomodimerization Stimulates the Production of PrP^CCleaved Fragments PrPN1 and PrPC1. Journal of Neuroscience, 2012, 32, 13255-13263.	3.6	52
34	An overlapping reading frame in the PRNP gene encodes a novel polypeptide distinct from the prion protein. FASEB Journal, 2011, 25, 2373-2386.	0.5	61
35	An Update on Prion Biology and Proteomics. Current Proteomics, 2010, 7, 36-48.	0.3	4
36	Aggregation and Amyloid Fibril Formation Induced by Chemical Dimerization of Recombinant Prion Protein in Physiological-like Conditions. Journal of Biological Chemistry, 2009, 284, 30907-30916.	3.4	26

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37	Reconstitution of chromatoid body-like particles in cultured cells: A novel approach to elucidate the mechanism of assembly and function of the chromatoid body. RNA Biology, 2009, 6, 165-168.	3.1	3
38	A large ribonucleoprotein particle induced by cytoplasmic PrP shares striking similarities with the chromatoid body, an RNA granule predicted to function in posttranscriptional gene regulation. Biochimica Et Biophysica Acta - Molecular Cell Research, 2009, 1793, 335-345.	4.1	30
39	Prion protein and RNA: a view from the cytoplasm. Frontiers in Bioscience - Landmark, 2009, 14, 5157.	3.0	8
40	Aggresomes do not represent a general cellular response to protein misfolding in mammalian cells. BMC Cell Biology, 2008, 9, 59.	3.0	20
41	Prion protein aggresomes are poly(A)+ ribonucleoprotein complexes that induce a PKR-mediated deficient cell stress response. Biochimica Et Biophysica Acta - Molecular Cell Research, 2008, 1783, 479-491.	4.1	49
42	Aggregation of cellular prion protein is initiated by proximity-induced dimerization. Journal of Neurochemistry, 2007, 102, 1195-1205.	3.9	11
43	Molecular morphology and toxicity of cytoplasmic prion protein aggregates in neuronal and non-neuronal cells. Journal of Neurochemistry, 2006, 97, 1456-1466.	3.9	58
44	Prion protein prevents Bax-mediated cell death in the absence of other Bcl-2 family members inSaccharomyces cerevisiae. FEMS Yeast Research, 2006, 6, 1204-1212.	2.3	28
45	Cellular prion protein inhibits proapoptotic Bax conformational change in human neurons and in breast carcinoma MCF-7 cells. Cell Death and Differentiation, 2005, 12, 783-795.	11.2	150
46	Cellular prion protein neuroprotective function: implications in prion diseases. Journal of Molecular Medicine, 2005, 83, 3-11.	3.9	131
47	Neuroprotective functions of prion protein. Journal of Neuroscience Research, 2004, 75, 153-161.	2.9	156
48	The Molecular Neighborhood of Subunit 8 of Yeast Mitochondrial F1F0-ATP Synthase Probed by Cysteine Scanning Mutagenesis and Chemical Modification. Journal of Biological Chemistry, 2003, 278, 17867-17875.	3.4	36
49	Toxicity and Protection in Prions. Science, 2003, 301, 168-169.	12.6	4
50	Cytosolic Prion Protein Is Not Toxic and Protects against Bax-mediated Cell Death in Human Primary Neurons. Journal of Biological Chemistry, 2003, 278, 40877-40881.	3.4	150
51	p75 Neurotrophin Receptor Protects Primary Cultures of Human Neurons against Extracellular Amyloid Î² Peptide Cytotoxicity. Journal of Neuroscience, 2003, 23, 7385-7394.	3.6	83
52	Bax oligomerization in mitochondrial membranes requires tBid (caspase-8-cleaved Bid) and a mitochondrial protein. Biochemical Journal, 2002, 368, 915-921.	3.7	172
53	On the Release of Cytochrome c from Mitochondria during Cell Death Signaling. Journal of Biomedical Science, 2002, 9, 488-506.	7.0	40
54	Bid induces cytochrome c-impermeable Bax channels in liposomes. Biochemical Journal, 2002, 363, 547-552.	3.7	68

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55	On the release of cytochromec from mitochondria during cell death signaling. Journal of Biomedical Science, 2002, 9, 488-506.	7.0	67
56	INVOLVEMENT OF MITOCHONDRIA IN APOPTOSIS. Cardiology Clinics, 2001, 19, 45-55.	2.2	38
57	Expression of Protein Tyrosine Phosphatase-like Molecule ICA512/IA-2 Induces Growth Arrest in Yeast Cells and Transfected Mammalian Cell Lines. Journal of Autoimmunity, 2001, 17, 51-61.	6.5	2
58	Conformational change of Bax: a question of life or death. Cell Death and Differentiation, 2001, 8, 875-877.	11.2	44
59	Topology and proximity relationships of yeast mitochondrial ATP synthase subunit 8 determined by unique introduced cysteine residues. FEBS Journal, 2000, 267, 6443-6451.	0.2	20
60	Modulation at a distance of proton conductance through the Saccharomyces cerevisiae mitochondrial F1F0-ATP synthase by variants of the oligomycin sensitivity-conferring protein containing substitutions near the C-terminus. Journal of Bioenergetics and Biomembranes, 2000, 32, 595-607.	2.3	10
61	Insights into ATP synthase assembly and function through the molecular genetic manipulation of subunits of the yeast mitochondrial enzyme complex. Biochimica Et Biophysica Acta - Bioenergetics, 2000, 1458, 428-442.	1.0	89
62	A cytochromec-GFP fusion is not released from mitochondria into the cytoplasm upon expression of Bax in yeast cells. FEBS Letters, 2000, 471, 235-239.	2.8	44
63	Bioenergetic and structural consequences of allotopic expression of subunit 8 of yeast mitochondrial ATP synthase. The hydrophobic character of residues 23 and 24 is essential for maximal activity and structural stability of the enzyme complex. FEBS Journal, 1999, 261, 444-451.	0.2	22
64	Identification of subunit g of yeast mitochondrial F1F0-ATP synthase, a protein required for maximal activity of cytochrome c oxidase. FEBS Journal, 1999, 262, 315-323.	0.2	49
65	Characterization of the yeast mitochondria unselective channel: a counterpart to the mammalian permeability transition pore?. Journal of Bioenergetics and Biomembranes, 1998, 30, 419-429.	2.3	65
66	Conditions allowing different states of ATP- and GDP-induced permeability in mitochondria from different strains of Saccharomyces cerevisiae. Biochimica Et Biophysica Acta - Biomembranes, 1997, 1324, 120-132.	2.6	30
67	Modulation of the electrophoretic ATPâ€induced K â€transport in yeast mitochondria by Î”pH. IUBMB Life, 1997, 43, 53-61.	3.4	9
68	Investigations of the inhibitory effect of propranolol, chlorpromazine, quinine, and dicyclohexylcarbodiimide on the swelling of yeast mitochondria in potassium acetate. Evidences for indirect effects mediated by the lipid phase. Journal of Bioenergetics and Biomembranes, 1995, 27, 353-362.	2.3	5
69	Stimulation of oxidative phosphorylation by electrophoretic K+ entry associated to electroneutral K+/H+ exchange in yeast mitochondria. Biochimica Et Biophysica Acta - Bioenergetics, 1995, 1231, 282-288.	1.0	11
70	ATP opens an electrophoretic potassium transport pathway in respiring yeast mitochondria. FEBS Letters, 1995, 364, 161-164.	2.8	17