

# Stefano Toppo

## List of Publications by Year in descending order

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107  
papers

9,895  
citations

87888

38  
h-index

38395

95  
g-index

124  
all docs

124  
docs citations

124  
times ranked

14764  
citing authors

#	ARTICLE	IF	CITATIONS
1	Vimentin binds to G-quadruplex repeats found at telomeres and gene promoters. <i>Nucleic Acids Research</i> , 2022, 50, 1370-1381.	14.5	13
2	Rapid SARS-CoV-2 Intra-Host and Within-Household Emergence of Novel Haplotypes. <i>Viruses</i> , 2022, 14, 399.	3.3	5
3	Phylogeography and genomic epidemiology of SARS-CoV-2 in Italy and Europe with newly characterized Italian genomes between February-June 2020. <i>Scientific Reports</i> , 2022, 12, 5736.	3.3	6
4	Longitudinal analysis of T cell receptor repertoires reveals shared patterns of antigen-specific response to SARS-CoV-2 infection. <i>JCI Insight</i> , 2022, 7, .	5.0	15
5	A Circadian Hygiene Education Initiative Covering the Pre-pandemic and Pandemic Period Resulted in Earlier Get-Up Times in Italian University Students: An Ecological Study. <i>Frontiers in Neuroscience</i> , 2022, 16, 848602.	2.8	3
6	The glutathione peroxidase family: Discoveries and mechanism. <i>Free Radical Biology and Medicine</i> , 2022, 187, 113-122.	2.9	64
7	Human Virus Genomes Are Enriched in Conserved Adenine/Thymine/Uracil Multiple Tracts That Pause Polymerase Progression. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	0
8	Neutralising reactivity against SARS-CoV-2 Delta and Omicron variants by vaccination and infection history. <i>Genome Medicine</i> , 2022, 14, .	8.2	15
9	A white paper on Phospholipid Hydroperoxide Glutathione Peroxidase (GPx4) forty years later. <i>Free Radical Biology and Medicine</i> , 2022, 188, 117-133.	2.9	33
10	Aerobic pyruvate metabolism sensitizes cells to ferroptosis primed by GSH depletion. <i>Free Radical Biology and Medicine</i> , 2021, 167, 45-53.	2.9	19
11	SARS-CoV-2 antibody dynamics and transmission from community-wide serological testing in the Italian municipality of Voâ€™. <i>Nature Communications</i> , 2021, 12, 4383.	12.8	33
12	QPARSE: searching for long-looped or multimeric G-quadruplexes potentially distinctive and druggable. <i>Bioinformatics</i> , 2020, 36, 393-399.	4.1	16
13	Insight into the mechanism of ferroptosis inhibition by ferrostatin-1. <i>Redox Biology</i> , 2020, 28, 101328.	9.0	369
14	Inactivation of the glutathione peroxidase GPx4 by the ferroptosisâ€™inducing molecule RSL3 requires the adaptor protein 14â€™. <i>FEBS Letters</i> , 2020, 594, 611-624.	2.8	41
15	Lack of glutathione peroxidase-8 in the ER impacts on lipid composition of HeLa cells microsomal membranes. <i>Free Radical Biology and Medicine</i> , 2020, 147, 80-89.	2.9	13
16	Suppression of a SARS-CoV-2 outbreak in the Italian municipality of Voâ€™. <i>Nature</i> , 2020, 584, 425-429.	27.8	872
17	Evolutionary Study of the Crassphage Virus at Gene Level. <i>Viruses</i> , 2020, 12, 1035.	3.3	8
18	Copper/Zinc Superoxide Dismutase from the Crocodile Icefish <i>Chionodraco hamatus</i> : Antioxidant Defense at Constant Sub-Zero Temperature. <i>Antioxidants</i> , 2020, 9, 325.	5.1	22

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19	Molecular characterization of novel mitochondrial peroxiredoxins from the Antarctic emerald rockcod and their gene expression in response to environmental warming. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2019, 225, 108580.	2.6	20
20	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
21	NeSSie: a tool for the identification of approximate DNA sequence symmetries. <i>Bioinformatics</i> , 2018, 34, 2503-2505.	4.1	11
22	Loss of cardiac Wnt/ $\beta$ -catenin signalling in desmoplakin-deficient AC8 zebrafish models is rescuable by genetic and pharmacological intervention. <i>Cardiovascular Research</i> , 2018, 114, 1082-1097.	3.8	39
23	G-quadruplex forming sequences in the genome of all known human viruses: A comprehensive guide. <i>PLoS Computational Biology</i> , 2018, 14, e1006675.	3.2	106
24	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. <i>BMC Bioinformatics</i> , 2018, 19, 343.	2.6	39
25	Transcriptome and Cell Physiological Analyses in Different Rice Cultivars Provide New Insights Into Adaptive and Salinity Stress Responses. <i>Frontiers in Plant Science</i> , 2018, 9, 204.	3.6	65
26	Pathway Inspector: a pathway based web application for RNAseq analysis of model and non-model organisms. <i>Bioinformatics</i> , 2017, 33, 453-455.	4.1	20
27	Glutathione peroxidase 4-catalyzed reduction of lipid hydroperoxides in membranes: The polar head of membrane phospholipids binds the enzyme and addresses the fatty acid hydroperoxide group toward the redox center. <i>Free Radical Biology and Medicine</i> , 2017, 112, 1-11.	2.9	97
28	Mapping and characterization of G-quadruplexes in <i>Mycobacterium tuberculosis</i> gene promoter regions. <i>Scientific Reports</i> , 2017, 7, 5743.	3.3	77
29	Redox status in a model of cancer stem cells. <i>Archives of Biochemistry and Biophysics</i> , 2017, 617, 120-128.	3.0	10
30	Sox10 contributes to the balance of fate choice in dorsal root ganglion progenitors. <i>PLoS ONE</i> , 2017, 12, e0172947.	2.5	24
31	Characterization of Intra-Type Variants of Oncogenic Human Papillomaviruses by Next-Generation Deep Sequencing of the E6/E7 Region. <i>Viruses</i> , 2016, 8, 79.	3.3	17
32	Identification of novel X-linked gain-of-function RPGR-ORF15 mutation in Italian family with retinitis pigmentosa and pathologic myopia. <i>Scientific Reports</i> , 2016, 6, 39179.	3.3	15
33	Eliciting the Functional Taxonomy from protein annotations and taxa. <i>Scientific Reports</i> , 2016, 6, 31971.	3.3	14
34	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
35	Glutathione Peroxidase 4. , 2016, , 223-234.		5
36	Third generation sequencing technologies applied to diagnostic microbiology: benefits and challenges in applications and data analysis. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 1011-1023.	3.1	33

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37	Enhancing protein function prediction with taxonomic constraints – The Argot2.5 web server. <i>Methods</i> , 2016, 93, 15-23.	3.8	54
38	Peroxiredoxin 6 from the Antarctic emerald rockcod: molecular characterization of its response to warming. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2016, 186, 59-71.	1.5	41
39	Full Genome Sequence-Based Comparative Study of Wild-Type and Vaccine Strains of Infectious Laryngotracheitis Virus from Italy. <i>PLoS ONE</i> , 2016, 11, e0149529.	2.5	20
40	Glutathione peroxidase 8 is transcriptionally regulated by HIF1 $\alpha$ and modulates growth factor signaling in HeLa cells. <i>Free Radical Biology and Medicine</i> , 2015, 81, 58-68.	2.9	28
41	Selenocysteine oxidation in glutathione peroxidase catalysis: an MS-supported quantum mechanics study. <i>Free Radical Biology and Medicine</i> , 2015, 87, 1-14.	2.9	100
42	Understanding mammalian glutathione peroxidase 7 in the light of its homologs. <i>Free Radical Biology and Medicine</i> , 2015, 83, 352-360.	2.9	35
43	Phylogenetic characterization of Central/Southern European lineage 2 West Nile virus: analysis of human outbreaks in Italy and Greece, 2013–2014. <i>Clinical Microbiology and Infection</i> , 2015, 21, 1122.e1-1122.e10.	6.0	49
44	Quantitative label-free redox proteomics of reversible cysteine oxidation in red blood cell membranes. <i>Free Radical Biology and Medicine</i> , 2014, 71, 90-98.	2.9	15
45	Reducing bias in RNA sequencing data: a novel approach to compute counts. <i>BMC Bioinformatics</i> , 2014, 15, S7.	2.6	51
46	keeSeek: searching distant non-existing words in genomes for PCR-based applications. <i>Bioinformatics</i> , 2014, 30, 2662-2664.	4.1	6
47	Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 10-14.	2.0	54
48	Organochalcogen peroxidase mimetics as potential drugs: a long story of a promise still unfulfilled. <i>Free Radical Biology and Medicine</i> , 2014, 66, 65-74.	2.9	115
49	Next-generation sequencing technologies in diagnostic virology. <i>Journal of Clinical Virology</i> , 2013, 58, 346-350.	3.1	117
50	In praise of open research measures. <i>Nature</i> , 2013, 498, 170-170.	27.8	11
51	Protein disulfide isomerase and glutathione are alternative substrates in the one Cys catalytic cycle of glutathione peroxidase 7. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 3846-3857.	2.4	53
52	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
53	Accurate human papillomavirus genotyping by 454 pyrosequencing. <i>Clinical Microbiology and Infection</i> , 2013, 19, E428-E434.	6.0	21
54	Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. <i>BMC Infectious Diseases</i> , 2013, 13, 554.	2.9	18

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55	Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. <i>Big Data</i> , 2013, 1, 196-201.	3.4	5
56	Whole genome sequencing and phylogenetic analysis of West Nile virus lineage 1 and lineage 2 from human cases of infection, Italy, August 2013. <i>Eurosurveillance</i> , 2013, 18, .	7.0	49
57	Studying Interactions by Molecular Dynamics Simulations at High Concentration. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-9.	3.0	16
58	Antimicrobial Treatment and Containment Measures for an Extremely Drug-Resistant <i>Klebsiella pneumoniae</i> ST101 Isolate Carrying pKPN101-IT, a Novel Fully Sequenced <i>bla</i> KPC-2 Plasmid. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3768-3772.	3.9	39
59	Novel West Nile virus lineage 1a full genome sequences from human cases of infection in north-eastern Italy, 2011. <i>Clinical Microbiology and Infection</i> , 2012, 18, E541-E544.	6.0	27
60	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. <i>Briefings in Bioinformatics</i> , 2012, 13, 269-280.	6.5	23
61	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. <i>BMC Bioinformatics</i> , 2012, 13, S14.	2.6	137
62	A strategy to reduce technical variability and bias in RNA sequencing data. <i>EMBnet Journal</i> , 2012, 18, 65.	0.6	2
63	New endemic West Nile virus lineage 1a in northern Italy, July 2012. <i>Eurosurveillance</i> , 2012, 17, .	7.0	25
64	Clinical and virological findings in the ongoing outbreak of West Nile virus Livenza strain in northern Italy, July to September 2012. <i>Eurosurveillance</i> , 2012, 17, .	7.0	22
65	Clinical and virological findings in the ongoing outbreak of West Nile virus Livenza strain in northern Italy, July to September 2012. <i>Eurosurveillance</i> , 2012, 17, 20260.	7.0	14
66	A Comparison of Thiol Peroxidase Mechanisms. <i>Antioxidants and Redox Signaling</i> , 2011, 15, 763-780.	5.4	190
67	Applications of Next-Generation Sequencing Technologies to Diagnostic Virology. <i>International Journal of Molecular Sciences</i> , 2011, 12, 7861-7884.	4.1	241
68	Human papillomavirus genotyping by 454 next generation sequencing technology. <i>Journal of Clinical Virology</i> , 2011, 52, 93-97.	3.1	67
69	The genome of the domesticated apple ( <i>Malus domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	21.4	1,891
70	Draft Genome Sequences of Two <i>Neisseria meningitidis</i> Serogroup C Clinical Isolates. <i>Journal of Bacteriology</i> , 2010, 192, 5270-5271.	2.2	2
71	Identification by MS/MS of Disulfides Produced by a Functional Redox Transition. <i>Methods in Enzymology</i> , 2010, 473, 217-225.	1.0	7
72	OC.03.1 ANALYSIS OF MICRORNA EXPRESSION PROFILES IN CHRONIC HEPATITIS AND DEVELOPMENT OF BIOINFORMATIC METHODS FOR PREDICTION OF MICRORNA TARGETS. <i>Digestive and Liver Disease</i> , 2010, 42, S75.	0.9	0

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73	Matching up Phosphosites to Kinases: A Survey of Available Predictive Programs. <i>Current Bioinformatics</i> , 2010, 5, 141-152.	1.5	4
74	Human cytomegalovirus productively infects adrenocortical cells and induces an early cortisol response. <i>Journal of Cellular Physiology</i> , 2009, 221, 629-641.	4.1	14
75	Transcriptome analysis of <i>Medicago truncatula</i> leaf senescence: similarities and differences in metabolic and transcriptional regulations as compared with <i>Arabidopsis</i> , nodule senescence and nitric oxide signalling. <i>New Phytologist</i> , 2009, 181, 563-575.	7.3	52
76	Catalytic mechanisms and specificities of glutathione peroxidases: Variations of a basic scheme. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2009, 1790, 1486-1500.	2.4	301
77	Rapid Annotation of Anonymous Sequences from Genome Projects Using Semantic Similarities and a Weighting Scheme in Gene Ontology. <i>PLoS ONE</i> , 2009, 4, e4619.	2.5	33
78	Genome sequence analysis of the first human West Nile virus isolated in Italy in 2009. <i>Eurosurveillance</i> , 2009, 14, .	7.0	28
79	Differential liquid phase proteomic analysis of the effect of selenium supplementation in LNCaP cells. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2008, 865, 63-73.	2.3	5
80	MPA: A multiple peak alignment algorithm to perform multiple comparisons of liquid-phase proteomic profiles. <i>Proteomics</i> , 2008, 8, 250-253.	2.2	8
81	Comparative analysis of [FeFe] hydrogenase from Thermotogales indicates the molecular basis of resistance to oxygen inactivation. <i>International Journal of Hydrogen Energy</i> , 2008, 33, 570-578.	7.1	16
82	Evolutionary and Structural Insights Into the Multifaceted Glutathione Peroxidase (Gpx) Superfamily. <i>Antioxidants and Redox Signaling</i> , 2008, 10, 1501-1514.	5.4	205
83	The Catalytic Site of Glutathione Peroxidases. <i>Antioxidants and Redox Signaling</i> , 2008, 10, 1515-1526.	5.4	151
84	Characterization of a novel complex BRAF mutation in a follicular variant papillary thyroid carcinoma.. <i>European Journal of Endocrinology</i> , 2008, 159, 77-80.	3.7	21
85	Mass Spectrometry Data Analysis in the Proteomics Era. <i>Current Bioinformatics</i> , 2007, 2, 63-93.	1.5	30
86	Linear motifs in the C-terminus of <i>D. melanogaster</i> cryptochrome. <i>Biochemical and Biophysical Research Communications</i> , 2007, 355, 531-537.	2.1	54
87	The Thioredoxin Specificity of <i>Drosophila</i> GPx: A Paradigm for a Peroxiredoxin-like Mechanism of many Glutathione Peroxidases. <i>Journal of Molecular Biology</i> , 2007, 365, 1033-1046.	4.2	113
88	A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety. <i>PLoS ONE</i> , 2007, 2, e1326.	2.5	945
89	Zebrafish <i>spata2</i> is expressed at early developmental stages. <i>International Journal of Developmental Biology</i> , 2007, 51, 241-246.	0.6	7
90	Improving the quality of protein structure models by selecting from alignment alternatives. <i>BMC Bioinformatics</i> , 2006, 7, 364.	2.6	17

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91	Large-Scale Prediction of Protein Structure and Function from Sequence. <i>Current Pharmaceutical Design</i> , 2006, 12, 2067-2086.	1.9	12
92	Align: a C++ Class Library and Web Server for Rapid Sequence Alignment Prototyping. <i>Current Drug Discovery Technologies</i> , 2006, 3, 167-173.	1.2	1
93	Functional Interaction of Phospholipid Hydroperoxide Glutathione Peroxidase with Sperm Mitochondrion-associated Cysteine-rich Protein Discloses the Adjacent Cysteine Motif as a New Substrate of the Selenoperoxidase. <i>Journal of Biological Chemistry</i> , 2005, 280, 38395-38402.	3.4	81
94	The SSEA server for protein secondary structure alignment. <i>Bioinformatics</i> , 2005, 21, 393-395.	4.1	35
95	Primary structure of the nuclear forms of phospholipid hydroperoxide glutathione peroxidase (PHGPx) in rat spermatozoa. <i>FEBS Letters</i> , 2005, 579, 667-670.	2.8	20
96	Pattern recognition in gene expression profiling using DNA array: a comparative study of different statistical methods applied to cancer classification. <i>Human Molecular Genetics</i> , 2003, 12, 823-836.	2.9	51
97	TRAIT (TRANscript Integrated Table): a knowledgebase of human skeletal muscle transcripts. <i>Bioinformatics</i> , 2003, 19, 661-662.	4.1	4
98	Simplifying amino acid alphabets by means of a branch and bound algorithm and substitution matrices. <i>Bioinformatics</i> , 2002, 18, 1102-1108.	4.1	35
99	A two-step strategy for constructing specifically self-subtracted cDNA libraries. <i>Nucleic Acids Research</i> , 2002, 30, 38e-38.	14.5	13
100	Development and production of an oligonucleotide MuscleChip: use for validation of ambiguous ESTs. <i>BMC Bioinformatics</i> , 2002, 3, 33.	2.6	8
101	Characterization of 16 novel human genes showing high similarity to yeast sequences. <i>Yeast</i> , 2001, 18, 69-80.	1.7	25
102	Characterization of 16 novel human genes showing high similarity to yeast sequences. <i>Yeast</i> , 2001, 18, 69-80.	1.7	1
103	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 820-823.	27.8	188
104	A Comprehensive, High-Resolution Genomic Transcript Map of Human Skeletal Muscle. <i>Genome Research</i> , 1998, 8, 817-825.	5.5	69
105	Telethonin, a novel sarcomeric protein of heart and skeletal muscle. <i>FEBS Letters</i> , 1997, 415, 163-168.	2.8	171
106	Semi-Multiplex PCR Technique for Screening of Abundant Transcripts During Systematic Sequencing of cDNA Libraries. <i>BioTechniques</i> , 1996, 21, 644-649.	1.8	7
107	Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization.. <i>Genome Research</i> , 1996, 6, 35-42.	5.5	52