Gian Gaetano Tartaglia

List of Publications by Year
in descending order

129 papers	9,950 citations	43973 48 h-index	42291 92 g-index
162 all docs	162 docs citations	162 times ranked	11584 citing authors

#	Article	IF	Citations
1	ALS/FTD Mutation-Induced Phase Transition of FUS Liquid Droplets and Reversible Hydrogels into Irreversible Hydrogels Impairs RNP Granule Function. Neuron, 2015, 88, 678-690.	3.8	716
2	FUS Phase Separation Is Modulated by a Molecular Chaperone and Methylation of Arginine Cation-Ï€ Interactions. Cell, 2018, 173, 720-734.e15.	13.5	662
3	Amyloid-like Aggregates Sequester Numerous Metastable Proteins with Essential Cellular Functions. Cell, 2011, 144, 67-78.	13.5	604
4	Prediction of Aggregation-Prone Regions in Structured Proteins. Journal of Molecular Biology, 2008, 380, 425-436.	2.0	420
5	Metastability of Native Proteins and the Phenomenon of Amyloid Formation. Journal of the American Chemical Society, 2011, 133, 14160-14163.	6.6	369
6	Predicting protein associations with long noncoding RNAs. Nature Methods, 2011, 8, 444-445.	9.0	335
7	DnaK Functions as a Central Hub in the E. coli Chaperone Network. Cell Reports, 2012, 1, 251-264.	2.9	308
8	The Zyggregator method for predicting protein aggregation propensities. Chemical Society Reviews, 2008, 37, 1395.	18.7	307
9	Life on the edge: a link between gene expression levels and aggregation rates of human proteins. Trends in Biochemical Sciences, 2007, 32, 204-206.	3.7	266
10	<i>cat</i>RAPID <i>omics</i>: a web server for large-scale prediction of protein–RNA interactions. Bioinformatics, 2013, 29, 2928-2930.	1.8	247
11	Widespread Aggregation and Neurodegenerative Diseases Are Associated with Supersaturated Proteins. Cell Reports, 2013, 5, 781-790.	2.9	245
12	A Concentration-Dependent Liquid Phase Separation Can Cause Toxicity upon Increased Protein Expression. Cell Reports, 2016, 16, 222-231.	2.9	230
13	Prediction of aggregation rate and aggregation-prone segments in polypeptide sequences. Protein Science, 2005, 14, 2723-2734.	3.1	201
14	Systematic In Vivo Analysis of the Intrinsic Determinants of Amyloid Î² Pathogenicity. PLoS Biology, 2007, 5, e290.	2.6	171
15	The role of aromaticity, exposed surface, and dipole moment in determining protein aggregation rates. Protein Science, 2004, 13, 1939-1941.	3.1	162
16	Physicochemical principles that regulate the competition between functional and dysfunctional association of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10159-10164.	3.3	148
17	ALS mutations in FUS cause neuronal dysfunction and death in Caenorhabditis elegans by a dominant gain-of-function mechanism. Human Molecular Genetics, 2012, 21, 1-9.	1.4	148
18	<i>cat</i>RAPID <i>signature</i>: identification of ribonucleoproteins and RNA-binding regions. Bioinformatics, 2016, 32, 773-775.	1.8	129

#	Article	IF	Citations
19	RNA structure drives interaction with proteins. Nature Communications, 2019, 10, 3246.	5.8	123
20	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. Nature Medicine, 2021, 27, 668-676.	15.2	120
21	The mutational landscape of a prion-like domain. Nature Communications, 2019, 10, 4162.	5.8	116
22	Proteome-wide observation of the phenomenon of life on the edge of solubility. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1015-1020.	3.3	115
23	Quantitative predictions of protein interactions with long noncoding RNAs. Nature Methods, 2017, 14, 5-6.	9.0	113
24	Phase separation drives X-chromosome inactivation: a hypothesis. Nature Structural and Molecular Biology, 2019, 26, 331-334.	3.6	98
25	Amyloid Formation by the Pro-Inflammatory S100A8/A9 Proteins in the Ageing Prostate. PLoS ONE, 2009, 4, e5562.	1.1	95
26	Characterisation of Amyloid Fibril Formation by Small Heat-shock Chaperone Proteins Human α-, βB- and R120G βB-Crystallins. Journal of Molecular Biology, 2007, 372, 470-484.	2.0	93
27	Molecular determinants of the aggregation behavior of α- and β-synuclein. Protein Science, 2008, 17, 887-898.	3.1	91
28	Spinal motor neuron protein supersaturation patterns are associated with inclusion body formation in ALS. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3935-E3943.	3.3	91
29	Advances in the characterization of RNA-binding proteins. Wiley Interdisciplinary Reviews RNA, 2016, 7, 793-810.	3.2	89
30	Sequence-Based Prediction of Protein Solubility. Journal of Molecular Biology, 2012, 421, 237-241.	2.0	85
31	SAMMSON fosters cancer cell fitness by concertedly enhancing mitochondrial and cytosolic translation. Nature Structural and Molecular Biology, 2018, 25, 1035-1046.	3.6	84
32	RNAct: Protein-RNA interaction predictions for model organisms with supporting experimental data. Nucleic Acids Research, 2019, 47, D601-D606.	6.5	80
33	*cat*RAPID*omics v2.0*: going deeper and wider in the prediction of protein-RNA interactions. Nucleic Acids Research, 2021, 49, W72-W79.	6.5	79
34	*cc* SOL *omics* : a webserver for solubility prediction of endogenous and heterologous expression in *Escherichia coli*. Bioinformatics, 2014, 30, 2975-2977.	1.8	78
35	Competition between Folding, Native-State Dimerisation and Amyloid Aggregation in β-Lactoglobulin. Journal of Molecular Biology, 2009, 386, 878-890.	2.0	77
36	Protein complex scaffolding predicted as a prevalent function of long non-coding RNAs. Nucleic Acids Research, 2018, 46, 917-928.	6.5	76

#	Article	IF	Citations
37	Structural analysis of SARS-CoV-2 genome and predictions of the human interactome. Nucleic Acids Research, 2020, 48, 11270-11283.	6.5	73
38	Neurodegenerative diseases: Quantitative predictions of protein–RNA interactions. Rna, 2013, 19, 129-140.	1.6	69
39	Competition between Intramolecular and Intermolecular Interactions in an Amyloid-Forming Protein. Journal of Molecular Biology, 2009, 389, 776-786.	2.0	68
40	Insights on protein thermal stability: a graph representation of molecular interactions. Bioinformatics, 2019, 35, 2569-2577.	1.8	66
41	The H50Q Mutation Induces a 10-fold Decrease in the Solubility of α-Synuclein. Journal of Biological Chemistry, 2015, 290, 2395-2404.	1.6	65
42	RNA as a key factor in driving or preventing self-assembly of the TAR DNA-binding protein 43. Journal of Molecular Biology, 2019, 431, 1671-1688.	2.0	65
43	An Integrative Study of Protein-RNA Condensates Identifies Scaffolding RNAs and Reveals Players in Fragile X-Associated Tremor/Ataxia Syndrome. Cell Reports, 2018, 25, 3422-3434.e7.	2.9	62
44	RNA-binding and prion domains: the Yin and Yang of phase separation. Nucleic Acids Research, 2020, 48, 9491-9504.	6.5	57
45	Prediction of Local Structural Stabilities of Proteins from Their Amino Acid Sequences. Structure, 2007, 15, 139-143.	1.6	56
46	Correlation between mRNA expression levels and protein aggregation propensities in subcellular localisations. Molecular BioSystems, 2009, 5, 1873.	2.9	56
47	The Distribution of Residues in a Polypeptide Sequence Is a Determinant of Aggregation Optimized by Evolution. Biophysical Journal, 2007, 93, 4382-4391.	0.2	55
48	Similarities in the thermodynamics and kinetics of aggregation of disease-related Aβ(1-40) peptides. Protein Science, 2007, 16, 1214-1222.	3.1	55
49	A Relationship between mRNA Expression Levels and Protein Solubility in E. coli. Journal of Molecular Biology, 2009, 388, 381-389.	2.0	53
50	Disulfide Bonds Reduce the Toxicity of the Amyloid Fibrils Formed by an Extracellular Protein. Angewandte Chemie - International Edition, 2011, 50, 7048-7051.	7.2	53
51	Physicochemical Determinants of Chaperone Requirements. Journal of Molecular Biology, 2010, 400, 579-588.	2.0	52
52	Proteome-Level Interplay between Folding and Aggregation Propensities of Proteins. Journal of Molecular Biology, 2010, 402, 919-928.	2.0	52
53	Neurodegeneration as an RNA disorder. Progress in Neurobiology, 2012, 99, 293-315.	2.8	52
54	A high-throughput approach to profile RNA structure. Nucleic Acids Research, 2017, 45, e35-e35.	6.5	52

#	Article	IF	Citations
55	X-inactivation: quantitative predictions of protein interactions in the Xist network. Nucleic Acids Research, 2013, 41, e31-e31.	6.5	49
56	Effects of the Known Pathogenic Mutations on the Aggregation Pathway of the Amyloidogenic Peptide of Apolipoprotein A-I. Journal of Molecular Biology, 2011, 407, 465-476.	2.0	48
57	The cleverSuite approach for protein characterization: predictions of structural properties, solubility, chaperone requirements and RNA-binding abilities. Bioinformatics, 2014, 30, 1601-1608.	1.8	48
58	Position‐Dependent Electrostatic Protection against Protein Aggregation. ChemBioChem, 2009, 10, 1309-1312.	1.3	47
59	Intrinsic Determinants of Neurotoxic Aggregate Formation by the Amyloid β Peptide. Biophysical Journal, 2010, 98, 1677-1684.	0.2	45
60	Neuronal intranuclear (hyaline) inclusion disease and fragile X-associated tremor/ataxia syndrome: a morphological and molecular dilemma. Brain, 2017, 140, e51-e51.	3.7	43
61	Neurodegeneration and Cancer: Where the Disorder Prevails. Scientific Reports, 2015, 5, 15390.	1.6	42
62	Translationally optimal codons associate with aggregation‐prone sites in proteins. Proteomics, 2010, 10, 4163-4171.	1.3	40
63	Detection of early locomotor abnormalities in a Drosophila model of Alzheimer's disease. Journal of Neuroscience Methods, 2011, 197, 186-189.	1.3	40
64	Expression in Drosophila of Tandem Amyloid β Peptides Provides Insights into Links between Aggregation and Neurotoxicity. Journal of Biological Chemistry, 2012, 287, 20748-20754.	1.6	40
65	Principles of self-organization in biological pathways: a hypothesis on the autogenous association of alpha-synuclein. Nucleic Acids Research, 2013, 41, 9987-9998.	6.5	40
66	Organism complexity anti-correlates with proteomic β-aggregation propensity. Protein Science, 2005, 14, 2735-2740.	3.1	39
67	Design and Functional Validation of a Mutant Variant of the LncRNA <i>HOTAIR</i> to Counteract Snail Function in Epithelial-to-Mesenchymal Transition. Cancer Research, 2021, 81, 103-113.	0.4	38
68	Constitutive patterns of gene expression regulated by RNA-binding proteins. Genome Biology, 2014, 15, R13.	13.9	35
69	Non-random distribution of homo-repeats: links with biological functions and human diseases. Scientific Reports, 2016, 6, 26941.	1.6	32
70	Discovering the 3′ UTR-mediated regulation of alpha-synuclein. Nucleic Acids Research, 2017, 45, 12888-12903.	6.5	32
71	Cerebrospinal fluid levels of coenzyme Q10 are reduced in multiple system atrophy. Parkinsonism and Related Disorders, 2018, 46, 16-23.	1.1	32
72	The moonlighting RNA-binding activity of cytosolic serine hydroxymethyltransferase contributes to control compartmentalization of serine metabolism. Nucleic Acids Research, 2019, 47, 4240-4254.	6.5	32

#	Article	IF	Citations
73	ALMOST: An all atom molecular simulation toolkit for protein structure determination. Journal of Computational Chemistry, 2014, 35, 1101-1105.	1.5	31
74	HOTAIRM1 regulates neuronal differentiation by modulating NEUROGENIN 2 and the downstream neurogenic cascade. Cell Death and Disease, 2020, 11, 527.	2.7	28
75	Long nonâ€coding RNA uc.291 controls epithelial differentiation by interfering with the ACTL6A/BAF complex. EMBO Reports, 2020, 21, e46734.	2.0	28
76	Computational analysis of the S. cerevisiae proteome reveals the function and cellular localization of the least and most amyloidogenic proteins. Proteins: Structure, Function and Bioinformatics, 2007, 68, 273-278.	1.5	27
77	Cerebrospinal fluid cytokines in multiple system atrophy: A cross-sectional Catalan MSA registry study. Parkinsonism and Related Disorders, 2019, 65, 3-12.	1.1	26
78	RNA as the stone guest of protein aggregation. Nucleic Acids Research, 2020, 48, 11880-11889.	6.5	25
79	SeAMotE: a method for high-throughput motif discovery in nucleic acid sequences. BMC Genomics, 2014, 15, 925.	1.2	23
80	A Rationally Designed Six-Residue Swap Generates Comparability in the Aggregation Behavior of Î±-Synuclein and Î²-Synuclein. Biochemistry, 2012, 51, 8771-8778.	1.2	22
81	Characterization of Novel Paternal ncRNAs at the Plagl1 Locus, Including Hymai, Predicted to Interact with Regulators of Active Chromatin. PLoS ONE, 2012, 7, e38907.	1.1	21
82	Posttranscriptional regulation of colonic epithelial repair by <scp>RNA</scp> binding protein <scp>IMP</scp> 1/ <scp>IGF</scp> 2 <scp>BP</scp> 1. EMBO Reports, 2019, 20, .	2.0	21
83	Post-transcriptional regulatory patterns revealed by protein-RNA interactions. Scientific Reports, 2019, 9, 4302.	1.6	21
84	Protein Syndesmos is a novel RNA-binding protein that regulates primary cilia formation. Nucleic Acids Research, 2018, 46, 12067-12086.	6.5	20
85	Predictions of proteinâ€"RNA interactions. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2013, 3, 161-175.	6.2	19
86	Discovery of proteinâ€"RNA networks. Molecular BioSystems, 2014, 10, 1632-1642.	2.9	18
87	<i>omiXcore</i>: a web server for prediction of protein interactions with large RNA. Bioinformatics, 2017, 33, 3104-3106.	1.8	18
88	Towards quantitative predictions in cell biology using chemical properties of proteins. Molecular BioSystems, 2008, 4, 1170.	2.9	17
89	Long non-coding RNA-polycomb intimate rendezvous. Open Biology, 2020, 10, 200126.	1.5	17
90	RNAâ€protein interactions: Central players in coordination of regulatory networks. BioEssays, 2021, 43, e2000118.	1.2	17

#	Article	IF	Citations
91	Physicochemical Principles of Protein Aggregation. Progress in Molecular Biology and Translational Science, 2013, 117, 53-72.	0.9	16
92	A Method for RNA Structure Prediction Shows Evidence for Structure in lncRNAs. Frontiers in Molecular Biosciences, 2018, 5, 111.	1.6	16
93	A metastable subproteome underlies inclusion formation in muscle proteinopathies. Acta Neuropathologica Communications, 2019, 7, 197.	2.4	16
94	Phase separation drives X-chromosome inactivation. Nature Structural and Molecular Biology, 2022, 29, 183-185.	3.6	16
95	Probing TDP-43 condensation using an in silico designed aptamer. Nature Communications, 2022, 13, .	5.8	16
96	Molecular Pathophysiology of Fragile X-Associated Tremor/Ataxia Syndrome and Perspectives for Drug Development. Cerebellum, 2016, 15, 599-610.	1.4	15
97	<scp>MicroRNA</scp> Deregulation in Blood Serum Identifies Multiple System Atrophy Altered Pathways. Movement Disorders, 2020, 35, 1873-1879.	2.2	15
98	The Interplay Between Disordered Regions in RNAs and Proteins Modulates Interactions Within Stress Granules and Processing Bodies. Journal of Molecular Biology, 2022, 434, 167159.	2.0	15
99	Protein aggregation, structural disorder and RNA-binding ability: a new approach for physico-chemical and gene ontology classification of multiple datasets. BMC Genomics, 2015, 16, 1071.	1.2	14
100	<i>CROSSalive</i>: a web server for predicting the<i>in vivo</i>structure of RNA molecules. Bioinformatics, 2020, 36, 940-941.	1.8	14
101	RNA-centric approaches to study RNA-protein interactions in vitro and in silico. Methods, 2020, 178, 11-18.	1.9	14
102	Mutational Analysis of the Aggregation-Prone and Disaggregation-Prone Regions of Acylphosphatase. Journal of Molecular Biology, 2009, 387, 965-974.	2.0	12
103	Interactions in the native state of monellin, which play a protective role against aggregation. Molecular BioSystems, 2011, 7, 521-532.	2.9	12
104	By the company they keep: interaction networks define the binding ability of transcription factors. Nucleic Acids Research, 2015, 43, e125-e125.	6.5	12
105	The Grand Challenge of Characterizing Ribonucleoprotein Networks. Frontiers in Molecular Biosciences, 2016, 3, 24.	1.6	12
106	Prediction of Time Series Gene Expression and Structural Analysis of Gene Regulatory Networks Using Recurrent Neural Networks. Entropy, 2022, 24, 141.	1.1	12
107	DualSeqDB: the hostâ€"pathogen dual RNA sequencing database for infection processes. Nucleic Acids Research, 2021, 49, D687-D693.	6.5	11
108	Zooming in on proteinâ€"RNA interactions: a multi-level workflow to identify interaction partners. Biochemical Society Transactions, 2020, 48, 1529-1543.	1.6	11

#	Article	IF	Citations
109	Matrix-screening reveals a vast potential for direct protein-protein interactions among RNA binding proteins. Nucleic Acids Research, 2021, 49, 6702-6721.	6.5	10
110	BacFITBase: a database to assess the relevance of bacterial genes during host infection. Nucleic Acids Research, 2019, 48, D511-D516.	6.5	9
111	In silico, in vitro, and in vivo Approaches to Identify Molecular Players in Fragile X Tremor and Ataxia Syndrome. Frontiers in Molecular Biosciences, 2020, 7, 31.	1.6	9
112	Modelling of SHMT1 riboregulation predicts dynamic changes of serine and glycine levels across cellular compartments. Computational and Structural Biotechnology Journal, 2021, 19, 3034-3041.	1.9	9
113	Computational optimization of angiotensin-converting enzyme 2 for SARS-CoV-2 Spike molecular recognition. Computational and Structural Biotechnology Journal, 2021, 19, 3006-3014.	1.9	9
114	Aggregation is a Context-Dependent Constraint on Protein Evolution. Frontiers in Molecular Biosciences, 2021, 8, 678115.	1.6	9
115	Thermometer: a webserver to predict protein thermal stability. Bioinformatics, 2022, 38, 2060-2061.	1.8	9
116	Assembly of Proteins by Free RNA during the Early Phase of Proteostasis Stress. Journal of Proteome Research, 2019, 18, 2835-2847.	1.8	8
117	New lessons on TDPâ€43 from old <i>N.Âfurzeri</i> killifish. Aging Cell, 2022, 21, e13517.	3.0	7
118	iASiS: Towards Heterogeneous Big Data Analysis for Personalized Medicine. , 2019, , .		6
119	Determination of primary microRNA processing in clinical samples by targeted pri-miR-sequencing. Rna, 2020, 26, 1726-1730.	1.6	5
120	A Computational Approach to Investigate TDP-43 RNA-Recognition Motif 2 C-Terminal Fragments Aggregation in Amyotrophic Lateral Sclerosis. Biomolecules, 2021, 11, 1905.	1.8	5
121	The seesaw between normal function and protein aggregation: How functional interactions may increase protein solubility. BioEssays, 2021, 43, 2100031.	1.2	4
122	A Computational Approach for the Discovery of Proteinâ€"RNA Networks. Methods in Molecular Biology, 2016, 1358, 29-39.	0.4	3
123	Interactive Extreme-Scale Analytics: Towards Battling Cancer. IEEE Technology and Society Magazine, 2019, 38, 54-61.	0.6	3
124	Machine learning methods applied to genotyping data capture interactions between single nucleotide variants in late onset Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2022, 14, e12300.	1.2	3
125	Phase Separation Drives SARS-CoV-2 Replication: A Hypothesis. Frontiers in Molecular Biosciences, 2022, 9, .	1.6	3
126	Proteome Metastability in Health, Aging, and Disease. Biophysical Journal, 2014, 106, 59a.	0.2	2

#	ARTICLE	IF	CITATIONS
127	The quest for long non-coding RNAs involved in aging. Nature Aging, 2021, 1, 418-419.	5.3	1
128	Homage to Chris Dobson. Frontiers in Molecular Biosciences, 2019, 6, 137.	1.6	0
129	Predicting RNA Secondary Using In Vitro and In Vivo Data. Methods in Molecular Biology, 2022, 2404, 43-52.	0.4	0