

Gian Gaetano Tartaglia

List of Publications by Citations

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130
papers

7,127
citations

44
h-index

83
g-index

162
ext. papers

8,777
ext. citations

10.3
avg, IF

5.94
L-index

#	Paper	IF	Citations
130	Amyloid-like aggregates sequester numerous metastable proteins with essential cellular functions. <i>Cell</i> , 2011 , 144, 67-78	56.2	520
129	ALS/FTD Mutation-Induced Phase Transition of FUS Liquid Droplets and Reversible Hydrogels into Irreversible Hydrogels Impairs RNP Granule Function. <i>Neuron</i> , 2015 , 88, 678-90	13.9	503
128	FUS Phase Separation Is Modulated by a Molecular Chaperone and Methylation of Arginine Cation- π Interactions. <i>Cell</i> , 2018 , 173, 720-734.e15	56.2	409
127	Prediction of aggregation-prone regions in structured proteins. <i>Journal of Molecular Biology</i> , 2008 , 380, 425-36	6.5	377
126	Metastability of native proteins and the phenomenon of amyloid formation. <i>Journal of the American Chemical Society</i> , 2011 , 133, 14160-3	16.4	305
125	The Zyggregator method for predicting protein aggregation propensities. <i>Chemical Society Reviews</i> , 2008 , 37, 1395-401	58.5	258
124	Predicting protein associations with long noncoding RNAs. <i>Nature Methods</i> , 2011 , 8, 444-5	21.6	235
123	DnaK functions as a central hub in the E. coli chaperone network. <i>Cell Reports</i> , 2012 , 1, 251-64	10.6	233
122	Life on the edge: a link between gene expression levels and aggregation rates of human proteins. <i>Trends in Biochemical Sciences</i> , 2007 , 32, 204-6	10.3	215
121	Widespread aggregation and neurodegenerative diseases are associated with supersaturated proteins. <i>Cell Reports</i> , 2013 , 5, 781-90	10.6	182
120	Prediction of aggregation rate and aggregation-prone segments in polypeptide sequences. <i>Protein Science</i> , 2005 , 14, 2723-34	6.3	181
119	catRAPID omics: a web server for large-scale prediction of protein-RNA interactions. <i>Bioinformatics</i> , 2013 , 29, 2928-30	7.2	173
118	Systematic in vivo analysis of the intrinsic determinants of amyloid Beta pathogenicity. <i>PLoS Biology</i> , 2007 , 5, e290	9.7	152
117	The role of aromaticity, exposed surface, and dipole moment in determining protein aggregation rates. <i>Protein Science</i> , 2004 , 13, 1939-41	6.3	145
116	Physicochemical principles that regulate the competition between functional and dysfunctional association of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 10159-64	11.5	125
115	A Concentration-Dependent Liquid Phase Separation Can Cause Toxicity upon Increased Protein Expression. <i>Cell Reports</i> , 2016 , 16, 222-231	10.6	122
114	ALS mutations in FUS cause neuronal dysfunction and death in <i>Caenorhabditis elegans</i> by a dominant gain-of-function mechanism. <i>Human Molecular Genetics</i> , 2012 , 21, 1-9	5.6	121

113	Characterisation of amyloid fibril formation by small heat-shock chaperone proteins human alphaA-, alphaB- and R120G alphaB-crystallins. <i>Journal of Molecular Biology</i> , 2007 , 372, 470-84	6.5	85
112	Molecular determinants of the aggregation behavior of alpha- and beta-synuclein. <i>Protein Science</i> , 2008 , 17, 887-98	6.3	84
111	Amyloid formation by the pro-inflammatory S100A8/A9 proteins in the ageing prostate. <i>PLoS ONE</i> , 2009 , 4, e5562	3.7	83
110	Quantitative predictions of protein interactions with long noncoding RNAs. <i>Nature Methods</i> , 2016 , 14, 5-6	21.6	80
109	Spinal motor neuron protein supersaturation patterns are associated with inclusion body formation in ALS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E3935-E3943	11.5	72
108	Sequence-based prediction of protein solubility. <i>Journal of Molecular Biology</i> , 2012 , 421, 237-41	6.5	71
107	Phase separation drives X-chromosome inactivation: a hypothesis. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 331-334	17.6	66
106	Advances in the characterization of RNA-binding proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016 , 7, 793-810	9.3	66
105	The mutational landscape of a prion-like domain. <i>Nature Communications</i> , 2019 , 10, 4162	17.4	65
104	Competition between folding, native-state dimerisation and amyloid aggregation in beta-lactoglobulin. <i>Journal of Molecular Biology</i> , 2009 , 386, 878-90	6.5	65
103	Competition between intramolecular and intermolecular interactions in an amyloid-forming protein. <i>Journal of Molecular Biology</i> , 2009 , 389, 776-86	6.5	62
102	SAMMSON fosters cancer cell fitness by concertedly enhancing mitochondrial and cytosolic translation. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 1035-1046	17.6	57
101	catRAPID signature: identification of ribonucleoproteins and RNA-binding regions. <i>Bioinformatics</i> , 2016 , 32, 773-5	7.2	55
100	RNA structure drives interaction with proteins. <i>Nature Communications</i> , 2019 , 10, 3246	17.4	55
99	Proteome-wide observation of the phenomenon of life on the edge of solubility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 1015-1020	11.5	52
98	Protein complex scaffolding predicted as a prevalent function of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2018 , 46, 917-928	20.1	51
97	The H50Q mutation induces a 10-fold decrease in the solubility of β -synuclein. <i>Journal of Biological Chemistry</i> , 2015 , 290, 2395-404	5.4	51
96	Neurodegenerative diseases: quantitative predictions of protein-RNA interactions. <i>Rna</i> , 2013 , 19, 129-40	5.8	50

95	The distribution of residues in a polypeptide sequence is a determinant of aggregation optimized by evolution. <i>Biophysical Journal</i> , 2007 , 93, 4382-91	2.9	50
94	A relationship between mRNA expression levels and protein solubility in <i>E. coli</i> . <i>Journal of Molecular Biology</i> , 2009 , 388, 381-9	6.5	49
93	Correlation between mRNA expression levels and protein aggregation propensities in subcellular localisations. <i>Molecular BioSystems</i> , 2009 , 5, 1873-6		49
92	Prediction of local structural stabilities of proteins from their amino acid sequences. <i>Structure</i> , 2007 , 15, 139-43	5.2	49
91	Similarities in the thermodynamics and kinetics of aggregation of disease-related Abeta(1-40) peptides. <i>Protein Science</i> , 2007 , 16, 1214-22	6.3	49
90	ccSOL omics: a webserver for solubility prediction of endogenous and heterologous expression in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2014 , 30, 2975-7	7.2	48
89	Disulfide bonds reduce the toxicity of the amyloid fibrils formed by an extracellular protein. <i>Angewandte Chemie - International Edition</i> , 2011 , 50, 7048-51	16.4	48
88	Proteome-level interplay between folding and aggregation propensities of proteins. <i>Journal of Molecular Biology</i> , 2010 , 402, 919-28	6.5	45
87	Neurodegeneration as an RNA disorder. <i>Progress in Neurobiology</i> , 2012 , 99, 293-315	10.9	44
86	Intrinsic determinants of neurotoxic aggregate formation by the amyloid beta peptide. <i>Biophysical Journal</i> , 2010 , 98, 1677-84	2.9	44
85	Position-dependent electrostatic protection against protein aggregation. <i>ChemBioChem</i> , 2009 , 10, 1309-12	3.8	43
84	Effects of the known pathogenic mutations on the aggregation pathway of the amyloidogenic peptide of apolipoprotein A-I. <i>Journal of Molecular Biology</i> , 2011 , 407, 465-76	6.5	42
83	An Integrative Study of Protein-RNA Condensates Identifies Scaffolding RNAs and Reveals Players in Fragile X-Associated Tremor/Ataxia Syndrome. <i>Cell Reports</i> , 2018 , 25, 3422-3434.e7	10.6	42
82	Physicochemical determinants of chaperone requirements. <i>Journal of Molecular Biology</i> , 2010 , 400, 579-88	8.5	39
81	RNA as a key factor in driving or preventing self-assembly of the TAR DNA-binding protein 43. <i>Journal of Molecular Biology</i> , 2019 , 431, 1671-1688	6.5	37
80	Translationally optimal codons associate with aggregation-prone sites in proteins. <i>Proteomics</i> , 2010 , 10, 4163-71	4.8	36
79	Structural analysis of SARS-CoV-2 genome and predictions of the human interactome. <i>Nucleic Acids Research</i> , 2020 , 48, 11270-11283	20.1	36
78	Expression in <i>Drosophila</i> of tandem amyloid peptides provides insights into links between aggregation and neurotoxicity. <i>Journal of Biological Chemistry</i> , 2012 , 287, 20748-54	5.4	34

77	Organism complexity anti-correlates with proteomic beta-aggregation propensity. <i>Protein Science</i> , 2005 , 14, 2735-40	6.3	34
76	X-inactivation: quantitative predictions of protein interactions in the Xist network. <i>Nucleic Acids Research</i> , 2013 , 41, e31	20.1	33
75	Principles of self-organization in biological pathways: a hypothesis on the autogenous association of alpha-synuclein. <i>Nucleic Acids Research</i> , 2013 , 41, 9987-98	20.1	32
74	Constitutive patterns of gene expression regulated by RNA-binding proteins. <i>Genome Biology</i> , 2014 , 15, R13	18.3	31
73	The cleverSuite approach for protein characterization: predictions of structural properties, solubility, chaperone requirements and RNA-binding abilities. <i>Bioinformatics</i> , 2014 , 30, 1601-8	7.2	31
72	Neurodegeneration and Cancer: Where the Disorder Prevails. <i>Scientific Reports</i> , 2015 , 5, 15390	4.9	30
71	Detection of early locomotor abnormalities in a Drosophila model of Alzheimer's disease. <i>Journal of Neuroscience Methods</i> , 2011 , 197, 186-9	3	29
70	ALMOST: an all atom molecular simulation toolkit for protein structure determination. <i>Journal of Computational Chemistry</i> , 2014 , 35, 1101-5	3.5	28
69	Neuronal intranuclear (hyaline) inclusion disease and fragile X-associated tremor/ataxia syndrome: a morphological and molecular dilemma. <i>Brain</i> , 2017 , 140, e51	11.2	27
68	RNAct: Protein-RNA interaction predictions for model organisms with supporting experimental data. <i>Nucleic Acids Research</i> , 2019 , 47, D601-D606	20.1	27
67	A high-throughput approach to profile RNA structure. <i>Nucleic Acids Research</i> , 2017 , 45, e35	20.1	26
66	Insights on protein thermal stability: a graph representation of molecular interactions. <i>Bioinformatics</i> , 2019 , 35, 2569-2577	7.2	26
65	Discovering the 3'UTR-mediated regulation of alpha-synuclein. <i>Nucleic Acids Research</i> , 2017 , 45, 12888-12903	20.1	23
64	Characterization of novel paternal ncRNAs at the Plagl1 locus, including Hymai, predicted to interact with regulators of active chromatin. <i>PLoS ONE</i> , 2012 , 7, e38907	3.7	21
63	RNA-binding and prion domains: the Yin and Yang of phase separation. <i>Nucleic Acids Research</i> , 2020 , 48, 9491-9504	20.1	21
62	SeAMotE: a method for high-throughput motif discovery in nucleic acid sequences. <i>BMC Genomics</i> , 2014 , 15, 925	4.5	20
61	A rationally designed six-residue swap generates comparability in the aggregation behavior of Eynuclein and Eynuclein. <i>Biochemistry</i> , 2012 , 51, 8771-8	3.2	20
60	Computational analysis of the S. cerevisiae proteome reveals the function and cellular localization of the least and most amyloidogenic proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 273-8	4.2	20

59	Non-random distribution of homo-repeats: links with biological functions and human diseases. <i>Scientific Reports</i> , 2016 , 6, 26941	4.9	20
58	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. <i>Nature Medicine</i> , 2021 , 27, 668-676	50.5	19
57	Design and Functional Validation of a Mutant Variant of the LncRNA to Counteract Snail Function in Epithelial-to-Mesenchymal Transition. <i>Cancer Research</i> , 2021 , 81, 103-113	10.1	18
56	Discovery of protein-RNA networks. <i>Molecular BioSystems</i> , 2014 , 10, 1632-42		16
55	omiXcore: a web server for prediction of protein interactions with large RNA. <i>Bioinformatics</i> , 2017 , 33, 3104-3106	7.2	15
54	Predictions of protein-RNA interactions. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2013 , 3, 161-175	7.9	15
53	Cerebrospinal fluid levels of coenzyme Q10 are reduced in multiple system atrophy. <i>Parkinsonism and Related Disorders</i> , 2018 , 46, 16-23	3.6	15
52	Post-transcriptional regulatory patterns revealed by protein-RNA interactions. <i>Scientific Reports</i> , 2019 , 9, 4302	4.9	14
51	Towards quantitative predictions in cell biology using chemical properties of proteins. <i>Molecular BioSystems</i> , 2008 , 4, 1170-5		14
50	Cerebrospinal fluid cytokines in multiple system atrophy: A cross-sectional Catalan MSA registry study. <i>Parkinsonism and Related Disorders</i> , 2019 , 65, 3-12	3.6	12
49	The moonlighting RNA-binding activity of cytosolic serine hydroxymethyltransferase contributes to control compartmentalization of serine metabolism. <i>Nucleic Acids Research</i> , 2019 , 47, 4240-4254	20.1	12
48	Molecular Pathophysiology of Fragile X-Associated Tremor/Ataxia Syndrome and Perspectives for Drug Development. <i>Cerebellum</i> , 2016 , 15, 599-610	4.3	12
47	Protein aggregation, structural disorder and RNA-binding ability: a new approach for physico-chemical and gene ontology classification of multiple datasets. <i>BMC Genomics</i> , 2015 , 16, 1071	4.5	12
46	Physicochemical principles of protein aggregation. <i>Progress in Molecular Biology and Translational Science</i> , 2013 , 117, 53-72	4	12
45	HOTAIRM1 regulates neuronal differentiation by modulating NEUROGENIN 2 and the downstream neurogenic cascade. <i>Cell Death and Disease</i> , 2020 , 11, 527	9.8	12
44	A Method for RNA Structure Prediction Shows Evidence for Structure in lncRNAs. <i>Frontiers in Molecular Biosciences</i> , 2018 , 5, 111	5.6	12
43	Protein Syndesmos is a novel RNA-binding protein that regulates primary cilia formation. <i>Nucleic Acids Research</i> , 2018 , 46, 12067-12086	20.1	12
42	Long non-coding RNA uc.291 controls epithelial differentiation by interfering with the ACTL6A/BAF complex. <i>EMBO Reports</i> , 2020 , 21, e46734	6.5	11

41	Interactions in the native state of monellin, which play a protective role against aggregation. <i>Molecular BioSystems</i> , 2011 , 7, 521-32		11
40	Long non-coding RNA-polycomb intimate rendezvous. <i>Open Biology</i> , 2020 , 10, 200126	7	11
39	The Grand Challenge of Characterizing Ribonucleoprotein Networks. <i>Frontiers in Molecular Biosciences</i> , 2016 , 3, 24	5.6	11
38	By the company they keep: interaction networks define the binding ability of transcription factors. <i>Nucleic Acids Research</i> , 2015 , 43, e125	20.1	10
37	RNA as the stone guest of protein aggregation. <i>Nucleic Acids Research</i> , 2020 , 48, 11880-11889	20.1	10
36	A metastable subproteome underlies inclusion formation in muscle proteinopathies. <i>Acta Neuropathologica Communications</i> , 2019 , 7, 197	7.3	10
35	RNA-centric approaches to study RNA-protein interactions in vitro and in silico. <i>Methods</i> , 2020 , 178, 11-18.6	18.6	10
34	Structural analysis of SARS-CoV-2 genome and predictions of the human interactome		9
33	catRAPID omics v2.0: going deeper and wider in the prediction of protein-RNA interactions. <i>Nucleic Acids Research</i> , 2021 , 49, W72-W79	20.1	9
32	Posttranscriptional regulation of colonic epithelial repair by RNA binding protein IMP1/IGF2BP1. <i>EMBO Reports</i> , 2019 , 20,	6.5	8
31	Mutational analysis of the aggregation-prone and disaggregation-prone regions of acylphosphatase. <i>Journal of Molecular Biology</i> , 2009 , 387, 965-74	6.5	8
30	, and Approaches to Identify Molecular Players in Fragile X Tremor and Ataxia Syndrome. <i>Frontiers in Molecular Biosciences</i> , 2020 , 7, 31	5.6	6
29	MicroRNA Deregulation in Blood Serum Identifies Multiple System Atrophy Altered Pathways. <i>Movement Disorders</i> , 2020 , 35, 1873-1879	7	6
28	Assembly of Proteins by Free RNA during the Early Phase of Proteostasis Stress. <i>Journal of Proteome Research</i> , 2019 , 18, 2835-2847	5.6	5
27	BacFITBase: a database to assess the relevance of bacterial genes during host infection. <i>Nucleic Acids Research</i> , 2020 , 48, D511-D516	20.1	5
26	RNA-protein interactions: Central players in coordination of regulatory networks. <i>BioEssays</i> , 2021 , 43, e2000118	4.1	5
25	CROSSalive: a web server for predicting the in vivo structure of RNA molecules. <i>Bioinformatics</i> , 2020 , 36, 940-941	7.2	4
24	The seesaw between normal function and protein aggregation: How functional interactions may increase protein solubility. <i>BioEssays</i> , 2021 , 43, e2100031	4.1	4

23	The Interplay Between Disordered Regions in RNAs and Proteins Modulates Interactions Within Stress Granules and Processing Bodies. <i>Journal of Molecular Biology</i> , 2021 , 167159	6.5	4
22	iASiS: Towards Heterogeneous Big Data Analysis for Personalized Medicine 2019 ,		3
21	A Computational Approach for the Discovery of Protein-RNA Networks. <i>Methods in Molecular Biology</i> , 2016 , 1358, 29-39	1.4	3
20	Zooming in on protein-RNA interactions: a multi-level workflow to identify interaction partners. <i>Biochemical Society Transactions</i> , 2020 , 48, 1529-1543	5.1	3
19	DualSeqDB: the host-pathogen dual RNA sequencing database for infection processes. <i>Nucleic Acids Research</i> , 2021 , 49, D687-D693	20.1	3
18	Xist lncRNA forms silencing granules that induce heterochromatin formation and repressive complexes recruitment by phase separation		2
17	Determination of primary microRNA processing in clinical samples by targeted pri-miR-sequencing. <i>Rna</i> , 2020 , 26, 1726-1730	5.8	2
16	Matrix-screening reveals a vast potential for direct protein-protein interactions among RNA binding proteins. <i>Nucleic Acids Research</i> , 2021 , 49, 6702-6721	20.1	2
15	Interactive Extreme-Scale Analytics: Towards Battling Cancer. <i>IEEE Technology and Society Magazine</i> , 2019 , 38, 54-61	0.8	1
14	Thermometer: a webserver to predict protein thermal stability.. <i>Bioinformatics</i> , 2022 ,	7.2	1
13	An integrative study on ribonucleoprotein condensates identifies scaffolding RNAs and reveals a new player in Fragile X-associated Tremor/Ataxia Syndrome		1
12	RNA-Binding and Prion Domains: The Yin and Yang of Phase Separation		1
11	rec-Y2H matrix screening reveals a vast potential for direct protein-protein interactions among RNA binding proteins		1
10	The mutational landscape of a prion-like domain		1
9	Aggregation is a Context-Dependent Constraint on Protein Evolution. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 678115	5.6	1
8	Modelling of SHMT1 riboregulation predicts dynamic changes of serine and glycine levels across cellular compartments. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 3034-3041	6.8	1
7	Computational optimization of angiotensin-converting enzyme 2 for SARS-CoV-2 Spike molecular recognition. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 3006-3014	6.8	1
6	Phase separation drives X-chromosome inactivation.. <i>Nature Structural and Molecular Biology</i> , 2022 , 29, 183-185	17.6	1

- 5 New lessons on TDP-43 from old N. furzeri killifish.. *Aging Cell*, **2021**, e13517 9.9 1
- 4 Sequence-Based Prediction of Protein Behavior **2013**, 167-182
- 3 Predicting RNA Secondary Structure Using In Vitro and In Vivo Data. *Methods in Molecular Biology*, **2022**, 2404, 43-52 1.4
- 2 Homage to Chris Dobson. *Frontiers in Molecular Biosciences*, **2019**, 6, 137 5.6
- 1 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 5.2