

Vince Grolmusz

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

97
papers

918
citations

17
h-index

24
g-index

103
ext. papers

1,133
ext. citations

2.6
avg, IF

4.91
L-index

#	Paper	IF	Citations
97	AmphoraNet: the webserver implementation of the AMPHORA2 metagenomic workflow suite. <i>Gene</i> , 2014 , 533, 538-40	3.8	61
96	Superpolynomial Size Set-systems with Restricted Intersections mod 6 and Explicit Ramsey Graphs. <i>Combinatorica</i> , 2000 , 20, 71-86	0.9	60
95	When the Web meets the cell: using personalized PageRank for analyzing protein interaction networks. <i>Bioinformatics</i> , 2011 , 27, 405-7	7.2	56
94	Parameterizable consensus connectomes from the Human Connectome Project: the Budapest Reference Connectome Server v3.0. <i>Cognitive Neurodynamics</i> , 2017 , 11, 113-116	4.2	31
93	The Bns Lower-Bound for Multiparty Protocols Is Nearly Optimal. <i>Information and Computation</i> , 1994 , 112, 51-54	0.8	31
92	Graph Theoretical Analysis Reveals: Women's Brains Are Better Connected than Men's. <i>PLoS ONE</i> , 2015 , 10, e0130045	3.7	28
91	Enhanced cellular uptake of a new, in silico identified antitubercular candidate by peptide conjugation. <i>Bioconjugate Chemistry</i> , 2012 , 23, 900-7	6.3	24
90	Equal opportunity for low-degree network nodes: a PageRank-based method for protein target identification in metabolic graphs. <i>PLoS ONE</i> , 2013 , 8, e54204	3.7	24
89	Antimycobacterial activity of peptide conjugate of pyridopyrimidine derivative against <i>Mycobacterium tuberculosis</i> in a series of in vitro and in vivo models. <i>Tuberculosis</i> , 2015 , 95 Suppl 1, S207-11	2.6	23
88	The Budapest Reference Connectome Server v2.0. <i>Neuroscience Letters</i> , 2015 , 595, 60-2	3.3	23
87	Near perfect protein multi-label classification with deep neural networks. <i>Methods</i> , 2018 , 132, 50-56	4.6	22
86	How to Direct the Edges of the Connectomes: Dynamics of the Consensus Connectomes and the Development of the Connections in the Human Brain. <i>PLoS ONE</i> , 2016 , 11, e0158680	3.7	22
85	The braingraph.org database of high resolution structural connectomes and the brain graph tools. <i>Cognitive Neurodynamics</i> , 2017 , 11, 483-486	4.2	21
84	The "Giant Virus Finder" discovers an abundance of giant viruses in the Antarctic dry valleys. <i>Archives of Virology</i> , 2017 , 162, 1671-1676	2.6	20
83	A note on the PageRank of undirected graphs. <i>Information Processing Letters</i> , 2015 , 115, 633-634	0.8	20
82	On k-wise set-intersections and k-wise Hamming-distances. <i>Journal of Combinatorial Theory - Series A</i> , 2002 , 99, 180-190	1	20
81	1987 ,		18

80	Constructing set systems with prescribed intersection sizes. <i>Journal of Algorithms</i> , 2002 , 44, 321-337		17
79	Comparative connectomics: Mapping the inter-individual variability of connections within the regions of the human brain. <i>Neuroscience Letters</i> , 2018 , 662, 17-21	3.3	16
78	SECLAF: a webserver and deep neural network design tool for hierarchical biological sequence classification. <i>Bioinformatics</i> , 2018 , 34, 2487-2489	7.2	15
77	Four spatial points that define enzyme families. <i>Biochemical and Biophysical Research Communications</i> , 2009 , 383, 417-20	3.4	15
76	High-resolution directed human connectomes and the Consensus Connectome Dynamics. <i>PLoS ONE</i> , 2019 , 14, e0215473	3.7	14
75	Circuits and multi-party protocols. <i>Computational Complexity</i> , 1998 , 7, 1-18	0.6	14
74	Lower Bounds for (MODp - MODm) Circuits. <i>SIAM Journal on Computing</i> , 2000 , 29, 1209-1222	1.1	14
73	Life without dUTPase. <i>Frontiers in Microbiology</i> , 2016 , 7, 1768	5.7	14
72	The Robustness and the Doubly-Preferential Attachment Simulation of the Consensus Connectome Dynamics of the Human Brain. <i>Scientific Reports</i> , 2017 , 7, 16118	4.9	12
71	The dorsal striatum and the dynamics of the consensus connectomes in the frontal lobe of the human brain. <i>Neuroscience Letters</i> , 2018 , 673, 51-55	3.3	12
70	A weight-size trade-off for circuits with MOD m gates 1994 ,		12
69	High throughput processing of the structural information in the protein data bank. <i>Journal of Molecular Graphics and Modelling</i> , 2007 , 25, 831-6	2.8	11
68	Brain size bias compensated graph-theoretical parameters are also better in women's structural connectomes. <i>Brain Imaging and Behavior</i> , 2018 , 12, 663-673	4.1	10
67	Mapping correlations of psychological and structural connectome properties of the dataset of the human connectome project with the maximum spanning tree method. <i>Brain Imaging and Behavior</i> , 2019 , 13, 1185-1192	4.1	10
66	On dimension reduction of clustering results in structural bioinformatics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 2277-83	4	10
65	Identifying combinatorial biomarkers by association rule mining in the CAMD Alzheimer's database. <i>Archives of Gerontology and Geriatrics</i> , 2017 , 73, 300-307	4	10
64	Discovery of novel MDR-Mycobacterium tuberculosis inhibitor by new FRIGATE computational screen. <i>PLoS ONE</i> , 2011 , 6, e28428	3.7	10
63	Low Rank Co-Diagonal Matrices and Ramsey Graphs. <i>Electronic Journal of Combinatorics</i> , 2000 , 7,	1.1	10

62	The frequent subgraphs of the connectome of the human brain. <i>Cognitive Neurodynamics</i> , 2019 , 13, 453-460	4.6	9
61	A hybrid clustering of protein binding sites. <i>FEBS Journal</i> , 2010 , 277, 1494-502	5.7	9
60	On the power of circuits with gates of low L1 norms. <i>Theoretical Computer Science</i> , 1997 , 188, 117-128	1.1	9
59	Building a structured PDB: the RS-PDB database. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2006 , 2006, 5755-8		9
58	3-d brownian motion simulator for high-sensitivity nanobiotechnological applications. <i>IEEE Transactions on Nanobioscience</i> , 2011 , 10, 248-9	3.4	8
57	Visual analysis of the quantitative composition of metagenomic communities: the AmphoraVizu webserver. <i>Microbial Ecology</i> , 2015 , 69, 695-7	4.4	7
56	Giant viruses of the Kutch Desert. <i>Archives of Virology</i> , 2016 , 161, 721-4	2.6	7
55	Computing Elementary Symmetric Polynomials with a Subpolynomial Number of Multiplications. <i>SIAM Journal on Computing</i> , 2003 , 32, 1475-1487	1.1	7
54	Incomparability in parallel computation. <i>Discrete Applied Mathematics</i> , 1990 , 29, 63-78	1	7
53	The Frequent Network Neighborhood Mapping of the human hippocampus shows much more frequent neighbor sets in males than in females. <i>PLoS ONE</i> , 2020 , 15, e0227910	3.7	6
52	Comparing advanced graph-theoretical parameters of the connectomes of the lobes of the human brain. <i>Cognitive Neurodynamics</i> , 2018 , 12, 549-559	4.2	6
51	PDB_Amyloid: an extended live amyloid structure list from the PDB. <i>FEBS Open Bio</i> , 2019 , 9, 185-190	2.7	5
50	Evaluating the Quantitative Capabilities of Metagenomic Analysis Software. <i>Current Microbiology</i> , 2016 , 72, 612-6	2.4	5
49	Identifying diabetes-related important protein targets with few interacting partners with the PageRank algorithm. <i>Royal Society Open Science</i> , 2015 , 2, 140252	3.3	5
48	Analyzing the simplicial decomposition of spatial protein structures. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 1, S11	3.6	5
47	Set-Systems with Restricted Multiple Intersections. <i>Electronic Journal of Combinatorics</i> , 2002 , 9,	1.1	5
46	Being a binding site: characterizing residue composition of binding sites on proteins. <i>Bioinformatics</i> , 2007 , 2, 216-21	1.1	5
45	The frequent complete subgraphs in the human connectome. <i>PLoS ONE</i> , 2020 , 15, e0236883	3.7	5

44	Fast and exact sequence alignment with the Smith-Waterman algorithm: The SwissAlign webserver. <i>Gene Reports</i> , 2016 , 4, 26-28	1.4	4
43	MetaHMM: A webserver for identifying novel genes with specified functions in metagenomic samples. <i>Genomics</i> , 2019 , 111, 883-885	4.3	4
42	The metagenomic telescope. <i>PLoS ONE</i> , 2014 , 9, e101605	3.7	4
41	A lower bound for depth-3 circuits with MOD m gates. <i>Information Processing Letters</i> , 1998 , 67, 87-90	0.8	4
40	A Note on Non-Deterministic Communication Complexity with Few Witnesses. <i>Theory of Computing Systems</i> , 2003 , 36, 387-391	0.6	4
39	Harmonic Analysis, Real Approximation, and the Communication Complexity of Boolean Functions. <i>Algorithmica</i> , 1999 , 23, 341-353	0.9	4
38	On set systems with restricted intersections modulo a composite number. <i>Lecture Notes in Computer Science</i> , 1997 , 82-90	0.9	3
37	. <i>Chicago Journal of Theoretical Computer Science</i> , 1995 , 1, 1-8	1	3
36	Good neighbors, bad neighbors: the frequent network neighborhood mapping of the hippocampus enlightens several structural factors of the human intelligence on a 414-subject cohort. <i>Scientific Reports</i> , 2020 , 10, 11967	4.9	3
35	The Budapest Amyloid Predictor and Its Applications. <i>Biomolecules</i> , 2021 , 11,	5.9	3
34	The Graph of Our Mind. <i>Brain Sciences</i> , 2021 , 11,	3.4	3
33	How to Find Non Hub Important Nodes in Protein Networks?. <i>Biophysical Journal</i> , 2012 , 102, 184a	2.9	2
32	Cysteine and tryptophan anomalies found when scanning all the binding sites in the Protein Data Bank. <i>International Journal of Bioinformatics Research and Applications</i> , 2010 , 6, 594	0.9	2
31	Modular Representations of Polynomials: Hyperdense Coding and Fast Matrix Multiplication. <i>IEEE Transactions on Information Theory</i> , 2008 , 54, 3687-3692	2.8	2
30	Evaluating Genetic Algorithms in Protein-Ligand Docking 2008 , 402-413		2
29	On a ramsey-theoretic property of orders. <i>Journal of Combinatorial Theory - Series A</i> , 1992 , 61, 243-251	1	2
28	Characterizing the functional similarity of enzymes with high co-citation in interaction networks. <i>Protein and Peptide Letters</i> , 2013 , 20, 1181-7	1.9	2
27	NASCENT: an automatic protein interaction network generation tool for non-model organisms. <i>Bioinformatics</i> , 2009 , 3, 361-3	1.1	2

26	DECOMP: a PDB decomposition tool on the web. <i>Bioinformation</i> , 2009 , 3, 413-4	1.1	2
25	The braingraph.org database with more than 1000 robust human connectomes in five resolutions. <i>Cognitive Neurodynamics</i> , 2021 , 15, 915-919	4.2	2
24	Cysteine and tryptophan anomalies found when scanning all the binding sites in the Protein Data Bank. <i>International Journal of Bioinformatics Research and Applications</i> , 2010 , 6, 594-608	0.9	2
23	Nucleotide 9-mers characterize the type II diabetic gut metagenome. <i>Genomics</i> , 2016 , 107, 120-3	4.3	1
22	An intuitive graphical webserver for multiple-choice protein sequence search. <i>Gene</i> , 2014 , 539, 152-3	3.8	1
21	The Erdős webgraph server. <i>Discrete Applied Mathematics</i> , 2014 , 167, 315-317	1	1
20	On the asymmetry of the residue compositions of the binding sites on protein surfaces. <i>Journal of Bioinformatics and Computational Biology</i> , 2009 , 7, 931-8	1	1
19	Pairs of codes with prescribed Hamming distances and coincidences. <i>Designs, Codes, and Cryptography</i> , 2006 , 41, 87-99	1.2	1
18	Secure routerless routing 2004 ,		1
17	A degree-decreasing Lemma for (MOD q, MOD p) circuits. <i>Lecture Notes in Computer Science</i> , 1998 , 215-228		1
16	The Frequent Complete Subgraphs in the Human Connectome. <i>Lecture Notes in Computer Science</i> , 2019 , 908-920	0.9	1
15	Identifying super-feminine, super-masculine and sex-defining connections in the human braingraph. <i>Cognitive Neurodynamics</i> , 2021 , 15, 949-959	4.2	1
14	Harmonic analysis, real approximation, and the communication complexity of Boolean functions. <i>Lecture Notes in Computer Science</i> , 1996 , 142-151	0.9	1
13	Significant differences found in short nucleotide sequences of human intestinal metagenomes of Northern-European and Chinese Origin. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 3627-3631 ⁰		
12	The multiple alignments of very short sequences. <i>FASEB BioAdvances</i> , 2021 , 3, 523-530	2.8	0
11	Mathematical modelling and computer simulation of Brownian motion and hybridisation of nanoparticle-probe-polymer complexes in the low concentration limit. <i>Molecular Simulation</i> , 2012 , 38, 66-71	2	
10	THE RAMACHANDRAN MAP OF MORE THAN 6,500 PERFECT POLYPEPTIDE CHAINS. <i>Biophysical Reviews and Letters</i> , 2007 , 02, 267-271	1.2	
9	Co-Orthogonal Codes. <i>Designs, Codes, and Cryptography</i> , 2006 , 38, 363-372	1.2	

- 8 A Note on Explicit Ramsey Graphs and Modular Sieves. *Combinatorics Probability and Computing*, **2003**, 12, 565-569 0.6
- 7 Generalized Secure Routerless Routing. *Lecture Notes in Computer Science*, **2005**, 454-462 0.9
- 6 Constructive Upper Bounds for Intersecting Set Systems. *Electronic Notes in Discrete Mathematics*, **2001**, 7, 54-57 0.3
- 5 Large parallel machines can be extremely slow for small problems. *Algorithmica*, **1991**, 6, 479-489 0.9
- 4 Co-orthogonal Codes. *Lecture Notes in Computer Science*, **2002**, 144-152 0.9
- 3 Amyloids and pre-amyloids from the PDB. *FASEB Journal*, **2018**, 32, lb111 0.9
- 2 On the Bond Graphs in the Delaunay-Tetrahedra of the Simplicial Decomposition of Spatial Protein Structures. *Lecture Notes in Computer Science*, **2009**, 1162-1169 0.9
- 1 Introducing and applying Newtonian blurring: an augmented dataset of 126,000 human connectomes at braingraph.org.. *Scientific Reports*, **2022**, 12, 3102 4.9