

# Alessandra Carbone

## List of Publications by Year in descending order

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Version: 2024-02-01

105  
papers

2,712  
citations

218677

26  
h-index

223800

46  
g-index

128  
all docs

128  
docs citations

128  
times ranked

3377  
citing authors

#	ARTICLE	IF	CITATIONS
1	Codon adaptation index as a measure of dominating codon bias. <i>Bioinformatics</i> , 2003, 19, 2005-2015.	4.1	274
2	NCIPLOT4: Fast, Robust, and Quantitative Analysis of Noncovalent Interactions. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 4150-4158.	5.3	151
3	MIReNA: finding microRNAs with high accuracy and no learning at genome scale and from deep sequencing data. <i>Bioinformatics</i> , 2010, 26, 2226-2234.	4.1	141
4	Diatom Phytochromes Reveal the Existence of Far-Red-Light-Based Sensing in the Ocean. <i>Plant Cell</i> , 2016, 28, 616-628.	6.6	105
5	Blind prediction of homo- and hetero-protein complexes: The CASP13 CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	2.6	99
6	SynChro: A Fast and Easy Tool to Reconstruct and Visualize Synteny Blocks along Eukaryotic Chromosomes. <i>PLoS ONE</i> , 2014, 9, e92621.	2.5	98
7	Reconstruction of ancestral chromosome architecture and gene repertoire reveals principles of genome evolution in a model yeast genus. <i>Genome Research</i> , 2016, 26, 918-932.	5.5	95
8	New Highly Divergent rRNA Sequence among Biodiverse Genotypes of <i>Enterocytozoon bieneusi</i> Strains Isolated from Humans in Gabon and Cameroon. <i>Journal of Clinical Microbiology</i> , 2007, 45, 2580-2589.	3.9	88
9	Circuits and programmable self-assembling DNA structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12577-12582.	7.1	85
10	Joint Evolutionary Trees: A Large-Scale Method To Predict Protein Interfaces Based on Sequence Sampling. <i>PLoS Computational Biology</i> , 2009, 5, e1000267.	3.2	79
11	Codon Bias Signatures, Organization of Microorganisms in Codon Space, and Lifestyle. <i>Molecular Biology and Evolution</i> , 2005, 22, 547-561.	8.9	73
12	Codon Bias is a Major Factor Explaining Phage Evolution in Translationally Biased Hosts. <i>Journal of Molecular Evolution</i> , 2008, 66, 210-223.	1.8	71
13	GEMME: A Simple and Fast Global Epistatic Model Predicting Mutational Effects. <i>Molecular Biology and Evolution</i> , 2019, 36, 2604-2619.	8.9	71
14	<scp>NCIPLOT</scp> and the analysis of noncovalent interactions using the reduced density gradient. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2021, 11, e1497.	14.6	56
15	Identification of Protein Interaction Partners and Protein-Protein Interaction Sites. <i>Journal of Molecular Biology</i> , 2008, 382, 1276-1289.	4.2	52
16	Local Geometry and Evolutionary Conservation of Protein Surfaces Reveal the Multiple Recognition Patches in Protein-Protein Interactions. <i>PLoS Computational Biology</i> , 2015, 11, e1004580.	3.2	52
17	Large scale chromosomal mapping of human microRNA structural clusters. <i>Nucleic Acids Research</i> , 2013, 41, 4392-4408.	14.5	48
18	Protein-Protein Interactions in a Crowded Environment: An Analysis via Cross-Docking Simulations and Evolutionary Information. <i>PLoS Computational Biology</i> , 2013, 9, e1003369.	3.2	48

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19	A multi-objective optimization approach accurately resolves protein domain architectures. <i>Bioinformatics</i> , 2016, 32, 345-353.	4.1	45
20	BIS2Analyzer: a server for co-evolution analysis of conserved protein families. <i>Nucleic Acids Research</i> , 2017, 45, W307-W314.	14.5	43
21	A multi-source domain annotation pipeline for quantitative metagenomic and metatranscriptomic functional profiling. <i>Microbiome</i> , 2018, 6, 149.	11.1	41
22	The diversity of small non-coding RNAs in the diatom <i>Phaeodactylum tricornutum</i> . <i>BMC Genomics</i> , 2014, 15, 698.	2.8	40
23	Improvement in Protein Domain Identification Is Reached by Breaking Consensus, with the Agreement of Many Profiles and Domain Co-occurrence. <i>PLoS Computational Biology</i> , 2016, 12, e1005038.	3.2	38
24	Interpolants, cut elimination and flow graphs for the propositional calculus. <i>Annals of Pure and Applied Logic</i> , 1997, 83, 249-299.	0.5	35
25	Chromosomal periodicity and positional networks of genes in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2010, 6, 366.	7.2	34
26	Protein-protein interaction specificity is captured by contact preferences and interface composition. <i>Bioinformatics</i> , 2018, 34, 459-468.	4.1	29
27	Phylogenetic Reconstruction Based on Synteny Block and Gene Adjacencies. <i>Molecular Biology and Evolution</i> , 2020, 37, 2747-2762.	8.9	29
28	Computational Prediction of Genomic Functional Cores Specific to Different Microbes. <i>Journal of Molecular Evolution</i> , 2006, 63, 733-746.	1.8	28
29	Marine diatoms change their gene expression profile when exposed to microscale turbulence under nutrient replete conditions. <i>Scientific Reports</i> , 2017, 7, 3826.	3.3	27
30	Coevolution analysis of Hepatitis C virus genome to identify the structural and functional dependency network of viral proteins. <i>Scientific Reports</i> , 2016, 6, 26401.	3.3	26
31	Local Interaction Signal Analysis Predicts Protein-Protein Binding Affinity. <i>Structure</i> , 2018, 26, 905-915.e4.	3.3	24
32	A Combinatorial Approach to Detect Coevolved Amino Acid Networks in Protein Families of Variable Divergence. <i>PLoS Computational Biology</i> , 2009, 5, e1000488.	3.2	23
33	Protein Fragments: Functional and Structural Roles of Their Coevolution Networks. <i>PLoS ONE</i> , 2012, 7, e48124.	2.5	22
34	Dissecting protein architecture with communication blocks and communicating segment pairs. <i>BMC Bioinformatics</i> , 2016, 17, 13.	2.6	20
35	Infostery-analysis of short molecular dynamics simulations identifies highly sensitive residues and predicts deleterious mutations. <i>Scientific Reports</i> , 2018, 8, 16126.	3.3	20
36	A protein coevolution method uncovers critical features of the Hepatitis C Virus fusion mechanism. <i>PLoS Pathogens</i> , 2018, 14, e1006908.	4.7	20

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37	Coding and geometrical shapes in nanostructures: A fractal DNA-assembly. <i>Natural Computing</i> , 2003, 2, 133-151.	3.0	18
38	CLAG: an unsupervised non hierarchical clustering algorithm handling biological data. <i>BMC Bioinformatics</i> , 2012, 13, 194.	2.6	18
39	Great interactions: How binding incorrect partners can teach us about protein recognition and function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1408-1421.	2.6	18
40	Protein social behavior makes a stronger signal for partner identification than surface geometry. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 137-154.	2.6	18
41	Multiple protein-DNA interfaces unravelled by evolutionary information, physico-chemical and geometrical properties. <i>PLoS Computational Biology</i> , 2020, 16, e1007624.	3.2	18
42	Duplication of directed graphs and exponential blow up of proofs. <i>Annals of Pure and Applied Logic</i> , 1999, 100, 1-67.	0.5	16
43	3D Fractal DNA Assembly from Coding, Geometry and Protection. <i>Natural Computing</i> , 2004, 3, 235-252.	3.0	16
44	Identification of Plasmodium falciparum nuclear proteins by mass spectrometry and proposed protein annotation. <i>PLoS ONE</i> , 2018, 13, e0205596.	2.5	16
45	Decrypting protein surfaces by combining evolution, geometry, and molecular docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 952-965.	2.6	16
46	A route to fractal DNA-assembly. <i>Natural Computing</i> , 2002, 1, 469-480.	3.0	15
47	INTerface Builder: A Fast Protein-Protein Interface Reconstruction Tool. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 2613-2617.	5.4	15
48	JET2 Viewer: a database of predicted multiple, possibly overlapping, protein-protein interaction sites for PDB structures. <i>Nucleic Acids Research</i> , 2017, 45, D236-D242.	14.5	15
49	The complexity of protein interactions unravelled from structural disorder. <i>PLoS Computational Biology</i> , 2021, 17, e1008546.	3.2	15
50	Making proofs without Modus Ponens: An introduction to the combinatorics and complexity of cut elimination. <i>Bulletin of the American Mathematical Society</i> , 1997, 34, 131-160.	1.5	14
51	Hidden partners: Using cross-docking calculations to predict binding sites for proteins with multiple interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 723-737.	2.6	14
52	Insights on the Evolution of Metabolic Networks of Unicellular Translationally Biased Organisms from Transcriptomic Data and Sequence Analysis. <i>Journal of Molecular Evolution</i> , 2005, 61, 456-469.	1.8	13
53	Molecular Tiling and DNA Self-assembly. <i>Lecture Notes in Computer Science</i> , 2003, , 61-83.	1.3	13
54	Periodic distributions of hydrophobic amino acids allows the definition of fundamental building blocks to align distantly related proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 695-708.	2.6	12

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55	Combinatorics of chromosomal rearrangements based on synteny blocks and synteny packs. Journal of Logic and Computation, 2013, 23, 815-838.	0.8	12
56	A fusion peptide in preS1 and the human protein disulfide isomerase ERp57 are involved in hepatitis B virus membrane fusion process. ELife, 2021, 10, .	6.0	12
57	Cycling in proofs and feasibility. Transactions of the American Mathematical Society, 1999, 352, 2049-2075.	0.9	11
58	Turning cycles into spirals. Annals of Pure and Applied Logic, 1999, 96, 57-73.	0.5	10
59	Asymptotic Cyclic Expansion and Bridge Groups of Formal Proofs. Journal of Algebra, 2001, 242, 109-145.	0.7	9
60	Co-evolution and information signals in biological sequences. Theoretical Computer Science, 2011, 412, 2486-2495.	0.9	9
61	From complete cross-docking to partners identification and binding sites predictions. PLoS Computational Biology, 2022, 18, e1009825.	3.2	9
62	A discriminative method for family-based protein remote homology detection that combines inductive logic programming and propositional models. BMC Bioinformatics, 2011, 12, 83.	2.6	8
63	The cost of a cycle is a square. Journal of Symbolic Logic, 2002, 67, 35-60.	0.5	7
64	Multiple Profile Models Extract Features from Protein Sequence Data and Resolve Functional Diversity of Very Different Protein Families. Molecular Biology and Evolution, 2022, 39, .	8.9	7
65	Inconsistent Distances in Substitution Matrices can be Avoided by Properly Handling Hydrophobic Residues. Evolutionary Bioinformatics, 2008, 4, EBO.S885.	1.2	6
66	A new mapping between combinatorial proofs and sequent calculus proofs read out from logical flow graphs. Information and Computation, 2010, 208, 500-509.	0.7	6
67	Much shorter proofs: A bimodal investigation. Zeitschrift Für Mathematische Logik Und Grundlagen Der Mathematik, 1990, 36, 47-66.	0.2	5
68	Looking From The Inside And From The Outside. Synthese, 2000, 125, 385-416.	1.1	5
69	Streams and strings in formal proofs. Theoretical Computer Science, 2002, 288, 45-83.	0.9	5
70	Plasmobase: a comparative database of predicted domain architectures for Plasmodium genomes. Malaria Journal, 2017, 16, 241.	2.3	5
71	Rosser Orderings in Bimodal Logics. Zeitschrift Für Mathematische Logik Und Grundlagen Der Mathematik, 1989, 35, 343-358.	0.2	4
72	Coevolution analysis of amino-acids reveals diversified drug-resistance solutions in viral sequences: a case study of hepatitis B virus. Virus Evolution, 2020, 6, veaa006.	4.9	4

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73	Meet-U: Educating through research immersion. PLoS Computational Biology, 2018, 14, e1005992.	3.2	4
74	Crystal structure of chloroplast fructose-1,6-bisphosphate aldolase from the green alga Chlamydomonas reinhardtii. Journal of Structural Biology, 2022, 214, 107873.	2.8	4
75	Logical structures and genus of proofs. Annals of Pure and Applied Logic, 2009, 161, 139-149.	0.5	3
76	iBIS2Analyzer: a web server for a phylogeny-driven coevolution analysis of protein families. Nucleic Acids Research, 0, , .	14.5	3
77	Functional labels and syntactic entropy on DNA strings and proteins. Theoretical Computer Science, 2003, 303, 35-51.	0.9	2
78	SPoRE: a mathematical model to predict double strand breaks and axis protein sites in meiosis. BMC Bioinformatics, 2014, 15, 391.	2.6	2
79	Targeted domain assembly for fast functional profiling of metagenomic datasets with S3A. Bioinformatics, 2020, 36, 3975-3981.	4.1	2
80	COVTree: Coevolution in OVERlapped sequences by Tree analysis server. Nucleic Acids Research, 2020, 48, W558-W565.	14.5	2
81	MyCLADE: a multi-source domain annotation server for sequence functional exploration. Nucleic Acids Research, 2021, 49, W452-W458.	14.5	2
82	Group Cancellation and Resolution. Studia Logica, 2006, 82, 73-93.	0.6	1
83	Co-evolution and Information Signals in Biological Sequences. Lecture Notes in Computer Science, 2009, , 6-17.	1.3	1
84	Provable fixed points in $\{m\}\Delta_0+\Omega_1$ .. Notre Dame Journal of Formal Logic, 1991, 32, .	0.4	1
85	PATHWAYS OF DEDUCTION. , 2005, , 383-400.		1
86	Provable Fixed Points.. Journal of Symbolic Logic, 1993, 58, 715.	0.5	0
87	Predicted human structural clusters of miRNAs target cancer genes. Atlas of Genetics and Cytogenetics in Oncology and Haematology, 2014, , .	0.1	0
88	Computability in Europe 2010. Journal of Logic and Computation, 2015, 25, 983-985.	0.8	0
89	Local Geometry and Evolutionary Conservation of Protein Surfaces Reveal the Multiple Recognition Patches in Protein-Protein Interactions. Biophysical Journal, 2016, 110, 347a-348a.	0.5	0
90	Great Interactions: Binding Incorrect Partners to Learn about Protein Recognition and Function. Biophysical Journal, 2017, 112, 200a-201a.	0.5	0

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91	A Question of Time. , 2008, , 165-167.		0
92	Information Content of Sets of Biological Sequences Revisited. Natural Computing Series, 2009, , 31-42.	2.2	0
93	Identification of Protein Interaction Partners from Shape Complementarity Molecular Cross-Docking. Lecture Notes in Computer Science, 2013, , 318-325.	1.3	0
94	Extracting Coevolving Characters from a Tree of Species. Natural Computing Series, 2014, , 45-65.	2.2	0
95	Predicting substitutions to modulate disorder and stability in coiled-coils. BMC Bioinformatics, 2020, 21, 573.	2.6	0
96	Title is missing!. , 2020, 16, e1007624.		0
97	Title is missing!. , 2020, 16, e1007624.		0
98	Title is missing!. , 2020, 16, e1007624.		0
99	Title is missing!. , 2020, 16, e1007624.		0
100	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
101	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
102	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
103	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
104	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
105	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0