

# Alessandra Carbone

## List of Publications by Year in descending order

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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	From complete cross-docking to partners identification and binding sites predictions. PLoS Computational Biology, 2022, 18, e1009825.	3.2	9
2	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
3	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
4	<scp>NCIPLOT</scp> and the analysis of noncovalent interactions using the reduced density gradient. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2021, 11, e1497.	14.6	56
5	The complexity of protein interactions unravelled from structural disorder. PLoS Computational Biology, 2021, 17, e1008546.	3.2	15
6	MyCLADE: a multi-source domain annotation server for sequence functional exploration. Nucleic Acids Research, 2021, 49, W452-W458.	14.5	2
7	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
8	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
9	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
10	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
11	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
12	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
13	The complexity of protein interactions unravelled from structural disorder. , 2021, 17, e1008546.		0
14	Targeted domain assembly for fast functional profiling of metagenomic datasets with S3A. Bioinformatics, 2020, 36, 3975-3981.	4.1	2
15	Phylogenetic Reconstruction Based on Synteny Block and Gene Adjacencies. Molecular Biology and Evolution, 2020, 37, 2747-2762.	8.9	29
16	NCIPLOT4: Fast, Robust, and Quantitative Analysis of Noncovalent Interactions. Journal of Chemical Theory and Computation, 2020, 16, 4150-4158.	5.3	151
17	COVTree: Coevolution in OVERlapped sequences by Tree analysis server. Nucleic Acids Research, 2020, 48, W558-W565.	14.5	2
18	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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19	Multiple protein-DNA interfaces unravelled by evolutionary information, physico-chemical and geometrical properties. <i>PLoS Computational Biology</i> , 2020, 16, e1007624.	3.2	18
20	Predicting substitutions to modulate disorder and stability in coiled-coils. <i>BMC Bioinformatics</i> , 2020, 21, 573.	2.6	0
21	Title is missing!. , 2020, 16, e1007624.		0
22	Title is missing!. , 2020, 16, e1007624.		0
23	Title is missing!. , 2020, 16, e1007624.		0
24	Title is missing!. , 2020, 16, e1007624.		0
25	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	2.6	99
26	GEMME: A Simple and Fast Global Epistatic Model Predicting Mutational Effects. <i>Molecular Biology and Evolution</i> , 2019, 36, 2604-2619.	8.9	71
27	Decrypting protein surfaces by combining evolution, geometry, and molecular docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 952-965.	2.6	16
28	Hidden partners: Using crossâ€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
29	Proteinâ€protein interaction specificity is captured by contact preferences and interface composition. <i>Bioinformatics</i> , 2018, 34, 459-468.	4.1	29
30	â€Infosteryâ€analysis of short molecular dynamics simulations identifies highly sensitive residues and predicts deleterious mutations. <i>Scientific Reports</i> , 2018, 8, 16126.	3.3	20
31	Identification of <i>Plasmodium falciparum</i> nuclear proteins by mass spectrometry and proposed protein annotation. <i>PLoS ONE</i> , 2018, 13, e0205596.	2.5	16
32	A multi-source domain annotation pipeline for quantitative metagenomic and metatranscriptomic functional profiling. <i>Microbiome</i> , 2018, 6, 149.	11.1	41
33	Local Interaction Signal Analysis Predicts Protein-Protein Binding Affinity. <i>Structure</i> , 2018, 26, 905-915.e4.	3.3	24
34	Meet-U: Educating through research immersion. <i>PLoS Computational Biology</i> , 2018, 14, e1005992.	3.2	4
35	A protein coevolution method uncovers critical features of the Hepatitis C Virus fusion mechanism. <i>PLoS Pathogens</i> , 2018, 14, e1006908.	4.7	20
36	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

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37	Great Interactions: Binding Incorrect Partners to Learn about Protein Recognition and Function. <i>Biophysical Journal</i> , 2017, 112, 200a-201a.	0.5	0
38	INTErface Builder: A Fast Protein-Protein Interface Reconstruction Tool. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 2613-2617.	5.4	15
39	Plasmobase: a comparative database of predicted domain architectures for Plasmodium genomes. <i>Malaria Journal</i> , 2017, 16, 241.	2.3	5
40	BIS2Analyzer: a server for co-evolution analysis of conserved protein families. <i>Nucleic Acids Research</i> , 2017, 45, W307-W314.	14.5	43
41	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
42	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
43	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
44	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
45	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
46	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
47	Local Geometry and Evolutionary Conservation of Protein Surfaces Reveal the Multiple Recognition Patches in Protein-Protein Interactions. <i>Biophysical Journal</i> , 2016, 110, 347a-348a.	0.5	0
48	Dissecting protein architecture with communication blocks and communicating segment pairs. <i>BMC Bioinformatics</i> , 2016, 17, 13.	2.6	20
49	A multi-objective optimization approach accurately resolves protein domain architectures. <i>Bioinformatics</i> , 2016, 32, 345-353.	4.1	45
50	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
51	Computability in Europe 2010. <i>Journal of Logic and Computation</i> , 2015, 25, 983-985.	0.8	0
52	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
53	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
54	Predicted human structural clusters of miRNAs target cancer genes. <i>Atlas of Genetics and Cytogenetics in Oncology and Haematology</i> , 2014, , .	0.1	0

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55	The diversity of small non-coding RNAs in the diatom <i>Phaeodactylum tricornutum</i> . BMC Genomics, 2014, 15, 698.	2.8	40
56	SPoRE: a mathematical model to predict double strand breaks and axis protein sites in meiosis. BMC Bioinformatics, 2014, 15, 391.	2.6	2
57	Extracting Coevolving Characters from a Tree of Species. Natural Computing Series, 2014, , 45-65.	2.2	0
58	Large scale chromosomal mapping of human microRNA structural clusters. Nucleic Acids Research, 2013, 41, 4392-4408.	14.5	48
59	Protein-Protein Interactions in a Crowded Environment: An Analysis via Cross-Docking Simulations and Evolutionary Information. PLoS Computational Biology, 2013, 9, e1003369.	3.2	48
60	Combinatorics of chromosomal rearrangements based on synteny blocks and synteny packs. Journal of Logic and Computation, 2013, 23, 815-838.	0.8	12
61	Identification of Protein Interaction Partners from Shape Complementarity Molecular Cross-Docking. Lecture Notes in Computer Science, 2013, , 318-325.	1.3	0
62	CLAG: an unsupervised non hierarchical clustering algorithm handling biological data. BMC Bioinformatics, 2012, 13, 194.	2.6	18
63	Protein Fragments: Functional and Structural Roles of Their Coevolution Networks. PLoS ONE, 2012, 7, e48124.	2.5	22
64	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
65	Co-evolution and information signals in biological sequences. Theoretical Computer Science, 2011, 412, 2486-2495.	0.9	9
66	Chromosomal periodicity and positional networks of genes in <i>Escherichia coli</i> . Molecular Systems Biology, 2010, 6, 366.	7.2	34
67	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
68	MIReNA: finding microRNAs with high accuracy and no learning at genome scale and from deep sequencing data. Bioinformatics, 2010, 26, 2226-2234.	4.1	141
69	Joint Evolutionary Trees: A Large-Scale Method To Predict Protein Interfaces Based on Sequence Sampling. PLoS Computational Biology, 2009, 5, e1000267.	3.2	79
70	A Combinatorial Approach to Detect Coevolved Amino Acid Networks in Protein Families of Variable Divergence. PLoS Computational Biology, 2009, 5, e1000488.	3.2	23
71	Logical structures and genus of proofs. Annals of Pure and Applied Logic, 2009, 161, 139-149.	0.5	3
72	Co-evolution and Information Signals in Biological Sequences. Lecture Notes in Computer Science, 2009, , 6-17.	1.3	1

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73	Information Content of Sets of Biological Sequences Revisited. Natural Computing Series, 2009, , 31-42.	2.2	0
74	Codon Bias is a Major Factor Explaining Phage Evolution in Translationally Biased Hosts. Journal of Molecular Evolution, 2008, 66, 210-223.	1.8	71
75	Identification of Protein Interaction Partners and Proteinâ€Protein Interaction Sites. Journal of Molecular Biology, 2008, 382, 1276-1289.	4.2	52
76	Inconsistent Distances in Substitution Matrices can be Avoided by Properly Handling Hydrophobic Residues. Evolutionary Bioinformatics, 2008, 4, EBO.S885.	1.2	6
77	A Question of Time. , 2008, , 165-167.		0
78	New Highly Divergent rRNA Sequence among Biodiverse Genotypes of Enterocytozoon bienersi Strains Isolated from Humans in Gabon and Cameroon. Journal of Clinical Microbiology, 2007, 45, 2580-2589.	3.9	88
79	Periodic distributions of hydrophobic amino acids allows the definition of fundamental building blocks to align distantly related proteins. Proteins: Structure, Function and Bioinformatics, 2007, 67, 695-708.	2.6	12
80	Group Cancellation and Resolution. Studia Logica, 2006, 82, 73-93.	0.6	1
81	Computational Prediction of Genomic Functional Cores Specific to Different Microbes. Journal of Molecular Evolution, 2006, 63, 733-746.	1.8	28
82	Codon Bias Signatures, Organization of Microorganisms in Codon Space, and Lifestyle. Molecular Biology and Evolution, 2005, 22, 547-561.	8.9	73
83	Insights on the Evolution of Metabolic Networks of Unicellular Translationally Biased Organisms from Transcriptomic Data and Sequence Analysis. Journal of Molecular Evolution, 2005, 61, 456-469.	1.8	13
84	PATHWAYS OF DEDUCTION. , 2005, , 383-400.		1
85	3D Fractal DNA Assembly from Coding, Geometry and Protection. Natural Computing, 2004, 3, 235-252.	3.0	16
86	Coding and geometrical shapes in nanostructures: A fractal DNA-assembly. Natural Computing, 2003, 2, 133-151.	3.0	18
87	Functional labels and syntactic entropy on DNA strings and proteins. Theoretical Computer Science, 2003, 303, 35-51.	0.9	2
88	Codon adaptation index as a measure of dominating codon bias. Bioinformatics, 2003, 19, 2005-2015.	4.1	274
89	Molecular Tiling and DNA Self-assembly. Lecture Notes in Computer Science, 2003, , 61-83.	1.3	13
90	Circuits and programmable self-assembling DNA structures. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12577-12582.	7.1	85

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91	The cost of a cycle is a square. <i>Journal of Symbolic Logic</i> , 2002, 67, 35-60.	0.5	7
92	Streams and strings in formal proofs. <i>Theoretical Computer Science</i> , 2002, 288, 45-83.	0.9	5
93	A route to fractal DNA-assembly. <i>Natural Computing</i> , 2002, 1, 469-480.	3.0	15
94	Asymptotic Cyclic Expansion and Bridge Groups of Formal Proofs. <i>Journal of Algebra</i> , 2001, 242, 109-145.	0.7	9
95	Looking From The Inside And From The Outside. <i>Synthese</i> , 2000, 125, 385-416.	1.1	5
96	Turning cycles into spirals. <i>Annals of Pure and Applied Logic</i> , 1999, 96, 57-73.	0.5	10
97	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
98	Cycling in proofs and feasibility. <i>Transactions of the American Mathematical Society</i> , 1999, 352, 2049-2075.	0.9	11
99	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
100	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
101	Provable Fixed Points.. <i>Journal of Symbolic Logic</i> , 1993, 58, 715.	0.5	0
102	Provable fixed points in $\{\Delta_0 + \Omega_1\}$ . <i>Notre Dame Journal of Formal Logic</i> , 1991, 32, .	0.4	1
103	Much shorter proofs: A bimodal investigation. <i>Zeitschrift für Mathematische Logik Und Grundlagen Der Mathematik</i> , 1990, 36, 47-66.	0.2	5
104	Rosser Orderings in Bimodal Logics. <i>Zeitschrift für Mathematische Logik Und Grundlagen Der Mathematik</i> , 1989, 35, 343-358.	0.2	4
105	iBIS2Analyzer: a web server for a phylogeny-driven coevolution analysis of protein families. <i>Nucleic Acids Research</i> , 0, , .	14.5	3