

# Charles Delisi

## List of Publications by Year in Descending Order

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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.

44  
papers

4,002  
citations

29  
h-index

45  
g-index

45  
ext. papers

4,280  
ext. citations

10.1  
avg, IF

4.8  
L-index

#	Paper	IF	Citations
44	VisANT 4.0: Integrative network platform to connect genes, drugs, diseases and therapies. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, W225-31	20.1	105
43	Gene set enrichment analysis: performance evaluation and usage guidelines. <i>Briefings in Bioinformatics</i> , <b>2012</b> , 13, 281-91	13.4	142
42	Identification of functional modules that correlate with phenotypic difference: the influence of network topology. <i>Genome Biology</i> , <b>2010</b> , 11, R23	18.3	60
41	VisANT 3.5: multi-scale network visualization, analysis and inference based on the gene ontology. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W115-21	20.1	154
40	VisANT: an integrative framework for networks in systems biology. <i>Briefings in Bioinformatics</i> , <b>2008</b> , 9, 317-25	13.4	89
39	High expression of lymphocyte-associated genes in node-negative HER2+ breast cancers correlates with lower recurrence rates. <i>Cancer Research</i> , <b>2007</b> , 67, 10669-76	10.1	167
38	Towards zoomable multidimensional maps of the cell. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 547-54	44.5	73
37	Portraits of breast cancer progression. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 291	3.6	29
36	VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W625-32	20.1	58
35	Comparative assessment of performance and genome dependence among phylogenetic profiling methods. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 420	3.6	40
34	VisANT: data-integrating visual framework for biological networks and modules. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W352-7	20.1	155
33	VisANT: an online visualization and analysis tool for biological interaction data. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 17	3.6	166
32	Analyzing networks with VisANT. <i>Current Protocols in Bioinformatics</i> , <b>2004</b> , Chapter 8, Unit 8.8	24.2	9
31	ELISA: structure-function inferences based on statistically significant and evolutionarily inspired observations. <i>BMC Bioinformatics</i> , <b>2003</b> , 4, 34	3.6	15
30	Protein therapeutics: promises and challenges for the 21st century. <i>Trends in Biotechnology</i> , <b>2002</b> , 20, 29-35	15.1	57
29	Predictome: a database of putative functional links between proteins. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 306-9	20.1	106
28	The society of genes: networks of functional links between genes from comparative genomics. <i>Genome Biology</i> , <b>2002</b> , 3, research0064	18.3	24

27	Neural network method for predicting peptides that bind major histocompatibility complex molecules. <i>Methods in Molecular Biology</i> , <b>2001</b> , 156, 201-9	1.4	6
26	Kinetics of desolvation-mediated protein-protein binding. <i>Biophysical Journal</i> , <b>2000</b> , 78, 1094-105	2.9	131
25	Protein-protein recognition: exploring the energy funnels near the binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1999</b> , 34, 255-267	4.2	63
24	Free energy landscapes of encounter complexes in protein-protein association. <i>Biophysical Journal</i> , <b>1999</b> , 76, 1166-78	2.9	164
23	Toward a predictive understanding of molecular recognition. <i>Immunological Reviews</i> , <b>1998</b> , 163, 251-66	11.3	14
22	Determination of atomic desolvation energies from the structures of crystallized proteins. <i>Journal of Molecular Biology</i> , <b>1997</b> , 267, 707-26	6.5	433
21	Two complementary methods for predicting peptides binding major histocompatibility complex molecules. <i>Journal of Molecular Biology</i> , <b>1997</b> , 267, 1258-67	6.5	224
20	Consistency in structural energetics of protein folding and peptide recognition. <i>Protein Science</i> , <b>1997</b> , 6, 1057-64	6.3	45
19	Empirical free energy calculation: comparison to calorimetric data. <i>Protein Science</i> , <b>1997</b> , 6, 1976-84	6.3	27
18	Empirical free energy as a target function in docking and design: application to HIV-1 protease inhibitors. <i>FEBS Letters</i> , <b>1996</b> , 384, 87-91	3.8	18
17	HLA allele selection for designing peptide vaccines. <i>Genetic Analysis, Techniques and Applications</i> , <b>1996</b> , 13, 81-6		31
16	Peptide docking using dynamic programming <b>1996</b> , 17, 418-428		18
15	RNA loop structure prediction via bond scaling and relaxation. <i>Biopolymers</i> , <b>1996</b> , 38, 769-79	2.2	5
14	Free energy mapping of class I MHC molecules and structural determination of bound peptides. <i>Protein Science</i> , <b>1996</b> , 5, 1272-81	6.3	43
13	Effect of conformational flexibility and solvation on receptor-ligand binding free energies. <i>Biochemistry</i> , <b>1994</b> , 33, 13977-88	3.2	149
12	Reflections on Mathematical Contributions to Understanding the Molecular Basis of Life: From 1970 to the 21st Century. <i>Lecture Notes in Biomathematics</i> , <b>1994</b> , 2-27		
11	Exhaustive conformational search and simulated annealing for models of lattice peptides. <i>Biopolymers</i> , <b>1993</b> , 33, 329-34	2.2	30
10	Loop closure via bond scaling and relaxation. <i>Journal of Computational Chemistry</i> , <b>1993</b> , 14, 556-565	3.5	42

9	Toward computational determination of peptide-receptor structure. <i>Protein Science</i> , <b>1993</b> , 2, 1827-43	6.3	28
8	Characterization of a helper T cell epitope recognized by mice of a low responder major histocompatibility type. <i>Molecular Immunology</i> , <b>1990</b> , 27, 941-6	4.3	5
7	Identification of T-cell epitopes and use in construction of synthetic vaccines. <i>Methods in Enzymology</i> , <b>1989</b> , 178, 611-34	1.7	23
6	Hydrophobicity scales and computational techniques for detecting amphipathic structures in proteins. <i>Journal of Molecular Biology</i> , <b>1987</b> , 195, 659-85	6.5	566
5	Protein antigenic structures recognized by T cells: potential applications to vaccine design. <i>Immunological Reviews</i> , <b>1987</b> , 98, 9-52	11.3	127
4	Prediction of protein structural class from the amino acid sequence. <i>Biopolymers</i> , <b>1986</b> , 25, 1659-72	2.2	160
3	The magnitude of signal amplification by ligand-induced receptor clustering. <i>Nature</i> , <b>1981</b> , 289, 322-3	50.4	52
2	The biophysics of ligand-receptor interactions. <i>Quarterly Reviews of Biophysics</i> , <b>1980</b> , 13, 201-30	7	128
1	Theory of ligand binding to heterogeneous receptor populations: Characterization of the free-energy distribution function. <i>Biopolymers</i> , <b>1978</b> , 17, 1075-1089	2.2	20