

Charles Delisi

List of Publications by Citations

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|-------------------|-------------------------|-----------------|----------------|
| 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 | Hydrophobicity scales and computational techniques for detecting amphipathic structures in proteins. <i>Journal of Molecular Biology</i> , 1987 , 195, 659-85 | 6.5 | 566 |
| 43 | Determination of atomic desolvation energies from the structures of crystallized proteins. <i>Journal of Molecular Biology</i> , 1997 , 267, 707-26 | 6.5 | 433 |
| 42 | Two complementary methods for predicting peptides binding major histocompatibility complex molecules. <i>Journal of Molecular Biology</i> , 1997 , 267, 1258-67 | 6.5 | 224 |
| 41 | High expression of lymphocyte-associated genes in node-negative HER2+ breast cancers correlates with lower recurrence rates. <i>Cancer Research</i> , 2007 , 67, 10669-76 | 10.1 | 167 |
| 40 | VisANT: an online visualization and analysis tool for biological interaction data. <i>BMC Bioinformatics</i> , 2004 , 5, 17 | 3.6 | 166 |
| 39 | Free energy landscapes of encounter complexes in protein-protein association. <i>Biophysical Journal</i> , 1999 , 76, 1166-78 | 2.9 | 164 |
| 38 | Prediction of protein structural class from the amino acid sequence. <i>Biopolymers</i> , 1986 , 25, 1659-72 | 2.2 | 160 |
| 37 | VisANT: data-integrating visual framework for biological networks and modules. <i>Nucleic Acids Research</i> , 2005 , 33, W352-7 | 20.1 | 155 |
| 36 | VisANT 3.5: multi-scale network visualization, analysis and inference based on the gene ontology. <i>Nucleic Acids Research</i> , 2009 , 37, W115-21 | 20.1 | 154 |
| 35 | Effect of conformational flexibility and solvation on receptor-ligand binding free energies. <i>Biochemistry</i> , 1994 , 33, 13977-88 | 3.2 | 149 |
| 34 | Gene set enrichment analysis: performance evaluation and usage guidelines. <i>Briefings in Bioinformatics</i> , 2012 , 13, 281-91 | 13.4 | 142 |
| 33 | Kinetics of desolvation-mediated protein-protein binding. <i>Biophysical Journal</i> , 2000 , 78, 1094-105 | 2.9 | 131 |
| 32 | The biophysics of ligand-receptor interactions. <i>Quarterly Reviews of Biophysics</i> , 1980 , 13, 201-30 | 7 | 128 |
| 31 | Protein antigenic structures recognized by T cells: potential applications to vaccine design. <i>Immunological Reviews</i> , 1987 , 98, 9-52 | 11.3 | 127 |
| 30 | Predictome: a database of putative functional links between proteins. <i>Nucleic Acids Research</i> , 2002 , 30, 306-9 | 20.1 | 106 |
| 29 | VisANT 4.0: Integrative network platform to connect genes, drugs, diseases and therapies. <i>Nucleic Acids Research</i> , 2013 , 41, W225-31 | 20.1 | 105 |
| 28 | VisANT: an integrative framework for networks in systems biology. <i>Briefings in Bioinformatics</i> , 2008 , 9, 317-25 | 13.4 | 89 |

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| 27 | Towards zoomable multidimensional maps of the cell. <i>Nature Biotechnology</i> , 2007 , 25, 547-54 | 44.5 | 73 |
| 26 | Protein-protein recognition: exploring the energy funnels near the binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 34, 255-267 | 4.2 | 63 |
| 25 | Identification of functional modules that correlate with phenotypic difference: the influence of network topology. <i>Genome Biology</i> , 2010 , 11, R23 | 18.3 | 60 |
| 24 | VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. <i>Nucleic Acids Research</i> , 2007 , 35, W625-32 | 20.1 | 58 |
| 23 | Protein therapeutics: promises and challenges for the 21st century. <i>Trends in Biotechnology</i> , 2002 , 20, 29-35 | 15.1 | 57 |
| 22 | The magnitude of signal amplification by ligand-induced receptor clustering. <i>Nature</i> , 1981 , 289, 322-3 | 50.4 | 52 |
| 21 | Consistency in structural energetics of protein folding and peptide recognition. <i>Protein Science</i> , 1997 , 6, 1057-64 | 6.3 | 45 |
| 20 | Free energy mapping of class I MHC molecules and structural determination of bound peptides. <i>Protein Science</i> , 1996 , 5, 1272-81 | 6.3 | 43 |
| 19 | Loop closure via bond scaling and relaxation. <i>Journal of Computational Chemistry</i> , 1993 , 14, 556-565 | 3.5 | 42 |
| 18 | Comparative assessment of performance and genome dependence among phylogenetic profiling methods. <i>BMC Bioinformatics</i> , 2006 , 7, 420 | 3.6 | 40 |
| 17 | HLA allele selection for designing peptide vaccines. <i>Genetic Analysis, Techniques and Applications</i> , 1996 , 13, 81-6 | | 31 |
| 16 | Exhaustive conformational search and simulated annealing for models of lattice peptides. <i>Biopolymers</i> , 1993 , 33, 329-34 | 2.2 | 30 |
| 15 | Portraits of breast cancer progression. <i>BMC Bioinformatics</i> , 2007 , 8, 291 | 3.6 | 29 |
| 14 | Toward computational determination of peptide-receptor structure. <i>Protein Science</i> , 1993 , 2, 1827-43 | 6.3 | 28 |
| 13 | Empirical free energy calculation: comparison to calorimetric data. <i>Protein Science</i> , 1997 , 6, 1976-84 | 6.3 | 27 |
| 12 | The society of genes: networks of functional links between genes from comparative genomics. <i>Genome Biology</i> , 2002 , 3, research0064 | 18.3 | 24 |
| 11 | Identification of T-cell epitopes and use in construction of synthetic vaccines. <i>Methods in Enzymology</i> , 1989 , 178, 611-34 | 1.7 | 23 |
| 10 | Theory of ligand binding to heterogeneous receptor populations: Characterization of the free-energy distribution function. <i>Biopolymers</i> , 1978 , 17, 1075-1089 | 2.2 | 20 |

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| 9 | Empirical free energy as a target function in docking and design: application to HIV-1 protease inhibitors. <i>FEBS Letters</i> , 1996 , 384, 87-91 | 3.8 | 18 |
| 8 | Peptide docking using dynamic programming 1996 , 17, 418-428 | | 18 |
| 7 | ELISA: structure-function inferences based on statistically significant and evolutionarily inspired observations. <i>BMC Bioinformatics</i> , 2003 , 4, 34 | 3.6 | 15 |
| 6 | Toward a predictive understanding of molecular recognition. <i>Immunological Reviews</i> , 1998 , 163, 251-66 | 11.3 | 14 |
| 5 | Analyzing networks with VisANT. <i>Current Protocols in Bioinformatics</i> , 2004 , Chapter 8, Unit 8.8 | 24.2 | 9 |
| 4 | Neural network method for predicting peptides that bind major histocompatibility complex molecules. <i>Methods in Molecular Biology</i> , 2001 , 156, 201-9 | 1.4 | 6 |
| 3 | RNA loop structure prediction via bond scaling and relaxation. <i>Biopolymers</i> , 1996 , 38, 769-79 | 2.2 | 5 |
| 2 | Characterization of a helper T cell epitope recognized by mice of a low responder major histocompatibility type. <i>Molecular Immunology</i> , 1990 , 27, 941-6 | 4.3 | 5 |
| 1 | Reflections on Mathematical Contributions to Understanding the Molecular Basis of Life: From 1970 to the 21st Century. <i>Lecture Notes in Biomathematics</i> , 1994 , 2-27 | | |