Irene Nobeli

List of Publications by Year
in descending order

41 papers	1,725 citations	361296 20 h-index	315616 38 g-index
49 all docs	49 docs citations	49 times ranked	2643 citing authors

#	Article	IF	Citations
1	Challenges in defining the functional, nonâ€coding, expressed genome of members of the Mycobacterium tuberculosis complex. Molecular Microbiology, 2022, 117, 20-31.	1.2	7
2	Defining the Genes Required for Survival of Mycobacterium bovis in the Bovine Host Offers Novel Insights into the Genetic Basis of Survival of Pathogenic Mycobacteria. MBio, 2022, 13, .	1.8	3
3	flexiMAP: a regression-based method for discovering differential alternative polyadenylation events in standard RNA-seq data. Bioinformatics, 2021, 37, 1461-1464.	1.8	1
4	Probing Differences in Gene Essentiality Between the Human and Animal Adapted Lineages of the Mycobacterium tuberculosis Complex Using TnSeq. Frontiers in Veterinary Science, 2021, 8, 760717.	0.9	6
5	baerhunter: an R package for the discovery and analysis of expressed non-coding regions in bacterial RNA-seq data. Bioinformatics, 2020, 36, 966-969.	1.8	8
6	Molecular dynamics simulations of the interaction of wild type and mutant human CYP2J2 with polyunsaturated fatty acids. BMC Research Notes, 2019, 12, 760.	0.6	2
7	Cell-wall synthesis and ribosome maturation are co-regulated by an RNA switch in Mycobacterium tuberculosis. Nucleic Acids Research, 2018, 46, 5837-5849.	6.5	19
8	In praise of slow. Science, 2018, 359, 602-602.	6.0	1
9	Cmr is a redox-responsive regulator of DosR that contributes to M. tuberculosis virulence. Nucleic Acids Research, 2017, 45, 6600-6612.	6.5	22
10	KSHV SOX mediated host shutoff: the molecular mechanism underlying mRNA transcript processing. Nucleic Acids Research, 2017, 45, gkw1340.	6.5	14
11	Untranslated Parts of Genes Interpreted: Making Heads or Tails of Highâ€Throughput Transcriptomic Data via Computational Methods. BioEssays, 2017, 39, 1700090.	1.2	14
12	Dysregulation of Alternative Poly-adenylation as a Potential Player in Autism Spectrum Disorder. Frontiers in Molecular Neuroscience, 2017, 10, 279.	1.4	13
13	Computational modelling of the binding of arachidonic acid to the human monooxygenase CYP2J2. Journal of Molecular Modeling, 2016, 22, 279.	0.8	10
14	Prokaryotic NavMs channel as a structural and functional model for eukaryotic sodium channel antagonism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8428-8433.	3.3	120
15	A text-mining system for extracting metabolic reactions from full-text articles. BMC Bioinformatics, 2012, 13, 172.	1.2	32
16	Visualisation of variable binding pockets on protein surfaces by probabilistic analysis of related structure sets. BMC Bioinformatics, 2012, 13, 39.	1.2	13
17	In Silico Assessment of Potential Druggable Pockets on the Surface of Î±1-Antitrypsin Conformers. PLoS ONE, 2012, 7, e36612.	1.1	39
18	SERAPhiC: A Benchmark for in Silico Fragment-Based Drug Design. Journal of Chemical Information and Modeling, 2011, 51, 2882-2896.	2.5	20

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19	Therapeutic target-site variability in Î±₁-antitrypsin characterized at high resolution. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1492-1497.	0.7	39
20	Interaction of N-methyl-2-alkenyl-4-quinolones with ATP-dependent MurE ligase of Mycobacterium tuberculosis: antibacterial activity, molecular docking and inhibition kinetics. Journal of Antimicrobial Chemotherapy, 2011, 66, 1766-1772.	1.3	37
21	Targeting Serpins in High-Throughput and Structure-Based Drug Design. Methods in Enzymology, 2011, 501, 139-175.	0.4	15
22	Protein promiscuity and its implications for biotechnology. Nature Biotechnology, 2009, 27, 157-167.	9.4	434
23	Crystallographic and Cellular Characterisation of Two Mechanisms Stabilising the Native Fold of Î±1-Antitrypsin: Implications for Disease and Drug Design. Journal of Molecular Biology, 2009, 387, 857-868.	2.0	34
24	Mapping Human Metabolic Pathways in the Small Molecule Chemical Space. Journal of Chemical Information and Modeling, 2009, 49, 2272-2289.	2.5	14
25	Molecular Docking for Substrate Identification: The Short-Chain Dehydrogenases/Reductases. Journal of Molecular Biology, 2008, 375, 855-874.	2.0	60
26	PROCOGNATE: a cognate ligand domain mapping for enzymes. Nucleic Acids Research, 2007, 36, D618-D622.	6.5	42
27	Cognate Ligand Domain Mapping for Enzymes. Journal of Molecular Biology, 2006, 364, 836-852.	2.0	26
28	A bioinformatician's view of the metabolome. BioEssays, 2006, 28, 534-545.	1.2	76
29	A Ligand-centric Analysis of the Diversity and Evolution of Proteinâ€“Ligand Relationships in E.coli. Journal of Molecular Biology, 2005, 347, 415-436.	2.0	24
30	Ligand selectivity and competition between enzymes in silico. Nature Biotechnology, 2004, 22, 1039-1045.	9.4	80
31	A Structure-based Anatomy of the E.coli Metabolome. Journal of Molecular Biology, 2003, 334, 697-719.	2.0	103
32	Using structural motif templates to identify proteins with DNA binding function. Nucleic Acids Research, 2003, 31, 2811-2823.	6.5	57
33	Evaluation of a knowledge-based potential of mean force for scoring docked protein-ligand complexes. Journal of Computational Chemistry, 2001, 22, 673-688.	1.5	22
34	On the molecular discrimination between adenine and guanine by proteins. Nucleic Acids Research, 2001, 29, 4294-4309.	6.5	77
35	Are all short Oâ€“HÂ·Â·Â·O contacts hydrogen bonds? A quantitative look at the nature of Oâ€“HÂ·Â·Â·O intermolecular hydrogen bonds. New Journal of Chemistry, 2000, 24, 5-8.	1.4	48
36	A Non-Empirical Intermolecular Potential for Oxalic Acid Crystal Structures. Journal of Physical Chemistry A, 1999, 103, 6448-6457.	1.1	38

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37	Use of molecular overlap to predict intermolecular repulsion in N Â·Â·Â· Hâ€”O hydrogen bonds. Molecular Physics, 1998, 95, 525-537.	0.8	17
38	Use of molecular overlap to predict intermolecular repulsion in N... H-O hydrogen bonds. Molecular Physics, 1998, 95, 525-537.	0.8	4
39	Hydrogen bonding properties of oxygen and nitrogen acceptors in aromatic heterocycles. , 1997, 18, 2060-2074.		113
40	On the hydrogen bonding abilities of phenols and anisoles. Chemical Physics Letters, 1997, 280, 196-202.	1.2	14
41	Hydrogen bonding properties of oxygen and nitrogen acceptors in aromatic heterocycles. , 1997, 18, 2060.		1