## Vittorio Limongelli

List of Publications by Year in descending order

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101384 114278 4,329 71 36 citations h-index papers

g-index 75 75 75 5132 docs citations times ranked citing authors all docs

63

#	Article	IF	CITATIONS
1	Promoting transparency and reproducibility in enhanced molecular simulations. Nature Methods, 2019, 16, 670-673.	9.0	655
2	Funnel metadynamics as accurate binding free-energy method. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6358-6363.	3.3	337
3	Kinetics of protein–ligand unbinding: Predicting pathways, rates, and rate-limiting steps. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E386-91.	3.3	311
4	Molecular basis of cyclooxygenase enzymes (COXs) selective inhibition. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5411-5416.	3.3	187
5	Unbinding Kinetics of a p38 MAP Kinase Type II Inhibitor from Metadynamics Simulations. Journal of the American Chemical Society, 2017, 139, 4780-4788.	6.6	187
6	Protein–ligand binding with the coarse-grained Martini model. Nature Communications, 2020, 11, 3714.	5.8	139
7	The Gâ€Triplex DNA. Angewandte Chemie - International Edition, 2013, 52, 2269-2273.	7.2	133
8	Structural and Conformational Requisites in DNA Quadruplex Groove Binding: Another Piece to the Puzzle. Journal of the American Chemical Society, 2010, 132, 6425-6433.	6.6	111
9	Conformational Changes in the Epidermal Growth Factor Receptor: Role of the Transmembrane Domain Investigated by Coarse-Grained MetaDynamics Free Energy Calculations. Journal of the American Chemical Society, 2016, 138, 10611-10622.	6.6	103
10	Sampling protein motion and solvent effect during ligand binding. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1467-1472.	3.3	100
11	Ligand binding free-energy calculations with funnel metadynamics. Nature Protocols, 2020, 15, 2837-2866.	5.5	96
12	Ligand binding to telomeric G-quadruplex DNA investigated by funnel-metadynamics simulations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2136-E2145.	3.3	91
13	Ligand binding free energy and kinetics calculation in 2020. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2020, 10, e1455.	6.2	86
14	Mechanistic insight into ligand binding to G-quadruplex DNA. Nucleic Acids Research, 2014, 42, 5447-5455.	6.5	79
15	Design, Synthesis, and Biological Evaluation of Potent Dual Agonists of Nuclear and Membrane Bile Acid Receptors. Journal of Medicinal Chemistry, 2014, 57, 937-954.	2.9	79
16	G-triplex structure and formation propensity. Nucleic Acids Research, 2014, 42, 13393-13404.	6.5	71
17	Design, Synthesis, and Biological Evaluation of Novel Aminobisphosphonates Possessing an in Vivo Antitumor Activity Through a Î Î T Lymphocytes-Mediated Activation Mechanism. Journal of Medicinal Chemistry, 2008, 51, 6800-6807.	2.9	70
18	Investigating the Mechanism of Substrate Uptake and Release in the Glutamate Transporter Homologue Glt <sub>Ph</sub> through Metadynamics Simulations. Journal of the American Chemical Society, 2012, 134, 453-463.	6.6	66

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19	Modeling of Cdc25B Dual Specifity Protein Phosphatase Inhibitors: Docking of Ligands and Enzymatic Inhibition Mechanism. ChemMedChem, 2006, 1, 540-550.	1.6	64
20	Modification on Ursodeoxycholic Acid (UDCA) Scaffold. Discovery of Bile Acid Derivatives As Selective Agonists of Cell-Surface G-Protein Coupled Bile Acid Receptor 1 (GP-BAR1). Journal of Medicinal Chemistry, 2014, 57, 7687-7701.	2.9	62
21	Design, Synthesis and Biological Evaluation of Carboxy Analogues of Arginine Methyltransferase Inhibitor 1 (AMIâ€1). ChemMedChem, 2010, 5, 398-414.	1.6	60
22	Molecular Modeling for Nanomaterial–Biology Interactions: Opportunities, Challenges, and Perspectives. Frontiers in Bioengineering and Biotechnology, 2019, 7, 268.	2.0	55
23	Novel <i>N</i> <sup>2</sup> -Substituted Pyrazolo[3,4- <i>d</i> ]pyrimidine Adenosine A <sub>3</sub> Receptor Antagonists: Inhibition of A <sub>3</sub> -Mediated Human Glioblastoma Cell Proliferation <sup>â€</sup> . Journal of Medicinal Chemistry, 2010, 53, 3954-3963.	2.9	50
24	Energetics and Structural Characterization of the large-scale Functional Motion of Adenylate Kinase. Scientific Reports, 2015, 5, 8425.	1.6	50
25	Binding Mechanism of the Farnesoid X Receptor Marine Antagonist Suvanine Reveals a Strategy To Forestall Drug Modulation on Nuclear Receptors. Design, Synthesis, and Biological Evaluation of Novel Ligands. Journal of Medicinal Chemistry, 2013, 56, 4701-4717.	2.9	49
26	Acetic Acid Aldose Reductase Inhibitors Bearing a Five-Membered Heterocyclic Core with Potent Topical Activity in a Visual Impairment Rat Model. Journal of Medicinal Chemistry, 2008, 51, 3182-3193.	2.9	47
27	The Molecular Mechanism Underlying Ligand Binding to the Membrane-Embedded Site of a G-Protein-Coupled Receptor. Journal of Chemical Theory and Computation, 2018, 14, 2761-2770.	2.3	46
28	New Insight into the Central Benzodiazepine Receptorâ€"Ligand Interactions: Design, Synthesis, Biological Evaluation, and Molecular Modeling of 3-Substituted 6-Phenyl-4 <i>H</i> i>imidazo[1,5- <i>a</i> ][1,4]benzodiazepines and Related Compounds. Journal of Medicinal Chemistry, 2011, 54, 5694-5711.	2.9	45
29	Funnel-Metadynamics and Solution NMR to Estimate Protein–Ligand Affinities. Journal of the American Chemical Society, 2015, 137, 1273-1281.	6.6	44
30	Accelerating the Calculation of Protein–Ligand Binding Free Energy and Residence Times Using Dynamically Optimized Collective Variables. Journal of Chemical Theory and Computation, 2019, 15, 743-750.	2.3	44
31	Ensemble-Docking Approach on BACE-1: Pharmacophore Perception and Guidelines for Drug Design. ChemMedChem, 2007, 2, 667-678.	1.6	43
32	Indolylarylsulfones Carrying a Heterocyclic Tail as Very Potent and Broad Spectrum HIV-1 Non-nucleoside Reverse Transcriptase Inhibitors. Journal of Medicinal Chemistry, 2014, 57, 9945-9957.	2.9	42
33	Ligand Binding, Unbinding, and Allosteric Effects: Deciphering Small-Molecule Modulation of HSP90. Journal of Chemical Theory and Computation, 2019, 15, 6368-6381.	2.3	42
34	The Free Energy Landscape of GABA Binding to a Pentameric Ligand-Gated Ion Channel and Its Disruption by Mutations. Journal of Chemical Theory and Computation, 2016, 12, 3398-3406.	2.3	41
35	Homology Modeling of NR2B Modulatory Domain of NMDA Receptor and Analysis of Ifenprodil Binding. ChemMedChem, 2007, 2, 1498-1510.	1.6	38
36	Ethyl 8-Fluoro-6-(3-nitrophenyl)-4 <i>H</i> -imidazo[1,5- <i>a</i> ][1,4]benzodiazepine-3-carboxylate as Novel, Highly Potent, and Safe Antianxiety Agent. Journal of Medicinal Chemistry, 2008, 51, 4730-4743.	2.9	38

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37	Potent Arylsulfonamide Inhibitors of Tumor Necrosis Factor-α Converting Enzyme Able to Reduce Activated Leukocyte Cell Adhesion Molecule Shedding in Cancer Cell Models. Journal of Medicinal Chemistry, 2010, 53, 2622-2635.	2.9	37
38	Breaking the Dogma of the Metalâ€Coordinating Carboxylate Group in Integrin Ligands: Introducing Hydroxamic Acids to the MIDAS To Tune Potency and Selectivity. Angewandte Chemie - International Edition, 2009, 48, 4436-4440.	7.2	35
39	Bioinformatics and Biosimulations as Toolbox for Peptides and Peptidomimetics Design: Where Are We?. Frontiers in Molecular Biosciences, 2020, 7, 66.	1.6	34
40	Stop Fitan: Antispasmodic Effect of Natural Extract of Chestnut Wood in Guinea Pig Ileum and Proximal Colon Smooth Muscle. Journal of Medicinal Food, 2010, 13, 1104-1110.	0.8	33
41	Steroidal scaffolds as FXR and GPBAR1 ligands: from chemistry to therapeutical application. Future Medicinal Chemistry, 2015, 7, 1109-1135.	1.1	32
42	Hyodeoxycholic acid derivatives as liver X receptor $\hat{l}_{\pm}$ and G-protein-coupled bile acid receptor agonists. Scientific Reports, 2017, 7, 43290.	1.6	30
43	Investigation around the Oxadiazole Core in the Discovery of a New Chemotype of Potent and Selective FXR Antagonists. ACS Medicinal Chemistry Letters, 2019, 10, 504-510.	1.3	27
44	Novel Isoxazole Derivatives with Potent FXR Agonistic Activity Prevent Acetaminophen-Induced Liver Injury. ACS Medicinal Chemistry Letters, 2019, 10, 407-412.	1.3	27
45	Disruption of TFGÎ <sup>2</sup> -SMAD3 pathway by the nuclear receptor SHP mediates the antifibrotic activities of BAR704, a novel highly selective FXR ligand. Pharmacological Research, 2018, 131, 17-31.	3.1	25
46	Perspectives on High-Throughput Ligand/Protein Docking With Martini MD Simulations. Frontiers in Molecular Biosciences, 2021, 8, 657222.	1.6	25
47	Membrane charge dependent states of the β-amyloid fragment Aβ (16–35) with differently charged micelle aggregates. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 660-671.	1.4	24
48	Structure-based drug design targeting the cell membrane receptor GPBAR1: exploiting the bile acid scaffold towards selective agonism. Scientific Reports, 2015, 5, 16605.	1.6	23
49	Targeting Bile Acid Receptors: Discovery of a Potent and Selective Farnesoid X Receptor Agonist as a New Lead in the Pharmacological Approach to Liver Diseases. Frontiers in Pharmacology, 2017, 8, 162.	1.6	23
50	Discovery of Bile Acid Derivatives as Potent ACE2 Activators by Virtual Screening and Essential Dynamics. Journal of Chemical Information and Modeling, 2022, 62, 196-209.	2.5	15
51	Insights on pregnane-X-receptor modulation. Natural and semisynthetic steroids from Theonella marine sponges. European Journal of Medicinal Chemistry, 2014, 73, 126-134.	2.6	14
52	Incisterols, highly degraded marine sterols, are a new chemotype of PXR agonists. Steroids, 2014, 83, 80-85.	0.8	14
53	Marine and Semi-Synthetic Hydroxysteroids as New Scaffolds for Pregnane X Receptor Modulation. Marine Drugs, 2014, 12, 3091-3115.	2.2	13
54	The Glycan Role in the Glycopeptide Immunogenicity Revealed by Atomistic Simulations and Spectroscopic Experiments on the Multiple Sclerosis Biomarker CSF114(Glc). Scientific Reports, 2015, 5, 9200.	1.6	13

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55	Discovery of ((1,2,4-oxadiazol-5-yl)pyrrolidin-3-yl)ureidyl derivatives as selective non-steroidal agonists of the G-protein coupled bile acid receptor-1. Scientific Reports, 2019, 9, 2504.	1.6	13
56	Tailoring of Integrin Ligands: Probing the Charge Capability of the Metal Ion-Dependent Adhesion Site. Journal of Medicinal Chemistry, 2012, 55, 871-882.	2.9	12
57	Structural Insight into the Binding Mode of FXR and GPBAR1 Modulators. Handbook of Experimental Pharmacology, 2019, 256, 111-136.	0.9	8
58	GPBAR1 Activation by C6-Substituted Hyodeoxycholane Analogues Protect against Colitis. ACS Medicinal Chemistry Letters, 2020, 11, 818-824.	1.3	8
59	Improving Small-Molecule Force Field Parameters in Ligand Binding Studies. Frontiers in Molecular Biosciences, 2021, 8, 760283.	1.6	8
60	DDT - Drug Discovery Tool: a fast and intuitive graphics user interface for docking and molecular dynamics analysis. Bioinformatics, 2019, 35, 5328-5330.	1.8	7
61	Identification of cysteinyl-leukotriene-receptor 1 antagonists as ligands for the bile acid receptor GPBAR1. Biochemical Pharmacology, 2020, 177, 113987.	2.0	5
62	$\hat{I}^3$ -Glutamyl 16-diaminopropane derivative of vasoactive intestinal peptide: a potent anti-oxidative agent for human epidermoid cancer cells. Amino Acids, 2010, 39, 661-670.	1.2	4
63	Epoxide functionalization on cholane side chains in the identification of G-protein coupled bile acid receptor (GPBAR1) selective agonists. RSC Advances, 2017, 7, 32877-32885.	1.7	4
64	Drug Repurposing on G Protein-Coupled Receptors Using a Computational Profiling Approach. Frontiers in Molecular Biosciences, 2021, 8, 673053.	1.6	4
65	Discovery of a Potent and Orally Active Dual GPBAR1/CysLT1R Modulator for the Treatment of Metabolic Fatty Liver Disease. Frontiers in Pharmacology, 2022, 13, 858137.	1.6	4
66	Introduction of Nonacidic Side Chains on 6-Ethylcholane Scaffolds in the Identification of Potent Bile Acid Receptor Agonists with Improved Pharmacokinetic Properties. Molecules, 2019, 24, 1043.	1.7	3
67	Structural Basis for Developing Multitarget Compounds Acting on Cysteinyl Leukotriene Receptor 1 and G-Protein-Coupled Bile Acid Receptor 1. Journal of Medicinal Chemistry, 2021, 64, 16512-16529.	2.9	3
68	Binding of the Anti-FIV Peptide C8 to Differently Charged Membrane Models: From First Docking to Membrane Tubulation. Frontiers in Chemistry, 2020, 8, 493.	1.8	2
69	Homo and Heterodimeric Structures of CCR5 and CXCR4: Molecular Dynamics Simulation as an Alternative to X-Ray Diffraction. Biophysical Journal, 2019, 116, 344a.	0.2	1
70	Cover Picture: Breaking the Dogma of the Metal-Coordinating Carboxylate Group in Integrin Ligands: Introducing Hydroxamic Acids to the MIDAS To Tune Potency and Selectivity (Angew. Chem. Int. Ed.) Tj ETQq0 0	0 rg/BT /O\	verdock 10 Tf
71	Highly Enhanced Conformational Sampling of the Transmembrane Domain of Egf Receptor Sheds Light on the Activation Mechanism. Biophysical Journal, 2014, 106, 307a.	0.2	0