Giorgio Amendola

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9226595/publications.pdf

Version: 2024-02-01

20	366	840119 11	794141 19
papers	citations	h-index	g-index

20	20	20	585
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Development of novel dipeptide nitriles as inhibitors of rhodesain of Trypanosoma brucei rhodesiense. European Journal of Medicinal Chemistry, 2022, 236, 114328.	2.6	11
2	Structureâ€“Activity Relationship Studies on Oxazolo[3,4-a]pyrazine Derivatives Leading to the Discovery of a Novel Neuropeptide S Receptor Antagonist with Potent In Vivo Activity. Journal of Medicinal Chemistry, 2021, 64, 4089-4108.	2.9	5
3	Lead Discovery of SARS-CoV-2 Main Protease Inhibitors through Covalent Docking-Based Virtual Screening. Journal of Chemical Information and Modeling, 2021, 61, 2062-2073.	2.5	37
4	Quinolinonyl Non-Diketo Acid Derivatives as Inhibitors of HIV-1 Ribonuclease H and Polymerase Functions of Reverse Transcriptase. Journal of Medicinal Chemistry, 2021, 64, 8579-8598.	2.9	8
5	PyRMD: A New Fully Automated AI-Powered Ligand-Based Virtual Screening Tool. Journal of Chemical Information and Modeling, 2021, 61, 3835-3845.	2.5	21
6	Inhibition studies on carbonic anhydrase isoforms I, II, IV and IX with N-arylsubstituted secondary sulfonamides featuring a bicyclic tetrahydroindazole scaffold. European Journal of Medicinal Chemistry, 2021, 220, 113490.	2.6	9
7	FEPrepare: A Web-Based Tool for Automating the Setup of Relative Binding Free Energy Calculations. Journal of Chemical Information and Modeling, 2021, 61, 4131-4138.	2.5	15
8	Peptidyl Vinyl Ketone Irreversible Inhibitors of Rhodesain: Modifications of the P2 Fragment. ChemMedChem, 2020, 15, 1552-1561.	1.6	17
9	Pyrrolyl Pyrazoles as Non-Diketo Acid Inhibitors of the HIV-1 Ribonuclease H Function of Reverse Transcriptase. ACS Medicinal Chemistry Letters, 2020, 11, 798-805.	1.3	25
10	Development of Novel Benzodiazepineâ€Based Peptidomimetics as Inhibitors of Rhodesain from Trypanosoma brucei rhodesiense. ChemMedChem, 2020, 15, 995-1001.	1.6	10
11	Optimization Strategy of Novel Peptide-Based Michael Acceptors for the Treatment of Human African Trypanosomiasis. Journal of Medicinal Chemistry, 2019, 62, 10617-10629.	2.9	22
12	Novel 2-substituted-benzimidazole-6-sulfonamides as carbonic anhydrase inhibitors: synthesis, biological evaluation against isoforms I, II, IX and XII and molecular docking studies. Journal of Enzyme Inhibition and Medicinal Chemistry, 2019, 34, 1697-1710.	2.5	28
13	Discovery of Pyrido[3â€²,2â€²:5,6]thiopyrano[4,3-d]pyrimidine-Based Antiproliferative Multikinase Inhibitors. ACS Medicinal Chemistry Letters, 2019, 10, 457-462.	1.3	3
14	Discovery of a Novel Chemotype of Histone Lysine Methyltransferase EHMT1/2 (GLP/G9a) Inhibitors: Rational Design, Synthesis, Biological Evaluation, and Co-crystal Structure. Journal of Medicinal Chemistry, 2019, 62, 2666-2689.	2.9	33
15	New insights in the structure-activity relationships of 2-phenylamino-substituted benzothiopyrano[4,3-d]pyrimidines as kinase inhibitors. European Journal of Medicinal Chemistry, 2018, 150, 446-456.	2.6	7
16	4-Substituted Benzenesulfonamides Incorporating Bi/Tricyclic Moieties Act as Potent and Isoform-Selective Carbonic Anhydrase II/IX Inhibitors. Journal of Medicinal Chemistry, 2018, 61, 5765-5770.	2.9	18
17	Development of Novel Peptide-Based Michael Acceptors Targeting Rhodesain and Falcipain-2 for the Treatment of Neglected Tropical Diseases (NTDs). Journal of Medicinal Chemistry, 2017, 60, 6911-6923.	2.9	46
18	Dual MET and SMO Negative Modulators Overcome Resistance to EGFR Inhibitors in Human Nonsmall Cell Lung Cancer. Journal of Medicinal Chemistry, 2017, 60, 7447-7458.	2.9	25

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19	Discovery of the first dual G-triplex/G-quadruplex stabilizing compound: a new opportunity in the targeting of G-rich DNA structures?. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 1271-1280.	1.1	23
20	Best Matching Protein Conformations and Docking Programs for a Virtual Screening Campaign Against SMO Receptor. Molecular Informatics, 2016, 35, 340-349.	1.4	3