

# Mahmoud E S Soliman

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2691149/publications.pdf>

Version: 2024-02-01

268  
papers

4,532  
citations

147801

31  
h-index

182427

51  
g-index

270  
all docs

270  
docs citations

270  
times ranked

5679  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering the molecular mechanisms of selective non-covalency demonstrated differentially by 9-Allylnaphtho[1,8-ef]isoindole-7,8,10(9H)-trione (C11) against fibroblast growth factor receptors 1â€“4. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 2419-2430.	3.5	2
2	Impact of compound mutations I1171Nâ€“+â€“F1174I and I1171Nâ€“+â€“L1198H on the structure of ALK in NSCLC pathogenesis: atomistic insights. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 4735-4743.	3.5	6
3	Structural Insights into the Role of Pseudouridimycin Binding in Disruption of Bacterial RNA Polymerase Bridge Helix Conformational Arrangement. <i>Current Pharmaceutical Biotechnology</i> , 2023, 24, 562-569.	1.6	1
4	Comparative Dynamic Features of Apo and Bound MDM2 Protein Reveal the Mechanism of Inhibitor Recognition for Anti-Cancer Activity. <i>Current Medicinal Chemistry</i> , 2023, 30, 1193-1206.	2.4	0
5	Natural phyto, compounds as possible noncovalent inhibitors against SARS-CoV2 protease: computational approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 2284-2301.	3.5	19
6	In silico design and analysis of NS4B inhibitors against hepatitis C virus. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 1915-1929.	3.5	11
7	Weak spots inhibition in the <i>Mycobacterium tuberculosis</i> antigen 85C target for antitubercular drug design through selective irreversible covalent inhibitor-SER124. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 2934-2954.	3.5	12
8	<i>In silico</i> screening of phytopolyphenolics for the identification of bioactive compounds as novel protease inhibitors effective against SARS-CoV-2. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 10437-10453.	3.5	49
9	A meta-analysis of <i>Cryptosporidium</i> species in humans from southern Africa (2000â€“2020). <i>Journal of Parasitic Diseases</i> , 2022, 46, 304-316.	1.0	6
10	Ï€-hole interactions of group IIIâ€“VI elements with Ï€-systems and Lewis bases: a comparative study. <i>Structural Chemistry</i> , 2022, 33, 9-21.	2.0	9
11	Unusual chalcogenâ€“chalcogen interactions in likeâ€“like and unlike YÏ€Ï€Yâ€“YÏ€Ï€Y complexes (Y = O, S, and Se). <i>Physical Chemistry Chemical Physics</i> , 2022, 24, 3386-3399.	2.8	11
12	A synergistic multitargeted of BET and HDAC: an intra-molecular mechanism of communication in treatment of Waldenström macroglobulinemia. <i>Molecular Simulation</i> , 2022, 48, 197-208.	2.0	3
13	Râ€“hole interactions of group IV-VII radical-containing molecules: A comparative study. <i>Journal of Molecular Graphics and Modelling</i> , 2022, 111, 108097.	2.4	5
14	Highlighting the mechanistic role of Olutasidenib (FT-2102) in the selective inhibition of mutated isocitrate dehydrogenase 1 (IDH1) in cancer therapy. <i>Informatics in Medicine Unlocked</i> , 2022, 28, 100829.	3.4	8
15	Prioritizing the Catalytic Gatekeepers through Pan- Inhibitory Mechanism of Entrectinib against ALK, ROS1 and TRKA Tyrosine Kinases. <i>Cell Biochemistry and Biophysics</i> , 2022, 80, 11-21.	1.8	3
16	An Allosteric Inhibitory Potential of Triterpenes from <i>Combretum racemosum</i> on the Structural and Functional Dynamics of <i>Plasmodium falciparum</i> Lactate Dehydrogenase Binding Landscape. <i>Chemistry and Biodiversity</i> , 2022, 19, e202100646.	2.1	10
17	Dual enzymatic inhibitory mechanism of WM382 on plasmepsin IX and X: Atomistic perspectives from dynamic analysis. <i>Informatics in Medicine Unlocked</i> , 2022, 29, 100874.	3.4	1
18	Conjugated Dienones from Differently Substituted Cinnamaldehyde as Highly Potent Monoamine Oxidase-B Inhibitors: Synthesis, Biochemistry, and Computational Chemistry. <i>ACS Omega</i> , 2022, 7, 8184-8197.	3.5	10

#	ARTICLE	IF	CITATIONS
19	Simulation Models for Prediction of Bioavailability of Medicinal Drugs—the Interface Between Experiment and Computation. <i>AAPS PharmSciTech</i> , 2022, 23, 86.	3.3	12
20	Multi-catalytic Sites Inhibition of Bcl2 Induces Expanding of Hydrophobic Groove: A New Avenue Towards Waldenström Macroglobulinemia Therapy. <i>Protein Journal</i> , 2022, 41, 201-215.	1.6	2
21	π-Hole and LP-Hole Interactions of Pnicogen–Pnicogen Homodimers under the External Electric Field Effect: A Quantum Mechanical Study. <i>ACS Omega</i> , 2022, 7, 11264-11275.	3.5	2
22	Nature-Inspired O-Benzyl Oxime-Based Derivatives as New Dual-Acting Agents Targeting Aldose Reductase and Oxidative Stress. <i>Biomolecules</i> , 2022, 12, 448.	4.0	11
23	Type I–IV Halogen–Halogen Interactions: A Comparative Theoretical Study in Halobenzene–Halobenzene Homodimers. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3114.	4.1	21
24	Lipid traits and type 2 diabetes risk in African ancestry individuals: A Mendelian Randomization study. <i>EBioMedicine</i> , 2022, 78, 103953.	6.1	23
25	Novel Sunifiram-carbamate hybrids as potential dual acetylcholinesterase inhibitor and NMDAR co-agonist: simulation-guided analogue design and pharmacological screening. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2022, 37, 1241-1256.	5.2	6
26	Inside the cracked kernel: establishing the molecular basis of AMG510 and MRTX849 in destabilising KRASG12C mutant switch I and II in cancer treatment. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, , 1-13.	3.5	4
27	External Electric Field Effect on the Strength of π-Hole Interactions: A Theoretical Perspective in Like–Like Carbon-Containing Complexes. <i>Molecules</i> , 2022, 27, 2963.	3.8	4
28	Talazoparib Dual-targeting on Poly (ADP-ribose) Polymerase-1 and -16 Enzymes Offers a Promising Therapeutic Strategy in Small Cell Lung Cancer Therapy: Insight from Biophysical Computations. <i>Cell Biochemistry and Biophysics</i> , 2022, 80, 495-504.	1.8	2
29	From a Computational Perspective: Elucidating the Neurotherapeutic and Inhibitory properties of LRRK2 Kinase Domain by a benzothiazole-based compound. <i>Current Pharmaceutical Biotechnology</i> , 2022, 23, .	1.6	0
30	Revealing the role of fluorine pharmacophore in chalcone scaffold for shifting the MAO-B selectivity: investigation of a detailed molecular dynamics and quantum chemical study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 6126-6139.	3.5	5
31	Molecular Basis of P131 Cryptosporidial-IMPDPH Selectivity—A Structural, Dynamical and Mechanistic Stance. <i>Cell Biochemistry and Biophysics</i> , 2021, 79, 11-24.	1.8	1
32	Investigating the Mechanistic Inhibitory Discrepancies of Novel Halogen and Alkyl Di-substituted Oxadiazole-Based Dibenzoazepine-Dione Derivatives on Poly (ADP-ribose) Polymerase-1. <i>Chemistry and Biodiversity</i> , 2021, 18, e2000802.	2.1	0
33	Could chroman-4-one derivative be a better inhibitor of PTR1? — Reason for the identified disparity in its inhibitory potency in <i>Trypanosoma brucei</i> and <i>Leishmania major</i> . <i>Computational Biology and Chemistry</i> , 2021, 90, 107412.	2.3	4
34	Design, synthesis, and evaluation of dual-site-binding diarylpyrimidines targeting both NNIBP and the NNRTI adjacent site of the HIV-1 reverse transcriptase. <i>European Journal of Medicinal Chemistry</i> , 2021, 211, 113063.	5.5	15
35	Functional Analysis of Single Nucleotide Polymorphism in ZUFSP Protein and Implication in Pathogenesis. <i>Protein Journal</i> , 2021, 40, 28-40.	1.6	1
36	A Mechanistic Probe into the Dual Inhibition of <i>T. cruzi</i> Glucokinase and Hexokinase in Chagas Disease Treatment — A Stone Killing Two Birds?. <i>Chemistry and Biodiversity</i> , 2021, 18, e2000863.	2.1	1

#	ARTICLE	IF	CITATIONS
37	A probable means to an end: exploring P131 pharmacophoric scaffold to identify potential inhibitors of <i>Cryptosporidium parvum</i> inosine monophosphate dehydrogenase. <i>Journal of Molecular Modeling</i> , 2021, 27, 35.	1.8	2
38	Update and Potential Opportunities in CBP [Cyclic Adenosine Monophosphate (cAMP) Response Element-Binding Protein (CREB)-Binding Protein] Research Using Computational Techniques. <i>Protein Journal</i> , 2021, 40, 19-27.	1.6	4
39	Transcription-translation error: In-silico investigation of the structural and functional impact of deleterious single nucleotide polymorphisms in GULP1 gene. <i>Informatics in Medicine Unlocked</i> , 2021, 22, 100503.	3.4	0
40	Exploring the effect of ritonavir and TMC-310911 on SARS-CoV-2 and SARS-CoV main proteases: potential from a molecular perspective. <i>Future Science OA</i> , 2021, 7, FSO640.	1.9	3
41	East to West not North-West: Structure-Based Mechanistic Resolution of 8-Hydroxyl Replacement and Resulting Effects on the Activities of Imidazole-Based Heme Oxygenase-1 Inhibitors. <i>Protein Journal</i> , 2021, 40, 166-174.	1.6	1
42	Piecing the fragments together: Dynamical insights into the enhancement of BRD4-BD1 (BET protein) druggability in cancer chemotherapy using novel 8-methyl-pyrrolo[1,2-a]pyrazin-1(2H)-one derivatives. <i>Current Pharmaceutical Biotechnology</i> , 2021, 22, .	1.6	0
43	Targeting Protein Degradation in Cancer Treatment. <i>Current Chemical Biology</i> , 2021, 15, 5-18.	0.5	0
44	Piece of the puzzle: Remdesivir disassembles the multimeric SARS-CoV-2 RNA-dependent RNA polymerase complex. <i>Cell Biochemistry and Biophysics</i> , 2021, 79, 175-187.	1.8	6
45	Distinguishing the optimal binding mechanism through reversible and irreversible inhibition analysis of HSP72 protein in cancer therapy. <i>Computers in Biology and Medicine</i> , 2021, 132, 104301.	7.0	1
46	Development of Halogenated Pyrazolines as Selective Monoamine Oxidase-B Inhibitors: Deciphering via Molecular Dynamics Approach. <i>Molecules</i> , 2021, 26, 3264.	3.8	9
47	Immunoinformatics prediction of potential B-cell and T-cell epitopes as effective vaccine candidates for eliciting immunogenic responses against Epstein-Barr virus. <i>Biomedical Journal</i> , 2021, 44, 317-337.	3.1	11
48	Dual-Knockout of Mutant Isocitrate Dehydrogenase 1 and 2 Subtypes Towards Glioma Therapy: Structural Mechanistic Insights on the Role of Vorasidenib. <i>Chemistry and Biodiversity</i> , 2021, 18, e2100110.	2.1	7
49	Leveraging on Active Site Similarities; Identification of Potential Inhibitors of Zinc-Finger and UFSP domain Protein (ZUFSP). <i>Current Pharmaceutical Biotechnology</i> , 2021, 22, 995-1004.	1.6	0
50	On the Potentiality of X-T-X <sub>3</sub> Compounds (T = C, Si, and Ge, and X = F, Cl, and Br) as Tetrel- and Halogen-Bond Donors. <i>ACS Omega</i> , 2021, 6, 19330-19341.	3.5	11
51	Prospecting the therapeutic edge of a novel compound (B12) over berberine in the selective targeting of Retinoid X Receptor in colon cancer. <i>Journal of Molecular Modeling</i> , 2021, 27, 231.	1.8	6
52	Comparison of irreversible inhibition targeting HSP72 protein: the resurgence of covalent drug developments. <i>Molecular Simulation</i> , 2021, 47, 1093-1103.	2.0	2
53	Blue Biotechnology: Computational Screening of Sarcophyton Cembranoid Diterpenes for SARS-CoV-2 Main Protease Inhibition. <i>Marine Drugs</i> , 2021, 19, 391.	4.6	22
54	Insight into the Therapeutic Potential of a Bicyclic Hydroxypyridone Compound 2-(2,4-dichlorophenyl)methyl-7-hydroxy-1,2,3,4-tetrahydro-8H-pyrrolo[1,2-a]pyrazin-8-one as COMT Inhibitor in the Treatment of Parkinson's Disease: A Molecular Dynamic Simulation Approach. <i>Chemistry and Biodiversity</i> , 2021, 18, e2100204.	2.1	2

#	ARTICLE	IF	CITATIONS
55	The Binding of Remdesivir to SARS-CoV-2 RNA-Dependent RNA Polymerase May Pave The Way Towards the Design of Potential Drugs for COVID-19 Treatment. <i>Current Pharmaceutical Biotechnology</i> , 2021, 22, 1520-1537.	1.6	4
56	Unveiling the mechanistic roles of chlorine substituted phthalazinone-based compounds containing chlorophenyl moiety towards the differential inhibition of poly (ADP-ribose) polymerase-1 in the treatment of lung cancer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-9.	3.5	1
57	Closing the Gap: An Atomistic Structural and Functional Perspective of S. mansoni Universal Stress G4LZ13 Protein in Complex with Phenolic Compounds. <i>Current Drug Discovery Technologies</i> , 2021, 18, e01102020186453.	1.2	0
58	Effect of External Electric Field on Tetrel Bonding Interactions in (FTF <sub>3</sub> - $\hat{A}$ - $\hat{A}$ -FH) Complexes (T) Tj ETQq,0,0 rgBT <sub>9</sub> /Overlock	3.5	9
59	Structure-based identification of novel scaffolds as potential HIV-1 entry inhibitors involving CCR5. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-12.	3.5	0
60	Diagnostic, Prognostic and Therapeutic Potential of Heat Shock Proteins in Schistosomiasis and Bladder Cancer: A Review. <i>Letters in Drug Design and Discovery</i> , 2021, 18, 650-665.	0.7	2
61	Glioma-Targeted Therapeutics: Computer-Aided Drug Design Prospective. <i>Protein Journal</i> , 2021, 40, 601-655.	1.6	9
62	Selective SIRT2 inhibitors as promising anticancer therapeutics: An update from 2016 to 2020. <i>European Journal of Medicinal Chemistry</i> , 2021, 224, 113709.	5.5	16
63	Structural alterations in the catalytic core of hSIRT2 enzyme predict therapeutic benefits of <i>Garcinia mangostana</i> derivatives in Alzheimer's disease: molecular dynamics simulation study. <i>RSC Advances</i> , 2021, 11, 8003-8018.	3.6	7
64	Atomistic insights into the selective therapeutic activity of 6-(2,4-difluorophenoxy)-5-((ethylmethyl)pyridine-3-yl)-8-methylpyrrolo[1,2-a]pyrazin-1(2H)-one towards bromodomain-containing proteins. <i>Computational Biology and Chemistry</i> , 2021, 95, 107592.	2.3	0
65	Mechanistic Insights into the Selective Dual BET and PLK1 Inhibitory Activity of a Novel Benzamide Compound in Castration-Resistant Prostate Cancer. <i>Chemistry and Biodiversity</i> , 2021, 18, e2100519.	2.1	1
66	$\pi$ -Hole Interactions of Tetrahedral Group IV-VIII Lewis Acid Centers with Lewis Bases: A Comparative Study. <i>ChemistrySelect</i> , 2021, 6, 11856-11864.	1.5	5
67	Genome-Wide Association and Mendelian Randomization Analysis Reveal the Causal Relationship Between White Blood Cell Subtypes and Asthma in Africans. <i>Frontiers in Genetics</i> , 2021, 12, 749415.	2.3	4
68	Dual-Inhibition of Human N-Myristoyltransferase Subtypes Halts Common Cold Pathogenesis: Atomistic Perspectives from the Case of IMP-1088**. <i>Chemistry and Biodiversity</i> , 2021, , .	2.1	1
69	Dual targeting approach for Mycobacterium tuberculosis drug discovery: insights from DFT calculations and molecular dynamics simulations. <i>Structural Chemistry</i> , 2020, 31, 557-571.	2.0	12
70	An analogue of a kinase inhibitor exhibits subjective characteristics that contribute to its inhibitory activities as a potential anti-cancer candidate: insights through computational biomolecular modelling of UM-164 binding with lyn protein. <i>RSC Advances</i> , 2020, 10, 145-161.	3.6	11
71	Human Rhinovirus Inhibition Through Capsid $\epsilon$ -Canyon-Perturbation: Structural Insights into The Role of a Novel Benzothioephene Derivative. <i>Cell Biochemistry and Biophysics</i> , 2020, 78, 3-13.	1.8	9
72	Leaving no stone unturned: Allosteric targeting of SARS-CoV-2 spike protein at putative druggable sites disrupts human angiotensin-converting enzyme interactions at the receptor binding domain. <i>Informatics in Medicine Unlocked</i> , 2020, 21, 100451.	3.4	17

#	ARTICLE	IF	CITATIONS
73	Probing the Highly Disparate Dual Inhibitory Mechanisms of Novel Quinazoline Derivatives against Mycobacterium tuberculosis Protein Kinases A and B. <i>Molecules</i> , 2020, 25, 4247.	3.8	1
74	A brief overview on recent advances in spiro[chromane-2,4-piperidine]-4(3H)-one-functionalized compounds in medicinal chemistry research. <i>Bioorganic and Medicinal Chemistry</i> , 2020, 28, 115813.	3.0	16
75	Computational and drug target analysis of functional single nucleotide polymorphisms associated with Haemoglobin Subunit Beta (HBB) gene. <i>Computers in Biology and Medicine</i> , 2020, 125, 104018.	7.0	1
76	Identification of potential SARS-CoV-2 inhibitors from South African medicinal plant extracts using molecular modelling approaches. <i>South African Journal of Botany</i> , 2020, 133, 273-284.	2.5	24
77	Supramolecular self-assembled drug delivery system (SADDs) of vancomycin and tocopherol succinate as an antibacterial agent: <i>in vitro</i> , <i>in silico</i> and <i>in vivo</i> evaluations. <i>Pharmaceutical Development and Technology</i> , 2020, 25, 1090-1108.	2.4	7
78	Formulation of pH-Responsive Quatsomes from Quaternary Bicephalic Surfactants and Cholesterol for Enhanced Delivery of Vancomycin against Methicillin Resistant Staphylococcus aureus. <i>Pharmaceutics</i> , 2020, 12, 1093.	4.5	21
79	Natural Products Database Screening for the Discovery of Naturally Occurring SARS-CoV-2 Spike Glycoprotein Blockers. <i>ChemistrySelect</i> , 2020, 5, 13309-13317.	1.5	24
80	Coupling of HSP72 $\pm$ -Helix Subdomains by the Unexpected Irreversible Targeting of Lysine-56 over Cysteine-17; Coevolution of Covalent Bonding. <i>Molecules</i> , 2020, 25, 4239.	3.8	0
81	Polymorphism-aided Selective Targeting and Inhibition of Caspase-6 by a Novel Allosteric Inhibitor Towards Efficient Alzheimer's Disease Treatment. <i>Cell Biochemistry and Biophysics</i> , 2020, 78, 291-299.	1.8	1
82	Druggability and drug-likeness concepts in drug design: are biomodelling and predictive tools having their say?. <i>Journal of Molecular Modeling</i> , 2020, 26, 120.	1.8	45
83	Antibiotic resistance: bioinformatics-based understanding as a functional strategy for drug design. <i>RSC Advances</i> , 2020, 10, 18451-18468.	3.6	45
84	Thompson loop: opportunities for antitubercular drug design by targeting the weak spot in demethylmenaquinone methyltransferase protein. <i>RSC Advances</i> , 2020, 10, 23466-23483.	3.6	14
85	Delving into the Characteristic Features of Menace-Mycobacterium tuberculosis Homologs: A Structural Dynamics and Proteomics Perspectives. <i>Protein Journal</i> , 2020, 39, 118-132.	1.6	7
86	Covalent Versus Non-covalent Enzyme Inhibition: Which Route Should We Take? A Justification of the Good and Bad from Molecular Modelling Perspective. <i>Protein Journal</i> , 2020, 39, 97-105.	1.6	36
87	Exploring the ring potential of 2,4-diaminopyrimidine derivatives towards the identification of novel caspase-1 inhibitors in Alzheimer's disease therapy. <i>Journal of Molecular Modeling</i> , 2020, 26, 68.	1.8	16
88	Lipid-Embedded Molecular Dynamics Simulation Model for Exploring the Reverse Prostaglandin D2 Agonism of CT133 towards CRTH2 in the Treatment of Type 2 Inflammation Dependent Diseases. <i>Chemistry and Biodiversity</i> , 2020, 17, e1900548.	2.1	4
89	The Dual-Targeting Activity of the Metabolite Substrate of Para-amino Salicylic Acid in the Mycobacterial Folate Pathway: Atomistic and Structural Perspectives. <i>Protein Journal</i> , 2020, 39, 106-117.	1.6	2
90	Triple Mycobacterial ATP-synthase mutations impedes Bedaquiline binding: Atomistic and structural perspectives. <i>Computational Biology and Chemistry</i> , 2020, 85, 107204.	2.3	7

#	ARTICLE	IF	CITATIONS
91	InÂvitro, in silico studies of newly isolated tetrahydro-4-(7-hydroxy-10-methoxy-6,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 747 Td boonei stem bark. Journal of Molecular Structure, 2020, 1216, 128225.	3.6	3
92	Exploring the Role of Asp1116 in Selective Drug Targeting of CREBcAMP- Responsive Element-binding Protein Implicated in Prostate Cancer. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 178-184.	1.1	5
93	Integrating Bioinformatics Strategies in Cancer Immunotherapy: Current and Future Perspectives. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 687-698.	1.1	7
94	Tweaking Î±-Galactoceramides: Probing the Dynamical Mechanisms of Improved Recognition for Invariant Natural Killer T-cell Receptor in Cancer Immunotherapeutics. Current Pharmaceutical Biotechnology, 2020, 21, 1354-1367.	1.6	2
95	Zoning in on Tankyrases: A Brief Review on the Past, Present and Prospective Studies. Anti-Cancer Agents in Medicinal Chemistry, 2020, 19, 1920-1934.	1.7	2
96	In Silico Repurposing of J147 for Neonatal Encephalopathy Treatment: Exploring Molecular Mechanisms of Mutant Mitochondrial ATP Synthase. Current Pharmaceutical Biotechnology, 2020, 21, 1551-1566.	1.6	5
97	Withdrawal Notice: Elucidating the Disparate Inhibitory Mechanisms of Novel 1-Heteroaryl-1,3-Propanediamine Derivatives and Maraviroc towards C-C Chemokine Receptor 5: Insights for Structural Modifications in HIV-1 Drug Discovery. Medicinal Chemistry, 2020, 17, .	1.5	1
98	DFT Study of the Structural and Electronic Properties of Selected Organogold(III) Compounds with Characteristic Anticancer Activity. Russian Journal of Physical Chemistry A, 2019, 93, 1543-1558.	0.6	15
99	Probing Binding Landscapes and Molecular Recognition Mechanisms of Atypical Antipsychotic Drugs towards the Selective Targeting of D<sub>2</sub> Dopamine Receptor. Molecular Informatics, 2019, 38, e1900044.	2.5	5
100	From genomic variation to protein aberration: Mutational analysis of single nucleotide polymorphism present in ULBP6 gene and implication in immune response. Computers in Biology and Medicine, 2019, 111, 103354.	7.0	7
101	â€Piperazingâ€™™ the catalytic gatekeepers: unraveling the pan-inhibition of SRC kinases; LYN, FYN and BLK by masitinib. Future Medicinal Chemistry, 2019, 11, 2365-2380.	2.3	2
102	CF3â€Pyridinyl Substitution on Antimalarial Therapeutics: Probing Differential Ligand Binding and Dynamical Inhibitory Effects of a Novel Triazolopyrimidineâ€Based Inhibitor on Plasmodium falciparum Dihydroorotate Dehydrogenase. Chemistry and Biodiversity, 2019, 16, e1900365.	2.1	12
103	Selective Covalent Inhibition of â€Allosteric Cys121â€Distort the Binding of PTP1B Enzyme: A Novel Therapeutic Approach for Cancer Treatment. Cell Biochemistry and Biophysics, 2019, 77, 203-211.	1.8	13
104	Tracing Potential Covalent Inhibitors of an E3 Ubiquitin Ligase through Target-Focused Modelling. Molecules, 2019, 24, 3125.	3.8	4
105	Identification of highly potent and selective Cdc25 protein phosphatases inhibitors from miniaturization click-chemistry-based combinatorial libraries. European Journal of Medicinal Chemistry, 2019, 183, 111696.	5.5	26
106	Unveiling a New Era in Malaria Therapeutics: A Tailored Molecular Approach Towards the Design of Plasmeprin IX Inhibitors. Protein Journal, 2019, 38, 616-627.	1.6	11
107	The irony of chirality â€ unveiling the distinct mechanistic binding and activities of 1-(3-(4-amino-5-(7-methoxy-5-methylbenzo[<i>b</i>]thiophen-2-yl)-7<i>H</i>-pyrrolo[2,3-<i>d</i>]pyrimidin-7-yl)pyrrolidin-1-yl)prop-2-ene enantiomers as irreversible covalent FGFR4 inhibitors. Organic and Biomolecular Chemistry, 2019, 17, 1176-1190.	2.8	24
108	Molecular mechanism of resveratrol inhibition of Zika virus NS3 helicase: behind the scenes. Future Virology, 2019, 14, 73-84.	1.8	5

#	ARTICLE	IF	CITATIONS
109	Halting ionic shuttle to disrupt the synthetic machinery—Structural and molecular insights into the inhibitory roles of Bedaquiline towards <i>Mycobacterium tuberculosis</i> ATP synthase in the treatment of tuberculosis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 16108-16119.	2.6	9
110	Revealing the distinct mechanistic binding and activity of 5-(1-(3,5-dichloropyridin-4-yl)ethoxy)-3-(5-(4-methylpiperazin-1-yl)-1 <i>H</i> -benzo[ <i>d</i> ]imidazol-2-yl)-1 <i>H</i> -indazole enantiomers against FGFR1. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 15120-15132.		
111	Drug promiscuity: Exploring the polypharmacology potential of 1, 3, 6-trisubstituted 1, 4-diazepane-7-ones as an inhibitor of the “god father” of immune checkpoint. <i>Computational Biology and Chemistry</i> , 2019, 80, 433-440.	2.3	14
112	Deciphering the canonical blockade of activated Hageman factor (FXIIa) by benzamidine in the coagulation cascade: A thorough dynamical perspective. <i>Chemical Biology and Drug Design</i> , 2019, 94, 1905-1918.	3.2	2
113	Broadening the horizon: Integrative pharmacophore-based and cheminformatics screening of novel chemical modulators of mitochondria ATP synthase towards interventive Alzheimer’s disease therapy. <i>Medical Hypotheses</i> , 2019, 130, 109277.	1.5	12
114	Deciphering the “Elixir of Life”: Dynamic Perspectives into the Allosteric Modulation of Mitochondrial ATP Synthase by J147, a Novel Drug in the Treatment of Alzheimer’s Disease. <i>Chemistry and Biodiversity</i> , 2019, 16, e1900085.	2.1	12
115	A Synergistic Combination Against Chronic Myeloid Leukemia: An Intra-molecular Mechanism of Communication in BCR-ABL1 Resistance. <i>Protein Journal</i> , 2019, 38, 142-150.	1.6	3
116	Recruiting monomer for dimer formation: resolving the antagonistic mechanisms of novel immune check point inhibitors against Programmed Death Ligand-1 in cancer immunotherapy. <i>Molecular Simulation</i> , 2019, 45, 777-789.	2.0	17
117	Distinguishing the optimal binding mechanism of an E3 ubiquitin ligase: Covalent versus noncovalent inhibition. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 12859-12869.	2.6	4
118	From a computational point of view: deciphering the molecular synergism between oxidative stress-induced lipid peroxidation products and metabolic dysfunctionality of human liver mitochondrial aldehyde dehydrogenase-2. <i>Molecular Simulation</i> , 2019, 45, 652-665.	2.0	1
119	Tracing Potential Covalent Inhibitors of an E3 Ubiquitin Ligase Through Target-Focused Modelling. <i>Proceedings (mdpi)</i> , 2019, 22, 103.	0.2	0
120	Dynamic perspectives into the mechanisms of mutation-induced p53-DNA binding loss and inactivation using active perturbation theory: Structural and molecular insights toward the design of potent reactivators in cancer therapy. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 951-966.	2.6	18
121	Probing Gallate-Mediated Selectivity and High-Affinity Binding of Epigallocatechin Gallate: a Way-Forward in the Design of Selective Inhibitors for Anti-apoptotic Bcl-2 Proteins. <i>Applied Biochemistry and Biotechnology</i> , 2019, 187, 1061-1080.	2.9	24
122	Covalent vs. Non-Covalent Inhibition: Tackling Drug Resistance in EGFR—A Thorough Dynamic Perspective. <i>Chemistry and Biodiversity</i> , 2019, 16, e1800518.	2.1	8
123	Noteworthy effect of slight variation in aliphatic chain length of trisubstituted imidazole inhibitors against epidermal growth factor receptor L858R/T790M/C797S mutant in cancer therapy. <i>Chemical Biology and Drug Design</i> , 2019, 93, 798-810.	3.2	7
124	Probing the Dynamic Mechanism of Uncommon Allosteric Inhibitors Optimized to Enhance Drug Selectivity of SHP2 with Therapeutic Potential for Cancer Treatment. <i>Applied Biochemistry and Biotechnology</i> , 2019, 188, 260-281.	2.9	11
125	A dual target of Plasmeprin IX and X: Unveiling the atomistic superiority of a core chemical scaffold in malaria therapy. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 7876-7887.	2.6	16
126	Domperidone nanocrystals with boosted oral bioavailability: fabrication, evaluation and molecular insight into the polymer-domperidone nanocrystal interaction. <i>Drug Delivery and Translational Research</i> , 2019, 9, 284-297.	5.8	32

#	ARTICLE	IF	CITATIONS
127	Microbes, not humans: exploring the molecular basis of Pseudouridimycin selectivity towards bacterial and not human RNA polymerase. <i>Biotechnology Letters</i> , 2019, 41, 115-128.	2.2	7
128	Navigating Research Toward the Re-emerging Nipah Virus- A New Piece to the Puzzle. <i>Current Pharmaceutical Design</i> , 2019, 25, 1392-1401.	1.9	1
129	Same Target, Different Therapeutic Outcomes: The Case of CAY10471 and Fevipiprant on CRTh2 Receptor in Treatment of Allergic Rhinitis and Asthma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2019, 22, 521-533.	1.1	7
130	Exploring the Lapse in Druggability: Sequence Analysis, Structural Dynamics and Binding Site Characterization of K-RasG12C Variant, a Feasible Oncotherapeutics Target. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2019, 18, 1540-1550.	1.7	7
131	Turning to Computer-aided Drug Design in the Treatment of Diffuse Large B-cell Lymphoma: Has it been Helpful?. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2019, 19, 1325-1339.	1.7	2
132	From the Explored to the Unexplored: Computer-Tailored Drug Design Attempts in the Discovery of Selective Caspase Inhibitors. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2019, 22, 432-444.	1.1	4
133	The Perplexity of Synergistic Duality: Inter-molecular Mechanisms of Communication in BCR-ABL1. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2019, 19, 1642-1650.	1.7	3
134	Reversible versus irreversible inhibition modes of ERK2: a comparative analysis for ERK2 protein kinase in cancer therapy. <i>Future Medicinal Chemistry</i> , 2018, 10, 1003-1015.	2.3	38
135	Alcohol Metabolic Inefficiency: Structural Characterization of Polymorphism-Induced ALDH2 Dysfunctionality and Allosteric Site Identification for Design of Potential Wildtype Reactivators. <i>Protein Journal</i> , 2018, 37, 216-222.	1.6	12
136	Allosteric inhibition abrogates dysregulated LFA-1 activation: Structural insight into mechanisms of diminished immunologic disease. <i>Computational Biology and Chemistry</i> , 2018, 73, 49-56.	2.3	26
137	An "All-In-One" Pharmacophoric Architecture for the Discovery of Potential Broad-Spectrum Anti-Flavivirus Drugs. <i>Applied Biochemistry and Biotechnology</i> , 2018, 185, 799-814.	2.9	8
138	Emergence of a Promising Lead Compound in the Treatment of Triple Negative Breast Cancer: An Insight into Conformational Features and Ligand Binding Landscape of c-Src Protein with UM-164. <i>Applied Biochemistry and Biotechnology</i> , 2018, 185, 655-675.	2.9	10
139	Dual Drug Targeting of Mutant BcrAbl Induces Inactive Conformation: New Strategy for the Treatment of Chronic Myeloid Leukemia and Overcoming Monotherapy Resistance. <i>Chemistry and Biodiversity</i> , 2018, 15, e1700533.	2.1	10
140	Hybrid 2D/3D-quantitative structure-activity relationship and modeling studies perspectives of pepstatin A analogs as cathepsin D inhibitors. <i>Future Medicinal Chemistry</i> , 2018, 10, 5-26.	2.3	5
141	Re-emergence of an orphan therapeutic target for the treatment of resistant prostate cancer a thorough conformational and binding analysis for ROR- $\beta$ protein. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 335-350.	3.5	5
142	Zika virus NS5 protein potential inhibitors: an enhanced <i>in silico</i> approach in drug discovery. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 1118-1133.	3.5	61
143	From mutational inactivation to aberrant gain-of-function: Unraveling the structural basis of mutant p53 oncogenic transition. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 2646-2652.	2.6	39
144	Ligand- and structure-based <i>in silico</i> studies to identify kinesin spindle protein (KSP) inhibitors as potential anticancer agents. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 3687-3704.	3.5	26

#	ARTICLE	IF	CITATIONS
145	Discovery of new class of methoxy carrying isoxazole derivatives as COX-II inhibitors: Investigation of a detailed molecular dynamics study. <i>Journal of Molecular Structure</i> , 2018, 1157, 19-28.	3.6	10
146	Using bioinformatics tools for the discovery of Dengue RNA-dependent RNA polymerase inhibitors. <i>PeerJ</i> , 2018, 6, e5068.	2.0	8
147	Allosteric inhibition induces an open WPD-loop: a new avenue towards glioblastoma therapy. <i>RSC Advances</i> , 2018, 8, 40187-40197.	3.6	20
148	Targeting HCV polymerase: a structural and dynamic perspective into the mechanism of selective covalent inhibition. <i>RSC Advances</i> , 2018, 8, 42210-42222.	3.6	14
149	Does Size Really Matter? Probing the Efficacy of Structural Reduction in the Optimization of Bioderived Compounds – A Computational –Proof-of-Concept–. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 573-586.	4.1	17
150	Covalent simulations of covalent/irreversible enzyme inhibition in drug discovery: a reliable technical protocol. <i>Future Medicinal Chemistry</i> , 2018, 10, 2265-2275.	2.3	9
151	Exploring the C-terminal Tail Dynamics: Structural and Molecular Perspectives into the Therapeutic Activities of Novel CRMP-2 Inhibitors, Naringenin and Naringenin-7-O-glucuronide, in the Treatment of Alzheimer's Disease. <i>Chemistry and Biodiversity</i> , 2018, 15, e1800437.	2.1	14
152	Exploring the Structural Mechanism of Covalently Bound E3 Ubiquitin Ligase: Catalytic or Allosteric Inhibition?. <i>Protein Journal</i> , 2018, 37, 500-509.	1.6	9
153	In Silico SAR Studies of HIV-1 Inhibitors. <i>Pharmaceuticals</i> , 2018, 11, 69.	3.8	13
154	An update on the discovery and development of selective heat shock protein inhibitors as anti-cancer therapy. <i>Expert Opinion on Drug Discovery</i> , 2018, 13, 903-918.	5.0	16
155	Across the blood-brain barrier: Neurotherapeutic screening and characterization of naringenin as a novel CRMP-2 inhibitor in the treatment of Alzheimer's disease using bioinformatics and computational tools. <i>Computers in Biology and Medicine</i> , 2018, 98, 168-177.	7.0	49
156	Bioinformatics-based tools in drug discovery: the cartography from single gene to integrative biological networks. <i>Drug Discovery Today</i> , 2018, 23, 1658-1665.	6.4	14
157	Co-inhibition as a strategic therapeutic approach to overcome rifampin resistance in tuberculosis therapy: atomistic insights. <i>Future Medicinal Chemistry</i> , 2018, 10, 1665-1675.	2.3	27
158	Induced Mutation Proves a Potential Target for TB Therapy: A Molecular Dynamics Study on LprG. <i>Cell Biochemistry and Biophysics</i> , 2018, 76, 345-356.	1.8	32
159	Solving the riddle: Unraveling the mechanisms of blocking the binding of leukotoxin by therapeutic antagonists in periodontal diseases. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 9364-9379.	2.6	7
160	A panoptic uncovering of the dynamical evolution of the Zika Virus NS5 methyltransferase binding site loops – zeroing in on the molecular landscape. <i>Chemical Biology and Drug Design</i> , 2018, 92, 1838-1850.	3.2	5
161	Egress and invasion machinery of malaria: an in-depth look into the structural and functional features of the flap dynamics of plasmeprin IX and X. <i>RSC Advances</i> , 2018, 8, 21829-21840.	3.6	15
162	Review on the Biological Mechanisms Associated with Depo-Provera and HIV-1 Risk Acquisition in Women. <i>Cell Biochemistry and Biophysics</i> , 2018, 76, 73-82.	1.8	1

#	ARTICLE	IF	CITATIONS
163	Synergistic Interplay of The Co-administration of Rifampin And Newly Developed Anti-TB Drug: Could It Be a Promising New Line of TB Therapy?. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2018, 21, 453-460.	1.1	15
164	Covalent Inhibition in Drug Discovery: Filling the Void in Literature. <i>Current Topics in Medicinal Chemistry</i> , 2018, 18, 1135-1145.	2.1	12
165	Diabetes mellitus caused by mutations in human insulin: analysis of impaired receptor binding of insulins <i>Wakayama</i> , <i>Los Angeles</i> and <i>Chicago</i> using pharmacoinformatics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 724-737.	3.5	13
166	Identification of Novel Potential gp120 of HIV-1 Antagonist Using Per-Residue Energy Contribution-Based Pharmacophore modelling. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 406-418.	3.6	6
167	VP40 of the Ebola Virus as a Target for EboV Therapy: Comprehensive Conformational and Inhibitor Binding Landscape from Accelerated Molecular Dynamics. <i>Cell Biochemistry and Biophysics</i> , 2017, 75, 65-78.	1.8	9
168	Pharmacophore-Based 3D-QSAR Analysis of Thienyl Chalcones as a New Class of Human MAO-B Inhibitors: Investigation of Combined Quantum Chemical and Molecular Dynamics Approach. <i>Journal of Physical Chemistry B</i> , 2017, 121, 1186-1203.	2.6	40
169	Potential Ebola drug targets "filling the gap: a critical step forward towards the design and discovery of potential drugs. <i>Biologia (Poland)</i> , 2017, 72, 1-13.	1.5	18
170	Non-active site mutations disturb the loop dynamics, dimerization, viral budding and egress of VP40 of the Ebola virus. <i>Molecular BioSystems</i> , 2017, 13, 585-597.	2.9	16
171	The impact of Thr91 mutation on c-Src resistance to UM-164: molecular dynamics study revealed a new opportunity for drug design. <i>Molecular BioSystems</i> , 2017, 13, 1157-1171.	2.9	48
172	Comprehensive Computational and Experimental Analysis of Biomaterial toward the Behavior of Imidazolium-Based Ionic Liquids: An Interplay between Hydrophilic and Hydrophobic Interactions. <i>Journal of Physical Chemistry B</i> , 2017, 121, 4909-4922.	2.6	17
173	An unexplored remarkable PNIPAM-osmolyte interaction study: An integrated experimental and simulation approach. <i>Journal of Colloid and Interface Science</i> , 2017, 504, 417-428.	9.4	33
174	Delving into Zika virus structural dynamics "a closer look at NS3 helicase loop flexibility and its role in drug discovery. <i>RSC Advances</i> , 2017, 7, 22133-22144.	3.6	28
175	Anti-oxidant behavior of functionalized chalcone-a combined quantum chemical and crystallographic structural investigation. <i>Journal of Molecular Structure</i> , 2017, 1146, 301-308.	3.6	31
176	Hybrid Receptor-Bound/MM-GBSA-Per-residue Energy-Based Pharmacophore Modelling: Enhanced Approach for Identification of Selective LTA4H Inhibitors as Potential Anti-inflammatory Drugs. <i>Cell Biochemistry and Biophysics</i> , 2017, 75, 35-48.	1.8	11
177	Preparation and Optimization of Meropenem-Loaded Solid Lipid Nanoparticles: In Vitro Evaluation and Molecular Modeling. <i>AAPS PharmSciTech</i> , 2017, 18, 2011-2025.	3.3	18
178	Identification of Binding Mode and Prospective Structural Features of Novel Nef Protein Inhibitors as Potential Anti-HIV Drugs. <i>Cell Biochemistry and Biophysics</i> , 2017, 75, 49-64.	1.8	9
179	Brain grants permission of access to Zika virus but denies entry to drugs: a molecular modeling perspective to infiltrate the boundary. <i>RSC Advances</i> , 2017, 7, 47416-47424.	3.6	6
180	Road Map for the Structure-Based Design of Selective Covalent HCV NS3/4A Protease Inhibitors. <i>Protein Journal</i> , 2017, 36, 397-406.	1.6	6

#	ARTICLE	IF	CITATIONS
181	Dynamics of allosteric modulation of lymphocyte function associated antigen-1 closure-open switch: unveiling the structural mechanisms associated with outside-in signaling activation. <i>Biotechnology Letters</i> , 2017, 39, 1843-1851.	2.2	11
182	Tailored-pharmacophore model to enhance virtual screening and drug discovery: a case study on the identification of potential inhibitors against drug-resistant <i>Mycobacterium tuberculosis</i> (3R)-hydroxyacyl-ACP dehydratases. <i>Future Medicinal Chemistry</i> , 2017, 9, 1055-1071.	2.3	8
183	Sequence, Structural Analysis and Metrics to Define the Unique Dynamic Features of the Flap Regions Among Aspartic Proteases. <i>Protein Journal</i> , 2017, 36, 385-396.	1.6	13
184	Characterization of Thienylchalcones as hMAO-B Inhibitors: Synthesis, Biochemistry and Molecular Dynamics Studies. <i>ChemistrySelect</i> , 2017, 2, 11113-11119.	1.5	23
185	The Identification of potential human rhinovirus inhibitors: exploring the binding landscape of HRV-3C protease through PRED pharmacophore screening. <i>Future Virology</i> , 2017, 12, 747-759.	1.8	1
186	Novel quinazolinone-based 2,4-thiazolidinedione-3-acetic acid derivatives as potent aldose reductase inhibitors. <i>Future Medicinal Chemistry</i> , 2017, 9, 2147-2166.	2.3	14
187	Implementing QM in docking calculations: is it a waste of computational time?. <i>Drug Discovery Today</i> , 2017, 22, 1216-1223.	6.4	35
188	Characterizing the ligand-binding landscape of Zika NS3 helicase-promising lead compounds as potential inhibitors. <i>Future Virology</i> , 2017, 12, 261-273.	1.8	17
189	Can We Rely on Computational Predictions To Correctly Identify Ligand Binding Sites on Novel Protein Drug Targets? Assessment of Binding Site Prediction Methods and a Protocol for Validation of Predicted Binding Sites. <i>Cell Biochemistry and Biophysics</i> , 2017, 75, 15-23.	1.8	46
190	Recent advancements in the development of anti-tuberculosis drugs. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 370-386.	2.2	97
191	Ebola virus: A gap in drug design and discovery – experimental and computational perspective. <i>Chemical Biology and Drug Design</i> , 2017, 89, 297-308.	3.2	17
192	Metal complexes in cancer therapy – an update from drug design perspective. <i>Drug Design, Development and Therapy</i> , 2017, Volume 11, 599-616.	4.3	668
193	Quantum mechanics implementation in drug-design workflows: does it really help?. <i>Drug Design, Development and Therapy</i> , 2017, Volume 11, 2551-2564.	4.3	39
194	Therapeutic, Molecular and Computational Aspects of Novel Monoamine Oxidase (MAO) Inhibitors. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 492-509.	1.1	13
195	Homology Modeling in Drug Discovery-an Update on the Last Decade. <i>Letters in Drug Design and Discovery</i> , 2017, 14, .	0.7	13
196	Per-residue energy decomposition pharmacophore model to enhance virtual screening in drug discovery: a study for identification of reverse transcriptase inhibitors as potential anti-HIV agents. <i>Drug Design, Development and Therapy</i> , 2016, 10, 1365.	4.3	21
197	Mechanism of Inhibition of Hsp90 Dimerization by Gyrase B Inhibitor Coumermycin A1 (C <sub>6</sub> A1) Revealed by Molecular Dynamics Simulations and Thermodynamic Calculations. <i>Cell Biochemistry and Biophysics</i> , 2016, 74, 353-363.	1.8	6
198	Sliding Clamp of DNA Polymerase III as a Drug Target for TB Therapy: Comprehensive Conformational and Binding Analysis from Molecular Dynamic Simulations. <i>Cell Biochemistry and Biophysics</i> , 2016, 74, 473-481.	1.8	16

#	ARTICLE	IF	CITATIONS
199	Zika virus drug targets: a missing link in drug design and discovery – a route map to fill the gap. RSC Advances, 2016, 6, 68719-68731.	3.6	22
200	Exploration of chlorinated thienyl chalcones: A new class of monoamine oxidase-B inhibitors. International Journal of Biological Macromolecules, 2016, 91, 680-695.	7.5	69
201	Molecular Dynamics Simulations of Ligand-Induced Flap Conformational Changes in Cathepsin-A Comparative Study. Journal of Cellular Biochemistry, 2016, 117, 2643-2657.	2.6	13
202	Multi-drug resistance profile of PR20 HIV-1 protease is attributed to distorted conformational and drug binding landscape: molecular dynamics insights. Journal of Biomolecular Structure and Dynamics, 2016, 34, 135-151.	3.5	26
203	Co-encapsulation of multi-lipids and polymers enhances the performance of vancomycin in lipid-polymer hybrid nanoparticles: In vitro and in silico studies. Materials Science and Engineering C, 2016, 61, 616-630.	7.3	64
204	New drug design with covalent modifiers. Expert Opinion on Drug Discovery, 2016, 11, 79-90.	5.0	33
205	Î <sup>3</sup> -Cyclodextrin capped silver nanoparticles for molecular recognition and enhancement of antibacterial activity of chloramphenicol. Journal of Inorganic Biochemistry, 2016, 157, 15-24.	3.5	39
206	Dual anti-inflammatory and selective inhibition mechanism of leukotriene A <sub>4</sub> hydrolase/aminopeptidase: insights from comparative molecular dynamics and binding free energy analyses. Journal of Biomolecular Structure and Dynamics, 2016, 34, 2418-2433.	3.5	8
207	Polyelectrolyte complex of vancomycin as a nanoantibiotic: Preparation, in vitro and in silico studies. Materials Science and Engineering C, 2016, 63, 489-498.	7.3	26
208	Ultra-small lipid-dendrimer hybrid nanoparticles as a promising strategy for antibiotic delivery: In vitro and in silico studies. International Journal of Pharmaceutics, 2016, 504, 1-10.	5.2	55
209	A comparative molecular dynamics study on BACE1 and BACE2 flap flexibility. Journal of Receptor and Signal Transduction Research, 2016, 36, 505-514.	2.5	26
210	The binding landscape of plasmepsin V and the implications for flap dynamics. Molecular BioSystems, 2016, 12, 1457-1467.	2.9	12
211	Synthesis, characterization and molecular modelling of a novel dipyrindamole supramolecule – X-ray structure, quantum mechanics and molecular dynamics study to comprehend the hydrogen bond structure-activity relationship. Journal of Molecular Structure, 2016, 1105, 194-204.	3.6	13
212	Adenosine Monophosphate-Activated Protein Kinase (AMPK) as a Diverse Therapeutic Target: A Computational Perspective. Applied Biochemistry and Biotechnology, 2016, 178, 810-830.	2.9	14
213	Per-Residue Energy Footprints-Based Pharmacophore Modeling as an Enhanced In Silico Approach in Drug Discovery: A Case Study on the Identification of Novel Î <sup>2</sup> -Secretase1 (BACE1) Inhibitors as Anti-Alzheimer Agents. Cellular and Molecular Bioengineering, 2016, 9, 175-189.	2.1	37
214	Single Active Site Mutation Causes Serious Resistance of HIV Reverse Transcriptase to Lamivudine: Insight from Multiple Molecular Dynamics Simulations. Cell Biochemistry and Biophysics, 2016, 74, 35-48.	1.8	8
215	A broad spectrum anti-HIV inhibitor significantly disturbs V1/V2 domain rearrangements of HIV-1 gp120 and inhibits virus entry. Journal of Receptor and Signal Transduction Research, 2016, 36, 119-129.	2.5	3
216	Investigation of flap flexibility of Î <sup>2</sup> -secretase using molecular dynamic simulations. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1008-1019.	3.5	33

#	ARTICLE	IF	CITATIONS
217	Binding Free Energy-Based Footprint Pharmacophore Model to Enhance Virtual Screening and Drug Discovery: A Case on Glycosidases as Anti-influenza Drug Targets. <i>Letters in Drug Design and Discovery</i> , 2016, 13, 1033-1046.	0.7	4
218	Flap flexibility amongst plasmepsins I, II, III, IV, and V: Sequence, structural, and molecular dynamics analyses. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1693-1705.	2.6	21
219	Understanding the cross-resistance of oseltamivir to H1N1 and H5N1 influenza A neuraminidase mutations using multidimensional computational analyses. <i>Drug Design, Development and Therapy</i> , 2015, 9, 4137.	4.3	11
220	Could the FDA-approved anti-HIV PR inhibitors be promising anticancer agents? An answer from enhanced docking approach and molecular dynamics analyses. <i>Drug Design, Development and Therapy</i> , 2015, 9, 6055.	4.3	6
221	Dynamics of the thumb-finger regions in a GH11 xylanase <i>Bacillus circulans</i> : comparison between the Michaelis and covalent intermediate. <i>RSC Advances</i> , 2015, 5, 82381-82394.	3.6	23
222	Insight into the binding theme of CA-074Me to cathepsin B: molecular dynamics simulations and scaffold hopping to identify potential analogues as anti-neurodegenerative diseases. <i>Medicinal Chemistry Research</i> , 2015, 24, 701-713.	2.4	4
223	Antipyrine- $\gamma$ cyclodextrin inclusion complex: Molecular modeling, preparation, characterization and cytotoxicity studies. <i>Journal of Molecular Structure</i> , 2015, 1089, 38-47.	3.6	13
224	Possible allosteric binding site on Gyrase B, a key target for novel anti-TB drugs: homology modelling and binding site identification using molecular dynamics simulation and binding free energy calculations. <i>Medicinal Chemistry Research</i> , 2015, 24, 2055-2074.	2.4	28
225	Dynamic features of apo and bound HIV-Nef protein reveal the anti-HIV dimerization inhibition mechanism. <i>Journal of Receptor and Signal Transduction Research</i> , 2015, 35, 346-356.	2.5	3
226	Chikungunya virus (CHIKV) inhibitors from natural sources: a medicinal chemistry perspective. <i>Journal of Natural Medicines</i> , 2015, 69, 451-462.	2.3	25
227	Theory and Applications of Covalent Docking in Drug Discovery: Merits and Pitfalls. <i>Molecules</i> , 2015, 20, 1984-2000.	3.8	112
228	Single H5N1 influenza A neuraminidase mutation develops resistance to oseltamivir due to distorted conformational and drug binding landscape: multiple molecular dynamics analyses. <i>RSC Advances</i> , 2015, 5, 10849-10861.	3.6	15
229	Flap dynamics of plasmepsin proteases: insight into proposed parameters and molecular dynamics. <i>Molecular BioSystems</i> , 2015, 11, 1061-1066.	2.9	31
230	Heat Shock Protein 90 (Hsp90) as Anticancer Target for Drug Discovery: An Ample Computational Perspective. <i>Chemical Biology and Drug Design</i> , 2015, 86, 1131-1160.	3.2	14
231	Monoamine oxidase inhibitory activity of 2-aryl-4H-chromen-4-ones. <i>Bioorganic Chemistry</i> , 2015, 58, 72-80.	4.1	41
232	<i>In Silico</i> Identification of Irreversible Cathepsin B Inhibitors as Anti- Cancer Agents: Virtual Screening, Covalent Docking Analysis and Molecular Dynamics Simulations. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2015, 18, 399-410.	1.1	6
233	G-Protein Coupled Receptors (GPCRs): A Comprehensive Computational Perspective. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2015, 18, 346-364.	1.1	6
234	Anti-cancer Glycosidase Inhibitors from Natural Products: A Computational and Molecular Modelling Perspective. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2015, 15, 933-946.	1.7	10

#	ARTICLE	IF	CITATIONS
235	Identification of Novel GSK1070916 Analogs as Potential Aurora B Inhibitors: Insights from Molecular Dynamics and MM/GBSA Based Rescoring. <i>Letters in Drug Design and Discovery</i> , 2014, 12, 2-13.	0.7	6
236	Integrated Computational Tools for Identification of CCR5 Antagonists as Potential HIV-1 Entry Inhibitors: Homology Modeling, Virtual Screening, Molecular Dynamics Simulations and 3D QSAR Analysis. <i>Molecules</i> , 2014, 19, 5243-5265.	3.8	13
237	Integrated Approach to Structure-Based Enzymatic Drug Design: Molecular Modeling, Spectroscopy, and Experimental Bioactivity. <i>Chemical Reviews</i> , 2014, 114, 493-537.	47.7	100
238	Dual acting HIV inhibitors: integrated rational in silico design strategy. <i>Medicinal Chemistry Research</i> , 2014, 23, 682-689.	2.4	8
239	Identification of irreversible protein splicing inhibitors as potential anti-TB drugs: insight from hybrid non-covalent/covalent docking virtual screening and molecular dynamics simulations. <i>Medicinal Chemistry Research</i> , 2014, 23, 2312-2323.	2.4	16
240	Target-Bound Generated Pharmacophore Model to Improve the Pharmacophore-Based Virtual Screening: Identification of G-Protein Coupled Human CCR2 Receptors Inhibitors as Anti-Inflammatory Drugs. <i>Cellular and Molecular Bioengineering</i> , 2014, 7, 45-57.	2.1	12
241	An integrated molecular dynamics, principal component analysis and residue interaction network approach reveals the impact of M184V mutation on HIV reverse transcriptase resistance to lamivudine. <i>Molecular BioSystems</i> , 2014, 10, 2215-2228.	2.9	52
242	Compensatory Role of Double Mutation N348I/M184V on Nevirapine Binding Landscape: Insight from Molecular Dynamics Simulation. <i>Protein Journal</i> , 2014, 33, 432-446.	1.6	15
243	A critical survey of average distances between catalytic carboxyl groups in glycoside hydrolases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1747-1755.	2.6	19
244	A perspective on targeting non-structural proteins to combat neglected tropical diseases: Dengue, West Nile and Chikungunya viruses. <i>European Journal of Medicinal Chemistry</i> , 2014, 87, 677-702.	5.5	34
245	Computer-Aided Perspective for the Design of Flexible HIV Non- Nucleoside Reverse Transcriptase Inhibitors (NNRTIs): de-novo Drug Design, Virtual Screening and Molecular Dynamics Simulations. <i>Letters in Drug Design and Discovery</i> , 2014, 11, 513-524.	0.7	3
246	A Hybrid Structure/Pharmacophore-Based Virtual Screening Approach to Design Potential Leads: A Computer-Aided Design of South African HIV-1 Subtype C Protease Inhibitors. <i>Drug Development Research</i> , 2013, 74, 283-295.	2.9	16
247	Novel PCU cage diol peptides as potential targets against wild-type CSA HIV-1 protease: synthesis, biological screening and molecular modelling studies. <i>Medicinal Chemistry Research</i> , 2013, 22, 3918-3933.	2.4	4
248	Linear and cyclic glycopeptide as HIV protease inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2013, 60, 144-154.	5.5	9
249	Synthesis, 2D-NMR and molecular modelling studies of pentacycloundecane lactam-peptides and peptoids as potential HIV-1 wild type C-SA protease inhibitors. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2013, 28, 78-88.	5.2	19
250	Comparison of the Molecular Dynamics and Calculated Binding Free Energies for Nine FDA-Approved HIV-1 PR Drugs Against Subtype B and CSA HIV PR. <i>Chemical Biology and Drug Design</i> , 2013, 81, 208-218.	3.2	32
251	Identification of Novel Gyrase B Inhibitors as Potential Anti-TB drugs: Homology Modelling, Hybrid Virtual Screening and Molecular Dynamics Simulations. <i>Chemical Biology and Drug Design</i> , 2013, 82, 205-215.	3.2	16
252	Structural insights into the South African HIV-1 subtype C protease: impact of hinge region dynamics and flap flexibility in drug resistance. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 1370-1380.	3.5	36

#	ARTICLE	IF	CITATIONS
253	Bifunctional Anti-HIV/TB Inhibitors: Perspective from In-Silico Design and Molecular Dynamics Simulations. <i>Letters in Drug Design and Discovery</i> , 2013, 10, 706-712.	0.7	3
254	Theoretical study on the molecular electronic properties of salicylic acid derivatives as anti-inflammatory drugs. <i>Journal of Structural Chemistry</i> , 2012, 53, 574-581.	1.0	3
255	Synthesis, screening and computational investigation of pentacycloundecane-peptoids as potent CSA-HIV PR inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2012, 57, 459-467.	5.5	15
256	Pentacycloundecane-diol-Based HIV-1 Protease Inhibitors: Biological Screening, 2D NMR, and Molecular Simulation Studies. <i>ChemMedChem</i> , 2012, 7, 1009-1019.	3.2	15
257	Inside Cover: Pentacycloundecane-diol-Based HIV-1 Protease Inhibitors: Biological Screening, 2D NMR, and Molecular Simulation Studies ( <i>ChemMedChem</i> 6/2012). <i>ChemMedChem</i> , 2012, 7, 938-938.	3.2	0
258	Synthesis and molecular modelling studies of novel carbapeptide analogs for inhibition of HIV-1 protease. <i>European Journal of Medicinal Chemistry</i> , 2012, 53, 13-21.	5.5	16
259	Pentacycloundecane derived hydroxy acid peptides: A new class of irreversible non-scissile ether bridged type isoster as potential HIV-1 wild type C-SA protease inhibitors. <i>Bioorganic Chemistry</i> , 2012, 40, 19-29.	4.1	22
260	Synthesis and structural studies of pentacycloundecane-based HIV-1 PR inhibitors: A hybrid 2D NMR and docking/QM/MM/MD approach. <i>European Journal of Medicinal Chemistry</i> , 2011, 46, 3976-3985.	5.5	38
261	Pentacycloundecane-based inhibitors of wild-type C-South African HIV-protease. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 2274-2277.	2.2	32
262	Computational mutagenesis reveals the role of active-site tyrosine in stabilising a boat conformation for the substrate: QM/MM molecular dynamics studies of wild-type and mutant xylanases. <i>Organic and Biomolecular Chemistry</i> , 2009, 7, 460-468.	2.8	36
263	Mechanism of glycoside hydrolysis: A comparative QM/MM molecular dynamics analysis for wild type and Y69F mutant retaining xylanases. <i>Organic and Biomolecular Chemistry</i> , 2009, 7, 5236.	2.8	28
264	"Finding the needle in the haystack"™- will natural products fit for purpose in the treatment of cryptosporidiosis? A theoretical perspective. <i>Molecular Simulation</i> , 0, , 1-14.	2.0	0
265	Synthesis, Biological Evaluation and Molecular Docking of Novel N-Acyl/Aroyl Spiro[Chromane-2,4-Piperidin]-4(3H)-One as Potent Anti-Microbial Agents. <i>Polycyclic Aromatic Compounds</i> , 0, , 1-17.	2.6	3
266	Could the spanning of NAM-AD subsites by poly (ADP ribose) polymerase inhibitors potentiate their selective inhibitory activity in breast cancer treatment? Insight from biophysical computations. <i>Molecular Simulation</i> , 0, , 1-9.	2.0	0
267	Unravelling the Structural Mechanism of Action of 5-methyl-5-[4-(4-oxo-3H-quinazolin-2-yl)phenyl]imidazolidine-2,4-dione in Dual-Targeting Tankyrase 1 and 2: A Novel Avenue in Cancer Therapy. <i>Cell Biochemistry and Biophysics</i> , 0, , .	1.8	0
268	Co-binding of JQ1 and Venetoclax exhibited synergetic inhibitory effect for cancer therapy; Potential line of treatment for the Waldenström macroglobulinemia lymphoma. <i>Chemistry and Biodiversity</i> , 0, , .	2.1	1