Gugan Kothandan

List of Publications by Year in descending order

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1040056 839539 21 341 9 18 citations h-index g-index papers 21 21 21 536 docs citations times ranked citing authors all docs

| # | Article | IF | CITATIONS |
|----|--|-------------------|--------------|
| 1 | Understanding the dual mechanism of bioactive peptides targeting the enzymes involved in Renin Angiotensin System (RAS): An <i>in-silico</i> approach. Journal of Biomolecular Structure and Dynamics, 2020, 38, 5044-5061. | 3.5 | 8 |
| 2 | Berberine and Emodin abrogates breast cancer growth and facilitates apoptosis through inactivation of SIK3-induced mTOR and Akt signaling pathway. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165897. | 3.8 | 35 |
| 3 | In-silico studies on Myo inositol-1-phosphate synthase of Leishmania donovani in search of anti-leishmaniasis. Journal of Biomolecular Structure and Dynamics, 2020, , 1-14. | 3.5 | 5 |
| 4 | Insights of structure-based pharmacophore studies and inhibitor design against Gal3 receptor through molecular dynamics simulations. Journal of Biomolecular Structure and Dynamics, 2020, 39, 1-13. | 3.5 | 2 |
| 5 | Proposing the Promiscuous Protein Structures in JNK1 and JNK3 for Virtual Screening in Pursuit of Potential Leads. ACS Omega, 2020, 5, 3969-3978. | 3.5 | 2 |
| 6 | Synthesis, X-ray crystal structure and DFT calculations of $2\hat{a}\in^2$, $4\hat{a}\in^2$ -dihydro-10H-spiro [anthracene-9,3 $\hat{a}\in^2$ -benzo[b][1,4]thiazin]-10-amine and 1,3,5 -triindolyl benzene. Chemical Data Collections, 2019, 21, 100227. | 2.3 | 3 |
| 7 | Application of docking and active site analysis for enzyme linked biodegradation of textile dyes. Environmental Pollution, 2019, 248, 599-608. | 7.5 | 77 |
| 8 | Unveiling the Accuracy of Homology Modeling to Elucidate the Structure of GPCRs-HIV Co-receptor-CCR5 as a Case Study. Letters in Drug Design and Discovery, 2018, 15, 1068-1078. | 0.7 | 1 |
| 9 | Structural insights into the <i>Aedes aegypti</i> aquaporins and aquaglyceroporins – an <i>in silico</i> study. Journal of Receptor and Signal Transduction Research, 2016, 36, 543-557. | 2.5 | 2 |
| 10 | In silico study of 1-(4-Phenylpiperazin-1-yl)-2-(1H-pyrazol-1-yl) ethanones derivatives as CCR1 antagonist: Homology modeling, docking and 3D-QSAR approach. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 928-933. | 2.2 | 14 |
| 11 | The nociceptin receptor (NOPR) and its interaction with clinically important agonist molecules: a membrane molecular dynamics simulation study. Molecular BioSystems, 2014, 10, 3188-3198. | 2.9 | 9 |
| 12 | Enhancement of P-gylcoprotein modulators of arylmethylamine-phenyl derivatives: an integrative modeling approach. Medicinal Chemistry Research, 2013, 22, 2511-2523. | 2.4 | 2 |
| 13 | Theoretical Characterization of Galanin Receptor Type 3 (<scp>G</scp> al ₃) and Its Interaction with Agonist (<scp>GALANIN</scp>) and Antagonists (<scp>SNAP</scp> 37889 and) Tj ETQq1 1 0.7 | '84314 rgl 3.2 | BT_{Overlock |
| 14 | A combined 3D QSAR and pharmacophore-based virtual screening for the identification of potent p38 MAP kinase inhibitors: an in silico approach. Medicinal Chemistry Research, 2013, 22, 1773-1787. | 2.4 | 15 |
| 15 | Large variation in electrostatic contours upon addition of steric parameters and the effect of charge calculation schemes in CoMFA on mutagenicity of MX analogues. Molecular Simulation, 2012, 38, 861-871. | 2.0 | 30 |
| 16 | Various atomic charge calculation schemes of CoMFA on HIFâ€1 inhibitors of moracin analogs. International Journal of Quantum Chemistry, 2012, 112, 995-1005. | 2.0 | 8 |
| 17 | QSAR analysis on PfPK7 inhibitors using HQSAR, CoMFA, and CoMSIA. Medicinal Chemistry Research, 2012, 21, 681-693. | 2.4 | 9 |
| 18 | Molecular modeling study of HIV-1 gp120 attachment inhibitors. Medicinal Chemistry Research, 2012, 21, 1892-1904. | 2.4 | 6 |

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|----|--|-----|----------|
| 19 | Structural Insights from Binding Poses of CCR2 and CCR5 with Clinically Important Antagonists: A Combined In Silico Study. PLoS ONE, 2012, 7, e32864. | 2.5 | 43 |
| 20 | Binding Site Analysis of CCR2 Through <i>In Silico</i> Methodologies: Docking, CoMFA, and CoMSIA. Chemical Biology and Drug Design, 2011, 78, 161-174. | 3.2 | 16 |
| 21 | Docking and 3D-QSAR (quantitative structure activity relationship) studies of flavones, the potent inhibitors of p-glycoprotein targeting the nucleotide binding domain. European Journal of Medicinal Chemistry, 2011, 46, 4078-4088. | 5.5 | 50 |