

Allosteric Methods and Their Applications: Facilitating and the Investigation of Allosteric Mechanisms

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Citation Report

#	ARTICLE	IF	CITATIONS
1	How calcium ion binding induces the conformational transition of the calmodulin N-terminal domain—an atomic level characterization. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 19795-19804.	2.8	7
2	Deactivation Pathway of Ras GTPase Underlies Conformational Substates as Targets for Drug Design. <i>ACS Catalysis</i> , 2019, 9, 7188-7196.	11.2	77
3	The Observation of Ligand-Binding-Relevant Open States of Fatty Acid Binding Protein by Molecular Dynamics Simulations and a Markov State Model. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3476.	4.1	18
4	Data-driven computational analysis of allosteric proteins by exploring protein dynamics, residue coevolution and residue interaction networks. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, , .	2.4	17
5	Key Factors in Conformation Transformation of an Important Neuronic Protein Glucose Transport 3 Revealed by Molecular Dynamics Simulation. <i>ACS Chemical Neuroscience</i> , 2019, 10, 4444-4448.	3.5	3
6	CTCF-dependent chromatin boundaries formed by asymmetric nucleosome arrays with decreased linker length. <i>Nucleic Acids Research</i> , 2019, 47, 11181-11196.	14.5	44
7	Unraveling allosteric landscapes of allosterome with ASD. <i>Nucleic Acids Research</i> , 2020, 48, D394-D401.	14.5	29
8	Drugging K-RasG12C through covalent inhibitors: Mission possible?. , 2019, 202, 1-17.		63
9	Chemical conversion of nicotinamide into type I positive allosteric modulator of $\alpha 7$ nAChRs. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2019, 29, 1928-1933.	2.2	2
10	AlloDriver: a method for the identification and analysis of cancer driver targets. <i>Nucleic Acids Research</i> , 2019, 47, W315-W321.	14.5	31
11	The structural basis of the autoinhibition mechanism of glycogen synthase kinase 3 β (GSK3 β): molecular modeling and molecular dynamics simulation studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 1-10.	3.5	3
12	Emerging roles of allosteric modulators in the regulation of protein-protein interactions (PPIs): A new paradigm for PPI drug discovery. <i>Medicinal Research Reviews</i> , 2019, 39, 2314-2342.	10.5	77
13	Computational investigation of a ternary model of SnoN-SMAD3-SMAD4 complex. <i>Computational Biology and Chemistry</i> , 2019, 83, 107159.	2.3	5
14	In Silico Discovery of JMJD6 Inhibitors for Cancer Treatment. <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 1609-1613.	2.8	12
15	Emergence of allosteric drug-resistance mutations: new challenges for allosteric drug discovery. <i>Drug Discovery Today</i> , 2020, 25, 177-184.	6.4	67
16	Role of protein-protein interactions in allosteric drug design for DNA methyltransferases. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 121, 49-84.	2.3	5
17	Microsecond molecular dynamics simulations reveal the allosteric regulatory mechanism of p53 R249S mutation in p53-associated liver cancer. <i>Computational Biology and Chemistry</i> , 2020, 84, 107194.	2.3	13
18	Analysis of allosteric communication in a multienzyme complex by ancestral sequence reconstruction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 346-354.	7.1	26

#	ARTICLE	IF	CITATIONS
19	New Promise and Opportunities for Allosteric Kinase Inhibitors. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 13764-13776.	13.8	109
20	Identification of potential platelet-derived growth factor receptor β inhibitors by computational screening and binding simulations. <i>Journal of Molecular Graphics and Modelling</i> , 2020, 96, 107527.	2.4	2
21	Identify old drugs as selective bacterial β -glucosidase inhibitors by structural-based virtual screening and bioassay evaluations. <i>Chemical Biology and Drug Design</i> , 2020, 95, 368-379.	3.2	7
22	Autoinhibition can identify rare driver mutations and advise pharmacology. <i>FASEB Journal</i> , 2020, 34, 16-29.	0.5	23
23	Probing the Structural Dynamics of the Plasmodium falciparum Tunneling-Fold Enzyme 6-Pyruvoyl Tetrahydropterin Synthase to Reveal Allosteric Drug Targeting Sites. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 575196.	3.5	3
24	Wrangling Shape-Shifting Morpheins to Tackle Disease and Approach Drug Discovery. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 582966.	3.5	9
25	Discovery of Evodiamine Derivatives as Highly Selective PDE5 Inhibitors Targeting a Unique Allosteric Pocket. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 9828-9837.	6.4	27
26	Recent advances in the development of protein-protein interactions modulators: mechanisms and clinical trials. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 213.	17.1	387
27	Bcr-Abl Allosteric Inhibitors: Where We Are and Where We Are Going to. <i>Molecules</i> , 2020, 25, 4210.	3.8	13
28	Zinc-mediated conformational preselection mechanism in the allosteric control of DNA binding to the zinc transcriptional regulator (ZitR). <i>Scientific Reports</i> , 2020, 10, 13276.	3.3	6
29	How Parkinson's disease-related mutations disrupt the dimerization of WD40 domain in LRRK2: a comparative molecular dynamics simulation study. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 20421-20433.	2.8	13
30	Allosteric inhibition explained through conformational ensembles sampling distinct "mixed" states. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3803-3818.	4.1	29
31	Identification of the New Covalent Allosteric Binding Site of Fructose-1,6-bisphosphatase with Disulfiram Derivatives toward Glucose Reduction. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 6238-6247.	6.4	17
32	Protein-protein complexes as targets for drug discovery against infectious diseases. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 121, 237-251.	2.3	2
33	In silico study reveals existing drugs as β -glucosidase inhibitors: Structure-based virtual screening validated by experimental investigation. <i>Journal of Molecular Structure</i> , 2020, 1218, 128532.	3.6	7
34	Discovery of aryl-piperidine derivatives as potential antipsychotic agents using molecular hybridization strategy. <i>European Journal of Medicinal Chemistry</i> , 2020, 193, 112214.	5.5	16
35	Exploration of the selective binding mechanism of GSK3 β via molecular modeling and molecular dynamics simulation studies. <i>Medicinal Chemistry Research</i> , 2020, 29, 690-698.	2.4	3
36	Combining Allosteric and Orthosteric Drugs to Overcome Drug Resistance. <i>Trends in Pharmacological Sciences</i> , 2020, 41, 336-348.	8.7	60

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37	Binding Interactions of Ergotamine and Dihydroergotamine to 5-Hydroxytryptamine Receptor 1B (5-HT _{1b}) Using Molecular Dynamics Simulations and Dynamic Network Analysis. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1749-1765.	5.4	8
38	Computational Insight into the Allosteric Activation Mechanism of Farnesoid X Receptor. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1540-1550.	5.4	5
39	Revealing the binding and drug resistance mechanism of amprenavir, indinavir, ritonavir, and nelfinavir complexed with HIV-1 protease due to double mutations G48T/L89M by molecular dynamics simulations and free energy analyses. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 4464-4480.	2.8	20
40	Allosterische Kinaseinhibitoren – Erwartungen und Chancen. <i>Angewandte Chemie</i> , 2020, 132, 13868-13881.	2.0	2
41	Allostery of multidomain proteins with disordered linkers. <i>Current Opinion in Structural Biology</i> , 2020, 62, 175-182.	5.7	28
42	Recent advances suggest increased influence of selective pressure in allostery. <i>Current Opinion in Structural Biology</i> , 2020, 62, 183-188.	5.7	13
43	Discovery of cryptic allosteric sites using reversed allosteric communication by a combined computational and experimental strategy. <i>Chemical Science</i> , 2021, 12, 464-476.	7.4	84
44	Mechanism of allosteric activation of SIRT6 revealed by the action of rationally designed activators. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 1355-1361.	12.0	57
45	Emerging roles of SIRT6 in human diseases and its modulators. <i>Medicinal Research Reviews</i> , 2021, 41, 1089-1137.	10.5	75
46	Deciphering the resistance mechanism of RET kinase mutant against vandetanib and nintedanib using molecular dynamics simulations. <i>Journal of Experimental Nanoscience</i> , 2021, 16, 278-293.	2.4	3
47	Mechanistic insights into the effect of phosphorylation on Ras conformational dynamics and its interactions with cell signaling proteins. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1184-1199.	4.1	51
48	Targeting RAS phosphorylation in cancer therapy: Mechanisms and modulators. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 3433-3446.	12.0	20
49	Conformational Selection Mechanism Provides Structural Insights into the Optimization of APC-Asef Inhibitors. <i>Molecules</i> , 2021, 26, 962.	3.8	11
50	Untangling Dual-Targeting Therapeutic Mechanism of Epidermal Growth Factor Receptor (EGFR) Based on Reversed Allosteric Communication. <i>Pharmaceutics</i> , 2021, 13, 747.	4.5	42
51	Approach in Improving Potency and Selectivity of Kinase Inhibitors: Allosteric Kinase Inhibitors. <i>Mini-Reviews in Medicinal Chemistry</i> , 2021, 21, 991-1003.	2.4	4
52	Allosteric Type and Pathways Are Governed by the Forces of Protein-Ligand Binding. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 5404-5412.	4.6	20
53	Chemical and Biophysical Approaches to Allosteric Modulation. <i>European Journal of Organic Chemistry</i> , 2021, 2021, 4245-4259.	2.4	2
54	Targeting a cryptic allosteric site of SIRT6 with small-molecule inhibitors that inhibit the migration of pancreatic cancer cells. <i>Acta Pharmaceutica Sinica B</i> , 2022, 12, 876-889.	12.0	32

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55	From Selection to Instruction and Back: Competing Conformational Selection and Induced Fit Pathways in Abiotic Hosts. <i>Angewandte Chemie</i> , 2021, 133, 20095-20101.	2.0	4
56	Fragment-based drug design facilitates selective kinase inhibitor discovery. <i>Trends in Pharmacological Sciences</i> , 2021, 42, 551-565.	8.7	22
57	From Selection to Instruction and Back: Competing Conformational Selection and Induced Fit Pathways in Abiotic Hosts. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 19942-19948.	13.8	18
58	Structure-Activity Studies of Novel Di-substituted [1,2,5]oxadiazolo [3,4-b]pyrazine Analogs Targeting the A-loop Regulatory Site of p38 MAP Kinase. <i>Current Medicinal Chemistry</i> , 2022, 29, 1640-1653.	2.4	1
59	Allosteric Mechanism of Human Mitochondrial Phenylalanyl-tRNA Synthetase: An Atomistic MD Simulation and a Mutual Information-Based Network Study. <i>Journal of Physical Chemistry B</i> , 2021, 125, 7651-7661.	2.6	5
60	Molecular Insights into the Recruiting Between UCP2 and DDX5/UBAP2L in the Metabolic Plasticity of Non-Small-Cell Lung Cancer. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 3978-3987.	5.4	8
61	Activation pathway of a G protein-coupled receptor uncovers conformational intermediates as targets for allosteric drug design. <i>Nature Communications</i> , 2021, 12, 4721.	12.8	124
62	Recent advances in the design and discovery of synthetic tyrosinase inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2021, 224, 113744.	5.5	57
63	Computational identification of potential chemoprophylactic agents according to dynamic behavior of peroxisome proliferator-activated receptor gamma. <i>RSC Advances</i> , 2021, 11, 147-159.	3.6	5
64	Along the allosteric stream: Recent advances in computational methods for allosteric drug discovery. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2022, 12, e1585.	14.6	23
65	How does nintedanib overcome cancer drug-resistant mutation of RET protein-tyrosine kinase: insights from molecular dynamics simulations. <i>Journal of Molecular Modeling</i> , 2021, 27, 337.	1.8	9
66	Assessment of the Contribution of a Thermodynamic and Mechanical Destabilization of Myosin-Binding Protein C Domain C2 to the Pathomechanism of Hypertrophic Cardiomyopathy-Causing Double Mutation MYBPC3I ^{255p} /D389V. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11949.	4.1	2
67	Wandering beyond small molecules: peptides as allosteric protein modulators. <i>Trends in Pharmacological Sciences</i> , 2021, , .	8.7	9
68	Multiple Molecular Dynamics Simulations and Free-Energy Predictions Uncover the Susceptibility of Variants of HIV-1 Protease against Inhibitors Darunavir and KNI-1657. <i>Langmuir</i> , 2021, 37, 14407-14418.	3.5	7
69	Drug discovery is an eternal challenge for the biomedical sciences. , 2022, 1, .		48
70	Allosteric binding on nuclear receptors: Insights on screening of non-competitive endocrine-disrupting chemicals. <i>Environment International</i> , 2022, 159, 107009.	10.0	7
71	Atomic-scale insights into allosteric inhibition and evolutionary rescue mechanism of <i>Streptococcus thermophilus</i> Cas9 by the anti-CRISPR protein AcrIIA6. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6108-6124.	4.1	35
72	Challenges in Discovering Drugs That Target the Protein-Protein Interactions of Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1550.	4.1	16

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73	Explaining and Predicting Allostery with Allosteric Database and Modern Analytical Techniques. <i>Journal of Molecular Biology</i> , 2022, 434, 167481.	4.2	10
74	Elucidation of the conformational dynamics and assembly of Argonauteâ€“RNA complexes by distinct yet coordinated actions of the supplementary microRNA. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1352-1365.	4.1	13
75	Structure and chemistry of enzymatic active sites that play a role in the switch and conformation mechanism. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 130, 59-83.	2.3	5
76	Mechanistic Insights Into Co-Administration of Allosteric and Orthosteric Drugs to Overcome Drug-Resistance in T315I BCR-ABL1. <i>Frontiers in Pharmacology</i> , 2022, 13, 862504.	3.5	11
77	From Data to Knowledge: Systematic Review of Tools for Automatic Analysis of Molecular Dynamics Output. <i>Frontiers in Pharmacology</i> , 2022, 13, 844293.	3.5	1
78	Computational elucidation of allosteric communication in proteins for allosteric drug design. <i>Drug Discovery Today</i> , 2022, 27, 2226-2234.	6.4	14
79	A molecular perspective for the use of type IV tyrosine kinase inhibitors as anticancer therapeutics. <i>Drug Discovery Today</i> , 2022, 27, 808-821.	6.4	3
80	Harnessing Reversed Allosteric Communication: A Novel Strategy for Allosteric Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 17728-17743.	6.4	29
81	An overview of kinase downregulators and recent advances in discovery approaches. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 423.	17.1	21
82	Deciphering the Mechanism of Gilteritinib Overcoming Lorlatinib Resistance to the Double Mutant I1171N/F1174I in Anaplastic Lymphoma Kinase. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 808864.	3.7	14
83	CDK9 inhibitors in cancer research. <i>RSC Medicinal Chemistry</i> , 2022, 13, 688-710.	3.9	10
84	Allosteric pluripotency: challenges and opportunities. <i>Biochemical Journal</i> , 2022, 479, 825-838.	3.7	5
94	Allostery and Missense Mutations as Intermittently Linked Promising Aspects of Modern Computational Drug Discovery. <i>Journal of Molecular Biology</i> , 2022, 434, 167610.	4.2	8
95	Computational Design of Inhibitors Targeting the Catalytic Î² Subunit of Escherichia coli FOF1-ATP Synthase. <i>Antibiotics</i> , 2022, 11, 557.	3.7	3
96	Delineating the conformational landscape and intrinsic properties of the angiotensin II type 2 receptor using a computational study. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2268-2279.	4.1	4
97	Understanding the P-Loop Conformation in the Determination of Inhibitor Selectivity Toward the Hepatocellular Carcinoma-Associated Dark Kinase STK17B. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	3.5	6
98	Medicinal Chemistry Strategies for the Development of Brutonâ€™s Tyrosine Kinase Inhibitors against Resistance. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 7415-7437.	6.4	18
99	Therapeutic Targeting the Allosteric Cysteinome of RAS and Kinase Families. <i>Journal of Molecular Biology</i> , 2022, 434, 167626.	4.2	4

#	ARTICLE	IF	CITATIONS
100	Unmasking allosteric-binding sites: novel targets for GPCR drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2022, 17, 897-923.	5.0	7
101	Insights into the Allosteric Effect of SENP1 Q597A Mutation on the Hydrolytic Reaction of SUMO1 via an Integrated Computational Study. <i>Molecules</i> , 2022, 27, 4149.	3.8	4
102	Allosteric modulation of GPCRs: From structural insights to in silico drug discovery. , 2022, 237, 108242.		15
103	The Role of Conformational Dynamics and Allostery in the Control of Distinct Efficacies of Agonists to the Glucocorticoid Receptor. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	7
104	Mechanistic insights into the clinical Y96D mutation with acquired resistance to AMG510 in the KRASG12C. <i>Frontiers in Oncology</i> , 0, 12, .	2.8	5
105	Mechanistic Insights into the Long-range Allosteric Regulation of KRAS Via Neurofibromatosis Type 1 (NF1) Scaffold Upon SPRED1 Loading. <i>Journal of Molecular Biology</i> , 2022, 434, 167730.	4.2	17
106	Design, synthesis and biological evaluation of 2-aminopyridine derivatives as USP7 inhibitors. <i>Bioorganic Chemistry</i> , 2022, 129, 106128.	4.1	3
108	Probing Mechanisms of Binding and Allostery in the SARS-CoV-2 Spike Omicron Variant Complexes with the Host Receptor: Revealing Functional Roles of the Binding Hotspots in Mediating Epistatic Effects and Communication with Allosteric Pockets. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11542.	4.1	15
109	Halide ion directed templation effect of quadruple-stranded helicates. <i>Cell Reports Physical Science</i> , 2022, 3, 101056.	5.6	3
110	Computer-Aided Drug Design Boosts RAS Inhibitor Discovery. <i>Molecules</i> , 2022, 27, 5710.	3.8	6
111	Exploring the druggability of the binding site of aurovertin, an exogenous allosteric inhibitor of FOF1-ATP synthase. <i>Frontiers in Pharmacology</i> , 0, 13, .	3.5	2
112	Molecular Insights into the Heterotropic Allosteric Mechanism in Cytochrome P450 3A4-Mediated Midazolam Metabolism. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 5762-5770.	5.4	3
113	Intrinsic disorder and allosteric regulation. , 2023, , 327-352.		0
114	Machine learning and protein allostery. <i>Trends in Biochemical Sciences</i> , 2023, 48, 375-390.	7.5	7
115	Recent applications of computational methods to allosteric drug discovery. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	2
116	Fragment-based drug discovery supports drugging "undruggable" protein-protein interactions. <i>Trends in Biochemical Sciences</i> , 2023, 48, 539-552.	7.5	7
117	Research progress of indole-fused derivatives as allosteric modulators: Opportunities for drug development. <i>Biomedicine and Pharmacotherapy</i> , 2023, 162, 114574.	5.6	3
118	From Deep Mutational Mapping of Allosteric Protein Landscapes to Deep Learning of Allostery and Hidden Allosteric Sites: Zooming in on "Allosteric Intersection" of Biochemical and Big Data Approaches. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7747.	4.1	6

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120	Decoupling the dynamic mechanism revealed by FGFR2 mutation-induced population shift. <i>Journal of Biomolecular Structure and Dynamics</i> , 2024, 42, 1940-1951.	3.5	1
121	Glycomimetics for the inhibition and modulation of lectins. <i>Chemical Society Reviews</i> , 2023, 52, 3663-3740.	38.1	13
122	Markov State Models and Perturbation-Based Approaches Reveal Distinct Dynamic Signatures and Hidden Allosteric Pockets in the Emerging SARS-Cov-2 Spike Omicron Variant Complexes with the Host Receptor: The Interplay of Dynamics and Convergent Evolution Modulates Allostery and Functional Mechanisms. <i>Journal of Chemical Information and Modeling</i> , 2023, 63, 5272-5296.	5.4	6
123	PASSerRank: Prediction of allosteric sites with learning to rank. <i>Journal of Computational Chemistry</i> , 2023, 44, 2223-2229.	3.3	8
124	Designing drugs and chemical probes with the dualsteric approach. <i>Chemical Society Reviews</i> , 2023, 52, 8651-8677.	38.1	1
125	Advances of Predicting Allosteric Mechanisms Through Protein Contact in New Technologies and Their Application. <i>Molecular Biotechnology</i> , 0, , .	2.4	1
126	Characterisation of a phosphatase-like nanozyme developed by baking cysteine and its application in reviving mung bean sprouts damaged by ash. <i>Environmental Science: Nano</i> , 0, , .	4.3	0
127	Protein-Protein Interaction for Drug Discovery. <i>Engineering Materials</i> , 2024, , 255-269.	0.6	0
128	Prospects for the use of allosteric drugs in real-world clinical practice. , 2023, 3, 15-21.		0
129	Biophysical Insights into Drug Discovery: Leveraging Phase Transitions and Protein Behavior for Therapeutic Innovation. <i>Biophysical Reviews and Letters</i> , 0, , 1-6.	0.8	0
130	Allo-targeting of the kinase domain: Insights from in silico studies and comparison with experiments. <i>Current Opinion in Structural Biology</i> , 2024, 84, 102770.	5.7	0
131	Allosteric Sites and Allosteric Regulators of G Protein-Coupled Receptors: Gray Cardinals of Signal Transduction. <i>Journal of Evolutionary Biochemistry and Physiology</i> , 2023, 59, S1-S106.	0.6	0
132	Allosteric Activation of $\alpha 7$ Nicotinic Acetylcholine Receptors by Novel 2-Arylamino-thiazole-5-carboxylic Acid Amide Derivatives for the Improvement of Cognitive Deficits in Mice. <i>Journal of Medicinal Chemistry</i> , 2024, 67, 6344-6364.	6.4	0