Avner Schlessinger

List of Publications by Year
in descending order

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87	5,444	94433	91884
papers	citations	37 h-index	69 g-index

101	101	101	8308
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Maternal health around pregnancy and autism risk: a diagnosis-wide, population-based study. Psychological Medicine, 2022, 52, 4076-4084.	4.5	10
2	Alanine serine cysteine transporter (ASCT) substrate binding site properties probed with hydroxyhomoserine esters. Journal of Physical Organic Chemistry, 2022, 35, .	1.9	4
3	Exploring the conformational diversity of proteins. ELife, 2022, 11, .	6.0	10
4	SLC16 Family: From Atomic Structure to Human Disease. Trends in Biochemical Sciences, 2021, 46, 28-40.	7.5	15
5	The Effects of Prodrug Size and a Carbonyl Linker on <scp>l</scp>â€Type Amino Acid Transporter 1â€Targeted Cellular and Brain Uptake. ChemMedChem, 2021, 16, 869-880.	3.2	5
6	Artificial intelligence and machine learningâ€aided drug discovery in central nervous system diseases: Stateâ€ofâ€theâ€arts and future directions. Medicinal Research Reviews, 2021, 41, 1427-1473.	10.5	120
7	Type II Binders Targeting the â€œGLR-Outâ€•Conformation of the Pseudokinase STRADÎ±. Biochemistry, 2021, 60, 289-302.	2.5	6
8	Exploiting Allosteric Properties of RAF and MEK Inhibitors to Target Therapy-Resistant Tumors Driven by Oncogenic BRAF Signaling. Cancer Discovery, 2021, 11, 1716-1735.	9.4	30
9	Human neurons from Christianson syndrome iPSCs reveal mutation-specific responses to rescue strategies. Science Translational Medicine, 2021, 13, .	12.4	21
10	Inside Back Cover Image, Volume 41, Issue 3. Medicinal Research Reviews, 2021, 41, iii.	10.5	0
11	Protein structureâ€“based gene expression signatures. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	5
12	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	14.5	135
13	Crowdsourced mapping of unexplored target space of kinase inhibitors. Nature Communications, 2021, 12, 3307.	12.8	41
14	Dual targeting of salt inducible kinases and CSF1R uncouples bone formation and bone resorption. ELife, 2021, 10, .	6.0	12
15	An Overview of Cell-Based Assay Platforms for the Solute Carrier Family of Transporters. Frontiers in Pharmacology, 2021, 12, 722889.	3.5	31
16	Crowdsourced identification of multi-target kinase inhibitors for RET- and TAU- based disease: The Multi-Targeting Drug DREAM Challenge. PLoS Computational Biology, 2021, 17, e1009302.	3.2	7
17	Rational design of ASCT2 inhibitors using an integrated experimental-computational approach. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	35
18	Identification of discriminative gene-level and protein-level features associated with pathogenic gain-of-function and loss-of-function variants. American Journal of Human Genetics, 2021, 108, 2301-2318.	6.2	21

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19	High-Resolution Structure and Inhibition of the Schizophrenia-Linked Pseudokinase ULK4. Journal of the American Chemical Society, 2020, 142, 33-37.	13.7	24
20	Transcriptomic profiling of human cardiac cells predicts protein kinase inhibitor-associated cardiotoxicity. Nature Communications, 2020, 11, 4809.	12.8	28
21	Identification of a G-Protein-Independent Activator of GIRK Channels. Cell Reports, 2020, 31, 107770.	6.4	20
22	Identification of newborns at risk for autism using electronic medical records and machine learning. European Psychiatry, 2020, 63, e22.	0.2	24
23	Interaction of the neutral amino acid transporter ASCT2 with basic amino acids. Biochemical Journal, 2020, 477, 1443-1457.	3.7	4
24	Advances and Challenges in Rational Drug Design for SLCs. Trends in Pharmacological Sciences, 2019, 40, 790-800.	8.7	40
25	An IRAK1â€“PIN1 signalling axis drives intrinsic tumour resistance to radiation therapy. Nature Cell Biology, 2019, 21, 203-213.	10.3	38
26	l-Type amino acid transporter 1 activity of 1,2,3-triazolyl analogs of l-histidine and l-tryptophan. Bioorganic and Medicinal Chemistry Letters, 2019, 29, 2254-2258.	2.2	13
27	Integrated computational and Drosophila cancer model platform captures previously unappreciated chemicals perturbing a kinase network. PLoS Computational Biology, 2019, 15, e1006878.	3.2	10
28	Structures of ligand-occupied Î²-Klotho complexes reveal a molecular mechanism underlying endocrine FGF specificity and activity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7819-7824.	7.1	27
29	Functional and structural analysis of rare SLC2A2 variants associated with Fanconiâ€Bickel syndrome and metabolic traits. Human Mutation, 2019, 40, 983-995.	2.5	13
30	Novel alanine serine cysteine transporter 2 (ASCT2) inhibitors based on sulfonamide and sulfonic acid ester scaffolds. Journal of General Physiology, 2019, 151, 357-368.	1.9	24
31	Encounter and React: Computer-Guided Design of Covalent Inhibitors. Cell Chemical Biology, 2019, 26, 6-8.	5.2	14
32	SLC13A3 variants cause acute reversible leukoencephalopathy and Î±â€ketoglutarate accumulation. Annals of Neurology, 2019, 85, 385-395.	5.3	22
33	KinaMetrix: a web resource to investigate kinase conformations and inhibitor space. Nucleic Acids Research, 2019, 47, D361-D366.	14.5	28
34	A whole-animal platform to advance a clinical kinase inhibitor into new disease space. Nature Chemical Biology, 2018, 14, 291-298.	8.0	56
35	Association of Autism Spectrum Disorder With Prenatal Exposure to Medication Affecting Neurotransmitter Systems. JAMA Psychiatry, 2018, 75, 1217.	11.0	28
36	Redefining the Protein Kinase Conformational Space with Machine Learning. Cell Chemical Biology, 2018, 25, 916-924.e2.	5.2	65

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37	Reevaluating the Substrate Specificity of the L-Type Amino Acid Transporter (LAT1). Journal of Medicinal Chemistry, 2018, 61, 7358-7373.	6.4	54
38	Homology Modeling Informs Ligand Discovery for the Glutamine Transporter ASCT2. Frontiers in Chemistry, 2018, 6, 279.	3.6	21
39	Molecular Modeling of Drugâ€“Transporter Interactionsâ€”An International Transporter Consortium Perspective. Clinical Pharmacology and Therapeutics, 2018, 104, 818-835.	4.7	43
40	Effects of Mutations and Ligands on the Thermostability of the l-Arginine/Agmatine Antiporter AdiC and Deduced Insights into Ligand-Binding of Human l-Type Amino Acid Transporters. International Journal of Molecular Sciences, 2018, 19, 918.	4.1	29
41	Novel selective thiadiazine DYRK1A inhibitor lead scaffold with human pancreatic Î²-cell proliferation activity. European Journal of Medicinal Chemistry, 2018, 157, 1005-1016.	5.5	36
42	Structure activity relationships of benzylproline-derived inhibitors of the glutamine transporter ASCT2. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 398-402.	2.2	29
43	Mapping Functionally Important Residues in the Na⁺/Dicarboxylate Cotransporter, NaDC1. Biochemistry, 2017, 56, 4432-4441.	2.5	10
44	Human Concentrative Nucleoside Transporter 3 (hCNT3, SLC28A3) Forms a Cyclic Homotrimer. Biochemistry, 2017, 56, 3475-3483.	2.5	15
45	Chemical Modulation of the Human Oligopeptide Transporter 1, hPepT1. Molecular Pharmaceutics, 2017, 14, 4685-4693.	4.6	20
46	Multi-targeting Drug Community Challenge. Cell Chemical Biology, 2017, 24, 1434-1435.	5.2	13
47	Generation of G protein-coupled receptor antibodies differentially sensitive to conformational states. PLoS ONE, 2017, 12, e0187306.	2.5	10
48	Mutations in the Na+/Citrate Cotransporter NaCT (SLC13A5) in Pediatric Patients with Epilepsy and Developmental Delay. Molecular Medicine, 2016, 22, 310-321.	4.4	59
49	Impaired Amino Acid Transport at the Blood Brain Barrier Is a Cause of Autism Spectrum Disorder. Cell, 2016, 167, 1481-1494.e18.	28.9	265
50	Systems Pharmacology: An Overview. AAPS Advances in the Pharmaceutical Sciences Series, 2016, , 53-80.	0.6	7
51	Computing Substrate Selectivity in a Peptide Transporter. Cell Chemical Biology, 2016, 23, 211-213.	5.2	6
52	Inhibitor Discovery for the Human GLUT1 from Homology Modeling and Virtual Screening. ACS Chemical Biology, 2016, 11, 1908-1916.	3.4	49
53	LAT-1 activity of meta-substituted phenylalanine and tyrosine analogs. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 2616-2621.	2.2	53
54	Molecular Basis for Redox Activation of Epidermal Growth Factor Receptor Kinase. Cell Chemical Biology, 2016, 23, 837-848.	5.2	100

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55	GEN3VA: aggregation and analysis of gene expression signatures from related studies. BMC Bioinformatics, 2016, 17, 461.	2.6	17
56	LAT1 activity of carboxylic acid bioisosteres: Evaluation of hydroxamic acids as substrates. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 5000-5006.	2.2	54
57	Interaction of Bacillus subtilis Polynucleotide Phosphorylase and RNase Y. Journal of Biological Chemistry, 2016, 291, 6655-6663.	3.4	24
58	SLC transporters: structure, function, and drug discovery. MedChemComm, 2016, 7, 1069-1081.	3.4	152
59	Ligand Discovery for the Alanine-Serine-Cysteine Transporter (ASCT2, SLC1A5) from Homology Modeling and Virtual Screening. PLoS Computational Biology, 2015, 11, e1004477.	3.2	62
60	Loss-of-function variants of SETD5 cause intellectual disability and the core phenotype of microdeletion 3p25.3 syndrome. European Journal of Human Genetics, 2015, 23, 753-760.	2.8	73
61	Structure-Based Identification of Inhibitors for the SLC13 Family of Na+/Dicarboxylate Cotransporters. Biochemistry, 2015, 54, 4900-4908.	2.5	26
62	DFGmodel: Predicting Protein Kinase Structures in Inactive States for Structure-Based Discovery of Type-II Inhibitors. ACS Chemical Biology, 2015, 10, 269-278.	3.4	37
63	Environmental Pressure May Change the Composition Protein Disorder in Prokaryotes. PLoS ONE, 2015, 10, e0133990.	2.5	11
64	PredictProteinâ€”an open resource for online prediction of protein structural and functional features. Nucleic Acids Research, 2014, 42, W337-W343.	14.5	589
65	Determinants of Substrate and Cation Transport in the Human Na+/Dicarboxylate Cotransporter NaDC3. Journal of Biological Chemistry, 2014, 289, 16998-17008.	3.4	24
66	Co-expression and co-localization of hub proteins and their partners are encoded in protein sequence. Molecular BioSystems, 2014, 10, 787.	2.9	1
67	Coordinating the impact of structural genomics on the human Î±-helical transmembrane proteome. Nature Structural and Molecular Biology, 2013, 20, 135-138.	8.2	64
68	Crystal structure of a eukaryotic phosphate transporter. Nature, 2013, 496, 533-536.	27.8	202
69	Structural basis for alternating access of a eukaryotic calcium/proton exchanger. Nature, 2013, 499, 107-110.	27.8	87
70	Evolution of modular intraflagellar transport from a coatomer-like progenitor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6943-6948.	7.1	144
71	Structure-based ligand discovery for the Large-neutral Amino Acid Transporter 1, LAT-1. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5480-5485.	7.1	173
72	Molecular Modeling and Ligand Docking for Solute Carrier (SLC) Transporters. Current Topics in Medicinal Chemistry, 2013, 13, 843-856.	2.1	85

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73	High Selectivity of the Î³-Aminobutyric Acid Transporter 2 (GAT-2, SLC6A13) Revealed by Structure-based Approach. Journal of Biological Chemistry, 2012, 287, 37745-37756.	3.4	49
74	Structure-based discovery of prescription drugs that interact with the norepinephrine transporter, NET. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15810-15815.	7.1	120
75	Ligand discovery from a dopamine D3 receptor homology model and crystal structure. Nature Chemical Biology, 2011, 7, 769-778.	8.0	285
76	Comparison of human solute carriers. Protein Science, 2010, 19, 412-428.	7.6	99
77	Function of human Rh based on structure of RhCG at 2.1Âå„«. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9638-9643.	7.1	178
78	Genetic Polymorphisms in Organic Cation Transporter 1 (OCT1) in Chinese and Japanese Populations Exhibit Altered Function. Journal of Pharmacology and Experimental Therapeutics, 2010, 335, 42-50.	2.5	72
79	Integrative Structure Modeling of Macromolecular Assemblies from Proteomics Data. Molecular and Cellular Proteomics, 2010, 9, 1689-1702.	3.8	64
80	Large-Scale Analysis of Thermostable, Mammalian Proteins Provides Insights into the Intrinsically Disordered Proteome. Journal of Proteome Research, 2009, 8, 211-226.	3.7	76
81	Improved Disorder Prediction by Combination of Orthogonal Approaches. PLoS ONE, 2009, 4, e4433.	2.5	170
82	Automated Identification of Complementarity Determining Regions (CDRs) Reveals Peculiar Characteristics of CDRs and B Cell Epitopes. Journal of Immunology, 2008, 181, 6230-6235.	0.8	73
83	Natively Unstructured Loops Differ from Other Loops. PLoS Computational Biology, 2007, 3, e140.	3.2	84
84	Natively unstructured regions in proteins identified from contact predictions. Bioinformatics, 2007, 23, 2376-2384.	4.1	118
85	Epitome: database of structure-inferred antigenic epitopes. Nucleic Acids Research, 2006, 34, D777-D780.	14.5	78
86	PROFbval: predict flexible and rigid residues in proteins. Bioinformatics, 2006, 22, 891-893.	4.1	135
87	Protein flexibility and rigidity predicted from sequence. Proteins: Structure, Function and Bioinformatics, 2005, 61, 115-126.	2.6	161