

Nieng Yan

List of Publications by Year in descending order

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97
papers

12,474
citations

30070

54
h-index

37204

96
g-index

113
all docs

113
docs citations

113
times ranked

13118
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural advances in sterol-sensing domain-containing proteins. Trends in Biochemical Sciences, 2022, 47, 289-300.	7.5	13
2	Structural basis for pore blockade of human voltage-gated calcium channel Cav1.3 by motion sickness drug cinnarizine. Cell Research, 2022, 32, 946-948.	12.0	30
3	High-resolution structures of human Nav1.7 reveal gating modulation through α -helical transition of S6IV. Cell Reports, 2022, 39, 110735.	6.4	35
4	Molecular basis for inhibiting human glucose transporters by exofacial inhibitors. Nature Communications, 2022, 13, 2632.	12.8	10
5	Cryo-EM structure of human glucose transporter GLUT4. Nature Communications, 2022, 13, 2671.	12.8	31
6	Structural Basis of the Modulation of the Voltage-Gated Calcium Ion Channel $Ca_{v1.1}$ by Dihydropyridine Compounds**. Angewandte Chemie, 2021, 133, 3168-3174.	2.0	3
7	Structural Basis of the Modulation of the Voltage-Gated Calcium Ion Channel $Ca_{v1.1}$ by Dihydropyridine Compounds**. Angewandte Chemie - International Edition, 2021, 60, 3131-3137.	13.8	42
8	Structural determination of human Nav1.4 and Nav1.7 using single particle cryo-electron microscopy. Methods in Enzymology, 2021, 653, 103-120.	1.0	5
9	Orthosteric allosteric dual inhibitors of PfHT1 as selective antimalarial agents. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	17
10	Structure of human $Na_{v1.5}$ reveals the fast inactivation-related segments as a mutational hotspot for the long QT syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	44
11	Comparative structural analysis of human $Na_{v1.1}$ and $Na_{v1.5}$ reveals mutational hotspots for sodium channelopathies. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	56
12	A structure of human Scap bound to Insig-2 suggests how their interaction is regulated by sterols. Science, 2021, 371, .	12.6	44
13	Atomistic Details of Charge/Space Competition in the Ca_{v2+} Selectivity of Ryanodine Receptors. Journal of Physical Chemistry Letters, 2021, 12, 4286-4291.	4.6	10
14	Structural Basis for Pore Blockade of the Human Cardiac Sodium Channel $Na_{v1.5}$ by the Antiarrhythmic Drug Quinidine**. Angewandte Chemie, 2021, 133, 11575-11581.	2.0	6
15	Structural Basis for Pore Blockade of the Human Cardiac Sodium Channel $Na_{v1.5}$ by the Antiarrhythmic Drug Quinidine**. Angewandte Chemie - International Edition, 2021, 60, 11474-11480.	13.8	63
16	Structural Basis for the Modulation of Ryanodine Receptors. Trends in Biochemical Sciences, 2021, 46, 489-501.	7.5	9
17	Structural basis for sterol sensing by Scap and Insig. Cell Reports, 2021, 35, 109299.	6.4	16
18	Structure of human Cav2.2 channel blocked by the painkiller ziconotide. Nature, 2021, 596, 143-147.	27.8	85

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19	High-yield monolayer graphene grids for near-atomic resolution cryoelectron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1009-1014.	7.1	84
20	Structural and functional diversity calls for a new classification of ABC transporters. FEBS Letters, 2020, 594, 3767-3775.	2.8	169
21	Structural Basis for Blocking Sugar Uptake into the Malaria Parasite Plasmodium falciparum. Cell, 2020, 183, 258-268.e12.	28.9	42
22	Cryo-EM analysis of a membrane protein embedded in the liposome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18497-18503.	7.1	89
23	Structural basis of ion transport and inhibition in ferroportin. Nature Communications, 2020, 11, 5686.	12.8	42
24	Structure and mechanism of human diacylglycerol O-acyltransferase \hat{A} 1. Nature, 2020, 581, 329-332.	27.8	72
25	Structural basis for catalysis and substrate specificity of human ACAT1. Nature, 2020, 581, 333-338.	27.8	66
26	Structural Basis of Low-pH-Dependent Lysosomal Cholesterol Egress by NPC1 and NPC2. Cell, 2020, 182, 98-111.e18.	28.9	107
27	Employing NaChBac for cryo-EM analysis of toxin action on voltage-gated Na ⁺ channels in nanodisc. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14187-14193.	7.1	33
28	Modulation of cardiac ryanodine receptor 2 by calmodulin. Nature, 2019, 572, 347-351.	27.8	110
29	Inhibition of tetrameric Patched1 by Sonic Hedgehog through an asymmetric paradigm. Nature Communications, 2019, 10, 2320.	12.8	77
30	Molecular Basis for Ligand Modulation of a Mammalian Voltage-Gated Ca ²⁺ Channel. Cell, 2019, 177, 1495-1506.e12.	28.9	172
31	Engineered XylE as a tool for mechanistic investigation and ligand discovery of the glucose transporters GLUTs. Cell Discovery, 2019, 5, 14.	6.7	18
32	Structures of human Na ^v 1.7 channel in complex with auxiliary subunits and animal toxins. Science, 2019, 363, 1303-1308.	12.6	318
33	Molecular basis for pore blockade of human Na ⁺ channel Na ^v 1.2 by the \hat{I} -4-conotoxin KIIIA. Science, 2019, 363, 1309-1313.	12.6	197
34	Molecular basis for allosteric regulation of the type 2 ryanodine receptor channel gating by key modulators. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25575-25582.	7.1	39
35	Cryo-EM structures of apo and antagonist-bound human Cav3.1. Nature, 2019, 576, 492-497.	27.8	116
36	Cryo-EM structure of L-fucokinase/GDP-fucose pyrophosphorylase (FKP) in Bacteroides fragilis. Protein and Cell, 2019, 10, 365-369.	11.0	6

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37	Crystallization and Structural Determination of the Human Glucose Transporters GLUT1 and GLUT3. <i>Methods in Molecular Biology</i> , 2018, 1713, 15-29.	0.9	0
38	Simulating the ion permeation and ion selection for a eukaryotic voltage-gated sodium channel NaVPaS. <i>Protein and Cell</i> , 2018, 9, 580-585.	11.0	17
39	Human SEIPIN Binds Anionic Phospholipids. <i>Developmental Cell</i> , 2018, 47, 248-256.e4.	7.0	159
40	Structure of the human plasma membrane Ca ²⁺ -ATPase 1 in complex with its obligatory subunit neuroplastin. <i>Nature Communications</i> , 2018, 9, 3623.	12.8	71
41	Structure of the human voltage-gated sodium channel Na ^v 1.4 in complex with β 1. <i>Science</i> , 2018, 362, .	12.6	333
42	Structural basis for the recognition of Sonic Hedgehog by human Patched1. <i>Science</i> , 2018, 361, .	12.6	168
43	Structural basis for the modulation of voltage-gated sodium channels by animal toxins. <i>Science</i> , 2018, 362, .	12.6	200
44	Structure of a eukaryotic voltage-gated sodium channel at near-atomic resolution. <i>Science</i> , 2017, 355, .	12.6	351
45	Structure-based assessment of disease-related mutations in human voltage-gated sodium channels. <i>Protein and Cell</i> , 2017, 8, 401-438.	11.0	126
46	Dimeric structure of the uracil:proton symporter UraA provides mechanistic insights into the SLC4/23/26 transporters. <i>Cell Research</i> , 2017, 27, 1020-1033.	12.0	91
47	Structure of the Human Lipid Exporter ABCA1. <i>Cell</i> , 2017, 169, 1228-1239.e10.	28.9	214
48	Structure of the Nav1.4- β 1 Complex from Electric Eel. <i>Cell</i> , 2017, 170, 470-482.e11.	28.9	272
49	A Glimpse of Membrane Transport through Structures—Advances in the Structural Biology of the GLUT Glucose Transporters. <i>Journal of Molecular Biology</i> , 2017, 429, 2710-2725.	4.2	61
50	Structure-Function Relationship of the Voltage-Gated Calcium Channel Cav1.1 Complex. <i>Advances in Experimental Medicine and Biology</i> , 2017, 981, 23-39.	1.6	9
51	Molecular determinants for the thermodynamic and functional divergence of uniporter GLUT1 and proton symporter Xyle. <i>PLoS Computational Biology</i> , 2017, 13, e1005603.	3.2	29
52	GLUT, SGLT, and SWEET: Structural and mechanistic investigations of the glucose transporters. <i>Protein Science</i> , 2016, 25, 546-558.	7.6	198
53	Structural Insights into the Niemann-Pick C1 (NPC1)-Mediated Cholesterol Transfer and Ebola Infection. <i>Cell</i> , 2016, 165, 1467-1478.	28.9	266
54	The Central domain of RyR1 is the transducer for long-range allosteric gating of channel opening. <i>Cell Research</i> , 2016, 26, 995-1006.	12.0	93

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55	Structural basis for the gating mechanism of the type 2 ryanodine receptor RyR2. <i>Science</i> , 2016, 354, .	12.6	221
56	Structure of the voltage-gated calcium channel Cav1.1 at 3.6Å resolution. <i>Nature</i> , 2016, 537, 191-196.	27.8	398
57	Complex structure of the fission yeast SREBP-SCAP binding domains reveals an oligomeric organization. <i>Cell Research</i> , 2016, 26, 1197-1211.	12.0	19
58	Crystal structure of a LacY nanobody complex in a periplasmic-open conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12420-12425.	7.1	38
59	Structure of the voltage-gated calcium channel Ca _v 1.1 complex. <i>Science</i> , 2015, 350, aad2395.	12.6	270
60	Crystal structure of a mycobacterial Insig homolog provides insight into how these sensors monitor sterol levels. <i>Science</i> , 2015, 349, 187-191.	12.6	32
61	Molecular basis of ligand recognition and transport by glucose transporters. <i>Nature</i> , 2015, 526, 391-396.	27.8	305
62	Structural Biology of the Major Facilitator Superfamily Transporters. <i>Annual Review of Biophysics</i> , 2015, 44, 257-283.	10.0	370
63	Structure of the WD40 domain of SCAP from fission yeast reveals the molecular basis for SREBP recognition. <i>Cell Research</i> , 2015, 25, 401-411.	12.0	15
64	Structure of the rabbit ryanodine receptor RyR1 at near-atomic resolution. <i>Nature</i> , 2015, 517, 50-55.	27.8	391
65	Identification and Characterization of ABA Receptors in <i>Oryza sativa</i> . <i>PLoS ONE</i> , 2014, 9, e95246.	2.5	103
66	Crystal structure of a bacterial homologue of SWEET transporters. <i>Cell Research</i> , 2014, 24, 1486-1489.	12.0	71
67	Examination of the Dimerization States of the Single-stranded RNA Recognition Protein Pentatricopeptide Repeat 10 (PPR10). <i>Journal of Biological Chemistry</i> , 2014, 289, 31503-31512.	3.4	16
68	Functional architecture of MFS -glucose transporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E719-27.	7.1	95
69	Crystal structure of the human glucose transporter GLUT1. <i>Nature</i> , 2014, 510, 121-125.	27.8	592
70	The recombinant expression systems for structure determination of eukaryotic membrane proteins. <i>Protein and Cell</i> , 2014, 5, 658-672.	11.0	87
71	Revisiting the TALE repeat. <i>Protein and Cell</i> , 2014, 5, 297-306.	11.0	36
72	Structural basis for the modular recognition of single-stranded RNA by PPR proteins. <i>Nature</i> , 2013, 504, 168-171.	27.8	281

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73	The Mechanism of Na ⁺ /K ⁺ Selectivity in Mammalian Voltage-Gated Sodium Channels Based on Molecular Dynamics Simulation. <i>Biophysical Journal</i> , 2013, 104, 2401-2409.	0.5	41
74	Structural investigation of the proton-coupled secondary transporters. <i>Current Opinion in Structural Biology</i> , 2013, 23, 483-491.	5.7	11
75	Structural advances for the major facilitator superfamily (MFS) transporters. <i>Trends in Biochemical Sciences</i> , 2013, 38, 151-159.	7.5	329
76	Molecular basis for the selective and ABA-independent inhibition of PP2CA by PYL13. <i>Cell Research</i> , 2013, 23, 1369-1379.	12.0	80
77	The conformational shifts of the voltage sensing domains between NavRh and NavAb. <i>Cell Research</i> , 2013, 23, 444-447.	12.0	14
78	Molecular Mechanism for Inhibition of a Critical Component in the Arabidopsis thaliana Abscisic Acid Signal Transduction Pathways, SnRK2.6, by Protein Phosphatase ABI1. <i>Journal of Biological Chemistry</i> , 2012, 287, 794-802.	3.4	76
79	Dynamics of the α -fucose/H ⁺ symporter revealed by fluorescence spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14847-14851.	7.1	18
80	Specific DNA-RNA Hybrid Recognition by TAL Effectors. <i>Cell Reports</i> , 2012, 2, 707-713.	6.4	28
81	Structural Basis for Sequence-Specific Recognition of DNA by TAL Effectors. <i>Science</i> , 2012, 335, 720-723.	12.6	528
82	Recognition of methylated DNA by TAL effectors. <i>Cell Research</i> , 2012, 22, 1502-1504.	12.0	113
83	Crystal structure of a bacterial homologue of glucose transporters GLUT1 ⁴ . <i>Nature</i> , 2012, 490, 361-366.	27.8	435
84	Crystal structure of an orthologue of the NaChBac voltage-gated sodium channel. <i>Nature</i> , 2012, 486, 130-134.	27.8	439
85	The Molecular Basis of ABA-Independent Inhibition of PP2Cs by a Subclass of PYL Proteins. <i>Molecular Cell</i> , 2011, 42, 662-672.	9.7	241
86	Structure and mechanism of the uracil transporter UraA. <i>Nature</i> , 2011, 472, 243-246.	27.8	186
87	Structure of a fucose transporter in an outward-open conformation. <i>Nature</i> , 2010, 467, 734-738.	27.8	272
88	Structure of the formate transporter FocA reveals a pentameric aquaporin-like channel. <i>Nature</i> , 2009, 462, 467-472.	27.8	148
89	Structural insights into the mechanism of abscisic acid signaling by PYL proteins. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1230-1236.	8.2	381
90	Allosteric Activation of a Bacterial Stress Sensor. <i>Cell</i> , 2007, 131, 441-443.	28.9	2

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91	Structure of a Site-2 Protease Family Intramembrane Metalloprotease. <i>Science</i> , 2007, 318, 1608-1612.	12.6	218
92	2:1 Stoichiometry of the CED4â€“CED9 Complex and the Tetrameric CED-4: Insights into the Regulation of CED-3 Activation. <i>Cell Cycle</i> , 2006, 5, 31-34.	2.6	19
93	Structure and Activation Mechanism of the Drosophila Initiator Caspase Dronc. <i>Journal of Biological Chemistry</i> , 2006, 281, 8667-8674.	3.4	45
94	Structure of the CED-4â€“CED-9 complex provides insights into programmed cell death in <i>Caenorhabditis elegans</i> . <i>Nature</i> , 2005, 437, 831-837.	27.8	207
95	MECHANISMS OF APOPTOSIS THROUGH STRUCTURAL BIOLOGY. <i>Annual Review of Cell and Developmental Biology</i> , 2005, 21, 35-56.	9.4	166
96	Molecular mechanisms of DrICE inhibition by DIAP1 and removal of inhibition by Reaper, Hid and Grim. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 420-428.	8.2	94
97	Structural, Biochemical, and Functional Analyses of CED-9 Recognition by the Proapoptotic Proteins EGL-1 and CED-4. <i>Molecular Cell</i> , 2004, 15, 999-1006.	9.7	92