

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	Crystal structure of the human glucose transporter GLUT1. <i>Nature</i> , 2014, 510, 121-125.	27.8	592
2	Structural Basis for Sequence-Specific Recognition of DNA by TAL Effectors. <i>Science</i> , 2012, 335, 720-723.	12.6	528
3	Crystal structure of an orthologue of the NaChBac voltage-gated sodium channel. <i>Nature</i> , 2012, 486, 130-134.	27.8	439
4	Crystal structure of a bacterial homologue of glucose transporters GLUT1 ⁴ . <i>Nature</i> , 2012, 490, 361-366.	27.8	435
5	Structure of the voltage-gated calcium channel Cav1.1 at 3.6Å resolution. <i>Nature</i> , 2016, 537, 191-196.	27.8	398
6	Structure of the rabbit ryanodine receptor RyR1 at near-atomic resolution. <i>Nature</i> , 2015, 517, 50-55.	27.8	391
7	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
8	Structural Biology of the Major Facilitator Superfamily Transporters. <i>Annual Review of Biophysics</i> , 2015, 44, 257-283.	10.0	370
9	Structure of a eukaryotic voltage-gated sodium channel at near-atomic resolution. <i>Science</i> , 2017, 355, .	12.6	351
10	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
11	Structural advances for the major facilitator superfamily (MFS) transporters. <i>Trends in Biochemical Sciences</i> , 2013, 38, 151-159.	7.5	329
12	Structures of human Na ^v 1.7 channel in complex with auxiliary subunits and animal toxins. <i>Science</i> , 2019, 363, 1303-1308.	12.6	318
13	Molecular basis of ligand recognition and transport by glucose transporters. <i>Nature</i> , 2015, 526, 391-396.	27.8	305
14	Structural basis for the modular recognition of single-stranded RNA by PPR proteins. <i>Nature</i> , 2013, 504, 168-171.	27.8	281
15	Structure of a fucose transporter in an outward-open conformation. <i>Nature</i> , 2010, 467, 734-738.	27.8	272
16	Structure of the Nav1.4- β 1 Complex from Electric Eel. <i>Cell</i> , 2017, 170, 470-482.e11.	28.9	272
17	Structure of the voltage-gated calcium channel Ca ^v 1.1 complex. <i>Science</i> , 2015, 350, aad2395.	12.6	270
18	Structural Insights into the Niemann-Pick C1 (NPC1)-Mediated Cholesterol Transfer and Ebola Infection. <i>Cell</i> , 2016, 165, 1467-1478.	28.9	266

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19	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
20	Structural basis for the gating mechanism of the type 2 ryanodine receptor RyR2. <i>Science</i> , 2016, 354, .	12.6	221
21	Structure of a Site-2 Protease Family Intramembrane Metalloprotease. <i>Science</i> , 2007, 318, 1608-1612.	12.6	218
22	Structure of the Human Lipid Exporter ABCA1. <i>Cell</i> , 2017, 169, 1228-1239.e10.	28.9	214
23	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
24	Structural basis for the modulation of voltage-gated sodium channels by animal toxins. <i>Science</i> , 2018, 362, .	12.6	200
25	<scp>GLUT</scp>, <scp>SGLT</scp>, and <scp>SWEET</scp>: Structural and mechanistic investigations of the glucose transporters. <i>Protein Science</i> , 2016, 25, 546-558.	7.6	198
26	Molecular basis for pore blockade of human Na ⁺ channel Na _v 1.2 by the Î¼-conotoxin KIIIA. <i>Science</i> , 2019, 363, 1309-1313.	12.6	197
27	Structure and mechanism of the uracil transporter UraA. <i>Nature</i> , 2011, 472, 243-246.	27.8	186
28	Molecular Basis for Ligand Modulation of a Mammalian Voltage-Gated Ca ²⁺ Channel. <i>Cell</i> , 2019, 177, 1495-1506.e12.	28.9	172
29	Structural and functional diversity calls for a new classification of ABC transporters. <i>FEBS Letters</i> , 2020, 594, 3767-3775.	2.8	169
30	Structural basis for the recognition of Sonic Hedgehog by human Patched1. <i>Science</i> , 2018, 361, .	12.6	168
31	MECHANISMS OF APOPTOSIS THROUGH STRUCTURAL BIOLOGY. <i>Annual Review of Cell and Developmental Biology</i> , 2005, 21, 35-56.	9.4	166
32	Human SEIPIN Binds Anionic Phospholipids. <i>Developmental Cell</i> , 2018, 47, 248-256.e4.	7.0	159
33	Structure of the formate transporter FocA reveals a pentameric aquaporin-like channel. <i>Nature</i> , 2009, 462, 467-472.	27.8	148
34	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
35	Cryo-EM structures of apo and antagonist-bound human Cav3.1. <i>Nature</i> , 2019, 576, 492-497.	27.8	116
36	Recognition of methylated DNA by TAL effectors. <i>Cell Research</i> , 2012, 22, 1502-1504.	12.0	113

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37	Modulation of cardiac ryanodine receptor 2 by calmodulin. <i>Nature</i> , 2019, 572, 347-351.	27.8	110
38	Structural Basis of Low-pH-Dependent Lysosomal Cholesterol Egress by NPC1 and NPC2. <i>Cell</i> , 2020, 182, 98-111.e18.	28.9	107
39	Identification and Characterization of ABA Receptors in <i>Oryza sativa</i> . <i>PLoS ONE</i> , 2014, 9, e95246.	2.5	103
40	Functional architecture of MFS d -glucose transporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E719-27.	7.1	95
41	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
42	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
43	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
44	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
45	Cryo-EM analysis of a membrane protein embedded in the liposome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18497-18503.	7.1	89
46	The recombinant expression systems for structure determination of eukaryotic membrane proteins. <i>Protein and Cell</i> , 2014, 5, 658-672.	11.0	87
47	Structure of human Cav2.2 channel blocked by the painkiller ziconotide. <i>Nature</i> , 2021, 596, 143-147.	27.8	85
48	High-yield monolayer graphene grids for near-atomic resolution cryoelectron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1009-1014.	7.1	84
49	Molecular basis for the selective and ABA-independent inhibition of PP2CA by PYL13. <i>Cell Research</i> , 2013, 23, 1369-1379.	12.0	80
50	Inhibition of tetrameric Patched1 by Sonic Hedgehog through an asymmetric paradigm. <i>Nature Communications</i> , 2019, 10, 2320.	12.8	77
51	Molecular Mechanism for Inhibition of a Critical Component in the <i>Arabidopsis thaliana</i> Abscisic Acid Signal Transduction Pathways, SnRK2.6, by Protein Phosphatase ABI1. <i>Journal of Biological Chemistry</i> , 2012, 287, 794-802.	3.4	76
52	Structure and mechanism of human diacylglycerol O-acyltransferase \hat{A} 1. <i>Nature</i> , 2020, 581, 329-332.	27.8	72
53	Crystal structure of a bacterial homologue of SWEET transporters. <i>Cell Research</i> , 2014, 24, 1486-1489.	12.0	71
54	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

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55	Structural basis for catalysis and substrate specificity of human ACAT1. <i>Nature</i> , 2020, 581, 333-338.	27.8	66
56	Structural Basis for Pore Blockade of the Human Cardiac Sodium Channel Na _v 1.5 by the Antiarrhythmic Drug Quinidine**. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 11474-11480.	13.8	63
57	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
58	Comparative structural analysis of human Na _v 1.1 and Na _v 1.5 reveals mutational hotspots for sodium channelopathies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	56
59	Structure and Activation Mechanism of the Drosophila Initiator Caspase Dronc. <i>Journal of Biological Chemistry</i> , 2006, 281, 8667-8674.	3.4	45
60	Structure of human Na _v 1.5 reveals the fast inactivation-related segments as a mutational hotspot for the long QT syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	44
61	A structure of human Scap bound to Insig-2 suggests how their interaction is regulated by sterols. <i>Science</i> , 2021, 371, .	12.6	44
62	Structural Basis for Blocking Sugar Uptake into the Malaria Parasite Plasmodium falciparum. <i>Cell</i> , 2020, 183, 258-268.e12.	28.9	42
63	Structural basis of ion transport and inhibition in ferroportin. <i>Nature Communications</i> , 2020, 11, 5686.	12.8	42
64	Structural Basis of the Modulation of the Voltage-Gated Calcium Ion Channel Ca _v 1.1 by Dihydropyridine Compounds**. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 3131-3137.	13.8	42
65	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
66	Molecular basis for allosteric regulation of the type 2 ryanodine receptor channel gating by key modulators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25575-25582.	7.1	39
67	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
68	Revisiting the TALE repeat. <i>Protein and Cell</i> , 2014, 5, 297-306.	11.0	36
69	High-resolution structures of human Nav1.7 reveal gating modulation through α -helical transition of S6IV. <i>Cell Reports</i> , 2022, 39, 110735.	6.4	35
70	Employing NaChBac for cryo-EM analysis of toxin action on voltage-gated Na ⁺ channels in nanodisc. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14187-14193.	7.1	33
71	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
72	Cryo-EM structure of human glucose transporter GLUT4. <i>Nature Communications</i> , 2022, 13, 2671.	12.8	31

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73	Structural basis for pore blockade of human voltage-gated calcium channel Cav1.3 by motion sickness drug cinnarizine. <i>Cell Research</i> , 2022, 32, 946-948.	12.0	30
74	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
75	Specific DNA-RNA Hybrid Recognition by TAL Effectors. <i>Cell Reports</i> , 2012, 2, 707-713.	6.4	28
76	2:1 Stoichiometry of the CED4/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
77	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
78	Dynamics of the α -D-glucose/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
79	Engineered Xyle as a tool for mechanistic investigation and ligand discovery of the glucose transporters GLUTs. <i>Cell Discovery</i> , 2019, 5, 14.	6.7	18
80	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
81	Orthosteric allosteric dual inhibitors of PfHT1 as selective antimalarial agents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	17
82	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
83	Structural basis for sterol sensing by Scap and Insig. <i>Cell Reports</i> , 2021, 35, 109299.	6.4	16
84	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
85	The conformational shifts of the voltage sensing domains between NavRh and NavAb. <i>Cell Research</i> , 2013, 23, 444-447.	12.0	14
86	Structural advances in sterol-sensing domain-containing proteins. <i>Trends in Biochemical Sciences</i> , 2022, 47, 289-300.	7.5	13
87	Structural investigation of the proton-coupled secondary transporters. <i>Current Opinion in Structural Biology</i> , 2013, 23, 483-491.	5.7	11
88	Atomistic Details of Charge/Space Competition in the Ca ²⁺ Selectivity of Ryanodine Receptors. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 4286-4291.	4.6	10
89	Molecular basis for inhibiting human glucose transporters by exofacial inhibitors. <i>Nature Communications</i> , 2022, 13, 2632.	12.8	10
90	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

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91	Structural Basis for the Modulation of Ryanodine Receptors. Trends in Biochemical Sciences, 2021, 46, 489-501.	7.5	9
92	Cryo-EM structure of L-fucokinase/GDP-fucose pyrophosphorylase (FKP) in Bacteroides fragilis. Protein and Cell, 2019, 10, 365-369.	11.0	6
93	Structural Basis for Pore Blockade of the Human Cardiac Sodium Channel Na _v 1.5 by the Antiarrhythmic Drug Quinidine**. Angewandte Chemie, 2021, 133, 11575-11581.	2.0	6
94	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
95	Structural Basis of the Modulation of the Voltage-Gated Calcium Ion Channel Ca _v 1.1 by Dihydropyridine Compounds**. Angewandte Chemie, 2021, 133, 3168-3174.	2.0	3
96	Allosteric Activation of a Bacterial Stress Sensor. Cell, 2007, 131, 441-443.	28.9	2
97	Crystallization and Structural Determination of the Human Glucose Transporters GLUT1 and GLUT3. Methods in Molecular Biology, 2018, 1713, 15-29.	0.9	0