

Norimichi Nomura

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,771
citations

430874

18
h-index

501196

28
g-index

34
all docs

34
docs citations

34
times ranked

2780
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Structural basis for channel conduction in the pump-like channelrhodopsin ChRmine. <i>Cell</i> , 2022, 185, 672-689.e23. | 28.9 | 72 |
| 2 | Structure, mechanism and lipid-mediated remodeling of the mammalian Na ⁺ /H ⁺ exchanger NHA2. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 108-120. | 8.2 | 27 |
| 3 | Structural insights into the HBV receptor and bile acid transporter NTCP. <i>Nature</i> , 2022, 606, 1027-1031. | 27.8 | 44 |
| 4 | Structure of the bile acid transporter and HBV receptor NTCP. <i>Nature</i> , 2022, 606, 1021-1026. | 27.8 | 45 |
| 5 | Isolation and thermal stabilization of mouse ferroportin. <i>FEBS Open Bio</i> , 2021, 11, 26-34. | 2.3 | 1 |
| 6 | Cryo-EM Structure of the Prostaglandin E Receptor EP4 Coupled to G Protein. <i>Structure</i> , 2021, 29, 252-260.e6. | 3.3 | 32 |
| 7 | The structure of MgtE in the absence of magnesium provides new insights into channel gating. <i>PLoS Biology</i> , 2021, 19, e3001231. | 5.6 | 8 |
| 8 | The structural basis of bacterial manganese import. <i>Science Advances</i> , 2021, 7, . | 10.3 | 17 |
| 9 | Cryo-EM structure of the human MT1α-Gi signaling complex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 694-701. | 8.2 | 31 |
| 10 | Molecular mechanism of SbmA, a promiscuous transporter exploited by antimicrobial peptides. <i>Science Advances</i> , 2021, 7, eabj5363. | 10.3 | 27 |
| 11 | The Intervening Removable Affinity Tag (iRAT) System for the Production of Recombinant Antibody Fragments. <i>Methods in Molecular Biology</i> , 2021, 2247, 77-103. | 0.9 | 0 |
| 12 | The Crystal Structure of Angiotensin II Type 2 Receptor with Endogenous Peptide Hormone. <i>Structure</i> , 2020, 28, 418-425.e4. | 3.3 | 40 |
| 13 | Atg9 is a lipid scramblase that mediates autophagosomal membrane expansion. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 1185-1193. | 8.2 | 253 |
| 14 | Structural insights into tetraspanin CD9 function. <i>Nature Communications</i> , 2020, 11, 1606. | 12.8 | 114 |
| 15 | Structure of the dopamine D2 receptor in complex with the antipsychotic drug spiperone. <i>Nature Communications</i> , 2020, 11, 6442. | 12.8 | 47 |
| 16 | Crystallographic approaches to study the interaction modes of PD-1- and CTLA-4-blocking antibodies. <i>Methods in Enzymology</i> , 2019, 629, 383-399. | 1.0 | 1 |
| 17 | FRET-assisted photoactivation of flavoproteins for in vivo two-photon optogenetics. <i>Nature Methods</i> , 2019, 16, 1029-1036. | 19.0 | 32 |
| 18 | Structures of the 5-HT _{2A} receptor in complex with the antipsychotics risperidone and zotepine. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 121-128. | 8.2 | 133 |

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|----|--|------|-----------|
| 19 | Ligand binding to human prostaglandin E receptor EP4 at the lipid-bilayer interface. <i>Nature Chemical Biology</i> , 2019, 15, 18-26. | 8.0 | 85 |
| 20 | Structural basis for tumor necrosis factor blockade with the therapeutic antibody golimumab. <i>Protein Science</i> , 2018, 27, 1038-1046. | 7.6 | 18 |
| 21 | Generation of Conformation-Specific Antibody Fragments for Crystallization of the Multidrug Resistance Transporter MdfA. <i>Methods in Molecular Biology</i> , 2018, 1700, 97-109. | 0.9 | 13 |
| 22 | Outward open conformation of a Major Facilitator Superfamily multidrug/H ⁺ antiporter provides insights into switching mechanism. <i>Nature Communications</i> , 2018, 9, 4005. | 12.8 | 46 |
| 23 | Crystal structure of the human angiotensin II type 2 receptor bound to an angiotensin II analog. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 570-576. | 8.2 | 58 |
| 24 | The multidrug-resistance transporter MdfA from <i>Escherichia coli</i> : crystallization and X-ray diffraction analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 423-430. | 0.8 | 8 |
| 25 | The intervening removable affinity tag (iRAT) production system facilitates Fv antibody fragment-mediated crystallography. <i>Protein Science</i> , 2016, 25, 2268-2276. | 7.6 | 7 |
| 26 | High-resolution crystal structure of the therapeutic antibody pembrolizumab bound to the human PD-1. <i>Scientific Reports</i> , 2016, 6, 35297. | 3.3 | 77 |
| 27 | Structure and Molecular Mechanism of the Mammalian Fructose Transporter GLUT5. <i>Nihon Kessho Gakkaishi</i> , 2016, 58, 133-138. | 0.0 | 1 |
| 28 | Structure and mechanism of the mammalian fructose transporter GLUT5. <i>Nature</i> , 2015, 526, 397-401. | 27.8 | 202 |
| 29 | Platform for the rapid construction and evaluation of GPCRs for crystallography in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012, 11, 78. | 4.0 | 43 |
| 30 | G-protein-coupled receptor inactivation by an allosteric inverse-agonist antibody. <i>Nature</i> , 2012, 482, 237-240. | 27.8 | 274 |