Daniel Hilger

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/85659/publications.pdf

Version: 2024-02-01

36 6,048 25 34 papers citations h-index g-index

43 43 43 6688
all docs docs citations times ranked citing authors

| # | Article | IF | CITATIONS |
|----------------------------|--|-----------------------------|------------------------------|
| 1 | Allosteric modulation of GPCRs: From structural insights to in silico drug discovery., 2022, 237, 108242. | | 15 |
| 2 | The role of structural dynamics in GPCRâ€mediated signaling. FEBS Journal, 2021, 288, 2461-2489. | 4.7 | 58 |
| 3 | Structures of active melanocortin-4 receptor–Gs-protein complexes with NDP-α-MSH and setmelanotide. Cell Research, 2021, 31, 1176-1189. | 12.0 | 40 |
| 4 | Viewing rare conformations of the \hat{l}^2 ₂ adrenergic receptor with pressure-resolved DEER spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31824-31831. | 7.1 | 31 |
| 5 | Structural insights into differences in G protein activation by family A and family B GPCRs. Science, 2020, 369, . | 12.6 | 103 |
| 6 | Time-resolved Conformational Analysis during GPCR-Gs Coupling. Proceedings for Annual Meeting of the Japanese Pharmacological Society, 2020, 93, 3-S28-3. | 0.0 | 1 |
| 7 | Structures of Gα Proteins in Complex with Their Chaperone Reveal Quality Control Mechanisms. Cell Reports, 2020, 30, 3699-3709.e6. | 6.4 | 18 |
| 8 | Conformational transitions of a neurotensin receptorÂ1–Gi1Âcomplex. Nature, 2019, 572, 80-85. | 27.8 | 199 |
| 9 | Structural Insights into the Process of GPCR-G Protein Complex Formation. Cell, 2019, 177, 1243-1251.e12. | 28.9 | 121 |
| | 1245-1251:e12. | | |
| 10 | Assembly of a GPCR-G Protein Complex. Cell, 2019, 177, 1232-1242.e11. | 28.9 | 163 |
| | | 28.9 | 163 57 |
| 10 | Assembly of a GPCR-G Protein Complex. Cell, 2019, 177, 1232-1242.e11. Local membrane charge regulates Î ² 2 adrenergic receptor coupling to Gi3. Nature Communications, | | |
| 10 | Assembly of a GPCR-G Protein Complex. Cell, 2019, 177, 1232-1242.e11. Local membrane charge regulates Î ² 2 adrenergic receptor coupling to Gi3. Nature Communications, 2019, 10, 2234. Comparison of the functional properties of trimeric and monomeric CaiT of Escherichia coli. | 12.8 | 57 |
| 10 11 12 | Assembly of a GPCR-G Protein Complex. Cell, 2019, 177, 1232-1242.e11. Local membrane charge regulates Î ² 2 adrenergic receptor coupling to Gi3. Nature Communications, 2019, 10, 2234. Comparison of the functional properties of trimeric and monomeric CaiT of Escherichia coli. Scientific Reports, 2019, 9, 3787. | 12.8 3.3 | 4 |
| 10 11 12 13 | Assembly of a GPCR-G Protein Complex. Cell, 2019, 177, 1232-1242.e11. Local membrane charge regulates β2 adrenergic receptor coupling to Gi3. Nature Communications, 2019, 10, 2234. Comparison of the functional properties of trimeric and monomeric CaiT of Escherichia coli. Scientific Reports, 2019, 9, 3787. Structure of a Signaling Cannabinoid Receptor 1-G Protein Complex. Cell, 2019, 176, 448-458.e12. Angiotensin Analogs with Divergent Bias Stabilize Distinct Receptor Conformations. Cell, 2019, 176, | 12.8 3.3 28.9 | 57 4 323 |
| 10 11 12 13 | Assembly of a GPCR-G Protein Complex. Cell, 2019, 177, 1232-1242.e11. Local membrane charge regulates î²2 adrenergic receptor coupling to Gi3. Nature Communications, 2019, 10, 2234. Comparison of the functional properties of trimeric and monomeric CaiT of Escherichia coli. Scientific Reports, 2019, 9, 3787. Structure of a Signaling Cannabinoid Receptor 1-G Protein Complex. Cell, 2019, 176, 448-458.e12. Angiotensin Analogs with Divergent Bias Stabilize Distinct Receptor Conformations. Cell, 2019, 176, 468-478.e11. | 12.8 3.3 28.9 28.9 | 57 4 323 194 |
| 10 11 12 13 14 | Assembly of a GPCR-G Protein Complex. Cell, 2019, 177, 1232-1242.e11. Local membrane charge regulates î²2 adrenergic receptor coupling to Gi3. Nature Communications, 2019, 10, 2234. Comparison of the functional properties of trimeric and monomeric CaiT of Escherichia coli. Scientific Reports, 2019, 9, 3787. Structure of a Signaling Cannabinoid Receptor 1-G Protein Complex. Cell, 2019, 176, 448-458.e12. Angiotensin Analogs with Divergent Bias Stabilize Distinct Receptor Conformations. Cell, 2019, 176, 468-478.e11. Yeast surface display platform for rapid discovery of conformationally selective nanobodies. Nature Structural and Molecular Biology, 2018, 25, 289-296. Structure and dynamics of GPCR signaling complexes. Nature Structural and Molecular Biology, 2018, | 12.8 3.3 28.9 28.9 | 57 4 323 194 360 |

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Structure of the µ-opioid receptor–Gi protein complex. Nature, 2018, 558, 547-552. | 27.8 | 527 |
| 20 | Single-molecule analysis of ligand efficacy in β2AR–G-protein activation. Nature, 2017, 547, 68-73. | 27.8 | 265 |
| 21 | Structural Insights into the Dynamic Process of Î ² 2-Adrenergic Receptor Signaling. Cell, 2015, 162, 1431. | 28.9 | 8 |
| 22 | Structural basis for nucleotide exchange in heterotrimeric G proteins. Science, 2015, 348, 1361-1365. | 12.6 | 250 |
| 23 | Structural Insights into the Dynamic Process of \hat{l}^2 2 -Adrenergic Receptor Signaling. Cell, 2015, 161, 1101-1111. | 28.9 | 562 |
| 24 | Extracellular Loop 4 of the Proline Transporter PutP Controls the Periplasmic Entrance to Ligand Binding Sites. Structure, 2014, 22, 769-780. | 3.3 | 19 |
| 25 | Structure of active \hat{I}^2 -arrestin-1 bound to a G-protein-coupled receptor phosphopeptide. Nature, 2013, 497, 137-141. | 27.8 | 393 |
| 26 | The Sodium/Proline Transporter PutP of Helicobacter pylori. PLoS ONE, 2013, 8, e83576. | 2.5 | 14 |
| 27 | Initial Steps of Photosystem II de Novo Assembly and Preloading with Manganese Take Place in Biogenesis Centers in <i>Synechocystis</i> . Plant Cell, 2012, 24, 660-675. | 6.6 | 86 |
| 28 | The Na+/L-proline transporter PutP. Frontiers in Bioscience - Landmark, 2012, 17, 745. | 3.0 | 29 |
| 29 | Homology Model of the Na+/Proline Transporter PutP of Escherichia coli and Its Functional Implications. Journal of Molecular Biology, 2011, 406, 59-74. | 4.2 | 23 |
| 30 | Backbone Structure of Transmembrane Domain IX of the Na+/Proline Transporter PutP of Escherichia coli. Biophysical Journal, 2009, 96, 217-225. | 0.5 | 38 |
| 31 | Function of Transmembrane Domain IX in the Na+/Proline Transporter PutP. Journal of Molecular Biology, 2008, 382, 884-893. | 4.2 | 20 |
| 32 | Role of Ser-340 and Thr-341 in Transmembrane Domain IX of the Na+/Proline Transporter PutP of Escherichia coli in Ligand Binding and Transport. Journal of Biological Chemistry, 2008, 283, 4921-4929. | 3.4 | 26 |
| 33 | High-Resolution Structure of a Na+/H+ Antiporter Dimer Obtained by Pulsed Electron Paramagnetic Resonance Distance Measurements. Biophysical Journal, 2007, 93, 3675-3683. | 0.5 | 101 |
| 34 | Secondary Transport of Amino Acids in Prokaryotes. Journal of Membrane Biology, 2006, 213, 119-133. | 2.1 | 17 |
| 35 | DeerAnalysis2006—a comprehensive software package for analyzing pulsed ELDOR data. Applied Magnetic Resonance, 2006, 30, 473-498. | 1.2 | 941 |
| 36 | Assessing Oligomerization of Membrane Proteins by Four-Pulse DEER: pH-Dependent Dimerization of NhaA Na+/H+ Antiporter of E. coli. Biophysical Journal, 2005, 89, 1328-1338. | 0.5 | 133 |