

Thomas D Grant

List of Publications by Year in descending order

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56
papers

2,312
citations

394421

19
h-index

345221

36
g-index

62
all docs

62
docs citations

62
times ranked

3520
citing authors

#	ARTICLE	IF	CITATIONS
1	Time-resolved serial crystallography captures high-resolution intermediates of photoactive yellow protein. <i>Science</i> , 2014, 346, 1242-1246.	12.6	418
2	Femtosecond structural dynamics drives the trans/cis isomerization in photoactive yellow protein. <i>Science</i> , 2016, 352, 725-729.	12.6	348
3	Structures of riboswitch RNA reaction states by mix-and-inject XFEL serial crystallography. <i>Nature</i> , 2017, 541, 242-246.	27.8	251
4	Structure of the full-length glucagon class B G-protein-coupled receptor. <i>Nature</i> , 2017, 546, 259-264.	27.8	179
5	Ab initio electron density determination directly from solution scattering data. <i>Nature Methods</i> , 2018, 15, 191-193.	19.0	169
6	Structural basis of ligand recognition at the human MT1 melatonin receptor. <i>Nature</i> , 2019, 569, 284-288.	27.8	140
7	Enzyme intermediates captured on the fly by mix-and-inject serial crystallography. <i>BMC Biology</i> , 2018, 16, 59.	3.8	117
8	Structural enzymology using X-ray free electron lasers. <i>Structural Dynamics</i> , 2017, 4, 044003.	2.3	92
9	Snapshot of an oxygen intermediate in the catalytic reaction of cytochrome <i>c</i> oxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3572-3577.	7.1	70
10	Small angle X-ray scattering as a complementary tool for high-throughput structural studies. <i>Biopolymers</i> , 2011, 95, 517-530.	2.4	69
11	Crystal structure of CO-bound cytochrome <i>c</i> oxidase determined by serial femtosecond X-ray crystallography at room temperature. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8011-8016.	7.1	51
12	Membrane protein megahertz crystallography at the European XFEL. <i>Nature Communications</i> , 2019, 10, 5021.	12.8	47
13	The accurate assessment of small-angle X-ray scattering data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 45-56.	2.5	34
14	A hybrid NMR/SAXS-based approach for discriminating oligomeric protein interfaces using <i>scPOSETTA</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 309-317.	2.6	33
15	The Structure of the PanD/PanZ Protein Complex Reveals Negative Feedback Regulation of Pantothenate Biosynthesis by Coenzyme A. <i>Chemistry and Biology</i> , 2015, 22, 492-503.	6.0	30
16	Segmented flow generator for serial crystallography at the European X-ray free electron laser. <i>Nature Communications</i> , 2020, 11, 4511.	12.8	27
17	Microfluidic sorting of protein nanocrystals by size for X-ray free-electron laser diffraction. <i>Structural Dynamics</i> , 2015, 2, 041719.	2.3	24
18	Structural and Functional Characterization of Aerobactin Synthetase <i>lucA</i> from a Hypervirulent Pathotype of <i>Klebsiella pneumoniae</i> . <i>Biochemistry</i> , 2016, 55, 3559-3570.	2.5	21

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19	A fixed-target platform for serial femtosecond crystallography in a hydrated environment. IUCr, 2020, 7, 30-41.	2.2	21
20	3D printed droplet generation devices for serial femtosecond crystallography enabled by surface coating. Journal of Applied Crystallography, 2019, 52, 997-1008.	4.5	19
21	Synchronous RNA conformational changes trigger ordered phase transitions in crystals. Nature Communications, 2021, 12, 1762.	12.8	17
22	Structural conservation of an ancient tRNA sensor in eukaryotic glutamyl-tRNA synthetase. Nucleic Acids Research, 2012, 40, 3723-3731.	14.5	14
23	Comparing Chemistry to Outcome: The Development of a Chemical Distance Metric, Coupled with Clustering and Hierarchal Visualization Applied to Macromolecular Crystallography. PLoS ONE, 2014, 9, e100782.	2.5	14
24	The Structure of Yeast Glutamyl-tRNA Synthetase and Modeling of Its Interaction with tRNA. Journal of Molecular Biology, 2013, 425, 2480-2493.	4.2	13
25	Purification and SAXS Analysis of the Integrin Linked Kinase, PINCH, Parvin (IPP) Heterotrimeric Complex. PLoS ONE, 2013, 8, e55591.	2.5	12
26	Co-flow injection for serial crystallography at X-ray free-electron lasers. Journal of Applied Crystallography, 2022, 55, 1-13.	4.5	12
27	Serial femtosecond X-ray diffraction of enveloped virus microcrystals. Structural Dynamics, 2015, 2, 041720.	2.3	11
28	Structural consequences of transforming growth factor beta-1 activation from near-therapeutic X-ray doses. Journal of Synchrotron Radiation, 2019, 26, 967-979.	2.4	10
29	X-ray Emission Spectroscopy at X-ray Free Electron Lasers: Limits to Observation of the Classical Spectroscopic Response for Electronic Structure Analysis. Journal of Physical Chemistry Letters, 2019, 10, 441-446.	4.6	8
30	XFEL and NMR Structures of Francisella Lipoprotein Reveal Conformational Space of Drug Target against Tularemia. Structure, 2020, 28, 540-547.e3.	3.3	8
31	Examples of Biological Small Angle Scattering. , 2018, , .		8
32	Biological Small Angle Scattering. , 2018, , .		7
33	Crystallization of ApoA1 and ApoE4 Nanolipoprotein Particles and Initial XFEL-Based Structural Studies. Crystals, 2020, 10, 886.	2.2	6
34	Reply to: Limitations of the iterative electron density reconstruction algorithm from solution scattering data. Nature Methods, 2021, 18, 246-248.	19.0	5
35	A new view on crystal harvesting. Journal of Applied Crystallography, 2014, 47, 1158-1161.	4.5	2
36	Membrane Protein Dynamics Revealed by X-Ray Scattering with a Femtosecond Free-Electron Laser. Biophysical Journal, 2020, 118, 365a.	0.5	1

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37	Pushing the Envelope. , 2018, , .		1
38	Towards a generalised approach for the time-resolved crystallographic study of enzymes. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s25-s25.	0.1	0
39	FRET, SAXS and Molecular Simulations Resolve the Solution Structures of Three Coexisting Conformers of Flexible RNA Four-Way Junction. Biophysical Journal, 2017, 112, 367a.	0.5	0
40	Study of Ultra-Fast Rhodopsin Activation Dynamics with Molecular Dynamics Simulations. Biophysical Journal, 2019, 116, 205a.	0.5	0
41	AB Initio Electron Density Determination Directly from Solution Scattering Data. Biophysical Journal, 2020, 118, 487a.	0.5	0
42	Rhodopsin's Ultra-Fast Activation Dynamics in Bilayer and Micelle Environments. Biophysical Journal, 2020, 118, 92a.	0.5	0
43	Chemical clustering and visualization applied to macromolecular crystallography. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1145-C1145.	0.1	0
44	Solving the phase problem in solution scattering. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a158-a158.	0.1	0
45	Using X-ray free-electron laser to capture intermediate states. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a15-a15.	0.1	0
46	Developments on the Horizon. , 2018, , .		0
47	Examples of Data Collection and Processing. , 2018, , .		0
48	Making the Best Use of Beamtime. , 2018, , .		0
49	Instrumental and Experimental Considerations. , 2018, , .		0
50	Distinct Instrumental Approaches to SAXS. , 2018, , .		0
51	Shape Reconstructions from Small Angle Scattering Data. , 2018, , .		0
52	Before the Beamtime. , 2018, , .		0
53	Quantities Directly Measurable by Scattering. , 2018, , .		0
54	Superposition of Macromolecular Electron Density Maps in X-ray Solution Scattering (SAXS). FASEB Journal, 2019, 33, 779.27.	0.5	0

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55	Structural studies on low-dose X-ray radiation induced transforming growth factor beta-1 (TGF β -1) activation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, a82-a82.	0.1	0
56	Structural consequences on transforming growth factor beta-1 activation from near-therapeutic X-ray doses. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, a233-a233.	0.1	0