

Helen M Ginn

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,486
citations

471371

17
h-index

677027

22
g-index

23
all docs

23
docs citations

23
times ranked

3291
citing authors

#	ARTICLE	IF	CITATIONS
1	The antigenic anatomy of SARS-CoV-2 receptor binding domain. <i>Cell</i> , 2021, 184, 2183-2200.e22.	13.5	331
2	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. <i>Science</i> , 2021, 372, 642-646.	6.0	240
3	Segmented flow generator for serial crystallography at the European X-ray free electron laser. <i>Nature Communications</i> , 2020, 11, 4511.	5.8	27
4	Pre-clustering data sets using <i>cluster4</i> improves the signal-to-noise ratio of high-throughput crystallography drug-screening analysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1134-1144.	1.1	19
5	Proteins' Knotty Problems. <i>Journal of Molecular Biology</i> , 2019, 431, 244-257.	2.0	36
6	Towards in cellulo virus crystallography. <i>Scientific Reports</i> , 2018, 8, 3771.	1.6	11
7	Megahertz serial crystallography. <i>Nature Communications</i> , 2018, 9, 4025.	5.8	147
8	Machining protein microcrystals for structure determination by electron diffraction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9569-9573.	3.3	69
9	Femtosecond X-ray coherent diffraction of aligned amyloid fibrils on low background graphene. <i>Nature Communications</i> , 2018, 9, 1836.	5.8	34
10	Where is crystallography going?. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 152-166.	1.1	54
11	High-speed fixed-target serial virus crystallography. <i>Nature Methods</i> , 2017, 14, 805-810.	9.0	106
12	Development of tools to automate quantitative analysis of radiation damage in SAXS experiments. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 63-72.	1.0	28
13	The slip-and-slide algorithm: a refinement protocol for detector geometry. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 1152-1162.	1.0	5
14	<i>TakeTwo</i> : an indexing algorithm suited to still images with known crystal parameters. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 956-965.	1.1	35
15	Fixed target combined with spectral mapping: approaching 100% hit rates for serial crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 944-955.	1.1	71
16	Recovery of data from perfectly twinned virus crystals revisited. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 817-822.	1.1	7
17	On the release of <i>cppxfel</i> for processing X-ray free-electron laser images. <i>Journal of Applied Crystallography</i> , 2016, 49, 1065-1072.	1.9	28
18	Structure of CPV17 polyhedrin determined by the improved analysis of serial femtosecond crystallographic data. <i>Nature Communications</i> , 2015, 6, 6435.	5.8	56

#	ARTICLE	IF	CITATIONS
19	A revised partiality model and post-refinement algorithm for X-ray free-electron laser data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1400-1410.	2.5	60
20	Structure-based energetics of protein interfaces guides foot-and-mouth disease virus vaccine design. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 788-794.	3.6	89
21	Polyhedra structures and the evolution of the insect viruses. <i>Journal of Structural Biology</i> , 2015, 192, 88-99.	1.3	25
22	<i>SynchLink</i> : an iOS app for ISPyB. <i>Journal of Applied Crystallography</i> , 2014, 47, 1781-1783.	1.9	5