Claudia Milln

List of Publications by Year in Descending Order

26 papers	962 citations	13 h-index	28 g-index
28 ext. papers	2,286 ext. citations	7.8 avg, IF	4.21 L-index

#	Paper	IF	Citations
26	Structure of the class XI myosin globular tail reveals evolutionary hallmarks for cargo recognition in plants. *Acta Crystallographica Section D: Structural Biology*, **2021**, 77, 522-533	5.5	
25	Accurate prediction of protein structures and interactions using a three-track neural network. *Science*, **2021**, 373, 871-876	33.3	522
24	Assessing the utility of CASP14 models for molecular replacement. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1752-1769	4.2	18
23	SEQUENCE SLIDER: expanding polyalanine fragments for phasing with multiple side-chain hypotheses. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 221-237	5.5	5
22	ALIXE: a phase-combination tool for fragment-based molecular replacement. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 209-220	5.5	7
21	ALEPH: a network-oriented approach for the generation of fragment-based libraries and for structure interpretation. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 193-208	5.5	9
20	Fragment-based determination of a proteinase K structure from MicroED data using ARCIMBOLDO_SHREDDER. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 703-712	5.5	6
19	Ega3 from the fungal pathogen is an endo-β1,4-galactosaminidase that disrupts microbial biofilms. *Journal of Biological Chemistry*, **2019**, 294, 13833-13849	5.4	18
18	Exolytic and endolytic turnover of peptidoglycan by lytic transglycosylase Slt of. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 4393-4398	11.5	18
17	ARCIMBOLDO on coiled coils. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 194-204	5.5	20
16	Structural basis of meiotic chromosome synapsis through SYCP1 self-assembly. *Nature Structural and Molecular Biology*, **2018**, 25, 557-569	17.6	38
15	Gyre and gimble: a maximum-likelihood replacement for Patterson correlation refinement. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 279-289	5.5	13
14	On the application of the expected log-likelihood gain to decision making in molecular replacement. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 245-255	5.5	22
13	Exploiting distant homologues for phasing through the generation of compact fragments, local fold refinement and partial solution combination. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 290-304	5.5	19
12	Structure and mechanism of a bacterial host-protein citrullinating virulence factor, Porphyromonas gingivalis peptidylarginine deiminase. *Scientific Reports*, **2015**, 5, 11969	4.9	57
11	ARCIMBOLDO_LITE: single-workstation implementation and use. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 1921-30		37
10	Combining phase information in reciprocal space for molecular replacement with partial models. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 1931-45		10

List of Publications

9	Macromolecular ab initio phasing enforcing secondary and tertiary structure. *IUCrJ*, **2015**, 2, 95-105	4.7	35
8	Crystallographic structure solution. *Arbor*, **2015**, 191, a218	0.2	
7	Structure of a 13-fold superhelix (almost) determined from first principles. *IUCrJ*, **2015**, 2, 177-87	4.7	2
6	A highly conserved region essential for NMD in the Upf2 N-terminal domain. *Journal of Molecular Biology*, **2014**, 426, 3689-3702	6.5	10
5	Structure solution with ARCIMBOLDO using fragments derived from distant homology models. *FEBS Journal*, **2014**, 281, 4029-45	5.7	33
4	Exploiting tertiary structure through local folds for crystallographic phasing. *Nature Methods*, **2013**, 10, 1099-101	21.6	51
3	Improving AlphaFold modeling using implicit information from experimental density maps		2
2	Accurate prediction of protein structures and interactions using a 3-track network		9
1	Assessing the utility of CASP14 models for molecular replacement		1