

# Alessandro Costa

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

2,939  
citations

186265  
28  
h-index

233421  
45  
g-index

50  
all docs

50  
docs citations

50  
times ranked

2730  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | The structural basis for MCM2-7 helicase activation by GINS and Cdc45. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 471-477.   | 8.2  | 290       |
| 2  | The mechanism of eukaryotic CMG helicase activation. <i>Nature</i> , 2018, 555, 265-268.   | 27.8 | 196       |
| 3  | A Ctf4 trimer couples the CMG helicase to DNA polymerase $\epsilon$ in the eukaryotic replisome. <i>Nature</i> , 2014, 510, 293-297.   | 27.8 | 186       |
| 4  | Mechanisms for Initiating Cellular DNA Replication. <i>Annual Review of Biochemistry</i> , 2013, 82, 25-54.  | 11.1 | 161       |
| 5  | Structural basis for retroviral integration into nucleosomes. <i>Nature</i> , 2015, 523, 366-369.  | 27.8 | 133       |
| 6  | Ctf4 Links DNA Replication with Sister Chromatid Cohesion Establishment by Recruiting the Chl1 Helicase to the Replisome. <i>Molecular Cell</i> , 2016, 63, 371-384.   | 9.7  | 113       |
| 7  | A Structure-Based Mechanism for DNA Entry into the Cohesin Ring. <i>Molecular Cell</i> , 2020, 79, 917-933.e9.   | 9.7  | 112       |
| 8  | Cryo-EM structures of the eukaryotic replicative helicase bound to a translocation substrate. <i>Nature Communications</i> , 2016, 7, 10708.   | 12.8 | 109       |
| 9  | Mechanism of head-to-head MCM double-hexamer formation revealed by cryo-EM. <i>Nature</i> , 2019, 575, 704-710.  | 27.8 | 105       |
| 10 | DNA binding polarity, dimerization, and ATPase ring remodeling in the CMG helicase of the eukaryotic replisome. <i>ELife</i> , 2014, 3, e03273.  | 6.0  | 103       |
| 11 | Microtubule Nucleation Properties of Single Human $\beta$ TuRCs Explained by Their Cryo-EM Structure. <i>Developmental Cell</i> , 2020, 53, 603-617.e8.  | 7.0  | 99        |
| 12 | A supramolecular assembly mediates lentiviral DNA integration. <i>Science</i> , 2017, 355, 93-95.  | 12.6 | 96        |
| 13 | Structure of DNA-CMG-Pol epsilon elucidates the roles of the non-catalytic polymerase modules in the eukaryotic replisome. <i>Nature Communications</i> , 2018, 9, 5061.   | 12.8 | 96        |
| 14 | CMG-Pol epsilon dynamics suggests a mechanism for the establishment of leading-strand synthesis in the eukaryotic replisome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4141-4146.    | 7.1  | 88        |
| 15 | Cdc45 (cell division cycle protein 45) guards the gate of the Eukaryote Replisome helicase stabilizing leading strand engagement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E249-58. | 7.1  | 78        |
| 16 | Cryo-EM structure of a licensed DNA replication origin. <i>Nature Communications</i> , 2017, 8, 2241.  | 12.8 | 75        |
| 17 | Molecular Basis for ATP-Hydrolysis-Driven DNA Translocation by the CMG Helicase of the Eukaryotic Replisome. <i>Cell Reports</i> , 2019, 28, 2673-2688.e8.   | 6.4  | 74        |
| 18 | Cdt1 stabilizes an open MCM ring for helicase loading. <i>Nature Communications</i> , 2017, 8, 15720.  | 12.8 | 69        |

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|----|---|------|-----------|
| 19 | The Initiation of Eukaryotic DNA Replication. <i>Annual Review of Biochemistry</i> , 2022, 91, 107-131.   | 11.1 | 68        |
| 20 | ATP-dependent conformational dynamics underlie the functional asymmetry of the replicative helicase from a minimalist eukaryote. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11999-12004. | 7.1  | 65        |
| 21 | Structural Studies Reveal the Functional Modularity of the Scc2-Scc4 Cohesin Loader. <i>Cell Reports</i> , 2015, 12, 719-725.   | 6.4  | 60        |
| 22 | The FA Core Complex Contains a Homo-dimeric Catalytic Module for the Symmetric Mono-ubiquitination of FANCI-FANCD2. <i>Cell Reports</i> , 2017, 18, 611-623.  | 6.4  | 55        |
| 23 | Structural biology of MCM helicases. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2009, 44, 326-342.   | 5.2  | 54        |
| 24 | Insights into the Architecture of the Replicative Helicase from the Structure of an Archaeal MCM Homolog. <i>Structure</i> , 2009, 17, 211-222.   | 3.3  | 51        |
| 25 | Human RECQ1 helicase-driven DNA unwinding, annealing, and branch migration: Insights from DNA complex structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4286-4291.                  | 7.1  | 47        |
| 26 | New Insights into the Mechanism of DNA Duplication by the Eukaryotic Replisome. <i>Trends in Biochemical Sciences</i> , 2016, 41, 859-871.  | 7.5  | 47        |
| 27 | Intersubunit allosteric communication mediated by a conserved loop in the MCM helicase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1051-1056.  | 7.1  | 43        |
| 28 | Retroviral integration into nucleosomes through DNA looping and sliding along the histone octamer. <i>Nature Communications</i> , 2019, 10, 4189.   | 12.8 | 43        |
| 29 | Mechanism of replication origin melting nucleated by CMG helicase assembly. <i>Nature</i> , 2022, 606, 1007-1014.   | 27.8 | 34        |
| 30 | The MCM Helicase Motor of the Eukaryotic Replisome. <i>Journal of Molecular Biology</i> , 2016, 428, 1822-1832.   | 4.2  | 32        |
| 31 | Architecture and DNA Recognition Elements of the Fanconi Anemia FANCM-FAAP24 Complex. <i>Structure</i> , 2013, 21, 1648-1658.   | 3.3  | 26        |
| 32 | Structural mechanism for the selective phosphorylation of DNA-loaded MCM double hexamers by the Dbf4-dependent kinase. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 10-20.  | 8.2  | 21        |
| 33 | The architecture and function of the chromatin replication machinery. <i>Current Opinion in Structural Biology</i> , 2017, 47, 9-16.  | 5.7  | 20        |
| 34 | Cryo-electron microscopy of chromatin biology. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 541-548.   | 2.3  | 20        |
| 35 | Caught in the act: structural dynamics of replication origin activation and fork progression. <i>Biochemical Society Transactions</i> , 2020, 48, 1057-1066.  | 3.4  | 14        |
| 36 | A combined structural and biochemical approach reveals translocation and stalling of UvrB on the DNA lesion as a mechanism of damage verification in bacterial nucleotide excision repair. <i>DNA Repair</i> , 2020, 85, 102746.                  | 2.8  | 13        |

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|----|--|-----|-----------|
| 37 | Mechanism of Bloom syndrome complex assembly required for double Holliday junction dissolution and genome stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, . | 7.1 | 12        |
| 38 | A structural framework for DNA replication and transcription through chromatin. <i>Current Opinion in Structural Biology</i> , 2021, 71, 51-58.  | 5.7 | 6         |
| 39 | Escorting Client Proteins to the Hsp90 Molecular Chaperone. <i>Structure</i> , 2017, 25, 964-965.  | 3.3 | 4         |
| 40 | DNA replication and inter-strand crosslink repair: Symmetric activation of dimeric nanomachines?. <i>Biophysical Chemistry</i> , 2017, 225, 15-19.   | 2.8 | 2         |
| 41 | In silico reconstitution of DNA replication. Lessons from single-molecule imaging and cryo-tomography applied to single-particle cryo-EM. <i>Current Opinion in Structural Biology</i> , 2022, 72, 279-286.                | 5.7 | 2         |
| 42 | Preparing Frozen-Hydrated Protein–Nucleic Acid Assemblies for High-Resolution Cryo-EM Imaging. <i>Methods in Molecular Biology</i> , 2018, 1814, 287-296.  | 0.9 | 1         |
| 43 | A Different Twist on Centromeric Chromatin. <i>Structure</i> , 2020, 28, 3-5.  | 3.3 | 1         |
| 44 | Towards a Structural Mechanism for Sister Chromatid Cohesion Establishment at the Eukaryotic Replication Fork. <i>Biology</i> , 2021, 10, 466.   | 2.8 | 1         |
| 45 | Preparing to unwind. <i>ELife</i> , 2014, 3, e02618.   | 6.0 | 1         |
| 46 | Multiple roles of Pol epsilon in eukaryotic chromosome replication. <i>Biochemical Society Transactions</i> , 2022, , .  | 3.4 | 1         |
| 47 | ReconSil: An electron microscopy toolbox to study helicase function at an origin of replication. <i>Methods in Enzymology</i> , 2022, , 203-231.   | 1.0 | 0         |