

Gino Cingolani

List of Publications by Year in descending order

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85
papers

5,443
citations

101543

36
h-index

88630

70
g-index

86
all docs

86
docs citations

86
times ranked

6180
citing authors

#	ARTICLE	IF	CITATIONS
1	Viral Ejection Proteins: Mosaically Conserved, Conformational Gymnasts. <i>Microorganisms</i> , 2022, 10, 504.	3.6	5
2	Differential recognition of canonical NF- κ B dimers by Importin β 3. <i>Nature Communications</i> , 2022, 13, 1207.	12.8	23
3	Cryo-EM Structure of a Kinetically Trapped Dodecameric Portal Protein from the Pseudomonas-phage PaP3. <i>Journal of Molecular Biology</i> , 2022, 434, 167537.	4.2	6
4	A periplasmic cinched protein is required for siderophore secretion and virulence of <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2022, 13, 2255.	12.8	8
5	Recognition of the TDP-43 nuclear localization signal by importin β 1/ β 2. <i>Cell Reports</i> , 2022, 39, 111007.	6.4	32
6	Three-dimensional structure of human cyclooxygenase (hCOX)-1. <i>Scientific Reports</i> , 2021, 11, 4312.	3.3	29
7	Learning from Nature: From a Marine Natural Product to Synthetic Cyclooxygenase-1 Inhibitors by Automated De Novo Design. <i>Advanced Science</i> , 2021, 8, e2100832.	11.2	17
8	Cryo-EM structure of the periplasmic tunnel of T7 DNA-ejectosome at 2.7Å... resolution. <i>Molecular Cell</i> , 2021, 81, 3145-3159.e7.	9.7	17
9	Expression and purification of phage T7 ejection proteins for cryo-EM analysis. <i>STAR Protocols</i> , 2021, 2, 100960.	1.2	4
10	Lyssavirus Vaccine with a Chimeric Glycoprotein Protects across Phylogroups. <i>Cell Reports</i> , 2020, 32, 107920.	6.4	10
11	Biophysical analysis of <i>Pseudomonas</i> -phage PaP3 small terminase suggests a mechanism for sequence-specific DNA-binding by lateral interdigitation. <i>Nucleic Acids Research</i> , 2020, 48, 11721-11736.	14.5	14
12	Recognition of an α -helical hairpin in P22 large terminase by a synthetic antibody fragment. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 876-888.	2.3	5
13	Selective inhibition of Ph-positive ALL cell growth through kinase-dependent and -independent effects by CDK6-specific PROTACs. <i>Blood</i> , 2020, 135, 1560-1573.	1.4	53
14	Portal Protein: The Orchestrator of Capsid Assembly for the dsDNA Tailed Bacteriophages and Herpesviruses. <i>Annual Review of Virology</i> , 2019, 6, 141-160.	6.7	64
15	Heme and hemoglobin utilization by <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2019, 10, 4260.	12.8	55
16	Structural basis for the homotypic fusion of chlamydial inclusions by the SNARE-like protein IncA. <i>Nature Communications</i> , 2019, 10, 2747.	12.8	16
17	DNA Conformational Changes Play a Force-Generating Role during Bacteriophage Genome Packaging. <i>Biophysical Journal</i> , 2019, 116, 2172-2180.	0.5	13
18	Molecular Architecture of the Inositol Phosphatase Siw14. <i>Biochemistry</i> , 2019, 58, 534-545.	2.5	7

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19	RNA Recognition-like Motifs Activate a Mitogen-Activated Protein Kinase. <i>Biochemistry</i> , 2018, 57, 6878-6887.	2.5	3
20	A Tail of Phage Adhesins. <i>Structure</i> , 2018, 26, 1565-1567.	3.3	3
21	Breaking Symmetry in Viral Icosahedral Capsids as Seen through the Lenses of X-ray Crystallography and Cryo-Electron Microscopy. <i>Viruses</i> , 2018, 10, 67.	3.3	34
22	Nuclear Pores Promote Lethal Prostate Cancer by Increasing POM121-Driven E2F1, MYC, and AR Nuclear Import. <i>Cell</i> , 2018, 174, 1200-1215.e20.	28.9	96
23	Portal protein functions akin to a DNA-sensor that couples genome-packaging to icosahedral capsid maturation. <i>Nature Communications</i> , 2017, 8, 14310.	12.8	90
24	Cleavage of DFNA5 by caspase-3 during apoptosis mediates progression to secondary necrotic/pyroptotic cell death. <i>Nature Communications</i> , 2017, 8, 14128.	12.8	953
25	Three-dimensional context rather than NLS amino acid sequence determines importin $\hat{\iota}$ subtype specificity for RCC1. <i>Nature Communications</i> , 2017, 8, 979.	12.8	54
26	Synergy of two low-affinity NLSs determines the high avidity of influenza A virus nucleoprotein NP for human importin $\hat{\iota}$ isoforms. <i>Scientific Reports</i> , 2017, 7, 11381.	3.3	20
27	Structural basis for selective inhibition of Cyclooxygenase-1 (COX-1) by diarylisoxazoles mofezolac and 3-(5-chlorofuran-2-yl)-5-methyl-4-phenylisoxazole (P6). <i>European Journal of Medicinal Chemistry</i> , 2017, 138, 661-668.	5.5	63
28	A viral scaffolding protein triggers portal ring oligomerization and incorporation during procapsid assembly. <i>Science Advances</i> , 2017, 3, e1700423.	10.3	36
29	Divergent Evolution of Nuclear Localization Signal Sequences in Herpesvirus Terminase Subunits. <i>Journal of Biological Chemistry</i> , 2016, 291, 11420-11433.	3.4	22
30	Structural Plasticity of the Protein Plug That Traps Newly Packaged Genomes in Podoviridae Virions. <i>Journal of Biological Chemistry</i> , 2016, 291, 215-226.	3.4	14
31	PARP-2 domain requirements for DNA damage-dependent activation and localization to sites of DNA damage. <i>Nucleic Acids Research</i> , 2016, 44, 1691-1702.	14.5	72
32	A Greasy Aid to Capsid Assembly: Lessons from a Salty Virus. <i>Structure</i> , 2015, 23, 1777-1779.	3.3	1
33	Conservation of inner nuclear membrane targeting sequences in mammalian Pom121 and yeast Heh2 membrane proteins. <i>Molecular Biology of the Cell</i> , 2015, 26, 3301-3312.	2.1	24
34	Dimeric Quaternary Structure of Human Laforin. <i>Journal of Biological Chemistry</i> , 2015, 290, 4552-4559.	3.4	18
35	Diversification of importin- $\hat{\iota}$ isoforms in cellular trafficking and disease states. <i>Biochemical Journal</i> , 2015, 466, 13-28.	3.7	187
36	Molecular Determinants for Nuclear Import of Influenza A PB2 by Importin $\hat{\iota}$ Isoforms 3 and 7. <i>Structure</i> , 2015, 23, 374-384.	3.3	87

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37	Distinctive Properties of the Nuclear Localization Signals of Inner Nuclear Membrane Proteins Heh1 and Heh2. <i>Structure</i> , 2015, 23, 1305-1316.	3.3	31
38	The tuberculosis necrotizing toxin kills macrophages by hydrolyzing NAD. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 672-678.	8.2	114
39	IPO3-mediated Nonclassical Nuclear Import of NF- κ B Essential Modulator (NEMO) Drives DNA Damage-dependent NF- κ B Activation. <i>Journal of Biological Chemistry</i> , 2015, 290, 17967-17984.	3.4	26
40	Architecture of the Complex Formed by Large and Small Terminase Subunits from Bacteriophage P22. <i>Journal of Molecular Biology</i> , 2015, 427, 3285-3299.	4.2	30
41	Exploring the atomic structure and conformational flexibility of a 320-Å long engineered viral fiber using X-ray crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 342-353.	2.5	9
42	Architecture of viral genome-delivery molecular machines. <i>Current Opinion in Structural Biology</i> , 2014, 25, 1-8.	5.7	51
43	Structure of Human PIR1, an Atypical Dual-Specificity Phosphatase. <i>Biochemistry</i> , 2014, 53, 862-871.	2.5	15
44	Jamming Up the α -Staple Regulation of SIRT1 Activity by Its C-Terminal Regulatory Segment (CTR). <i>Journal of Molecular Biology</i> , 2014, 426, 507-509.	4.2	1
45	Atomic Structure of Dual-Specificity Phosphatase 26, a Novel p53 Phosphatase. <i>Biochemistry</i> , 2013, 52, 938-948.	2.5	22
46	The Tip of the Tail Needle Affects the Rate of DNA Delivery by Bacteriophage P22. <i>PLoS ONE</i> , 2013, 8, e70936.	2.5	26
47	Nucleoporin Nup50 Stabilizes Closed Conformation of Armadillo repeat 10 in Importin β 5. <i>Journal of Biological Chemistry</i> , 2012, 287, 2022-2031.	3.4	22
48	Structure of P22 Headful Packaging Nuclease. <i>Journal of Biological Chemistry</i> , 2012, 287, 28196-28205.	3.4	50
49	Improved crystallization of <i>Escherichia coli</i> ATP synthase catalytic complex (F1) by introducing a phosphomimetic mutation in subunit δ . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1229-1233.	0.7	16
50	Small Terminase Couples Viral DNA Binding to Genome-Packaging ATPase Activity. <i>Structure</i> , 2012, 20, 1403-1413.	3.3	60
51	Three-dimensional structure of a viral genome-delivery portal vertex. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 597-603.	8.2	142
52	Structure of the ATP synthase catalytic complex (F1) from <i>Escherichia coli</i> in an autoinhibited conformation. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 701-707.	8.2	219
53	Peering Down the Barrel of a Bacteriophage Portal: The Genome Packaging and Release Valve in P22. <i>Structure</i> , 2011, 19, 496-502.	3.3	101
54	The importin β 2 binding domain as a master regulator of nucleocytoplasmic transport. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2011, 1813, 1578-1592.	4.1	155

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55	Crystallization of the nonameric small terminase subunit of bacteriophage P22. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 104-110.	0.7	17
56	Atomic Structure of Bacteriophage Sf6 Tail Needle Knob. <i>Journal of Biological Chemistry</i> , 2011, 286, 30867-30877.	3.4	33
57	A Minimal Nuclear Localization Signal (NLS) in Human Phospholipid Scramblase 4 That Binds Only the Minor NLS-binding Site of Importin β 1. <i>Journal of Biological Chemistry</i> , 2011, 286, 28160-28169.	3.4	57
58	Dimerization of Vaccinia Virus VH1 Is Essential for Dephosphorylation of STAT1 at Tyrosine 701. <i>Journal of Biological Chemistry</i> , 2011, 286, 14373-14382.	3.4	29
59	Phosphorylation meets nuclear import: a review. <i>Cell Communication and Signaling</i> , 2010, 8, 32.	6.5	196
60	The Importin β 2 Binding Domain Modulates the Avidity of Importin β 2 for the Nuclear Pore Complex. <i>Journal of Biological Chemistry</i> , 2010, 285, 13769-13780.	3.4	38
61	Molecular Basis for the Recognition of Phosphorylated STAT1 by Importin β 5. <i>Journal of Molecular Biology</i> , 2010, 402, 83-100.	4.2	70
62	Dimeric Quaternary Structure of the Prototypical Dual Specificity Phosphatase VH1. <i>Journal of Biological Chemistry</i> , 2009, 284, 10129-10137.	3.4	38
63	Structural plasticity of the phage P22 tail needle gp26 probed with xenon gas. <i>Protein Science</i> , 2009, 18, 537-548.	7.6	24
64	An Evolutionarily Conserved Family of Virion Tail Needles Related to Bacteriophage P22 gp26: Correlation between Structural Stability and Length of the α -Helical Trimeric Coiled Coil. <i>Journal of Molecular Biology</i> , 2009, 391, 227-245.	4.2	15
65	A unique conformation of the inhibitory μ subunit in a crystal structure of the Escherichia coli F1 α -ATPase. <i>FASEB Journal</i> , 2009, 23, 504.6.	0.5	0
66	Foldonâ€“guided selfâ€“assembly of ultraâ€“stable protein fibers. <i>Protein Science</i> , 2008, 17, 1475-1485.	7.6	30
67	Determination of Stoichiometry and Conformational Changes in the First Step of the P22 Tail Assembly. <i>Journal of Molecular Biology</i> , 2008, 379, 385-396.	4.2	68
68	A Conformational Switch in Bacteriophage P22 Portal Protein Primes Genome Injection. <i>Molecular Cell</i> , 2008, 29, 376-383.	9.7	40
69	Molecular Basis for the Recognition of Snurportin 1 by Importin β 2. <i>Journal of Biological Chemistry</i> , 2008, 283, 7877-7884.	3.4	65
70	Domain Organization and Polarity of Tail Needle GP26 in the Portal Vertex Structure of Bacteriophage P22. <i>Journal of Molecular Biology</i> , 2007, 371, 374-387.	4.2	32
71	Role of Gene 10 Protein in the Hierarchical Assembly of the Bacteriophage P22 Portal Vertex Structure. <i>Biochemistry</i> , 2007, 46, 8776-8784.	2.5	36
72	Structure of phage P22 cell envelopeâ€“penetrating needle. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1221-1226.	8.2	74

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73	Binding-induced Stabilization and Assembly of the Phage P22 Tail Accessory Factor Gp4. <i>Journal of Molecular Biology</i> , 2006, 363, 558-576.	4.2	47
74	Crystallography of bacteriophage P22 tail accessory factor gp26 at acidic and neutral pH. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 477-482.	0.7	5
75	Three-dimensional structure of the bacteriophage P22 tail machine. <i>EMBO Journal</i> , 2005, 24, 2087-2095.	7.8	76
76	Bacteriophage P22 Tail Accessory Factor GP26 Is a Long Triple-stranded Coiled-coil. <i>Journal of Biological Chemistry</i> , 2005, 280, 5929-5933.	3.4	27
77	Phospholipid Scramblase 1 Contains a Nonclassical Nuclear Localization Signal with Unique Binding Site in Importin $\hat{1}\pm$. <i>Journal of Biological Chemistry</i> , 2005, 280, 10599-10606.	3.4	97
78	Nucleocytoplasmic Transport: Navigating the Channel. <i>Traffic</i> , 2003, 4, 127-135.	2.7	137
79	Synergy of Silent and Hot Spot Mutations in Importin $\hat{1}^2$ Reveals a Dynamic Mechanism for Recognition of a Nuclear Localization Signal. <i>Journal of Biological Chemistry</i> , 2003, 278, 16216-16221.	3.4	19
80	Importin $\hat{1}^2$ contains a COOH-terminal nucleoporin binding region important for nuclear transport. <i>Journal of Cell Biology</i> , 2003, 162, 391-401.	5.2	126
81	Molecular Basis for Nucleocytoplasmic Transport. , 2003, , 419-430.		1
82	Preliminary crystallographic analysis of the bacteriophage P22 portal protein. <i>Journal of Structural Biology</i> , 2002, 139, 46-54.	2.8	46
83	Molecular Basis for the Recognition of a Nonclassical Nuclear Localization Signal by Importin $\hat{1}^2$. <i>Molecular Cell</i> , 2002, 10, 1345-1353.	9.7	177
84	Nuclear import factors importin $\hat{1}\pm$ and importin $\hat{1}^2$ undergo mutually induced conformational changes upon association. <i>FEBS Letters</i> , 2000, 484, 291-298.	2.8	48
85	Structure of importin- $\hat{1}^2$ bound to the IBB domain of importin- $\hat{1}\pm$. <i>Nature</i> , 1999, 399, 221-229.	27.8	530