Gino Cingolani

List of Publications by Year
in descending order

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Version: 2024-02-01

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	Cleavage of DFNA5 by caspase-3 during apoptosis mediates progression to secondary necrotic/pyroptotic cell death. Nature Communications, 2017, 8, 14128.	12.8	953
2	Structure of importin-Î² bound to the IBB domain of importin-Î±. Nature, 1999, 399, 221-229.	27.8	530
3	Structure of the ATP synthase catalytic complex (F1) from Escherichia coli in an autoinhibited conformation. Nature Structural and Molecular Biology, 2011, 18, 701-707.	8.2	219
4	Phosphorylation meets nuclear import: a review. Cell Communication and Signaling, 2010, 8, 32.	6.5	196
5	Diversification of importin-Î± isoforms in cellular trafficking and disease states. Biochemical Journal, 2015, 466, 13-28.	3.7	187
6	Molecular Basis for the Recognition of a Nonclassical Nuclear Localization Signal by Importin Î². Molecular Cell, 2002, 10, 1345-1353.	9.7	177
7	The importin Î² binding domain as a master regulator of nucleocytoplasmic transport. Biochimica Et Biophysica Acta - Molecular Cell Research, 2011, 1813, 1578-1592.	4.1	155
8	Three-dimensional structure of a viral genome-delivery portal vertex. Nature Structural and Molecular Biology, 2011, 18, 597-603.	8.2	142
9	Nucleocytoplasmic Transport: Navigating the Channel. Traffic, 2003, 4, 127-135.	2.7	137
10	Importin Î² contains a COOH-terminal nucleoporin binding region important for nuclear transport. Journal of Cell Biology, 2003, 162, 391-401.	5.2	126
11	The tuberculosis necrotizing toxin kills macrophages by hydrolyzing NAD. Nature Structural and Molecular Biology, 2015, 22, 672-678.	8.2	114
12	Peering Down the Barrel of a Bacteriophage Portal: The Genome Packaging and Release Valve in P22. Structure, 2011, 19, 496-502.	3.3	101
13	Phospholipid Scramblase 1 Contains a Nonclassical Nuclear Localization Signal with Unique Binding Site in Importin Î±. Journal of Biological Chemistry, 2005, 280, 10599-10606.	3.4	97
14	Nuclear Pores Promote Lethal Prostate Cancer by Increasing POM121-Driven E2F1, MYC, and AR Nuclear Import. Cell, 2018, 174, 1200-1215.e20.	28.9	96
15	Portal protein functions akin to a DNA-sensor that couples genome-packaging to icosahedral capsid maturation. Nature Communications, 2017, 8, 14310.	12.8	90
16	Molecular Determinants for Nuclear Import of Influenza A PB2 by Importin Î± Isoforms 3 and 7. Structure, 2015, 23, 374-384.	3.3	87
17	Three-dimensional structure of the bacteriophage P22 tail machine. EMBO Journal, 2005, 24, 2087-2095.	7.8	76
18	Structure of phage P22 cell envelopeâ€“penetrating needle. Nature Structural and Molecular Biology, 2007, 14, 1221-1226.	8.2	74

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19	PARP-2 domain requirements for DNA damage-dependent activation and localization to sites of DNA damage. Nucleic Acids Research, 2016, 44, 1691-1702.	14.5	72
20	Molecular Basis for the Recognition of Phosphorylated STAT1 by Importin Î±5. Journal of Molecular Biology, 2010, 402, 83-100.	4.2	70
21	Determination of Stoichiometry and Conformational Changes in the First Step of the P22 Tail Assembly. Journal of Molecular Biology, 2008, 379, 385-396.	4.2	68
22	Molecular Basis for the Recognition of Snurportin 1 by Importin Î². Journal of Biological Chemistry, 2008, 283, 7877-7884.	3.4	65
23	Portal Protein: The Orchestrator of Capsid Assembly for the dsDNA Tailed Bacteriophages and Herpesviruses. Annual Review of Virology, 2019, 6, 141-160.	6.7	64
24	Structural basis for selective inhibition of Cyclooxygenase-1 (COX-1) by diarylisoxazoles mofezolac and 3-(5-chlorofuran-2-yl)-5-methyl-4-phenylisoxazole (P6). European Journal of Medicinal Chemistry, 2017, 138, 661-668.	5.5	63
25	Small Terminase Couples Viral DNA Binding to Genome-Packaging ATPase Activity. Structure, 2012, 20, 1403-1413.	3.3	60
26	A Minimal Nuclear Localization Signal (NLS) in Human Phospholipid Scramblase 4 That Binds Only the Minor NLS-binding Site of Importin Î±1. Journal of Biological Chemistry, 2011, 286, 28160-28169.	3.4	57
27	Heme and hemoglobin utilization by Mycobacterium tuberculosis. Nature Communications, 2019, 10, 4260.	12.8	55
28	Three-dimensional context rather than NLS amino acid sequence determines importin Î± subtype specificity for RCC1. Nature Communications, 2017, 8, 979.	12.8	54
29	Selective inhibition of Ph-positive ALL cell growth through kinase-dependent and -independent effects by CDK6-specific PROTACs. Blood, 2020, 135, 1560-1573.	1.4	53
30	Architecture of viral genome-delivery molecular machines. Current Opinion in Structural Biology, 2014, 25, 1-8.	5.7	51
31	Structure of P22 Headful Packaging Nuclease. Journal of Biological Chemistry, 2012, 287, 28196-28205.	3.4	50
32	Nuclear import factors importin Î± and importin Î² undergo mutually induced conformational changes upon association. FEBS Letters, 2000, 484, 291-298.	2.8	48
33	Binding-induced Stabilization and Assembly of the Phage P22 Tail Accessory Factor Gp4. Journal of Molecular Biology, 2006, 363, 558-576.	4.2	47
34	Preliminary crystallographic analysis of the bacteriophage P22 portal protein. Journal of Structural Biology, 2002, 139, 46-54.	2.8	46
35	A Conformational Switch in Bacteriophage P22 Portal Protein Primes Genome Injection. Molecular Cell, 2008, 29, 376-383.	9.7	40
36	Dimeric Quaternary Structure of the Prototypical Dual Specificity Phosphatase VH1. Journal of Biological Chemistry, 2009, 284, 10129-10137.	3.4	38

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37	The Importin Î² Binding Domain Modulates the Avidity of Importin Î² for the Nuclear Pore Complex. Journal of Biological Chemistry, 2010, 285, 13769-13780.	3.4	38
38	Role of Gene 10 Protein in the Hierarchical Assembly of the Bacteriophage P22 Portal Vertex Structure. Biochemistry, 2007, 46, 8776-8784.	2.5	36
39	A viral scaffolding protein triggers portal ring oligomerization and incorporation during procapsid assembly. Science Advances, 2017, 3, e1700423.	10.3	36
40	Breaking Symmetry in Viral Icosahedral Capsids as Seen through the Lenses of X-ray Crystallography and Cryo-Electron Microscopy. Viruses, 2018, 10, 67.	3.3	34
41	Atomic Structure of Bacteriophage Sf6 Tail Needle Knob. Journal of Biological Chemistry, 2011, 286, 30867-30877.	3.4	33
42	Domain Organization and Polarity of Tail Needle GP26 in the Portal Vertex Structure of Bacteriophage P22. Journal of Molecular Biology, 2007, 371, 374-387.	4.2	32
43	Recognition of the TDP-43 nuclear localization signal by importin Î±1/Î². Cell Reports, 2022, 39, 111007.	6.4	32
44	Distinctive Properties of the Nuclear Localization Signals of Inner Nuclear Membrane Proteins Heh1 and Heh2. Structure, 2015, 23, 1305-1316.	3.3	31
45	Foldonâ€guided selfâ€assembly of ultraâ€stable protein fibers. Protein Science, 2008, 17, 1475-1485.	7.6	30
46	Architecture of the Complex Formed by Large and Small Terminase Subunits from Bacteriophage P22. Journal of Molecular Biology, 2015, 427, 3285-3299.	4.2	30
47	Dimerization of Vaccinia Virus VH1 Is Essential for Dephosphorylation of STAT1 at Tyrosine 701. Journal of Biological Chemistry, 2011, 286, 14373-14382.	3.4	29
48	Three-dimensional structure of human cyclooxygenase (hCOX)-1. Scientific Reports, 2021, 11, 4312.	3.3	29
49	Bacteriophage P22 Tail Accessory Factor GP26 Is a Long Triple-stranded Coiled-coil. Journal of Biological Chemistry, 2005, 280, 5929-5933.	3.4	27
50	IPO3-mediated Nonclassical Nuclear Import of NF-ÎºB Essential Modulator (NEMO) Drives DNA Damage-dependent NF-ÎºB Activation. Journal of Biological Chemistry, 2015, 290, 17967-17984.	3.4	26
51	The Tip of the Tail Needle Affects the Rate of DNA Delivery by Bacteriophage P22. PLoS ONE, 2013, 8, e70936.	2.5	26
52	Structural plasticity of the phage P22 tail needle gp26 probed with xenon gas. Protein Science, 2009, 18, 537-548.	7.6	24
53	Conservation of inner nuclear membrane targeting sequences in mammalian Pom121 and yeast Heh2 membrane proteins. Molecular Biology of the Cell, 2015, 26, 3301-3312.	2.1	24
54	Differential recognition of canonical NF-ÎºB dimers by Importin Î±3. Nature Communications, 2022, 13, 1207.	12.8	23

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55	Nucleoporin Nup50 Stabilizes Closed Conformation of Armadillo repeat 10 in Importin Î±5. Journal of Biological Chemistry, 2012, 287, 2022-2031.	3.4	22
56	Atomic Structure of Dual-Specificity Phosphatase 26, a Novel p53 Phosphatase. Biochemistry, 2013, 52, 938-948.	2.5	22
57	Divergent Evolution of Nuclear Localization Signal Sequences in Herpesvirus Terminase Subunits. Journal of Biological Chemistry, 2016, 291, 11420-11433.	3.4	22
58	Synergy of two low-affinity NLSs determines the high avidity of influenza A virus nucleoprotein NP for human importin Î± isoforms. Scientific Reports, 2017, 7, 11381.	3.3	20
59	Synergy of Silent and Hot Spot Mutations in Importin Î² Reveals a Dynamic Mechanism for Recognition of a Nuclear Localization Signal. Journal of Biological Chemistry, 2003, 278, 16216-16221.	3.4	19
60	Dimeric Quaternary Structure of Human Laforin. Journal of Biological Chemistry, 2015, 290, 4552-4559.	3.4	18
61	Crystallization of the nonameric small terminase subunit of bacteriophage P22. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 104-110.	0.7	17
62	Learning from Nature: From a Marine Natural Product to Synthetic Cyclooxygenaseâ€1 Inhibitors by Automated De Novo Design. Advanced Science, 2021, 8, e2100832.	11.2	17
63	Cryo-EM structure of the periplasmic tunnel of T7 DNA-ejectosome at 2.7ÂÃ... resolution. Molecular Cell, 2021, 81, 3145-3159.e7.	9.7	17
64	Improved crystallization ofEscherichia coliATP synthase catalytic complex (F1) by introducing a phosphomimetic mutation in subunit âˆŠ. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1229-1233.	0.7	16
65	Structural basis for the homotypic fusion of chlamydial inclusions by the SNARE-like protein IncA. Nature Communications, 2019, 10, 2747.	12.8	16
66	An Evolutionarily Conserved Family of Virion Tail Needles Related to Bacteriophage P22 gp26: Correlation between Structural Stability and Length of the Î±-Helical Trimeric Coiled Coil. Journal of Molecular Biology, 2009, 391, 227-245.	4.2	15
67	Structure of Human PIR1, an Atypical Dual-Specificity Phosphatase. Biochemistry, 2014, 53, 862-871.	2.5	15
68	Structural Plasticity of the Protein Plug That Traps Newly Packaged Genomes in Podoviridae Virions. Journal of Biological Chemistry, 2016, 291, 215-226.	3.4	14
69	Biophysical analysis ofPseudomonas-phage PaP3 small terminase suggests a mechanism for sequence-specific DNA-binding by lateral interdigitation. Nucleic Acids Research, 2020, 48, 11721-11736.	14.5	14
70	DNA Conformational Changes Play a Force-Generating Role during Bacteriophage Genome Packaging. Biophysical Journal, 2019, 116, 2172-2180.	0.5	13
71	Lyssavirus Vaccine with a Chimeric Glycoprotein Protects across Phylogroups. Cell Reports, 2020, 32, 107920.	6.4	10
72	Exploring the atomic structure and conformational flexibility of a 320â€...Ã... long engineered viral fiber using X-ray crystallography. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 342-353.	2.5	9

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73	A periplasmic cinched protein is required for siderophore secretion and virulence of Mycobacterium tuberculosis. Nature Communications, 2022, 13, 2255.	12.8	8
74	Molecular Architecture of the Inositol Phosphatase Siw14. Biochemistry, 2019, 58, 534-545.	2.5	7
75	Cryo-EM Structure of a Kinetically Trapped Dodecameric Portal Protein from the Pseudomonas-phage PaP3. Journal of Molecular Biology, 2022, 434, 167537.	4.2	6
76	Crystallogenesis of bacteriophage P22 tail accessory factor gp26 at acidic and neutral pH. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 477-482.	0.7	5
77	Recognition of an Î±-helical hairpin in P22 large terminase by a synthetic antibody fragment. Acta Crystallographica Section D: Structural Biology, 2020, 76, 876-888.	2.3	5
78	Viral Ejection Proteins: Mosaically Conserved, Conformational Gymnasts. Microorganisms, 2022, 10, 504.	3.6	5
79	Expression and purification of phage T7 ejection proteins for cryo-EM analysis. STAR Protocols, 2021, 2, 100960.	1.2	4
80	RNA Recognition-like Motifs Activate a Mitogen-Activated Protein Kinase. Biochemistry, 2018, 57, 6878-6887.	2.5	3
81	A Tail of Phage Adhesins. Structure, 2018, 26, 1565-1567.	3.3	3
82	Jamming Up the â€œÎ²-Stapleâ€• Regulation of SIRT1 Activity by Its C-Terminal Regulatory Segment (CTR). Journal of Molecular Biology, 2014, 426, 507-509.	4.2	1
83	A Greasy Aid to Capsid Assembly: Lessons from a Salty Virus. Structure, 2015, 23, 1777-1779.	3.3	1
84	Molecular Basis for Nucleocytoplasmic Transport. , 2003, , 419-430.		1
85	A unique conformation of the inhibitory Îµ subunit in a crystal structure of the Escherichia coli F 1 â€ATPase. FASEB Journal, 2009, 23, 504.6.	0.5	0