

Christopher P Hill

List of Publications by Year in descending order

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64
papers

5,492
citations

109321

35
h-index

133252

59
g-index

79
all docs

79
docs citations

79
times ranked

5367
citing authors

#	ARTICLE	IF	CITATIONS
1	Somatostatin venom analogs evolved by fish-hunting cone snails: From prey capture behavior to identifying drug leads. <i>Science Advances</i> , 2022, 8, eabk1410.	10.3	12
2	Symmetric and asymmetric receptor conformation continuum induced by a new insulin. <i>Nature Chemical Biology</i> , 2022, 18, 511-519.	8.0	20
3	The interaction between the Spt6-tSH2 domain and Rpb1 affects multiple functions of RNA Polymerase II. <i>Nucleic Acids Research</i> , 2022, 50, 784-802.	14.5	6
4	Active conformation of the p97-p47 unfoldase complex. <i>Nature Communications</i> , 2022, 13, 2640.	12.8	18
5	Cleavage and Polyadenylation Specificity Factor 6 Is Required for Efficient HIV-1 Latency Reversal. <i>MBio</i> , 2021, 12, e0109821.	4.1	2
6	Activation of the Anti-Oxidative Stress Response Reactivates Latent HIV-1 Through the Mitochondrial Antiviral Signaling Protein Isoform MiniMAVS. <i>Frontiers in Immunology</i> , 2021, 12, 682182.	4.8	3
7	Peptoid Residues Make Diverse, Hyperstable Collagen Triple-Helices. <i>Journal of the American Chemical Society</i> , 2021, 143, 10910-10919.	13.7	28
8	Structure-Based Optimization of Small Molecule Human Galactokinase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 13551-13571.	6.4	2
9	Branched ubiquitin chain binding and deubiquitination by UCH37 facilitate proteasome clearance of stress-induced inclusions. <i>ELife</i> , 2021, 10, .	6.0	20
10	Novel four-disulfide insulin analog with high aggregation stability and potency. <i>Chemical Science</i> , 2020, 11, 195-200.	7.4	20
11	Structure of spastin bound to a glutamate-rich peptide implies a hand-over-hand mechanism of substrate translocation. <i>Journal of Biological Chemistry</i> , 2020, 295, 435-443.	3.4	38
12	Same structure, different mechanisms?. <i>ELife</i> , 2020, 9, .	6.0	12
13	Structure of the Cdc48 segregase in the act of unfolding an authentic substrate. <i>Science</i> , 2019, 365, 502-505.	12.6	138
14	Characterization of resistance to a potent d-peptide HIV entry inhibitor. <i>Retrovirology</i> , 2019, 16, 28.	2.0	5
15	Structure and mechanism of the ESCRT pathway AAA+ ATPase Vps4. <i>Biochemical Society Transactions</i> , 2019, 47, 37-45.	3.4	25
16	Phosphorylation of Tyr-950 in the proteasome scaffolding protein RPN2 modulates its interaction with the ubiquitin receptor RPN13. <i>Journal of Biological Chemistry</i> , 2019, 294, 9659-9665.	3.4	13
17	Selective Kinase Inhibition Shows That Bur1 (Cdk9) Phosphorylates the Rpb1 Linker <i>In Vivo</i> . <i>Molecular and Cellular Biology</i> , 2019, 39, .	2.3	20
18	Structure of Vps4 with circular peptides and implications for translocation of two polypeptide chains by AAA+ ATPases. <i>ELife</i> , 2019, 8, .	6.0	41

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19	Recruitment and Regulation of RPN13 in the 26S Proteasome. <i>FASEB Journal</i> , 2019, 33, 466.1.	0.5	0
20	Vms1p is a release factor for the ribosome-associated quality control complex. <i>Nature Communications</i> , 2018, 9, 2197.	12.8	80
21	Structure and energetics of pairwise interactions between proteasome subunits RPN2, RPN13, and ubiquitin clarify a substrate recruitment mechanism. <i>Journal of Biological Chemistry</i> , 2017, 292, 9493-9504.	3.4	42
22	Sterol Oxidation Mediates Stress-Responsive Vms1 Translocation to Mitochondria. <i>Molecular Cell</i> , 2017, 68, 673-685.e6.	9.7	33
23	Structural basis of protein translocation by the Vps4-Vta1 AAA ATPase. <i>ELife</i> , 2017, 6, .	6.0	123
24	A novel SH2 recognition mechanism recruits Spt6 to the doubly phosphorylated RNA polymerase II linker at sites of transcription. <i>ELife</i> , 2017, 6, .	6.0	61
25	The AAA ATPase Vps4 binds ESCRT-III substrates through a repeating array of dipeptide-binding pockets. <i>ELife</i> , 2017, 6, .	6.0	80
26	Meiotic Clade AAA ATPases: Protein Polymer Disassembly Machines. <i>Journal of Molecular Biology</i> , 2016, 428, 1897-1911.	4.2	56
27	Binding of Substrates to the Central Pore of the Vps4 ATPase Is Autoinhibited by the Microtubule Interacting and Trafficking (MIT) Domain and Activated by MIT Interacting Motifs (MIMs). <i>Journal of Biological Chemistry</i> , 2015, 290, 13490-13499.	3.4	35
28	FACT Disrupts Nucleosome Structure by Binding H2A-H2B with Conserved Peptide Motifs. <i>Molecular Cell</i> , 2015, 60, 294-306.	9.7	143
29	Structural Basis for the Activation and Inhibition of the UCH37 Deubiquitylase. <i>Molecular Cell</i> , 2015, 57, 901-911.	9.7	96
30	Editorial overview: Macromolecular machines and assemblies: Rise and fall at the molecular level. <i>Current Opinion in Structural Biology</i> , 2015, 31, vii-viii.	5.7	2
31	The Oligomeric State of the Active Vps4 AAA ATPase. <i>Journal of Molecular Biology</i> , 2014, 426, 510-525.	4.2	51
32	Structure of the Spt16 Middle Domain Reveals Functional Features of the Histone Chaperone FACT. <i>Journal of Biological Chemistry</i> , 2013, 288, 10188-10194.	3.4	53
33	Building a super elongation complex for HIV. <i>ELife</i> , 2013, 2, e00577.	6.0	3
34	Structure and function of the membrane deformation AAA ATPase Vps4. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 172-181.	4.1	47
35	Crystal Structures of the <i>S. cerevisiae</i> Spt6 Core and C-Terminal Tandem SH2 Domain. <i>Journal of Molecular Biology</i> , 2011, 408, 697-713.	4.2	54
36	Structure of the Bro1 Domain Protein BROX and Functional Analyses of the ALIX Bro1 Domain in HIV-1 Budding. <i>PLoS ONE</i> , 2011, 6, e27466.	2.5	28

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37	Structure and Biological Importance of the Spn1-Spt6 Interaction, and Its Regulatory Role in Nucleosome Binding. <i>Molecular Cell</i> , 2010, 40, 725-735.	9.7	66
38	Structural basis for ESCRT-III protein autoinhibition. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 754-762.	8.2	203
39	Cryo-EM Structure of Dodecameric Vps4p and Its 2:1 Complex with Vta1p. <i>Journal of Molecular Biology</i> , 2008, 377, 364-377.	4.2	68
40	Crystal Structure and RNA Binding of the Tex Protein from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2008, 377, 1460-1473.	4.2	39
41	Biochemical and Structural Studies of Yeast Vps4 Oligomerization. <i>Journal of Molecular Biology</i> , 2008, 384, 878-895.	4.2	58
42	Structural and Functional Analysis of the Spt16p N-terminal Domain Reveals Overlapping Roles of γ FACT Subunits. <i>Journal of Biological Chemistry</i> , 2008, 283, 5058-5068.	3.4	78
43	Crystal Structure and RNA Binding of the Tex Protein from <i>Pseudomonas aeruginosa</i> . <i>FASEB Journal</i> , 2008, 22, 205-205.	0.5	0
44	Structural Basis for Proteasome Activation. <i>FASEB Journal</i> , 2007, 21, A208.	0.5	0
45	The Structure of the γ FACT Pob3-M Domain, Its Interaction with the DNA Replication Factor RPA, and a Potential Role in Nucleosome Deposition. <i>Molecular Cell</i> , 2006, 22, 363-374.	9.7	128
46	Ubiquitin-binding domains. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 610-621.	37.0	696
47	Structural and mechanistic studies of VPS4 proteins. <i>EMBO Journal</i> , 2005, 24, 3658-3669.	7.8	199
48	Crystal Structure of Coproporphyrinogen Oxidase (CPO). <i>Blood</i> , 2004, 104, 52-52.	1.4	0
49	Proteasome degradation: enter the substrate. <i>Trends in Cell Biology</i> , 2003, 13, 550-553.	7.9	56
50	Two-stepping with E1. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 244-246.	8.2	9
51	Crystal Structure of a Biliverdin IX α Reductase Enzyme Cofactor Complex. <i>Journal of Molecular Biology</i> , 2002, 319, 1199-1210.	4.2	56
52	Structural basis of ubiquitylation. <i>Current Opinion in Structural Biology</i> , 2002, 12, 822-830.	5.7	57
53	Defining polyubiquitin chain topology. <i>Nature</i> , 2001, 8, 650-652.		20
54	Image reconstructions of helical assemblies of the HIV-1 CA protein. <i>Nature</i> , 2000, 407, 409-413.	27.8	461

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55	Structural basis for the activation of 20S proteasomes by 11S regulators. <i>Nature</i> , 2000, 408, 115-120.	27.8	476
56	Structure of the C-terminal domain of FliG, a component of the rotor in the bacterial flagellar motor. <i>Nature</i> , 1999, 400, 472-475.	27.8	105
57	Structural basis for the specificity of ubiquitin C-terminal hydrolases. <i>EMBO Journal</i> , 1999, 18, 3877-3887.	7.8	280
58	Crystal Structure of <i>Trichomonas foetus</i> Inosine-5- α -monophosphate Dehydrogenase and the Enzyme-Product Complex. <i>Biochemistry</i> , 1997, 36, 10666-10674.	2.5	57
59	Structure of the Carboxyl-Terminal Dimerization Domain of the HIV-1 Capsid Protein. <i>Science</i> , 1997, 278, 849-853.	12.6	559
60	Structure of the proteasome activator REG γ (PA28 γ). <i>Nature</i> , 1997, 390, 639-643.	27.8	179
61	Characterization and crystallization of human uroporphyrinogen decarboxylase. <i>Protein Science</i> , 1997, 6, 1343-1346.	7.6	37
62	Crystal structure of cyclophilin A complexed with a binding site peptide from the HIV-1 capsid protein. <i>Protein Science</i> , 1997, 6, 2297-2307.	7.6	84
63	The proteasome 11S regulator subunit REG γ (PA28 γ) is a heptamer. <i>Protein Science</i> , 1997, 6, 2469-2473.	7.6	35
64	Comparison of the NMR and X-ray structures of the HIV-1 matrix protein: Evidence for conformational changes during viral assembly. <i>Protein Science</i> , 1996, 5, 2391-2398.	7.6	67