

Yunje Cho

List of Publications by Year in descending order

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31
papers

1,405
citations

394421

19
h-index

434195

31
g-index

32
all docs

32
docs citations

32
times ranked

1977
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the Human Telo2-TTI1-TTI2 Complex. <i>Journal of Molecular Biology</i> , 2022, 434, 167370.	4.2	8
2	Structure Basis for Shaping the Nse4 Protein by the Nse1 and Nse3 Dimer within the Smc5/6 Complex. <i>Journal of Molecular Biology</i> , 2021, 433, 166910.	4.2	12
3	Polyimide mesh-based sample holder with irregular crystal mounting holes for fixed-target serial crystallography. <i>Scientific Reports</i> , 2021, 11, 13115.	3.3	17
4	Structure of the class C orphan GPCR GPR158 in complex with RGS7-G β 25. <i>Nature Communications</i> , 2021, 12, 6805.	12.8	19
5	Structural Basis for Activation of the Heterodimeric GABAB Receptor. <i>Journal of Molecular Biology</i> , 2020, 432, 5966-5984.	4.2	33
6	Structural basis of the fanconi anemia-associated mutations within the FANCA and FANCG complex. <i>Nucleic Acids Research</i> , 2020, 48, 3328-3342.	14.5	9
7	Application of a high-throughput microcrystal delivery system to serial femtosecond crystallography. <i>Journal of Applied Crystallography</i> , 2020, 53, 477-485.	4.5	25
8	Structural Basis for the Antibiotic Resistance of Eukaryotic Isoleucyl-tRNA Synthetase. <i>Molecules and Cells</i> , 2020, 43, 350-359.	2.6	3
9	Structural mechanism of DNA interstrand cross-link unhooking by the bacterial FAN1 nuclease. <i>Journal of Biological Chemistry</i> , 2018, 293, 6482-6496.	3.4	3
10	Eukaryotic Rad50 functions as a rod-shaped dimer. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 248-257.	8.2	63
11	Structural and functional relationships of FAN1. <i>DNA Repair</i> , 2017, 56, 135-143.	2.8	19
12	Interactions between Transmembrane Helices within Monomers of the Aquaporin AtPIP2;1 Play a Crucial Role in Tetramer Formation. <i>Molecular Plant</i> , 2016, 9, 1004-1017.	8.3	19
13	<sc>ATP</sc>-dependent <sc>DNA</sc> binding, unwinding, and resection by the Mre11/Rad50 complex. <i>EMBO Journal</i> , 2016, 35, 743-758.	7.8	99
14	Crystal Structure of the Rad3/XPD Regulatory Domain of Ssl1/p44. <i>Journal of Biological Chemistry</i> , 2015, 290, 8321-8330.	3.4	12
15	Crystal structures of the structure-selective nuclease Mus81-Eme1 bound to flap DNA substrates. <i>EMBO Journal</i> , 2014, 33, 1061-1072.	7.8	29
16	Crystal structure of a Fanconi anemia-associated nuclease homolog bound to 5' flap DNA: basis of interstrand cross-link repair by FAN1. <i>Genes and Development</i> , 2014, 28, 2276-2290.	5.9	19
17	Structure of the ArgRS-GlnRS-AIMP1 complex and its implications for mammalian translation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15084-15089.	7.1	50
18	<sc>DNA</sc> end recognition by the Mre11 nuclease dimer: insights into resection and repair of damaged <sc>DNA</sc>. <i>EMBO Journal</i> , 2014, 33, 2422-2435.	7.8	40

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19	An Ankyrin Repeat Domain of AKR2 Drives Chloroplast Targeting through Coincident Binding of Two Chloroplast Lipids. <i>Developmental Cell</i> , 2014, 30, 598-609.	7.0	49
20	Crystal structure of the NurA-dAMP-Mn ²⁺ complex. <i>Nucleic Acids Research</i> , 2012, 40, 2258-2270.	14.5	17
21	Crystal Structure of Human Mre11: Understanding Tumorigenic Mutations. <i>Structure</i> , 2011, 19, 1591-1602.	3.3	78
22	Crystal structure of the Mre11-Rad50-ATP γ S complex: understanding the interplay between Mre11 and Rad50. <i>Genes and Development</i> , 2011, 25, 1091-1104.	5.9	118
23	Structure of the Cdt1 C-terminal domain: Conservation of the winged helix fold in replication licensing factors. <i>Protein Science</i> , 2009, 18, 2252-2264.	7.6	33
24	Crystal structure of the Mus81-Eme1 complex. <i>Genes and Development</i> , 2008, 22, 1093-1106.	5.9	50
25	Probing the Roles of Active Site Residues in the 3 ϵ -5 ϵ Exonuclease of the Werner Syndrome Protein. <i>Journal of Biological Chemistry</i> , 2007, 282, 9941-9951.	3.4	20
26	Structural basis for inhibition of the replication licensing factor Cdt1 by geminin. <i>Nature</i> , 2004, 430, 913-917.	27.8	130
27	Structural basis for the recognition of the E2F transactivation domain by the retinoblastoma tumor suppressor. <i>Genes and Development</i> , 2002, 16, 3199-3212.	5.9	132
28	Interactions of SV40 large T antigen and other viral proteins with retinoblastoma tumour suppressor. <i>Reviews in Medical Virology</i> , 2002, 12, 81-92.	8.3	44
29	Structure-based identification of a novel NTPase from <i>Methanococcus jannaschii</i> . <i>Nature Structural Biology</i> , 1999, 6, 691-696.	9.7	128
30	Structure and mechanism of glutamate racemase from <i>Aquifex pyrophilus</i> . <i>Nature Structural Biology</i> , 1999, 6, 422-426.	9.7	93
31	Structural similarity between the pocket region of retinoblastoma tumour suppressor and the cyclin-box. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 390-395.	8.2	34