

# Ashwin Chari

## List of Publications by Year in descending order

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38  
papers

3,163  
citations

218677

26  
h-index

315739

38  
g-index

41  
all docs

41  
docs citations

41  
times ranked

4540  
citing authors

#	ARTICLE	IF	CITATIONS
1	Conformational rearrangements upon start codon recognition in human 48S translation initiation complex. <i>Nucleic Acids Research</i> , 2022, 50, 5282-5298.	14.5	15
2	Ground-state destabilization by electrostatic repulsion is not a driving force in orotidine-5 $\alpha$ -monophosphate decarboxylase catalysis. <i>Nature Catalysis</i> , 2022, 5, 332-341.	34.4	12
3	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. <i>Science</i> , 2021, 372, 642-646.	12.6	240
4	Chromatography-Free Purification Strategies for Large Biological Macromolecular Complexes Involving Fractionated PEG Precipitation and Density Gradients. <i>Life</i> , 2021, 11, 1289.	2.4	3
5	Atomic-resolution protein structure determination by cryo-EM. <i>Nature</i> , 2020, 587, 157-161.	27.8	454
6	Proteasomal degradation of the intrinsically disordered protein tau at single-residue resolution. <i>Science Advances</i> , 2020, 6, eaba3916.	10.3	31
7	Discovery of a Regulatory Subunit of the Yeast Fatty Acid Synthase. <i>Cell</i> , 2020, 180, 1130-1143.e20.	28.9	40
8	The copper(II)-binding tripeptide GHK, a valuable crystallization and phasing tag for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1222-1232.	2.3	2
9	Structural and Functional Analyses of the Human PDH Complex Suggest a $\alpha$ Division-of-Labor Mechanism by Local E1 and E3 Clusters. <i>Structure</i> , 2019, 27, 1124-1136.e4.	3.3	23
10	Cryo-EM in drug discovery: achievements, limitations and prospects. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 471-492.	46.4	304
11	Long-range allosteric regulation of the human 26S proteasome by 20S proteasome-targeting cancer drugs. <i>Nature Communications</i> , 2017, 8, 15578.	12.8	63
12	The Ribosome Cooperates with the Assembly Chaperone pICln to Initiate Formation of snRNPs. <i>Cell Reports</i> , 2016, 16, 3103-3112.	6.4	23
13	The inhibition mechanism of human 20 <i>S</i> proteasomes enables next-generation inhibitor design. <i>Science</i> , 2016, 353, 594-598.	12.6	170
14	Molecular architecture of the <i>Saccharomyces cerevisiae</i> activated spliceosome. <i>Science</i> , 2016, 353, 1399-1405.	12.6	165
15	Sample preparation of biological macromolecular assemblies for the determination of high-resolution structures by cryo-electron microscopy. <i>Microscopy (Oxford, England)</i> , 2016, 65, 23-34.	1.5	43
16	Reconstitution of the human U sn RNP assembly machinery reveals stepwise Sm protein organization. <i>EMBO Journal</i> , 2015, 34, 1925-1941.	7.8	47
17	The catalytically inactive tyrosine phosphatase HD-PTP/PTPN23 is a novel regulator of SMN complex localization. <i>Molecular Biology of the Cell</i> , 2015, 26, 161-171.	2.1	22
18	Assembly of RNPs: help needed. <i>Rna</i> , 2015, 21, 613-614.	3.5	3

#	ARTICLE	IF	CITATIONS
19	ProteoPlex: stability optimization of macromolecular complexes by sparse-matrix screening of chemical space. <i>Nature Methods</i> , 2015, 12, 859-865.	19.0	87
20	Phosphoregulation of the human SMN complex. <i>European Journal of Cell Biology</i> , 2014, 93, 106-117.	3.6	24
21	Translation Initiation Factor eIF3b Contains a Nine-Bladed $\hat{\nu}$ -Propeller and Interacts with the 40S Ribosomal Subunit. <i>Structure</i> , 2014, 22, 923-930.	3.3	33
22	Structural Basis of Assembly Chaperone-Mediated snRNP Formation. <i>Molecular Cell</i> , 2013, 49, 692-703.	9.7	82
23	Biogenesis of spliceosomal small nuclear ribonucleoproteins. <i>Wiley Interdisciplinary Reviews RNA</i> , 2011, 2, 718-731.	6.4	116
24	Cellular strategies for the assembly of molecular machines. <i>Trends in Biochemical Sciences</i> , 2010, 35, 676-683.	7.5	37
25	A crystallization screen based on alternative polymeric precipitants. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 685-697.	2.5	17
26	LSm1-7 complexes bind to specific sites in viral RNA genomes and regulate their translation and replication. <i>Rna</i> , 2010, 16, 817-827.	3.5	41
27	Arginine methylation in subunits of mammalian pre-mRNA cleavage factor I. <i>Rna</i> , 2010, 16, 1646-1659.	3.5	27
28	IGHMBP2 is a ribosome-associated helicase inactive in the neuromuscular disorder distal SMA type 1 (DSMA1). <i>Human Molecular Genetics</i> , 2009, 18, 1288-1300.	2.9	88
29	Translation and replication of hepatitis C virus genomic RNA depends on ancient cellular proteins that control mRNA fates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13517-13522.	7.1	127
30	The role of RNP biogenesis in spinal muscular atrophy. <i>Current Opinion in Cell Biology</i> , 2009, 21, 387-393.	5.4	84
31	Deciphering the assembly pathway of Sm-class U snRNPs. <i>FEBS Letters</i> , 2008, 582, 1997-2003.	2.8	99
32	An Assembly Chaperone Collaborates with the SMN Complex to Generate Spliceosomal SnRNPs. <i>Cell</i> , 2008, 135, 497-509.	28.9	189
33	Evolution of an RNP assembly system: A minimal SMN complex facilitates formation of U snRNPs in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10045-10050.	7.1	92
34	A Comprehensive Interaction Map of the Human Survival of Motor Neuron (SMN) Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 5825-5833.	3.4	123
35	A $5\hat{\nu}$ -fluorosulfonylbenzoyladenine-based method to identify physiological substrates of a <i>Drosophila</i> p21-activated kinase. <i>Analytical Biochemistry</i> , 2007, 368, 178-184.	2.4	6
36	Spinal muscular atrophy: the RNP connection. <i>Trends in Molecular Medicine</i> , 2006, 12, 113-121.	6.7	97

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37	Unrip, a factor implicated in cap-independent translation, associates with the cytosolic SMN complex and influences its intracellular localization. <i>Human Molecular Genetics</i> , 2005, 14, 3099-3111.	2.9	70
38	Toward an Assembly Line for U7 snRNPs. <i>Journal of Biological Chemistry</i> , 2005, 280, 34435-34440.	3.4	38