

Arnaud Poterszman

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

61
papers

2,261
citations

25
h-index

47
g-index

62
ext. papers

2,440
ext. citations

7.7
avg, IF

4.03
L-index

#	Paper	IF	Citations
61	Insect Cells-Baculovirus System for the Production of Difficult to Express Proteins: From Expression Screening for Soluble Constructs to Protein Quality Control.. <i>Methods in Molecular Biology</i> , 2022 , 2406, 281-317	1.4	1
60	HR-Bac, a toolbox based on homologous recombination for expression, screening and production of multiprotein complexes using the baculovirus expression system.. <i>Scientific Reports</i> , 2022 , 12, 2030	4.9	1
59	Production of Multiprotein Complexes Using the Baculovirus Expression System: Homology-Based and Restriction-Free Cloning Strategies for Construct Design. <i>Methods in Molecular Biology</i> , 2021 , 2247, 17-38	1.4	2
58	Community-Wide Experimental Evaluation of the PROSS Stability-Design Method. <i>Journal of Molecular Biology</i> , 2021 , 433, 166964	6.5	8
57	Tagging Proteins with Fluorescent Reporters Using the CRISPR/Cas9 System and Double-Stranded DNA Donors. <i>Methods in Molecular Biology</i> , 2021 , 2247, 39-57	1.4	
56	Gene Tagging with the CRISPR-Cas9 System to Facilitate Macromolecular Complex Purification. <i>Methods in Molecular Biology</i> , 2021 , 2305, 153-174	1.4	
55	A Novel Nanobody Precisely Visualizes Phosphorylated Histone H2AX in Living Cancer Cells under Drug-Induced Replication Stress. <i>Cancers</i> , 2021 , 13,	6.6	4
54	In TFIIH the Arch domain of XPD is mechanistically essential for transcription and DNA repair. <i>Nature Communications</i> , 2020 , 11, 1667	17.4	15
53	Functional interplay between TFIIH and KAT2A regulates higher-order chromatin structure and class II gene expression. <i>Nature Communications</i> , 2019 , 10, 1288	17.4	7
52	Identification and characterization of the Onchocerca volvulus Excretory Secretory Product Ov28CRP, a putative GM2 activator protein. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007591	4.8	5
51	TFIIH: A multi-subunit complex at the cross-roads of transcription and DNA repair. <i>Advances in Protein Chemistry and Structural Biology</i> , 2019 , 115, 21-67	5.3	28
50	Crystallization and Preliminary X-Ray Diffraction Analysis of a Mammal Inositol 1,3,4,5,6-Pentakisphosphate 2-Kinase. <i>Protein Journal</i> , 2017 , 36, 240-248	3.9	2
49	The intricate network between the p34 and p44 subunits is central to the activity of the transcription/DNA repair factor TFIIH. <i>Nucleic Acids Research</i> , 2017 , 45, 10872-10883	20.1	16
48	An evolutionary conserved Hexim1 peptide binds to the Cdk9 catalytic site to inhibit P-TEFb. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 12721-12726	11.5	28
47	Baculovirus expression: old dog, new tricks. <i>Bioengineered</i> , 2015 , 6, 316-22	5.7	12
46	Insect cells-baculovirus system for the production of difficult to express proteins. <i>Methods in Molecular Biology</i> , 2015 , 1258, 181-205	1.4	9
45	The production of multiprotein complexes in insect cells using the baculovirus expression system. <i>Methods in Molecular Biology</i> , 2015 , 1261, 91-114	1.4	11

44	In TFIIH, XPD helicase is exclusively devoted to DNA repair. <i>PLoS Biology</i> , 2014 , 12, e1001954	9.7	57
43	ARCH domain of XPD, an anchoring platform for CAK that conditions TFIIH DNA repair and transcription activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E633-42	11.5	52
42	Expression of functional full-length hSRC-1 in eukaryotic cells using modified vaccinia virus Ankara and baculovirus. <i>Analytical Biochemistry</i> , 2012 , 426, 106-8	3.1	0
41	Robots, pipelines, polyproteins: enabling multiprotein expression in prokaryotic and eukaryotic cells. <i>Journal of Structural Biology</i> , 2011 , 175, 198-208	3.4	80
40	Structural insights into transcription complexes. <i>Journal of Structural Biology</i> , 2011 , 175, 135-46	3.4	13
39	Interacting partners of the Tfb2 subunit from yeast TFIIH. <i>DNA Repair</i> , 2010 , 9, 33-9	4.3	9
38	Analysis of recombinant phosphoprotein complexes with complementary mass spectrometry approaches. <i>Analytical Biochemistry</i> , 2010 , 407, 34-43	3.1	4
37	Structure determination of the minimal complex between Tfb5 and Tfb2, two subunits of the yeast transcription/DNA-repair factor TFIIH: a retrospective study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 745-55		3
36	A set of baculovirus transfer vectors for screening of affinity tags and parallel expression strategies. <i>Analytical Biochemistry</i> , 2009 , 385, 383-5	3.1	47
35	Structural basis for group A trichothiodystrophy. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 980-47.6		48
34	Structural Proteomics in Relation to Signaling Pathways 2008 , 331-345		
33	Solution structure and self-association properties of the p8 TFIIH subunit responsible for trichothiodystrophy. <i>Journal of Molecular Biology</i> , 2007 , 368, 473-80	6.5	28
32	Biophysical characterization of an indolinone inhibitor in the ATP-binding site of DNA gyrase. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 349, 1206-13	3.4	14
31	First steps towards effective methods in exploiting high-throughput technologies for the determination of human protein structures of high biomedical value. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1208-17		27
30	Eukaryotic expression: developments for structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1114-24		67
29	Co-expression of protein complexes in prokaryotic and eukaryotic hosts: experimental procedures, database tracking and case studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1232-42		94
28	Structure and oligomeric state of human transcription factor TFIIIE. <i>EMBO Reports</i> , 2006 , 7, 500-5	6.5	23
27	Solution structure of the C-terminal domain of TFIIH P44 subunit reveals a novel type of C4C4 ring domain involved in protein-protein interactions. <i>Journal of Biological Chemistry</i> , 2005 , 280, 20785-92	5.4	25

26	TFIIH contains a PH domain involved in DNA nucleotide excision repair. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 616-22	17.6	69
25	Domain architecture of the p62 subunit from the human transcription/repair factor TFIIH deduced by limited proteolysis and mass spectrometry analysis. <i>Biochemistry</i> , 2004 , 43, 14420-30	3.2	24
24	p52 Mediates XPB function within the transcription/repair factor TFIIH. <i>Journal of Biological Chemistry</i> , 2002 , 277, 31761-7	5.4	48
23	Expression of FLAG fusion proteins in insect cells: application to the multi-subunit transcription/DNA repair factor TFIIH. <i>Protein Expression and Purification</i> , 2002 , 24, 513-23	2	14
22	Solution structure of the N-terminal domain of the human TFIIH MAT1 subunit: new insights into the RING finger family. <i>Journal of Biological Chemistry</i> , 2001 , 276, 7457-64	5.4	39
21	Dissecting the interaction network of multiprotein complexes by pairwise coexpression of subunits in <i>E. coli</i> . <i>Journal of Molecular Biology</i> , 2001 , 306, 363-73	6.5	60
20	The structure of human aldose reductase bound to the inhibitor IDD384. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 536-40		22
19	Characterization of crystal content by ESI-MS and MALDI-MS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 1583-90		11
18	Structural characterization of the cysteine-rich domain of TFIIH p44 subunit. <i>Journal of Biological Chemistry</i> , 2000 , 275, 31963-71	5.4	27
17	Distinct regions of MAT1 regulate cdk7 kinase and TFIIH transcription activities. <i>Journal of Biological Chemistry</i> , 2000 , 275, 22815-23	5.4	59
16	An intermediate step in the recognition of tRNA(Asp) by aspartyl-tRNA synthetase. <i>Journal of Molecular Biology</i> , 2000 , 299, 1051-60	6.5	43
15	Molecular structure of human TFIIH. <i>Cell</i> , 2000 , 102, 599-607	56.2	155
14	Production of crystals of human aldose reductase with very high resolution diffraction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 721-3		21
13	Crystals of <i>Thermus thermophilus</i> tRNA ^{Asp} complexed with its cognate aspartyl-tRNA synthetase have a solvent content of 75%. Comparison with other aminoacylation systems. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1382-6		3
12	Expression in <i>Escherichia coli</i> : purification and characterization of cyclin H, a subunit of the human general transcription/DNA repair factor TFIIH. <i>Protein Expression and Purification</i> , 1997 , 9, 153-8	2	1
11	A eukaryotic XPB/ERCC3-like helicase in <i>Mycobacterium leprae</i> ?. <i>Trends in Biochemical Sciences</i> , 1997 , 22, 418-9	10.3	13
10	The structure of cyclin H: common mode of kinase activation and specific features. <i>EMBO Journal</i> , 1997 , 16, 958-67	13	65
9	The crystal structure of human cyclin H. <i>FEBS Letters</i> , 1996 , 397, 65-9	3.8	27

8	Getting into the major groove. Protein-RNA interactions. <i>Current Biology</i> , 1996 , 6, 530-2	6.3	13
7	Crystallization of Escherichia coli aspartyl-tRNA synthetase in its free state and in a complex with yeast tRNA(Asp). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996 , 52, 211-4		6
6	Genomic structure of the human TATA-box-binding protein (TBP). <i>Gene</i> , 1995 , 161, 277-82	3.8	15
5	RNA-protein interactions. Diverse modes of recognition. <i>Current Biology</i> , 1995 , 5, 249-51	6.3	17
4	Synthesis and recognition of aspartyl-adenylate by <i>Thermus thermophilus</i> aspartyl-tRNA synthetase. <i>Journal of Molecular Biology</i> , 1994 , 244, 158-67	6.5	68
3	Sequence, overproduction and crystallization of aspartyl-tRNA synthetase from <i>Thermus thermophilus</i> . Implications for the structure of prokaryotic aspartyl-tRNA synthetases. <i>FEBS Letters</i> , 1993 , 325, 183-6	3.8	27
2	Class II aminoacyl transfer RNA synthetases: crystal structure of yeast aspartyl-tRNA synthetase complexed with tRNA(Asp). <i>Science</i> , 1991 , 252, 1682-9	33.3	669
1	The Transcription/DNA Repair Factor TFIIH		1