

Arnaud Poterszman

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

2,647
citations

218662

26
h-index

189881

50
g-index

62
all docs

62
docs citations

62
times ranked

2397
citing authors

#	ARTICLE	IF	CITATIONS
1	Class II aminoacyl transfer RNA synthetases: crystal structure of yeast aspartyl-tRNA synthetase complexed with tRNA(Asp). <i>Science</i> , 1991, 252, 1682-1689.	12.6	710
2	Molecular Structure of Human TFIIH. <i>Cell</i> , 2000, 102, 599-607.	28.9	175
3	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, 1232-1242.	2.5	113
4	Robots, pipelines, polyproteins: Enabling multiprotein expression in prokaryotic and eukaryotic cells. <i>Journal of Structural Biology</i> , 2011, 175, 198-208.	2.8	92
5	The structure of cyclin H: common mode of kinase activation and specific features. <i>EMBO Journal</i> , 1997, 16, 958-967.	7.8	81
6	Eukaryotic expression: developments for structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1114-1124.	2.5	79
7	In TFIIH, XPD Helicase Is Exclusively Devoted to DNA Repair. <i>PLoS Biology</i> , 2014, 12, e1001954.	5.6	79
8	TFIIH contains a PH domain involved in DNA nucleotide excision repair. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 616-622.	8.2	78
9	Synthesis and Recognition of Aspartyl-adenylate by <i>Thermus thermophilus</i> Aspartyl-tRNA Synthetase. <i>Journal of Molecular Biology</i> , 1994, 244, 158-167.	4.2	73
10	Distinct Regions of MAT1 Regulate cdk7 Kinase and TFIIH Transcription Activities. <i>Journal of Biological Chemistry</i> , 2000, 275, 22815-22823.	3.4	71
11	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.	7.1	67
12	A set of baculovirus transfer vectors for screening of affinity tags and parallel expression strategies. <i>Analytical Biochemistry</i> , 2009, 385, 383-385.	2.4	66
13	Dissecting the interaction network of multiprotein complexes by pairwise coexpression of subunits in <i>E. coli</i> 11 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 2001, 306, 363-373.	4.2	64
14	Structural basis for group A trichothiodystrophy. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 980-984.	8.2	54
15	p52 Mediates XPB Function within the Transcription/Repair Factor TFIIH. <i>Journal of Biological Chemistry</i> , 2002, 277, 31761-31767.	3.4	53
16	Solution Structure of the N-terminal Domain of the Human TFIIH MAT1 Subunit. <i>Journal of Biological Chemistry</i> , 2001, 276, 7457-7464.	3.4	44
17	An intermediate step in the recognition of tRNA Asp by aspartyl-tRNA synthetase 1 1 Edited by J. Doudna. <i>Journal of Molecular Biology</i> , 2000, 299, 1051-1060.	4.2	43
18	Community-Wide Experimental Evaluation of the PROSS Stability-Design Method. <i>Journal of Molecular Biology</i> , 2021, 433, 166964.	4.2	42

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19	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.	7.1	40
20	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.	2.3	39
21	Sequence, overproduction and crystallization of aspartyl-tRNA synthetase from <i>Thermus thermophilus</i> . <i>FEBS Letters</i> , 1993, 325, 183-186.	2.8	36
22	In TFIIH the Arch domain of XPD is mechanistically essential for transcription and DNA repair. <i>Nature Communications</i> , 2020, 11, 1667.	12.8	32
23	Solution Structure and Self-association Properties of the p8 TFIIH Subunit Responsible for Trichothiodystrophy. <i>Journal of Molecular Biology</i> , 2007, 368, 473-480.	4.2	31
24	The crystal structure of human cyclin H. <i>FEBS Letters</i> , 1996, 397, 65-69.	2.8	29
25	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, 1208-1217.	2.5	29
26	Structural Characterization of the Cysteine-rich Domain of TFIIH p44 Subunit. <i>Journal of Biological Chemistry</i> , 2000, 275, 31963-31971.	3.4	28
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, 20785-20792.	3.4	28
28	Production of crystals of human aldose reductase with very high resolution diffraction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 721-723.	2.5	26
29	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, 14420-14430.	2.5	26
30	The structure of human aldose reductase bound to the inhibitor IDD384. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 536-540.	2.5	25
31	Structure and oligomeric state of human transcription factor TFIIH. <i>EMBO Reports</i> , 2006, 7, 500-505.	4.5	24
32	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.	14.5	21
33	RNA-Protein Interactions: Diverse modes of recognition. <i>Current Biology</i> , 1995, 5, 249-251.	3.9	19
34	Protein-RNA interactions: Getting into the major groove. <i>Current Biology</i> , 1996, 6, 530-532.	3.9	17
35	Genomic structure of the human TATA-box-binding protein (TBP). <i>Gene</i> , 1995, 161, 277-282.	2.2	16
36	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, 513-523.	1.3	15

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37	A eukaryotic SPB/ERCC3-like helicase in <i>Mycobacterium leprae</i> ?. <i>Trends in Biochemical Sciences</i> , 1997, 22, 418-419.	7.5	14
38	Biophysical characterization of an indolinone inhibitor in the ATP-binding site of DNA gyrase. <i>Biochemical and Biophysical Research Communications</i> , 2006, 349, 1206-1213.	2.1	14
39	Structural insights into transcription complexes. <i>Journal of Structural Biology</i> , 2011, 175, 135-146.	2.8	14
40	Baculovirus expression: old dog, new tricks. <i>Bioengineered</i> , 2015, 6, 316-322.	3.2	14
41	A Novel Nanobody Precisely Visualizes Phosphorylated Histone H2AX in Living Cancer Cells under Drug-Induced Replication Stress. <i>Cancers</i> , 2021, 13, 3317.	3.7	14
42	The Production of Multiprotein Complexes in Insect Cells Using the Baculovirus Expression System. <i>Methods in Molecular Biology</i> , 2015, 1261, 91-114.	0.9	14
43	Characterization of crystal content by ESI-MS and MALDI-MS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1583-1590.	2.5	13
44	Interacting partners of the Tfb2 subunit from yeast TFIIH. <i>DNA Repair</i> , 2010, 9, 33-39.	2.8	13
45	Insect Cells-Baculovirus System for the Production of Difficult to Express Proteins. <i>Methods in Molecular Biology</i> , 2015, 1258, 181-205.	0.9	12
46	Identification and characterization of the <i>Onchocerca volvulus</i> Excretory Secretory Product Ov28CRP, a putative GM2 activator protein. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007591.	3.0	10
47	Functional interplay between TFIIH and KAT2A regulates higher-order chromatin structure and class II gene expression. <i>Nature Communications</i> , 2019, 10, 1288.	12.8	10
48	Crystallization of <i>Escherichia coli</i> 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, 211-214.	2.5	6
49	Analysis of recombinant phosphoprotein complexes with complementary mass spectrometry approaches. <i>Analytical Biochemistry</i> , 2010, 407, 34-43.	2.4	5
50	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.	3.3	5
51	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, 745-755.	2.5	4
52	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, 1382-1386.	2.5	3
53	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.	1.6	3
54	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.	0.9	3

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55	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.	0.9	3
56	Expression in <i>Escherichia coli</i> : Purification and Characterization of Cyclin H, a Subunit of the Human General Transcription/DNA Repair Factor TFIIF. <i>Protein Expression and Purification</i> , 1997, 9, 153-158.	1.3	1
57	Expression of functional full-length hSRC-1 in eukaryotic cells using modified vaccinia virus Ankara and baculovirus. <i>Analytical Biochemistry</i> , 2012, 426, 106-108.	2.4	1
58	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.	0.9	1
59	Gene Tagging with the CRISPR-Cas9 System to Facilitate Macromolecular Complex Purification. <i>Methods in Molecular Biology</i> , 2021, 2305, 153-174.	0.9	0
60	Structural Proteomics in Relation to Signaling Pathways. , 2008, , 331-345.		0