

# Laurence H Pearl

## List of Publications by Year in descending order

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223  
papers

26,920  
citations

4960

84  
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6300

158  
g-index

251  
all docs

251  
docs citations

251  
times ranked

23432  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and Structural Characterization of the ATP/ADP-Binding Site in the Hsp90 Molecular Chaperone. <i>Cell</i> , 1997, 90, 65-75.	28.9	1,203
2	Structure and Mechanism of the Hsp90 Molecular Chaperone Machinery. <i>Annual Review of Biochemistry</i> , 2006, 75, 271-294.	11.1	988
3	Structural Basis for Inhibition of the Hsp90 Molecular Chaperone by the Antitumor Antibiotics Radicol and Geldanamycin. <i>Journal of Medicinal Chemistry</i> , 1999, 42, 260-266.	6.4	948
4	Crystal structure of an Hsp90- $\alpha$ -nucleotide- $\beta$ 23/Sba1 closed chaperone complex. <i>Nature</i> , 2006, 440, 1013-1017.	27.8	857
5	GSK-3-Selective Inhibitors Derived from Tyrian Purple Indirubins. <i>Chemistry and Biology</i> , 2003, 10, 1255-1266.	6.0	720
6	ATP binding and hydrolysis are essential to the function of the Hsp90 molecular chaperone in vivo. <i>EMBO Journal</i> , 1998, 17, 4829-4836.	7.8	662
7	A structural model for the retroviral proteases. <i>Nature</i> , 1987, 329, 351-354.	27.8	638
8	Crystal Structure of Glycogen Synthase Kinase 3 $\beta$ . <i>Cell</i> , 2001, 105, 721-732.	28.9	610
9	DNA repair, genome stability and cancer: a historical perspective. <i>Nature Reviews Cancer</i> , 2016, 16, 35-42.	28.4	575
10	Activation of the ATPase Activity of Hsp90 by the Stress-Regulated Cochaperone Aha1. <i>Molecular Cell</i> , 2002, 10, 1307-1318.	9.7	487
11	Therapeutic opportunities within the DNA damage response. <i>Nature Reviews Cancer</i> , 2015, 15, 166-180.	28.4	442
12	Structural and Functional Analysis of the Middle Segment of Hsp90: Implications for ATP Hydrolysis and Client Protein and Cochaperone Interactions. <i>Molecular Cell</i> , 2003, 11, 647-658.	9.7	434
13	NVP-AUY922: A Novel Heat Shock Protein 90 Inhibitor Active against Xenograft Tumor Growth, Angiogenesis, and Metastasis. <i>Cancer Research</i> , 2008, 68, 2850-2860.	0.9	433
14	The ATPase cycle of Hsp90 drives a molecular clamp' via transient dimerization of the N-terminal domains. <i>EMBO Journal</i> , 2000, 19, 4383-4392.	7.8	418
15	The structural basis of specific base-excision repair by uracil-DNA glycosylase. <i>Nature</i> , 1995, 373, 487-493.	27.8	413
16	The Hsp90 molecular chaperone: an open and shut case for treatment. <i>Biochemical Journal</i> , 2008, 410, 439-453.	3.7	410
17	4,5-Diarylisoazole Hsp90 Chaperone Inhibitors: Potential Therapeutic Agents for the Treatment of Cancer. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 196-218.	6.4	386
18	Chaperoned Ubiquitylation-Crystal Structures of the CHIP U Box E3 Ubiquitin Ligase and a CHIP-Ubc13-Uev1a Complex. <i>Molecular Cell</i> , 2005, 20, 525-538.	9.7	382

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19	Regulation of Hsp90 ATPase activity by tetratricopeptide repeat (TPR)-domain co-chaperones. <i>EMBO Journal</i> , 1999, 18, 754-762.	7.8	376
20	Structural Basis for the Synthesis of Indirubins as Potent and Selective Inhibitors of Glycogen Synthase Kinase-3 and Cyclin-Dependent Kinases. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 935-946.	6.4	343
21	The Mechanism of Hsp90 Regulation by the Protein Kinase-Specific Cochaperone p50cdc37. <i>Cell</i> , 2004, 116, 87-98.	28.9	319
22	Structure and in vivo function of Hsp90. <i>Current Opinion in Structural Biology</i> , 2000, 10, 46-51.	5.7	294
23	Structure of an Hsp90-Cdc37-Cdk4 Complex. <i>Molecular Cell</i> , 2006, 23, 697-707.	9.7	288
24	Structural basis for recruitment of glycogen synthase kinase 3beta to the axin-APC scaffold complex. <i>EMBO Journal</i> , 2003, 22, 494-501.	7.8	269
25	Structure and function in the uracil-DNA glycosylase superfamily. <i>Mutation Research DNA Repair</i> , 2000, 460, 165-181.	3.7	268
26	Regulation of Hsp90 ATPase Activity by the Co-chaperone Cdc37p/p50. <i>Journal of Biological Chemistry</i> , 2002, 277, 20151-20159.	3.4	246
27	The active site of aspartic proteinases. <i>FEBS Letters</i> , 1984, 174, 96-101.	2.8	242
28	Structure and Functional Relationships of Hsp90. <i>Current Cancer Drug Targets</i> , 2003, 3, 301-323.	1.6	242
29	Crystal Structure of a G:T/U Mismatch-Specific DNA Glycosylase. <i>Cell</i> , 1998, 92, 117-129.	28.9	240
30	Hsp90 and Cdc37 – a chaperone cancer conspiracy. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 55-61.	3.3	238
31	Crystal structure of the Î <sup>2</sup> -glycosidase from the hyperthermophilic archeon <i>Sulfolobus solfataricus</i> : resilience as a key factor in thermostability. <i>Journal of Molecular Biology</i> , 1997, 271, 789-802.	4.2	235
32	Three-dimensional structure, specificity and catalytic mechanism of renin. <i>Nature</i> , 1983, 304, 273-275.	27.8	229
33	The identification, synthesis, protein crystal structure and in vitro biochemical evaluation of a new 3,4-diarylpyrazole class of Hsp90 inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2005, 15, 3338-3343.	2.2	228
34	Three-Dimensional Structure of the Human DNA-PKcs/Ku70/Ku80 Complex Assembled on DNA and Its Implications for DNA DSB Repair. <i>Molecular Cell</i> , 2006, 22, 511-519.	9.7	223
35	Human BRCA1-BARD1 ubiquitin ligase activity counteracts chromatin barriers to DNA resection. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 647-655.	8.2	222
36	Recursive PCR: a novel technique for total gene synthesis. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 827-829.	2.1	217

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37	A molecular clamp in the crystal structure of the N-terminal domain of the yeast Hsp90 chaperone. <i>Nature Structural Biology</i> , 1997, 4, 477-482.	9.7	214
38	The zinc-finger domains of PARP1 cooperate to recognize DNA strand breaks. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 685-692.	8.2	214
39	Structural basis for recruitment of translesion DNA polymerase Pol IV/DinB to the $\beta$ -clamp. <i>EMBO Journal</i> , 2003, 22, 5883-5892.	7.8	212
40	Structure of the Ire1 autophosphorylation complex and implications for the unfolded protein response. <i>EMBO Journal</i> , 2011, 30, 894-905.	7.8	201
41	High-throughput screening assay for inhibitors of heat-shock protein 90 ATPase activity. <i>Analytical Biochemistry</i> , 2004, 327, 176-183.	2.4	192
42	Hsp90-Dependent Activation of Protein Kinases Is Regulated by Chaperone-Targeted Dephosphorylation of Cdc37. <i>Molecular Cell</i> , 2008, 31, 886-895.	9.7	184
43	Co-chaperone Regulation of Conformational Switching in the Hsp90 ATPase Cycle. <i>Journal of Biological Chemistry</i> , 2004, 279, 51989-51998.	3.4	183
44	Structural basis for recruitment of the ATPase activator Aha1 to the Hsp90 chaperone machinery. <i>EMBO Journal</i> , 2004, 23, 1402-1410.	7.8	179
45	Selectivity, Cocrystal Structures, and Neuroprotective Properties of Leucettines, a Family of Protein Kinase Inhibitors Derived from the Marine Sponge Alkaloid Leucettamine B. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 9312-9330.	6.4	174
46	Structure, function, and mechanism of the Hsp90 molecular chaperone. <i>Advances in Protein Chemistry</i> , 2001, 59, 157-186.	4.4	172
47	Swe1Wee1-Dependent Tyrosine Phosphorylation of Hsp90 Regulates Distinct Facets of Chaperone Function. <i>Molecular Cell</i> , 2010, 37, 333-343.	9.7	165
48	Structural basis for recruitment of the ATPase activator Aha1 to the Hsp90 chaperone machinery. <i>EMBO Journal</i> , 2004, 23, 511-519.	7.8	164
49	A Two-Hybrid Screen of the Yeast Proteome for Hsp90 Interactors Uncovers a Novel Hsp90 Chaperone Requirement in the Activity of a Stress-Activated Mitogen-Activated Protein Kinase, Slt2p (Mpk1p). <i>Eukaryotic Cell</i> , 2005, 4, 849-860.	3.4	159
50	Structural basis for recruitment of BRCA2 by PALB2. <i>EMBO Reports</i> , 2009, 10, 990-996.	4.5	154
51	Activation segment dimerization: a mechanism for kinase autophosphorylation of non-consensus sites. <i>EMBO Journal</i> , 2008, 27, 704-714.	7.8	147
52	Structural basis for uracil recognition by archaeal family B DNA polymerases. <i>Nature Structural Biology</i> , 2002, 9, 922-927.	9.7	146
53	Threonine 22 Phosphorylation Attenuates Hsp90 Interaction with Cochaperones and Affects Its Chaperone Activity. <i>Molecular Cell</i> , 2011, 41, 672-681.	9.7	146
54	Review: The HSP90 molecular chaperone—“an enigmatic ATPase. <i>Biopolymers</i> , 2016, 105, 594-607.	2.4	144

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55	High resolution X-ray analyses of renin inhibitor-aspartic proteinase complexes. <i>Nature</i> , 1987, 327, 349-352.	27.8	143
56	Inhibition of the heat shock protein 90 molecular chaperone in vitro and in vivo by novel, synthetic, potent resorcinolic pyrazole/isoxazole amide analogues. <i>Molecular Cancer Therapeutics</i> , 2007, 6, 1198-1211.	4.1	141
57	Regulation of DNA Replication through Sld3-Dpb11 Interaction Is Conserved from Yeast to Humans. <i>Current Biology</i> , 2011, 21, 1152-1157.	3.9	135
58	Molecular Recognition of Transcriptional Repressor Motifs by the WD Domain of the Groucho/TLE Corepressor. <i>Molecular Cell</i> , 2006, 22, 645-655.	9.7	134
59	ATP-competitive inhibitors block protein kinase recruitment to the Hsp90-Cdc37 system. <i>Nature Chemical Biology</i> , 2013, 9, 307-312.	8.0	132
60	Trans-activation of the DNA-damage signalling protein kinase Chk2 by T-loop exchange. <i>EMBO Journal</i> , 2006, 25, 3179-3190.	7.8	131
61	Crystal Structure of Alanine:Glyoxylate Aminotransferase and the Relationship Between Genotype and Enzymatic Phenotype in Primary Hyperoxaluria Type 1. <i>Journal of Molecular Biology</i> , 2003, 331, 643-652.	4.2	129
62	Structural and Mechanistic Insights into Ras Association Domains of Phospholipase C Epsilon. <i>Molecular Cell</i> , 2006, 21, 495-507.	9.7	129
63	Structure and Specificity of the Vertebrate Anti-Mutator Uracil-DNA Glycosylase SMUG1. <i>Molecular Cell</i> , 2003, 11, 1647-1659.	9.7	127
64	Crystal Structure of an Octameric RuvA-Holliday Junction Complex. <i>Molecular Cell</i> , 1998, 2, 361-372.	9.7	126
65	Crystal structure of a thwarted mismatch glycosylase DNA repair complex. <i>EMBO Journal</i> , 1999, 18, 6599-6609.	7.8	122
66	X-ray analyses of aspartic proteinases. <i>Journal of Molecular Biology</i> , 1990, 211, 919-941.	4.2	120
67	Insights into histone code syntax from structural and biochemical studies of CARM1 methyltransferase. <i>EMBO Journal</i> , 2007, 26, 4402-4412.	7.8	117
68	Identification of the Axin and Frat Binding Region of Glycogen Synthase Kinase-3. <i>Journal of Biological Chemistry</i> , 2002, 277, 2176-2185.	3.4	112
69	Crystal Structure of the Rad9-Rad1-Hus1 DNA Damage Checkpoint Complex—Implications for Clamp Loading and Regulation. <i>Molecular Cell</i> , 2009, 34, 735-745.	9.7	112
70	In vitro Biological Characterization of a Novel, Synthetic Diaryl Pyrazole Resorcinol Class of Heat Shock Protein 90 Inhibitors. <i>Cancer Research</i> , 2007, 67, 2206-2216.	0.9	111
71	Structural model of full-length human Ku70-Ku80 heterodimer and its recognition of DNA and DNA-PCs. <i>EMBO Reports</i> , 2007, 8, 56-62.	4.5	111
72	Structural Basis for Assembly of Hsp90-Sgt1-CHORD Protein Complexes: Implications for Chaperoning of NLR Innate Immunity Receptors. <i>Molecular Cell</i> , 2010, 39, 269-281.	9.7	108

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73	Structural and functional coupling of Hsp90- and Sgt1-centred multi-protein complexes. <i>EMBO Journal</i> , 2008, 27, 2789-2798.	7.8	104
74	Glycogen Synthase Kinase-3 Inhibition by Lithium and Beryllium Suggests the Presence of Two Magnesium Binding Sites. <i>Biochemical and Biophysical Research Communications</i> , 2002, 290, 967-972.	2.1	102
75	Reciprocal "flipping" underlies substrate recognition and catalytic activation by the human 8-oxo-guanine DNA glycosylase. <i>Journal of Molecular Biology</i> , 2002, 317, 171-177.	4.2	101
76	Crystal structure of the catalytic fragment of murine poly(ADP-ribose) polymerase-2. <i>Nucleic Acids Research</i> , 2004, 32, 456-464.	14.5	101
77	Three-Dimensional Structure and Regulation of the DNA-Dependent Protein Kinase Catalytic Subunit (DNA-PKcs). <i>Structure</i> , 2005, 13, 243-255.	3.3	98
78	MDC1 Interacts with TOPBP1 to Maintain Chromosomal Stability during Mitosis. <i>Molecular Cell</i> , 2019, 74, 571-583.e8.	9.7	97
79	CCT241533 Is a Potent and Selective Inhibitor of CHK2 that Potentiates the Cytotoxicity of PARP Inhibitors. <i>Cancer Research</i> , 2011, 71, 463-472.	0.9	96
80	<i>Plasmodium falciparum</i> glycogen synthase kinase-3: molecular model, expression, intracellular localisation and selective inhibitors. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1697, 181-196.	2.3	95
81	The ATPase-dependent chaperoning activity of Hsp90a regulates thick filament formation and integration during skeletal muscle myofibrillogenesis. <i>Development (Cambridge)</i> , 2008, 135, 1147-1156.	2.5	94
82	The crystal structure of yeast CCT reveals intrinsic asymmetry of eukaryotic cytosolic chaperonins. <i>EMBO Journal</i> , 2011, 30, 3078-3090.	7.8	94
83	A Mechanism for the Inhibition of DNA-PK-Mediated DNA Sensing by a Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003649.	4.7	94
84	Visualization of a DNA-PK/PARP1 complex. <i>Nucleic Acids Research</i> , 2012, 40, 4168-4177.	14.5	89
85	Nucleotide mimicry in the crystal structure of the uracil-DNA glycosylase-uracil glycosylase inhibitor protein complex. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 752-757.	8.2	87
86	Activation segment exchange: a common mechanism of kinase autophosphorylation?. <i>Trends in Biochemical Sciences</i> , 2007, 32, 351-356.	7.5	86
87	Structural Basis for Phosphorylation-Dependent Recruitment of Tel2 to Hsp90 by Pih1. <i>Structure</i> , 2014, 22, 805-818.	3.3	86
88	Crystal structure and induction mechanism of AmiC-AmiR: a ligand-regulated transcription antitermination complex. <i>EMBO Journal</i> , 1999, 18, 5175-5186.	7.8	83
89	Optimizing Natural Products by Biosynthetic Engineering: Discovery of Nonquinone Hsp90 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 5494-5497.	6.4	79
90	Specific recognition of a multiply phosphorylated motif in the DNA repair scaffold XRCC1 by the FHA domain of human PNK. <i>Nucleic Acids Research</i> , 2009, 37, 1701-1712.	14.5	75

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91	Crystal Structure of the CCT <sup>3</sup> Apical Domain: Implications for Substrate Binding to the Eukaryotic Cytosolic Chaperonin. <i>Journal of Molecular Biology</i> , 2002, 318, 1367-1379.	4.2	72
92	Structure and function of the Rad9-binding region of the DNA-damage checkpoint adaptor TopBP1. <i>Nucleic Acids Research</i> , 2011, 39, 313-324.	14.5	72
93	Enzyme thermostability and thermoactivity. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 629-630.	2.1	68
94	Crystal Structure of the Retinoblastoma Protein N Domain Provides Insight into Tumor Suppression, Ligand Interaction, and Holo-protein Architecture. <i>Molecular Cell</i> , 2007, 28, 371-385.	9.7	68
95	Cooperation of local motions in the Hsp90 molecular chaperone ATPase mechanism. <i>Nature Chemical Biology</i> , 2016, 12, 628-635.	8.0	68
96	Visualization of DNA-induced conformational changes in the DNA repair kinase DNA-PKcs. <i>EMBO Journal</i> , 2003, 22, 5875-5882.	7.8	67
97	Structural Insights into Formation of an Active Signaling Complex between Rac and Phospholipase C Gamma 2. <i>Molecular Cell</i> , 2009, 34, 223-233.	9.7	67
98	An Iron-Sulfur Cluster in the Family 4 Uracil-DNA Glycosylases. <i>Journal of Biological Chemistry</i> , 2002, 277, 16936-16940.	3.4	66
99	Regulation of protein kinases in insulin, growth factor and Wnt signalling. <i>Current Opinion in Structural Biology</i> , 2002, 12, 761-767.	5.7	66
100	Structural and functional analysis of the Crb2 <sup>BRCT</sup> domain reveals distinct roles in checkpoint signaling and DNA damage repair. <i>Genes and Development</i> , 2008, 22, 2034-2047.	5.9	65
101	Destabilized SMC5/6 complex leads to chromosome breakage syndrome with severe lung disease. <i>Journal of Clinical Investigation</i> , 2016, 126, 2881-2892.	8.2	65
102	Structure of an archaeal PCNA1 <sup>PCNA2</sup> <sup>FEN1</sup> complex: elucidating PCNA subunit and client enzyme specificity. <i>Nucleic Acids Research</i> , 2006, 34, 4515-4526.	14.5	64
103	Inhibition of Hsp90 with Synthetic Macrolactones: Synthesis and Structural and Biological Evaluation of Ring and Conformational Analogs of Radicol. <i>Chemistry and Biology</i> , 2006, 13, 1203-1215.	6.0	64
104	Crystal Structure of the C-Terminal WD40 Repeat Domain of the Human Groucho/TLE1 Transcriptional Corepressor. <i>Structure</i> , 2002, 10, 751-761.	3.3	63
105	Crystal structure of the fission yeast mitochondrial Holliday junction resolvase Ydc2. <i>EMBO Journal</i> , 2001, 20, 6601-6611.	7.8	62
106	ATM Localization and Heterochromatin Repair Depend on Direct Interaction of the 53BP1-BRCT 2 Domain with <sup>1</sup> H2AX. <i>Cell Reports</i> , 2015, 13, 2081-2089.	6.4	61
107	Specialized interfaces of Smc5/6 control hinge stability and DNA association. <i>Nature Communications</i> , 2017, 8, 14011.	12.8	61
108	Expressed in the Yeast <i>Saccharomyces cerevisiae</i> , Human ERK5 Is a Client of the Hsp90 Chaperone That Complements Loss of the Slf2p (Mpk1p) Cell Integrity Stress-Activated Protein Kinase. <i>Eukaryotic Cell</i> , 2006, 5, 1914-1924.	3.4	60

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109	PARP3 is a sensor of nicked nucleosomes and monoribosylates histone H2B <sup>Glu2</sup> . <i>Nature Communications</i> , 2016, 7, 12404.	12.8	60
110	Molecular modelling of the interactions of tetra-(4-N-methylpyridyl) porphyrin with TA and CG sites on DNA. <i>Nucleic Acids Research</i> , 1987, 15, 6553-6562.	14.5	59
111	The catalytic mechanism of aspartic proteinases. <i>FEBS Letters</i> , 1987, 214, 8-12.	2.8	59
112	Efficient Single-Strand Break Repair Requires Binding to Both Poly(ADP-Ribose) and DNA by the Central BRCT Domain of XRCC1. <i>Cell Reports</i> , 2019, 26, 573-581.e5.	6.4	58
113	The Ku-binding motif is a conserved module for recruitment and stimulation of non-homologous end-joining proteins. <i>Nature Communications</i> , 2016, 7, 11242.	12.8	57
114	Molecular Characterization of Macbecin as an Hsp90 Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 2853-2857.	6.4	56
115	The 3D Solution Structure of the C-terminal Region of Ku86 (Ku86CTR). <i>Journal of Molecular Biology</i> , 2004, 335, 573-582.	4.2	55
116	3,6-Diamino-4-(2-halophenyl)-2-benzoylthieno[2,3- <i>b</i> ]pyridine-5-carbonitriles Are Selective Inhibitors of Plasmodium falciparum Glycogen Synthase Kinase-3. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 264-275.	6.4	54
117	RPAP3 provides a flexible scaffold for coupling HSP90 to the human R2TP co-chaperone complex. <i>Nature Communications</i> , 2018, 9, 1501.	12.8	54
118	A second front against AIDS. <i>Nature</i> , 1989, 337, 596-597.	27.8	53
119	Structural Basis of the Radicol Resistance Displayed by a Fungal Hsp90. <i>ACS Chemical Biology</i> , 2009, 4, 289-297.	3.4	53
120	Sensitivity to Hsp90-targeting drugs can arise with mutation to the Hsp90 chaperone, cochaperones and plasma membrane ATP binding cassette transporters of yeast. <i>FEBS Journal</i> , 2003, 270, 4689-4695.	0.2	52
121	Yeast is selectively hypersensitized to heat shock protein 90 (Hsp90)-targeting drugs with heterologous expression of the human Hsp90 <sup>Δ2</sup> , a property that can be exploited in screens for new Hsp90 chaperone inhibitors. <i>Gene</i> , 2003, 302, 165-170.	2.2	51
122	MoKCa database <sup>2</sup> mutations of kinases in cancer. <i>Nucleic Acids Research</i> , 2009, 37, D824-D831.	14.5	51
123	A common conformationally coupled ATPase mechanism for yeast and human cytoplasmic HSP90s. <i>FEBS Journal</i> , 2009, 276, 199-209.	4.7	51
124	Generation of molecular surfaces for graphic display. <i>Journal of Molecular Graphics</i> , 1983, 1, 9-12.	1.1	50
125	Identification and characterisation of 2-aminopyridine inhibitors of checkpoint kinase 2. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 707-718.	3.0	50
126	Differential Regulation of G1 CDK Complexes by the Hsp90-Cdc37 Chaperone System. <i>Cell Reports</i> , 2017, 21, 1386-1398.	6.4	49



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127	Direct Measurement of the Substrate Preference of Uracil-DNA Glycosylase. <i>Journal of Biological Chemistry</i> , 1998, 273, 45-50.	3.4	48
128	The Structure of the R2TP Complex Defines a Platform for Recruiting Diverse Client Proteins to the HSP90 Molecular Chaperone System. <i>Structure</i> , 2017, 25, 1145-1152.e4.	3.3	48
129	The crystal structure of the DNA-binding drug berenil: molecular modelling studies of berenil-DNA complexes. <i>Nucleic Acids Research</i> , 1987, 15, 3469-3478.	14.5	46
130	Chaperone ligand-discrimination by the TPR-domain protein Tah1. <i>Biochemical Journal</i> , 2008, 413, 261-268.	3.7	46
131	Structure-Based Design of Potent and Selective 2-(Quinazolin-2-yl)phenol Inhibitors of Checkpoint Kinase 2. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 580-590.	6.4	46
132	Uracil-DNA glycosylase activities in hyperthermophilic micro-organisms. <i>FEMS Microbiology Letters</i> , 1996, 143, 267-271.	1.8	44
133	Qri2/Nse4, a component of the essential Smc5/6 DNA repair complex. <i>Molecular Microbiology</i> , 2005, 55, 1735-1750.	2.5	43
134	Selective cleavage of glycol bonds by papaya proteinase IV. <i>FEBS Letters</i> , 1990, 260, 195-197.	2.8	42
135	Investigating the protein-protein interactions of the yeast Hsp90 chaperone system by two-hybrid analysis: potential uses and limitations of this approach. <i>Cell Stress and Chaperones</i> , 2004, 9, 359.	2.9	41
136	Phosphorylation-mediated interactions with TOPBP1 couple 53BP1 and 9-1-1 to control the G1 DNA damage checkpoint. <i>ELife</i> , 2019, 8, .	6.0	40
137	Power frequency magnetic field and illness in multistorey blocks. <i>Public Health</i> , 1988, 102, 11-18.	2.9	39
138	The problem with pyrimidines. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 485-487.	8.2	39
139	Restricting direct interaction of CDC37 with HSP90 does not compromise chaperoning of client proteins. <i>Oncogene</i> , 2015, 34, 15-26.	5.9	39
140	Towards meeting the paracelsus challenge: The design, synthesis, and characterization of paracelsin-43, an $\alpha$ -helical protein with over 50% sequence identity to an $\alpha$ - $\beta$ protein. , 1996, 24, 502-513.		36
141	Improving dideoxynucleotide-triphosphate utilisation by the hyper-thermophilic DNA polymerase from the archaeon <i>Pyrococcus furiosus</i> . <i>Nucleic Acids Research</i> , 2000, 28, 1059-1066.	14.5	36
142	Power frequency magnetic field; depressive illness and myocardial infarction. <i>Public Health</i> , 1989, 103, 177-180.	2.9	35
143	Thermostable $\beta$ -Glycosidase from <i>Sulfolobus Solfatarius</i> . <i>Biocatalysis</i> , 1994, 11, 89-103.	0.9	34
144	Combinatorial Domain Hunting: An effective approach for the identification of soluble protein domains adaptable to high-throughput applications. <i>Protein Science</i> , 2006, 15, 2356-2365.	7.6	34

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145	BRCT domains of the DNA damage checkpoint proteins TOPBP1/Rad4 display distinct specificities for phosphopeptide ligands. <i>ELife</i> , 2018, 7, .	6.0	34
146	A novel expression system of domain I of human beta2 glycoprotein I in <i>Escherichia coli</i> . <i>BMC Biotechnology</i> , 2006, 6, 8.	3.3	33
147	An Artemis polymorphic variant reduces Artemis activity and confers cellular radiosensitivity. <i>DNA Repair</i> , 2010, 9, 1003-1010.	2.8	33
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