

Laurence H Pearl

List of Publications by Year in descending order

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223
papers

26,920
citations

4960

84
h-index

6300

158
g-index

251
all docs

251
docs citations

251
times ranked

23432
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the human RAD17-RFC clamp loader and 911 checkpoint clamp bound to a dsDNA/ssDNA junction. <i>Nucleic Acids Research</i> , 2022, 50, 8279-8289.	14.5	13
2	Uncovering an allosteric mode of action for a selective inhibitor of human Bloom syndrome protein. <i>ELife</i> , 2021, 10, .	6.0	18
3	Structural basis for recruitment of the CHK1 DNA damage kinase by the CLASPIN scaffold protein. <i>Structure</i> , 2021, 29, 531-539.e3.	3.3	8
4	Structure of the TELO2-TTI1-TTI2 complex and its function in TOR recruitment to the R2TP chaperone. <i>Cell Reports</i> , 2021, 36, 109317.	6.4	20
5	Phosphorylation-dependent assembly of DNA damage response systems and the central roles of TOPBP1. <i>DNA Repair</i> , 2021, 108, 103232.	2.8	21
6	CK2 Phosphorylation of Human Papillomavirus 16 E2 on Serine 23 Promotes Interaction with TopBP1 and Is Critical for E2 Interaction with Mitotic Chromatin and the Viral Life Cycle. <i>MBio</i> , 2021, 12, e0116321.	4.1	16
7	Solution structure of the Hop TPR2A domain and investigation of target druggability by NMR, biochemical and in silico approaches. <i>Scientific Reports</i> , 2020, 10, 16000.	3.3	8
8	The structure-function relationship of oncogenic LMTK3. <i>Science Advances</i> , 2020, 6, .	10.3	18
9	Modeling of a 14 kDa RUVBL2-Binding Domain with Medium Resolution Cryo-EM Density. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2541-2551.	5.4	3
10	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
11	Structural mechanism for regulation of the AAA-ATPases RUVBL1-RUVBL2 in the R2TP co-chaperone revealed by cryo-EM. <i>Science Advances</i> , 2019, 5, eaaw1616.	10.3	33
12	MDC1 Interacts with TOPBP1 to Maintain Chromosomal Stability during Mitosis. <i>Molecular Cell</i> , 2019, 74, 571-583.e8.	9.7	97
13	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
14	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
15	Advances on the Structure of the R2TP/Prefoldin-like Complex. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1106, 73-83.	1.6	15
16	BRCT domains of the DNA damage checkpoint proteins TOPBP1/Rad4 display distinct specificities for phosphopeptide ligands. <i>ELife</i> , 2018, 7, .	6.0	34
17	Specialized interfaces of Smc5/6 control hinge stability and DNA association. <i>Nature Communications</i> , 2017, 8, 14011.	12.8	61
18	HECTD3 Mediates an HSP90-Dependent Degradation Pathway for Protein Kinase Clients. <i>Cell Reports</i> , 2017, 19, 2515-2528.	6.4	23

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19	Differential Regulation of G1 CDK Complexes by the Hsp90-Cdc37 Chaperone System. <i>Cell Reports</i> , 2017, 21, 1386-1398.	6.4	49
20	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
21	The structure of FKBP38 in complex with the MEEVD tetratricopeptide binding-motif of Hsp90. <i>PLoS ONE</i> , 2017, 12, e0173543.	2.5	25
22	A first generation inhibitor of human Greatwall kinase, enabled by structural and functional characterisation of a minimal kinase domain construct. <i>Oncotarget</i> , 2016, 7, 71182-71197.	1.8	30
23	Mode of action of DNA-competitive small molecule inhibitors of tyrosyl DNA phosphodiesterase 2. <i>Biochemical Journal</i> , 2016, 473, 1869-1879.	3.7	30
24	Review: The HSP90 molecular chaperone—“an enigmatic ATPase. <i>Biopolymers</i> , 2016, 105, 594-607.	2.4	144
25	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
26	PARP3 is a sensor of nicked nucleosomes and monoribosylates histone H2BGlu2. <i>Nature Communications</i> , 2016, 7, 12404.	12.8	60
27	Cooperation of local motions in the Hsp90 molecular chaperone ATPase mechanism. <i>Nature Chemical Biology</i> , 2016, 12, 628-635.	8.0	68
28	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
29	DNA repair, genome stability and cancer: a historical perspective. <i>Nature Reviews Cancer</i> , 2016, 16, 35-42.	28.4	575
30	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
31	ATM Localization and Heterochromatin Repair Depend on Direct Interaction of the 53BP1-BRCT 2 Domain with γ H2AX. <i>Cell Reports</i> , 2015, 13, 2081-2089.	6.4	61
32	Restricting direct interaction of CDC37 with HSP90 does not compromise chaperoning of client proteins. <i>Oncogene</i> , 2015, 34, 15-26.	5.9	39
33	Therapeutic opportunities within the DNA damage response. <i>Nature Reviews Cancer</i> , 2015, 15, 166-180.	28.4	442
34	Tah1 helix-swap dimerization prevents mixed Hsp90 co-chaperone complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1197-1206.	2.5	13
35	Design and discovery of 3-aryl-5-substituted-isoquinolin-1-ones as potent tankyrase inhibitors. <i>MedChemComm</i> , 2015, 6, 1687-1692.	3.4	11
36	Development of an oligonucleotide-based fluorescence assay for the identification of tyrosyl-DNA phosphodiesterase 1 (TDP1) inhibitors. <i>Analytical Biochemistry</i> , 2014, 454, 17-22.	2.4	14

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37	Structural Basis for Phosphorylation-Dependent Recruitment of Tel2 to Hsp90 by Pih1. <i>Structure</i> , 2014, 22, 805-818.	3.3	86
38	Phosphorylation-Dependent Assembly and Coordination of the DNA Damage Checkpoint Apparatus by Rad4TopBP1. <i>Molecular Cell</i> , 2013, 51, 723-736.	9.7	27
39	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
40	ATP-competitive inhibitors block protein kinase recruitment to the Hsp90-Cdc37 system. <i>Nature Chemical Biology</i> , 2013, 9, 307-312.	8.0	132
41	A Mechanism for the Inhibition of DNA-PK-Mediated DNA Sensing by a Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003649.	4.7	94
42	The BAH domain of Rsc2 is a histone H3 binding domain. <i>Nucleic Acids Research</i> , 2013, 41, 9168-9182.	14.5	31
43	Visualization of a DNA-PK/PARP1 complex. <i>Nucleic Acids Research</i> , 2012, 40, 4168-4177.	14.5	89
44	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
45	Engineering human MEK-1 for structural studies: A case study of combinatorial domain hunting. <i>Journal of Structural Biology</i> , 2012, 177, 329-334.	2.8	19
46	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
47	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
48	Targeting the Hsp90 Molecular Chaperone with Novel Macrolactams. Synthesis, Structural, Binding, and Cellular Studies. <i>ACS Chemical Biology</i> , 2011, 6, 1339-1347.	3.4	27
49	Threonine 22 Phosphorylation Attenuates Hsp90 Interaction with Cochaperones and Affects Its Chaperone Activity. <i>Molecular Cell</i> , 2011, 41, 672-681.	9.7	146
50	The Structural Basis for Substrate Recognition by Mammalian Polynucleotide Kinase 3 ^{â€²} Phosphatase. <i>Molecular Cell</i> , 2011, 44, 385-396.	9.7	32
51	Structure of the Ire1 autophosphorylation complex and implications for the unfolded protein response. <i>EMBO Journal</i> , 2011, 30, 894-905.	7.8	201
52	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
53	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
54	Features of the <i>Streptomyces hygrosopicus</i> HtpG reveal how partial geldanamycin resistance can arise with mutation to the ATP binding pocket of a eukaryotic Hsp90. <i>FASEB Journal</i> , 2011, 25, 3828-3837.	0.5	32

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55	A combinatorial method to enable detailed investigation of protein-protein interactions. <i>Future Medicinal Chemistry</i> , 2011, 3, 271-282.	2.3	5
56	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
57	Cyclin-Cyclin-dependent Kinase Regulatory Response Is Linked to Substrate Recognition. <i>Journal of Biological Chemistry</i> , 2011, 286, 9713-9725.	3.4	3
58	p185, an Immunodominant Epitope, Is an Autoantigen Mimotope. <i>Journal of Biological Chemistry</i> , 2011, 286, 26220-26227.	3.4	5
59	Evidence for a remodelling of DNA-PK upon autophosphorylation from electron microscopy studies. <i>Nucleic Acids Research</i> , 2011, 39, 5757-5767.	14.5	20
60	The crystal structure of yeast CCT reveals intrinsic asymmetry of eukaryotic cytosolic chaperonins. <i>EMBO Journal</i> , 2011, 30, 3078-3090.	7.8	94
61	An Artemis polymorphic variant reduces Artemis activity and confers cellular radiosensitivity. <i>DNA Repair</i> , 2010, 9, 1003-1010.	2.8	33
62	Inhibition of Hsp90 with Resorcylic Acid Macrolactones: Synthesis and Binding Studies. <i>Chemistry - A European Journal</i> , 2010, 16, 10366-10372.	3.3	22
63	Identification and characterisation of 2-aminopyridine inhibitors of checkpoint kinase 2. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 707-718.	3.0	50
64	Detection of the ATPase Activity of the Molecular Chaperones Hsp90 and Hsp72 Using the Transcreener [®] , [®] ADP Assay Kit. <i>Journal of Biomolecular Screening</i> , 2010, 15, 279-286.	2.6	29
65	Swe1Wee1-Dependent Tyrosine Phosphorylation of Hsp90 Regulates Distinct Facets of Chaperone Function. <i>Molecular Cell</i> , 2010, 37, 333-343.	9.7	165
66	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
67	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
68	MoKCa database [®] mutations of kinases in cancer. <i>Nucleic Acids Research</i> , 2009, 37, D824-D831.	14.5	51
69	Electron microscopy of Xrcc4 and the DNA ligase IV [®] Xrcc4 DNA repair complex. <i>DNA Repair</i> , 2009, 8, 1380-1389.	2.8	24
70	Structural basis for recruitment of BRCA2 by PALB2. <i>EMBO Reports</i> , 2009, 10, 990-996.	4.5	154
71	A common conformationally coupled ATPase mechanism for yeast and human cytoplasmic HSP90s. <i>FEBS Journal</i> , 2009, 276, 199-209.	4.7	51
72	Structural [®] Thermodynamic Relationships of Interactions in the N-Terminal ATP-Binding Domain of Hsp90. <i>Journal of Molecular Biology</i> , 2009, 392, 923-936.	4.2	19

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73	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
74	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
75	Structural Basis of the Radicicol Resistance Displayed by a Fungal Hsp90. <i>ACS Chemical Biology</i> , 2009, 4, 289-297.	3.4	53
76	Structural and functional coupling of Hsp90- and Sgt1-centred multi-protein complexes. <i>EMBO Journal</i> , 2008, 27, 2789-2798.	7.8	104
77	Activation segment dimerization: a mechanism for kinase autophosphorylation of non-consensus sites. <i>EMBO Journal</i> , 2008, 27, 704-714.	7.8	147
78	4,5-Diarylisoxazole Hsp90 Chaperone Inhibitors: Potential Therapeutic Agents for the Treatment of Cancer. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 196-218.	6.4	386
79	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
80	Optimizing Natural Products by Biosynthetic Engineering: Discovery of Nonquinone Hsp90 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 5494-5497.	6.4	79
81	Molecular Characterization of Macbecin as an Hsp90 Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 2853-2857.	6.4	56
82	The Hsp90 molecular chaperone: an open and shut case for treatment. <i>Biochemical Journal</i> , 2008, 410, 439-453.	3.7	410
83	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
84	Structural and functional analysis of the Crb2—BRCT ₂ domain reveals distinct roles in checkpoint signaling and DNA damage repair. <i>Genes and Development</i> , 2008, 22, 2034-2047.	5.9	65
85	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
86	Chaperone ligand-discrimination by the TPR-domain protein Tah1. <i>Biochemical Journal</i> , 2008, 413, 261-268.	3.7	46
87	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
88	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
89	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
90	Insights into histone code syntax from structural and biochemical studies of CARM1 methyltransferase. <i>EMBO Journal</i> , 2007, 26, 4402-4412.	7.8	117

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91	Structural model of full-length human Ku70-Ku80 heterodimer and its recognition of DNA and DNA-PKcs. <i>EMBO Reports</i> , 2007, 8, 56-62.	4.5	111
92	Activation segment exchange: a common mechanism of kinase autophosphorylation?. <i>Trends in Biochemical Sciences</i> , 2007, 32, 351-356.	7.5	86
93	Structure and Mechanism of the Hsp90 Molecular Chaperone Machinery. <i>Annual Review of Biochemistry</i> , 2006, 75, 271-294.	11.1	988
94	Structural and Mechanistic Insights into Ras Association Domains of Phospholipase C Epsilon. <i>Molecular Cell</i> , 2006, 21, 495-507.	9.7	129
95	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
96	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
97	Structure of an Hsp90-Cdc37-Cdk4 Complex. <i>Molecular Cell</i> , 2006, 23, 697-707.	9.7	288
98	Structure of an archaeal PCNA1-PCNA2-FEN1 complex: elucidating PCNA subunit and client enzyme specificity. <i>Nucleic Acids Research</i> , 2006, 34, 4515-4526.	14.5	64
99	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
100	Crystal structure of an Hsp90-nucleotide-p23/Sba1 closed chaperone complex. <i>Nature</i> , 2006, 440, 1013-1017.	27.8	857
101	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
102	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
103	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
104	Expressed in the Yeast <i>Saccharomyces cerevisiae</i> , Human ERK5 Is a Client of the Hsp90 Chaperone That Complements Loss of the Slt2p (Mpk1p) Cell Integrity Stress-Activated Protein Kinase. <i>Eukaryotic Cell</i> , 2006, 5, 1914-1924.	3.4	60
105	Crystal structure of the proximal BAH domain of the polybromo protein. <i>Biochemical Journal</i> , 2005, 389, 657-664.	3.7	23
106	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
107	Qri2/Nse4, a component of the essential Smc5/6 DNA repair complex. <i>Molecular Microbiology</i> , 2005, 55, 1735-1750.	2.5	43
108	Lupus autoantibodies to native DNA preferentially bind DNA presented on PolIV. <i>Immunology</i> , 2005, 114, 418-427.	4.4	7

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109	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
110	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
111	Chaperoned Ubiquitylationâ€”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
112	Beta-2-glycoprotein specificity of human anti-phospholipid antibody resides on the light chain: a novel mechanism for acquisition of cross-reactivity by an autoantibody. <i>Molecular Immunology</i> , 2005, 42, 39-48.	2.2	3
113	Hsp90 and Cdc37 â€” a chaperone cancer conspiracy. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 55-61.	3.3	238
114	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
115	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
116	Co-chaperone Regulation of Conformational Switching in the Hsp90 ATPase Cycle. <i>Journal of Biological Chemistry</i> , 2004, 279, 51989-51998.	3.4	183
117	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
118	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
119	High-throughput screening assay for inhibitors of heat-shock protein 90 ATPase activity. <i>Analytical Biochemistry</i> , 2004, 327, 176-183.	2.4	192
120	Electron microscopy studies on DNA recognition by DNA-PK. <i>Micron</i> , 2004, 35, 625-633.	2.2	14
121	Plasmodium falciparum 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
122	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
123	Fine binding characteristics of human autoantibodies?partial molecular characterization. <i>Molecular Immunology</i> , 2004, 41, 495-495.	2.2	0
124	Fine binding characteristics of human autoantibodiesâ€”partial molecular characterization. <i>Molecular Immunology</i> , 2004, 41, 495-510.	2.2	4
125	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
126	The Mechanism of Hsp90 Regulation by the Protein Kinase-Specific Cochaperone p50cdc37. <i>Cell</i> , 2004, 116, 87-98.	28.9	319

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127	Structural basis for recruitment of glycogen synthase kinase 3beta to the axin-APC scaffold complex. EMBO Journal, 2003, 22, 494-501.	7.8	269
128	Structural basis for recruitment of translesion DNA polymerase Pol IV/DinB to the Å-clamp. EMBO Journal, 2003, 22, 5883-5892.	7.8	212
129	GSK-3-Selective Inhibitors Derived from Tyrian Purple Indirubins. Chemistry and Biology, 2003, 10, 1255-1266.	6.0	720
130	Sensitivity to Hsp90-targeting drugs can arise with mutation to the Hsp90 chaperone, cochaperones and plasma membrane ATP binding cassette transporters of yeast. FEBS Journal, 2003, 270, 4689-4695.	0.2	52
131	Assays for HSP90 and Inhibitors. , 2003, 85, 149-162.		14
132	Visualization of DNA-induced conformational changes in the DNA repair kinase DNA-PKcs. EMBO Journal, 2003, 22, 5875-5882.	7.8	67
133	Crystal Structure of Alanine:Glyoxylate Aminotransferase and the Relationship Between Genotype and Enzymatic Phenotype in Primary Hyperoxaluria Type 1. Journal of Molecular Biology, 2003, 331, 643-652.	4.2	129
134	Yeast is selectively hypersensitised to heat shock protein 90 (Hsp90)-targetting drugs with heterologous expression of the human Hsp90 α , a property that can be exploited in screens for new Hsp90 chaperone inhibitors. Gene, 2003, 302, 165-170.	2.2	51
135	Anti-cardiolipin β -2 glycoprotein activities co-exist on human anti-DNA antibody light chains. Molecular Immunology, 2003, 40, 517-530.	2.2	7
136	Structural and Functional Analysis of the Middle Segment of Hsp90: Implications for ATP Hydrolysis and Client Protein and Cochaperone Interactions. Molecular Cell, 2003, 11, 647-658.	9.7	434
137	Structure and Specificity of the Vertebrate Anti-Mutator Uracil-DNA Glycosylase SMUG1. Molecular Cell, 2003, 11, 1647-1659.	9.7	127
138	Crystal structure of the Escherichia coli dcm very-short-patch DNA repair endonuclease bound to its reaction product-site in a DNA superhelix. Nucleic Acids Research, 2003, 31, 1633-1639.	14.5	26
139	Structure and Functional Relationships of Hsp90. Current Cancer Drug Targets, 2003, 3, 301-323.	1.6	242
140	An Iron-Sulfur Cluster in the Family 4 Uracil-DNA Glycosylases. Journal of Biological Chemistry, 2002, 277, 16936-16940.	3.4	66
141	Regulation of Hsp90 ATPase Activity by the Co-chaperone Cdc37/p50. Journal of Biological Chemistry, 2002, 277, 20151-20159.	3.4	246
142	Identification of the Axin and Frat Binding Region of Glycogen Synthase Kinase-3. Journal of Biological Chemistry, 2002, 277, 2176-2185.	3.4	112
143	Reciprocal "flipping" underlies substrate recognition and catalytic activation by the human 8-oxo-guanine DNA glycosylase. Journal of Molecular Biology, 2002, 317, 171-177.	4.2	101
144	Glycogen Synthase Kinase-3 Inhibition by Lithium and Beryllium Suggests the Presence of Two Magnesium Binding Sites. Biochemical and Biophysical Research Communications, 2002, 290, 967-972.	2.1	102

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145	Crystal Structure of the CCT ¹ Apical Domain: Implications for Substrate Binding to the Eukaryotic Cytosolic Chaperonin. <i>Journal of Molecular Biology</i> , 2002, 318, 1367-1379.	4.2	72
146	Activation of the ATPase Activity of Hsp90 by the Stress-Regulated Cochaperone Aha1. <i>Molecular Cell</i> , 2002, 10, 1307-1318.	9.7	487
147	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
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