

Laurence H Pearl

List of Publications by Year in descending order

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223
papers

26,920
citations

4942

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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. | 13.5 | 1,203 |
| 2 | Structure and Mechanism of the Hsp90 Molecular Chaperone Machinery. <i>Annual Review of Biochemistry</i> , 2006, 75, 271-294. | 5.0 | 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. | 2.9 | 948 |
| 4 | Crystal structure of an Hsp90 nucleotide-p23/Sba1 closed chaperone complex. <i>Nature</i> , 2006, 440, 1013-1017. | 13.7 | 857 |
| 5 | GSK-3-Selective Inhibitors Derived from Tyrian Purple Indirubins. <i>Chemistry and Biology</i> , 2003, 10, 1255-1266. | 6.2 | 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. | 3.5 | 662 |
| 7 | A structural model for the retroviral proteases. <i>Nature</i> , 1987, 329, 351-354. | 13.7 | 638 |
| 8 | Crystal Structure of Glycogen Synthase Kinase 3 β . <i>Cell</i> , 2001, 105, 721-732. | 13.5 | 610 |
| 9 | DNA repair, genome stability and cancer: a historical perspective. <i>Nature Reviews Cancer</i> , 2016, 16, 35-42. | 12.8 | 575 |
| 10 | Activation of the ATPase Activity of Hsp90 by the Stress-Regulated Cochaperone Aha1. <i>Molecular Cell</i> , 2002, 10, 1307-1318. | 4.5 | 487 |
| 11 | Therapeutic opportunities within the DNA damage response. <i>Nature Reviews Cancer</i> , 2015, 15, 166-180. | 12.8 | 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. | 4.5 | 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. | 0.4 | 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. | 3.5 | 418 |
| 15 | The structural basis of specific base-excision repair by uracil DNA glycosylase. <i>Nature</i> , 1995, 373, 487-493. | 13.7 | 413 |
| 16 | The Hsp90 molecular chaperone: an open and shut case for treatment. <i>Biochemical Journal</i> , 2008, 410, 439-453. | 1.7 | 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. | 2.9 | 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. | 4.5 | 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. | 3.5 | 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. | 2.9 | 343 |
| 21 | The Mechanism of Hsp90 Regulation by the Protein Kinase-Specific Cochaperone p50cdc37. <i>Cell</i> , 2004, 116, 87-98. | 13.5 | 319 |
| 22 | Structure and in vivo function of Hsp90. <i>Current Opinion in Structural Biology</i> , 2000, 10, 46-51. | 2.6 | 294 |
| 23 | Structure of an Hsp90-Cdc37-Cdk4 Complex. <i>Molecular Cell</i> , 2006, 23, 697-707. | 4.5 | 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. | 3.5 | 269 |
| 25 | Structure and function in the uracil-DNA glycosylase superfamily. <i>Mutation Research DNA Repair</i> , 2000, 460, 165-181. | 3.8 | 268 |
| 26 | Regulation of Hsp90 ATPase Activity by the Co-chaperone Cdc37p/p50. <i>Journal of Biological Chemistry</i> , 2002, 277, 20151-20159. | 1.6 | 246 |
| 27 | The active site of aspartic proteinases. <i>FEBS Letters</i> , 1984, 174, 96-101. | 1.3 | 242 |
| 28 | Structure and Functional Relationships of Hsp90. <i>Current Cancer Drug Targets</i> , 2003, 3, 301-323. | 0.8 | 242 |
| 29 | Crystal Structure of a G:T/U Mismatch-Specific DNA Glycosylase. <i>Cell</i> , 1998, 92, 117-129. | 13.5 | 240 |
| 30 | Hsp90 and Cdc37 – a chaperone cancer conspiracy. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 55-61. | 1.5 | 238 |
| 31 | Crystal structure of the Î ² -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. | 2.0 | 235 |
| 32 | Three-dimensional structure, specificity and catalytic mechanism of renin. <i>Nature</i> , 1983, 304, 273-275. | 13.7 | 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. | 1.0 | 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. | 4.5 | 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. | 3.6 | 222 |
| 36 | Recursive PCR: a novel technique for total gene synthesis. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 827-829. | 1.0 | 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. | 3.6 | 214 |
| 39 | Structural basis for recruitment of translesion DNA polymerase Pol IV/DinB to the β -clamp. <i>EMBO Journal</i> , 2003, 22, 5883-5892. | 3.5 | 212 |
| 40 | Structure of the Ire1 autophosphorylation complex and implications for the unfolded protein response. <i>EMBO Journal</i> , 2011, 30, 894-905. | 3.5 | 201 |
| 41 | High-throughput screening assay for inhibitors of heat-shock protein 90 ATPase activity. <i>Analytical Biochemistry</i> , 2004, 327, 176-183. | 1.1 | 192 |
| 42 | Hsp90-Dependent Activation of Protein Kinases Is Regulated by Chaperone-Targeted Dephosphorylation of Cdc37. <i>Molecular Cell</i> , 2008, 31, 886-895. | 4.5 | 184 |
| 43 | Co-chaperone Regulation of Conformational Switching in the Hsp90 ATPase Cycle. <i>Journal of Biological Chemistry</i> , 2004, 279, 51989-51998. | 1.6 | 183 |
| 44 | Structural basis for recruitment of the ATPase activator Aha1 to the Hsp90 chaperone machinery. <i>EMBO Journal</i> , 2004, 23, 1402-1410. | 3.5 | 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. | 2.9 | 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. | 4.5 | 165 |
| 48 | Structural basis for recruitment of the ATPase activator Aha1 to the Hsp90 chaperone machinery. <i>EMBO Journal</i> , 2004, 23, 511-519. | 3.5 | 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. | 2.0 | 154 |
| 51 | Activation segment dimerization: a mechanism for kinase autophosphorylation of non-consensus sites. <i>EMBO Journal</i> , 2008, 27, 704-714. | 3.5 | 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. | 4.5 | 146 |
| 54 | Review: The HSP90 molecular chaperone—“an enigmatic ATPase. <i>Biopolymers</i> , 2016, 105, 594-607. | 1.2 | 144 |

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| 55 | High resolution X-ray analyses of renin inhibitor-aspartic proteinase complexes. <i>Nature</i> , 1987, 327, 349-352. | 13.7 | 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. | 1.9 | 141 |
| 57 | Regulation of DNA Replication through Sld3-Dpb11 Interaction Is Conserved from Yeast to Humans. <i>Current Biology</i> , 2011, 21, 1152-1157. | 1.8 | 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. | 4.5 | 134 |
| 59 | ATP-competitive inhibitors block protein kinase recruitment to the Hsp90-Cdc37 system. <i>Nature Chemical Biology</i> , 2013, 9, 307-312. | 3.9 | 132 |
| 60 | Trans-activation of the DNA-damage signalling protein kinase Chk2 by T-loop exchange. <i>EMBO Journal</i> , 2006, 25, 3179-3190. | 3.5 | 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. | 2.0 | 129 |
| 62 | Structural and Mechanistic Insights into Ras Association Domains of Phospholipase C Epsilon. <i>Molecular Cell</i> , 2006, 21, 495-507. | 4.5 | 129 |
| 63 | Structure and Specificity of the Vertebrate Anti-Mutator Uracil-DNA Glycosylase SMUG1. <i>Molecular Cell</i> , 2003, 11, 1647-1659. | 4.5 | 127 |
| 64 | Crystal Structure of an Octameric RuvA-Holliday Junction Complex. <i>Molecular Cell</i> , 1998, 2, 361-372. | 4.5 | 126 |
| 65 | Crystal structure of a thwarted mismatch glycosylase DNA repair complex. <i>EMBO Journal</i> , 1999, 18, 6599-6609. | 3.5 | 122 |
| 66 | X-ray analyses of aspartic proteinases. <i>Journal of Molecular Biology</i> , 1990, 211, 919-941. | 2.0 | 120 |
| 67 | Insights into histone code syntax from structural and biochemical studies of CARM1 methyltransferase. <i>EMBO Journal</i> , 2007, 26, 4402-4412. | 3.5 | 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. | 1.6 | 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. | 4.5 | 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. | 0.4 | 111 |
| 71 | Structural model of full-length human Ku70-Ku80 heterodimer and its recognition of DNA and DNA- ϵ PKcs. <i>EMBO Reports</i> , 2007, 8, 56-62. | 2.0 | 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. | 4.5 | 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. | 3.5 | 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. | 1.0 | 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. | 2.0 | 101 |
| 76 | Crystal structure of the catalytic fragment of murine poly(ADP-ribose) polymerase-2. <i>Nucleic Acids Research</i> , 2004, 32, 456-464. | 6.5 | 101 |
| 77 | Three-Dimensional Structure and Regulation of the DNA-Dependent Protein Kinase Catalytic Subunit (DNA-PKcs). <i>Structure</i> , 2005, 13, 243-255. | 1.6 | 98 |
| 78 | MDC1 Interacts with TOPBP1 to Maintain Chromosomal Stability during Mitosis. <i>Molecular Cell</i> , 2019, 74, 571-583.e8. | 4.5 | 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. | 0.4 | 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. | 1.1 | 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. | 1.2 | 94 |
| 82 | The crystal structure of yeast CCT reveals intrinsic asymmetry of eukaryotic cytosolic chaperonins. <i>EMBO Journal</i> , 2011, 30, 3078-3090. | 3.5 | 94 |
| 83 | A Mechanism for the Inhibition of DNA-PK-Mediated DNA Sensing by a Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003649. | 2.1 | 94 |
| 84 | Visualization of a DNA-PK/PARP1 complex. <i>Nucleic Acids Research</i> , 2012, 40, 4168-4177. | 6.5 | 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. | 3.6 | 87 |
| 86 | Activation segment exchange: a common mechanism of kinase autophosphorylation?. <i>Trends in Biochemical Sciences</i> , 2007, 32, 351-356. | 3.7 | 86 |
| 87 | Structural Basis for Phosphorylation-Dependent Recruitment of Tel2 to Hsp90 by Pih1. <i>Structure</i> , 2014, 22, 805-818. | 1.6 | 86 |
| 88 | Crystal structure and induction mechanism of AmiC-AmiR: a ligand-regulated transcription antitermination complex. <i>EMBO Journal</i> , 1999, 18, 5175-5186. | 3.5 | 83 |
| 89 | Optimizing Natural Products by Biosynthetic Engineering: Discovery of Nonquinone Hsp90 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 5494-5497. | 2.9 | 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. | 6.5 | 75 |

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| 91 | Crystal Structure of the CCT ³ Apical Domain: Implications for Substrate Binding to the Eukaryotic Cytosolic Chaperonin. <i>Journal of Molecular Biology</i> , 2002, 318, 1367-1379. | 2.0 | 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. | 6.5 | 72 |
| 93 | Enzyme thermostability and thermoactivity. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 629-630. | 1.0 | 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. | 4.5 | 68 |
| 95 | Cooperation of local motions in the Hsp90 molecular chaperone ATPase mechanism. <i>Nature Chemical Biology</i> , 2016, 12, 628-635. | 3.9 | 68 |
| 96 | Visualization of DNA-induced conformational changes in the DNA repair kinase DNA-PKcs. <i>EMBO Journal</i> , 2003, 22, 5875-5882. | 3.5 | 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. | 4.5 | 67 |
| 98 | An Iron-Sulfur Cluster in the Family 4 Uracil-DNA Glycosylases. <i>Journal of Biological Chemistry</i> , 2002, 277, 16936-16940. | 1.6 | 66 |
| 99 | Regulation of protein kinases in insulin, growth factor and Wnt signalling. <i>Current Opinion in Structural Biology</i> , 2002, 12, 761-767. | 2.6 | 66 |
| 100 | Structural and functional analysis of the Crb2 ^{BRCT} domain reveals distinct roles in checkpoint signaling and DNA damage repair. <i>Genes and Development</i> , 2008, 22, 2034-2047. | 2.7 | 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. | 3.9 | 65 |
| 102 | Structure of an archaeal PCNA1 ^{PCNA2} ^{FEN1} complex: elucidating PCNA subunit and client enzyme specificity. <i>Nucleic Acids Research</i> , 2006, 34, 4515-4526. | 6.5 | 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. | 6.2 | 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. | 1.6 | 63 |
| 105 | Crystal structure of the fission yeast mitochondrial Holliday junction resolvase Ydc2. <i>EMBO Journal</i> , 2001, 20, 6601-6611. | 3.5 | 62 |
| 106 | ATM Localization and Heterochromatin Repair Depend on Direct Interaction of the 53BP1-BRCT 2 Domain with ³ H2AX. <i>Cell Reports</i> , 2015, 13, 2081-2089. | 2.9 | 61 |
| 107 | Specialized interfaces of Smc5/6 control hinge stability and DNA association. <i>Nature Communications</i> , 2017, 8, 14011. | 5.8 | 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 ^{Glu2} . <i>Nature Communications</i> , 2016, 7, 12404. | 5.8 | 60 |
| 110 | Molecular modelling of the interactions of tetra-(4-N-methylpyridyl) porphin with TA and CG sites on DNA. <i>Nucleic Acids Research</i> , 1987, 15, 6553-6562. | 6.5 | 59 |
| 111 | The catalytic mechanism of aspartic proteinases. <i>FEBS Letters</i> , 1987, 214, 8-12. | 1.3 | 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. | 2.9 | 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. | 5.8 | 57 |
| 114 | Molecular Characterization of Macbecin as an Hsp90 Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 2853-2857. | 2.9 | 56 |
| 115 | The 3D Solution Structure of the C-terminal Region of Ku86 (Ku86CTR). <i>Journal of Molecular Biology</i> , 2004, 335, 573-582. | 2.0 | 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. | 2.9 | 54 |
| 117 | RPAP3 provides a flexible scaffold for coupling HSP90 to the human R2TP co-chaperone complex. <i>Nature Communications</i> , 2018, 9, 1501. | 5.8 | 54 |
| 118 | A second front against AIDS. <i>Nature</i> , 1989, 337, 596-597. | 13.7 | 53 |
| 119 | Structural Basis of the Radicol Resistance Displayed by a Fungal Hsp90. <i>ACS Chemical Biology</i> , 2009, 4, 289-297. | 1.6 | 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 ^{Δ2} , a property that can be exploited in screens for new Hsp90 chaperone inhibitors. <i>Gene</i> , 2003, 302, 165-170. | 1.0 | 51 |
| 122 | MoKCa database ² mutations of kinases in cancer. <i>Nucleic Acids Research</i> , 2009, 37, D824-D831. | 6.5 | 51 |
| 123 | A common conformationally coupled ATPase mechanism for yeast and human cytoplasmic HSP90s. <i>FEBS Journal</i> , 2009, 276, 199-209. | 2.2 | 51 |
| 124 | Generation of molecular surfaces for graphic display. <i>Journal of Molecular Graphics</i> , 1983, 1, 9-12. | 1.7 | 50 |
| 125 | Identification and characterisation of 2-aminopyridine inhibitors of checkpoint kinase 2. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 707-718. | 1.4 | 50 |
| 126 | Differential Regulation of G1 CDK Complexes by the Hsp90-Cdc37 Chaperone System. <i>Cell Reports</i> , 2017, 21, 1386-1398. | 2.9 | 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. | 1.6 | 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. | 1.6 | 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. | 6.5 | 46 |
| 130 | Chaperone ligand-discrimination by the TPR-domain protein Tah1. <i>Biochemical Journal</i> , 2008, 413, 261-268. | 1.7 | 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. | 2.9 | 46 |
| 132 | Uracil-DNA glycosylase activities in hyperthermophilic micro-organisms. <i>FEMS Microbiology Letters</i> , 1996, 143, 267-271. | 0.7 | 44 |
| 133 | Qri2/Nse4, a component of the essential Smc5/6 DNA repair complex. <i>Molecular Microbiology</i> , 2005, 55, 1735-1750. | 1.2 | 43 |
| 134 | Selective cleavage of glycol bonds by papaya proteinase IV. <i>FEBS Letters</i> , 1990, 260, 195-197. | 1.3 | 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. | 1.2 | 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, . | 2.8 | 40 |
| 137 | Power frequency magnetic field and illness in multistorey blocks. <i>Public Health</i> , 1988, 102, 11-18. | 1.4 | 39 |
| 138 | The problem with pyrimidines. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 485-487. | 3.6 | 39 |
| 139 | Restricting direct interaction of CDC37 with HSP90 does not compromise chaperoning of client proteins. <i>Oncogene</i> , 2015, 34, 15-26. | 2.6 | 39 |
| 140 | Towards meeting the paracelsus challenge: The design, synthesis, and characterization of paracelsin-43, an α -helical protein with over 50% sequence identity to an α - β 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. | 6.5 | 36 |
| 142 | Power frequency magnetic field; depressive illness and myocardial infarction. <i>Public Health</i> , 1989, 103, 177-180. | 1.4 | 35 |
| 143 | Thermostable β -Glycosidase from <i>Sulfolobus Solfataricus</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. | 3.1 | 34 |

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