Paul A Bates

List of Publications by Year
in descending order

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194	13,222	25034	26613
papers	citations	57 h-index	107 g-index

235	235	235	17211
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Spatial patterns of tumour growth impact clonal diversification in a computational model and the TRACERx Renal study. Nature Ecology and Evolution, 2022, 6, 88-102.	7.8	30
2	Emergence of novel cephalopod gene regulation and expression through large-scale genome reorganization. Nature Communications, 2022, 13, 2172.	12.8	21
3	Application of deep learning methods: From molecular modelling to patient classification. Experimental Cell Research, 2022, 418, 113278.	2.6	3
4	Comparison of loop extrusion and diffusion capture as mitotic chromosome formation pathways in fission yeast. Nucleic Acids Research, 2021, 49, 1294-1312.	14.5	27
5	A FIJI macro for quantifying pattern in extracellular matrix. Life Science Alliance, 2021, 4, e202000880.	2.8	75
6	Toward Patient-Specific Prediction of Ablation Strategies for Atrial Fibrillation Using Deep Learning. Frontiers in Physiology, 2021, 12, 674106.	2.8	13
7	Selection of metastasis competent subclones in the tumour interior. Nature Ecology and Evolution, 2021, 5, 1033-1045.	7.8	50
8	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	2.6	73
9	Extracellular matrix anisotropy is determined by TFAP2C-dependent regulation of cell collisions. Nature Materials, 2020, 19, 227-238.	27.5	82
10	Enhanced sampling of protein conformational states for dynamic crossâ€docking within the proteinâ€protein docking server SwarmDock. Proteins: Structure, Function and Bioinformatics, 2020, 88, 962-972.	2.6	16
11	Fission yeast condensin contributes to interphase chromatin organization and prevents transcription-coupled DNA damage. Genome Biology, 2020, 21, 272.	8.8	19
12	Butyrophilin-2A1 Directly Binds Germline-Encoded Regions of the Vγ9Vδ2 TCR and Is Essential for Phosphoantigen Sensing. Immunity, 2020, 52, 487-498.e6.	14.3	164
13	A Guide for Proteinâ€“Protein Docking Using SwarmDock. Methods in Molecular Biology, 2020, 2165, 199-216.	0.9	1
14	Development of a Deep Learning Method to Predict Optimal Ablation Patterns for Atrial Fibrillation. , 2019, , .		3
15	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
16	Matrix feedback enables diverse higher-order patterning of the extracellular matrix. PLoS Computational Biology, 2019, 15, e1007251.	3.2	20
17	Refinement of proteinâ€protein complexes in contact map space with metadynamics simulations. Proteins: Structure, Function and Bioinformatics, 2019, 87, 12-22.	2.6	13
18	Flexible Protein-Protein Docking with SwarmDock. Methods in Molecular Biology, 2018, 1764, 413-428.	0.9	20

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19	The Î³Î´TCR combines innate immunity with adaptive immunity by utilizing spatially distinct regions for agonist selection and antigen responsiveness. Nature Immunology, 2018, 19, 1352-1365.	14.5	163
20	Predicting improved protein conformations with a temporal deep recurrent neural network. PLoS ONE, 2018, 13, e0202652.	2.5	14
21	A machine learning approach for ranking clusters of docked proteinâ€protein complexes by pairwise cluster comparison. Proteins: Structure, Function and Bioinformatics, 2017, 85, 528-543.	2.6	18
22	IRaPPA: information retrieval based integration of biophysical models for protein assembly selection. Bioinformatics, 2017, 33, 1806-1813.	4.1	36
23	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
24	Optimisation of a Molecular Dynamics Simulation of Chromosome Condensation. , 2016, , .		0
25	Extracellular matrix anisotropy in breast cancer invasion and metastasis. European Journal of Cancer, 2016, 61, S102.	2.8	0
26	Ctf4 Links DNA Replication with Sister Chromatid Cohesion Establishment by Recruiting the Chl1 Helicase to the Replisome. Molecular Cell, 2016, 63, 371-384.	9.7	113
27	Opposing effects of Elk-1 multisite phosphorylation shape its response to ERK activation. Science, 2016, 354, 233-237.	12.6	100
28	Costâ€“benefit analysis of the mechanisms that enable migrating cells to sustain motility upon changes in matrix environments. Journal of the Royal Society Interface, 2015, 12, 20141355.	3.4	26
29	SETD2 loss-of-function promotes renal cancer branched evolution through replication stress and impaired DNA repair. Oncogene, 2015, 34, 5699-5708.	5.9	147
30	The structural basis for enhancerâ€dependent assembly and activation of the AAA transcriptional activator NorR. Molecular Microbiology, 2015, 95, 17-30.	2.5	13
31	Updates to the Integrated Proteinâ€“Protein Interaction Benchmarks: Docking Benchmark Version 5 and Affinity Benchmark Version 2. Journal of Molecular Biology, 2015, 427, 3031-3041.	4.2	348
32	Relapse models for clear cell renal carcinoma. Lancet Oncology, The, 2015, 16, e376-e378.	10.7	3
33	STRIPAK components determine mode of cancer cell migration and metastasis. Nature Cell Biology, 2015, 17, 68-80.	10.3	158
34	A simple biophysical model emulates budding yeast chromosome condensation. ELife, 2015, 4, e05565.	6.0	87
35	Development of synchronous VHL syndrome tumors reveals contingencies and constraints to tumor evolution. Genome Biology, 2014, 15, 433.	8.8	69
36	Systematic Evaluation of the Prognostic Impact and Intratumour Heterogeneity of Clear Cell Renal Cell Carcinoma Biomarkers. European Urology, 2014, 66, 936-948.	1.9	141

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37	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. Nature Genetics, 2014, 46, 225-233.	21.4	1,103
38	Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632.	2.6	50
39	Predicting the Structure of Proteinâ€“Protein Complexes Using the SwarmDock Web Server. Methods in Molecular Biology, 2014, 1137, 181-197.	0.9	27
40	SwarmDock: a server for flexible proteinâ€“protein docking. Bioinformatics, 2013, 29, 807-809.	4.1	259
41	Modeling protein association mechanisms and kinetics. Current Opinion in Structural Biology, 2013, 23, 887-893.	5.7	87
42	The scoring of poses in protein-protein docking: current capabilities and future directions. BMC Bioinformatics, 2013, 14, 286.	2.6	98
43	Matrix geometry determines optimal cancer cell migration strategy and modulates response to interventions. Nature Cell Biology, 2013, 15, 751-762.	10.3	282
44	Cancer networks and beyond: Interpreting mutations using the human interactome and protein structure. Seminars in Cancer Biology, 2013, 23, 219-226.	9.6	23
45	RaTrav: a tool for calculating mean first-passage times on biochemical networks. BMC Systems Biology, 2013, 7, 130.	3.0	3
46	Characterizing Changes in the Rate of Protein-Protein Dissociation upon Interface Mutation Using Hotspot Energy and Organization. PLoS Computational Biology, 2013, 9, e1003216.	3.2	29
47	A Markovâ€chain model description of binding funnels to enhance the ranking of docked solutions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2143-2149.	2.6	32
48	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87
49	A Structural Systems Biology Approach for Quantifying the Systemic Consequences of Missense Mutations in Proteins. PLoS Computational Biology, 2012, 8, e1002738.	3.2	19
50	Understanding cancer mechanisms through network dynamics. Briefings in Functional Genomics, 2012, 11, 543-560.	2.7	35
51	Kinetic Rate Constant Prediction Supports the Conformational Selection Mechanism of Protein Binding. PLoS Computational Biology, 2012, 8, e1002351.	3.2	48
52	Mean first-passage time calculations: comparison of the deterministic Hillâ€™s algorithm with Monte Carlo simulations. European Physical Journal B, 2012, 85, 1.	1.5	2
53	Rational engineering of L-asparaginase reveals importance of dual activity for cancer cell toxicity. Blood, 2011, 117, 1614-1621.	1.4	122
54	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131

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55	An siRNA screen identifies RSK1 as a key modulator of lung cancer metastasis. Oncogene, 2011, 30, 3513-3521.	5.9	78
56	A structureâ€based benchmark for proteinâ€“protein binding affinity. Protein Science, 2011, 20, 482-491.	7.6	252
57	Planar polarization of the atypical myosin Dachs orients cell divisions in Drosophila. Genes and Development, 2011, 25, 131-136.	5.9	205
58	Proteinâ€“protein binding affinity prediction on a diverse set of structures. Bioinformatics, 2011, 27, 3002-3009.	4.1	103
59	Abstract LB-356: An siRNA screen identifies Rsk1 as a key modulator of lung cancer metastasis. , 2011, , .		1
60	Bridging the gaps: atomic simulation of macromolecular environment brings together protein docking, interaction kinetics and the crowding effects. BMC Bioinformatics, 2010, 11, .	2.6	1
61	Detection and refinement of encounter complexes for proteinâ€“protein docking: Taking account of macromolecular crowding. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3189-3196.	2.6	59
62	SwarmDock and the Use of Normal Modes in Protein-Protein Docking. International Journal of Molecular Sciences, 2010, 11, 3623-3648.	4.1	154
63	Mechanism of Cohesin Loading onto Chromosomes: A Conformational Dynamics Study. Biophysical Journal, 2010, 99, 1212-1220.	0.5	10
64	A dyad of lymphoblastic lysosomal cysteine proteases degrades the antileukemic drug l-asparaginase. Journal of Clinical Investigation, 2009, 119, 1964-73.	8.2	69
65	Tipping the Balance: Robustness of Tip Cell Selection, Migration and Fusion in Angiogenesis. PLoS Computational Biology, 2009, 5, e1000549.	3.2	187
66	Agent-based simulation of notch-mediated tip cell selection in angiogenic sprout initialisation. Journal of Theoretical Biology, 2008, 250, 25-36.	1.7	234
67	Alternating evolutionary pressure in a genetic algorithm facilitates protein model selection. BMC Structural Biology, 2008, 8, 34.	2.3	14
68	Mathematical modeling identifies Smad nucleocytoplasmic shuttling as a dynamic signal-interpreting system. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6608-6613.	7.1	168
69	Flexible relaxation of rigid-body docking solutions. Proteins: Structure, Function and Bioinformatics, 2007, 68, 159-169.	2.6	44
70	Implicit flexibility in protein docking: Crossâ€docking and local refinement. Proteins: Structure, Function and Bioinformatics, 2007, 69, 750-757.	2.6	53
71	Repair of alkylated DNA: Recent advances. DNA Repair, 2007, 6, 429-442.	2.8	262
72	Lymphoblasts Produce a Lysosomal Protease That Rapidly Degrades L-Asparaginase - Implications for Therapy in Childhood Acute Lymphoblastic Leukemia.. Blood, 2007, 110, 2791-2791.	1.4	0

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73	Probability-based model of protein-protein interactions on biological timescales. Algorithms for Molecular Biology, 2006, 1, 25.	1.2	7
74	Macroscopic pKa Calculations for Fluorescein and Its Derivatives. Journal of Chemical Theory and Computation, 2006, 2, 1520-1529.	5.3	49
75	Cluster analysis of networks generated through homology: automatic identification of important protein communities involved in cancer metastasis. BMC Bioinformatics, 2006, 7, 2.	2.6	148
76	Can MM-PBSA calculations predict the specificities of protein kinase inhibitors?. Journal of Computational Chemistry, 2006, 27, 1990-2007.	3.3	55
77	Global topological features of cancer proteins in the human interactome. Bioinformatics, 2006, 22, 2291-2297.	4.1	458
78	Developing a move-set for protein model refinement. Bioinformatics, 2006, 22, 1838-1845.	4.1	19
79	Incorporation of flexibility into rigid-body docking: Applications in rounds 3-5 of CAPRI. Proteins: Structure, Function and Bioinformatics, 2005, 60, 263-268.	2.6	29
80	The Relationship between the Flexibility of Proteins and their Conformational States on Forming Proteinâ€“Protein Complexes with an Application to Proteinâ€“Protein Docking. Journal of Molecular Biology, 2005, 347, 1077-1101.	4.2	159
81	Recognition of Phosphorylated-Smad2-Containing Complexes by a Novel Smad Interaction Motif. Molecular and Cellular Biology, 2004, 24, 1106-1121.	2.3	59
82	A link between sequence conservation and domain motion within the AAA+ family. Journal of Structural Biology, 2004, 146, 189-204.	2.8	21
83	Guided docking: First step to locate potential binding sites. Proteins: Structure, Function and Bioinformatics, 2003, 52, 28-32.	2.6	30
84	Novel use of a genetic algorithm for protein structure prediction: Searching template and sequence alignment space. Proteins: Structure, Function and Bioinformatics, 2003, 53, 424-429.	2.6	29
85	OPCML at 11q25 is epigenetically inactivated and has tumor-suppressor function in epithelial ovarian cancer. Nature Genetics, 2003, 34, 337-343.	21.4	169
86	Functional Recycling of C2 Domains Throughout Evolution: A Comparative Study of Synaptotagmin, Protein Kinase C and Phospholipase C by Sequence, Structural and Modelling Approaches. Journal of Molecular Biology, 2003, 333, 621-639.	4.2	33
87	Structural Context of Exons in Protein Domains: Implications for Protein Modelling and Design. Journal of Molecular Biology, 2003, 333, 1045-1059.	4.2	9
88	In silico Protein Recombination: Enhancing Template and Sequence Alignment Selection for Comparative Protein Modelling. Journal of Molecular Biology, 2003, 328, 593-608.	4.2	39
89	Reversal of DNA alkylation damage by two human dioxygenases. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16660-16665.	7.1	357
90	Different Smad2 partners bind a common hydrophobic pocket in Smad2 via a defined proline-rich motif. EMBO Journal, 2002, 21, 145-156.	7.8	84

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91	Comparative modelling: an essential methodology for protein structure prediction in the post-genomic era. Applied Bioinformatics, 2002, 1, 177-90.	1.6	18
92	A region encompassing the FERM domain of Jak1 is necessary for binding to the cytokine receptor gp130. FEBS Letters, 2001, 505, 87-91.	2.8	43
93	BRCT Domain Interactions in the Heterodimeric DNA Repair Protein XRCC1â^'DNA Ligase III. Biochemistry, 2001, 40, 5906-5913.	2.5	59
94	Enhancement of protein modeling by human intervention in applying the automatic programs 3D-JIGSAW and 3D-PSSM. Proteins: Structure, Function and Bioinformatics, 2001, 45, 39-46.	2.6	504
95	The second domain of intercellular adhesion molecule-1 (ICAM-1) maintains the structural integrity of the leucocyte function-associated antigen-1 (LFA-1) ligand-binding site in the first domain. Biochemical Journal, 2000, 351, 79.	3.7	9
96	The second domain of intercellular adhesion molecule-1 (ICAM-1) maintains the structural integrity of the leucocyte function-associated antigen-1 (LFA-1) ligand-binding site in the first domain. Biochemical Journal, 2000, 351, 79-86.	3.7	13
97	The BRCA1 C-terminal domain: structure and function. Mutation Research DNA Repair, 2000, 460, 319-332.	3.7	128
98	Structure of the AAA ATPase p97. Molecular Cell, 2000, 6, 1473-1484.	9.7	394
99	Genetic analysis of integrin function in man: LAD-1 and other syndromes. Matrix Biology, 2000, 19, 211-222.	3.6	94
100	Conserved Residues of Human XPG Protein Important for Nuclease Activity and Function in Nucleotide Excision Repair. Journal of Biological Chemistry, 1999, 274, 5637-5648.	3.4	100
101	Humanisation and characterisation of PR1A3, a monoclonal antibody specific for cell-bound carcinoembryonic antigen. Cancer Immunology, Immunotherapy, 1999, 47, 299-306.	4.2	17
102	Model building by comparison at CASP3: Using expert knowledge and computer automation. Proteins: Structure, Function and Bioinformatics, 1999, 37, 47-54.	2.6	138
103	Model building by comparison at CASP3: Using expert knowledge and computer automation. Proteins: Structure, Function and Bioinformatics, 1999, 37, 47-54.	2.6	27
104	Model building by comparison at CASP3: Using expert knowledge and computer automation. Proteins: Structure, Function and Bioinformatics, 1999, 37, 47-54.	2.6	53
105	Structure of an XRCC1 BRCT domain: a new protein-protein interaction module. EMBO Journal, 1998, 17, 6404-6411.	7.8	223
106	Automated classification of antibody complementarity determining region 3 of the heavy chain (H3) loops into canonical forms and its application to protein structure prediction. Journal of Molecular Biology, 1998, 279, 1193-1210.	4.2	80
107	Crystal structure at 1.95 Ã¥ resolution of the breast tumour-specific antibody SM3 complexed with its peptide epitope reveals novel hypervariable loop recognition. Journal of Molecular Biology, 1998, 284, 713-728.	4.2	72
108	Conformational analysis of the first observed non-proline cis-peptide bond occurring within the complementarity determining region (CDR) of an antibody. Journal of Molecular Biology, 1998, 284, 549-555.	4.2	21

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109	The I Domain of Integrin Leukocyte Function-associated Antigen-1 Is Involved in a Conformational Change Leading to High Affinity Binding to Ligand Intercellular Adhesion Molecule 1 (ICAM-1). Journal of Biological Chemistry, 1998, 273, 27396-27403.	3.4	84
110	An automated classification of the structure of protein loops. Journal of Molecular Biology, 1997, 266, 814-830.	4.2	189
111	Recognition of analogous and homologous protein folds: analysis of sequence and structure conservation 1 1Edited by F. E. Cohen. Journal of Molecular Biology, 1997, 269, 423-439.	4.2	204
112	Model building by comparison: A combination of expert knowledge and computer automation. Proteins: Structure, Function and Bioinformatics, 1997, 29, 59-67.	2.6	12
113	Model building by comparison: A combination of expert knowledge and computer automation. Proteins: Structure, Function and Bioinformatics, 1997, 29, 59-67.	2.6	3
114	Analysis of the Binding Site on Intercellular Adhesion Molecule 3 for the Leukocyte Integrin Lymphocyte Function-associated Antigen 1. Journal of Biological Chemistry, 1995, 270, 877-884.	3.4	68
115	The protein folding problem and tertiary structure prediction. Trends in Biochemical Sciences, 1995, 20, 129-130.	7.5	0
116	Protein Determinants for Specific Polysialylation of the Neural Cell Adhesion Molecule. Journal of Biological Chemistry, 1995, 270, 17171-17179.	3.4	115
117	PECAM-1: Its Expression and Function as a Cell Adhesion Molecule on Hemopoietic and Endothelial Cells. Leukemia and Lymphoma, 1995, 17, 229-244.	1.3	134
118	Characterisation of the single copy trefoil peptides intestinal trefoil factor and pS2 and their ability to form covalent dimers. FEBS Letters, 1995, 357, 50-54.	2.8	54
119	Prediction of the three dimensional structure of activin. , 1995, , 214-216.		0
120	The sticking point: how integrins bind to their ligands. Trends in Cell Biology, 1994, 4, 379-382.	7.9	20
121	Structure of debrisoquinium sulfate. Acta Crystallographica Section C: Crystal Structure Communications, 1993, 49, 300-303.	0.4	2
122	Interations of the Plasmodium falciparumâ€"Infected Erythrocyte with ICAM-1. , 1993, , 92-103.		0
123	Towards an automatic method of predicting protein stucture by homology: an evaluation of suboptimal sequence alignments. Protein Engineering, Design and Selection, 1992, 5, 305-311.	2.1	19
124	Electron acceptor molecules: new, expedient synthesis of substituted 7,7,8,8-tetracyano-p-quinodimethane (TCNQ) derivatives and the X-ray crystal structure of 2,5-dibromo-TCNQ. Journal of the Chemical Society Perkin Transactions 1, 1992, , 611.	0.9	5
125	The binding site on ICAM-1 for plasmodium falciparum-infected erythrocytes overlaps, but is distinct from, the LFA-1-binding site. Cell, 1992, 68, 71-81.	28.9	277
126	A predicted three-dimensional structure for the carcinoembryonic antigen (CEA). FEBS Letters, 1992, 301, 207-214.	2.8	60

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127	Structure and Function of Intercellular Adhesion Molecule-1. Chemical Immunology and Allergy, 1991, 50, 98-115.	1.7	19
128	Structure and Function of Intercellular Adhesion Molecule-1. Chemical Immunology and Allergy, 1991, 50, 98-115.	1.7	33
129	Hydrogen bonding between free fluoride ions and water molecules: two X-ray structures. Journal of Molecular Structure, 1990, 220, 1-12.	3.6	31
130	The syntheses, structures, and stereodynamics of [3]-ferrocenophane complexes III. Rhenium tricarbonyl halide complexes, fac-[ReX(CO)3(C5H4ECH3)2Fe] (X î—» Cl, Br, I; E î—» S, Se). Crystal structure of chloro-1,1â€²-bis(methylthio)ferrocenetricarbonylrhenium. Journal of Organometallic Chemistry, 1990, 383, 253-269.	1.8	22
131	The syntheses, structures and stereodynamics of transition metal complexes of 1,1â€²-bis(methylthio)ruthenocene. Crystal structure of 1,1â€²-bis(methylthio)ruthenocene tetracarbonyltungsten. Journal of Organometallic Chemistry, 1990, 394, 455-468.	1.8	19
132	Cephalotaxine analogs: stereospecific synthesis of spiro-fused 3-benzazepine and 1,3-benzodiazepine derivatives. Journal of Organic Chemistry, 1990, 55, 1261-1266.	3.2	37
133	The heteronuclear cluster chemistry of the Group 1B metals. Part 13. Synthesis and structural characterization of the bimetallic hexanuclear Group 1B metal cluster compounds [M2Ru4(Âµ-CO)3(CO)10(PPh3)2] (M = Cu, Ag, or Au). X-Ray structure analyses of [M2Ru4(Âµ-CO)3(CO)10(PPh3)2] (M = Cu or Ag). Journal of the Chemical Society Dalton Transactions, 1990, , 799-805.	1.1	7
134	A predicted three-dimensional structure for the human immunodeficiency virus binding domains of CD4 antigen. Protein Engineering, Design and Selection, 1989, 3, 13-21.	2.1	24
135	Mixed-valence linear-chain complexes: X-ray structural characterization of a PdII/PdIVBr2 chain and of three mixed-metal chains, [NiPt(en)4Cl2]4+, [PdPt(pn)4Cl2]4+ and [NiPt(pn)4Cl2]4+, all as perchlorate salts. Acta Crystallographica Section B: Structural Science, 1989, 45, 147-152.	1.8	12
136	Fluoride-water hydrogen bonding: X-ray structure of tris(ethylenediamine)zinc(II) fluoride dihydrate. Inorganica Chimica Acta, 1989, 165, 191-195.	2.4	10
137	Î²-Diketone interactions. Journal of Molecular Structure, 1989, 196, 249-255.	3.6	5
138	The syntheses, structures, and stereodynamics of [3]ferrocenophane complexes. Journal of Organometallic Chemistry, 1989, 367, 275-289.	1.8	36
139	Cationic but-2-yne complexes of tungsten(II). Preparation and spectral properties of [WI(CO)L(dppm)(Î·2-MeC2Me)][BF4] (L = neutral monodentate oxygen and sulphur donor ligands). Crystal structure of [WI(CO){SC(NH2)2}(dppm)-(Î·2-MeC2Me)][ClO4]. Journal of Organometallic Chemistry, 1989, 372, 263-272.	1.8	12
140	The structure of 2,2-di-t-butyl-1,3,2-dioxa-, -oxathia-, and -dithia-stannolanes: a study by solution and solid state NMR and single crystal X-ray diffraction. Journal of Organometallic Chemistry, 1989, 363, 45-60.	1.8	46
141	Tris(ethylenediamine)zinc(II) fluoride dihydrate: X-ray structure reveals a strongly hydrogen bonded difluoride cluster, [F2(H2O)2]2?. Journal of the Chemical Society Chemical Communications, 1989, , 738.	2.0	9
142	Platinum metal complexes of potentially chelating alkene thioether and selenoether ligands: the synthesis and dynamic nuclear magnetic resonance study of [MX2{E[(CH2)nCRî€†CR2]2}](M = Pt or Pd; X =) Tj ETQq0 0 0 rgBT /Overlo cis-di-iodo-(5-thianona-1,8-diene)platinum(II), [PtI2{S[(CH2)2CHî€†CH2]2}]. Journal of the Chemical Society Dalton Transactions, 1989, , 2315-2321.	1.1	21
143	Syntheses, electrochemistry, and spectroscopy of dirhodium(II) tetra-acetamidate and tetrakis(trifluoroacetamide) complexes with axial Group 15 substituents. The X-ray crystal structures of [Rh2(CH3CONH)4(AsPh3)2] and [Rh2(CH3CONH)4 â€“n(CH3CO2)n(MPh3)2], M = As or Sb, nâ‰ˆ 1. Journal of the Chemical Society Dalton Transactions, 1989, , 581-588.	1.1	17
144	Î²-Diketone interactions. Part 8. The hydrogen bonding of the enol tautomers of some 3-substituted pentane-2,4-diones. Journal of the Chemical Society Perkin Transactions II, 1989, , 527-533.	0.9	47

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145	The heteronuclear cluster chemistry of the Group 1B metals. Part 11. Effect of the nature of the bidentate diphosphine ligand on the metal framework structures of the gold heteronuclear cluster compounds [Au2Ru4(Âµ3-H)(Âµ-H){Âµ-Ph2P(CH2)nPPh2}(CO)12](n= 1â€“6). X-Ray crystal structures of [Au2Ru4(Âµ3-H)(Âµ-H){Âµ-Ph2P(CH2)nPPh2}(CO)12](n= 1 or 2). Journal of the Chemical Society Dalton Transactions, 1989, , 1327-1336.	1.1	21
146	Platinum metal complexes of potentially chelating alkeneâ€“thioether and alkeneâ€“selenoether ligands: synthesis and dynamic nuclear magnetic resonance study of [MX2{MeE(CH2)nCHî€†CH2}](M = Pt or Pd; X) Tj ETQq0 0 0 rgBT /Overloc [PtBr2{{MeS(CH2)3CHî€†CH2}]. Journal of the Chemical Society Dalton Transactions, 1989, , 985-989.	1.1	14
147	Electrophile-mediated cyclisations: regioselective synthesis of substituted cyclic nitrones and crystal structures of the nitrone cycloadducts. Journal of the Chemical Society Perkin Transactions 1, 1989, , 2415.	0.9	43
148	Structure of Âµ-fluoro-bis[bis(2,2â€²-bipyridyl)fluoronickel(II)] fluorideâ€“ethanol (1/2) trihydrate, revealing several unique features including strong hydrogen bonds between fluoride ions and ethanol molecules. Journal of the Chemical Society Dalton Transactions, 1989, , 1273-1276.	1.1	16
149	A new type of pyridine-2-thionato bridge: X-ray crystal structure of the complex [Re2(MepyS)2(CO)6] where MepyS is the 6-methylpyridine-2-thionato ligand. Polyhedron, 1988, 7, 1401-1403.	2.2	64
150	Structure of the dinuclear compound [Mo2(C5H5)2(CO)4(Î¼-Ph2PCH2PPh2)] in the crystal and in solution. Polyhedron, 1988, 7, 1793-1799.	2.2	13
151	Trimethylplatenum(IV) complexes of the dimethyldithioarsinate(V) anion: Preparation and molecular structure of the dinuclear [(PtMe3)2(Me2AsS2)2] and its selective fission to mononuclear [PtMe3(Me2AsS2)L] (L = PPh3, PPh2Me, py) complexes. Polyhedron, 1988, 7, 1855-1859.	2.2	9
152	The hydrogen bonding of ligand fluoride: the X-ray crystal structure of difluoro(2,2â€²:6â€²,2â€³-terpyridine)copper(II) trihydrate. Inorganica Chimica Acta, 1988, 143, 25-29.	2.4	16
153	Reactions of 2-thiopyridone and related N-, S- and C-methylated derivatives with [Rh2Cl2(CO)4]: crystal and molecular structure of fac-[Rh(MeC5H3NS)3] containing 6-methyl-2-thiopyridonato ligands. Inorganica Chimica Acta, 1988, 142, 37-41.	2.4	9
154	Diaquabis(1,3-diaminopropane)copper(II) difluoride: X-ray structure reveals short hydrogen bonds between ligand waters and lattice fluorides. Inorganica Chimica Acta, 1988, 154, 17-20.	2.4	18
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