

# Ehmke Pohl

## List of Publications by Year in descending order

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129  
papers

4,401  
citations

159585

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docs citations

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citing authors

#	ARTICLE	IF	CITATIONS
1	CPR-C4 is a highly conserved novel protease from the Candidate Phyla Radiation with remote structural homology to human vasohibins. <i>Journal of Biological Chemistry</i> , 2022, 298, 101919.	3.4	2
2	Structure–functional relationship of cellular retinoic acid-binding proteins I and II interacting with natural and synthetic ligands. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 164-175.	2.3	6
3	Going to extremes – a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	16
4	Multiple Occurrences of a 168-Nucleotide Deletion in SARS-CoV-2 ORF8, Unnoticed by Standard Amplicon Sequencing and Variant Calling Pipelines. <i>Viruses</i> , 2021, 13, 1870.	3.3	7
5	Flavonoid-based inhibitors of the Phi-class glutathione transferase from black-grass to combat multiple herbicide resistance. <i>Organic and Biomolecular Chemistry</i> , 2021, 19, 9211-9222.	2.8	4
6	Chalcones identify cTXNPx as a potential antileishmanial drug target. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009951.	3.0	15
7	Preface. <i>Methods in Enzymology</i> , 2020, 637, xix-xx.	1.0	0
8	Classical pathways of gene regulation by retinoids. <i>Methods in Enzymology</i> , 2020, 637, 151-173.	1.0	7
9	GSP4PDB: a web tool to visualize, search and explore protein-ligand structural patterns. <i>BMC Bioinformatics</i> , 2020, 21, 85.	2.6	18
10	Obtaining Tertiary Protein Structures by the ab Initio Interpretation of Small Angle X-ray Scattering Data. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 1985-2001.	5.3	10
11	Crystal structure of the GDP-bound GTPase domain of Rab5a from <i>Leishmania donovani</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 544-556.	0.8	0
12	A C-terminal CXCL8 peptide based on chemokine–glycosaminoglycan interactions reduces neutrophil adhesion and migration during inflammation. <i>Immunology</i> , 2019, 157, 173-184.	4.4	19
13	How to Stabilize Protein: Stability Screens for Thermal Shift Assays and Nano Differential Scanning Fluorimetry in the Virus-X Project. <i>Journal of Visualized Experiments</i> , 2019, .	0.3	15
14	Relative Binding Energies Predict Crystallographic Binding Modes of Ethionamide Booster Lead Compounds. <i>Journal of Physical Chemistry Letters</i> , 2019, 10, 2244-2249.	4.6	5
15	A unique dynamin-related protein is essential for mitochondrial fission in <i>Toxoplasma gondii</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007512.	4.7	43
16	Fluorescent Retinoic Acid Analogues as Probes for Biochemical and Intracellular Characterization of Retinoid Signaling Pathways. <i>ACS Chemical Biology</i> , 2019, 14, 369-377.	3.4	16
17	Crystal structures of the <i>Bacillus subtilis</i> prophage lytic cassette proteins XepA and YomS. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 1028-1039.	2.3	9
18	Probing biological activity through structural modelling of ligand-receptor interactions of 2,4-disubstituted thiazole retinoids. <i>Bioorganic and Medicinal Chemistry</i> , 2018, 26, 1560-1572.	3.0	13

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19	The calcium-dependent protein kinase 1 from <i>Toxoplasma gondii</i> as target for structure-based drug design. <i>Parasitology</i> , 2018, 145, 210-218.	1.5	21
20	Novel Fluorescence Competition Assay for Retinoic Acid Binding Proteins. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 1297-1300.	2.8	8
21	Functional Analyses of a Putative, Membrane-Bound, Peroxisomal Protein Import Mechanism from the Apicomplexan Protozoan <i>Toxoplasma gondii</i> . <i>Genes</i> , 2018, 9, 434.	2.4	4
22	Mutantelec: An <i>In Silico</i> mutation simulation platform for comparative electrostatic potential profiling of proteins. <i>Journal of Computational Chemistry</i> , 2017, 38, 467-474.	3.3	6
23	The molecular basis of the interactions between synthetic retinoic acid analogues and the retinoic acid receptors. <i>MedChemComm</i> , 2017, 8, 578-592.	3.4	25
24	A tight tunable range for Ni(II) sensing and buffering in cells. <i>Nature Chemical Biology</i> , 2017, 13, 409-414.	8.0	37
25	Functional and phylogenetic evidence of a bacterial origin for the first enzyme in sphingolipid biosynthesis in a phylum of eukaryotic protozoan parasites. <i>Journal of Biological Chemistry</i> , 2017, 292, 12208-12219.	3.4	20
26	New active leads for tuberculosis booster drugs by structure-based drug discovery. <i>Organic and Biomolecular Chemistry</i> , 2017, 15, 10245-10255.	2.8	22
27	Air/Liquid Interfacial Nanoassembly of Molecular Building Blocks into Preferentially Oriented Porous Organic Nanosheet Crystals <i>via</i> Hydrogen Bonding. <i>ACS Nano</i> , 2017, 11, 10875-10882.	14.6	23
28	Practical synthetic strategies towards lipophilic 6-iodotetrahydroquinolines and -dihydroquinolines. <i>Beilstein Journal of Organic Chemistry</i> , 2016, 12, 1851-1862.	2.2	19
29	Conjugate Addition of 3-Buytn-2-one to Anilines in Ethanol: Alkene Geometric Insights through In Situ FTIR Monitoring. <i>Journal of Organic Chemistry</i> , 2016, 81, 7557-7565.	3.2	25
30	The Effectors and Sensory Sites of Formaldehyde-responsive Regulator FrmR and Metal-sensing Variant. <i>Journal of Biological Chemistry</i> , 2016, 291, 19502-19516.	3.4	25
31	Crystal Structure of a Hidden Protein, YcaC, a Putative Cysteine Hydrolase from <i>Pseudomonas aeruginosa</i> , with and without an Acrylamide Adduct. <i>International Journal of Molecular Sciences</i> , 2015, 16, 15971-15984.	4.1	6
32	Protein-ligand interactions investigated by thermal shift assays (TSA) and dual polarization interferometry (DPI). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 36-44.	2.5	72
33	A silk purse from a sow's ear—bioinspired materials based on $\alpha$ -helical coiled coils. <i>Current Opinion in Cell Biology</i> , 2015, 32, 131-137.	5.4	8
34	Global low-frequency motions in protein allostery: CAP as a model system. <i>Biophysical Reviews</i> , 2015, 7, 175-182.	3.2	21
35	Multi-scale Approaches to Dynamical Transmission of Protein Allostery. , 2015, , 141-152.		0
36	The Role of Protein-Ligand Contacts in Allosteric Regulation of the <i>Escherichia coli</i> Catabolite Activator Protein. <i>Journal of Biological Chemistry</i> , 2015, 290, 22225-22235.	3.4	37

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37	The Crystal Structures of Apo and cAMP-Bound GlxR from <i>Corynebacterium glutamicum</i> Reveal Structural and Dynamic Changes upon cAMP Binding in CRP/FNR Family Transcription Factors. <i>PLoS ONE</i> , 2014, 9, e113265.	2.5	27
38	A chemical potentiator of copper accumulation used to investigate the iron regulons of <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2014, 93, 317-330.	2.5	23
39	Structure solution of DNA-binding proteins and complexes with ARCIMBOLDO libraries. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1743-1757.	2.5	19
40	AFAL: a web service for profiling amino acids surrounding ligands in proteins. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 1069-1076.	2.9	8
41	The crystal structure of ferritin from <i>Chlorobium tepidum</i> reveals a new conformation of the 4-fold channel for this protein family. <i>Biochimie</i> , 2014, 106, 39-47.	2.6	13
42	A tale of tails: deciphering the contribution of terminal tails to the biochemical properties of two Dps proteins from <i>Streptomyces coelicolor</i> . <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 4911-4926.	5.4	14
43	Porphyrim-based Coordination Polymer Composed of Layered Pillarless Two-dimensional Networks. <i>Chemistry Letters</i> , 2014, 43, 1161-1163.	1.3	11
44	PT: a comprehensive toolbox for the analysis of protein motion. <i>BMC Bioinformatics</i> , 2013, 14, 183.	2.6	21
45	High-level over-expression, purification, and crystallization of a novel phospholipase C/sphingomyelinase from <i>Pseudomonas aeruginosa</i> . <i>Protein Expression and Purification</i> , 2013, 90, 40-46.	1.3	7
46	Modulation of Global Low-Frequency Motions Underlies Allosteric Regulation: Demonstration in CRP/FNR Family Transcription Factors. <i>PLoS Biology</i> , 2013, 11, e1001651.	5.6	71
47	Changes in the quaternary structure and function of MjHSP16.5 attributable to deletion of the IXI motif and introduction of the substitution, R107G, in the $\pm$ -crystallin domain. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120327.	4.0	18
48	Structural and docking studies of potent ethionamide boosters. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2013, 69, 1243-1250.	0.4	8
49	A Nucleotide Phosphatase Activity in the Nucleotide Binding Domain of an Orphan Resistance Protein from Rice. <i>Journal of Biological Chemistry</i> , 2012, 287, 4023-4032.	3.4	22
50	Metal-adeninate vertices for the construction of an exceptionally porous metal-organic framework. <i>Nature Communications</i> , 2012, 3, 604.	12.8	356
51	Synthesis and molecular structure of a perfluorinated pyridyl carbanion. <i>Journal of Fluorine Chemistry</i> , 2012, 133, 33-37.	1.7	6
52	The Crystal Structure of Non-Modified and Bipyridine-Modified PNA Duplexes. <i>Chemistry - A European Journal</i> , 2010, 16, 11867-11875.	3.3	26
53	Crystal Structure of the Caseinolytic Protease Gene Regulator, a Transcriptional Activator in <i>Actinomyces</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 5208-5216.	3.4	14
54	Crystallization and preliminary X-ray analysis of the <i>Thermoplasma acidophilum</i> 20S proteasome in complex with protein substrates. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 899-902.	0.7	0

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55	Crystal structure and stereochemical studies of KD(P)G aldolase from <i>Thermoproteus tenax</i> . Proteins: Structure, Function and Bioinformatics, 2008, 72, 35-43.	2.6	14
56	The Metal-Dependent Regulators FurA and FurB from Mycobacterium Tuberculosis. International Journal of Molecular Sciences, 2008, 9, 1548-1560.	4.1	26
57	Crystal Structure and Function of the Zinc Uptake Regulator FurB from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2007, 282, 9914-9922.	3.4	121
58	Reduction of X-ray-induced radiation damage of macromolecular crystals by data collection at 15Å: a systematic study. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 302-309.	2.5	28
59	Improvements in G protein-coupled receptor purification yield light stable rhodopsin crystals. Journal of Structural Biology, 2006, 156, 497-504.	2.8	52
60	Facility Update: The New Protein Crystallography Beamline X10SA at the Swiss Light Source. Synchrotron Radiation News, 2006, 19, 24-26.	0.8	11
61	The PILATUS 1M detector. Journal of Synchrotron Radiation, 2006, 13, 120-130.	2.4	439
62	Structural evidence for a proton transfer pathway coupled with haem reduction of cytochrome c <sub>3</sub> from Methylophilus methylotrophus. Journal of Biological Inorganic Chemistry, 2006, 11, 189-196.	2.6	12
63	The Crystal Structure of the Zinc Phosphodiesterase from Escherichia coli Provides Insight into Function and Cooperativity of tRNase Z-Family Proteins. Journal of Bacteriology, 2006, 188, 1607-1614.	2.2	68
64	Mechanism of the Schiff Base Forming Fructose-1,6-bisphosphate Aldolase: A Structural Analysis of Reaction Intermediates. Biochemistry, 2005, 44, 4222-4229.	2.5	62
65	Automation of the EMBL Hamburg protein crystallography beamline BW7B. Journal of Synchrotron Radiation, 2004, 11, 372-377.	2.4	46
66	Preparation and Properties of Centrally Bridgehead-Substituted Hexacyclo[4.4.0.0 <sup>2,1</sup> .0 <sup>3,5</sup> .0 <sup>4,8</sup> .0 <sup>7,9</sup> ]decanes (Diademanes) and Related (CH) <sub>10</sub> Hydrocarbons.. ChemInform, 2004, 35, no.	0.0	0
67	Structural Basis of Allosteric Regulation and Substrate Specificity of the Non-Phosphorylating Glyceraldehyde 3-Phosphate Dehydrogenase from Thermoproteus tenax. Journal of Molecular Biology, 2004, 341, 815-828.	4.2	48
68	Structure and Function of a Regulated Archaeal Triosephosphate Isomerase Adapted to High Temperature. Journal of Molecular Biology, 2004, 342, 861-875.	4.2	32
69	Structure, function and evolution of the Archaeal class I fructose-1,6-bisphosphate aldolase. Biochemical Society Transactions, 2004, 32, 259-263.	3.4	29
70	The TB structural genomics consortium: a resource for Mycobacterium tuberculosis biology. Tuberculosis, 2003, 83, 223-249.	1.9	95
71	Preparation and Properties of Centrally Bridgehead-Substituted Hexacyclo[4.4.0.0 <sup>2,1</sup> .0 <sup>3,5</sup> .0 <sup>4,8</sup> .0 <sup>7,9</sup> ]decanes (Diademanes) and Related (CH) <sub>10</sub> Hydrocarbons. Chemistry - A European Journal, 2003, 9, 5481-5488.	3.3	21
72	Architecture of a protein central to iron homeostasis: crystal structure and spectroscopic analysis of the ferric uptake regulator. Molecular Microbiology, 2003, 47, 903-915.	2.5	304

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73	Crystallization and preliminary X-ray characterization of cytochrome c <sub>2</sub> from the obligate methylotroph <i>Methylophilus methylotrophus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 580-583.	2.5	2
74	Crystal Structure of an Archaeal Class I Aldolase and the Evolution of (β <sup>2</sup> ) <sub>8</sub> Barrel Proteins. <i>Journal of Biological Chemistry</i> , 2003, 278, 47253-47260.	3.4	45
75	Structural Conservation between the Actin Monomer-binding Sites of Twinfilin and Actin-depolymerizing Factor (ADF)/Cofilin. <i>Journal of Biological Chemistry</i> , 2002, 277, 43089-43095.	3.4	44
76	The Crystal Structure of the Allosteric Non-phosphorylating Glyceraldehyde-3-phosphate Dehydrogenase from the Hyperthermophilic Archaeum <i>Thermoproteus tenax</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 19938-19945.	3.4	30
77	Multistate Binding in Pyridoxine 5'-Phosphate Synthase: Å 1.96 Å... Crystal Structure in Complex with 1-Deoxy-d-xylulose Phosphate. <i>Biochemistry</i> , 2002, 41, 11649-11657.	2.5	16
78	Differential Dimer Activities of the Transcription Factor Oct-1 by DNA-Induced Interface Swapping. <i>Molecular Cell</i> , 2001, 8, 569-580.	9.7	114
79	The Structure of the Chloroplast F1-ATPase at 3.2 Å... Resolution. <i>Journal of Biological Chemistry</i> , 2001, 276, 1345-1352.	3.4	118
80	Structures of three diphtheria toxin repressor (DtxR) variants with decreased repressor activity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 619-627.	2.5	11
81	Crystallization of redox-insensitive Oct1 POU domain with different DNA-response elements. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1634-1638.	2.5	11
82	Overview of the tunable beamlines for protein crystallography at the EMBL Hamburg Outstation; an analysis of current and future usage and developments. <i>Journal of Synchrotron Radiation</i> , 2001, 8, 1113-1120.	2.4	6
83	The Three-Dimensional Structure of Cystathionine β <sup>2</sup> -Lyase from <i>Arabidopsis</i> and Its Substrate Specificity. <i>Plant Physiology</i> , 2001, 126, 631-642.	4.8	47
84	Ab initio structure determination of the lantibiotic mersacidin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 705-713.	2.5	27
85	Absolute configurations of Emycin D, E and F; mimicry of centrosymmetric space groups by mixtures of chiral stereoisomers. <i>Acta Crystallographica Section B: Structural Science</i> , 1999, 55, 607-616.	1.8	21
86	1.7 Å... structure of the stabilized RELv mutant T39K. Application of local NCS restraints. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1158-1167.	2.5	29
87	A rapid method for positioning small flexible molecules, nucleic acids, and large protein fragments in experimental electron density maps. , 1999, 36, 512-525.		18
88	A database method for automated map interpretation in protein crystallography. , 1999, 36, 526-541.		16
89	Crystal Structure of the Iron-dependent Regulator (IdeR) from <i>Mycobacterium tuberculosis</i> Shows Both Metal Binding Sites Fully Occupied. <i>Journal of Molecular Biology</i> , 1999, 285, 1145-1156.	4.2	115
90	Crystal Structure of a Cobalt-activated Diphtheria Toxin Repressor-DNA Complex Reveals a Metal-binding SH3-like Domain. <i>Journal of Molecular Biology</i> , 1999, 292, 653-667.	4.2	132

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91	Anion-Coordinating Residues at Binding Site 1 Are Essential for the Biological Activity of the Diphtheria Toxin Repressor. <i>Infection and Immunity</i> , 1999, 67, 1806-1811.	2.2	24
92	Anion-Coordinating Residues at Binding Site 1 Are Essential for the Biological Activity of the Diphtheria Toxin Repressor. <i>Infection and Immunity</i> , 1999, 67, 1806-1811.	2.2	6
93	Motion of the DNA-binding Domain with Respect to the Core of the Diphtheria Toxin Repressor (DtxR) Revealed in the Crystal Structures of Apo- and Holo-DtxR. <i>Journal of Biological Chemistry</i> , 1998, 273, 22420-22427.	3.4	61
94	Comparison of high-resolution structures of the diphtheria toxin repressor in complex with cobalt and zinc at the cation-anion binding site. <i>Protein Science</i> , 1997, 6, 1114-1118.	7.6	40
95	High-Resolution Structure of the Diphtheria Toxin Repressor Complexed with Cobalt and Manganese Reveals an SH3-like Third Domain and Suggests a Possible Role of Phosphate as Co-corepressor. <i>Biochemistry</i> , 1996, 35, 12292-12302.	2.5	94
96	Contribution of the intramolecular disulfide bridge to the folding stability of REIv, the variable domain of a human immunoglobulin $\lambda$ light chain. <i>Folding &amp; Design</i> , 1996, 1, 431-440.	4.5	61
97	Crystal Structure and Packing of Isocyclosporin A. <i>Helvetica Chimica Acta</i> , 1996, 79, 1635-1642.	1.6	10
98	The Molecular and Crystal Structure of the Glycopeptide A-40926 Aglycone. <i>Helvetica Chimica Acta</i> , 1996, 79, 1916-1924.	1.6	22
99	(2E,4'S)-2-(4'-Benzyl-2'-oxo-3'-oxazolidinylcarbonyl)-3-phenylacrylic Acid Methyl Ester. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1996, 52, 246-248.	0.4	0
100	(2R)-3-[(4S)-4-Benzyl-2-oxo-3-oxazolidinyl]-3-oxo-2-[(1R,2S)-2-vinylcyclohexyl]propionic Acid Methyl Ester and (2R)-3-[(4S)-4-Benzyl-2-oxo-3-oxazolidinyl]-3-oxo-2-[(1R,2S)-2-vinylcyclopentyl]propionic Acid Methyl Ester. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1996, 52, 2029-2032.	0.4	0
101	rac-1,1,4-Trimethyl-5-trimethylsilyl-1,3,3a,4,6,7,8,9-octahydro-1-silanaphtho[1,2-c]furan at 153 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1995, 51, 891-892.	0.4	0
102	A Diaza-cyclo-tetradecadiene-Bis(pyrido-silafuran) Ring System. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1995, 51, 2145-2147.	0.4	1
103	Three $\eta^2$ -Unsaturated (Carbene)pentacarbonylchromium Complexes. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1995, 51, 2503-2508.	0.4	3
104	Structures of quinoxaline antibiotics. <i>Acta Crystallographica Section B: Structural Science</i> , 1995, 51, 987-999.	1.8	13
105	Structure of octreotide, a somatostatin analogue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 48-59.	2.5	47
106	Comparison of different X-ray data-collection systems using the crystal structure of octreotide. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 60-68.	2.5	5
107	Ab initio determination of the crystal structure of cytochrome c6 and comparison with plastocyanin. <i>Structure</i> , 1995, 3, 1159-1169.	3.3	146
108	Crystal Structures of Two Modifications of [3,O-didehydro-mebmt1, val2]-cyclosporin and comparison of three different X-ray data sets. <i>Helvetica Chimica Acta</i> , 1995, 78, 355-366.	1.6	9

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109	Self-assembly in the metallation of bis(aminoaryl) ethers. <i>Tetrahedron</i> , 1995, 51, 579-590.	1.9	5
110	Erste Kristallstruktur eines Selenans; Metall(II)-Komplexe mit dem 2,4,6-Tris(trifluormethyl)selenophenolat-Liganden. <i>Zeitschrift Fur Anorganische Und Allgemeine Chemie</i> , 1994, 620, 41-47.	1.2	38
111	Structure of cyclo-(L-threonyl-D-valyl-L-prolyl-sarcosyl-N-methyl-L-valyl-OThr) at 153 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1994, 50, 100-103.	0.4	4
112	(+)-N-Trichloroacetyl-7,8-dimethoxy-1-vinyl-2,3,4,5-tetrahydro-1H-3-benzazepine at 153 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1994, 50, 1978-1980.	0.4	0
113	Coordinated 1,3-butadienes: Stable Intermediates in the Formation of Pyridines from [(1-aminophenyl)carbene]chromium Complexes. <i>Chemische Berichte</i> , 1993, 126, 2535-2541.	0.2	33
114	Dilithiation of Two Diphenyl Ethers Each Containing Two NHCH <sub>2</sub> CH <sub>2</sub> Y (Y = OMe, NMe <sub>2</sub> ) Side Arms in ortho Positions: Assembly of ?Adamantanoid? Li <sub>4</sub> O <sub>2</sub> N <sub>4</sub> Cores. <i>Angewandte Chemie International Edition in English</i> , 1993, 32, 1182-1184.	4.4	13
115	The First Structure of a Lithiated Cyanamide; Synthesis of (PhNCNLi·HMPA) <sub>n</sub> by Extrusion of N <sub>2</sub> and S from 5-Phenylamino-1,2,3,4-thiaziazole with Li Reagents and HMPA. <i>Angewandte Chemie International Edition in English</i> , 1993, 32, 1769-1771.	4.4	17
116	Structure of 4,6-bis(trifluoromethyl)-2,2-bis[2,4,6-tris(trifluoromethyl)phenylthio]-1-thiabenzocyclobutene. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1993, 49, 1026-1028.	0.4	2
117	Structures of amino(triphenyl)phosphonium bromide and amino(triphenyl)phosphonium hexachloroantimonate. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1993, 49, 1280-1283.	0.4	4
118	Structure of bis-1/4-[(trimethylsilylmethanolato-O)-bis(trimethylsilylmethyl)gallium] and bis-1/4-[(trimethylsilylmethanolato-O)-bis(trimethylsilylmethyl)indium]. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1993, 49, 1309-1311.	0.4	6
119	Structure of (Δ±)-1 <sup>2</sup> -tert-butoxy-3a <sup>1±</sup> ,4 <sup>1±</sup> ,5,6,7,7a-hexahydro-7a <sup>1±</sup> -methyl-5-oxo-4 <sup>1±</sup> -indancarboxylic acid methyl ester at 153 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1993, 49, 1654-1655.	0.4	0
120	Structures of endo- and exo-3-acetoxy-2,4-diethoxy-6-(2-oxo-1,3-oxazolidin-3-ylcarbonyl)-3,4-dihydro-2H-pyran. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1993, 49, 1850-1852.	0.4	2
121	Structure of 2,4,6-tri(tert-butyl)aniline at 153 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1993, 49, 2141-2143.	0.4	2
122	Synthesis, characterization, and molecular structures of supermesitylgallium- and supermesitylindium dihalides. <i>Inorganic Chemistry</i> , 1993, 32, 3343-3346.	4.0	40
123	A new, simple access to pentacarbonyl(3-aminoallenylidene)chromium complexes. <i>Organometallics</i> , 1993, 12, 2556-2564.	2.3	79
124	Crystal structure of N-(3,5-bis(trifluoromethyl)-phenyl)-tert-butylsulfonamide, C <sub>12</sub> H <sub>13</sub> F <sub>6</sub> NOS. <i>Zeitschrift Fur Kristallographie - Crystalline Materials</i> , 1993, 207, 256-258.	0.8	0
125	Darstellung und Kristallstruktur von [(Me <sub>3</sub> SiCH <sub>2</sub> ) <sub>2</sub> InP(H)Ad] <sub>2</sub> . <i>Zeitschrift Fur Anorganische Und Allgemeine Chemie</i> , 1992, 611, 92-94.	1.2	6
126	Polycyclische Verbindungen aus 2,5-Norbornadien, Isopropylbenzol und Dehalogenierungsprodukten von Dihalogeno(diorganylamino)boranen. Reaktion von Bis(diisopropylamino)phenylboran mit Na/K-Legierung und Difluor(diisopropylamino)boran. <i>Chemische Berichte</i> , 1992, 125, 1559-1564.	0.2	6



#	ARTICLE	IF	CITATIONS
127	Michael Adducts of (Alkynylcarbene)pentacarbonylchromium Complexes: Formation, Stereochemistry, and Thermal Rearrangement. <i>Chemische Berichte</i> , 1992, 125, 2051-2065.	0.2	91
128	Darstellung und Struktur von Thallium(I)-2,4,6-Tris(trifluormethyl)thiophenolat, einer Verbindung mit faltblattartigem polymerem Aufbau. <i>Chemische Berichte</i> , 1991, 124, 1127-1129.	0.2	19
129	Zweifache Borylierung von Benzolderivaten mit (Diisoalkylamino)boradiyleinheiten. <i>Chemische Berichte</i> , 1991, 124, 1907-1912.	0.2	10