

Yves A Muller

List of Publications by Year in descending order

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papers

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citations

87723

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101
all docs

101
docs citations

101
times ranked

5991
citing authors

#	ARTICLE	IF	CITATIONS
1	Endothelium-protective sphingosine-1-phosphate provided by HDL-associated apolipoprotein M. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9613-9618.	3.3	512
2	Vascular endothelial growth factor: Crystal structure and functional mapping of the kinase domain receptor binding site. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 7192-7197.	3.3	402
3	VEGF and the Fab fragment of a humanized neutralizing antibody: crystal structure of the complex at 2.4 Å resolution and mutational analysis of the interface. Structure, 1998, 6, 1153-1167.	1.6	257
4	Structure of the thiamine- and flavin-dependent enzyme pyruvate oxidase. Science, 1993, 259, 965-967.	6.0	237
5	The crystal structure of vascular endothelial growth factor (VEGF) refined to 1.93 Å resolution: multiple copy flexibility and receptor binding. Structure, 1997, 5, 1325-1338.	1.6	222
6	A thiamin diphosphate binding fold revealed by comparison of the crystal structures of transketolase, pyruvate oxidase and pyruvate decarboxylase. Structure, 1993, 1, 95-103.	1.6	193
7	New aspects of electron transfer revealed by the crystal structure of a truncated bovine adrenodoxin, Adx(4â€“108). Structure, 1998, 6, 269-280.	1.6	167
8	Structure of the Extracellular Domain of Human Tissue Factor: Location of the Factor VIIa Binding Site. Biochemistry, 1994, 33, 10864-10870.	1.2	158
9	Crystal structure of human sex hormone-binding globulin: steroid transport by a laminin G-like domain. EMBO Journal, 2000, 19, 504-512.	3.5	144
10	The Opitz syndrome gene product, MID1, associates with microtubules. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 2794-2799.	3.3	116
11	Corticosteroid-binding Globulin, a Structural Basis for Steroid Transport and Proteinase-triggered Release. Journal of Biological Chemistry, 2007, 282, 29594-29603.	1.6	110
12	The Refined Structures of a Stabilized Mutant and of Wild-type Pyruvate Oxidase from Lactobacillus plantarum. Journal of Molecular Biology, 1994, 237, 315-335.	2.0	107
13	The Crystal Structure of the Extracellular Domain of Human Tissue Factor Refined to 1.7 Å Resolution. Journal of Molecular Biology, 1996, 256, 144-159.	2.0	106
14	Redirecting T Cells to Ewing's Sarcoma Family of Tumors by a Chimeric NKG2D Receptor Expressed by Lentiviral Transduction or mRNA Transfection. PLoS ONE, 2012, 7, e31210.	1.1	101
15	Comparison of the intermediate complexes of human growth hormone bound to the human growth hormone and prolactin receptors. Protein Science, 1994, 3, 1697-1705.	3.1	91
16	The CD83 Molecule â€“ An Important Immune Checkpoint. Frontiers in Immunology, 2020, 11, 721.	2.2	86
17	LG/LNS domains: multiple functions â€“ one business end?. Trends in Biochemical Sciences, 2001, 26, 363-368.	3.7	85
18	Molecular and structural basis of steroid hormone binding and release from corticosteroid-binding globulin. Molecular and Cellular Endocrinology, 2010, 316, 3-12.	1.6	75

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19	Crystal Structure of the Human Cytomegalovirus pUL50-pUL53 Core Nuclear Egress Complex Provides Insight into a Unique Assembly Scaffold for Virus-Host Protein Interactions. <i>Journal of Biological Chemistry</i> , 2015, 290, 27452-27458.	1.6	71
20	Structural analyses of sex hormone-binding globulin reveal novel ligands and function. <i>Molecular and Cellular Endocrinology</i> , 2010, 316, 13-23.	1.6	70
21	Ligand Recognition and Homophilic Interactions in Tyro3. <i>Journal of Biological Chemistry</i> , 2004, 279, 6952-6958.	1.6	65
22	Resolution of the Human Sex Hormone-binding Globulin Dimer Interface and Evidence for Two Steroid-binding Sites per Homodimer. <i>Journal of Biological Chemistry</i> , 2001, 276, 34453-34457.	1.6	62
23	Serendipitous Fatty Acid Binding Reveals the Structural Determinants for Ligand Recognition in Apolipoprotein M. <i>Journal of Molecular Biology</i> , 2009, 393, 920-936.	2.0	62
24	Steroid Ligands Bind Human Sex Hormone-binding Globulin in Specific Orientations and Produce Distinct Changes in Protein Conformation. <i>Journal of Biological Chemistry</i> , 2002, 277, 32086-32093.	1.6	61
25	Crystal Structure of Cytomegalovirus IE1 Protein Reveals Targeting of TRIM Family Member PML via Coiled-Coil Interactions. <i>PLoS Pathogens</i> , 2014, 10, e1004512.	2.1	60
26	Near-native, site-specific and purification-free protein labeling for quantitative protein interaction analysis by MicroScale Thermophoresis. <i>Scientific Reports</i> , 2018, 8, 4977.	1.6	60
27	The Crystal Structure of Progesterone 5 β -Reductase from <i>Digitalis lanata</i> Defines a Novel Class of Short Chain Dehydrogenases/Reductases. <i>Journal of Biological Chemistry</i> , 2008, 283, 17260-17269.	1.6	54
28	Crystal Structure Analysis and Solution Studies of Human Lck-SH3; Zinc-induced Homodimerization Competes with the Binding of Proline-rich Motifs. <i>Journal of Molecular Biology</i> , 2007, 365, 1417-1428.	2.0	51
29	Corticosteroid-Binding Globulin: Structure-Function Implications from Species Differences. <i>PLoS ONE</i> , 2012, 7, e52759.	1.1	51
30	Structural Insight into the Giant Ca ²⁺ -Binding Adhesin SiiE: Implications for the Adhesion of <i>Salmonella enterica</i> to Polarized Epithelial Cells. <i>Structure</i> , 2013, 21, 741-752.	1.6	46
31	The Human Cytomegalovirus IE1 Protein Antagonizes PML Nuclear Body-Mediated Intrinsic Immunity via the Inhibition of PML <i>De Novo</i> SUMOylation. <i>Journal of Virology</i> , 2017, 91, .	1.5	46
32	Crystallization of the receptor binding domain of vascular endothelial growth factor. , 1996, 26, 353-357.		45
33	Steroid-binding Specificity of Human Sex Hormone-binding Globulin Is Influenced by Occupancy of a Zinc-binding Site. <i>Journal of Biological Chemistry</i> , 2000, 275, 25920-25925.	1.6	45
34	The Cystine Knot Promotes Folding and Not Thermodynamic Stability in Vascular Endothelial Growth Factor. <i>Journal of Biological Chemistry</i> , 2002, 277, 43410-43416.	1.6	45
35	Nuclear trafficking of the anti-apoptotic <i>Coxiella burnetii</i> effector protein AnkG requires binding to p32 and Importin- β 1. <i>Cellular Microbiology</i> , 2017, 19, e12634.	1.1	45
36	Insight into the induction mechanism of the GntR/HutC bacterial transcription regulator YvoA. <i>Nucleic Acids Research</i> , 2010, 38, 2485-2497.	6.5	44

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37	Characterization of Recombinant Human Cytomegaloviruses Encoding IE1 Mutants L174P and 1-382 Reveals that Viral Targeting of PML Bodies Perturbs both Intrinsic and Innate Immune Responses. <i>Journal of Virology</i> , 2016, 90, 1190-1205.	1.5	42
38	Structural Basis for the Recognition of Human Cytomegalovirus Glycoprotein B by a Neutralizing Human Antibody. <i>PLoS Pathogens</i> , 2014, 10, e1004377.	2.1	41
39	Highly conserved progesterone 5 β -reductase genes (P5 β R) from 5 β -cardenolide-free and 5 β -cardenolide-producing angiosperms. <i>Phytochemistry</i> , 2010, 71, 1495-1505.	1.4	40
40	The VEP1 gene (At4g24220) encodes a short-chain dehydrogenase/reductase with 3-oxo- $\Delta^4,5$ -steroid 5 β -reductase activity in <i>Arabidopsis thaliana</i> L. <i>Biochimie</i> , 2009, 91, 517-525.	1.3	39
41	The human cytomegalovirus nuclear egress complex unites multiple functions: Recruitment of effectors, nuclear envelope rearrangement, and docking to nuclear capsids. <i>Reviews in Medical Virology</i> , 2017, 27, e1934.	3.9	39
42	The 1.85 Å... resolution crystal structures of tissue factor in complex with humanized fab d3h44 and of free humanized fab d3h44: revisiting the solvation of antigen combining sites 1 1 Edited by I. Wilson. <i>Journal of Molecular Biology</i> , 2001, 313, 83-97.	2.0	36
43	Residues in the Human Corticosteroid-binding Globulin Reactive Center Loop That Influence Steroid Binding before and after Elastase Cleavage. <i>Journal of Biological Chemistry</i> , 2009, 284, 884-896.	1.6	36
44	Structural insight into operator dre-sites recognition and effector binding in the GntR/HutC transcription regulator NagR. <i>Nucleic Acids Research</i> , 2015, 43, 1283-1296.	6.5	36
45	Specific Residues of a Conserved Domain in the N Terminus of the Human Cytomegalovirus pUL50 Protein Determine Its Intranuclear Interaction with pUL53. <i>Journal of Biological Chemistry</i> , 2012, 287, 24004-24016.	1.6	35
46	Identification of a Novel TGF- β -Binding Site in the Zona Pellucida C-terminal (ZP-C) Domain of TGF- β -Receptor-3 (TGFR-3). <i>PLoS ONE</i> , 2013, 8, e67214.	1.1	33
47	Ligand-binding sites in Ig-like domains of receptor tyrosine kinases. <i>Journal of Molecular Medicine</i> , 2000, 78, 247-260.	1.7	32
48	A protein functional leap: how a single mutation reverses the function of the transcription regulator TetR. <i>Nucleic Acids Research</i> , 2008, 36, 4390-4401.	6.5	32
49	Multiple allosteric effectors control the affinity of DasR for its target sites. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 324-329.	1.0	32
50	Crystal Structure of Human Sex Hormone-binding Globulin in Complex with 2-Methoxyestradiol Reveals the Molecular Basis for High Affinity Interactions with C-2 Derivatives of Estradiol. <i>Journal of Biological Chemistry</i> , 2002, 277, 45219-45225.	1.6	30
51	Hydration Structure and Dynamics of Inhibitor-Bound HIV-1 Protease. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 2784-2796.	2.3	28
52	High-resolution crystal structures of two prototypical β - and β -herpesviral nuclear egress complexes unravel the determinants of subfamily specificity. <i>Journal of Biological Chemistry</i> , 2020, 295, 3189-3201.	1.6	28
53	Three-dimensional model of the SHBG-like region of anticoagulant protein S: New structure-function insights. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 43, 203-216.	1.5	26
54	Folding screening assayed by proteolysis: application to various cysteine deletion mutants of vascular endothelial growth factor. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 183-188.	1.0	23

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55	How an Agonist Peptide Mimics the Antibiotic Tetracycline to Induce Tet-Repressor. <i>Journal of Molecular Biology</i> , 2007, 368, 780-790.	2.0	23
56	High Frequency of <i>SERPINA6</i> Polymorphisms that Reduce Plasma Corticosteroid-Binding Globulin Activity in Chinese Subjects. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2012, 97, E678-E686.	1.8	23
57	Nuclear Egress Complexes of HCMV and Other Herpesviruses: Solving the Puzzle of Sequence Coevolution, Conserved Structures and Subfamily-Spanning Binding Properties. <i>Viruses</i> , 2020, 12, 683.	1.5	23
58	Structure/function analyses of human sex hormone-binding globulin: effects of zinc on steroid-binding specificity. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2003, 85, 195-200.	1.2	22
59	Crystal Structures of the Global Regulator DasR from <i>Streptomyces coelicolor</i> : Implications for the Allosteric Regulation of GntR/HutC Repressors. <i>PLoS ONE</i> , 2016, 11, e0157691.	1.1	21
60	Resolution of a Disordered Region at the Entrance of the Human Sex Hormone-binding Globulin Steroid-binding Site. <i>Journal of Molecular Biology</i> , 2002, 318, 621-626.	2.0	20
61	Hinge bending within the cytokine receptor superfamily revealed by the 2.4 Å... crystal structure of the extracellular domain of rabbit tissue factor. <i>Protein Science</i> , 1998, 7, 1106-1115.	3.1	19
62	Expression, crystallization and structure elucidation of β -terpinene synthase from <i>Thymus vulgaris</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 16-23.	0.4	19
63	Disorder and twin refinement of RNA heptamer double helices. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1405-1413.	2.5	18
64	Structural and functional dissection reveals distinct roles of Ca ²⁺ -binding sites in the giant adhesin SiiE of <i>Salmonella enterica</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006418.	2.1	18
65	PRISEs (progesterone 5 β -reductase and/or iridoid synthase-like 1,4-enone reductases): Catalytic and substrate promiscuity allows for realization of multiple pathways in plant metabolism. <i>Phytochemistry</i> , 2018, 156, 9-19.	1.4	18
66	MUMBO: a protein-design approach to crystallographic model building and refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 648-658.	2.5	17
67	The complex formed between a synthetic RNA aptamer and the transcription repressor TetR is a structural and functional twin of the operator DNA-TetR regulator complex. <i>Nucleic Acids Research</i> , 2020, 48, 3366-3378.	6.5	17
68	An Exclusive β / α Code Directs Allostery in TetR-Peptide Complexes. <i>Journal of Molecular Biology</i> , 2012, 416, 46-56.	2.0	14
69	A PROSS-designed extensively mutated estrogen receptor β variant displays enhanced thermal stability while retaining native allosteric regulation and structure. <i>Scientific Reports</i> , 2021, 11, 10509.	1.6	14
70	Crystallization of the N-terminal domain of human sex hormone-binding globulin, the major sex steroid carrier in blood. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 2053-2055.	2.5	13
71	Controlled crystal dehydration triggers a space-group switch and shapes the tertiary structure of cytomegalovirus immediate-early 1 (IE1) protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1493-1504.	2.5	11
72	Crystal Structure of the Extracellular Domain of the Human Dendritic Cell Surface Marker CD83. <i>Journal of Molecular Biology</i> , 2017, 429, 1227-1243.	2.0	11

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73	Design of an allosterically modulated doxycycline and doxorubicin drug-binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5744-5749.	3.3	11
74	A Glucose Kinase from <i>Mycobacterium smegmatis</i> . Journal of Molecular Microbiology and Biotechnology, 2007, 12, 75-81.	1.0	10
75	Exploring the Human Cytomegalovirus Core Nuclear Egress Complex as a Novel Antiviral Target: A New Type of Small Molecule Inhibitors. Viruses, 2021, 13, 471.	1.5	10
76	Structural and functional characterization of SiiA, an auxiliary protein from the SPI4-encoded type 1 secretion system from <i>Salmonella enterica</i> . Molecular Microbiology, 2019, 112, 1403-1422.	1.2	9
77	Mouse ApoM Displays an Unprecedented Seven-Stranded Lipocalin Fold: Folding Decoy or Alternative Native Fold?. Journal of Molecular Biology, 2010, 404, 363-371.	2.0	8
78	The crystal structure of the varicella-zoster Orf24-Orf27 nuclear egress complex spotlights multiple determinants of herpesvirus subfamily specificity. Journal of Biological Chemistry, 2022, 298, 101625.	1.6	8
79	Crystallization and preliminary crystallographic analysis of the global nitrogen regulator AmtR from <i>Corynebacterium glutamicum</i> . Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1123-1127.	0.7	7
80	Computational Design of a Chain-Specific Tetracycline Repressor Heterodimer. Journal of Molecular Biology, 2010, 403, 371-385.	2.0	7
81	Unexpected features in the Protein Data Bank entries 3qd1 and 4i8e: the structural description of the binding of the serine-rich repeat adhesin GspB to host cell carbohydrate receptor is not a solved issue. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1071-1076.	0.7	7
82	Recombinant protein production and purification of SiiD, SiiE and SiiF - Components of the SPI4-encoded type I secretion system from <i>Salmonella Typhimurium</i> . Protein Expression and Purification, 2020, 172, 105632.	0.6	6
83	Crystallization and preliminary crystallographic analysis of selenomethionine-labelled progesterone 5 β -reductase from <i>Digitalis lanata</i> Ehrh. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 186-188.	0.7	5
84	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of YvoA from <i>Bacillus subtilis</i> . Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 410-414.	0.7	5
85	Structural origins for selectivity and specificity in an engineered bacterial repressor-inducer pair. FEBS Journal, 2009, 276, 5610-5621.	2.2	5
86	Crystallization and preliminary crystallographic analysis of an Ig-domain-encompassing fragment of the giant adhesion protein SiiE from <i>Salmonella enterica</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1371-1374.	0.7	4
87	Crystal structures of adenylylated and unadenylylated P _{II} protein GlnK from <i>Corynebacterium glutamicum</i> . Acta Crystallographica Section D: Structural Biology, 2021, 77, 325-335.	1.1	4
88	Cytomegalovirus immediate-early 1 proteins form a structurally distinct protein class with adaptations determining cross-species barriers. PLoS Pathogens, 2021, 17, e1009863.	2.1	4
89	Highly ordered crystals of channel-forming membrane proteins, of nucleoside-monophosphate kinases, of FAD-containing oxidoreductases and of sugar-processing enzymes and their mutants. Journal of Crystal Growth, 1992, 122, 385-392.	0.7	2
90	Crystallization and preliminary X-ray analysis of human nicotinamide mononucleotide adenylyltransferase (NMNAT). Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 140-142.	2.5	2

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91	Similarities in the structure of the transcriptional repressor AmtR in two different space groups suggest a model for the interaction with GlnK. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 146-151.	0.4	2
92	NewBG: A surrogate corticosteroid-binding globulin with an unprecedentedly high ligand release efficacy. <i>Journal of Structural Biology</i> , 2019, 207, 169-182.	1.3	2
93	Röntgenstrukturanalyse großer Biomoleküle. <i>Chemie in Unserer Zeit</i> , 1998, 32, 22-33.	0.1	1
94	Purification, crystallization and preliminary X-ray diffraction analysis of the Hsp40 protein CPIP1 from <i>Nicotiana tabacum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 236-239.	0.7	1
95	Crystallization of the receptor binding domain of vascular endothelial growth factor. , 1996, 26, 353.		1
96	Molekülmodelle und Modellmoleküle: Strukturanalyse großer biologischer Moleküle für die Medizin. , 2003, , 340-359.		0
97	Molekülmodelle und Modellmoleküle: Strukturanalyse großer biologischer Moleküle für die Medizin. , 2008, , 275-294.		0