

Yves A Muller

List of Publications by Year in descending order

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97
papers

5,206
citations

87723

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88477

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all docs

101
docs citations

101
times ranked

5991
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#	ARTICLE	IF	CITATIONS
1	The crystal structure of the varicella-zoster Orf24-Orf27 nuclear egress complex spotlights multiple determinants of herpesvirus subfamily specificity. <i>Journal of Biological Chemistry</i> , 2022, 298, 101625.	1.6	8
2	Crystal structures of adenylylated and unadenylylated P _{II} protein GlnK from <i>Corynebacterium glutamicum</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 325-335.	1.1	4
3	Exploring the Human Cytomegalovirus Core Nuclear Egress Complex as a Novel Antiviral Target: A New Type of Small Molecule Inhibitors. <i>Viruses</i> , 2021, 13, 471.	1.5	10
4	A PROSS-designed extensively mutated estrogen receptor $\hat{\pm}$ variant displays enhanced thermal stability while retaining native allosteric regulation and structure. <i>Scientific Reports</i> , 2021, 11, 10509.	1.6	14
5	Cytomegalovirus immediate-early 1 proteins form a structurally distinct protein class with adaptations determining cross-species barriers. <i>PLoS Pathogens</i> , 2021, 17, e1009863.	2.1	4
6	Recombinant protein production and purification of SiiD, SiiE and SiiF - Components of the SPI4-encoded type I secretion system from <i>Salmonella Typhimurium</i> . <i>Protein Expression and Purification</i> , 2020, 172, 105632.	0.6	6
7	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
8	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
9	The CD83 Molecule - An Important Immune Checkpoint. <i>Frontiers in Immunology</i> , 2020, 11, 721.	2.2	86
10	High-resolution crystal structures of two prototypical $\hat{2}$ - and $\hat{3}$ -herpesviral nuclear egress complexes unravel the determinants of subfamily specificity. <i>Journal of Biological Chemistry</i> , 2020, 295, 3189-3201.	1.6	28
11	Structural and functional characterization of SiiA, an auxiliary protein from the SPI4-encoded type 1 secretion system from <i>Salmonella enterica</i> . <i>Molecular Microbiology</i> , 2019, 112, 1403-1422.	1.2	9
12	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
13	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
14	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
15	PRISEs (progesterone $\hat{2}$ -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
16	Design of an allosterically modulated doxycycline and doxorubicin drug-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5744-5749.	3.3	11
17	Nuclear trafficking of the anti-apoptotic <i>Coxiella burnetii</i> effector protein AnkG requires binding to p32 and Importin- $\hat{1}$. <i>Cellular Microbiology</i> , 2017, 19, e12634.	1.1	45
18	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

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19	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
20	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
21	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
22	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
23	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
24	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
25	Expression, crystallization and structure elucidation of Î ³ -terpinene synthase from <i>Thymus vulgaris</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 16-23.	0.4	19
26	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
27	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
28	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
29	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
30	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
31	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
32	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
33	Identification of a Novel TGF-Î ² -Binding Site in the Zona Pellucida C-terminal (ZP-C) Domain of TGF-Î ² -Receptor-3 (TGFR-3). <i>PLoS ONE</i> , 2013, 8, e67214.	1.1	33
34	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. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1071-1076.	0.7	7
35	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
36	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

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37	An Exclusive $\hat{1}\pm/\hat{1}^2$ Code Directs Allostery in TetRâ€‘Peptide Complexes. <i>Journal of Molecular Biology</i> , 2012, 416, 46-56.	2.0	14
38	Redirecting T Cells to Ewing's Sarcoma Family of Tumors by a Chimeric NKG2D Receptor Expressed by Lentiviral Transduction or mRNA Transfection. <i>PLoS ONE</i> , 2012, 7, e31210.	1.1	101
39	Corticosteroid-Binding Globulin: Structure-Function Implications from Species Differences. <i>PLoS ONE</i> , 2012, 7, e52759.	1.1	51
40	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
41	Crystallization and preliminary crystallographic analysis of an Ig-domain-encompassing fragment of the giant adhesion protein SiiE from <i>Salmonella enterica</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1371-1374.	0.7	4
42	Endothelium-protective sphingosine-1-phosphate provided by HDL-associated apolipoprotein M. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9613-9618.	3.3	512
43	Highly conserved progesterone $5\hat{1}^2$ -reductase genes (P5 $\hat{1}^2$ R) from $5\hat{1}^2$ -cardenolide-free and $5\hat{1}^2$ -cardenolide-producing angiosperms. <i>Phytochemistry</i> , 2010, 71, 1495-1505.	1.4	40
44	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
45	Computational Design of a Chain-Specific Tetracycline Repressor Heterodimer. <i>Journal of Molecular Biology</i> , 2010, 403, 371-385.	2.0	7
46	Molecular and structural basis of steroid hormone binding and release from corticosteroid-binding globulin. <i>Molecular and Cellular Endocrinology</i> , 2010, 316, 3-12.	1.6	75
47	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
48	Mouse ApoM Displays an Unprecedented Seven-Stranded Lipocalin Fold: Folding Decoy or Alternative Native Fold?. <i>Journal of Molecular Biology</i> , 2010, 404, 363-371.	2.0	8
49	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
50	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of YvoA from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 410-414.	0.7	5
51	Crystallization and preliminary crystallographic analysis of the global nitrogen regulator AmtR from <i>Corynebacterium glutamicum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1123-1127.	0.7	7
52	Structural origins for selectivity and specificity in an engineered bacterial repressorâ€‘inducer pair. <i>FEBS Journal</i> , 2009, 276, 5610-5621.	2.2	5
53	The VEP1 gene (At4g24220) encodes a short-chain dehydrogenase/reductase with 3-oxo- $\hat{1}^2$ 4,5-steroid $5\hat{1}^2$ -reductase activity in <i>Arabidopsis thaliana</i> L.. <i>Biochimie</i> , 2009, 91, 517-525.	1.3	39
54	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

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55	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
56	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
57	Molekülmodelle und Modellmoleküle: Strukturanalyse großer biologischer Moleküle für die Medizin. , 2008, , 275-294.		0
58	A Glucose Kinase from <i>Mycobacterium smegmatis</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2007, 12, 75-81.	1.0	10
59	Corticosteroid-binding Globulin, a Structural Basis for Steroid Transport and Proteinase-triggered Release. <i>Journal of Biological Chemistry</i> , 2007, 282, 29594-29603.	1.6	110
60	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
61	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
62	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
63	Crystallization and preliminary crystallographic analysis of selenomethionine-labelled progesterone 5 β -reductase from <i>Digitalis lanata</i> Ehrh. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 186-188.	0.7	5
64	Ligand Recognition and Homophilic Interactions in Tyro3. <i>Journal of Biological Chemistry</i> , 2004, 279, 6952-6958.	1.6	65
65	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
66	Molekülmodelle und Modellmoleküle: Strukturanalyse großer biologischer Moleküle für die Medizin. , 2003, , 340-359.		0
67	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
68	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
69	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
70	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
71	Crystallization and preliminary X-ray analysis of human nicotinamide mononucleotide adenylyltransferase (NMNAT). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 140-142.	2.5	2
72	Folding screening assayed by proteolysis: application to various cystine 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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73	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 Edited by I. Wilson. Journal of Molecular Biology, 2001, 313, 83-97.	2.0	36
74	Three-dimensional model of the SHBG-like region of anticoagulant protein S: New structure-function insights. Proteins: Structure, Function and Bioinformatics, 2001, 43, 203-216.	1.5	26
75	LG/LNS domains: multiple functions "one business end?". Trends in Biochemical Sciences, 2001, 26, 363-368.	3.7	85
76	Resolution of the Human Sex Hormone-binding Globulin Dimer Interface and Evidence for Two Steroid-binding Sites per Homodimer. Journal of Biological Chemistry, 2001, 276, 34453-34457.	1.6	62
77	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
78	Ligand-binding sites in Ig-like domains of receptor tyrosine kinases. Journal of Molecular Medicine, 2000, 78, 247-260.	1.7	32
79	Steroid-binding Specificity of Human Sex Hormone-binding Globulin Is Influenced by Occupancy of a Zinc-binding Site. Journal of Biological Chemistry, 2000, 275, 25920-25925.	1.6	45
80	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
81	Disorder and twin refinement of RNA heptamer double helices. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1405-1413.	2.5	18
82	Crystallization of the N-terminal domain of human sex hormone-binding globulin, the major sex steroid carrier in blood. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 2053-2055.	2.5	13
83	New aspects of electron transfer revealed by the crystal structure of a truncated bovine adrenodoxin, Adx(4"108). Structure, 1998, 6, 269-280.	1.6	167
84	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
85	Röntgenstrukturanalyse großer Biomoleküle. Chemie in Unserer Zeit, 1998, 32, 22-33.	0.1	1
86	Hinge bending within the cytokine receptor superfamily revealed by the 2.4 Å... crystal structure of the extracellular domain of rabbit tissue factor. Protein Science, 1998, 7, 1106-1115.	3.1	19
87	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
88	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
89	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
90	Crystallization of the receptor binding domain of vascular endothelial growth factor. , 1996, 26, 353-357.		45

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91	Crystallization of the receptor binding domain of vascular endothelial growth factor. , 1996, 26, 353.		1
92	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
93	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
94	Structure of the Extracellular Domain of Human Tissue Factor: Location of the Factor VIIa Binding Site. Biochemistry, 1994, 33, 10864-10870.	1.2	158
95	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
96	Structure of the thiamine- and flavin-dependent enzyme pyruvate oxidase. Science, 1993, 259, 965-967.	6.0	237
97	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