

Hans Brandstetter

List of Publications by Year in descending order

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127
papers

5,756
citations

76294

40
h-index

82499

72
g-index

131
all docs

131
docs citations

131
times ranked

6027
citing authors

#	ARTICLE	IF	CITATIONS
1	X-ray structure of clotting factor IXa: active site and module structure related to Xase activity and hemophilia B.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 9796-9800.	3.3	295
2	The crystal structure of dipeptidyl peptidase IV (CD26) reveals its functional regulation and enzymatic mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5063-5068.	3.3	295
3	X-ray Structure of Active Site-inhibited Clotting Factor Xa. Journal of Biological Chemistry, 1996, 271, 29988-29992.	1.6	265
4	Structure and function of legumain in health and disease. Biochimie, 2016, 122, 126-150.	1.3	210
5	Refined 2Å-3Å...X-ray crystal structure of bovine thrombin complexes formed with the benzamidine and arginine-based thrombin inhibitors NAPAP, 4-TAPAP and MQPA. Journal of Molecular Biology, 1992, 226, 1085-1099.	2.0	203
6	Crystal structures of the methane monooxygenase hydroxylase from <i>Methylococcus capsulatus</i> (Bath): Implications for substrate gating and component interactions. Proteins: Structure, Function and Bioinformatics, 1997, 29, 141-152.	1.5	189
7	Molecular Machines for Protein Degradation. ChemBioChem, 2005, 6, 222-256.	1.3	176
8	Mechanistic and structural studies on legumain explain its zymogenicity, distinct activation pathways, and regulation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10940-10945.	3.3	160
9	Natural and synthetic inhibitors of kallikrein-related peptidases (KLKs). Biochimie, 2010, 92, 1546-1567.	1.3	129
10	Coagulation factor IXa: the relaxed conformation of Tyr99 blocks substrate binding. Structure, 1999, 7, 989-996.	1.6	123
11	Pyrimidine-2,4,6-Triones: A New Effective and Selective Class of Matrix Metalloproteinase Inhibitors. Biological Chemistry, 2001, 382, 1277-85.	1.2	121
12	Structural Basis of the Adaptive Molecular Recognition by MMP9. Journal of Molecular Biology, 2002, 320, 1065-1079.	2.0	120
13	The 1.8-Å... Crystal Structure of a Matrix Metalloproteinase 8-Barbiturate Inhibitor Complex Reveals a Previously Unobserved Mechanism for Collagenase Substrate Recognition. Journal of Biological Chemistry, 2001, 276, 17405-17412.	1.6	113
14	Enzyme flexibility, solvent and π -weak π ™ interactions characterize thrombin π -ligand interactions: implications for drug design. Structure, 1996, 4, 1353-1362.	1.6	110
15	Investigations on the Maturation and Regulation of Archaeobacterial Proteasomes. Journal of Molecular Biology, 2003, 327, 75-83.	2.0	99
16	Inhibition of delta-secretase improves cognitive functions in mouse models of Alzheimer π ™s disease. Nature Communications, 2017, 8, 14740.	5.8	96
17	Crystallographically Mapped Ligand Binding Differs in High and Low IgE Binding Isoforms of Birch Pollen Allergen Bet v 1. Journal of Molecular Biology, 2012, 422, 109-123.	2.0	93
18	Crystal structure of the tricorn protease reveals a protein disassembly line. Nature, 2001, 414, 466-470.	13.7	90

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19	Crystal Structure of the Catalytic Domain of Human Atypical Protein Kinase C- ι Reveals Interaction Mode of Phosphorylation Site in Turn Motif. <i>Journal of Molecular Biology</i> , 2005, 352, 918-931.	2.0	88
20	Changing Residue 338 in Human Factor IX from Arginine to Alanine Causes an Increase in Catalytic Activity. <i>Journal of Biological Chemistry</i> , 1998, 273, 12089-12094.	1.6	85
21	Structure of collagenase G reveals a chew-and-digest mechanism of bacterial collagenolysis. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1109-1114.	3.6	85
22	Structure-Based Design and Synthesis of Potent Matrix Metalloproteinase Inhibitors Derived from a 6H-1,3,4-Thiadiazine Scaffold. <i>Journal of Medicinal Chemistry</i> , 2001, 44, 3231-3243.	2.9	84
23	Comparative Analysis of Haemostatic Proteinases: Structural Aspects of Thrombin, Factor Xa, Factor IXa and Protein C. <i>Thrombosis and Haemostasis</i> , 1997, 78, 501-511.	1.8	83
24	Crystal Structures of the Tricorn Interacting Factor F3 from <i>Thermoplasma acidophilum</i> , a Zinc Aminopeptidase in Three Different Conformations. <i>Journal of Molecular Biology</i> , 2005, 349, 787-800.	2.0	77
25	Crystal Structures of Uninhibited Factor VIIa Link its Cofactor and Substrate-assisted Activation to Specific Interactions. <i>Journal of Molecular Biology</i> , 2002, 322, 591-603.	2.0	75
26	Structure and Mechanism of an Aspartimide-Dependent Peptide Ligase in Human Legumain. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 2917-2921.	7.2	75
27	Activation of legumain involves proteolytic and conformational events, resulting in a context- and substrate-dependent activity profile. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 24-31.	0.7	70
28	The Impact of Nitration on the Structure and Immunogenicity of the Major Birch Pollen Allergen Bet v 1.0101. <i>PLoS ONE</i> , 2014, 9, e104520.	1.1	70
29	X-ray Structures of Human Furin in Complex with Competitive Inhibitors. <i>ACS Chemical Biology</i> , 2014, 9, 1113-1118.	1.6	69
30	Fold stability during endolysosomal acidification is a key factor for allergenicity and immunogenicity of the major birch pollen allergen. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1525-1534.	1.5	69
31	Converting blood coagulation factor IXa into factor Xa: dramatic increase in amidolytic activity identifies important active site determinants. <i>EMBO Journal</i> , 1997, 16, 6626-6635.	3.5	68
32	Structural Basis for Activity Regulation and Substrate Preference of Clostridial Collagenases G, H, and T. <i>Journal of Biological Chemistry</i> , 2013, 288, 20184-20194.	1.6	64
33	Crystal Structure of Plant Legumain Reveals a Unique Two-Chain State with pH-Dependent Activity Regulation. <i>Plant Cell</i> , 2018, 30, 686-699.	3.1	62
34	Proteomic protease specificity profiling of clostridial collagenases reveals their intrinsic nature as dedicated degraders of collagen. <i>Journal of Proteomics</i> , 2014, 100, 102-114.	1.2	60
35	Structural Basis of the Cofactor- and Substrate-Assisted Activation of Human Coagulation Factor IXa. <i>Structure</i> , 2009, 17, 1669-1678.	1.6	51
36	Nitration of the Birch Pollen Allergen Bet v 1.0101: Efficiency and Site-Selectivity of Liquid and Gaseous Nitrating Agents. <i>Journal of Proteome Research</i> , 2014, 13, 1570-1577.	1.8	51

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37	Multiple roles of Bet v 1 ligands in allergen stabilization and modulation of endosomal protease activity. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019, 74, 2382-2393.	2.7	51
38	Structure of malonic acid-based inhibitors bound to human neutrophil collagenase. A new binding mode explains apparently anomalous data. <i>Protein Science</i> , 1998, 7, 1303-1309.	3.1	47
39	Distinct Roles of Catalytic Cysteine and Histidine in the Protease and Ligase Mechanisms of Human Legumain As Revealed by DFT-Based QM/MM Simulations. <i>ACS Catalysis</i> , 2017, 7, 5585-5593.	5.5	46
40	Surface loops of trypsin-like serine proteases as determinants of function. <i>Biochimie</i> , 2019, 166, 52-76.	1.3	46
41	Structures of the tricorn-interacting aminopeptidase F1 with different ligands explain its catalytic mechanism. <i>EMBO Journal</i> , 2002, 21, 5343-5352.	3.5	45
42	Structure of the N-Terminal Domain of the Adenylyl Cyclase-Associated Protein (CAP) from <i>Dictyostelium discoideum</i> . <i>Structure</i> , 2003, 11, 1171-1178.	1.6	44
43	Structural analyses of <i>Arabidopsis thaliana</i> legumain $\hat{1}^3$ reveal differential recognition and processing of proteolysis and ligation substrates. <i>Journal of Biological Chemistry</i> , 2018, 293, 8934-8946.	1.6	43
44	Small Peptides Blocking Inhibition of Factor Xa and Tissue Factor-Factor VIIa by Tissue Factor Pathway Inhibitor (TFPI). <i>Journal of Biological Chemistry</i> , 2014, 289, 1732-1741.	1.6	41
45	Physiological fIXa Activation Involves a Cooperative Conformational Rearrangement of the 99-Loop. <i>Journal of Biological Chemistry</i> , 2003, 278, 4121-4126.	1.6	40
46	Synthesis and biological evaluation of potential inhibitors of the cysteine proteases cruzain and rhodesain designed by molecular simplification. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 1889-1900.	1.4	39
47	Design and Synthesis of Malonic Acid-Based Inhibitors of Human Neutrophil Collagenase (MMP8). <i>Journal of Medicinal Chemistry</i> , 1998, 41, 339-345.	2.9	38
48	Protease recognition sites in Bet v 1a are cryptic, explaining its slow processing relevant to its allergenicity. <i>Scientific Reports</i> , 2015, 5, 12707.	1.6	37
49	Biochemical characterization of the catalytic domains of three different clostridial collagenases. <i>Biological Chemistry</i> , 2009, 390, 11-18.	1.2	35
50	Ligand Binding Modulates the Structural Dynamics and Compactness of the Major Birch Pollen Allergen. <i>Biophysical Journal</i> , 2014, 107, 2972-2981.	0.2	35
51	Mutational and structural analyses of the regulatory protein B of soluble methane monooxygenase from <i>Methylococcus capsulatus</i> (Bath). <i>Chemistry and Biology</i> , 1999, 6, 441-449.	6.2	33
52	Ligand Binding of PR-10 Proteins with a Particular Focus on the Bet v 1 Allergen Family. <i>Current Allergy and Asthma Reports</i> , 2020, 20, 25.	2.4	33
53	The influence of residue 190 in the S1 site of trypsin-like serine proteases on substrate selectivity is universally conserved. <i>FEBS Letters</i> , 2002, 530, 220-224.	1.3	32
54	Navigation Inside a Protease: Substrate Selection and Product Exit in the Tricorn Protease from <i>Thermoplasma acidophilum</i> . <i>Journal of Molecular Biology</i> , 2002, 324, 1041-1050.	2.0	32

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55	Do-it-yourself histidine-tagged bovine enterokinase: A handy member of the protein engineer's toolbox. <i>Journal of Biotechnology</i> , 2013, 168, 421-425.	1.9	30
56	Discovery of a Potent Inhibitor Class with High Selectivity toward Clostridial Collagenases. <i>Journal of the American Chemical Society</i> , 2017, 139, 12696-12703.	6.6	29
57	The stability and activity of recombinant <i>Helicobacter pylori</i> HtrA under stress conditions. <i>Journal of Basic Microbiology</i> , 2013, 53, 402-409.	1.8	28
58	Structure-Function Analyses of Human Kallikrein-related Peptidase 2 Establish the 99-Loop as Master Regulator of Activity. <i>Journal of Biological Chemistry</i> , 2014, 289, 34267-34283.	1.6	28
59	Stabilization of the Dimeric Birch Pollen Allergen Bet v 1 Impacts Its Immunological Properties. <i>Journal of Biological Chemistry</i> , 2014, 289, 540-551.	1.6	27
60	N-Aryl-3-mercaptosuccinimides as Antivirulence Agents Targeting <i>Pseudomonas aeruginosa</i> Elastase and <i>Clostridium</i> Collagenases. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 8359-8368.	2.9	27
61	Structural and functional analysis of cystatin E reveals enzymologically relevant dimer and amyloid fibril states. <i>Journal of Biological Chemistry</i> , 2018, 293, 13151-13165.	1.6	25
62	Structural and functional studies of <i>Arabidopsis thaliana</i> legumain beta reveal isoform specific mechanisms of activation and substrate recognition. <i>Journal of Biological Chemistry</i> , 2020, 295, 13047-13064.	1.6	24
63	X-ray Snapshots of Peptide Processing in Mutants of Tricorn-interacting Factor F1 from <i>Thermoplasma acidophilum</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 33387-33396.	1.6	23
64	Sweetened kallikrein-related peptidases (KLKs): glycan trees as potential regulators of activation and activity. <i>Biological Chemistry</i> , 2014, 395, 959-976.	1.2	22
65	A Single Glycan at the 99-Loop of Human Kallikrein-related Peptidase 2 Regulates Activation and Enzymatic Activity. <i>Journal of Biological Chemistry</i> , 2016, 291, 593-604.	1.6	21
66	Activation mechanisms of coagulation factor IX. <i>Biological Chemistry</i> , 2009, 390, 391-400.	1.2	20
67	A universal strategy for high-yield production of soluble and functional clostridial collagenases in <i>E. coli</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 83, 1055-1065.	1.7	20
68	Crystal Structures of the Viral Protease Npro Imply Distinct Roles for the Catalytic Water in Catalysis. <i>Structure</i> , 2013, 21, 929-938.	1.6	20
69	Role of the Cysteine 81 Residue of Macrophage Migration Inhibitory Factor as a Molecular Redox Switch. <i>Biochemistry</i> , 2018, 57, 1523-1532.	1.2	20
70	Structures of the NLRP14 pyrin domain reveal a conformational switch mechanism regulating its molecular interactions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2007-2018.	2.5	19
71	Discovery and characterization of trypanocidal cysteine protease inhibitors from the <i>Plasmodium falciparum</i> malaria box™. <i>European Journal of Medicinal Chemistry</i> , 2019, 179, 765-778.	2.6	19
72	The structure of a furin-antibody complex explains non-competitive inhibition by steric exclusion of substrate conformers. <i>Scientific Reports</i> , 2016, 6, 34303.	1.6	18

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73	Cloning, Purification and Characterization of the Collagenase ColA Expressed by <i>Bacillus cereus</i> ATCC 14579. <i>PLoS ONE</i> , 2016, 11, e0162433.	1.1	17
74	ExtENDING Proteome Coverage with Legumain as a Highly Specific Digestion Protease. <i>Analytical Chemistry</i> , 2020, 92, 2961-2971.	3.2	17
75	The X-Ray Crystal Structure of Thrombin in Complex with NÎ±-2-Naphthylsulfonyl-L-3-Amidino-Phenylalanyl-4-Methylpiperidide: The Beneficial Effect of Filling Out an Empty Cavity. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 1995, 9, 101-110.	0.5	16
76	Polycystic kidney disease-like domains of clostridial collagenases and their role in collagen recruitment. <i>Biological Chemistry</i> , 2011, 392, 1039-1045.	1.2	16
77	Crystallographic Determination of Thrombin Complexes With Small Synthetic Inhibitors as a Starting Point for the Receptor-Based Design of Antithrombotics. <i>Seminars in Thrombosis and Hemostasis</i> , 1993, 19, 352-360.	1.5	15
78	Structural Basis for the Processive Protein Degradation by Tricorn Protease. <i>Biological Chemistry</i> , 2002, 383, 1157-65.	1.2	15
79	The Peptide Ligase Activity of Human Legumain Depends on Fold Stabilization and Balanced Substrate Affinities. <i>ACS Catalysis</i> , 2021, 11, 11885-11896.	5.5	15
80	Bis-Substituted Malonic Acid Hydroxamate Derivatives as Inhibitors of Human Neutrophil Collagenase (MMP8). <i>Journal of Medicinal Chemistry</i> , 1998, 41, 3041-3047.	2.9	14
81	Crystal structure of the NADP-dependent mannitol dehydrogenase from <i>Cladosporium herbarum</i> : Implications for oligomerisation and catalysis. <i>Biochimie</i> , 2010, 92, 985-993.	1.3	14
82	Crystal structure of Pla I 1 reveals both structural similarity and allergenic divergence within the Ole e 1â€“like protein family. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 277-280.	1.5	14
83	Specificity profiling of human trypsin-isoenzymes. <i>Biological Chemistry</i> , 2018, 399, 997-1007.	1.2	14
84	Boiling down the cysteine-stabilized LTP fold - loss of structural and immunological integrity of allergenic Art v 3 and Pru p 3 as a consequence of irreversible lanthionine formation. <i>Molecular Immunology</i> , 2019, 116, 140-150.	1.0	14
85	Biochemical characterisation of a collagenase from <i>Bacillus cereus</i> strain Q1. <i>Scientific Reports</i> , 2021, 11, 4187.	1.6	14
86	Phosphonate as a Stable Zincâ€“Binding Group for â€œPathoblockerâ€“Inhibitors of Clostridial Collagenase H (ColH). <i>ChemMedChem</i> , 2021, 16, 1257-1267.	1.6	14
87	Crystallization and preliminary X-ray characterization of the catalytic domain of collagenase G from <i>Clostridium histolyticum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 419-421.	0.7	13
88	Molecular metamorphosis in polcalcin allergens by EFâ€“hand rearrangements and domain swapping. <i>FEBS Journal</i> , 2010, 277, 2598-2610.	2.2	13
89	A Short Synthesis of the Factor-Xa Inhibitor DX-9065a using palladium-catalyzed key steps. <i>Helvetica Chimica Acta</i> , 1997, 80, 892-896.	1.0	12
90	Complex Assemblies of Factors IX and X Regulate the Initiation, Maintenance, and Shutdown of Blood Coagulation. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 99, 51-103.	0.9	12

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91	Cruzain structures: apocruzain and cruzain bound to <i>S</i> -methyl thiomethanesulfonate and implications for drug design. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 419-427.	0.4	11
92	The Basicity Makes the Difference: Improved Canavanine-Derived Inhibitors of the Proprotein Convertase Furin. <i>ACS Medicinal Chemistry Letters</i> , 2021, 12, 426-432.	1.3	11
93	OFF-State-Specific Inhibition of the Proprotein Convertase Furin. <i>ACS Chemical Biology</i> , 2021, 16, 1692-1700.	1.6	10
94	Rayleigh and Brillouin scattering in a lysozyme-water mixture: An unusual behavior around 343K. <i>Journal of Molecular Liquids</i> , 2011, 158, 7-12.	2.3	9
95	Structural Integrity of the Antigen Is a Determinant for the Induction of T-Helper Type-1 Immunity in Mice by Gene Gun Vaccines against <i>E.coli</i> Beta-Galactosidase. <i>PLoS ONE</i> , 2014, 9, e102280.	1.1	9
96	Releasing the brakes in coagulation Factor IXa by co-operative maturation of the substrate-binding site. <i>Biochemical Journal</i> , 2016, 473, 2395-2411.	1.7	9
97	Endolysosomal Degradation of Allergenic Ole e 1-Like Proteins: Analysis of Proteolytic Cleavage Sites Revealing T Cell Epitope-Containing Peptides. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1780.	1.8	9
98	Structural basis for the Zn ²⁺ inhibition of the zymogen-like kallikrein-related peptidase 10. <i>Biological Chemistry</i> , 2016, 397, 1251-1264.	1.2	8
99	Sirtilins - the new old members of the vitamin K-dependent coagulation factor family. <i>Journal of Thrombosis and Haemostasis</i> , 2019, 17, 470-481.	1.9	8
100	Molecular metamorphosis in polcalcin allergens by EF-hand rearrangements and domain swapping. <i>FEBS Journal</i> , 2010, 277, 2598-2610.	2.2	8
101	Two Distinct Conformations in Bet v 2 Determine Its Proteolytic Resistance to Cathepsin S. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2156.	1.8	7
102	Activation and activity of glycosylated KLKs 3, 4 and 11. <i>Biological Chemistry</i> , 2018, 399, 1009-1022.	1.2	7
103	Structural determinants of specificity and regulation of activity in the allosteric loop network of human KLK8/neuropilin. <i>Scientific Reports</i> , 2018, 8, 10705.	1.6	7
104	Dichlorophenylpyridine-Based Molecules Inhibit Furin through an Induced-Fit Mechanism. <i>ACS Chemical Biology</i> , 2022, 17, 816-821.	1.6	7
105	Proteolytic Profiling of Streptococcal Pyrogenic Exotoxin B (SpeB) by Complementary HPLC-MS Approaches. <i>International Journal of Molecular Sciences</i> , 2022, 23, 412.	1.8	7
106	Structure-Based Design of $\hat{\pm}$ -Substituted Mercaptoacetamides as Inhibitors of the Virulence Factor LasB from <i>Pseudomonas aeruginosa</i> . <i>ACS Infectious Diseases</i> , 2022, 8, 1010-1021.	1.8	7
107	The nanotopography of SiO ₂ particles impacts the selectivity and 3D fold of bound allergens. <i>Nanoscale</i> , 2021, 13, 20508-20520.	2.8	6
108	Production of Functional Plant Legumain Proteases Using the <i>Leishmania tarentolae</i> Expression System. <i>Methods in Molecular Biology</i> , 2022, 2447, 35-51.	0.4	6

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109	HAX1 deletion impairs BCR internalization and leads to delayed BCR-mediated apoptosis. Cellular and Molecular Immunology, 2016, 13, 451-461.	4.8	5
110	Identification and characterization of the proteolytic flagellin from the common freshwater bacterium Hylemonella gracilis. Scientific Reports, 2020, 10, 19052.	1.6	5
111	Inhibition and Activity Regulation of Bacterial Collagenases. Topics in Medicinal Chemistry, 2016, , 69-94.	0.4	4
112	Analytical Cascades of Enzymes for Sensitive Detection of Structural Variations in Protein Samples. Analytical Chemistry, 2018, 90, 5055-5065.	3.2	4
113	Inhibition of Collagenase Q1 of <i>Bacillus cereus</i> as a Novel Antivirulence Strategy for the Treatment of Skin Wound Infections. Advanced Therapeutics, 2022, 5, 2100222.	1.6	4
114	The activation peptide of coagulation factor IX and X serves as a high affinity receptor to cationic ligands. Thrombosis and Haemostasis, 2013, 110, 620-622.	1.8	3
115	Structural Alterations of Antigens at the Material Interface: An Early Decision Toolbox Facilitating Safe-by-Design Nanovaccine Development. International Journal of Molecular Sciences, 2021, 22, 10895.	1.8	3
116	Maturation of coagulation factor IX during Xase formation as deduced using factor VIII-derived peptides. FEBS Open Bio, 2019, 9, 1370-1378.	1.0	2
117	Structure of human factor VIIa soluble tissue factor with calcium, magnesium and rubidium. Acta Crystallographica Section D: Structural Biology, 2021, 77, 809-819.	1.1	2
118	Crystal structures of the methane monooxygenase hydroxylase from Methylococcus capsulatus (Bath): Implications for substrate gating and component interactions. Proteins: Structure, Function and Bioinformatics, 1997, 29, 141-152.	1.5	2
119	Research on MMP Inhibitors with Unusual Scaffolds. , 2001, , 223-243.		1
120	Real Space Refinement of Crystal Structures with Canonical Distributions of Electrons. Structure, 2011, 19, 1739-1743.	1.6	1
121	Npro autoprotease fusion technology (NAFT), a platform for industrial peptide/protein production in E. coli. New Biotechnology, 2012, 29, S240.	2.4	1
122	Struktur und Mechanismus einer Aspartimid-abhängigen Peptidligase in humanem Legumin. Angewandte Chemie, 2015, 127, 2959-2964.	1.6	1
123	HAX1 deletion impairs BCR internalization and leads to delayed BCR-mediated apoptosis. Cellular and Molecular Immunology, 2015, , .	4.8	1
124	Molecular Machines for Protein Degradation. , 2005, , 248-287.		0
125	Crystal Structure of the Antihaemophilic Clotting Factor IXa. Japanese Journal of Thrombosis and Hemostasis, 1996, 7, 165-175.	0.1	0
126	Molecular Characterization of the Synergistic Effect on TFPI Inhibition By Fusion of Two Inhibitory Peptides. Blood, 2014, 124, 1484-1484.	0.6	0

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127	Research on MMP Inhibitors with Unusual Scaffolds. , 0, , 223-243.		0