

# Hans Brandstetter

## List of Publications by Year in descending order

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127  
papers

5,756  
citations

76326

40  
h-index

82547

72  
g-index

131  
all docs

131  
docs citations

131  
times ranked

6027  
citing authors

#	ARTICLE	IF	CITATIONS
1	Inhibition of Collagenase Q1 of <i>Bacillus cereus</i> as a Novel Antivirulence Strategy for the Treatment of Skin Wound Infections. <i>Advanced Therapeutics</i> , 2022, 5, 2100222.	3.2	4
2	Dichlorophenylpyridine-Based Molecules Inhibit Furin through an Induced-Fit Mechanism. <i>ACS Chemical Biology</i> , 2022, 17, 816-821.	3.4	7
3	Proteolytic Profiling of Streptococcal Pyrogenic Exotoxin B (SpeB) by Complementary HPLC-MS Approaches. <i>International Journal of Molecular Sciences</i> , 2022, 23, 412.	4.1	7
4	Structure-Based Design of $\hat{\text{L}}\pm$ -Substituted Mercaptoacetamides as Inhibitors of the Virulence Factor LasB from <i>Pseudomonas aeruginosa</i> . <i>ACS Infectious Diseases</i> , 2022, 8, 1010-1021.	3.8	7
5	Production of Functional Plant Legumain Proteases Using the <i>Leishmania tarentolae</i> Expression System. <i>Methods in Molecular Biology</i> , 2022, 2447, 35-51.	0.9	6
6	The Basicity Makes the Difference: Improved Canavanine-Derived Inhibitors of the Proprotein Convertase Furin. <i>ACS Medicinal Chemistry Letters</i> , 2021, 12, 426-432.	2.8	11
7	Biochemical characterisation of a collagenase from <i>Bacillus cereus</i> strain Q1. <i>Scientific Reports</i> , 2021, 11, 4187.	3.3	14
8	Phosphonate as a Stable Zinc-Binding Group for Pathoblocker-Inhibitors of Clostridial Collagenase H (ColH). <i>ChemMedChem</i> , 2021, 16, 1257-1267.	3.2	14
9	Structure of human factor VIIa soluble tissue factor with calcium, magnesium and rubidium. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 809-819.	2.3	2
10	OFF-State-Specific Inhibition of the Proprotein Convertase Furin. <i>ACS Chemical Biology</i> , 2021, 16, 1692-1700.	3.4	10
11	The Peptide Ligase Activity of Human Legumain Depends on Fold Stabilization and Balanced Substrate Affinities. <i>ACS Catalysis</i> , 2021, 11, 11885-11896.	11.2	15
12	Structural Alterations of Antigens at the Material Interface: An Early Decision Toolbox Facilitating Safe-by-Design Nanovaccine Development. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10895.	4.1	3
13	The nanotopography of SiO <sub>2</sub> particles impacts the selectivity and 3D fold of bound allergens. <i>Nanoscale</i> , 2021, 13, 20508-20520.	5.6	6
14	Identification and characterization of the proteolytic flagellin from the common freshwater bacterium <i>Hylemonella gracilis</i> . <i>Scientific Reports</i> , 2020, 10, 19052.	3.3	5
15	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.	3.4	24
16	<i>N</i> -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.	6.4	27
17	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.	5.3	33
18	ExtENDING Proteome Coverage with Legumain as a Highly Specific Digestion Protease. <i>Analytical Chemistry</i> , 2020, 92, 2961-2971.	6.5	17

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19	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.	0.8	11
20	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.	2.2	14
21	Surface loops of trypsin-like serine proteases as determinants of function. <i>Biochimie</i> , 2019, 166, 52-76.	2.6	46
22	Discovery and characterization of trypanocidal cysteine protease inhibitors from the "malaria box"™. <i>European Journal of Medicinal Chemistry</i> , 2019, 179, 765-778.	5.5	19
23	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.	5.7	51
24	Maturation of coagulation factor IX during Xase formation as deduced using factor VIII-derived peptides. <i>FEBS Open Bio</i> , 2019, 9, 1370-1378.	2.3	2
25	Sirtilins - the new old members of the vitamin K-dependent coagulation factor family. <i>Journal of Thrombosis and Haemostasis</i> , 2019, 17, 470-481.	3.8	8
26	Structural analyses of <i>Arabidopsis thaliana</i> legumain <sup>13</sup> reveal differential recognition and processing of proteolysis and ligation substrates. <i>Journal of Biological Chemistry</i> , 2018, 293, 8934-8946.	3.4	43
27	Crystal Structure of Plant Legumain Reveals a Unique Two-Chain State with pH-Dependent Activity Regulation. <i>Plant Cell</i> , 2018, 30, 686-699.	6.6	62
28	Role of the Cysteine 81 Residue of Macrophage Migration Inhibitory Factor as a Molecular Redox Switch. <i>Biochemistry</i> , 2018, 57, 1523-1532.	2.5	20
29	Analytical Cascades of Enzymes for Sensitive Detection of Structural Variations in Protein Samples. <i>Analytical Chemistry</i> , 2018, 90, 5055-5065.	6.5	4
30	Specificity profiling of human trypsin-isoenzymes. <i>Biological Chemistry</i> , 2018, 399, 997-1007.	2.5	14
31	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.	3.4	25
32	Activation and activity of glycosylated KLKs 3, 4 and 11. <i>Biological Chemistry</i> , 2018, 399, 1009-1022.	2.5	7
33	Structural determinants of specificity and regulation of activity in the allosteric loop network of human KLK8/neuropsin. <i>Scientific Reports</i> , 2018, 8, 10705.	3.3	7
34	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.	3.0	39
35	Inhibition of delta-secretase improves cognitive functions in mouse models of Alzheimer's disease. <i>Nature Communications</i> , 2017, 8, 14740.	12.8	96
36	Crystal structure of Pla l 1 reveals both structural similarity and allergenic divergence within the Ole e 1-like protein family. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 277-280.	2.9	14

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37	Discovery of a Potent Inhibitor Class with High Selectivity toward Clostridial Collagenases. <i>Journal of the American Chemical Society</i> , 2017, 139, 12696-12703.	13.7	29
38	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.	11.2	46
39	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.	4.1	9
40	Two Distinct Conformations in Bet v 2 Determine Its Proteolytic Resistance to Cathepsin S. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2156.	4.1	7
41	Cloning, Purification and Characterization of the Collagenase ColA Expressed by <i>Bacillus cereus</i> ATCC 14579. <i>PLoS ONE</i> , 2016, 11, e0162433.	2.5	17
42	Inhibition and Activity Regulation of Bacterial Collagenases. <i>Topics in Medicinal Chemistry</i> , 2016, , 69-94.	0.8	4
43	HAX1 deletion impairs BCR internalization and leads to delayed BCR-mediated apoptosis. <i>Cellular and Molecular Immunology</i> , 2016, 13, 451-461.	10.5	5
44	Structural basis for the Zn <sup>2+</sup> inhibition of the zymogen-like kallikrein-related peptidase 10. <i>Biological Chemistry</i> , 2016, 397, 1251-1264.	2.5	8
45	Releasing the brakes in coagulation Factor IXa by co-operative maturation of the substrate-binding site. <i>Biochemical Journal</i> , 2016, 473, 2395-2411.	3.7	9
46	The structure of a furin-antibody complex explains non-competitive inhibition by steric exclusion of substrate conformers. <i>Scientific Reports</i> , 2016, 6, 34303.	3.3	18
47	Structure and function of legumain in health and disease. <i>Biochimie</i> , 2016, 122, 126-150.	2.6	210
48	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.	2.9	69
49	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.	3.4	21
50	Struktur und Mechanismus einer Aspartimidase-Abhängigen Peptidligase in humanem Legumain. <i>Angewandte Chemie</i> , 2015, 127, 2959-2964.	2.0	1
51	Protease recognition sites in Bet v 1a are cryptic, explaining its slow processing relevant to its allergenicity. <i>Scientific Reports</i> , 2015, 5, 12707.	3.3	37
52	HAX1 deletion impairs BCR internalization and leads to delayed BCR-mediated apoptosis. <i>Cellular and Molecular Immunology</i> , 2015, , .	10.5	1
53	Structure and Mechanism of an Aspartimide-Dependent Peptide Ligase in Human Legumain. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 2917-2921.	13.8	75
54	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.	2.5	9

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55	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.	2.5	70
56	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.	3.4	28
57	Stabilization of the Dimeric Birch Pollen Allergen Bet v 1 Impacts Its Immunological Properties. <i>Journal of Biological Chemistry</i> , 2014, 289, 540-551.	3.4	27
58	Ligand Binding Modulates the Structural Dynamics and Compactness of the Major Birch Pollen Allergen. <i>Biophysical Journal</i> , 2014, 107, 2972-2981.	0.5	35
59	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.	3.4	41
60	Sweetened kallikrein-related peptidases (KLKs): glycan trees as potential regulators of activation and activity. <i>Biological Chemistry</i> , 2014, 395, 959-976.	2.5	22
61	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
62	X-ray Structures of Human Furin in Complex with Competitive Inhibitors. <i>ACS Chemical Biology</i> , 2014, 9, 1113-1118.	3.4	69
63	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.	3.7	51
64	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.	2.4	60
65	Molecular Characterization of the Synergistic Effect on TFPI Inhibition By Fusion of Two Inhibitory Peptides. <i>Blood</i> , 2014, 124, 1484-1484.	1.4	0
66	The stability and activity of recombinant <i>Helicobacter pylori</i> HtrA under stress conditions. <i>Journal of Basic Microbiology</i> , 2013, 53, 402-409.	3.3	28
67	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.	3.8	30
68	Crystal Structures of the Viral Protease Npro Imply Distinct Roles for the Catalytic Water in Catalysis. <i>Structure</i> , 2013, 21, 929-938.	3.3	20
69	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.	3.4	64
70	Mechanistic and structural studies on legumain explain its zymogenicity, distinct activation pathways, and regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10940-10945.	7.1	160
71	The activation peptide of coagulation factor IX and X serves as a high affinity receptor to cationic ligands. <i>Thrombosis and Haemostasis</i> , 2013, 110, 620-622.	3.4	3
72	Crystallographically Mapped Ligand Binding Differs in High and Low IgE Binding Isoforms of Birch Pollen Allergen Bet v 1. <i>Journal of Molecular Biology</i> , 2012, 422, 109-123.	4.2	93

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73	Npro autoprotease fusion technology (NAFT), a platform for industrial peptide/protein production in <i>E. coli</i> . <i>New Biotechnology</i> , 2012, 29, S240.	4.4	1
74	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
75	Real Space Refinement of Crystal Structures with Canonical Distributions of Electrons. <i>Structure</i> , 2011, 19, 1739-1743.	3.3	1
76	Rayleigh and Brillouin scattering in a lysozyme-water mixture: An unusual behavior around 343K. <i>Journal of Molecular Liquids</i> , 2011, 158, 7-12.	4.9	9
77	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.	1.7	12
78	Polycystic kidney disease-like domains of clostridial collagenases and their role in collagen recruitment. <i>Biological Chemistry</i> , 2011, 392, 1039-1045.	2.5	16
79	Structure of collagenase G reveals a chew-and-digest mechanism of bacterial collagenolysis. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1109-1114.	8.2	85
80	Molecular metamorphosis in polcalcin allergens by EF-hand rearrangements and domain swapping. <i>FEBS Journal</i> , 2010, 277, 2598-2610.	4.7	13
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.	2.6	14
82	Natural and synthetic inhibitors of kallikrein-related peptidases (KLKs). <i>Biochimie</i> , 2010, 92, 1546-1567.	2.6	129
83	Molecular metamorphosis in polcalcin allergens by EF-hand rearrangements and domain swapping. <i>FEBS Journal</i> , 2010, 277, 2598-2610.	4.7	8
84	Activation mechanisms of coagulation factor IX. <i>Biological Chemistry</i> , 2009, 390, 391-400.	2.5	20
85	Structural Basis of the Cofactor- and Substrate-Assisted Activation of Human Coagulation Factor IXa. <i>Structure</i> , 2009, 17, 1669-1678.	3.3	51
86	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.	3.6	20
87	Biochemical characterization of the catalytic domains of three different clostridial collagenases. <i>Biological Chemistry</i> , 2009, 390, 11-18.	2.5	35
88	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
89	Molecular Machines for Protein Degradation. , 2005, , 248-287.		0
90	Molecular Machines for Protein Degradation. <i>ChemBioChem</i> , 2005, 6, 222-256.	2.6	176

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91	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.	3.4	23
92	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.	4.2	77
93	Crystal Structure of the Catalytic Domain of Human Atypical Protein Kinase C- $\iota$ Reveals Interaction Mode of Phosphorylation Site in Turn Motif. <i>Journal of Molecular Biology</i> , 2005, 352, 918-931.	4.2	88
94	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.	3.3	44
95	Investigations on the Maturation and Regulation of Archaeobacterial Proteasomes. <i>Journal of Molecular Biology</i> , 2003, 327, 75-83.	4.2	99
96	The crystal structure of dipeptidyl peptidase IV (CD26) reveals its functional regulation and enzymatic mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5063-5068.	7.1	295
97	Physiological FIXa Activation Involves a Cooperative Conformational Rearrangement of the 99-Loop. <i>Journal of Biological Chemistry</i> , 2003, 278, 4121-4126.	3.4	40
98	Structural Basis for the Processive Protein Degradation by Tricorn Protease. <i>Biological Chemistry</i> , 2002, 383, 1157-65.	2.5	15
99	Structures of the tricorn-interacting aminopeptidase F1 with different ligands explain its catalytic mechanism. <i>EMBO Journal</i> , 2002, 21, 5343-5352.	7.8	45
100	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.	2.8	32
101	Structural Basis of the Adaptive Molecular Recognition by MMP9. <i>Journal of Molecular Biology</i> , 2002, 320, 1065-1079.	4.2	120
102	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.	4.2	75
103	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.	4.2	32
104	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.	6.4	84
105	The 1.8-Å... Crystal Structure of a Matrix Metalloproteinase 8-Barbiturate Inhibitor Complex Reveals a Previously Unobserved Mechanism for Collagenase Substrate Recognition. <i>Journal of Biological Chemistry</i> , 2001, 276, 17405-17412.	3.4	113
106	Crystal structure of the tricorn protease reveals a protein disassembly line. <i>Nature</i> , 2001, 414, 466-470.	27.8	90
107	Pyrimidine-2,4,6-Triones: A New Effective and Selective Class of Matrix Metalloproteinase Inhibitors. <i>Biological Chemistry</i> , 2001, 382, 1277-85.	2.5	121
108	Research on MMP Inhibitors with Unusual Scaffolds. , 2001, , 223-243.		1

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109	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.	6.0	33
110	Coagulation factor IXa: the relaxed conformation of Tyr99 blocks substrate binding. <i>Structure</i> , 1999, 7, 989-996.	3.3	123
111	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.	7.6	47
112	Bis-Substituted Malonic Acid Hydroxamate Derivatives as Inhibitors of Human Neutrophil Collagenase (MMP8). <i>Journal of Medicinal Chemistry</i> , 1998, 41, 3041-3047.	6.4	14
113	Design and Synthesis of Malonic Acid-Based Inhibitors of Human Neutrophil Collagenase (MMP8). <i>Journal of Medicinal Chemistry</i> , 1998, 41, 339-345.	6.4	38
114	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.	3.4	85
115	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.	7.8	68
116	A Short Synthesis of the Factor-Xa Inhibitor DX-9065a using palladium-catalyzed key steps. <i>Helvetica Chimica Acta</i> , 1997, 80, 892-896.	1.6	12
117	Crystal structures of the methane monooxygenase hydroxylase from <i>Methylococcus capsulatus</i> (Bath): Implications for substrate gating and component interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 141-152.	2.6	189
118	Crystal structures of the methane monooxygenase hydroxylase from <i>Methylococcus capsulatus</i> (Bath): Implications for substrate gating and component interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 141-152.	2.6	2
119	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.	3.4	83
120	X-ray Structure of Active Site-inhibited Clotting Factor Xa. <i>Journal of Biological Chemistry</i> , 1996, 271, 29988-29992.	3.4	265
121	Enzyme flexibility, solvent and "weak" interactions characterize thrombin-ligand interactions: implications for drug design. <i>Structure</i> , 1996, 4, 1353-1362.	3.3	110
122	Crystal Structure of the Antihaemophilic Clotting Factor IXa. <i>Japanese Journal of Thrombosis and Hemostasis</i> , 1996, 7, 165-175.	0.1	0
123	X-ray structure of clotting factor IXa: active site and module structure related to Xase activity and hemophilia B.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 9796-9800.	7.1	295
124	The X-Ray Crystal Structure of Thrombin in Complex with N <sup>1</sup> -(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
125	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.	2.7	15
126	Refined 2.3 Å X-ray crystal structure of bovine thrombin complexes formed with the benzamidine and arginine-based thrombin inhibitors NAPAP, 4-TAPAP and MQPA. <i>Journal of Molecular Biology</i> , 1992, 226, 1085-1099.	4.2	203



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