Bruno O Villoutreix

List of Publications by Year in Descending Order

208 papers	7,409 citations	46 h-index	74 g-index
239 ext. papers	8,223 ext. citations	6.1 avg, IF	6.11 L-index

#	Paper	IF	Citations
208	Machine learning-driven identification of drugs inhibiting cytochrome P450 2C9.. *PLoS Computational Biology*, **2022**, 18, e1009820	5	2
207	A new ChEMBL dataset for the similarity-based target fishing engine FastTargetPred: Annotation of an exhaustive list of linear tetrapeptides.. *Data in Brief*, **2022**, 42, 108159	1.2	
206	The first laminin G-like domain of protein S is essential for binding and activation of Tyro3 receptor and intracellular signalling.. *Biochemistry and Biophysics Reports*, **2022**, 30, 101263	2.2	
205	Antihistamine and cationic amphiphilic drugs, old molecules as new tools against the COVID-19?. *Medical Hypotheses*, **2021**, 148, 110508	3.8	9
204	Chemoinformatic Analysis of Psychotropic and Antihistaminic Drugs in the Light of Experimental Anti-SARS-CoV-2 Activities. *Advances and Applications in Bioinformatics and Chemistry*, **2021**, 14, 71-85	1.5	7
203	Role of Gly197 in the structure and function of protein C. *Biochimica Et Biophysica Acta - General Subjects*, **2021**, 1865, 129892	4	
202	Virtual screening web servers: designing chemical probes and drug candidates in the cyberspace. *Briefings in Bioinformatics*, **2021**, 22, 1790-1818	13.4	36
201	Resources and computational strategies to advance small molecule SARS-CoV-2 discovery: Lessons from the pandemic and preparing for future health crises. *Computational and Structural Biotechnology Journal*, **2021**, 19, 2537-2548	6.8	9
200	In Silico Investigation of the New UK (B.1.1.7) and South African (501Y.V2) SARS-CoV-2 Variants with a Focus at the ACE2-Spike RBD Interface. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	54
199	PAK1-Dependent Antitumor Effect of AAC-11-Derived Peptides on S□ary Syndrome Malignant CD4 T Lymphocytes. *Journal of Investigative Dermatology*, **2021**, 141, 2261-2271.e5	4.3	0
198	Anti-Factor B Antibodies and Acute Postinfectious GN in Children. *Journal of the American Society of Nephrology: JASN*, **2020**, 31, 829-840	12.7	20
197	FastTargetPred: a program enabling the fast prediction of putative protein targets for input chemical databases. *Bioinformatics*, **2020**, 36, 4225-4226	7.2	3
196	Gly197Arg mutation in protein C causes recurrent thrombosis in a heterozygous carrier. *Journal of Thrombosis and Haemostasis*, **2020**, 18, 1141-1153	15.4	2
195	Thr90Ser Mutation in Antithrombin is Associated with Recurrent Thrombosis in a Heterozygous Carrier. *Thrombosis and Haemostasis*, **2020**, 120, 1045-1055	7	2
194	Analysis of protein missense alterations by combining sequence- and structure-based methods. *Molecular Genetics & Genomic Medicine*, **2020**, 8, e1166	2.3	16
193	ELA/APELA precursor cleaved by furin displays tumor suppressor function in renal cell carcinoma through mTORC1 activation. *JCI Insight*, **2020**, 5,	9.9	15
192	Demystifying the Molecular Basis of Pyrazoloquinolinones Recognition at the Extracellular □+/□- Interface of the GABA Receptor by Molecular Modeling. *Frontiers in Pharmacology*, **2020**, 11, 561834	5.6	1

191	Fast Rescoring Protocols to Improve the Performance of Structure-Based Virtual Screening Performed on Protein-Protein Interfaces. *Journal of Chemical Information and Modeling*, **2020**, 60, 3910-3934	6.1	6
190	Structure-based drug repositioning over the human TMPRSS2 protease domain: search for chemical probes able to repress SARS-CoV-2 Spike protein cleavages. *European Journal of Pharmaceutical Sciences*, **2020**, 153, 105495	5.1	28
189	Ile73Asn mutation in protein C introduces a new N-linked glycosylation site on the first EGF-domain of protein C and causes thrombosis. *Haematologica*, **2020**, 105, 1712-1722	6.6	4
188	Fr-PPIChem: An Academic Compound Library Dedicated to Protein-Protein Interactions. *ACS Chemical Biology*, **2020**, 15, 1566-1574	4.9	13
187	A Free Web-Based Protocol to Assist Structure-Based Virtual Screening Experiments. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	10
186	Rigorous sampling of docking poses unveils binding hypothesis for the halogenated ligands of L-type Amino acid Transporter 1 (LAT1). *Scientific Reports*, **2019**, 9, 15061	4.9	13
185	Analysis of solvent-exposed and buried co-crystallized ligands: a case study to support the design of novel protein-protein interaction inhibitors. *Drug Discovery Today*, **2019**, 24, 551-559	8.8	11
184	Breast Cancer Targeting through Inhibition of the Endoplasmic Reticulum-Based Apoptosis Regulator Nrh/BCL2L10. *Cancer Research*, **2018**, 78, 1404-1417	10.1	22
183	Expression and functional characterization of two natural heparin-binding site variants of antithrombin. *Journal of Thrombosis and Haemostasis*, **2018**, 16, 330-341	15.4	5
182	Insights into molecular mechanisms of drug metabolism dysfunction of human CYP2C9*30. *PLoS ONE*, **2018**, 13, e0197249	3.7	14
181	Online structure-based screening of purchasable approved drugs and natural compounds: retrospective examples of drug repositioning on cancer targets. *Oncotarget*, **2018**, 9, 32346-32361	3.3	15
180	Acute genetic ablation of pendrin lowers blood pressure in mice. *Nephrology Dialysis Transplantation*, **2017**, 32, 1137-1145	4.3	19
179	Computational Biology and Chemistry in MTi: Emphasis on the Prediction of Some ADMET Properties. *Molecular Informatics*, **2017**, 36, 1700008	3.8	2
178	Computational analysis of calculated physicochemical and ADMET properties of protein-protein interaction inhibitors. *Scientific Reports*, **2017**, 7, 46277	4.9	71
177	FAF-Drugs4: free ADME-tox filtering computations for chemical biology and early stages drug discovery. *Bioinformatics*, **2017**, 33, 3658-3660	7.2	141
176	In silico model of the human ClC-Kb chloride channel: pore mapping, biostructural pathology and drug screening. *Scientific Reports*, **2017**, 7, 7249	4.9	11
175	Identification of insulin-sensitizing molecules acting by disrupting the interaction between the Insulin Receptor and Grb14. *Scientific Reports*, **2017**, 7, 16901	4.9	3
174	AMMOS2: a web server for protein-ligand-water complexes refinement via molecular mechanics. *Nucleic Acids Research*, **2017**, 45, W350-W355	20.1	21

173	Pharmacogenomics of the cytochrome P450 2C family: impacts of amino acid variations on drug metabolism. *Drug Discovery Today*, **2017**, 22, 366-376	8.8	39
172	Gly74Ser mutation in protein C causes thrombosis due to a defect in protein S-dependent anticoagulant function. *Thrombosis and Haemostasis*, **2017**, 117, 1358-1369	7	5
171	Blockade of the malignant phenotype by β5-subunit selective noncovalent inhibition of immuno- and constitutive proteasomes. *Oncotarget*, **2017**, 8, 10437-10449	3.3	8
170	Combining bioinformatics, chemoinformatics and experimental approaches to design chemical probes: Applications in the field of blood coagulation. *Annales Pharmaceutiques Francaises*, **2016**, 74, 253-66	1.3	1
169	iPPI-DB: an online database of modulators of protein-protein interactions. *Nucleic Acids Research*, **2016**, 44, D542-7	20.1	38
168	A Cell-Penetrating Peptide Targeting AAC-11 Specifically Induces Cancer Cells Death. *Cancer Research*, **2016**, 76, 5479-90	10.1	36
167	Discoidin Domains as Emerging Therapeutic Targets. *Trends in Pharmacological Sciences*, **2016**, 37, 641-659	13.2	18
166	DNA damage-induced nuclear translocation of Apaf-1 is mediated by nucleoporin Nup107. *Cell Cycle*, **2015**, 14, 1242-51	4.7	19
165	Functional characterization of two novel non-synonymous alterations in CD46 and a Q950H change in factor H found in atypical hemolytic uremic syndrome patients. *Molecular Immunology*, **2015**, 65, 367-76	4.3	19
164	In silico design of low molecular weight protein-protein interaction inhibitors: Overall concept and recent advances. *Progress in Biophysics and Molecular Biology*, **2015**, 119, 20-32	4.7	46
163	Strategies in the Search for New Lead Compounds or Original Working Hypotheses **2015**, 73-99		6
162	Application Strategies for the Primary Structure–Activity Relationship Exploration **2015**, 301-318		2
161	MTiOpenScreen: a web server for structure-based virtual screening. *Nucleic Acids Research*, **2015**, 43, W448-54	20.1	101
160	Computational investigations of hERG channel blockers: New insights and current predictive models. *Advanced Drug Delivery Reviews*, **2015**, 86, 72-82	18.5	53
159	Therapeutic Targeting of Nuclear βIII-Tubulin in RB1-Negative Tumors. *Molecular Cancer Research*, **2015**, 13, 1073-82	6.6	11
158	Integrated structure- and ligand-based in silico approach to predict inhibition of cytochrome P450 2D6. *Bioinformatics*, **2015**, 31, 3930-7	7.2	12
157	An exploration of the 3D chemical space has highlighted a specific shape profile for the compounds intended to inhibit protein-protein interactions. *BMC Bioinformatics*, **2015**, 16, A5	3.6	2
156	In Silico Approaches Assisting the Rational Design of Low Molecular Weight Protein–Protein Interaction Modulators **2015**, 441-482		

155	Amino acid residues in the laminin G domains of protein S involved in tissue factor pathway inhibitor interaction. *Thrombosis and Haemostasis*, **2015**, 113, 976-87	7	8
154	Genetic polymorphisms associated with increased risk of developing chronic myelogenous leukemia. *Oncotarget*, **2015**, 6, 36269-77	3.3	23
153	FAF-Drugs3: a web server for compound property calculation and chemical library design. *Nucleic Acids Research*, **2015**, 43, W200-7	20.1	192
152	Theileria parasites secrete a prolyl isomerase to maintain host leukocyte transformation. *Nature*, **2015**, 520, 378-82	50.4	71
151	Which three-dimensional characteristics make efficient inhibitors of protein-protein interactions?. *Journal of Chemical Information and Modeling*, **2014**, 54, 3067-79	6.1	33
150	Identification of Small Inhibitory Molecules Targeting the Bfl-1 Anti-Apoptotic Protein That Alleviates Resistance to ABT-737. *Journal of Biomolecular Screening*, **2014**, 19, 1035-46		10
149	Ligand efficiency driven design of new inhibitors of Mycobacterium tuberculosis transcriptional repressor EthR using fragment growing, merging, and linking approaches. *Journal of Medicinal Chemistry*, **2014**, 57, 4876-88	8.3	50
148	Discovery of novel inhibitors of vascular endothelial growth factor-A-Neuropilin-1 interaction by structure-based virtual screening. *Bioorganic and Medicinal Chemistry*, **2014**, 22, 4042-8	3.4	30
147	Identification of novel small molecule inhibitors of activated protein C. *Thrombosis Research*, **2014**, 133, 1105-14	8.2	12
146	Rational design of small molecules targeting the C2 domain of coagulation factor VIII. *Blood*, **2014**, 123, 113-20	2.2	17
145	Drug-Like Protein-Protein Interaction Modulators: Challenges and Opportunities for Drug Discovery and Chemical Biology. *Molecular Informatics*, **2014**, 33, 414-437	3.8	84
144	EFFICIENCY OF A HIERARCHICAL DOCKING PROTOCOL FOR COMPUTATIONAL LIGAND SCREENING AGAINST HOMOLOGY MODELS. *Biomedical Engineering - Applications, Basis and Communications*, **2014**, 26, 1450024	0.6	1
143	1,2,4-Triazole derivatives as transient inactivators of kallikreins involved in skin diseases. *Bioorganic and Medicinal Chemistry Letters*, **2013**, 23, 4547-51	2.9	27
142	Identification by in silico and in vitro screenings of small organic molecules acting as reversible inhibitors of kallikreins. *European Journal of Medicinal Chemistry*, **2013**, 70, 661-8	6.8	17
141	Aggrecanase-2 inhibitors based on the acylthiosemicarbazide zinc-binding group. *European Journal of Medicinal Chemistry*, **2013**, 69, 244-61	6.8	10
140	A Leap into the Chemical Space of Protein–Protein Interaction Inhibitors **2013**, 63-83		1
139	iPPI-DB: a manually curated and interactive database of small non-peptide inhibitors of protein-protein interactions. *Drug Discovery Today*, **2013**, 18, 958-68	8.8	79
138	Molecular basis of coagulation factor V deficiency caused by the R1698W inter-domain mutation. *Thrombosis and Haemostasis*, **2013**, 110, 31-8	7	2

137	One hundred thousand mouse clicks down the road: selected online resources supporting drug discovery collected over a decade. *Drug Discovery Today*, **2013**, 18, 1081-9	8.8	68
136	Insights into an original pocket-ligand pair classification: a promising tool for ligand profile prediction. *PLoS ONE*, **2013**, 8, e63730	3.7	15
135	1,2,4-Oxadiazoles identified by virtual screening and their non-covalent inhibition of the human 20S proteasome. *Current Medicinal Chemistry*, **2013**, 20, 2351-62	4.3	23
134	In silico mechanistic profiling to probe small molecule binding to sulfotransferases. *PLoS ONE*, **2013**, 8, e73587	3.7	14
133	Toward in silico structure-based ADMET prediction in drug discovery. *Drug Discovery Today*, **2012**, 17, 44-55	8.8	171
132	Design and synthesis of novel bis-thiazolone derivatives as micromolar CDC25 phosphatase inhibitors: effect of dimerisation on phosphatase inhibition. *Bioorganic and Medicinal Chemistry Letters*, **2012**, 22, 7345-50	2.9	16
131	In silico prediction of aqueous solubility: a multimodel protocol based on chemical similarity. *Molecular Pharmaceutics*, **2012**, 9, 3127-35	5.6	22
130	Established and emerging trends in computational drug discovery in the structural genomics era. *Chemistry and Biology*, **2012**, 19, 29-41		54
129	Analysis of binding sites on complement factor I using artificial N-linked glycosylation. *Journal of Biological Chemistry*, **2012**, 287, 13572-83	5.4	8
128	A leap into the chemical space of protein-protein interaction inhibitors. *Current Pharmaceutical Design*, **2012**, 18, 4648-67	3.3	53
127	AMMOS software: method and application. *Methods in Molecular Biology*, **2012**, 819, 127-41	1.4	2
126	Tyrosine kinase syk non-enzymatic inhibitors and potential anti-allergic drug-like compounds discovered by virtual and in vitro screening. *PLoS ONE*, **2011**, 6, e21117	3.7	17
125	Targeting the proangiogenic VEGF-VEGFR protein-protein interface with drug-like compounds by in silico and in vitro screening. *Chemistry and Biology*, **2011**, 18, 1631-9		35
124	Three-dimensional structure generators of drug-like compounds: DG-AMMOS, an open-source package. *Expert Opinion on Drug Discovery*, **2011**, 6, 339-51	6.2	9
123	Target-Based Virtual Screening to Address Protein–Protein Interfaces. *Methods and Principles in Medicinal Chemistry*, **2011**, 435-465	0.4	
122	The FAF-Drugs2 server: a multistep engine to prepare electronic chemical compound collections. *Bioinformatics*, **2011**, 27, 2018-20	7.2	70
121	Analysis of binding sites on complement factor I that are required for its activity. *Journal of Biological Chemistry*, **2010**, 285, 6235-45	5.4	20
120	Mutations in components of complement influence the outcome of Factor I-associated atypical hemolytic uremic syndrome. *Kidney International*, **2010**, 77, 339-49	9.9	131

119	In Silico ADME/Tox Predictions **2010**, 29-124		4
118	Tensin2 reduces intracellular phosphatidylinositol 3,4,5-trisphosphate levels at the plasma membrane. *Biochemical and Biophysical Research Communications*, **2010**, 399, 396-401	3.4	12
117	Designing focused chemical libraries enriched in protein-protein interaction inhibitors using machine-learning methods. *PLoS Computational Biology*, **2010**, 6, e1000695	5	94
116	Mutations in complement factor I as found in atypical hemolytic uremic syndrome lead to either altered secretion or altered function of factor I. *European Journal of Immunology*, **2010**, 40, 172-85	6.1	48
115	Novel organic proteasome inhibitors identified by virtual and in vitro screening. *Journal of Medicinal Chemistry*, **2010**, 53, 509-13	8.3	40
114	How to choose relevant multiple receptor conformations for virtual screening: a test case of Cdk2 and normal mode analysis. *European Biophysics Journal*, **2010**, 39, 1365-72	1.9	65
113	In silico studies of blood coagulation proteins: from mosaic proteases to nonenzymatic cofactor inhibitors. *Current Opinion in Structural Biology*, **2010**, 20, 168-79	8.1	14
112	Rationalizing the chemical space of protein-protein interaction inhibitors. *Drug Discovery Today*, **2010**, 15, 220-9	8.8	158
111	Druggable pockets and binding site centric chemical space: a paradigm shift in drug discovery. *Drug Discovery Today*, **2010**, 15, 656-67	8.8	214
110	New non-hydroxamic ADAMTS-5 inhibitors based on the 1,2,4-triazole-3-thiol scaffold. *Bioorganic and Medicinal Chemistry Letters*, **2010**, 20, 6213-6	2.9	19
109	Zebrafish ProVEGF-C expression, proteolytic processing and inhibitory effect of unprocessed ProVEGF-C during fin regeneration. *PLoS ONE*, **2010**, 5, e11438	3.7	17
108	Characterization of the complement inhibitory function of rhesus rhadinovirus complement control protein (RCP). *Journal of Biological Chemistry*, **2009**, 284, 505-514	5.4	21
107	Development of novel thiazolopyrimidines as CDC25B phosphatase inhibitors. *ChemMedChem*, **2009**, 4, 633-48	3.7	71
106	Genetic, molecular and functional analyses of complement factor I deficiency. *European Journal of Immunology*, **2009**, 39, 310-23	6.1	39
105	DG-AMMOS: a new tool to generate 3d conformation of small molecules using distance geometry and automated molecular mechanics optimization for in silico screening. *BMC Chemical Biology*, **2009**, 9, 6		31
104	MED-3DMC: a new tool to generate 3D conformation ensembles of small molecules with a Monte Carlo sampling of the conformational space. *European Journal of Medicinal Chemistry*, **2009**, 44, 1405-9	6.8	23
103	Structure-based virtual ligand screening: recent success stories. *Combinatorial Chemistry and High Throughput Screening*, **2009**, 12, 1000-16	1.3	101
102	MS-DOCK: accurate multiple conformation generator and rigid docking protocol for multi-step virtual ligand screening. *BMC Bioinformatics*, **2008**, 9, 184	3.6	84

101	FAF-Drugs2: free ADME/tox filtering tool to assist drug discovery and chemical biology projects. *BMC Bioinformatics*, **2008**, 9, 396	3.6	192
100	AMMOS: Automated Molecular Mechanics Optimization tool for in silico Screening. *BMC Bioinformatics*, **2008**, 9, 438	3.6	39
99	A novel druglike spleen tyrosine kinase binder prevents anaphylactic shock when administered orally. *Journal of Allergy and Clinical Immunology*, **2008**, 122, 188-94, 194.e1-3	11.5	24
98	Receptor-based virtual ligand screening for the identification of novel CDC25 phosphatase inhibitors. *Journal of Chemical Information and Modeling*, **2008**, 48, 157-65	6.1	36
97	A novel non-synonymous polymorphism (p.Arg240His) in C4b-binding protein is associated with atypical hemolytic uremic syndrome and leads to impaired alternative pathway cofactor activity. *Journal of Immunology*, **2008**, 180, 6385-91	5.3	45
96	Mapping of the factor Xa binding site on factor Va by site-directed mutagenesis. *Journal of Biological Chemistry*, **2008**, 283, 20805-12	5.4	14
95	Defining the structure of membrane-bound human blood coagulation factor Va. *Journal of Thrombosis and Haemostasis*, **2008**, 6, 76-82	15.4	20
94	In silico-in vitro screening of protein-protein interactions: towards the next generation of therapeutics. *Current Pharmaceutical Biotechnology*, **2008**, 9, 103-22	2.6	47
93	Combining Ligand- and Structure-Based Methods in Drug Design Projects. *Current Computer-Aided Drug Design*, **2008**, 4, 250-258	1.4	21
92	Screening Outside the Catalytic Site: Inhibition of Macromolecular Inter-actions Through Structure-Based Virtual Ligand Screening Experiments. *The Open Biochemistry Journal*, **2008**, 2, 29-37	0.9	14
91	MED-SuMoLig: a new ligand-based screening tool for efficient scaffold hopping. *Journal of Chemical Information and Modeling*, **2007**, 47, 1097-110	6.1	31
90	Protein structure analysis online. *Current Protocols in Protein Science*, **2007**, Chapter 2, Unit 2.13	3.1	1
89	Structure-based virtual ligand screening with LigandFit: pose prediction and enrichment of compound collections. *Proteins: Structure, Function and Bioinformatics*, **2007**, 68, 712-25	4.2	41
88	Molecular characterization of the interaction between porins of Neisseria gonorrhoeae and C4b-binding protein. *Journal of Immunology*, **2007**, 179, 540-7	5.3	16
87	Free resources to assist structure-based virtual ligand screening experiments. *Current Protein and Peptide Science*, **2007**, 8, 381-411	2.8	91
86	Frog: a FRee Online druG 3D conformation generator. *Nucleic Acids Research*, **2007**, 35, W568-72	20.1	67
85	Kaposi's sarcoma-associated herpes virus complement control protein: KCP--complement inhibition and more. *Molecular Immunology*, **2007**, 44, 11-22	4.3	16
84	Design of protein membrane interaction inhibitors by virtual ligand screening, proof of concept with the C2 domain of factor V. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 12697-702	11.5	41

83	Functional analysis of the factor IX epidermal growth factor-like domain mutation Ile66Thr associated with mild hemophilia B. *Pathophysiology of Haemostasis and Thrombosis: International Journal on Haemostasis and Thrombosis Research*, **2006**, 35, 370-5		2
82	FAF-Drugs: free ADME/tox filtering of compound collections. *Nucleic Acids Research*, **2006**, 34, W738-44	20.1	96
81	Receptor-based computational screening of compound databases: the main docking-scoring engines. *Current Protein and Peptide Science*, **2006**, 7, 369-93	2.8	40
80	A formylated hexapeptide ligand mimics the ability of Wnt-5a to impair migration of human breast epithelial cells. *Journal of Biological Chemistry*, **2006**, 281, 2740-9	5.4	92
79	The Kaposi's sarcoma-associated herpesvirus complement control protein (KCP) binds to heparin and cell surfaces via positively charged amino acids in CCP1-2. *Molecular Immunology*, **2006**, 43, 1665-75	4.3	41
78	Prothrombin deficiency caused by compound heterozygosity for two novel mutations in the prothrombin gene associated with a bleeding tendency. *Thrombosis and Haemostasis*, **2006**, 95, 195-198	7	19
77	Proposed structural models of the prothrombinase (FXa-FVa) complex. *Proteins: Structure, Function and Bioinformatics*, **2006**, 63, 440-50	4.2	39
76	PCE: web tools to compute protein continuum electrostatics. *Nucleic Acids Research*, **2005**, 33, W372-5	20.1	49
75	RPBS: a web resource for structural bioinformatics. *Nucleic Acids Research*, **2005**, 33, W44-9	20.1	68
74	The anticoagulant protein C pathway. *FEBS Letters*, **2005**, 579, 3310-6	3.8	189
73	Noonan syndrome type I with PTPN11 3 bp deletion: structure-function implications. *Proteins: Structure, Function and Bioinformatics*, **2005**, 58, 7-13	4.2	13
72	The gamma-carboxyglutamic acid domain of anticoagulant protein S is involved in activated protein C cofactor activity, independently of phospholipid binding. *Blood*, **2005**, 105, 122-30	2.2	32
71	Fast structure-based virtual ligand screening combining FRED, DOCK, and Surflex. *Journal of Medicinal Chemistry*, **2005**, 48, 6012-22	8.3	96
70	A critical role for Gly25 in the B chain of human thrombin. *Journal of Thrombosis and Haemostasis*, **2005**, 3, 139-45	15.4	9
69	Molecular models of the procoagulant factor VIIIa-factor IXa complex. *Journal of Thrombosis and Haemostasis*, **2005**, 3, 2044-56	15.4	25
68	Regulation of blood coagulation by the protein C anticoagulant pathway: novel insights into structure-function relationships and molecular recognition. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2005**, 25, 1311-20	9.4	205
67	The Kaposi's sarcoma-associated herpesvirus complement control protein mimics human molecular mechanisms for inhibition of the complement system. *Journal of Biological Chemistry*, **2004**, 279, 45093-101	5.4	34
66	Altered inactivation pathway of factor Va by activated protein C in the presence of heparin. *FEBS Journal*, **2004**, 271, 2724-36		10

65	Structural stability and heat-induced conformational change of two complement inhibitors: C4b-binding protein and factor H. *Protein Science*, **2004**, 13, 1356-64	6.3	28
64	Functional properties of recombinant factor V mutated in a potential calcium-binding site. *Biochemistry*, **2004**, 43, 5803-10	3.2	10
63	Complement inhibitor C4b-binding protein-friend or foe in the innate immune system?. *Molecular Immunology*, **2004**, 40, 1333-46	4.3	147
62	Theoretical and experimental study of the D2194G mutation in the C2 domain of coagulation factor V. *Biophysical Journal*, **2004**, 86, 488-98	2.9	16
61	Functions of human complement inhibitor C4b-binding protein in relation to its structure. *Archivum Immunologiae Et Therapiae Experimentalis*, **2004**, 52, 83-95	4	25
60	Mutations in alpha-chain of C4BP that selectively affect its factor I cofactor function. *Journal of Biological Chemistry*, **2003**, 278, 43437-42	5.4	27
59	Factor V New Brunswick: Ala221Val associated with FV deficiency reproduced in vitro and functionally characterized. *Blood*, **2003**, 102, 1316-22	2.2	27
58	Antithrombin Phe229Leu: a new homozygous variant leading to spontaneous antithrombin polymerization in vivo associated with severe childhood thrombosis. *Blood*, **2003**, 102, 919-25	2.2	46
57	Role of CCP2 of the C4b-binding protein beta-chain in protein S binding evaluated by mutagenesis and monoclonal antibodies. *FEBS Journal*, **2003**, 270, 93-100		5
56	Probing plasma clearance of the thrombin-antithrombin complex with a monoclonal antibody against the putative serpin-enzyme complex receptor-binding site. *FEBS Journal*, **2003**, 270, 4059-69		8
55	Functional analysis of the EGF-like domain mutations Pro55Ser and Pro55Leu, which cause mild hemophilia B. *Journal of Thrombosis and Haemostasis*, **2003**, 1, 782-90	15.4	8
54	Molecular recognition in the protein C anticoagulant pathway. *Journal of Thrombosis and Haemostasis*, **2003**, 1, 1525-34	15.4	68
53	Mutations within the cyclooxygenase-1 gene in aspirin non-responders with recurrence of stroke. *Thrombosis Research*, **2003**, 112, 275-83	8.2	38
52	Protein C Deficiency caused by Homozygosity for a Novel PROC D180G Mutation In vitro Expression and Structural Analysis of the Mutation. *Thrombosis and Haemostasis*, **2002**, 88, 632-638	7	7
51	Structural requirements of anticoagulant protein S for its binding to the complement regulator C4b-binding protein. *Journal of Biological Chemistry*, **2002**, 277, 15099-106	5.4	19
50	Defining the factor Xa-binding site on factor Va by site-directed glycosylation. *Journal of Biological Chemistry*, **2002**, 277, 50022-9	5.4	32
49	A novel interaction of outer membrane protein A with C4b binding protein mediates serum resistance of Escherichia coli K1. *Journal of Immunology*, **2002**, 169, 6352-60	5.3	136
48	The N-terminal epidermal growth factor-like domain of coagulation factor IX. Probing its functions in the activation of factor IX and factor X with a monoclonal antibody. *Journal of Biological Chemistry*, **2002**, 277, 35616-24	5.4	13

47	3-Dimensional structure of membrane-bound coagulation factor VIII: modeling of the factor VIII heterodimer within a 3-dimensional density map derived by electron crystallography. *Blood*, **2002**, 99, 1215-23	2.2	137
46	Structural bioinformatics: methods, concepts and applications to blood coagulation proteins. *Current Protein and Peptide Science*, **2002**, 3, 341-64	2.8	16
45	Two clusters of charged residues located in the electropositive face of the von Willebrand factor A1 domain are essential for heparin binding. *Biochemistry*, **2002**, 41, 6668-78	3.2	22
44	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	4.2	23
43	Screening the molecular surface of human anticoagulant protein C: a search for interaction sites. *Journal of Computer-Aided Molecular Design*, **2001**, 15, 13-27	4.2	11
42	Localization of a hydrophobic binding site for anticoagulant protein S on the beta -chain of complement regulator C4b-binding protein. *Journal of Biological Chemistry*, **2001**, 276, 4330-7	5.4	18
41	Secondary substrate-binding exosite in the serine protease domain of activated protein C important for cleavage at Arg-506 but not at Arg-306 in factor Va. *Journal of Biological Chemistry*, **2001**, 276, 23105-8	5.4	38
40	Structural and energetic characteristics of the heparin-binding site in antithrombotic protein C. *Journal of Biological Chemistry*, **2001**, 276, 24122-8	5.4	44
39	Proposed lipocalin fold for apolipoprotein M based on bioinformatics and site-directed mutagenesis. *FEBS Letters*, **2001**, 499, 127-32	3.8	76
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