Bruno O Villoutreix

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5485759/publications.pdf

Version: 2024-02-01

221 papers	9,172 citations	36303 51 h-index	58581 82 g-index
239 all docs	239 docs citations	239 times ranked	10334 citing authors

#	Article	IF	Citations
1	Kinase signaling as a drug target modality for regulation of vascular hyperpermeability: A case for ARDS therapy development. Drug Discovery Today, 2022, , .	6.4	0
2	Machine learning-driven identification of drugs inhibiting cytochrome P450 2C9. PLoS Computational Biology, 2022, 18, e1009820.	3.2	11
3	Dominant negative mutation in oxalate transporterSLC26A6associated with enteric hyperoxaluria and nephrolithiasis. Journal of Medical Genetics, 2022, 59, 1035-1043.	3.2	7
4	Novel treatment strategy for NRAS-mutated melanoma through a selective inhibitor of CD147/VEGFR-2 interaction. Oncogene, 2022, 41, 2254-2264.	5.9	5
5	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.	1.0	2
6	Furin and COVID-19: Structure, Function and Chemoinformatic Analysis of Representative Active Site Inhibitors. Frontiers in Drug Discovery, 2022, 2, .	2.8	7
7	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.	1.3	0
8	Virtual screening web servers: designing chemical probes and drug candidates in the cyberspace. Briefings in Bioinformatics, 2021, 22, 1790-1818.	6.5	81
9	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.	4.1	18
10	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 ACE2â€“Spike RBD Interface. International Journal of Molecular Sciences, 2021, 22, 1695.	4.1	72
11	Antihistamine and cationic amphiphilic drugs, old molecules as new tools against the COVID-19?. Medical Hypotheses, 2021, 148, 110508.	1.5	9
12	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, Volume 14, 71-85.	2.6	12
13	Role of Gly197 in the structure and function of protein C. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129892.	2.4	1
14	Antithrombin Resistance Rescues Clotting Defect of Homozygous Prothrombin-Y510N Dysprothrombinemia. Thrombosis and Haemostasis, 2021, , .	3.4	0
15	PAK1-Dependent Antitumor Effect of AAC-11â€'Derived Peptides on SÃ©zary Syndrome Malignant CD4+ T Lymphocytes. Journal of Investigative Dermatology, 2021, 141, 2261-2271.e5.	0.7	3
16	Computational Analysis of Chemical Space of Natural Compounds Interacting with Sulfotransferases. Molecules, 2021, 26, 6360.	3.8	3
17	Anti-tumor effect of anti-apoptosis clone 11 protein-derived peptides on SÃ©zary syndrome malignant CD4+ T lymphocytes. European Journal of Cancer, 2021, 156, S14.	2.8	0
18	Demystifying the Molecular Basis of Pyrazoloquinolinones Recognition at the Extracellular Î±1+/Î²3-Interface of the GABAA Receptor by Molecular Modeling. Frontiers in Pharmacology, 2020, 11, 561834.	3.5	3

#	Article	IF	Citations
19	Fast Rescoring Protocols to Improve the Performance of Structure-Based Virtual Screening Performed on Proteinâ€“Protein Interfaces. Journal of Chemical Information and Modeling, 2020, 60, 3910-3934.	5.4	14
20	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.	4.0	40
21	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.	3.5	8
22	Anti-Factor B Antibodies and Acute Postinfectious GN in Children. Journal of the American Society of Nephrology: JASN, 2020, 31, 829-840.	6.1	50
23	FastTargetPred: a program enabling the fast prediction of putative protein targets for input chemical databases. Bioinformatics, 2020, 36, 4225-4226.	4.1	5
24	Gly197Arg mutation in protein C causes recurrent thrombosis in a heterozygous carrier. Journal of Thrombosis and Haemostasis, 2020, 18, 1141-1153.	3.8	5
25	Prevention of COVID-19 by drug repurposing: rationale from drugs prescribed for mental disorders. Drug Discovery Today, 2020, 25, 1287-1290.	6.4	26
26	Thr90Ser Mutation in Antithrombin is Associated with Recurrent Thrombosis in a Heterozygous Carrier. Thrombosis and Haemostasis, 2020, 120, 1045-1055.	3.4	5
27	Analysis of protein missense alterations by combining sequenceâ€•and structureâ€based methods. Molecular Genetics & Genomic Medicine, 2020, 8, e1166.	1.2	25
28	Fr-PPIChem: An Academic Compound Library Dedicated to Proteinâ€“Protein Interactions. ACS Chemical Biology, 2020, 15, 1566-1574.	3.4	29
29	ELA/APELA precursor cleaved by furin displays tumor suppressor function in renal cell carcinoma through mTORC1 activation. JCI Insight, 2020, 5, .	5.0	25
30	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.	3.3	23
31	A Free Web-Based Protocol to Assist Structure-Based Virtual Screening Experiments. International Journal of Molecular Sciences, 2019, 20, 4648.	4.1	16
32	Analysis of solvent-exposed and buried co-crystallized ligands: a case study to support the design of novel proteinâ€“protein interaction inhibitors. Drug Discovery Today, 2019, 24, 551-559.	6.4	20
33	Breast Cancer Targeting through Inhibition of the Endoplasmic Reticulum-Based Apoptosis Regulator Nrh/BCL2L10. Cancer Research, 2018, 78, 1404-1417.	0.9	34
34	Expression and functional characterization of two natural heparinâ€binding site variants of antithrombin. Journal of Thrombosis and Haemostasis, 2018, 16, 330-341.	3.8	7
35	Insights into molecular mechanisms of drug metabolism dysfunction of human CYP2C9*30. PLoS ONE, 2018, 13, e0197249.	2.5	24
36	Online structure-based screening of purchasable approved drugs and natural compounds: retrospective examples of drug repositioning on cancer targets. Oncotarget, 2018, 9, 32346-32361.	1.8	25

#	Article	IF	Citations
37	Acute genetic ablation of pendrin lowers blood pressure in mice. Nephrology Dialysis Transplantation, 2017, 32, gfw393.	0.7	31
38	Computational Biology and Chemistry in MTi: Emphasis on the Prediction of Some ADMET Properties. Molecular Informatics, 2017, 36, 1700008.	2.5	3
39	Computational analysis of calculated physicochemical and ADMET properties of protein-protein interaction inhibitors. Scientific Reports, 2017, 7, 46277.	3.3	128
40	FAF-Drugs4: free ADME-tox filtering computations for chemical biology and early stages drug discovery. Bioinformatics, 2017, 33, 3658-3660.	4.1	230
41	In silico model of the human ClC-Kb chloride channel: pore mapping, biostructural pathology and drug screening. Scientific Reports, 2017, 7, 7249.	3.3	15
42	Identification of insulin-sensitizing molecules acting by disrupting the interaction between the Insulin Receptor and Grb14. Scientific Reports, 2017, 7, 16901.	3.3	4
43	AMMOS2: a web server for proteinâ€“ligandâ€“water complexes refinement via molecular mechanics. Nucleic Acids Research, 2017, 45, W350-W355.	14.5	24
44	Pan-assay interference compounds (PAINS) that may not be too painful for chemical biology projects. Drug Discovery Today, 2017, 22, 1131-1133.	6.4	26
45	Pharmacogenomics of the cytochrome P450 2C family: impacts of amino acid variations on drug metabolism. Drug Discovery Today, 2017, 22, 366-376.	6.4	58
46	Gly74Ser mutation in protein C causes thrombosis due to a defect in protein S-dependent anticoagulant function. Thrombosis and Haemostasis, 2017, 117, 1358-1369.	3.4	8
47	Blockade of the malignant phenotype by Î²-subunit selective noncovalent inhibition of immuno- and constitutive proteasomes. Oncotarget, 2017, 8, 10437-10449.	1.8	13
48	A Cell-Penetrating Peptide Targeting AAC-11 Specifically Induces Cancer Cells Death. Cancer Research, 2016, 76, 5479-5490.	0.9	51
49	Discoidin Domains as Emerging Therapeutic Targets. Trends in Pharmacological Sciences, 2016, 37, 641-659.	8.7	21
50	Combining bioinformatics, chemoinformatics and experimental approaches to design chemical probes: Applications in the field of blood coagulation. Annales Pharmaceutiques Francaises, 2016, 74, 253-266.	1.0	2
51	iPPI-DB: an online database of modulators of proteinâ€“protein interactions. Nucleic Acids Research, 2016, 44, D542-D547.	14.5	49
52	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.	2.6	3
53	In Silico Approaches Assisting the Rational Design of Low Molecular Weight Proteinâ€“Protein Interaction Modulators. , 2015, , 441-482.		0
54	Amino acid residues in the laminin G domains of protein S involved in tissue factor pathway inhibitor interaction. Thrombosis and Haemostasis, 2015, 113, 976-987.	3.4	12

#	Article	IF	Citations
55	Genetic polymorphisms associated with increased risk of developing chronic myelogenous leukemia. Oncotarget, 2015, 6, 36269-36277.	1.8	27
56	FAF-Drugs3: a web server for compound property calculation and chemical library design. Nucleic Acids Research, 2015, 43, W200-W207.	14.5	237
57	Theileria parasites secrete a prolyl isomerase to maintain host leukocyte transformation. Nature, 2015, 520, 378-382.	27.8	100
58	DNA damage-induced nuclear translocation of Apaf-1 is mediated by nucleoporin Nup107. Cell Cycle, 2015, 14, 1242-1251.	2.6	26
59	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, 367-376.	2.2	24
60	In silico design of low molecular weight proteinâ€“protein interaction inhibitors: Overall concept and recent advances. Progress in Biophysics and Molecular Biology, 2015, 119, 20-32.	2.9	56
61	Strategies in the Search for New Lead Compounds or Original Working Hypotheses. , 2015, , 73-99.		15
62	Application Strategies for the Primary Structureâ€“Activity Relationship Exploration. , 2015, , 301-318.		2
63	MTiOpenScreen: a web server for structure-based virtual screening. Nucleic Acids Research, 2015, 43, W448-W454.	14.5	159
64	Computational investigations of hERG channel blockers: New insights and current predictive models. Advanced Drug Delivery Reviews, 2015, 86, 72-82.	13.7	82
65	Therapeutic Targeting of Nuclear Î³-Tubulin in RB1-Negative Tumors. Molecular Cancer Research, 2015, 13, 1073-1082.	3.4	13
66	Integrated structure- and ligand-based in silico approach to predict inhibition of cytochrome P450 2D6. Bioinformatics, 2015, 31, 3930-3937.	4.1	27
67	Drugâ€Like Proteinï£¿Protein Interaction Modulators: Challenges and Opportunities for Drug Discovery and Chemical Biology. Molecular Informatics, 2014, 33, 414-437.	2.5	93
68	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
69	Which Three-Dimensional Characteristics Make Efficient Inhibitors of Proteinâ€“Protein Interactions?. Journal of Chemical Information and Modeling, 2014, 54, 3067-3079.	5.4	38
70	Identification of Small Inhibitory Molecules Targeting the Bfl-1 Anti-Apoptotic Protein That Alleviates Resistance to ABT-737. Journal of Biomolecular Screening, 2014, 19, 1035-1046.	2.6	11
71	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, 4876-4888.	6.4	59
72	Discovery of novel inhibitors of vascular endothelial growth factor-Aâ€“Neuropilin-1 interaction by structure-based virtual screening. Bioorganic and Medicinal Chemistry, 2014, 22, 4042-4048.	3.0	35

#	Article	IF	Citations
73	Identification of novel small molecule inhibitors of activated protein C. Thrombosis Research, 2014, 133, 1105-1114.	1.7	14
74	Rational design of small molecules targeting the C2 domain of coagulation factor VIII. Blood, 2014, 123, 113-120.	1.4	22
75	1,2,4-Triazole derivatives as transient inactivators of kallikreins involved in skin diseases. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 4547-4551.	2.2	29
76	Identification by in silico and inÂvitro screenings of small organic molecules acting as reversible inhibitors of kallikreins. European Journal of Medicinal Chemistry, 2013, 70, 661-668.	5.5	19
77	Aggrecanase-2 inhibitors based on the acylthiosemicarbazide zinc-binding group. European Journal of Medicinal Chemistry, 2013, 69, 244-261.	5.5	13
78	iPPI-DB: a manually curated and interactive database of small non-peptide inhibitors of proteinâ€“protein interactions. Drug Discovery Today, 2013, 18, 958-968.	6.4	91
79	Molecular basis of coagulation factor V deficiency caused by the R1698W inter-domain mutation. Thrombosis and Haemostasis, 2013, 110, 31-38.	3.4	3
80	One hundred thousand mouse clicks down the road: selected online resources supporting drug discovery collected over a decade. Drug Discovery Today, 2013, 18, 1081-1089.	6.4	76
81	Insights into an Original Pocket-Ligand Pair Classification: A Promising Tool for Ligand Profile Prediction. PLoS ONE, 2013, 8, e63730.	2.5	18
82	1,2,4-Oxadiazoles Identified by Virtual Screening and their Non-Covalent Inhibition of the Human 20S Proteasome. Current Medicinal Chemistry, 2013, 20, 2351-2362.	2.4	25
83	In Silico Mechanistic Profiling to Probe Small Molecule Binding to Sulfotransferases. PLoS ONE, 2013, 8, e73587.	2.5	23
84	Analysis of Binding Sites on Complement Factor I Using Artificial N-Linked Glycosylation. Journal of Biological Chemistry, 2012, 287, 13572-13583.	3.4	9
85	A Leap into the Chemical Space of Protein-Protein Interaction Inhibitors. Current Pharmaceutical Design, 2012, 18, 4648-4667.	1.9	64
86	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, 7345-7350.	2.2	19
87	In Silico Prediction of Aqueous Solubility: A Multimodel Protocol Based on Chemical Similarity. Molecular Pharmaceutics, 2012, 9, 3127-3135.	4.6	33
88	Established and Emerging Trends in Computational Drug Discovery in the Structural Genomics Era. Chemistry and Biology, 2012, 19, 29-41.	6.0	57
89	Toward in silico structure-based ADMET prediction in drug discovery. Drug Discovery Today, 2012, 17, 44-55.	6.4	220
90	AMMOS Software: Method and Application. Methods in Molecular Biology, 2012, 819, 127-141.	0.9	2

#	Article	IF	Citations
91	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.	2.5	23
92	Targeting the Proangiogenic VEGF-VEGFR Protein-Protein Interface with Drug-like Compounds by In Silico and InÂVitro Screening. Chemistry and Biology, 2011, 18, 1631-1639.	6.0	38
93	Three-dimensional structure generators of drug-like compounds: DG-AMMOS, an open-source package. Expert Opinion on Drug Discovery, 2011, 6, 339-351.	5.0	9
94	The FAF-Drugs2 server: a multistep engine to prepare electronic chemical compound collections. Bioinformatics, 2011, 27, 2018-2020.	4.1	81
95	Chemical Libraries for Virtual Screening. , 2011, , 1-19.		1
96	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, 172-185.	2.9	58
97	Editorial [Hot topic: Structure-Based Virtual Screening (Guest Editor: Walter Filgueira De Azevedo) Tj ETQq1 1 0.784314 rgBT /Overlo	2.1	26
98	Novel Organic Proteasome Inhibitors Identified by Virtual and in Vitro Screening. Journal of Medicinal Chemistry, 2010, 53, 509-513.	6.4	42
99	How to choose relevant multiple receptor conformations for virtual screening: a test case of Cdk2 and normal mode analysis. European Biophysics Journal, 2010, 39, 1365-1372.	2.2	68
100	In silico studies of blood coagulation proteins: from mosaic proteases to nonenzymatic cofactor inhibitors. Current Opinion in Structural Biology, 2010, 20, 168-179.	5.7	14
101	Rationalizing the chemical space of proteinâ€“protein interaction inhibitors. Drug Discovery Today, 2010, 15, 220-229.	6.4	185
102	Druggable pockets and binding site centric chemical space: a paradigm shift in drug discovery. Drug Discovery Today, 2010, 15, 656-667.	6.4	249
103	New non-hydroxamic ADAMTS-5 inhibitors based on the 1,2,4-triazole-3-thiol scaffold. Bioorganic and Medicinal Chemistry Letters, 2010, 20, 6213-6216.	2.2	21
104	Analysis of Binding Sites on Complement Factor I That Are Required for Its Activity. Journal of Biological Chemistry, 2010, 285, 6235-6245.	3.4	28
105	Mutations in components of complement influence the outcome of Factor I-associated atypical hemolytic uremic syndrome. Kidney International, 2010, 77, 339-349.	5.2	163
106	Tensin2 reduces intracellular phosphatidylinositol 3,4,5-trisphosphate levels at the plasma membrane. Biochemical and Biophysical Research Communications, 2010, 399, 396-401.	2.1	15
107	Designing Focused Chemical Libraries Enriched in Protein-Protein Interaction Inhibitors using Machine-Learning Methods. PLoS Computational Biology, 2010, 6, e1000695.	3.2	110
108	Zebrafish ProVEGF-C Expression, Proteolytic Processing and Inhibitory Effect of Unprocessed ProVEGF-C during Fin Regeneration. PLoS ONE, 2010, 5, e11438.	2.5	20

#	Article	IF	Citations
109	Characterization of the Complement Inhibitory Function of Rhesus Rhadinovirus Complement Control Protein (RCP). Journal of Biological Chemistry, 2009, 284, 505-514.	3.4	23
110	Development of Novel Thiazolopyrimidines as CDC25B Phosphatase Inhibitors. ChemMedChem, 2009, 4, 633-648.	3.2	84
111	Genetic, molecular and functional analyses of complement factor I deficiency. European Journal of Immunology, 2009, 39, 310-323.	2.9	53
112	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.	1.6	38
113	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, 1405-1409.	5.5	26
114	Structure-Based Virtual Ligand Screening: Recent Success Stories. Combinatorial Chemistry and High Throughput Screening, 2009, 12, 1000-1016.	1.1	114
115	Defining the structure of membraneâ€bound human blood coagulation factor Va. Journal of Thrombosis and Haemostasis, 2008, 6, 76-82.	3.8	25
116	MS-DOCK: Accurate multiple conformation generator and rigid docking protocol for multi-step virtual ligand screening. BMC Bioinformatics, 2008, 9, 184.	2.6	102
117	FAF-Drugs2: Free ADME/tox filtering tool to assist drug discovery and chemical biology projects. BMC Bioinformatics, 2008, 9, 396.	2.6	221
118	AMMOS: Automated Molecular Mechanics Optimization tool for in silico Screening. BMC Bioinformatics, 2008, 9, 438.	2.6	44
119	A novel druglike spleen tyrosine kinase binder prevents anaphylactic shock when administered orally. Journal of Allergy and Clinical Immunology, 2008, 122, 188-194.e3.	2.9	27
120	Molecular and functional analysis of complement factor I mutations in atypical haemolytic uraemic syndrome patients. Molecular Immunology, 2008, 45, 4131.	2.2	0
121	Characterization of the complement inhibitory function of Rhesus rhadinovirus. Molecular Immunology, 2008, 45, 4172-4173.	2.2	0
122	Receptor-Based Virtual Ligand Screening for the Identification of Novel CDC25 Phosphatase Inhibitors. Journal of Chemical Information and Modeling, 2008, 48, 157-165.	5.4	43
123	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, 6385-6391.	0.8	50
124	Mapping of the Factor Xa Binding Site on Factor Va by Site-directed Mutagenesis. Journal of Biological Chemistry, 2008, 283, 20805-20812.	3.4	19
125	In Silico-In Vitro Screening of Protein-Protein Interactions: Towards the Next Generation of Therapeutics. Current Pharmaceutical Biotechnology, 2008, 9, 103-122.	1.6	59
126	Combining Ligand- and Structure-Based Methods in Drug Design Projects. Current Computer-Aided Drug Design, 2008, 4, 250-258.	1.2	27

#	Article	IF	Citations
127	Screening Outside the Catalytic Site: Inhibition of Macromolecular Interactions Through Structure-Based Virtual Ligand Screening Experiments. The Open Biochemistry Journal, 2008, 2, 29-37.	0.5	17
128	Editorial [Hot Topic: Virtual Screening (Guest Editor: Bruno O. Villoutreix)]. Current Computer-Aided Drug Design, 2008, 4, 154-155.	1.2	0
129	Molecular Characterization of the Interaction between Porins of Neisseria gonorrhoeae and C4b-Binding Protein. Journal of Immunology, 2007, 179, 540-547.	0.8	19
130	Free Resources to Assist Structure-Based Virtual Ligand Screening Experiments. Current Protein and Peptide Science, 2007, 8, 381-411.	1.4	104
131	Frog: a FRee Online druG 3D conformation generator. Nucleic Acids Research, 2007, 35, W568-W572.	14.5	86
132	Kaposi's sarcoma-associated herpes virus complement control protein: KCP â€“ complement inhibition and more. Molecular Immunology, 2007, 44, 11-22.	2.2	18
133	Design of proteinâ€“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, 12697-12702.	7.1	50
134	MED-SuMoLig:â€‰ A New Ligand-Based Screening Tool for Efficient Scaffold Hopping. Journal of Chemical Information and Modeling, 2007, 47, 1097-1110.	5.4	34
135	Protein Structure Analysis Online. Current Protocols in Protein Science, 2007, 50, Unit 2.13.	2.8	1
136	Structure-based virtual ligand screening with LigandFit: Pose prediction and enrichment of compound collections. Proteins: Structure, Function and Bioinformatics, 2007, 68, 712-725.	2.6	45
137	A Formylated Hexapeptide Ligand Mimics the Ability of Wnt-5a to Impair Migration of Human Breast Epithelial Cells. Journal of Biological Chemistry, 2006, 281, 2740-2749.	3.4	107
138	The Kaposi's sarcoma-associated herpesvirus complement control protein (KCP) binds to heparin and cell surfaces via positively charged amino acids in CCP1â€“2. Molecular Immunology, 2006, 43, 1665-1675.	2.2	42
139	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.	3.4	21
140	Proposed structural models of the prothrombinase (FXa-FVa) complex. Proteins: Structure, Function and Bioinformatics, 2006, 63, 440-450.	2.6	47
141	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, 370-375.	0.3	2
142	FAF-Drugs: free ADME/tox filtering of compound collections. Nucleic Acids Research, 2006, 34, W738-W744.	14.5	115
143	Receptor-Based Computational Screening of Compound Databases: The Main Docking-Scoring Engines. Current Protein and Peptide Science, 2006, 7, 369-393.	1.4	47
144	Editorial [Hot Topic: Structure-Based Virtual Ligand Screening (Guest Editor: Bruno O. Villoutreix)]. Current Protein and Peptide Science, 2006, 7, 367-367.	1.4	0

#	Article	IF	Citations
145	Noonan syndrome type I with PTPN11 3 bp deletion: Structureâ€“function implications. Proteins: Structure, Function and Bioinformatics, 2005, 58, 7-13.	2.6	15
146	The Î³-carboxyglutamic acid domain of anticoagulant protein S is involved in activated protein C cofactor activity, independently of phospholipid binding. Blood, 2005, 105, 122-130.	1.4	33
147	Fast Structure-Based Virtual Ligand Screening Combining FRED, DOCK, and Surflex. Journal of Medicinal Chemistry, 2005, 48, 6012-6022.	6.4	106
148	A critical role for Gly25 in the B chain of human thrombin. Journal of Thrombosis and Haemostasis, 2005, 3, 139-145.	3.8	9
149	Molecular models of the procoagulant Factor VIIIa-Factor IXa complex. Journal of Thrombosis and Haemostasis, 2005, 3, 2044-2056.	3.8	31
150	Regulation of Blood Coagulation by the Protein C Anticoagulant Pathway. Arteriosclerosis, Thrombosis, and Vascular Biology, 2005, 25, 1311-1320.	2.4	268
151	PCE: web tools to compute protein continuum electrostatics. Nucleic Acids Research, 2005, 33, W372-W375.	14.5	51
152	RPBS: a web resource for structural bioinformatics. Nucleic Acids Research, 2005, 33, W44-W49.	14.5	81
153	The anticoagulant protein C pathway. FEBS Letters, 2005, 579, 3310-3316.	2.8	239
154	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, 45093-45101.	3.4	35
155	Altered inactivation pathway of factor Va by activated protein C in the presence of heparin. FEBS Journal, 2004, 271, 2724-2736.	0.2	14
156	Structural stability and heat-induced conformational change of two complement inhibitors: C4b-binding protein and factor H. Protein Science, 2004, 13, 1356-1364.	7.6	31
157	Functional Properties of Recombinant Factor V Mutated in a Potential Calcium-Binding Site. Biochemistry, 2004, 43, 5803-5810.	2.5	10
158	Complement inhibitor C4b-binding proteinâ€”friend or foe in the innate immune system?. Molecular Immunology, 2004, 40, 1333-1346.	2.2	170
159	Theoretical and Experimental Study of the D2194G Mutation in the C2 Domain of Coagulation Factor V. Biophysical Journal, 2004, 86, 488-498.	0.5	18
160	Functions of human complement inhibitor C4b-binding protein in relation to its structure. Archivum Immunologiae Et Therapiae Experimentalis, 2004, 52, 83-95.	2.3	27
161	Role of CCP2 of the C4b-binding protein Î²-chain in protein S binding evaluated by mutagenesis and monoclonal antibodies. FEBS Journal, 2003, 270, 93-100.	0.2	5
162	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, 4059-4069.	0.2	8

#	Article	IF	Citations
163	Functional analysis of the EGF-like domain mutations Pro55Ser and Pro55Leu, which cause mild hemophilia B. Journal of Thrombosis and Haemostasis, 2003, 1, 782-790.	3.8	10
164	Molecular recognition in the protein C anticoagulant pathway. Journal of Thrombosis and Haemostasis, 2003, 1, 1525-1534.	3.8	76
165	Mutations within the cyclooxygenase-1 gene in aspirin non-responders with recurrence of stroke. Thrombosis Research, 2003, 112, 275-283.	1.7	41
166	Mutations in Î±-Chain of C4BP That Selectively Affect Its Factor I Cofactor Function. Journal of Biological Chemistry, 2003, 278, 43437-43442.	3.4	31
167	Factor V New Brunswick: Ala221Val associated with FV deficiency reproduced in vitro and functionally characterized. Blood, 2003, 102, 1316-1322.	1.4	31
168	Antithrombin Phe229Leu: a new homozygous variant leading to spontaneous antithrombin polymerization in vivo associated with severe childhood thrombosis. Blood, 2003, 102, 919-925.	1.4	61
169	Defining the Factor Xa-binding Site on Factor Va by Site-directed Glycosylation. Journal of Biological Chemistry, 2002, 277, 50022-50029.	3.4	36
170	A Novel Interaction of Outer Membrane Protein A with C4b Binding Protein Mediates Serum Resistance of Escherichia coli K1. Journal of Immunology, 2002, 169, 6352-6360.	0.8	159
171	The N-terminal Epidermal Growth Factor-like Domain of Coagulation Factor IX. Journal of Biological Chemistry, 2002, 277, 35616-35624.	3.4	14
172	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, 1215-1223.	1.4	154
173	Structural Bioinformatics: Methods, Concepts and Applications to Blood Coagulation Proteins. Current Protein and Peptide Science, 2002, 3, 341-364.	1.4	18
174	Two Clusters of Charged Residues Located in the Electropositive Face of the Von Willebrand Factor A1 Domain Are Essential for Heparin Bindingâ€. Biochemistry, 2002, 41, 6668-6678.	2.5	36
175	Protein C Deficiency caused by Homozygosity for a Novel PROC D180G Mutation â€“ in vitro Expression and Structural Analysis of the Mutation. Thrombosis and Haemostasis, 2002, 88, 632-638.	3.4	7
176	Structural Requirements of Anticoagulant Protein S for Its Binding to the Complement Regulator C4b-binding Protein. Journal of Biological Chemistry, 2002, 277, 15099-15106.	3.4	24
177	Proposed lipocalin fold for apolipoprotein M based on bioinformatics and site-directed mutagenesis. FEBS Letters, 2001, 499, 127-132.	2.8	83
178	Characterization and Structural Impact of Five Novel PROS1 Mutations in Eleven Protein S-deficient Families. Thrombosis and Haemostasis, 2001, 86, 1392-1399.	3.4	16
179	Defect of Heparin Binding in Plasma and Recombinant von Willebrand Factor with Type 2 von Willebrand Disease Mutations. Thrombosis and Haemostasis, 2001, 86, 1459-1465.	3.4	2
180	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.	2.6	26

#	Article	IF	Citations
181	Screening the molecular surface of human anticoagulant protein C: a search for interaction sites. Journal of Computer-Aided Molecular Design, 2001, 15, 13-27.	2.9	12
182	Localization of a Hydrophobic Binding Site for Anticoagulant Protein S on the Î²-Chain of Complement Regulator C4b-binding Protein. Journal of Biological Chemistry, 2001, 276, 4330-4337.	3.4	19
183	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, 23105-23108.	3.4	45
184	Structural and Energetic Characteristics of the Heparin-binding Site in Antithrombotic Protein C. Journal of Biological Chemistry, 2001, 276, 24122-24128.	3.4	52
185	Factor VIII Inhibitors in Two Families with Mild Haemophilia A: Structural Analysis of the Mutations. Pathophysiology of Haemostasis and Thrombosis: International Journal on Haemostasis and Thrombosis Research, 2000, 30, 268-279.	0.3	13
186	Human C4b-Binding Protein Has Overlapping, But Not Identical, Binding Sites for C4b and Streptococcal M Proteins. Journal of Immunology, 2000, 164, 5328-5336.	0.8	74
187	Positively charged amino acids at the interface between Î±-chain CCP1 and CCP2 of C4BP are required for regulation of the classical C3-convertase. Molecular Immunology, 2000, 37, 445-453.	2.2	31
188	Quaternary Structure of the HSC70 Cochaperone HIP. Biochemistry, 2000, 39, 307-315.	2.5	23
189	Tracking Structural Features Leading to Resistance of Activated Protein C to Î±1-antitrypsinâ€. Biochemistry, 2000, 39, 2853-2860.	2.5	17
190	Activated Protein Câ^'Protein C Inhibitor Complex Formation:Â Characterization of a Neoepitope Provides Evidence for Extensive Insertion of the Reactive Center Loop. Biochemistry, 2000, 39, 15713-15720.	2.5	20
191	Mutations in a potential phospholipid binding loop in the C2 domain of factor V affecting the assembly of the prothrombinase complex. Blood Coagulation and Fibrinolysis, 2000, 11, 89-100.	1.0	1
192	In Vitro Characterisation of Two Naturally Occurring Mutations in the Thrombin-sensitive Region of Anticoagulant Protein S. Thrombosis and Haemostasis, 1999, 82, 1627-1633.	3.4	17
193	Involvement of Lys 62[217] and Lys 63[218] of Human Anticoagulant Protein C in Heparin Stimulation of Inhibition by the Protein C Inhibitor. Thrombosis and Haemostasis, 1999, 82, 72-79.	3.4	29
194	Structural prediction and analysis of endothelial cell protein C/activated protein C receptor. Protein Engineering, Design and Selection, 1999, 12, 833-840.	2.1	22
195	A Cluster of Positively Charged Amino Acids in the C4BP Î±-Chain Is Crucial for C4b Binding and Factor I Cofactor Function. Journal of Biological Chemistry, 1999, 274, 19237-19245.	3.4	98
196	The complement regulator C4b-binding protein analyzed by molecular modeling, bioinformatics and computer-aided experimental design. Immunopharmacology, 1999, 42, 121-134.	2.0	19
197	Probing the activation of protein C by the thrombin-thrombomodulin complex using structural analysis, site-directed mutagenesis, and computer modeling. Proteins: Structure, Function and Bioinformatics, 1999, 35, 218-234.	2.6	34
198	Partial Glycosylation of Asn2181in Human Factor V as a Cause of Molecular and Functional Heterogeneity. Modulation of Glycosylation Efficiency by Mutagenesis of the Consensus Sequence for N-Linked Glycosylationâ€. Biochemistry, 1999, 38, 13584-13591.	2.5	64

#	Article	IF	Citations
199	Interspecies Loop Grafting in the Protease Domain of Human Protein C Yielding Enhanced Catalytic and Anticoagulant Activity. Thrombosis and Haemostasis, 1999, 82, 1078-1087.	3.4	20
200	The C4b-binding proteinâ€"protein S interaction is hydrophobic in nature. BBA - Proteins and Proteomics, 1998, 1388, 181-189.	2.1	18
201	Structural investigation of C4b-binding protein by molecular modeling: Localization of putative binding sites. , 1998, 31, 391-405.		39
202	Molecular Models for the two Discoidin Domains of Human Blood Coagulation Factor V. Journal of Molecular Modeling, 1998, 4, 268-275.	1.8	30
203	Molecular Model for the C-type Lectin Domain of Human Thrombomodulin. Journal of Molecular Modeling, 1998, 4, 310-322.	1.8	13
204	Determination and analysis of antigenic epitopes of prostate specific antigen (PSA) and human glandular kallikrein 2 (hK2) using synthetic peptides and computer modeling. Protein Science, 1998, 7, 259-269.	7.6	60
205	Structural investigation of the A domains of human blood coagulation factor V by molecular modeling. Protein Science, 1998, 7, 1317-1325.	7.6	82
206	Amino Acid Residues in Thrombin-sensitive Region and First Epidermal Growth Factor Domain of Vitamin K-dependent Protein S Determining Specificity of the Activated Protein C Cofactor Function. Journal of Biological Chemistry, 1998, 273, 27449-27458.	3.4	35
207	Topological Studies of the Amino Terminal Modules of Vitamin K-dependent Protein S Using Monoclonal Antibody Epitope Mapping and Molecular Modeling. Thrombosis and Haemostasis, 1998, 80, 798-804.	3.4	20
208	Structural analysis of an anti-estradiol antibody. Molecular Immunology, 1997, 34, 1215-1226.	2.2	20
209	A theoretical model for the Gla-TSR-EGF-1 region of the anticoagulant cofactor protein S: from biostructural pathology to species-specific cofactor activity. Journal of Computer-Aided Molecular Design, 1997, 11, 293-304.	2.9	35
210	Local electrostatic potentials in pyridoxal phosphate labelled horse heart cytochrome c. Journal of Photochemistry and Photobiology B: Biology, 1997, 37, 74-83.	3.8	9
211	SHBG region of the anticoagulant cofactor protein S: Secondary structure prediction, circular dichroism spectroscopy, and analysis of naturally occurring mutations. , 1997, 29, 478-491.		32
212	Calcium binding to tandem repeats of EGFâ€like modules. Expression and characterization of the EGFâ€like modules of human Notchâ€1 implicated in receptorâ€ligand interactions. Protein Science, 1997, 6, 2059-2071.	7.6	57
213	Structural investigation of the alphaâ€1â€antichymotrypsin: Prostateâ€specific antigen complex by comparative model building. Protein Science, 1996, 5, 836-851.	7.6	32
214	A Two-Allele Polymorphism in Protein C Inhibitor with Varying Frequencies in Different Ethnic Populations. Thrombosis and Haemostasis, 1996, 75, 062-069.	3.4	8
215	Comparative modeling of the three CP modules of the ÃŸ-chain of C4BP and evaluation of potential sites of interaction with protein S. Protein Engineering, Design and Selection, 1995, 8, 1253-1258.	2.1	15
216	Characterization of a cDNA for Rhesus Monkey Protein C Inhibitor â€" Evidence for N-Terminal Involvement in Heparin Stimulation. Thrombosis and Haemostasis, 1995, 74, 1079-1087.	3.4	8

#	Article	IF	Citations
217	A structural model for the prostate disease marker, human prostateâ€specific antigen. Protein Science, 1994, 3, 2033-2044.	7.6	71
218	Structural basis for type I and type II deficiencies of antithrombotic plasma protein C: Patterns revealed by three-dimensional molecular modelling of mutations of the protease domain. Proteins: Structure, Function and Bioinformatics, 1994, 18, 367-380.	2.6	42
219	Structural modeling and electrostatic properties of aspartate transcarbamylase fromSaccharomyces cerevisiae. Proteins: Structure, Function and Bioinformatics, 1994, 19, 230-243.	2.6	15
220	Analysis of Protein S C4b-Binding Protein Interactions by Homology Modeling and Inhibitory Antibodies. Biochemistry, 1994, 33, 11073-11078.	2.5	20
221	Post-Pandemic Drug Discovery and Development: Facing Present and Future Challenges. Frontiers in Drug Discovery, 0, 1, .	2.8	9