Alexandre G de Brevern

List of Publications by Year
in descending order

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128 papers	3,984 citations	126907 33 h-index	155660 55 g-index
133 all docs	133 docs citations	133 times ranked	4154 citing authors

#	Article	IF	Citations
1	New Î±IIbÎ²3 variants in 28 Turkish Glanzmann patients; structural hypothesis for complex activation by residues variations in I-EGF domains. Platelets, 2022, 33, 551-561.	2.3	2
2	Shaking the Î²-Bulges. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 14-18.	3.0	3
3	Analysis of Integrin Î±IIb Subunit Dynamics Reveals Long-Range Effects of Missense Mutations on Calf Domains. International Journal of Molecular Sciences, 2022, 23, 858.	4.1	6
4	VHH Structural Modelling Approaches: A Critical Review. International Journal of Molecular Sciences, 2022, 23, 3721.	4.1	9
5	SWORD2: hierarchical analysis of protein 3D structures. Nucleic Acids Research, 2022, 50, W732-W738.	14.5	13
6	CALR-ETdb, the database of calreticulin variants diversity in essential thrombocythemia. Platelets, 2021, , 1-11.	2.3	2
7	Insights into antiâ€D formation in carriers of RhD variants through studies of 3D intraprotein interactions. Transfusion, 2021, 61, 1286-1301.	1.6	12
8	ABCG2 Is Overexpressed on Red Blood Cells in Ph-Negative Myeloproliferative Neoplasms and Potentiates Ruxolitinib-Induced Apoptosis. International Journal of Molecular Sciences, 2021, 22, 3530.	4.1	3
9	Conformational Strain Indicated by Ramachandran Angles for the Protein Backbone Is Only Weakly Related to the Flexibility. Journal of Physical Chemistry B, 2021, 125, 2597-2606.	2.6	7
10	A Review of the Literature Organized Into a New Database: RHeference. Transfusion Medicine Reviews, 2021, 35, 70-77.	2.0	8
11	MEDUSA: Prediction of Protein Flexibility from Sequence. Journal of Molecular Biology, 2021, 433, 166882.	4.2	31
12	Structural and evolutionary exploration of the IL-3 family and its alpha subunit receptors. Amino Acids, 2021, 53, 1211-1227.	2.7	3
13	PYTHIA: Deep Learning Approach for Local Protein Conformation Prediction. International Journal of Molecular Sciences, 2021, 22, 8831.	4.1	6
14	Hierarchical Structure of Protein Sequence. International Journal of Molecular Sciences, 2021, 22, 8339.	4.1	7
15	Insights into Comparative Modeling of VHH Domains. International Journal of Molecular Sciences, 2021, 22, 9771.	4.1	3
16	Discrete analyses of protein dynamics. Journal of Biomolecular Structure and Dynamics, 2020, 38, 2988-3002.	3.5	20
17	Impact of protein dynamics on secondary structure prediction. Biochimie, 2020, 179, 14-22.	2.6	7
18	Analysis of Protein Disorder Predictions in the Light of a Protein Structural Alphabet. Biomolecules, 2020, 10, 1080.	4.0	9

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19	Investigating the Product Profiles and Structural Relationships of New Levansucrases with Conventional and Non-Conventional Substrates. International Journal of Molecular Sciences, 2020, 21, 5402.	4.1	9
20	Data set of intrinsically disordered proteins analysed at a local protein conformation level. Data in Brief, 2020, 29, 105383.	1.0	4
21	Combining In Silico Phylogenetic and Threading Approaches to Assist the in vitro Protein Engineering of BVMO Enzymes. Biophysical Journal, 2020, 118, 45a.	0.5	1
22	A structural entropy index to analyse local conformations in intrinsically disordered proteins. Journal of Structural Biology, 2020, 210, 107464.	2.8	13
23	Accurate Representation of Protein-Ligand Structural Diversity in the Protein Data Bank (PDB). International Journal of Molecular Sciences, 2020, 21, 2243.	4.1	4
24	Discrete analysis of camelid variable domains: sequences, structures, and in-silico structure prediction. PeerJ, 2020, 8, e8408.	2.0	15
25	Dimerization and phosphorylation of Lutheran/basal cell adhesion molecule are critical for its function in cell migration on laminin. Journal of Biological Chemistry, 2019, 294, 14911-14921.	3.4	7
26	In silico prediction of protein flexibility with local structure approach. Biochimie, 2019, 165, 150-155.	2.6	15
27	Structural variations within proteins can be as large as variations observed across their homologues. Biochimie, 2019, 167, 162-170.	2.6	4
28	Investigation of the impact of PTMs on the protein backbone conformation. Amino Acids, 2019, 51, 1065-1079.	2.7	17
29	Halogens in Proteinâ€“Ligand Binding Mechanism: A Structural Perspective. Journal of Medicinal Chemistry, 2019, 62, 9341-9356.	6.4	106
30	A minimum set of stable blocks for rational design of polypeptide chains. Biochimie, 2019, 160, 88-92.	2.6	13
31	iPBAvizu: a PyMOL plugin for an efficient 3D protein structure superimposition approach. Source Code for Biology and Medicine, 2019, 14, 5.	1.7	14
32	Prediction of the intestinal resistome by a three-dimensional structure-based method. Nature Microbiology, 2019, 4, 112-123.	13.3	129
33	Longâ€range molecular dynamics show that inactive forms of Protein Kinase A are more dynamic than active forms. Protein Science, 2019, 28, 543-560.	7.6	9
34	Dynamics and deformability of Î±-, 310- and Ï€-helices. Archives of Biological Sciences, 2018, 70, 21-31.	0.5	10
35	Short in-Frame Insertions/Deletions in the Coding Sequence of the Î±-Globin Gene. Consequences of the 3D Structure and Resulting Phenotypes: Hb Choisy as an Example. Hemoglobin, 2018, 42, 287-293.	0.8	1
36	Alloimmunization risk associated with amino acid 223 substitution in the RhD protein: analysis in the light of molecular modeling. Transfusion, 2018, 58, 2683-2692.	1.6	9

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37	Analysing the Structural Effect of Point Mutations of Cytotoxic Necrotizing Factor 1 (CNF1) on Lu/BCAM Adhesion Glycoprotein Association. Toxins, 2018, 10, 122.	3.4	1
38	Same but not alike: Structure, flexibility and energetics of domains in multi-domain proteins are influenced by the presence of other domains. PLoS Computational Biology, 2018, 14, e1006008.	3.2	41
39	Molecular characterization of 13 new RHD alleles. Transfusion, 2017, 57, 1089-1091.	1.6	2
40	Recent advances on polyproline II. Amino Acids, 2017, 49, 705-713.	2.7	22
41	Enhancing the Activity of a Dietzia sp. D5 Baeyerâ€Villiger Monooxygenase towards Cyclohexanone by Saturation Mutagenesis. ChemistrySelect, 2017, 2, 7169-7177.	1.5	7
42	In silico analysis of Glanzmann variants of Calf-1 domain of Î±IIbÎ²3 integrin revealed dynamic allosteric effect. Scientific Reports, 2017, 7, 8001.	3.3	30
43	Knowledge-based prediction of protein backbone conformation using a structural alphabet. PLoS ONE, 2017, 12, e0186215.	2.5	12
44	PBxplore: a tool to analyze local protein structure and deformability with Protein Blocks. PeerJ, 2017, 5, e4013.	2.0	29
45	Conservation of structural fluctuations in homologous protein kinases and its implications on functional sites. Proteins: Structure, Function and Bioinformatics, 2016, 84, 957-978.	2.6	7
46	ORION: a web server for protein fold recognition and structure prediction using evolutionary hybrid profiles. Scientific Reports, 2016, 6, 28268.	3.3	37
47	Global analysis of VHHs framework regions with a structural alphabet. Biochimie, 2016, 131, 11-19.	2.6	16
48	Extension of the classical classification of Î²-turns. Scientific Reports, 2016, 6, 33191.	3.3	74
49	Enzymatic Synthesis of Galactosylated Serine/Threonine Derivatives by Î²-Galactosidase from Escherichia coli. International Journal of Molecular Sciences, 2015, 16, 13714-13728.	4.1	4
50	Protein flexibility in the light of structural alphabets. Frontiers in Molecular Biosciences, 2015, 2, 20.	3.5	71
51	Trends in IT Innovation to Build a Next Generation Bioinformatics Solution to Manage and Analyse Biological Big Data Produced by NGS Technologies. BioMed Research International, 2015, 2015, 1-15.	1.9	26
52	Sequenceâ€“structure relationship study in all-Î± transmembrane proteins using an unsupervised learning approach. Amino Acids, 2015, 47, 2303-2322.	2.7	8
53	Improving protein fold recognition with hybrid profiles combining sequence and structure evolution. Bioinformatics, 2015, 31, 3782-3789.	4.1	36
54	Use of a structural alphabet to find compatible folds for amino acid sequences. Protein Science, 2015, 24, 145-153.	7.6	9

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55	Studies of a Murine Monoclonal Antibody Directed against DARC: Reappraisal of Its Specificity. PLoS ONE, 2015, 10, e0116472.	2.5	6
56	Correlation between local structural dynamics of proteins inferred from NMR ensembles and evolutionary dynamics of homologues of known structure. Journal of Biomolecular Structure and Dynamics, 2014, 32, 751-758.	3.5	6
57	PTM-SD: a database of structurally resolved and annotated posttranslational modifications in proteins. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau041-bau041.	3.0	44
58	From local structure to a global framework: recognition of protein folds. Journal of the Royal Society Interface, 2014, 11, 20131147.	3.4	11
59	Bioinformatic analysis of the protein/DNA interface. Nucleic Acids Research, 2014, 42, 3381-3394.	14.5	51
60	Local dynamics of proteins and DNA evaluated from crystallographicBfactors. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2413-2419.	2.5	38
61	Modeling and molecular dynamics simulations of the V33 variant of the integrin subunit Î²3: Structural comparison with the L33 (HPA-1a) and P33 (HPA-1b) variants. Biochimie, 2014, 105, 84-90.	2.6	20
62	mulPBA: an efficient multiple protein structure alignment method based on a structural alphabet. Journal of Biomolecular Structure and Dynamics, 2014, 32, 661-668.	3.5	28
63	Cisâ€“trans isomerization of omega dihedrals in proteins. Amino Acids, 2013, 45, 279-289.	2.7	60
64	Î²â€Bulges: Extensive structural analyses of Î²â€sheets irregularities. Protein Science, 2013, 22, 1366-1378.	7.6	27
65	Evolution study of the Baeyerâ€“Villiger monooxygenases enzyme family: Functional importance of the highly conserved residues. Biochimie, 2013, 95, 1394-1402.	2.6	19
66	Understanding the role of domainâ€“domain linkers in the spatial orientation of domains in multi-domain proteins. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1467-1480.	3.5	35
67	PRR Repeats in the Intracellular Domain of KISS1R Are Important for Its Export to Cell Membrane. Molecular Endocrinology, 2013, 27, 1004-1014.	3.7	18
68	DoSA: Database of Structural Alignments. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat048-bat048.	3.0	2
69	VLDP web server: a powerful geometric tool for analysing protein structures in their environment. Nucleic Acids Research, 2013, 41, W373-W378.	14.5	18
70	Selective Constraint on Human Pre-mRNA Splicing by Protein Structural Properties. Genome Biology and Evolution, 2012, 4, 966-975.	2.5	13
71	PredyFlexy: flexibility and local structure prediction from sequence. Nucleic Acids Research, 2012, 40, W317-W322.	14.5	78
72	Comparison of tertiary structures of proteins in protein-protein complexes with unbound forms suggests prevalence of allostery in signalling proteins. BMC Structural Biology, 2012, 12, 6.	2.3	19

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73	Progressive structure-based alignment of homologous proteins: Adopting sequence comparison strategies. Biochimie, 2012, 94, 2025-2034.	2.6	14
74	Cisâ€“trans peptide variations in structurally similar proteins. Amino Acids, 2012, 43, 1369-1381.	2.7	47
75	Local Structural Differences in Homologous Proteins: Specificities in Different SCOP Classes. PLoS ONE, 2012, 7, e38805.	2.5	13
76	Modeling and Molecular Dynamics of HPA-1a and -1b Polymorphisms: Effects on the Structure of the Î²3 Subunit of the Î±IIbÎ²3 Integrin. PLoS ONE, 2012, 7, e47304.	2.5	33
77	Comparative Analysis of Threshold and Tessellation Methods for Determining Protein Contacts. Journal of Chemical Information and Modeling, 2011, 51, 493-507.	5.4	25
78	Improvement of protein structure comparison using a structural alphabet. Biochimie, 2011, 93, 1434-1445.	2.6	37
79	Assignment of PolyProline II Conformation and Analysis of Sequence â€“ Structure Relationship. PLoS ONE, 2011, 6, e18401.	2.5	86
80	Predicting protein flexibility through the prediction of local structures. Proteins: Structure, Function and Bioinformatics, 2011, 79, 839-852.	2.6	107
81	Species specific amino acid sequenceâ€“protein local structure relationships: An analysis in the light of a structural alphabet. Journal of Theoretical Biology, 2011, 276, 209-217.	1.7	5
82	Protein Peeling 3D: new tools for analyzing protein structures. Bioinformatics, 2011, 27, 132-133.	4.1	16
83	iPBA: a tool for protein structure comparison using sequence alignment strategies. Nucleic Acids Research, 2011, 39, W18-W23.	14.5	96
84	Identification of Local Conformational Similarity in Structurally Variable Regions of Homologous Proteins Using Protein Blocks. PLoS ONE, 2011, 6, e17826.	2.5	6
85	A Dominant Mutation in the Gene Encoding the Erythroid Transcription Factor KLF1 Causes a Congenital Dyserythropoietic Anemia. American Journal of Human Genetics, 2010, 87, 721-727.	6.2	172
86	3D Structural Models of Transmembrane Proteins. Methods in Molecular Biology, 2010, 654, 387-401.	0.9	13
87	A recombinant dromedary antibody fragment (VHH or nanobody) directed against human Duffy antigen receptor for chemokines. Cellular and Molecular Life Sciences, 2010, 67, 3371-3387.	5.4	47
88	Influence of assignment on the prediction of transmembrane helices in protein structures. Amino Acids, 2010, 39, 1241-1254.	2.7	6
89	A short survey on protein blocks. Biophysical Reviews, 2010, 2, 137-145.	3.2	107
90	Comparative analysis of missing value imputation methods to improve clustering and interpretation of microarray experiments. BMC Genomics, 2010, 11, 15.	2.8	80

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91	Î±IIbÎ²3 integrin: new allelic variants in Glanzmann thrombasthenia, effects onITGA2BandITGB3mRNA splicing, expression, and structure-function. Human Mutation, 2010, 31, 237-246.	2.5	30
92	Fast and automated functional classification with MEDâ€SuMo: An application on purineâ€binding proteins. Protein Science, 2010, 19, 847-867.	7.6	15
93	A Novel Evaluation of Residue and Protein Volumes by Means of Laguerre Tessellation. Journal of Chemical Information and Modeling, 2010, 50, 947-960.	5.4	30
94	Multiple interests in structural models of DARC transmembrane protein. Transfusion Clinique Et Biologique, 2010, 17, 184-196.	0.4	13
95	Editorial [Hot Topic: In Silico (Guest Editor: Alexandre G. de Brevern)]. Infectious Disorders - Drug Targets, 2009, 9, 246-247.	0.8	9
96	Analysis of HSP90-related folds with MED-SuMo classification approach. Drug Design, Development and Therapy, 2009, 3, 59.	4.3	6
97	Computational fragment-based drug design to explore the hydrophobic sub-pocket of the mitotic kinesin Eg5 allosteric binding site. Journal of Computer-Aided Molecular Design, 2009, 23, 571-582.	2.9	8
98	A new prediction strategy for long local protein structures using an original description. Proteins: Structure, Function and Bioinformatics, 2009, 76, 570-587.	2.6	29
99	Analysis of loop boundaries using different local structure assignment methods. Protein Science, 2009, 18, 1869-1881.	7.6	27
100	Analyzing the sequenceâ€“structure relationship of a library of local structural prototypes. Journal of Theoretical Biology, 2009, 256, 215-226.	1.7	18
101	Protein short loop prediction in terms of a structural alphabet. Computational Biology and Chemistry, 2009, 33, 329-333.	2.3	21
102	Extension of a local backbone description using a structural alphabet: A new approach to the sequence-structure relationship. Protein Science, 2009, 11, 2871-2886.	7.6	54
103	Analysis of protein contacts into Protein Units. Biochimie, 2009, 91, 876-887.	2.6	15
104	In Silico Studies on DARC. Infectious Disorders - Drug Targets, 2009, 9, 289-303.	0.8	18
105	Analysis of protein chameleon sequence characteristics. Bioinformation, 2009, 3, 367-369.	0.5	22
106	In silico local structure approach: A case study on Outer Membrane Proteins. Proteins: Structure, Function and Bioinformatics, 2008, 71, 92-109.	2.6	12
107	Protein structure mining using a structural alphabet. Proteins: Structure, Function and Bioinformatics, 2008, 71, 920-937.	2.6	52
108	Protein contacts, inter-residue interactions and side-chain modelling. Biochimie, 2008, 90, 626-639.	2.6	55

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109	Corrigendum to â€œProtein contacts, inter-residue interactions and side-chain modellingâ€•[Biochimie 90 (4) (2008) 626â€“639]. Biochimie, 2008, 90, 1264.	2.6	0
110	Local Protein Structures. Current Bioinformatics, 2007, 2, 165-202.	1.5	73
111	A reduced amino acid alphabet for understanding and designing protein adaptation to mutation. European Biophysics Journal, 2007, 36, 1059-1069.	2.2	78
112	â€œPinning strategyâ€: a novel approach for predicting the backbone structure in terms of protein blocks from sequence. Journal of Biosciences, 2007, 32, 51-70.	1.1	28
113	Functional annotation strategy for protein structures. Bioinformation, 2007, 1, 357-359.	0.5	15
114	Protein Block Expert (PBE): a web-based protein structure analysis server using a structural alphabet. Nucleic Acids Research, 2006, 34, W119-W123.	14.5	52
115	A substitution matrix for structural alphabet based on structural alignment of homologous proteins and its applications. Proteins: Structure, Function and Bioinformatics, 2006, 65, 32-39.	2.6	50
116	Protein Peeling 2: a web server to convert protein structures into series of protein units. Nucleic Acids Research, 2006, 34, W75-W78.	14.5	16
117	â€˜Protein Peelingâ€™: an approach for splitting a 3D protein structure into compact fragments. Bioinformatics, 2006, 22, 129-133.	4.1	33
118	Protein beta-turn assignments. Bioinformation, 2006, 1, 153-155.	0.5	28
119	Protein secondary structure assignment revisited: a detailed analysis of different assignment methods. BMC Structural Biology, 2005, 5, 17.	2.3	144
120	A structural alphabet for local protein structures: Improved prediction methods. Proteins: Structure, Function and Bioinformatics, 2005, 59, 810-827.	2.6	98
121	Assessing a novel approach for predicting local 3D protein structures from sequence. Proteins: Structure, Function and Bioinformatics, 2005, 62, 865-880.	2.6	40
122	A structural model of a seven-transmembrane helix receptor: The Duffy antigen/receptor for chemokine (DARC). Biochimica Et Biophysica Acta - General Subjects, 2005, 1724, 288-306.	2.4	68
123	Influence of microarrays experiments missing values on the stability of gene groups by hierarchical clustering. BMC Bioinformatics, 2004, 5, 114.	2.6	80
124	Use of a structural alphabet for analysis of short loops connecting repetitive structures. BMC Bioinformatics, 2004, 5, 58.	2.6	57
125	'Hybrid Protein Model' for optimally defining 3D protein structure fragments. Bioinformatics, 2003, 19, 345-353.	4.1	44
126	Genome compartimentation by a Hybrid Chromosome Model (HÏ‡M). Application to Saccharomyces cerevisae subtelomeres. Computers & Chemistry, 2002, 26, 437-445.	1.2	3

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127	Compacting local protein folds with a "hybrid protein model". Theoretical Chemistry Accounts, 2001, 106, 36-47.	1.4	19
128	Bayesian probabilistic approach for predicting backbone structures in terms of protein blocks. Proteins: Structure, Function and Bioinformatics, 2000, 41, 271-287.	2.6	254