Frederic Rousseau

List of Publications by Year
in descending order

154 papers	16,392 citations	28242 55 h-index	17580 121 g-index
167 all docs	167 docs citations	167 times ranked	21172 citing authors

#	Article	IF	Citations
1	The FoldX web server: an online force field. Nucleic Acids Research, 2005, 33, W382-W388.	6.5	2,110
2	Protein Phase Separation: A New Phase in Cell Biology. Trends in Cell Biology, 2018, 28, 420-435.	3.6	1,439
3	Prediction of sequence-dependent and mutational effects on the aggregation of peptides and proteins. Nature Biotechnology, 2004, 22, 1302-1306.	9.4	1,435
4	Exploring the sequence determinants of amyloid structure using position-specific scoring matrices. Nature Methods, 2010, 7, 237-242.	9.0	566
5	Neurotoxicity of Alzheimer's disease Aβ peptides is induced by small changes in the Aβ42 to Aβ40 ratio. EMBO Journal, 2010, 29, 3408-3420.	3.5	455
6	Gain of function of mutant p53 by coaggregation with multiple tumor suppressors. Nature Chemical Biology, 2011, 7, 285-295.	3.9	450
7	Phase Separation of C9orf72 Dipeptide Repeats Perturbs Stress Granule Dynamics. Molecular Cell, 2017, 65, 1044-1055.e5.	4.5	437
8	The mechanism of γ-Secretase dysfunction in familial Alzheimer disease. EMBO Journal, 2012, 31, 2261-2274.	3.5	432
9	A Comparative Study of the Relationship Between Protein Structure and β-Aggregation in Globular and Intrinsically Disordered Proteins. Journal of Molecular Biology, 2004, 342, 345-353.	2.0	353
10	Protein aggregation and amyloidosis: confusion of the kinds?. Current Opinion in Structural Biology, 2006, 16, 118-126.	2.6	322
11	Prediction of water and metal binding sites and their affinities by using the Fold-X force field. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10147-10152.	3.3	315
12	Lipids revert inert Aβ amyloid fibrils to neurotoxic protofibrils that affect learning in mice. EMBO Journal, 2008, 27, 224-233.	3.5	303
13	A graphical interface for the FoldX forcefield. Bioinformatics, 2011, 27, 1711-1712.	1.8	288
14	Restricted Location of PSEN2/γ-Secretase Determines Substrate Specificity and Generates an Intracellular Aβ Pool. Cell, 2016, 166, 193-208.	13.5	260
15	How Evolutionary Pressure Against Protein Aggregation Shaped Chaperone Specificity. Journal of Molecular Biology, 2006, 355, 1037-1047.	2.0	242
16	Drosophila screen connects nuclear transport genes to DPR pathology in c9ALS/FTD. Scientific Reports, 2016, 6, 20877.	1.6	239
17	SNPeffect 4.0: on-line prediction of molecular and structural effects of protein-coding variants. Nucleic Acids Research, 2012, 40, D935-D939.	6.5	235
18	The Unfolding Story of Three-Dimensional Domain Swapping. Structure, 2003, 11, 243-251.	1.6	203

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19	Structural Basis for Increased Toxicity of Pathological $A\beta42:A\beta40$ Ratios in Alzheimer Disease. Journal of Biological Chemistry, 2012, 287, 5650-5660.	1.6	201
20	Alzheimer's-Causing Mutations Shift $A\beta$ Length by Destabilizing γ-Secretase-$A\beta$n Interactions. Cell, 2017, 170, 443-456.e14.	13.5	199
21	PupaSuite: finding functional single nucleotide polymorphisms for large-scale genotyping purposes. Nucleic Acids Research, 2006, 34, W621-W625.	6.5	194
22	Loss of *TBK1* is a frequent cause of frontotemporal dementia in a Belgian cohort. Neurology, 2015, 85, 2116-2125.	1.5	151
23	Computational design of peptide ligands. Trends in Biotechnology, 2011, 29, 231-239.	4.9	146
24	SNPeffect: a database mapping molecular phenotypic effects of human non-synonymous coding SNPs. Nucleic Acids Research, 2004, 33, D527-D532.	6.5	136
25	The Alzheimer Disease Protective Mutation A2T Modulates Kinetic and Thermodynamic Properties of Amyloid-β ($A\beta$) Aggregation. Journal of Biological Chemistry, 2014, 289, 30977-30989.	1.6	132
26	The culprit behind amyloid beta peptide related neurotoxicity in Alzheimer's disease: oligomer size or conformation?. Alzheimer's Research and Therapy, 2010, 2, 12.	3.0	131
27	Molecular Mechanism of SSR128129E, an Extracellularly Acting, Small-Molecule, Allosteric Inhibitor of FGF Receptor Signaling. Cancer Cell, 2013, 23, 489-501.	7.7	125
28	Accurate Prediction of DnaK-Peptide Binding via Homology Modelling and Experimental Data. PLoS Computational Biology, 2009, 5, e1000475.	1.5	118
29	Redox Proteomics of Protein-bound Methionine Oxidation. Molecular and Cellular Proteomics, 2011, 10, M110.006866.	2.5	117
30	Mutations other than null mutations producing a pathogenic loss of progranulin in frontotemporal dementia. Human Mutation, 2007, 28, 416-416.	1.1	116
31	Prediction and Reduction of the Aggregation of Monoclonal Antibodies. Journal of Molecular Biology, 2017, 429, 1244-1261.	2.0	112
32	Genetic variability in the mitochondrial serine protease *HTRA2* contributes to risk for Parkinson disease. Human Mutation, 2008, 29, 832-840.	1.1	107
33	Variable Glutamine-Rich Repeats Modulate Transcription Factor Activity. Molecular Cell, 2015, 59, 615-627.	4.5	103
34	Hsp90 Mediates Membrane Deformation and Exosome Release. Molecular Cell, 2018, 71, 689-702.e9.	4.5	103
35	PepX: a structural database of non-redundant protein–peptide complexes. Nucleic Acids Research, 2010, 38, D545-D551.	6.5	102
36	Recognizing and Defining True Ras Binding Domains II: In Silico Prediction Based on Homology Modelling and Energy Calculations. Journal of Molecular Biology, 2005, 348, 759-775.	2.0	101

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37	Rational Design of Amyloid–Like Fibrillary Structures for Tailoring Food Protein Techno–Functionality and Their Potential Health Implications. Comprehensive Reviews in Food Science and Food Safety, 2019, 18, 84-105.	5.9	101
38	A standardized and biocompatible preparation of aggregate-free amyloid beta peptide for biophysical and biological studies of Alzheimer's disease. Protein Engineering, Design and Selection, 2011, 24, 743-750.	1.0	97
39	Analysis of Protein Processing by N-terminal Proteomics Reveals Novel Species-specific Substrate Determinants of Granzyme B Orthologs. Molecular and Cellular Proteomics, 2009, 8, 258-272.	2.5	95
40	Increased Monomerization of Mutant HSPB1 Leads to Protein Hyperactivity in Charcot-Marie-Tooth Neuropathy. Journal of Biological Chemistry, 2010, 285, 12778-12786.	1.6	95
41	Implications of 3D Domain Swapping for Protein Folding, Misfolding and Function. Advances in Experimental Medicine and Biology, 2012, 747, 137-152.	0.8	91
42	What Makes a Protein Sequence a Prion?. PLoS Computational Biology, 2015, 11, e1004013.	1.5	88
43	Protein sequences encode safeguards against aggregation. Human Mutation, 2009, 30, 431-437.	1.1	86
44	Protein aggregation in bacteria: the thin boundary between functionality and toxicity. Microbiology (United Kingdom), 2013, 159, 1795-1806.	0.7	81
45	SNPeffect v2.0: a new step in investigating the molecular phenotypic effects of human non-synonymous SNPs. Bioinformatics, 2006, 22, 2183-2185.	1.8	80
46	Protein-Peptide Interactions Adopt the Same Structural Motifs as Monomeric Protein Folds. Structure, 2009, 17, 1128-1136.	1.6	79
47	PrionW: a server to identify proteins containing glutamine/asparagine rich prion-like domains and their amyloid cores. Nucleic Acids Research, 2015, 43, W331-W337.	6.5	74
48	Molecular Dissection of FUS Points at Synergistic Effect of Low-Complexity Domains in Toxicity. Cell Reports, 2018, 24, 529-537.e4.	2.9	74
49	Proteome-wide Substrate Analysis Indicates Substrate Exclusion as a Mechanism to Generate Caspase-7 Versus Caspase-3 Specificity. Molecular and Cellular Proteomics, 2009, 8, 2700-2714.	2.5	64
50	A comparative analysis of the aggregation behavior of amyloid–β peptide variants. FEBS Letters, 2012, 586, 4088-4093.	1.3	64
51	WALTZ-DB 2.0: an updated database containing structural information of experimentally determined amyloid-forming peptides. Nucleic Acids Research, 2020, 48, D389-D393.	6.5	64
52	De novo design of a biologically active amyloid. Science, 2016, 354, .	6.0	63
53	A systems biology perspective on protein structural dynamics and signal transduction. Current Opinion in Structural Biology, 2005, 15, 23-30.	2.6	61
54	WALTZ-DB: a benchmark database of amyloidogenic hexapeptides. Bioinformatics, 2015, 31, 1698-1700.	1.8	61

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55	Joint annotation of coding and non-coding single nucleotide polymorphisms and mutations in the SNPeffect and PupaSuite databases. Nucleic Acids Research, 2008, 36, D825-D829.	6.5	60
56	Protein-Peptide Complex Prediction through Fragment Interaction Patterns. Structure, 2013, 21, 789-797.	1.6	59
57	Post-translational Control of the Temporal Dynamics of Transcription Factor Activity Regulates Neurogenesis. Cell, 2016, 164, 460-475.	13.5	58
58	Structure of the Extracellular Domain of Matrix Protein 2 of Influenza A Virus in Complex with a Protective Monoclonal Antibody. Journal of Virology, 2015, 89, 3700-3711.	1.5	57
59	Structural hot spots for the solubility of globular proteins. Nature Communications, 2016, 7, 10816.	5.8	57
60	Conditions Governing Food Protein Amyloid Fibril Formation. Part II: Milk and Legume Proteins. Comprehensive Reviews in Food Science and Food Safety, 2019, 18, 1277-1291.	5.9	57
61	A guide to studying protein aggregation. FEBS Journal, 2023, 290, 554-583.	2.2	55
62	Nuclear inclusion bodies of mutant and wildâ€type p53 in cancer: a hallmark of p53 inactivation and proteostasis remodelling by p53 aggregation. Journal of Pathology, 2017, 242, 24-38.	2.1	54
63	Structure-based machine-guided mapping of amyloid sequence space reveals uncharted sequence clusters with higher solubilities. Nature Communications, 2020, 11, 3314.	5.8	54
64	Aggregating sequences that occur in many proteins constitute weak spots of bacterial proteostasis. Nature Communications, 2018, 9, 866.	5.8	53
65	Solubis: a webserver to reduce protein aggregation through mutation. Protein Engineering, Design and Selection, 2016, 29, 285-289.	1.0	51
66	Aggregation Prone Regions and Gatekeeping Residues in Protein Sequences. Current Topics in Medicinal Chemistry, 2013, 12, 2470-2478.	1.0	51
67	An Evolutionary Trade-Off between Protein Turnover Rate and Protein Aggregation Favors a Higher Aggregation Propensity in Fast Degrading Proteins. PLoS Computational Biology, 2011, 7, e1002090.	1.5	50
68	Observation of signal transduction in three-dimensional domain swapping. Nature Structural Biology, 2001, 8, 888-892.	9.7	48
69	BriX: a database of protein building blocks for structural analysis, modeling and design. Nucleic Acids Research, 2011, 39, D435-D442.	6.5	48
70	Amyloids or prions? That is the question. Prion, 2015, 9, 200-206.	0.9	47
71	Potential human transmission of amyloid Î² pathology: surveillance and risks. Lancet Neurology, The, 2020, 19, 872-878.	4.9	46
72	Protein aggregation as an antibiotic design strategy. Molecular Microbiology, 2016, 99, 849-865.	1.2	44

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73	Exploring the sequence–structure relationship for amyloid peptides. Biochemical Journal, 2013, 450, 275-283.	1.7	43
74	Conditions Governing Food Protein Amyloid Fibril Formation—Part I: Egg and Cereal Proteins. Comprehensive Reviews in Food Science and Food Safety, 2019, 18, 1256-1276.	5.9	43
75	Reconstruction of Protein Backbones from the BriX Collection of Canonical Protein Fragments. PLoS Computational Biology, 2008, 4, e1000083.	1.5	42
76	The Dynamic Transition of Persistence toward the Viable but Nonculturable State during Stationary Phase Is Driven by Protein Aggregation. MBio, 2021, 12, e0070321.	1.8	42
77	Structural Diversity of PDZ–Lipid Interactions. ChemBioChem, 2010, 11, 456-467.	1.3	41
78	Predicting aggregation-prone sequences in proteins. Essays in Biochemistry, 2014, 56, 41-52.	2.1	41
79	Bcl-xL acts as an inhibitor of IP3R channels, thereby antagonizing Ca2+-driven apoptosis. Cell Death and Differentiation, 2022, 29, 788-805.	5.0	41
80	Genome-Wide Prediction of SH2 Domain Targets Using Structural Information and the FoldX Algorithm. PLoS Computational Biology, 2008, 4, e1000052.	1.5	39
81	Increased Aggregation Is More Frequently Associated to Human Disease-Associated Mutations Than to Neutral Polymorphisms. PLoS Computational Biology, 2015, 11, e1004374.	1.5	38
82	Molecular Plasticity Regulates Oligomerization and Cytotoxicity of the Multipeptide-length Amyloid-β Peptide Pool. Journal of Biological Chemistry, 2012, 287, 36732-36743.	1.6	37
83	Loss of DPP6 in neurodegenerative dementia: a genetic player in the dysfunction of neuronal excitability. Acta Neuropathologica, 2019, 137, 901-918.	3.9	37
84	A Genome-Wide Sequence–Structure Analysis Suggests Aggregation Gatekeepers Constitute an Evolutionary Constrained Functional Class. Journal of Molecular Biology, 2014, 426, 2405-2412.	2.0	35
85	Frizzled 7 and PIP2 binding by syntenin PDZ2 domain supports Frizzled 7 trafficking and signalling. Nature Communications, 2016, 7, 12101.	5.8	35
86	Thermodynamic and Evolutionary Coupling between the Native and Amyloid State of Globular Proteins. Cell Reports, 2020, 31, 107512.	2.9	34
87	Processing Induced Changes in Food Proteins: Amyloid Formation during Boiling of Hen Egg White. Biomacromolecules, 2020, 21, 2218-2228.	2.6	34
88	Quantifying information transfer by protein domains: Analysis of the Fyn SH2 domain structure. BMC Structural Biology, 2008, 8, 43.	2.3	33
89	Aggregation gatekeepers modulate protein homeostasis of aggregating sequences and affect bacterial fitness. Protein Engineering, Design and Selection, 2012, 25, 357-366.	1.0	33
90	Autonomous aggregation suppression by acidic residues explains why chaperones favour basic residues. EMBO Journal, 2020, 39, e102864.	3.5	33

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91	Protein design with fragment databases. Current Opinion in Structural Biology, 2011, 21, 452-459.	2.6	32
92	Defective Sec61Î±1 underlies a novel cause of autosomal dominant severe congenital neutropenia. Journal of Allergy and Clinical Immunology, 2020, 146, 1180-1193.	1.5	32
93	Î±-Galactosidase Aggregation Is a Determinant of Pharmacological Chaperone Efficacy on Fabry Disease Mutants. Journal of Biological Chemistry, 2012, 287, 28386-28397.	1.6	31
94	Intermediates Control Domain Swapping during Folding of p13. Journal of Biological Chemistry, 2004, 279, 8368-8377.	1.6	25
95	Selectivity of Aggregation-Determining Interactions. Journal of Molecular Biology, 2015, 427, 236-247.	2.0	25
96	Structural Basis of the Subcellular Topology Landscape of Escherichia coli. Frontiers in Microbiology, 2019, 10, 1670.	1.5	25
97	Reverse engineering synthetic antiviral amyloids. Nature Communications, 2020, 11, 2832.	5.8	25
98	Domain Swapping in p13suc1 Results in Formation of Native-like, Cytotoxic Aggregates. Journal of Molecular Biology, 2006, 363, 496-505.	2.0	24
99	Sequence-specific protein aggregation generates defined protein knockdowns in plants. Plant Physiology, 2016, 171, pp.00335.2016.	2.3	24
100	Using structural bioinformatics to investigate the impact of non synonymous SNPs and disease mutations: scope and limitations. BMC Bioinformatics, 2009, 10, S9.	1.2	22
101	Sequence-dependent Internalization of Aggregating Peptides. Journal of Biological Chemistry, 2015, 290, 242-258.	1.6	22
102	Transcellular Spreading of Tau in Tauopathies. ChemBioChem, 2018, 19, 2424-2432.	1.3	22
103	Folding and Association of the Human Cell Cycle Regulatory Proteins ckshs1 and ckshs2. Biochemistry, 2002, 41, 1202-1210.	1.2	21
104	ALS precursor finally shaken into fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18649-18650.	3.3	21
105	The Structure of the Transition State for Folding of Domain-Swapped Dimeric p13suc1. Structure, 2002, 10, 649-657.	1.6	20
106	Mechanisms and therapeutic potential of interactions between human amyloids and viruses. Cellular and Molecular Life Sciences, 2021, 78, 2485-2501.	2.4	20
107	Solubis: optimize your protein. Bioinformatics, 2015, 31, 2580-2582.	1.8	19
108	Comprehensive subcellular topologies of polypeptides in Streptomyces. Microbial Cell Factories, 2018, 17, 43.	1.9	19

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109	Heterotypic Amyloid Î² interactions facilitate amyloid assembly and modify amyloid structure. EMBO Journal, 2022, 41, e108591.	3.5	19
110	Heating Wheat Gluten Promotes the Formation of Amyloid-like Fibrils. ACS Omega, 2021, 6, 1823-1833.	1.6	18
111	Heterotypic interactions in amyloid function and disease. FEBS Journal, 2022, 289, 2025-2046.	2.2	18
112	Information theoretical quantification of cooperativity in signalling complexes. BMC Systems Biology, 2009, 3, 9.	3.0	17
113	The structural basis for an onâ€"off switch controlling GÎ²Î³-mediated inhibition of TRPM3 channels. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29090-29100.	3.3	17
114	Hydrothermal Treatments Cause Wheat Gluten-Derived Peptides to Form Amyloid-like Fibrils. Journal of Agricultural and Food Chemistry, 2021, 69, 1963-1974.	2.4	16
115	Hybrid N-glycans on the host protective activation-associated secreted proteins of Ostertagia ostertagi and their importance in immunogenicity. Molecular and Biochemical Parasitology, 2008, 161, 67-71.	0.5	15
116	Drying mode and hydrothermal treatment conditions govern the formation of amyloid-like protein fibrils in solutions of dried hen egg white. Food Hydrocolloids, 2021, 112, 106276.	5.6	15
117	Impact of hydrothermal treatment on denaturation and aggregation of water-extractable quinoa (Chenopodium quinoa Willd.) protein. Food Hydrocolloids, 2021, 115, 106611.	5.6	15
118	The cellular modifier MOAGâ€4/SERF drives amyloid formation through charge complementation. EMBO Journal, 2021, 40, e107568.	3.5	15
119	<i>In silico</i> prediction of <i>in vitro</i> protein liquidâ€"liquid phase separation experiments outcomes with multi-head neural attention. Bioinformatics, 2021, 37, 3473-3479.	1.8	14
120	Surfing on protein folding energy landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15846-15848.	3.3	13
121	Adaption of human antibody Î» and Îº light chain architectures to CDR repertoires. Protein Engineering, Design and Selection, 2019, 32, 109-127.	1.0	12
122	Entropic Bristles Tune the Seeding Efficiency of Prion-Nucleating Fragments. Cell Reports, 2020, 30, 2834-2845.e3.	2.9	12
123	Peptides based on the presenilinâ€APP binding domain inhibit APP processing and AÎ² production through interfering with the APP transmembrane domain. FASEB Journal, 2012, 26, 3765-3778.	0.2	11
124	A rescue by chaperones. Nature Chemical Biology, 2016, 12, 58-59.	3.9	11
125	Mapping the sequence specificity of heterotypic amyloid interactions enables the identification of aggregation modifiers. Nature Communications, 2022, 13, 1351.	5.8	11
126	Thermodynamic analysis of amyloid fibril structures reveals a common framework for stability in amyloid polymorphs. Structure, 2022, 30, 1178-1189.e3.	1.6	11

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127	MAPRE2 mutations result in altered human cranial neural crest migration, underlying craniofacial malformations in CSC-KT syndrome. Scientific Reports, 2021, 11, 4976.	1.6	10
128	PyUUL provides an interface between biological structures and deep learning algorithms. Nature Communications, 2022, 13, 961.	5.8	10
129	Impact of heat and enzymatic treatment on ovalbumin amyloid-like fibril formation and enzyme-induced gelation. Food Hydrocolloids, 2022, 131, 107784.	5.6	10
130	SolubiS: Optimizing Protein Solubility by Minimal Point Mutations. Methods in Molecular Biology, 2019, 1873, 317-333.	0.4	9
131	Protein structure and aggregation: a marriage of necessity ruled by aggregation gatekeepers. Trends in Biochemical Sciences, 2022, 47, 194-205.	3.7	9
132	Investigating the mechanism of action of aggregation-inducing antimicrobial Pept-ins. Cell Chemical Biology, 2021, 28, 524-536.e4.	2.5	8
133	StAmP-DB: a platform for structures of polymorphic amyloid fibril cores. Bioinformatics, 2022, 38, 2636-2638.	1.8	8
134	Multiple Evolutionary Mechanisms Reduce Protein Aggregation~!2009-04-21~!2009-07-09~!2010-01-02~!. The Open Biology Journal, 2010, 2, 176-184.	0.5	7
135	Heterotypic amyloid interactions: Clues to polymorphic bias and selective cellular vulnerability?. Current Opinion in Structural Biology, 2022, 72, 176-186.	2.6	7
136	Differential proteostatic regulation of insoluble and abundant proteins. Bioinformatics, 2019, 35, 4098-4107.	1.8	6
137	Exposure of a cryptic Hsp70 binding site determines the cytotoxicity of the ALS-associated SOD1-mutant A4V. Protein Engineering, Design and Selection, 2019, 32, 443-457.	1.0	6
138	Targeting S100B with Peptides Encoding Intrinsic Aggregation-Prone Sequence Segments. Molecules, 2021, 26, 440.	1.7	6
139	Horizontal gene transfer from human host to HIV-1 reverse transcriptase confers drug resistance and partly compensates for replication deficits. Virology, 2014, 456-457, 310-318.	1.1	5
140	Assessing computational predictions of the phenotypic effect of cystathionine‐beta‐synthase variants. Human Mutation, 2019, 40, 1530-1545.	1.1	5
141	Bacterial Protein Homeostasis Disruption as a Therapeutic Intervention. Frontiers in Molecular Biosciences, 2021, 8, 681855.	1.6	5
142	Gene Erosion Can Lead to Gain-of-Function Alleles That Contribute to Bacterial Fitness. MBio, 2021, 12, e0112921.	1.8	5
143	From Binding-Induced Dynamic Effects in SH3 Structures to Evolutionary Conserved Sectors. PLoS Computational Biology, 2016, 12, e1004938.	1.5	5
144	Protein Domains as Information Processing Units. Current Protein and Peptide Science, 2009, 10, 133-145.	0.7	4

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145	Synthetic Pept-Ins as a Generic Amyloid-Like Aggregation-Based Platform for In Vivo PET Imaging of Intracellular Targets. Bioconjugate Chemistry, 2021, 32, 2052-2064.	1.8	4
146	MOTIF DISCOVERY WITH DATA MINING IN 3D PROTEIN STRUCTURE DATABASES: DISCOVERY, VALIDATION AND PREDICTION OF THE U-SHAPE ZINC BINDING ("HUF-ZINC") MOTIF. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340008.	0.3	3
147	Selective Knockdowns in Maize by Sequence-Specific Protein Aggregation. Methods in Molecular Biology, 2018, 1676, 109-127.	0.4	3
148	Protein Homeostasis Database: protein quality control in <i>E.coli</i>. Bioinformatics, 2020, 36, 948-949.	1.8	3
149	Multiple Evolutionary Mechanisms Reduce Protein Aggregation. The Open Biology Journal, 2009, 2, 176-184.	0.5	2
150	Brominated phenols as auxin-like molecules. European Journal of Soil Biology, 2009, 45, 81-87.	1.4	1
151	Modeling protein-peptide interactions using protein fragments: fitting the pieces?. BMC Bioinformatics, 2010, 11, .	1.2	1
152	Identifying rescuers of misfolding. Nature Biomedical Engineering, 2017, 1, 782-783.	11.6	1
153	Prediction of sequence-dependent and mutational effects on the aggregation of peptides and proteins. , 0, .		1
154	Aggregation Prone Regions and Gatekeeping Residues in Protein Sequences. Current Topics in Medicinal Chemistry, 2013, 999, 43-49.	1.0	0