

Evolutionarily conserved networks of residues mediate proteins

Nature Structural Biology

10, 59-69

DOI: [10.1038/nsb881](https://doi.org/10.1038/nsb881)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Cooperative organization in a macromolecular complex. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 718-724.	3.6	21
2	Evolutionary analysis of rhodopsin and cone pigments: connecting the three-dimensional structure with spectral tuning and signal transfer. <i>FEBS Letters</i> , 2003, 555, 151-159.	1.3	16
3	Switch-of-Function Mutants Based on Morphology Classification of Ras Superfamily Small GTPases. <i>Cell</i> , 2003, 113, 315-328.	13.5	102
4	Allosteric determinants in guanine nucleotide-binding proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14445-14450.	3.3	120
5	Chemical communication threatened by endocrine-disrupting chemicals.. <i>Environmental Health Perspectives</i> , 2004, 112, 648-653.	2.8	39
6	FamClash: A method for ranking the activity of engineered enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 4142-4147.	3.3	70
7	A perturbation-based method for calculating explicit likelihood of evolutionary co-variance in multiple sequence alignments. <i>Bioinformatics</i> , 2004, 20, 1565-1572.	1.8	114
8	Quantitative Analysis and Interpretation of Allosteric Behavior. <i>Methods in Enzymology</i> , 2004, 380, 187-203.	0.4	75
9	A Natural Prothrombin Mutant Reveals an Unexpected Influence of A-chain Structure on the Activity of Human α -Thrombin. <i>Journal of Biological Chemistry</i> , 2004, 279, 13035-13043.	1.6	21
10	On Evolutionary Conservation of Thermodynamic Coupling in Proteins. <i>Journal of Biological Chemistry</i> , 2004, 279, 19046-19050.	1.6	72
11	Evolutionary Trace of G Protein-coupled Receptors Reveals Clusters of Residues That Determine Global and Class-specific Functions. <i>Journal of Biological Chemistry</i> , 2004, 279, 8126-8132.	1.6	179
12	PCOAT: positional correlation analysis using multiple methods. <i>Bioinformatics</i> , 2004, 20, 3697-3699.	1.8	6
13	Searching for new allosteric sites in enzymes. <i>Current Opinion in Structural Biology</i> , 2004, 14, 706-715.	2.6	293
14	Influence of conservation on calculations of amino acid covariance in multiple sequence alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 211-221.	1.5	197
15	Is allostery an intrinsic property of all dynamic proteins?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 433-443.	1.5	779
16	Novel methods for directed evolution of enzymes: quality, not quantity. <i>Current Opinion in Biotechnology</i> , 2004, 15, 291-297.	3.3	214
17	An Evolutionarily Conserved Network of Amino Acids Mediates Gating in Voltage-dependent Potassium Channels. <i>Journal of Mathematical Analysis and Applications</i> , 2004, 294, .	0.5	0
18	Ligand-dependent Dynamics and Intramolecular Signaling in a PDZ Domain. <i>Journal of Molecular Biology</i> , 2004, 335, 1105-1115.	2.0	215

#	ARTICLE	IF	CITATIONS
19	Crystal Structure of a cAMP-dependent Protein Kinase Mutant at 1.26 Å...: New Insights into the Catalytic Mechanism. <i>Journal of Molecular Biology</i> , 2004, 336, 473-487.	2.0	78
20	An Evolutionarily Conserved Network of Amino Acids Mediates Gating in Voltage-dependent Potassium Channels. <i>Journal of Molecular Biology</i> , 2004, 340, 307-318.	2.0	59
21	Beyond Consensus: Statistical Free Energies Reveal Hidden Interactions in the Design of a TPR Motif. <i>Journal of Molecular Biology</i> , 2004, 343, 731-745.	2.0	77
22	Structural Determinants of Allosteric Ligand Activation in RXR Heterodimers. <i>Cell</i> , 2004, 116, 417-429.	13.5	293
23	Allostery and Coupled Sequence Variation in Nuclear Hormone Receptors. <i>Cell</i> , 2004, 116, 354-356.	13.5	15
24	Differential phospholipase C activation by phenylalkylamine serotonin 5-HT _{2A} receptor agonists. <i>Journal of Neurochemistry</i> , 2005, 95, 1575-1584.	2.1	38
25	Natural-like function in artificial WW domains. <i>Nature</i> , 2005, 437, 579-583.	13.7	231
26	Evolutionary information for specifying a protein fold. <i>Nature</i> , 2005, 437, 512-518.	13.7	374
27	Intrinsic dynamics of an enzyme underlies catalysis. <i>Nature</i> , 2005, 438, 117-121.	13.7	1,018
28	The study of G-protein coupled receptor oligomerization with computational modeling and bioinformatics. <i>FEBS Journal</i> , 2005, 272, 2926-2938.	2.2	103
29	The N-Terminal End of the Catalytic Domain of Src Kinase Hck Is a Conformational Switch Implicated in Long-Range Allosteric Regulation. <i>Structure</i> , 2005, 13, 1715-1723.	1.6	45
30	A systems biology perspective on protein structural dynamics and signal transduction. <i>Current Opinion in Structural Biology</i> , 2005, 15, 23-30.	2.6	61
31	Phenology of disease-linked proteins. <i>Human Mutation</i> , 2005, 25, 90-97.	1.1	11
32	Coupling of structural fluctuations to deamidation reaction in triosephosphate isomerase by Gaussian network model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 715-727.	1.5	5
33	Mutations Remote from the Human Gonadotropin-releasing Hormone (GnRH) Receptor-binding Sites Specifically Increase Binding Affinity for GnRH II but Not GnRH I. <i>Journal of Biological Chemistry</i> , 2005, 280, 29796-29803.	1.6	51
34	Inhibition of Human Type I Gonadotropin-Releasing Hormone Receptor (GnRHR) Function by Expression of a Human Type II GnRHR Gene Fragment. <i>Endocrinology</i> , 2005, 146, 2639-2649.	1.4	40
35	Graphical models of residue coupling in protein families. , 2005, , .		6
36	Statistical coevolution analysis and molecular dynamics: Identification of amino acid pairs essential for catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 994-999.	3.3	48

#	ARTICLE	IF	CITATIONS
37	Directed evolution of protein switches and their application to the creation of ligand-binding proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11224-11229.	3.3	191
38	Engineering allosteric protein switches by domain insertion. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 359-364.	1.0	123
39	Mechanistic insight into the allosteric activation of a ubiquitin-conjugating enzyme by RING-type ubiquitin ligases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18890-18895.	3.3	160
40	Site-saturation Mutagenesis is more Efficient than DNA Shuffling for the Directed Evolution of β -Fucosidase from β -Galactosidase. <i>Journal of Molecular Biology</i> , 2005, 352, 621-628.	2.0	84
41	Multilevel regulation of protein-protein interactions in biological circuitry. <i>Physical Biology</i> , 2005, 2, S67-S73.	0.8	10
42	iVici: Interrelational Visualization and Correlation Interface. <i>Genome Biology</i> , 2005, 6, R115.	13.9	10
43	Identifying and manipulating structural determinates linking catalytic specificities in terpene synthases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9826-9831.	3.3	195
44	Reconciling the "old" and "new" views of protein allostery: A molecular simulation study of chemotaxis Y protein (CheY). <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 846-867.	1.5	103
45	Relating Protein Motion to Catalysis. <i>Annual Review of Biochemistry</i> , 2006, 75, 519-541.	5.0	565
46	Characterization of the Fast Dynamics of Protein Amino Acid Side Chains Using NMR Relaxation in Solution. <i>Chemical Reviews</i> , 2006, 106, 1672-1699.	23.0	300
47	Residues crucial for maintaining short paths in network communication mediate signaling in proteins. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0019.	3.2	268
48	Massive Sequence Perturbation of the Raf ras Binding Domain Reveals Relationships between Sequence Conservation, Secondary Structure Propensity, Hydrophobic Core Organization and Stability. <i>Journal of Molecular Biology</i> , 2006, 362, 151-171.	2.0	10
49	Characterization of the family of Mistic homologues. <i>BMC Structural Biology</i> , 2006, 6, 10.	2.3	26
50	Evolutionary coupling of structural and functional sequence information in the intracellular lipid-binding protein family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 373-384.	1.5	35
51	Correlated mutations: Advances and limitations. A study on fusion proteins and on the Cohesin-Dockerin families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 832-845.	1.5	95
52	Pump-probe molecular dynamics as a tool for studying protein motion and long range coupling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 347-361.	1.5	96
53	Dynamically driven protein allostery. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 831-838.	3.6	574
54	A simple tool to explore the distance distribution of correlated mutations in proteins. <i>Biophysical Chemistry</i> , 2006, 119, 240-246.	1.5	7

#	ARTICLE	IF	CITATIONS
55	Molecular Interaction of Serotonin 5-HT _{2A} Receptor Residues Phe339(6.51) and Phe340(6.52) with Superpotent N-Benzyl Phenethylamine Agonists. <i>Molecular Pharmacology</i> , 2006, 70, 1956-1964.	1.0	194
56	Mining for allosteric information: Natural mutations and positional sequence conservation in pyruvate kinase. <i>IUBMB Life</i> , 2006, 58, 31-38.	1.5	26
57	Determination of network of residues that regulate allostery in protein families using sequence analysis. <i>Protein Science</i> , 2006, 15, 258-268.	3.1	84
58	Src kinase activation: A switched electrostatic network. <i>Protein Science</i> , 2006, 15, 1051-1062.	3.1	71
59	The changing landscape of protein allostery. <i>Current Opinion in Structural Biology</i> , 2006, 16, 102-108.	2.6	282
60	Knowledge-based potentials in protein design. <i>Current Opinion in Structural Biology</i> , 2006, 16, 508-513.	2.6	83
61	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. <i>Structure</i> , 2006, 14, 1801-1809.	1.6	103
62	Predicting residue contacts using pragmatic correlated mutations method: reducing the false positives. <i>BMC Bioinformatics</i> , 2006, 7, 503.	1.2	43
63	Role of Na ⁺ and K ⁺ in Enzyme Function. <i>Physiological Reviews</i> , 2006, 86, 1049-1092.	13.1	274
64	Common dynamical signatures of familial amyotrophic lateral sclerosis-associated structurally diverse Cu, Zn superoxide dismutase mutants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3147-3152.	3.3	94
65	Evolutionarily Conserved Allosteric Network in the Cys Loop Family of Ligand-gated Ion Channels Revealed by Statistical Covariance Analyses. <i>Journal of Biological Chemistry</i> , 2006, 281, 18184-18192.	1.6	23
66	Intersubunit signaling in glutamate-1-semialdehyde-aminomutase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13688-13693.	3.3	34
67	Structure-Guided Recombination Creates an Artificial Family of Cytochromes P450. <i>PLoS Biology</i> , 2006, 4, e112.	2.6	133
68	Improved mutants from directed evolution are biased to orthologous substitutions. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 245-253.	1.0	57
69	Low-frequency normal modes that describe allosteric transitions in biological nanomachines are robust to sequence variations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7664-7669.	3.3	248
70	Markov propagation of allosteric effects in biomolecular systems: application to GroEL and GroES. <i>Molecular Systems Biology</i> , 2006, 2, 36.	3.2	146
71	Coordinated effects of distal mutations on environmentally coupled tunneling in dihydrofolate reductase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15753-15758.	3.3	171
72	A Novel Method for Detecting Intramolecular Coevolution: Adding a Further Dimension to Selective Constraints Analyses. <i>Genetics</i> , 2006, 173, 9-23.	1.2	149

#	ARTICLE	IF	CITATIONS
73	Signal transduction pathway of TonB-dependent transporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 513-518.	3.3	102
74	The Immunoglobulin Heavy Chain Constant Region Affects Kinetic and Thermodynamic Parameters of Antibody Variable Region Interactions with Antigen. <i>Journal of Biological Chemistry</i> , 2007, 282, 13917-13927.	1.6	116
75	NMR Investigation of Tyr105 Mutants in TEM-1 β -Lactamase. <i>Journal of Biological Chemistry</i> , 2007, 282, 21448-21459.	1.6	33
76	Principles underlying energetic coupling along an allosteric communication trajectory of a voltage-activated K ⁺ channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19813-19818.	3.3	95
77	Structural and Thermodynamic Properties of Selective Ion Binding in a K ⁺ Channel. <i>PLoS Biology</i> , 2007, 5, e121.	2.6	206
78	Mechanochemical Coupling in the Myosin Motor Domain. I. Insights from Equilibrium Active-Site Simulations. <i>PLoS Computational Biology</i> , 2007, 3, e21.	1.5	44
79	Mechanochemical Coupling in the Myosin Motor Domain. II. Analysis of Critical Residues. <i>PLoS Computational Biology</i> , 2007, 3, e23.	1.5	63
80	The Origins of Specificity in Polyketide Synthase Protein Interactions. <i>PLoS Computational Biology</i> , 2007, 3, e186.	1.5	44
81	Multicopy Suppression Underpins Metabolic Evolvability. <i>Molecular Biology and Evolution</i> , 2007, 24, 2716-2722.	3.5	154
82	Correlated substitution analysis and the prediction of amino acid structural contacts. <i>Briefings in Bioinformatics</i> , 2007, 9, 46-56.	3.2	58
83	Co-evolving residues in membrane proteins. <i>Bioinformatics</i> , 2007, 23, 3312-3319.	1.8	65
84	Functional Coevolutionary Networks of the Hsp70-Hsp90 System Revealed through Computational Analyses. <i>Molecular Biology and Evolution</i> , 2007, 24, 1032-1044.	3.5	50
85	The Molecular Basis for Ligand Specificity in a Mouse Olfactory Receptor. <i>Journal of Biological Chemistry</i> , 2007, 282, 1216-1224.	1.6	105
86	Functional and structural characterization of a protein based on analysis of its hydrogen bonding network by hydrogen bonding plot. <i>Archives of Biochemistry and Biophysics</i> , 2007, 461, 225-234.	1.4	76
87	Propagation of Dynamic Changes in Barnase Upon Binding of Barstar: An NMR and Computational Study. <i>Journal of Molecular Biology</i> , 2007, 367, 1079-1092.	2.0	52
88	Multivariate Analysis of Conserved Sequence-Structure Relationships in Kinesins: Coupling of the Active Site and a Tubulin-binding Sub-domain. <i>Journal of Molecular Biology</i> , 2007, 368, 1231-1248.	2.0	47
89	Allosteric Communication in Dihydrofolate Reductase: Signaling Network and Pathways for Closed to Occluded Transition and Back. <i>Journal of Molecular Biology</i> , 2007, 374, 250-266.	2.0	69
90	Predicting Allosteric Communication in Myosin via a Pathway of Conserved Residues. <i>Journal of Molecular Biology</i> , 2007, 373, 1361-1373.	2.0	61

#	ARTICLE	IF	CITATIONS
91	Solution Structure of Inhibitor-Free Human Metalloelastase (MMP-12) Indicates an Internal Conformational Adjustment. <i>Journal of Molecular Biology</i> , 2007, 374, 1333-1344.	2.0	20
92	A Minimal TrpRS Catalytic Domain Supports Sense/Antisense Ancestry of Class I and II Aminoacyl-tRNA Synthetases. <i>Molecular Cell</i> , 2007, 25, 851-862.	4.5	87
93	Finding coevolving amino acid residues using row and column weighting of mutual information and multi-dimensional amino acid representation. <i>Algorithms for Molecular Biology</i> , 2007, 2, 12.	0.3	49
94	Determinants of protein function revealed by combinatorial entropy optimization. <i>Genome Biology</i> , 2007, 8, R232.	13.9	262
95	Modular architecture of protein structures and allosteric communications: potential implications for signaling proteins and regulatory linkages. <i>Genome Biology</i> , 2007, 8, R92.	13.9	86
96	Features of Protein-Protein Interactions in Two-Component Signaling Deduced from Genomic Libraries. <i>Methods in Enzymology</i> , 2007, 422, 75-101.	0.4	44
97	Screened Nonbonded Interactions in Native Proteins Manipulate Optimal Paths for Robust Residue Communication. <i>Biophysical Journal</i> , 2007, 92, 3052-3062.	0.2	53
98	How Directional Translocation is Regulated in a DNA Helicase Motor. <i>Biophysical Journal</i> , 2007, 93, 3783-3797.	0.2	30
99	Engineering the Melanocortin-4 Receptor to Control Constitutive and Ligand-Mediated Gs Signaling In Vivo. <i>PLoS ONE</i> , 2007, 2, e668.	1.1	15
100	Distinguishing Functional Amino Acid Covariation from Background Linkage Disequilibrium in HIV Protease and Reverse Transcriptase. <i>PLoS ONE</i> , 2007, 2, e814.	1.1	15
101	Local motions in a benchmark of allosteric proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 385-399.	1.5	103
102	Identifying allosteric fluctuation transitions between different protein conformational states as applied to Cyclin Dependent Kinase 2. <i>BMC Bioinformatics</i> , 2007, 8, 45.	1.2	10
103	The Signaling Pathway of Rhodopsin. <i>Structure</i> , 2007, 15, 611-623.	1.6	59
104	Exploring allosteric coupling in the $\hat{\beta}$ -subunit of Heterotrimeric G proteins using evolutionary and ensemble-based approaches. <i>BMC Structural Biology</i> , 2008, 8, 23.	2.3	16
105	Quantifying information transfer by protein domains: Analysis of the Fyn SH2 domain structure. <i>BMC Structural Biology</i> , 2008, 8, 43.	2.3	33
106	New insight into long-range nonadditivity within protein double-mutant cycles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 915-924.	1.5	52
107	Using scores derived from statistical coupling analysis to distinguish correct and incorrect folds in de novo protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 950-959.	1.5	20
108	Contact rearrangements form coupled networks from local motions in allosteric proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 455-466.	1.5	89

#	ARTICLE	IF	CITATIONS
109	Crystal structure of yeast hexokinase PI in complex with glucose: A classical α -induced fit example revised. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 731-740.	1.5	31
110	Analysis of the residue α residue coevolution network and the functionally important residues in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 863-872.	1.5	50
111	Protein Design by Directed Evolution. <i>Annual Review of Biophysics</i> , 2008, 37, 153-173.	4.5	344
112	Serotonin Receptors. <i>Chemical Reviews</i> , 2008, 108, 1614-1641.	23.0	751
113	Role of A-chain in functioning of the active site of human β -thrombin. <i>Biochemistry (Moscow)</i> , 2008, 73, 237-244.	0.7	4
114	Allosteric regulation and catalysis emerge via a common route. <i>Nature Chemical Biology</i> , 2008, 4, 474-482.	3.9	610
115	H2r: Identification of evolutionary important residues by means of an entropy based analysis of multiple sequence alignments. <i>BMC Bioinformatics</i> , 2008, 9, 151.	1.2	16
116	Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. <i>BMC Evolutionary Biology</i> , 2008, 8, 327.	3.2	25
117	Allostery: an illustrated definition for the α "second secret of life"™. <i>Trends in Biochemical Sciences</i> , 2008, 33, 420-425.	3.7	256
118	Allostery and cooperativity revisited. <i>Protein Science</i> , 2008, 17, 1295-1307.	3.1	603
119	An electrostatic network and long α range regulation of Src kinases. <i>Protein Science</i> , 2008, 17, 1871-1880.	3.1	54
120	Coevolving residues of (β / β) α -barrel proteins play roles in stabilizing active site architecture and coordinating protein dynamics. <i>Journal of Structural Biology</i> , 2008, 164, 281-292.	1.3	15
121	Allosteric Signaling in the Biotin Repressor Occurs via Local Folding Coupled to Global Dampening of Protein Dynamics. <i>Journal of Molecular Biology</i> , 2008, 381, 89-101.	2.0	22
122	An Allosteric Circuit in Caspase-1. <i>Journal of Molecular Biology</i> , 2008, 381, 1157-1167.	2.0	83
123	High-throughput Analysis of the Protein Sequence α Stability Landscape using a Quantitative Yeast Surface Two-hybrid System and Fragment Reconstitution. <i>Journal of Molecular Biology</i> , 2008, 382, 721-733.	2.0	20
124	Statistical Coupling Analysis of Aspartic Proteinases Based on Crystal Structures of the <i>Trichoderma reesei</i> Enzyme and Its Complex with Pepstatin A. <i>Journal of Molecular Biology</i> , 2008, 382, 763-778.	2.0	11
125	Potential Modes of Interaction of 9-Aminomethyl-9,10-dihydroanthracene (AMDA) Derivatives with the 5-HT α Receptor: A Ligand Structure-Affinity Relationship, Receptor Mutagenesis and Receptor Modeling Investigation. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 6808-6828.	2.9	34
126	Energy Flow in Proteins. <i>Annual Review of Physical Chemistry</i> , 2008, 59, 233-259.	4.8	268

#	ARTICLE	IF	CITATIONS
127	Surface Sites for Engineering Allosteric Control in Proteins. <i>Science</i> , 2008, 322, 438-442.	6.0	310
128	Graphical Models of Residue Coupling in Protein Families. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 183-197.	1.9	59
129	Characterization of the Dynamics of an Essential Helix in the U1A Protein by Time-Resolved Fluorescence Measurements. <i>Journal of Physical Chemistry B</i> , 2008, 112, 6122-6130.	1.2	13
130	Identification of Functionally Distinct Regions That Mediate Biological Activity of the Protein Kinase A Homolog Tpk2. <i>Journal of Biological Chemistry</i> , 2008, 283, 1084-1093.	1.6	5
131	Structural identification of the pathway of long-range communication in an allosteric enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1832-1837.	3.3	97
132	Molecular Architecture of the Major Histocompatibility Complex Class I-binding Site of Ly49 Natural Killer Cell Receptors. <i>Journal of Biological Chemistry</i> , 2008, 283, 16840-16849.	1.6	47
133	A helix scaffold for the assembly of active protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14377-14382.	3.3	371
134	Reassessing a sparse energetic network within a single protein domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4679-4684.	3.3	89
135	Phylogenetic profiles reveal evolutionary relationships within the " twilight zone " of sequence similarity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13474-13479.	3.3	34
136	Force-Clamp Spectroscopy Detects Residue Co-evolution in Enzyme Catalysis. <i>Journal of Biological Chemistry</i> , 2008, 283, 27121-27129.	1.6	16
137	Using inferred residue contacts to distinguish between correct and incorrect protein models. <i>Bioinformatics</i> , 2008, 24, 1575-1582.	1.8	44
138	Analysis of correlated mutations in HIV-1 protease using spectral clustering. <i>Bioinformatics</i> , 2008, 24, 1243-1250.	1.8	38
139	Cooperative Transition between Open and Closed Conformations in Potassium Channels. <i>PLoS Computational Biology</i> , 2008, 4, e1000164.	1.5	19
140	Identifying Cognate Binding Pairs among a Large Set of Paralogs: The Case of PE/PPE Proteins of <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2008, 4, e1000174.	1.5	37
141	Genome-wide hepatitis C virus amino acid covariance networks can predict response to antiviral therapy in humans. <i>Journal of Clinical Investigation</i> , 2008, 119, 225-36.	3.9	76
142	An integrated system for studying residue coevolution in proteins. <i>Bioinformatics</i> , 2008, 24, 290-292.	1.8	70
143	Advances in the development and application of computational methodologies for structural modeling of G-protein-coupled receptors. <i>Expert Opinion on Drug Discovery</i> , 2008, 3, 343-355.	2.5	17
144	Functional Motions in Biomolecules: Insights from Computational Studies at Multiple Scales. , 2008, , 253-297.		3

#	ARTICLE	IF	CITATIONS
145	Computing Highly Correlated Positions Using Mutual Information and Graph Theory for G Protein-Coupled Receptors. PLoS ONE, 2009, 4, e4681.	1.1	24
146	Correlated Mutation Analysis on the Catalytic Domains of Serine/Threonine Protein Kinases. PLoS ONE, 2009, 4, e5913.	1.1	9
147	Long-range energy transfer in proteins. Physical Biology, 2009, 6, 046014.	0.8	52
148	Traceless protein splicing utilizing evolved split inteins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10999-11004.	3.3	100
149	Polymorphisms in CD1d affect antigen presentation and the activation of CD1d-restricted T cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1909-1914.	3.3	33
150	Differential Behavior of Missense Mutations in the Intersubunit Contact Domain of the Human Pyruvate Kinase M2 Isozyme. Journal of Biological Chemistry, 2009, 284, 11971-11981.	1.6	21
151	Contribution of Non-catalytic Core Residues to Activity and Regulation in Protein Kinase A. Journal of Biological Chemistry, 2009, 284, 6241-6248.	1.6	44
152	The Effect of Sequence Evolution on Protein Structural Divergence. Molecular Biology and Evolution, 2009, 26, 1055-1065.	3.5	30
153	Coarse-grained modeling of allosteric regulation in protein receptors. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14253-14258.	3.3	43
154	Examining Cooperative Gating Phenomena in Voltage-Dependent Potassium Channels. Methods in Enzymology, 2009, 466, 179-209.	0.4	15
155	Intra and Inter-Molecular Communications Through Protein Structure Network. Current Protein and Peptide Science, 2009, 10, 146-160.	0.7	159
156	The Impact of Ions on Allosteric Functions in Human Liver Pyruvate Kinase. Methods in Enzymology, 2009, 466, 83-107.	0.4	32
157	TOWARD UNDERSTANDING ALLOSTERIC SIGNALING MECHANISMS IN THE ATPASE DOMAIN OF MOLECULAR CHAPERONES. , 2009, , 269-280.		10
158	Linear predictive coding representation of correlated mutation for protein sequence alignment. , 2009, , .		0
159	Mechanical Network in Titin Immunoglobulin from Force Distribution Analysis. PLoS Computational Biology, 2009, 5, e1000306.	1.5	62
160	Dynamic Allostery in the Methionine Repressor Revealed by Force Distribution Analysis. PLoS Computational Biology, 2009, 5, e1000574.	1.5	49
161	A Combinatorial Approach to Detect Coevolved Amino Acid Networks in Protein Families of Variable Divergence. PLoS Computational Biology, 2009, 5, e1000488.	1.5	23
162	Structure-Based Predictive Models for Allosteric Hot Spots. PLoS Computational Biology, 2009, 5, e1000531.	1.5	58

#	ARTICLE	IF	CITATIONS
163	Integration of Evolutionary Features for the Identification of Functionally Important Residues in Major Facilitator Superfamily Transporters. <i>PLoS Computational Biology</i> , 2009, 5, e1000522.	1.5	16
164	Identification of direct residue contacts in protein-protein interaction by message passing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 67-72.	3.3	902
165	A new method for revealing correlated mutations under the structural and functional constraints in proteins. <i>Bioinformatics</i> , 2009, 25, 2506-2513.	1.8	35
166	Amplification of signaling via cellular allosteric relay and protein disorder: Fig. 1.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6887-6888.	3.3	36
167	Evolutionary Basis for the Coupled-domain Motions in <i>Thermus thermophilus</i> Leucyl-tRNA Synthetase. <i>Journal of Biological Chemistry</i> , 2009, 284, 10088-10099.	1.6	20
168	The induction of folding cooperativity by ligand binding drives the allosteric response of tetracycline repressor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22263-22268.	3.3	99
169	Designing switchable enzymes. <i>Current Opinion in Structural Biology</i> , 2009, 19, 442-448.	2.6	64
170	The Origin of Allosteric Functional Modulation: Multiple Pre-existing Pathways. <i>Structure</i> , 2009, 17, 1042-1050.	1.6	347
171	Evolution based on domain combinations: the case of glutaredoxins. <i>BMC Evolutionary Biology</i> , 2009, 9, 66.	3.2	35
173	Engineering Allosteric Regulation into Biological Catalysts. <i>ChemBioChem</i> , 2009, 10, 2824-2835.	1.3	40
174	Pathogenic or not? And if so, then how? Studying the effects of missense mutations using bioinformatics methods. <i>Human Mutation</i> , 2009, 30, 703-714.	1.1	211
175	Allosteric Switches: Remote Controls for Proteins. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 3218-3220.	7.2	8
176	Coevolution in defining the functional specificity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 231-240.	1.5	62
177	Conserved amino acid networks involved in antibody variable domain interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 99-114.	1.5	43
178	Systematic structural studies of iron superoxide dismutases from human parasites and a statistical coupling analysis of metal binding specificity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 26-37.	1.5	35
179	Predicting structurally conserved contacts for homologous proteins using sequence conservation filters. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 448-453.	1.5	11
180	On the accuracy of inferring energetic coupling between distant sites in protein families from evolutionary imprints: Illustrations using lattice model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 823-831.	1.5	32
181	Large-scale evaluation of dynamically important residues in proteins predicted by the perturbation analysis of a coarse-grained elastic model. <i>BMC Structural Biology</i> , 2009, 9, 45.	2.3	56

#	ARTICLE	IF	CITATIONS
182	Modulation of the heme electronic structure and cystathionine β -synthase activity by second coordination sphere ligands: The role of heme ligand switching in redox regulation. <i>Journal of Inorganic Biochemistry</i> , 2009, 103, 689-697.	1.5	59
183	Specificity in lipases: A computational study of transesterification of sucrose. <i>Protein Science</i> , 2009, 13, 3092-3103.	3.1	21
184	Unnatural Amino Acid Substitution as a Probe of the Allosteric Coupling Pathway in a Mycobacterial Cu(I) Sensor. <i>Journal of the American Chemical Society</i> , 2009, 131, 18044-18045.	6.6	54
185	Quantifying Correlations Between Allosteric Sites in Thermodynamic Ensembles. <i>Journal of Chemical Theory and Computation</i> , 2009, 5, 2486-2502.	2.3	203
186	Energy Flow and Long-Range Correlations in Guanine-Binding Riboswitch: A Nonequilibrium Molecular Dynamics Study. <i>Journal of Physical Chemistry B</i> , 2009, 113, 9340-9347.	1.2	36
187	The Myosin C-Loop Is an Allosteric Actin Contact Sensor in Actomyosin. <i>Biochemistry</i> , 2009, 48, 5263-5275.	1.2	17
188	Protein Sectors: Evolutionary Units of Three-Dimensional Structure. <i>Cell</i> , 2009, 138, 774-786.	13.5	642
189	During Transitions Proteins Make Fleeting Bonds. <i>Cell</i> , 2009, 139, 1049-1051.	13.5	10
190	Allostery Wiring Diagrams in the Transitions that Drive the GroEL Reaction Cycle. <i>Journal of Molecular Biology</i> , 2009, 387, 390-406.	2.0	77
191	Amino acid substitutions in the sugar kinase/hsp70/actin superfamily conserved ATPase core of E. coli glycerol kinase modulate allosteric ligand affinity but do not alter allosteric coupling. <i>Archives of Biochemistry and Biophysics</i> , 2009, 481, 151-156.	1.4	7
192	Oligomeric interactions provide alternatives to direct steric modes of control of sugar kinase/actin/hsp70 superfamily functions by heterotropic allosteric effectors: Inhibition of E. coli glycerol kinase. <i>Archives of Biochemistry and Biophysics</i> , 2009, 492, 29-39.	1.4	4
193	Protein allostery, signal transmission and dynamics: a classification scheme of allosteric mechanisms. <i>Molecular BioSystems</i> , 2009, 5, 207.	2.9	299
194	Direct Observation of the Dynamic Process Underlying Allosteric Signal Transmission. <i>Journal of the American Chemical Society</i> , 2009, 131, 3063-3068.	6.6	111
196	Bioinformatic perspectives on NRPS/PKS megasynthases: Advances and challenges. <i>Natural Product Reports</i> , 2009, 26, 874.	5.2	67
197	Evolving a Polymerase for Hydrophobic Base Analogues. <i>Journal of the American Chemical Society</i> , 2009, 131, 14827-14837.	6.6	73
198	Allosteric Transitions in Biological Nanomachines are Described by Robust Normal Modes of Elastic Networks. <i>Current Protein and Peptide Science</i> , 2009, 10, 128-132.	0.7	43
199	An interdomain sector mediating allostery in Hsp70 molecular chaperones. <i>Molecular Systems Biology</i> , 2010, 6, 414.	3.2	118
200	Sequence signatures of allosteric proteins towards rational design. <i>Systems and Synthetic Biology</i> , 2010, 4, 271-280.	1.0	9

#	ARTICLE	IF	CITATIONS
201	The Third Conformation of p38 MAP Kinase Observed in Phosphorylated p38 and in Solution. <i>Structure</i> , 2010, 18, 1571-1578.	1.6	37
202	Structural synthetic biotechnology: from molecular structure to predictable design for industrial strain development. <i>Trends in Biotechnology</i> , 2010, 28, 534-542.	4.9	47
203	Linear predictive coding representation of correlated mutation for protein sequence alignment. <i>BMC Bioinformatics</i> , 2010, 11, S2.	1.2	3
204	Experimental and computational determination of tRNA dynamics. <i>FEBS Letters</i> , 2010, 584, 376-386.	1.3	63
205	Defining the conserved internal architecture of a protein kinase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 440-444.	1.1	222
206	Selecting sequences that fold into a defined 3D structure: A new approach for protein design based on molecular dynamics and energetics. <i>Biophysical Chemistry</i> , 2010, 146, 76-84.	1.5	15
207	Conserved tertiary couplings stabilize elements in the PDZ fold, leading to characteristic patterns of domain conformational flexibility. <i>Protein Science</i> , 2010, 19, 398-411.	3.1	36
208	Protein structure prediction enhanced with evolutionary diversity: SPEED. <i>Protein Science</i> , 2010, 19, 520-534.	3.1	23
209	Molecular mechanism of allosteric communication in the human PPAR α -RXR α heterodimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 873-887.	1.5	19
210	FoldGPCR: Structure prediction protocol for the transmembrane domain of G protein-coupled receptors from class A. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2189-2201.	1.5	33
211	iPatch: Interprotein contact prediction using local network information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2781-2797.	1.5	26
212	Structural polymorphism in F-actin. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1318-1323.	3.6	170
213	An allosteric inhibitor of substrate recognition by the SCFCdc4 ubiquitin ligase. <i>Nature Biotechnology</i> , 2010, 28, 733-737.	9.4	136
214	Validation of Coevolving Residue Algorithms via Pipeline Sensitivity Analysis: ELSC and OMES and ZNMI, Oh My!. <i>PLoS ONE</i> , 2010, 5, e10779.	1.1	31
215	Correlation Analysis for Protein Evolutionary Family Based on Amino Acid Position Mutations and Application in PDZ Domain. <i>PLoS ONE</i> , 2010, 5, e13207.	1.1	10
216	Understanding large multiprotein complexes: applying a multiple allosteric networks model to explain the function of the Mediator transcription complex. <i>Journal of Cell Science</i> , 2010, 123, 159-163.	1.2	6
217	An Online Approach for Mining Collective Behaviors from Molecular Dynamics Simulations. <i>Journal of Computational Biology</i> , 2010, 17, 309-324.	0.8	27
218	Disentangling Direct from Indirect Co-Evolution of Residues in Protein Alignments. <i>PLoS Computational Biology</i> , 2010, 6, e1000633.	1.5	171

#	ARTICLE	IF	CITATIONS
219	On the Conservation of the Slow Conformational Dynamics within the Amino Acid Kinase Family: NAGK the Paradigm. <i>PLoS Computational Biology</i> , 2010, 6, e1000738.	1.5	41
220	Pervasive Cryptic Epistasis in Molecular Evolution. <i>PLoS Genetics</i> , 2010, 6, e1001162.	1.5	147
221	Statistical Potentials for Improved Structurally Constrained Evolutionary Models. <i>Molecular Biology and Evolution</i> , 2010, 27, 1546-1560.	3.5	49
222	Enhancement of the latent 3-isopropylmalate dehydrogenase activity of promiscuous homoisocitrate dehydrogenase by directed evolution. <i>Biochemical Journal</i> , 2010, 431, 401-412.	1.7	11
223	Inference of Direct Residue Contacts in Two-Component Signaling. <i>Methods in Enzymology</i> , 2010, 471, 17-41.	0.4	40
224	Protein functional landscapes, dynamics, allostery: a tortuous path towards a universal theoretical framework. <i>Quarterly Reviews of Biophysics</i> , 2010, 43, 295-332.	2.4	131
225	Dynamics-Based Discovery of Allosteric Inhibitors: Selection of New Ligands for the C-terminal Domain of Hsp90. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 2978-2989.	2.3	83
226	Protein Dynamics and Drug Design: The Role of Molecular Simulations. , 2010, , 340-385.		0
227	Interaction fidelity in two-component signaling. <i>Current Opinion in Microbiology</i> , 2010, 13, 190-197.	2.3	53
228	Crystal structure and statistical coupling analysis of highly glycosylated peroxidase from royal palm tree (<i>Roystonea regia</i>). <i>Journal of Structural Biology</i> , 2010, 169, 226-242.	1.3	41
229	The Membrane Complex between Transducin and Dark-State Rhodopsin Exhibits Large-Amplitude Interface Dynamics on the Sub-Microsecond Timescale: Insights from All-Atom MD Simulations. <i>Journal of Molecular Biology</i> , 2010, 398, 161-173.	2.0	21
230	Probing the Transition State of the Allosteric Pathway of the Shaker Kv Channel Pore by Linear Free-Energy Relations. <i>Journal of Molecular Biology</i> , 2010, 403, 167-173.	2.0	11
231	Allosteric regulation of protease activity by small molecules. <i>Molecular BioSystems</i> , 2010, 6, 1431.	2.9	41
232	An Integrated View of Molecular Coevolution in Protein-Protein Interactions. <i>Molecular Biology and Evolution</i> , 2010, 27, 2567-2575.	3.5	119
233	Correlating allostery with rigidity. <i>Molecular BioSystems</i> , 2011, 7, 464-471.	2.9	41
234	Coevolutionary Analysis Enabled Rational Deregulation of Allosteric Enzyme Inhibition in <i>Corynebacterium glutamicum</i> for Lysine Production. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4352-4360.	1.4	61
235	Structure-Function Analysis from the Outside In: Long-Range Tertiary Contacts in RNA Exhibit Distinct Catalytic Roles. <i>Biochemistry</i> , 2011, 50, 8733-8755.	1.2	14
237	Catalytic Contributions from Remote Regions of Enzyme Structure. <i>Chemical Reviews</i> , 2011, 111, 7595-7624.	23.0	81

#	ARTICLE	IF	CITATIONS
239	Application of Recurrence Quantification Analysis (RQA) in Biosequence Pattern Recognition. Communications in Computer and Information Science, 2011, , 284-293.	0.4	4
240	Link between Allosteric Signal Transduction and Functional Dynamics in a Multisubunit Enzyme: <i>S</i> -Adenosylhomocysteine Hydrolase. Journal of the American Chemical Society, 2011, 133, 19807-19815.	6.6	17
241	Protein Allostery at the Solid-Liquid Interface: Endoglucanase Attachment to Cellulose Affects Glucan Clenching in the Binding Cleft. Journal of the American Chemical Society, 2011, 133, 16617-16624.	6.6	22
242	Hot Spots for Allosteric Regulation on Protein Surfaces. Cell, 2011, 147, 1564-1575.	13.5	311
243	Bioinformatics and mathematical modelling in the study of receptor-receptor interactions and receptor oligomerization. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 1267-1283.	1.4	17
244	Identification of distant co-evolving residues in antigen 85C from Mycobacterium tuberculosis using statistical coupling analysis of the esterase family proteins. Journal of Biomedical Research, 2011, 25, 165-169.	0.7	8
245	Using Amino Acid Correlation and Community Detection Algorithms to Identify Functional Determinants in Protein Families. PLoS ONE, 2011, 6, e27786.	1.1	25
246	The Energy Landscape Analysis of Cancer Mutations in Protein Kinases. PLoS ONE, 2011, 6, e26071.	1.1	39
247	Defining an allosteric circuit in the cysteine protease domain of Clostridium difficile toxins. Nature Structural and Molecular Biology, 2011, 18, 364-371.	3.6	66
248	Allostery in Protein Domains Reflects a Balance of Steric and Hydrophobic Effects. Structure, 2011, 19, 967-975.	1.6	30
249	Protein kinases: evolution of dynamic regulatory proteins. Trends in Biochemical Sciences, 2011, 36, 65-77.	3.7	753
250	Analyzing and visualizing residue networks of protein structures. Trends in Biochemical Sciences, 2011, 36, 179-182.	3.7	244
251	Allostery in pharmacology: Thermodynamics, evolution and design. Progress in Biophysics and Molecular Biology, 2011, 106, 463-473.	1.4	21
252	Direct correlation analysis improves fold recognition. Computational Biology and Chemistry, 2011, 35, 323-332.	1.1	21
253	Remodeling of actin filaments by ADF/cofilin proteins. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20568-20572.	3.3	194
254	Genetically engineered light sensors for control of bacterial gene expression. Biotechnology Journal, 2011, 6, 826-836.	1.8	15
255	Long-Range Effects of a Peripheral Mutation on the Enzymatic Activity of Cytochrome P450 1A2. Journal of Chemical Information and Modeling, 2011, 51, 1336-1346.	2.5	39
256	Use of mutual information arrays to predict coevolving sites in the full length HIV gp120 protein for subtypes B and C. Virologica Sinica, 2011, 26, 95-104.	1.2	2

#	ARTICLE	IF	CITATIONS
257	The self-organizing fractal theory as a universal discovery method: the phenomenon of life. <i>Theoretical Biology and Medical Modelling</i> , 2011, 8, 4.	2.1	50
258	Network approach for capturing ligand-induced subtle global changes in protein structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 429-439.	2.5	18
259	Modeling allosteric signal propagation using protein structure networks. <i>BMC Bioinformatics</i> , 2011, 12, S23.	1.2	20
260	Functionally important positions can comprise the majority of a protein's architecture. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1589-1608.	1.5	32
261	Identification of functional motions in the adenylate kinase (ADK) protein family by computational hybrid approaches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1662-1671.	1.5	17
262	Engineering an Allosteric Binding Site for Aminoglycosides into TEM1 β -Lactamase. <i>ChemBioChem</i> , 2011, 12, 904-913.	1.3	3
263	Integrating molecular dynamics and co-evolutionary analysis for reliable target prediction and deregulation of the allosteric inhibition of aspartokinase for amino acid production. <i>Journal of Biotechnology</i> , 2011, 154, 248-254.	1.9	49
264	Co-evolution and information signals in biological sequences. <i>Theoretical Computer Science</i> , 2011, 412, 2486-2495.	0.5	9
265	Possible new targets for GPCR modulation: allosteric interactions, plasma membrane domains, intercellular transfer and epigenetic mechanisms. <i>Journal of Receptor and Signal Transduction Research</i> , 2011, 31, 315-331.	1.3	20
266	Molecular Evolution of Protein Conformational Changes Revealed by a Network of Evolutionarily Coupled Residues. <i>Molecular Biology and Evolution</i> , 2011, 28, 2675-2685.	3.5	45
267	Relationships between ligand binding sites, protein architecture and correlated paths of energy and conformational fluctuations. <i>Physical Biology</i> , 2011, 8, 056003.	0.8	20
268	RING: networking interacting residues, evolutionary information and energetics in protein structures. <i>Bioinformatics</i> , 2011, 27, 2003-2005.	1.8	116
269	Moving Iron through Ferritin Protein Nanocages Depends on Residues throughout Each Four α -Helix Bundle Subunit. <i>Journal of Biological Chemistry</i> , 2011, 286, 25620-25627.	1.6	55
270	Sequence-specific Long Range Networks in PSD-95/Discs Large/ZO-1 (PDZ) Domains Tune Their Binding Selectivity. <i>Journal of Biological Chemistry</i> , 2011, 286, 27167-27175.	1.6	62
271	Using physicochemical properties of amino acids to induce graphical models of residue couplings. , 2011, , .		0
272	Computational Modeling of Allosteric Communication Reveals Organizing Principles of Mutation-Induced Signaling in ABL and EGFR Kinases. <i>PLoS Computational Biology</i> , 2011, 7, e1002179.	1.5	67
273	Changes in Dynamics upon Oligomerization Regulate Substrate Binding and Allostery in Amino Acid Kinase Family Members. <i>PLoS Computational Biology</i> , 2011, 7, e1002201.	1.5	49
274	Long-Range Intra-Protein Communication Can Be Transmitted by Correlated Side-Chain Fluctuations Alone. <i>PLoS Computational Biology</i> , 2011, 7, e1002168.	1.5	57

#	ARTICLE	IF	CITATIONS
275	Change in Allosteric Network Affects Binding Affinities of PDZ Domains: Analysis through Perturbation Response Scanning. PLoS Computational Biology, 2011, 7, e1002154.	1.5	156
276	“Fluctuograms” Reveal the Intermittent Intra-Protein Communication in Subtilisin Carlsberg and Correlate Mechanical Coupling with Co-Evolution. PLoS Computational Biology, 2011, 7, e1002023.	1.5	19
277	Rational Engineering of Enzyme Allosteric Regulation through Sequence Evolution Analysis. PLoS Computational Biology, 2012, 8, e1002612.	1.5	71
278	Convergent Transmission of RNAi Guide-Target Mismatch Information across Argonaute Internal Allosteric Network. PLoS Computational Biology, 2012, 8, e1002693.	1.5	10
279	Detecting coevolving positions in a molecule: why and how to account for phylogeny. Briefings in Bioinformatics, 2012, 13, 228-243.	3.2	41
280	A Critical Evaluation of Correlated Mutation Algorithms and Coevolution Within Allosteric Mechanisms. Methods in Molecular Biology, 2012, 796, 385-398.	0.4	35
281	Allostery. Methods in Molecular Biology, 2012, , .	0.4	5
282	Temperature-Sensitive Mutants and Revertants in the Coronavirus Nonstructural Protein 5 Protease (3CLpro) Define Residues Involved in Long-Distance Communication and Regulation of Protease Activity. Journal of Virology, 2012, 86, 4801-4810.	1.5	37
283	Correlation of Molecular and Functional Effects of Mutations in Cardiac Troponin T Linked to Familial Hypertrophic Cardiomyopathy. Journal of Biological Chemistry, 2012, 287, 14515-14523.	1.6	33
284	Transition Step during Assembly of HIV Tat:P-TEFb Transcription Complexes and Transfer to TAR RNA. Molecular and Cellular Biology, 2012, 32, 4780-4793.	1.1	46
285	Structural and Functional Analysis of Hemoglobin and Serum Albumin Through Protein Long-Range Interaction Networks. Current Proteomics, 2012, 9, 160-166.	0.1	12
286	NetworkView: 3D display and analysis of protein-RNA interaction networks. Bioinformatics, 2012, 28, 3000-3001.	1.8	186
287	Local motifs in proteins combine to generate global functional moves. Briefings in Functional Genomics, 2012, 11, 479-488.	1.3	17
288	Exploring Residue Component Contributions to Dynamical Network Models of Allostery. Journal of Chemical Theory and Computation, 2012, 8, 2949-2961.	2.3	152
289	The XNA world: progress towards replication and evolution of synthetic genetic polymers. Current Opinion in Chemical Biology, 2012, 16, 245-252.	2.8	164
290	Post-translational tools expand the scope of synthetic biology. Current Opinion in Chemical Biology, 2012, 16, 300-306.	2.8	43
291	Directed evolution to re-adapt a co-evolved network within an enzyme. Journal of Biotechnology, 2012, 157, 237-245.	1.9	27
292	Network-Based Models as Tools Hinting at Nonevident Protein Functionality. Annual Review of Biophysics, 2012, 41, 205-225.	4.5	54

#	ARTICLE	IF	CITATIONS
293	Experimental Assessment of the Importance of Amino Acid Positions Identified by an Entropy-Based Correlation Analysis of Multiple-Sequence Alignments. <i>Biochemistry</i> , 2012, 51, 5633-5641.	1.2	12
294	The spatial architecture of protein function and adaptation. <i>Nature</i> , 2012, 491, 138-142.	13.7	423
295	CLAG: an unsupervised non hierarchical clustering algorithm handling biological data. <i>BMC Bioinformatics</i> , 2012, 13, 194.	1.2	18
296	A minimal ligand binding pocket within a network of correlated mutations identified by multiple sequence and structural analysis of G protein coupled receptors. <i>BMC Biophysics</i> , 2012, 5, 13.	4.4	7
297	Identifying Allosteric Binding Sites in Proteins with a Two-State Go... Model for Novel Allosteric Effector Discovery. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 2962-2971.	2.3	46
298	The emergence of protein complexes: quaternary structure, dynamics and allostery. <i>Biochemical Society Transactions</i> , 2012, 40, 475-491.	1.6	75
299	4.3 Structure and Dynamic States of Actin Filaments. , 2012, , 15-30.		1
300	The Dynamic Structure of Thrombin in Solution. <i>Biophysical Journal</i> , 2012, 103, 79-88.	0.2	47
301	Mechanisms of Intramolecular Communication in a Hyperthermophilic Acylaminoacyl Peptidase: A Molecular Dynamics Investigation. <i>PLoS ONE</i> , 2012, 7, e35686.	1.1	40
302	Protein Fragments: Functional and Structural Roles of Their Coevolution Networks. <i>PLoS ONE</i> , 2012, 7, e48124.	1.1	22
303	Synthetic Genetic Polymers Capable of Heredity and Evolution. <i>Science</i> , 2012, 336, 341-344.	6.0	635
304	Simulating Dynamics in RNA-Protein Complexes. <i>Nucleic Acids and Molecular Biology</i> , 2012, , 213-238.	0.2	3
305	Chapter 13. Computational Strategies and Challenges for Targeting Protein-Protein Interactions with Small Molecules. <i>RSC Drug Discovery Series</i> , 2012, , 319-359.	0.2	3
306	A rigid network of long-range contacts increases thermostability in a mutant endoglucanase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 30, 628-637.	2.0	17
307	Fine-Tuning Multiprotein Complexes Using Small Molecules. <i>ACS Chemical Biology</i> , 2012, 7, 1311-1320.	1.6	87
308	Role of long- and short-range hydrophobic, hydrophilic and charged residues contact network in protein's structural organization. <i>BMC Bioinformatics</i> , 2012, 13, 142.	1.2	42
309	Actin Filaments as Tension Sensors. <i>Current Biology</i> , 2012, 22, R96-R101.	1.8	146
310	Shedding light on protein-ligand binding by graph theory: The topological nature of allostery. <i>Biophysical Chemistry</i> , 2012, 165-166, 21-29.	1.5	48

#	ARTICLE	IF	CITATIONS
311	Dynamics in Enzyme Catalysis. Topics in Current Chemistry, 2013, , .	4.0	13
312	Evolutionary biochemistry: revealing the historical and physical causes of protein properties. Nature Reviews Genetics, 2013, 14, 559-571.	7.7	305
313	Prediction of contacts from correlated sequence substitutions. Current Opinion in Structural Biology, 2013, 23, 473-479.	2.6	33
314	Fractal Symmetry of Protein Interior. SpringerBriefs in Biochemistry and Molecular Biology, 2013, , .	0.3	2
315	Evolution of protein structures and interactions from the perspective of residue contact networks. Current Opinion in Structural Biology, 2013, 23, 954-963.	2.6	33
316	Theoretical studies on the reaction mechanism of PP1 and the effects of different oxidation states of the Mn ²⁺ Mn center on the mechanism. Journal of Biological Inorganic Chemistry, 2013, 18, 451-459.	1.1	11
317	The Global Sequence Signature algorithm unveils a structural network surrounding heavy chain CDR3 loop in Camelidae variable domains. Biochimica Et Biophysica Acta - General Subjects, 2013, 1830, 3373-3381.	1.1	4
318	Helices 2 and 3 Are the Initiation Sites in the PrPC \rightarrow PrP ^{Sc} Transition. Biochemistry, 2013, 52, 310-319.	1.2	26
319	Statistical analyses of protein sequence alignments identify structures and mechanisms in signal activation of sensor histidine kinases. Molecular Microbiology, 2013, 87, 707-712.	1.2	12
320	A fast approximate method of identifying paths of allosteric communication in proteins. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1097-1101.	1.5	18
321	Exploring the Molecular Mechanism of Cross-Resistance to HIV-1 Integrase Strand Transfer Inhibitors by Molecular Dynamics Simulation and Residue Interaction Network Analysis. Journal of Chemical Information and Modeling, 2013, 53, 210-222.	2.5	75
322	A conserved interdomain communication pathway of pseudosymmetrically distributed residues affects substrate specificity of the fungal multidrug transporter Cdr1p. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 479-490.	1.4	17
323	Comparing proteins by their internal dynamics: Exploring structure \leftrightarrow function relationships beyond static structural alignments. Physics of Life Reviews, 2013, 10, 1-26.	1.5	89
324	Molecular signatures of G-protein-coupled receptors. Nature, 2013, 494, 185-194.	13.7	1,298
325	Impact of Mutations on the Allosteric Conformational Equilibrium. Journal of Molecular Biology, 2013, 425, 647-661.	2.0	48
326	Allosteric Inhibition of a Zinc-Sensing Transcriptional Repressor: Insights into the Arsenic Repressor (ArsR) Family. Journal of Molecular Biology, 2013, 425, 1143-1157.	2.0	35
327	Mapping the intramolecular signal propagation pathways in protein using Bayesian change point analysis of atomic motions. Computational Biology and Chemistry, 2013, 47, 89-95.	1.1	3
328	Protein co-evolution: how do we combine bioinformatics and experimental approaches?. Molecular BioSystems, 2013, 9, 175-181.	2.9	16

#	ARTICLE	IF	CITATIONS
329	Protein Contact Networks: An Emerging Paradigm in Chemistry. <i>Chemical Reviews</i> , 2013, 113, 1598-1613.	23.0	226
330	Emerging methods in protein co-evolution. <i>Nature Reviews Genetics</i> , 2013, 14, 249-261.	7.7	553
331	Structure-based network analysis of an evolved G protein-coupled receptor homodimer interface. <i>Protein Science</i> , 2013, 22, 745-754.	3.1	11
332	Volumetric properties underlying ligand binding in a monomeric hemoglobin: A high-pressure NMR study. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1910-1922.	1.1	12
333	Multiple Pathways Promote Dynamical Coupling between Catalytic Domains in <i>Escherichia coli</i> Prolyl-tRNA Synthetase. <i>Biochemistry</i> , 2013, 52, 4399-4412.	1.2	16
334	The Crystal Structure of <i>Mycobacterium tuberculosis</i> NrdH at 0.87 Å... Suggests a Possible Mode of Its Activity. <i>Biochemistry</i> , 2013, 52, 4056-4065.	1.2	12
335	Highly covarying residues have a functional role in antibody constant domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 884-895.	1.5	5
336	Allosteric Activation Transitions in Enzymes and Biomolecular Motors: Insights from Atomistic and Coarse-Grained Simulations. <i>Topics in Current Chemistry</i> , 2013, 337, 139-164.	4.0	12
337	Protein Engineering and Stabilization from Sequence Statistics. <i>Methods in Enzymology</i> , 2013, 523, 237-256.	0.4	25
338	Evolution-Based Design of Proteins. <i>Methods in Enzymology</i> , 2013, 523, 213-235.	0.4	37
339	Entropic Mechanism of Allosteric Communication in Conformational Transitions of Dihydrofolate Reductase. <i>Journal of Physical Chemistry B</i> , 2013, 117, 12864-12877.	1.2	12
340	Allosteric Communication in the KIX Domain Proceeds through Dynamic Repacking of the Hydrophobic Core. <i>ACS Chemical Biology</i> , 2013, 8, 1600-1610.	1.6	62
341	Role of Glycoside Phosphorylases in Mannose Foraging by Human Gut Bacteria. <i>Journal of Biological Chemistry</i> , 2013, 288, 32370-32383.	1.6	50
342	Correlated Motions and Residual Frustration in Thrombin. <i>Journal of Physical Chemistry B</i> , 2013, 117, 12857-12863.	1.2	37
343	MCPATH: Monte Carlo path generation approach to predict likely allosteric pathways and functional residues. <i>Nucleic Acids Research</i> , 2013, 41, W249-W255.	6.5	66
344	Computational Protein Design Quantifies Structural Constraints on Amino Acid Covariation. <i>PLoS Computational Biology</i> , 2013, 9, e1003313.	1.5	35
345	A Mechanistic Understanding of Allosteric Immune Escape Pathways in the HIV-1 Envelope Glycoprotein. <i>PLoS Computational Biology</i> , 2013, 9, e1003046.	1.5	53
346	Engineering alternate cooperative-communications in the lactose repressor protein scaffold. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 433-443.	1.0	27

#	ARTICLE	IF	CITATIONS
347	Rational design of a ligand-controlled protein conformational switch. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6800-6804.	3.3	111
348	Probing impact of active site residue mutations on stability and activity of <i>Neisseria polysaccharea</i> amylosucrase. Protein Science, 2013, 22, 1754-1765.	3.1	23
349	Adaptive Evolution of the Streptococcus pyogenes Regulatory Aldolase LacD.1. Journal of Bacteriology, 2013, 195, 1294-1304.	1.0	5
350	Kinetic response of a photoperturbed allosteric protein. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11725-11730.	3.3	93
351	A novel mechanism for fine-tuning open-state stability in a voltage-gated potassium channel. Nature Communications, 2013, 4, 1784.	5.8	15
352	Prediction of Protein Contacts from Correlated Sequence Substitutions. Science Progress, 2013, 96, 33-42.	1.0	4
353	A Tobacco Etch Virus Protease with Increased Substrate Tolerance at the P1' position. PLoS ONE, 2013, 8, e67915.	1.1	32
354	Development of Scoring Functions for Antibody Sequence Assessment and Optimization. PLoS ONE, 2013, 8, e76909.	1.1	23
355	Identifying Cytochrome P450 Functional Networks and Their Allosteric Regulatory Elements. PLoS ONE, 2013, 8, e81980.	1.1	27
356	Allo-Network Drugs: Extension of the Allosteric Drug Concept to Protein- Protein Interaction and Signaling Networks. Current Topics in Medicinal Chemistry, 2013, 13, 64-77.	1.0	68
357	Site-Directed Mutagenesis as Applied to Biocatalysts. , 2013, , .		1
358	Computational Study on the Inhibitor Binding Mode and Allosteric Regulation Mechanism in Hepatitis C Virus NS3/4A Protein. PLoS ONE, 2014, 9, e87077.	1.1	19
359	Sets of Covariant Residues Modulate the Activity and Thermal Stability of GH1 Î ² -Glucosidases. PLoS ONE, 2014, 9, e96627.	1.1	11
360	Atypical Signaling and Functional Desensitization Response of MAS Receptor to Peptide Ligands. PLoS ONE, 2014, 9, e103520.	1.1	39
361	A Unified View of "How Allostery Works": PLoS Computational Biology, 2014, 10, e1003394.	1.5	330
362	Communication Maps: Exploring Energy Transport through Proteins and Water. Israel Journal of Chemistry, 2014, 54, 1065-1073.	1.0	15
363	Computational Studies of Allosteric Regulation in the Hsp90 Molecular Chaperone: From Functional Dynamics and Protein Structure Networks to Allosteric Communications and Targeted Anti-Cancer Modulators. Israel Journal of Chemistry, 2014, 54, 1052-1064.	1.0	5
364	Mapping the intramolecular signal transduction of G-protein coupled receptors. Proteins: Structure, Function and Bioinformatics, 2014, 82, 727-743.	1.5	64

#	ARTICLE	IF	CITATIONS
365	Population shift of binding pocket size and dynamic correlation analysis shed new light on the anticooperative mechanism of P II protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1048-1059.	1.5	10
366	Identification of a New Hormone-Binding Site on the Surface of Thyroid Hormone Receptor. <i>Molecular Endocrinology</i> , 2014, 28, 534-545.	3.7	33
367	Crystallization and preliminary X-ray crystallographic analysis of an artificial molten-globular-like triosephosphate isomerase protein of mixed phylogenetic origin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1521-1525.	0.4	2
368	A novel allosteric mechanism in the cysteine peptidase cathepsin K discovered by computational methods. <i>Nature Communications</i> , 2014, 5, 3287.	5.8	77
369	Multiple conformational selection and induced fit events take place in allosteric propagation. <i>Biophysical Chemistry</i> , 2014, 186, 22-30.	1.5	105
370	The ensemble nature of allostery. <i>Nature</i> , 2014, 508, 331-339.	13.7	1,026
371	Unraveling structural mechanisms of allosteric drug action. <i>Trends in Pharmacological Sciences</i> , 2014, 35, 256-264.	4.0	111
372	Amino Acid Networks in a $(\beta\text{-barrel})_8$ Barrel Enzyme Change during Catalytic Turnover. <i>Journal of the American Chemical Society</i> , 2014, 136, 6818-6821.	6.6	41
373	Local packing modulates diversity of iron pathways and cooperative behavior in eukaryotic and prokaryotic ferritins. <i>Journal of Chemical Physics</i> , 2014, 140, 115104.	1.2	13
374	Mechanisms of Differential Allosteric Modulation in Homologous Proteins: Insights from the Analysis of Internal Dynamics and Energetics of PDZ Domains. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 5677-5689.	2.3	43
375	Evolutionary Aspects of Enzyme Dynamics. <i>Journal of Biological Chemistry</i> , 2014, 289, 30205-30212.	1.6	55
376	NMR mapping of protein conformational landscapes using coordinated behavior of chemical shifts upon ligand binding. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 6508-6518.	1.3	54
377	Conserved patterns in bacterial genomes: A conundrum physically tailored by evolutionary tinkering. <i>Computational Biology and Chemistry</i> , 2014, 53, 125-133.	1.1	14
378	Differences in Allosteric Communication Pipelines in the Inactive and Active States of a GPCR. <i>Biophysical Journal</i> , 2014, 107, 422-434.	0.2	103
379	Coevolutionary information, protein folding landscapes, and the thermodynamics of natural selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12408-12413.	3.3	126
380	A New Formulation of Protein Evolutionary Models that Account for Structural Constraints. <i>Molecular Biology and Evolution</i> , 2014, 31, 736-749.	3.5	25
381	Engineering allostery. <i>Trends in Genetics</i> , 2014, 30, 521-528.	2.9	64
382	Extension and Limits of the Network of Coupled Motions Correlated to Hydride Transfer in Dihydrofolate Reductase. <i>Journal of the American Chemical Society</i> , 2014, 136, 2575-2582.	6.6	51

#	ARTICLE	IF	CITATIONS
383	Broad-Spectrum Allosteric Inhibition of Herpesvirus Proteases. <i>Biochemistry</i> , 2014, 53, 4648-4660.	1.2	14
384	Protein motions and the activation of the CH bond catalyzed by dihydrofolate reductase. <i>Current Opinion in Chemical Biology</i> , 2014, 21, 19-24.	2.8	18
385	Engineering the allosteric properties of archaeal non-phosphorylating glyceraldehyde-3-phosphate dehydrogenases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 759-766.	1.1	3
386	Alteration of the C-Terminal Ligand Specificity of the Erbin PDZ Domain by Allosteric Mutational Effects. <i>Journal of Molecular Biology</i> , 2014, 426, 3500-3508.	2.0	17
387	Evolutionary imprint of activation: The design principles of VSDs. <i>Journal of General Physiology</i> , 2014, 143, 145-156.	0.9	57
388	Global connectivity of hub residues in Oncoprotein structures encodes genetic factors dictating personalized drug response to targeted Cancer therapy. <i>Scientific Reports</i> , 2015, 4, 7294.	1.6	4
389	The Phylogenetic Signature Underlying ATP Synthase c-Ring Compliance. <i>Biophysical Journal</i> , 2015, 109, 975-987.	0.2	11
390	Sparse networks of directly coupled, polymorphic, and functional side chains in allosteric proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 497-516.	1.5	5
391	Sequence and structure-based prediction of fructosyltransferase activity for functional subclassification of fungal <i>Glycosyltransferase</i> 32 enzymes. <i>FEBS Journal</i> , 2015, 282, 4782-4796.	2.2	35
392	Energy exchange network of inter-residue interactions within a thermally fluctuating protein molecule: A computational study. <i>Journal of Computational Chemistry</i> , 2015, 36, 1709-1718.	1.5	39
393	Linking Protein Motion to Enzyme Catalysis. <i>Molecules</i> , 2015, 20, 1192-1209.	1.7	25
394	Molecular Determinants Underlying Binding Specificities of the ABL Kinase Inhibitors: Combining Alanine Scanning of Binding Hot Spots with Network Analysis of Residue Interactions and Coevolution. <i>PLoS ONE</i> , 2015, 10, e0130203.	1.1	36
395	Amino acid interaction networks provide a new lens for therapeutic antibody discovery and anti-viral drug optimization. <i>Current Opinion in Virology</i> , 2015, 11, 122-129.	2.6	6
396	Global ITC fitting methods in studies of protein allostery. <i>Methods</i> , 2015, 76, 149-161.	1.9	36
397	Conformational changes and allosteric communications in human serum albumin due to ligand binding. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2192-2204.	2.0	12
398	Synthetic biology for the directed evolution of protein biocatalysts: navigating sequence space intelligently. <i>Chemical Society Reviews</i> , 2015, 44, 1172-1239.	18.7	316
399	Amino acid coevolution reveals three-dimensional structure and functional domains of insect odorant receptors. <i>Nature Communications</i> , 2015, 6, 6077.	5.8	113
400	Near-Atomic Resolution for One State of F-Actin. <i>Structure</i> , 2015, 23, 173-182.	1.6	121

#	ARTICLE	IF	CITATIONS
401	The Design of Covalent Allosteric Drugs. <i>Annual Review of Pharmacology and Toxicology</i> , 2015, 55, 249-267.	4.2	96
402	Discovery of multiple hidden allosteric sites by combining Markov state models and experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2734-2739.	3.3	183
403	Universal allosteric mechanism for G $\beta\gamma$ activation by GPCRs. <i>Nature</i> , 2015, 524, 173-179.	13.7	291
404	Evolution of sparsity and modularity in a model of protein allostery. <i>Physical Review E</i> , 2015, 91, 042704.	0.8	29
405	Comparative sequence analysis suggests a conserved gating mechanism for TRP channels. <i>Journal of General Physiology</i> , 2015, 146, 37-50.	0.9	57
406	Protein Sectors: Statistical Coupling Analysis versus Conservation. <i>PLoS Computational Biology</i> , 2015, 11, e1004091.	1.5	70
407	A new ensemble coevolution system for detecting HIV-1 protein coevolution. <i>Biology Direct</i> , 2015, 10, 1.	1.9	78
408	From local to global changes in proteins: a network view. <i>Current Opinion in Structural Biology</i> , 2015, 31, 1-8.	2.6	54
409	Protein contact network topology: a natural language for allostery. <i>Current Opinion in Structural Biology</i> , 2015, 31, 43-48.	2.6	141
410	Towards the computational design of protein post-translational regulation. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 2877-2882.	1.4	24
411	Endogenous Allosteric Modulators of G Protein-Coupled Receptors. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2015, 353, 246-260.	1.3	127
412	KrÄppel Expression Levels Are Maintained through Compensatory Evolution of Shadow Enhancers. <i>Cell Reports</i> , 2015, 12, 1740-1747.	2.9	55
413	Nuclear Receptors: From Structure to the Clinic. , 2015, , .		3
414	Dynamics-Driven Allostery in Protein Kinases. <i>Trends in Biochemical Sciences</i> , 2015, 40, 628-647.	3.7	237
415	Molecular interactions between general anesthetics and the 5HT _{2B} receptor. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 211-218.	2.0	10
416	Synthetic protein switches: design principles and applications. <i>Trends in Biotechnology</i> , 2015, 33, 101-110.	4.9	135
417	Rational coupled dynamics network manipulation rescues disease-relevant mutant cystic fibrosis transmembrane conductance regulator. <i>Chemical Science</i> , 2015, 6, 1237-1246.	3.7	49
418	Severing of a hydrogen bond disrupts amino acid networks in the catalytically active state of the alpha subunit of tryptophan synthase. <i>Protein Science</i> , 2015, 24, 484-494.	3.1	19

#	ARTICLE	IF	CITATIONS
419	Allosteric sites can be identified based on the residue-residue interaction energy difference. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1375-1384.	1.5	17
420	Protein residue networks from a local search perspective. <i>Journal of Complex Networks</i> , 2016, 4, 245-278.	1.1	6
421	Role of Conformational Motions in Enzyme Function: Selected Methodologies and Case Studies. <i>Catalysts</i> , 2016, 6, 81.	1.6	26
422	Evolution-Based Functional Decomposition of Proteins. <i>PLoS Computational Biology</i> , 2016, 12, e1004817.	1.5	119
423	Functional Sites Induce Long-Range Evolutionary Constraints in Enzymes. <i>PLoS Biology</i> , 2016, 14, e1002452.	2.6	94
424	The Context-Dependence of Mutations: A Linkage of Formalisms. <i>PLoS Computational Biology</i> , 2016, 12, e1004771.	1.5	95
425	Allostery: An Overview of Its History, Concepts, Methods, and Applications. <i>PLoS Computational Biology</i> , 2016, 12, e1004966.	1.5	194
426	Epistasis in protein evolution. <i>Protein Science</i> , 2016, 25, 1204-1218.	3.1	383
427	Correlated rigid modes in protein families. <i>Physical Biology</i> , 2016, 13, 025003.	0.8	1
428	Function changing mutations in glucocorticoid receptor evolution correlate with their relevance to mode coupling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 655-665.	1.5	3
429	Biophysical and computational methods to analyze amino acid interaction networks in proteins. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 245-251.	1.9	55
430	Peptide- and proton-driven allosteric clamps catalyze anthrax toxin translocation across membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9611-9616.	3.3	28
431	Vibrational resonance, allostery, and activation in rhodopsin-like G protein-coupled receptors. <i>Scientific Reports</i> , 2016, 6, 37290.	1.6	24
432	Improving the catalytic activity of isopentenyl phosphate kinase through protein coevolution analysis. <i>Scientific Reports</i> , 2016, 6, 24117.	1.6	28
433	Crystal structure of glutamate-1-semialdehyde-2,1-aminomutase from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 448-456.	0.4	8
434	Emerging Computational Methods for the Rational Discovery of Allosteric Drugs. <i>Chemical Reviews</i> , 2016, 116, 6370-6390.	23.0	176
435	Identifying Allosteric Hotspots with Dynamics: Application to Inter- and Intra-species Conservation. <i>Structure</i> , 2016, 24, 826-837.	1.6	55
436	Allosteric communication pipelines in G-protein-coupled receptors. <i>Current Opinion in Pharmacology</i> , 2016, 30, 76-83.	1.7	33

#	ARTICLE	IF	CITATIONS
437	A network of allosterically coupled residues in the bacteriophage T4 Mre11â€“Rad50 complex. <i>Protein Science</i> , 2016, 25, 2054-2065.	3.1	4
438	Motions of Allosteric and Orthosteric Ligand-Binding Sites in Proteins are Highly Correlated. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1725-1733.	2.5	70
439	Structural Determinants of Sleeping Beauty Transposase Activity. <i>Molecular Therapy</i> , 2016, 24, 1369-1377.	3.7	7
440	Coevolution analysis of Hepatitis C virus genome to identify the structural and functional dependency network of viral proteins. <i>Scientific Reports</i> , 2016, 6, 26401.	1.6	26
441	Adaptive Molecular Evolution: Detection Methods. , 2016, , 16-25.		0
442	Allosteric Communication Disrupted by a Small Molecule Binding to the Imidazole Glycerol Phosphate Synthase Proteinâ€“Protein Interface. <i>Biochemistry</i> , 2016, 55, 6484-6494.	1.2	33
443	OCoM-SOCoM. , 2016, , .		0
444	Allostery Wiring Map for Kinesin Energy Transduction and Its Evolution. <i>Journal of Biological Chemistry</i> , 2016, 291, 20932-20945.	1.6	11
445	Origins of Allostery and Evolvability in Proteins: A Case Study. <i>Cell</i> , 2016, 166, 468-480.	13.5	123
446	Peptide and Proton Driven Allosteric Clamps Catalyze Anthrax Toxin Translocation across Membranes. <i>Biophysical Journal</i> , 2016, 110, 224a.	0.2	8
447	Structure-based Markov random field model for representing evolutionary constraints on functional sites. <i>BMC Bioinformatics</i> , 2016, 17, 99.	1.2	7
448	UET: a database of evolutionarily-predicted functional determinants of protein sequences that cluster as functional sites in protein structures. <i>Nucleic Acids Research</i> , 2016, 44, D308-D312.	6.5	31
449	Protein structural robustness to mutations: an in silico investigation. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 13770-13780.	1.3	24
450	Intramolecular allosteric communication in dopamine D2 receptor revealed by evolutionary amino acid covariation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3539-3544.	3.3	38
451	Controlling Allosteric Networks in Proteins. <i>Chemical Reviews</i> , 2016, 116, 6463-6487.	23.0	207
452	Computational approaches to detect allosteric pathways in transmembrane molecular machines. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 1652-1662.	1.4	58
453	Protein Allostery and Conformational Dynamics. <i>Chemical Reviews</i> , 2016, 116, 6503-6515.	23.0	306
454	Calculated p<i>K</i></sub>a</sub> Variations Expose Dynamic Allosteric Communication Networks. <i>Journal of the American Chemical Society</i> , 2016, 138, 2036-2045.	6.6	18

#	ARTICLE	IF	CITATIONS
455	Early Folding Events, Local Interactions, and Conservation of Protein Backbone Rigidity. <i>Biophysical Journal</i> , 2016, 110, 572-583.	0.2	23
456	Engineering an allosteric transcription factor to respond to new ligands. <i>Nature Methods</i> , 2016, 13, 177-183.	9.0	274
457	Direct Calculation of Protein Fitness Landscapes through Computational Protein Design. <i>Biophysical Journal</i> , 2016, 110, 75-84.	0.2	7
458	A Chemical Perspective on Allostery. <i>Chemical Reviews</i> , 2016, 116, 6488-6502.	23.0	85
459	Using THz Spectroscopy, Evolutionary Network Analysis Methods, and MD Simulation to Map the Evolution of Allosteric Communication Pathways in c-Type Lysozymes. <i>Molecular Biology and Evolution</i> , 2016, 33, 40-61.	3.5	6
460	Evolutionary Covariance Combined with Molecular Dynamics Predicts a Framework for Allostery in the MutS DNA Mismatch Repair Protein. <i>Journal of Physical Chemistry B</i> , 2017, 121, 2049-2061.	1.2	17
461	NMR reveals a dynamic allosteric pathway in thrombin. <i>Scientific Reports</i> , 2017, 7, 39575.	1.6	21
463	An evolution-based strategy for engineering allosteric regulation. <i>Physical Biology</i> , 2017, 14, 025002.	0.8	13
464	Quantifying Allosteric Communication via Both Concerted Structural Changes and Conformational Disorder with CARDS. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 1509-1517.	2.3	46
465	Allosteric regulation of metabolism in cancer: endogenous mechanisms and considerations for drug design. <i>Current Opinion in Biotechnology</i> , 2017, 48, 102-110.	3.3	11
466	Structure-Activity Relationship in TLR4 Mutations: Atomistic Molecular Dynamics Simulations and Residue Interaction Network Analysis. <i>Scientific Reports</i> , 2017, 7, 43807.	1.6	54
467	Causality, transfer entropy, and allosteric communication landscapes in proteins with harmonic interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1056-1064.	1.5	27
468	Targeting S-adenosylmethionine biosynthesis with a novel allosteric inhibitor of Mat2A. <i>Nature Chemical Biology</i> , 2017, 13, 785-792.	3.9	82
469	High-Dimensional Mutant and Modular Thermodynamic Cycles, Molecular Switching, and Free Energy Transduction. <i>Annual Review of Biophysics</i> , 2017, 46, 433-453.	4.5	24
470	Synthetic Protein Switches: Theoretical and Experimental Considerations. <i>Methods in Molecular Biology</i> , 2017, 1596, 3-25.	0.4	3
471	A combination of mutational and computational scanning guides the design of an artificial ligand-binding controlled lipase. <i>Scientific Reports</i> , 2017, 7, 42592.	1.6	5
472	A General Mechanism for the Propagation of Mutational Effects in Proteins. <i>Biochemistry</i> , 2017, 56, 294-305.	1.2	53
473	Lighting up yeast cell factories by transcription factor-based biosensors. <i>FEMS Yeast Research</i> , 2017, 17, .	1.1	32

#	ARTICLE	IF	CITATIONS
474	Enabling tools for high-throughput detection of metabolites: Metabolic engineering and directed evolution applications. <i>Biotechnology Advances</i> , 2017, 35, 950-970.	6.0	97
475	Correlated Mutation in the Evolution of Catalysis in Uracil DNA Glycosylase Superfamily. <i>Scientific Reports</i> , 2017, 7, 45978.	1.6	12
476	Calcium-Mediated Control of S100 Proteins: Allosteric Communication via an Agitator/Signal Blocking Mechanism. <i>Journal of the American Chemical Society</i> , 2017, 139, 11460-11470.	6.6	16
477	Origins of coevolution between residues distant in protein 3D structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9122-9127.	3.3	167
478	Design of Elastic Networks with Evolutionary Optimized Long-Range Communication as Mechanical Models of Allosteric Proteins. <i>Biophysical Journal</i> , 2017, 113, 558-571.	0.2	49
479	A Cooperative Folding Unit as the Structural Link for Energetic Coupling within a Protein. <i>Biochemistry</i> , 2017, 56, 6555-6564.	1.2	3
480	Patterns of coevolving amino acids unveil structural and dynamical domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10612-E10621.	3.3	33
481	2D-IR Spectroscopy of an AHA Labeled Photoswitchable PDZ2 Domain. <i>Journal of Physical Chemistry A</i> , 2017, 121, 9435-9445.	1.1	18
482	BIS2Analyzer: a server for co-evolution analysis of conserved protein families. <i>Nucleic Acids Research</i> , 2017, 45, W307-W314.	6.5	43
483	Uncoupling of an ammonia channel as a mechanism of allosteric inhibition in anthranilate synthase of <i>Serratia marcescens</i> : dynamic and graph theoretical analysis. <i>Molecular BioSystems</i> , 2017, 13, 142-155.	2.9	13
484	Time-Resolved Resonance Raman Spectroscopy and Application to Studies on Ultrafast Protein Dynamics. <i>Bulletin of the Chemical Society of Japan</i> , 2017, 90, 1344-1371.	2.0	29
485	Implications of short time scale dynamics on long time processes. <i>Structural Dynamics</i> , 2017, 4, 061507.	0.9	24
486	Migration of small ligands in globins: Xe diffusion in truncated hemoglobin N. <i>PLoS Computational Biology</i> , 2017, 13, e1005450.	1.5	4
487	Translational regulation of ribosomal protein S15 drives characteristic patterns of protein-mRNA epistasis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 827-832.	1.5	4
488	Ligand-Triggered Structural Changes in the M ₂ Muscarinic Acetylcholine Receptor. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1074-1082.	2.5	7
489	Computational Exploration of Conformational Transitions in Protein Drug Targets. <i>Methods in Molecular Biology</i> , 2018, 1762, 339-365.	0.4	1
490	Coupled Mutations-Enabled Glycerol Transportation in an Aquaporin Z Mutant. <i>ACS Omega</i> , 2018, 3, 4113-4122.	1.6	3
492	Decoding Allosteric Networks in Biocatalysts: Rational Approach to Therapies and Biotechnologies. <i>ACS Catalysis</i> , 2018, 8, 2683-2692.	5.5	11

#	ARTICLE	IF	CITATIONS
493	Engineered control of enzyme structural dynamics and function. <i>Protein Science</i> , 2018, 27, 825-838.	3.1	30
494	The visualCMAT: A web-server to select and interpret correlated mutations/co-evolving residues in protein families. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840005.	0.3	16
495	ProteinAC: a frequency domain technique for analyzing protein dynamics. <i>Physical Biology</i> , 2018, 15, 026009.	0.8	5
496	Visualization and analysis of non-covalent contacts using the Protein Contacts Atlas. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 185-194.	3.6	103
497	Evolutionary analysis of mitochondrially encoded proteins of toad-headed lizards, <i>Phrynocephalus</i> , along an altitudinal gradient. <i>BMC Genomics</i> , 2018, 19, 185.	1.2	19
498	Green function of correlated genes in a minimal mechanical model of protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4559-E4568.	3.3	30
499	Structural Basis for a Bimodal Allosteric Mechanism of General Anesthetic Modulation in Pentameric Ligand-Gated Ion Channels. <i>Cell Reports</i> , 2018, 23, 993-1004.	2.9	33
500	Directed Evolution Mimics Allosteric Activation by Stepwise Tuning of the Conformational Ensemble. <i>Journal of the American Chemical Society</i> , 2018, 140, 7256-7266.	6.6	73
501	Understanding G Protein-Coupled Receptor Allostery via Molecular Dynamics Simulations: Implications for Drug Discovery. <i>Methods in Molecular Biology</i> , 2018, 1762, 455-472.	0.4	7
502	An evolutionary hotspot defines functional differences between CRYPTOCHROMES. <i>Nature Communications</i> , 2018, 9, 1138.	5.8	72
503	Proteinâ€™protein interaction specificity is captured by contact preferences and interface composition. <i>Bioinformatics</i> , 2018, 34, 459-468.	1.8	29
504	Twoâ€™domain analysis of JmjNâ€™mJc and PHDâ€™mJc lysine demethylases: Detecting an interâ€™domain evolutionary stress. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 3-12.	1.5	5
505	Applications of sequence coevolution in membrane protein biochemistry. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 895-908.	1.4	27
506	Biochemical and structural insights into a thermostable cellobiohydrolase from <i>Myceliophthora thermophila</i> . <i>FEBS Journal</i> , 2018, 285, 559-579.	2.2	26
507	Systems Approaches to Understanding and Designing Allosteric Proteins. <i>Biochemistry</i> , 2018, 57, 376-382.	1.2	17
508	Long-Range Changes in Neurolysin Dynamics Upon Inhibitor Binding. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 444-452.	2.3	11
509	Structure-based prediction of protein allostery. <i>Current Opinion in Structural Biology</i> , 2018, 50, 1-8.	2.6	90
511	Seeking allosteric networks in PDZ domains. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 367-373.	1.0	25

#	ARTICLE	IF	CITATIONS
512	Millisecond Timescale Motions Connect Amino Acid Interaction Networks in Alpha Tryptophan Synthase. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 92.	1.6	6
513	Engineering allosteric regulation in protein kinases. <i>Science Signaling</i> , 2018, 11, .	1.6	18
514	Mutations close to a hub residue affect the distant active site of a GH1 β -glucosidase. <i>PLoS ONE</i> , 2018, 13, e0198696.	1.1	6
516	Proteins across scales through graph partitioning: application to the major peanut allergen Ara h 1. <i>Journal of Complex Networks</i> , 2018, 6, 679-692.	1.1	0
517	The mechanistic insight of a specific interaction between 15d-Prostaglandin-J2 and eIF4A suggests an evolutionary conserved role across species. <i>Biology Open</i> , 2018, 7, .	0.6	4
518	Evolutionarily Conserved Allosteric Communication in Protein Tyrosine Phosphatases. <i>Biochemistry</i> , 2018, 57, 6443-6451.	1.2	32
519	Toward an understanding of the structural basis of allostery in muscarinic acetylcholine receptors. <i>Journal of General Physiology</i> , 2018, 150, 1360-1372.	0.9	38
520	Controlling Cells with Light and LOV. <i>Advanced Biology</i> , 2018, 2, 1800098.	3.0	19
521	Reprogramming G protein coupled receptor structure and function. <i>Current Opinion in Structural Biology</i> , 2018, 51, 187-194.	2.6	26
522	Estimating the contribution of folding stability to nonspecific epistasis in protein evolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1242-1250.	1.5	17
523	The Binding Mechanism Between Inositol Phosphate (InsP) and the Jasmonate Receptor Complex: A Computational Study. <i>Frontiers in Plant Science</i> , 2018, 9, 963.	1.7	9
524	Determining the Structural and Energetic Basis of Allostery in a De Novo Designed Metalloprotein Assembly. <i>Journal of the American Chemical Society</i> , 2018, 140, 10043-10053.	6.6	20
525	Singular value decomposition for the correlation of atomic fluctuations with arbitrary angle. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1075-1087.	1.5	5
526	Conformational dynamics and enzyme evolution. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180330.	1.5	140
527	Exploring the effect of E76K mutation on SHP2 cause gain-of-function activity by a molecular dynamics study. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 9941-9956.	1.2	7
528	High Thermal Stability of Oligomeric Assemblies of Thermophilic Rhodopsin in a Lipid Environment. <i>Journal of Physical Chemistry B</i> , 2018, 122, 6945-6953.	1.2	16
529	MISTIC2: comprehensive server to study coevolution in protein families. <i>Nucleic Acids Research</i> , 2018, 46, W323-W328.	6.5	30
530	Pareto Optimization of Combinatorial Mutagenesis Libraries. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1143-1153.	1.9	6

#	ARTICLE	IF	CITATIONS
531	Conservation of the behavioral and transcriptional response to social experience among <i>Drosophilids</i> . <i>Genes, Brain and Behavior</i> , 2019, 18, e12487.	1.1	11
532	Colloquium: Proteins: The physics of amorphous evolving matter. <i>Reviews of Modern Physics</i> , 2019, 91, .	16.4	27
533	Protein Allostery in Drug Discovery. <i>Advances in Experimental Medicine and Biology</i> , 2019, , .	0.8	11
534	Adaption of human antibody heavy and light chain architectures to CDR repertoires. <i>Protein Engineering, Design and Selection</i> , 2019, 32, 109-127.	1.0	12
535	Statistical coupling analysis uncovers sites crucial for the proton transfer in laccase Lac15. <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 894-900.	1.0	3
536	Nervous-Like Circuits in the Ribosome Facts, Hypotheses and Perspectives. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2911.	1.8	7
537	Engineering repressors with coevolutionary cues facilitates toggle switches with a master reset. <i>Nucleic Acids Research</i> , 2019, 47, 5449-5463.	6.5	22
538	Coevolution of Residues Provides Evidence of a Functional Heterodimer of 5-HT2AR and 5-HT2CR Involving Both Intracellular and Extracellular Domains. <i>Neuroscience</i> , 2019, 412, 48-59.	1.1	7
539	Revealing evolutionary constraints on proteins through sequence analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1007010.	1.5	18
540	Tuning the evolution of protein kinases: The role of dynamics-based allostery. <i>IUBMB Life</i> , 2019, 71, 685-696.	1.5	49
541	Symmetry, Rigidity, and Allosteric Signaling: From Monomeric Proteins to Molecular Machines. <i>Chemical Reviews</i> , 2019, 119, 6788-6821.	23.0	82
542	Ligand-Binding-Site Structure Shapes Allosteric Signal Transduction and the Evolution of Allostery in Protein Complexes. <i>Molecular Biology and Evolution</i> , 2019, 36, 1711-1727.	3.5	33
543	Dynamical important residue network (DIRN): network inference via conformational change. <i>Bioinformatics</i> , 2019, 35, 4664-4670.	1.8	12
544	Improved measures for evolutionary conservation that exploit taxonomy distances. <i>Nature Communications</i> , 2019, 10, 1556.	5.8	21
545	The Subtle Trade-Off between Evolutionary and Energetic Constraints in Protein-Protein Interactions. <i>Journal of Physical Chemistry Letters</i> , 2019, 10, 1489-1497.	2.1	20
546	Exploring Allosteric Pathways of a V-Type Enzyme with Dynamical Perturbation Networks. <i>Journal of Physical Chemistry B</i> , 2019, 123, 3452-3461.	1.2	29
547	Functional assays for transcription mechanisms in high-throughput. <i>Methods</i> , 2019, 159-160, 115-123.	1.9	9
548	A Species-Related Transitional Residue D132 on Human FMRP Plays a Role in Nuclear Localization via an RNA-Dependent Interaction With PABP1. <i>Neuroscience</i> , 2019, 404, 282-296.	1.1	3

#	ARTICLE	IF	CITATIONS
549	Quantifying correlations between mutational sites in the catalytic subunit of Î³-secretase. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 88, 221-227.	1.3	4
550	Understanding molecular mechanisms in cell signaling through natural and artificial sequence variation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 25-34.	3.6	28
551	The missing links within troponin. <i>Archives of Biochemistry and Biophysics</i> , 2019, 663, 95-100.	1.4	6
552	Analysis of Protein Structures Using Residue Interaction Networks. <i>Challenges and Advances in Computational Chemistry and Physics</i> , 2019, , 55-69.	0.6	2
553	A Biophysical Perspective on Enzyme Catalysis. <i>Biochemistry</i> , 2019, 58, 438-449.	1.2	104
554	Integration of network models and evolutionary analysis into high-throughput modeling of protein dynamics and allosteric regulation: theory, tools and applications. <i>Briefings in Bioinformatics</i> , 2020, 21, 815-835.	3.2	58
555	Spectral analysis of molecular dynamics simulations on PDZ: MD sectors. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 781-790.	2.0	8
556	Evolutionary coupling saturation mutagenesis: Coevolution-guided identification of distant sites influencing <i>Bacillus naganensis</i> pullulanase activity. <i>FEBS Letters</i> , 2020, 594, 799-812.	1.3	22
557	Strategies for Engineering and Rewiring Kinase Regulation. <i>Trends in Biochemical Sciences</i> , 2020, 45, 259-271.	3.7	16
558	Computational design of G Protein-Coupled Receptor allosteric signal transductions. <i>Nature Chemical Biology</i> , 2020, 16, 77-86.	3.9	57
559	Energy flow and intersubunit signalling in GSAM: A non-equilibrium molecular dynamics study. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1651-1663.	1.9	6
560	Generalized correlation-based dynamical network analysis: a new high-performance approach for identifying allosteric communications in molecular dynamics trajectories. <i>Journal of Chemical Physics</i> , 2020, 153, 134104.	1.2	81
561	Intra-Protein Coevolution Is Increasingly Functional with Greater Proximity to Fertilization. <i>Cytogenetic and Genome Research</i> , 2020, 160, 295-308.	0.6	1
562	A Time-Dependent Quantum Approach to Allostery and a Comparison With Light-Harvesting in Photosynthetic Phenomenon. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 156.	1.6	1
563	Non-equilibrium thermodynamic properties and internal dynamics of 32-residue beta amyloid fibrils. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2020, 557, 124873.	1.2	2
564	Identification of potential allosteric binding sites in cathepsin K based on intramolecular communication. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1675-1687.	1.5	3
565	Allosteric Regulation at the Crossroads of New Technologies: Multiscale Modeling, Networks, and Machine Learning. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 136.	1.6	44
566	Mapping allosteric communications within individual proteins. <i>Nature Communications</i> , 2020, 11, 3862.	5.8	101

#	ARTICLE	IF	CITATIONS
567	Shaping Polyclonal Responses via Antigen-Mediated Antibody Interference. <i>IScience</i> , 2020, 23, 101568.	1.9	4
568	Decoding the Functional Evolution of an Intramembrane Protease Superfamily by Statistical Coupling Analysis. <i>Structure</i> , 2020, 28, 1329-1336.e4.	1.6	6
569	Residue interaction dynamics in <i>Vaucheria</i> aureochrome1 light-oxygen-voltage: Bridging theory and experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1660-1674.	1.5	9
570	Characterization of the Topological Features of Catalytic Sites in Protein Coevolution Networks*. <i>Chinese Physics Letters</i> , 2020, 37, 068701.	1.3	2
571	Direct coupling analysis of epistasis in allosteric materials. <i>PLoS Computational Biology</i> , 2020, 16, e1007630.	1.5	14
572	Glutaminase: a database for improving the rational design of glucose-tolerant β -glucosidases. <i>BMC Molecular and Cell Biology</i> , 2020, 21, 50.	1.0	9
573	An allosteric pathway explains beneficial fitness in yeast for long-range mutations in an essential TIM barrel enzyme. <i>Protein Science</i> , 2020, 29, 1911-1923.	3.1	5
574	Engineering allosteric communication. <i>Current Opinion in Structural Biology</i> , 2020, 63, 115-122.	2.6	9
575	The Pierced Lasso Topology Leptin has a Bolt on Dynamic Domain Composed by the Disordered Loops I and III. <i>Journal of Molecular Biology</i> , 2020, 432, 3050-3063.	2.0	9
576	Residue-Level Allostery Propagates through the Effective Coarse-Grained Hessian. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 3385-3395.	2.3	21
577	D3Targets-2019-nCoV: a webserver for predicting drug targets and for multi-target and multi-site based virtual screening against COVID-19. <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 1239-1248.	5.7	65
578	N-Terminus of the Third PDZ Domain of PSD-95 Orchestrates Allosteric Communication for Selective Ligand Binding. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 347-357.	2.5	2
579	Long-range correlation and critical fluctuations in coevolution networks of protein sequences. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2021, 562, 125339.	1.2	5
580	Enlightening Allostery: Designing Switchable Proteins by Photoreceptor Fusion. <i>Advanced Biology</i> , 2021, 5, e2000181.	1.4	14
581	Co-evolutionary landscape at the interface and non-interface regions of protein-protein interaction complexes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3779-3795.	1.9	3
582	Rosetta design with co-evolutionary information retains protein function. <i>PLoS Computational Biology</i> , 2021, 17, e1008568.	1.5	12
583	Synchronous and Asynchronous Response in Dynamically Perturbed Proteins. <i>Journal of Physical Chemistry B</i> , 2021, 125, 729-739.	1.2	14
584	Computational investigations of allostery in aromatic amino acid biosynthetic enzymes. <i>Biochemical Society Transactions</i> , 2021, 49, 415-429.	1.6	3

#	ARTICLE	IF	CITATIONS
585	Probing biased activation of mu-opioid receptor by the biased agonist PZM21 using all atom molecular dynamics simulation. <i>Life Sciences</i> , 2021, 269, 119026.	2.0	13
586	A large-scale survey of pairwise epistasis reveals a mechanism for evolutionary expansion and specialization of PDZ domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 899-914.	1.5	14
587	Influence of Disease-Causing Mutations on Protein Structural Networks. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 620554.	1.6	23
590	Biomolecular Systems Engineering: Unlocking the Potential of Engineered Allostery via the Lactose Repressor Topology. <i>Annual Review of Biophysics</i> , 2021, 50, 303-321.	4.5	6
591	Roadmap on biology in time varying environments. <i>Physical Biology</i> , 2021, 18, 041502.	0.8	23
592	Step-by-step design of proteins for small molecule interaction: A review on recent milestones. <i>Protein Science</i> , 2021, 30, 1502-1520.	3.1	4
593	Hotspot Coevolution Is a Key Identifier of Near-Native Protein Complexes. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6058-6067.	1.2	1
594	Conserved allosteric ensembles in disordered proteins using TROSY/anti-TROSY R2-filtered spectroscopy. <i>Biophysical Journal</i> , 2021, 120, 2498-2510.	0.2	4
595	Rational design of allosteric modulators: Challenges and successes. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2021, 11, e1529.	6.2	39
596	Structurally distributed surface sites tune allosteric regulation. <i>ELife</i> , 2021, 10, .	2.8	23
597	Unraveling the Allosteric Cross-Talk between the Coactivator Peptide and the Ligand-Binding Site in the Glucocorticoid Receptor. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 3667-3680.	2.5	10
599	A Framework for Investigating Rules of Life by Establishing Zones of Influence. <i>Integrative and Comparative Biology</i> , 2021, , .	0.9	1
600	Allosteric Mechanism of Human Mitochondrial Phenylalanyl-tRNA Synthetase: An Atomistic MD Simulation and a Mutual Information-Based Network Study. <i>Journal of Physical Chemistry B</i> , 2021, 125, 7651-7661.	1.2	5
601	Revealing enzyme functional architecture via high-throughput microfluidic enzyme kinetics. <i>Science</i> , 2021, 373, .	6.0	105
602	The two redox states of the human NEET proteins' [2Fe-2S] clusters. <i>Journal of Biological Inorganic Chemistry</i> , 2021, 26, 763-774.	1.1	6
603	Probing allosteric regulations with coevolution-driven molecular simulations. <i>Science Advances</i> , 2021, 7, eabj0786.	4.7	8
604	Leri: A web-server for identifying protein functional networks from evolutionary couplings. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3556-3563.	1.9	10
605	Identification of Allosteric Effects in Proteins by Elastic Network Models. <i>Methods in Molecular Biology</i> , 2021, 2253, 21-35.	0.4	7

#	ARTICLE	IF	CITATIONS
606	Network Re-Wiring During Allostery and Protein-Protein Interactions: A Graph Spectral Approach. <i>Methods in Molecular Biology</i> , 2021, 2253, 89-112.	0.4	6
607	Community Network Analysis of Allosteric Proteins. <i>Methods in Molecular Biology</i> , 2021, 2253, 137-151.	0.4	15
608	Studying Protein Interior with Fractal Dimension. <i>SpringerBriefs in Biochemistry and Molecular Biology</i> , 2013, , 19-84.	0.3	1
609	Coordination and Control Inside Simple Biomolecular Machines. <i>Advances in Experimental Medicine and Biology</i> , 2014, 805, 353-384.	0.8	4
610	Allosteric Regulation and Intrinsic Disorder in Nuclear Hormone Receptors. , 2015, , 73-91.		2
611	An Online Approach for Mining Collective Behaviors from Molecular Dynamics Simulations. <i>Lecture Notes in Computer Science</i> , 2009, , 138-154.	1.0	6
612	Co-evolution and Information Signals in Biological Sequences. <i>Lecture Notes in Computer Science</i> , 2009, , 6-17.	1.0	1
613	Prediction of Functional Sites in Proteins by Evolutionary Methods. <i>Principles and Practice</i> , 2004, , 319-340.	0.3	8
614	Interrogating Regulatory Mechanisms in Signaling Proteins by Allosteric Inhibitors and Activators: A Dynamic View Through the Lens of Residue Interaction Networks. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1163, 187-223.	0.8	17
615	Predictive shifts in free energy couple mutations to their phenotypic consequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18275-18284.	3.3	27
616	Functional plasticity and evolutionary adaptation of allosteric regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25445-25454.	3.3	65
621	Two Separate Interfaces between the Voltage Sensor and Pore Are Required for the Function of Voltage-Dependent K ⁺ Channels. <i>PLoS Biology</i> , 2009, 7, e1000047.	2.6	138
622	Allosteric Communication across the Native and Mutated KIT Receptor Tyrosine Kinase. <i>PLoS Computational Biology</i> , 2012, 8, e1002661.	1.5	48
623	Prediction of Functionally Important Phospho-Regulatory Events in <i>Xenopus laevis</i> Oocytes. <i>PLoS Computational Biology</i> , 2015, 11, e1004362.	1.5	14
624	From Binding-Induced Dynamic Effects in SH3 Structures to Evolutionary Conserved Sectors. <i>PLoS Computational Biology</i> , 2016, 12, e1004938.	1.5	5
625	Computational Analysis of Residue Interaction Networks and Coevolutionary Relationships in the Hsp70 Chaperones: A Community-Hopping Model of Allosteric Regulation and Communication. <i>PLoS Computational Biology</i> , 2017, 13, e1005299.	1.5	91
626	Leveraging Hierarchical Population Structure in Discrete Association Studies. <i>PLoS ONE</i> , 2007, 2, e591.	1.1	33
627	Reciprocally Coupled Residues Crucial for Protein Kinase Pak2 Activity Calculated by Statistical Coupling Analysis. <i>PLoS ONE</i> , 2010, 5, e9455.	1.1	9

#	ARTICLE	IF	CITATIONS
628	The Substrate-Driven Transition to an Inward-Facing Conformation in the Functional Mechanism of the Dopamine Transporter. PLoS ONE, 2011, 6, e16350.	1.1	107
629	Positive Darwinian Selection in the Piston That Powers Proton Pumps in Complex I of the Mitochondria of Pacific Salmon. PLoS ONE, 2011, 6, e24127.	1.1	84
630	Discovery of Intramolecular Signal Transduction Network Based on a New Protein Dynamics Model of Energy Dissipation. PLoS ONE, 2012, 7, e31529.	1.1	11
631	Accurate Simulation and Detection of Coevolution Signals in Multiple Sequence Alignments. PLoS ONE, 2012, 7, e47108.	1.1	12
632	Rheostats and Toggle Switches for Modulating Protein Function. PLoS ONE, 2013, 8, e83502.	1.1	51
633	Multiple Co-Evolutionary Networks Are Supported by the Common Tertiary Scaffold of the LacI/GalR Proteins. PLoS ONE, 2013, 8, e84398.	1.1	26
634	Integrated Analysis of Residue Coevolution and Protein Structures Capture Key Protein Sectors in HIV-1 Proteins. PLoS ONE, 2015, 10, e0117506.	1.1	11
635	Exploring Molecular Mechanisms of Paradoxical Activation in the BRAF Kinase Dimers: Atomistic Simulations of Conformational Dynamics and Modeling of Allosteric Communication Networks and Signaling Pathways. PLoS ONE, 2016, 11, e0166583.	1.1	28
636	Protein Inter-Residue Contacts Prediction: Methods, Performances and Applications. Current Bioinformatics, 2019, 14, 178-189.	0.7	11
637	Identification of Alternative Allosteric Sites in Glycolytic Enzymes for Potential Use as Species-Specific Drug Targets. Frontiers in Molecular Biosciences, 2020, 7, 88.	1.6	17
638	Integrated Computational Approaches and Tools for Allosteric Drug Discovery. International Journal of Molecular Sciences, 2020, 21, 847.	1.8	73
639	Ferritin protein nanocages—the story. Nanotechnology Perceptions, 2012, 8, 7-16.	0.1	36
640	Bioinformatic approaches for the structure and function of membrane proteins. BMB Reports, 2009, 42, 697-704.	1.1	32
641	Allosteric signalling in the outer membrane translocation domain of PapC usher. ELife, 2014, 3, .	2.8	18
642	Coevolution-based inference of amino acid interactions underlying protein function. ELife, 2018, 7, .	2.8	101
643	Unique features of different classes of <scp>Gâ€proteinâ€coupled</scp> receptors revealed from sequence coevolutionary and structural analysis. Proteins: Structure, Function and Bioinformatics, 2022, 90, 601-614.	1.5	4
644	Molecular Coevolution and the Three-Dimensionality of Natural Selection. , 2009, , 237-251.		0
645	Information Content of Sets of Biological Sequences Revisited. Natural Computing Series, 2009, , 31-42.	2.2	0

#	ARTICLE	IF	CITATIONS
646	In Silico-Screening Approaches for Lead Generation: Identification of Novel Allosteric Modulators of Human-Erythrocyte Pyruvate Kinase. <i>Methods in Molecular Biology</i> , 2012, 796, 351-367.	0.4	0
647	<i>Subcellular Systems.</i> , 2012, , 297-390.		0
649	Extracting Coevolving Characters from a Tree of Species. <i>Natural Computing Series</i> , 2014, , 45-65.	2.2	0
651	Rational Designing of Novel Proteins Through Computational Approaches. <i>SpringerBriefs in Applied Sciences and Technology</i> , 2017, , 61-83.	0.2	2
652	Using n-dimensional Mutual Information to Measure Protein Multiple Residues Coevolution. , 0, , .		0
659	Advances in NMR Methods to Identify Allosteric Sites and Allosteric Ligands. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1163, 171-186.	0.8	4
667	Towards the Idea of Molecular Brains. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11868.	1.8	19
668	Locating and Navigating in Proteins. <i>Methods in Molecular Biology</i> , 2021, 2253, 37-59.	0.4	0
675	Distinct allosteric pathways in imidazole glycerol phosphate synthase from yeast and bacteria. <i>Biophysical Journal</i> , 2022, 121, 119-130.	0.2	8
676	Improvement of the Stability and Activity of an LPMO Through Rational Disulfide Bonds Design. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 815990.	2.0	8
677	Linking protein structural and functional change to mutation using amino acid networks. <i>PLoS ONE</i> , 2022, 17, e0261829.	1.1	21
678	Structural evolution of the ancient enzyme, dissimilatory sulfite reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1331-1345.	1.5	5
680	Hidden allosteric sites and De-Novo drug design. <i>Expert Opinion on Drug Discovery</i> , 2022, 17, 283-295.	2.5	13
687	Information flow and allosteric communication in proteins. <i>Journal of Chemical Physics</i> , 2022, 156, 185101.	1.2	2
689	Infection Dynamics of ATG8 in Leishmania: Balancing Autophagy for Therapeutics. <i>Molecules</i> , 2022, 27, 3142.	1.7	6
690	Validation of an Allosteric Binding Site of Src Kinase Identified by Unbiased Ligand Binding Simulations. <i>Journal of Molecular Biology</i> , 2022, 434, 167628.	2.0	6
691	Vanilloid-dependent TRPV1 opening trajectory from cryoEM ensemble analysis. <i>Nature Communications</i> , 2022, 13, .	5.8	24
692	iBIS2Analyzer: a web server for a phylogeny-driven coevolution analysis of protein families. <i>Nucleic Acids Research</i> , 0, , .	6.5	3

#	ARTICLE	IF	CITATIONS
693	Molecular Dynamics Simulations Establish the Molecular Basis for the Broad Allostery Hotspot Distributions in the Tetracycline Repressor. <i>Journal of the American Chemical Society</i> , 2022, 144, 10870-10887.	6.6	16
694	Prediction of allosteric communication pathways in proteins. <i>Bioinformatics</i> , 2022, 38, 3590-3599.	1.8	8
695	Simulation and Machine Learning Methods for Ion-Channel Structure Determination, Mechanistic Studies and Drug Design. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
696	Functional roles of enzyme dynamics in accelerating active site chemistry: Emerging techniques and changing concepts. <i>Current Opinion in Structural Biology</i> , 2022, 75, 102434.	2.6	14
697	Dynamics of integrin $\alpha 5 \beta 1$, fibronectin, and their complex reveal sites of interaction and conformational change. <i>Journal of Biological Chemistry</i> , 2022, 298, 102323.	1.6	5
698	<sc>N</sc>â€glycosylation induced changes in tau protein dynamics reveal its role in tau misfolding and aggregation: A microsecond long molecular dynamics study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2023, 91, 147-160.	1.5	5
699	Mutual information analysis of mutation, nonlinearity, and triple interactions in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2023, 91, 121-133.	1.5	2
700	Simple mechanisms for the evolution of protein complexity. <i>Protein Science</i> , 2022, 31, .	3.1	9
701	Specifics of Metabolite-Protein Interactions and Their Computational Analysis and Prediction. <i>Methods in Molecular Biology</i> , 2023, , 179-197.	0.4	3
702	Deep mutational scanning and machine learning reveal structural and molecular rules governing allosteric hotspots in homologous proteins. <i>ELife</i> , 0, 11, .	2.8	17
703	Binding and Functional Folding (BFF): A Physiological Framework for Studying Biomolecular Interactions and Allostery. <i>Journal of Molecular Biology</i> , 2022, 434, 167872.	2.0	2
704	Intragenic compensation through the lens of deep mutational scanning. <i>Biophysical Reviews</i> , 2022, 14, 1161-1182.	1.5	4
705	Variable Regions of p53 Isoforms Allosterically Hard Code DNA Interaction. <i>Journal of Physical Chemistry B</i> , 2022, 126, 8495-8507.	1.2	0
706	Dynamical activation of function in metalloenzymes. <i>FEBS Letters</i> , 2023, 597, 79-91.	1.3	3
707	Allostery Frustrates the Experimentalist. <i>Journal of Molecular Biology</i> , 2023, 435, 167934.	2.0	8
708	Undersampling and the inference of coevolution in proteins. <i>Cell Systems</i> , 2023, 14, 210-219.e7.	2.9	0
709	Systematic analysis reveals novel insight into the molecular determinants of function, diversity and evolution of sweet taste receptors T1R2/T1R3 in primates. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	1
711	Chasing long-range evolutionary couplings in the <sc>AlphaFold</sc> era. <i>Biopolymers</i> , 2023, 114, .	1.2	4

#	ARTICLE	IF	CITATIONS
712	Coevolution-based prediction of key allosteric residues for protein function regulation. <i>ELife</i> , 0, 12, .	2.8	7
713	The quaternary question: Determining allostery in spastin through dynamics classification learning and bioinformatics. <i>Journal of Chemical Physics</i> , 2023, 158, 125102.	1.2	0
714	An Assessment of Quaternary Structure Functionality in Homomer Protein Complexes. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	2
715	Study of the Allosteric Mechanism of Human Mitochondrial Phenylalanyl-tRNA Synthetase by Transfer Entropy via an Improved Gaussian Network Model and Co-evolution Analyses. <i>Journal of Physical Chemistry Letters</i> , 2023, 14, 3452-3460.	2.1	1
716	Atomistic description of the relationship between protein dynamics and catalysis with transition path sampling. <i>Methods in Enzymology</i> , 2023, , 319-340.	0.4	0