

# ConSurf 2016: an improved methodology to estimate and conservation in macromolecules

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Structural determinants of adhesion by Protocadherin-19 and implications for its role in epilepsy. <i>ELife</i> , 2016, 5, .	2.8	70
2	Crystal Structure of the Substrate-Binding Domain from <i>Listeria monocytogenes</i> Bile-Resistance Determinant Bile. <i>Crystals</i> , 2016, 6, 162.	1.0	7
3	Phylogenetic-Derived Insights into the Evolution of Sialylation in Eukaryotes: Comprehensive Analysis of Vertebrate $\beta$ -Galactoside $\alpha$ 2,3/6-Sialyltransferases (ST3Gal and ST6Gal). <i>International Journal of Molecular Sciences</i> , 2016, 17, 1286.	1.8	25
4	High-Resolution Identification of Specificity Determining Positions in the LacI Protein Family Using Ensembles of Sub-Sampled Alignments. <i>PLoS ONE</i> , 2016, 11, e0162579.	1.1	9
5	Elucidating the druggable interface of protein-protein interactions using fragment docking and coevolutionary analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E8051-E8058.	3.3	65
6	Crystal structure of the ADP-ribosylating component of BEC, the binary enterotoxin of <i>Clostridium perfringens</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 480, 261-267.	1.0	8
7	Contribution of intertwined loop to membrane association revealed by Zika virus full-length NS5 structure. <i>EMBO Journal</i> , 2016, 35, 2170-2178.	3.5	126
8	Insect odorant receptor trafficking requires calmodulin. <i>BMC Biology</i> , 2016, 14, 83.	1.7	27
9	The Chromatin Remodelling Protein CHD1 Contains a Previously Unrecognised C-Terminal Helical Domain. <i>Journal of Molecular Biology</i> , 2016, 428, 4298-4314.	2.0	14
10	In silico characterization of TTHA0596: A potential Zn <sup>2+</sup> binding protein of ATP-binding cassette transporter. <i>Gene Reports</i> , 2017, 6, 132-141.	0.4	2
11	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. <i>Structure</i> , 2017, 25, 434-445.	1.6	61
12	M1 aminopeptidases as drug targets: broad applications or therapeutic niche?. <i>FEBS Journal</i> , 2017, 284, 1473-1488.	2.2	53
13	HFB7 – A novel orphan hydrophobin of the Harzianum and Virens clades of <i>Trichoderma</i> , is involved in response to biotic and abiotic stresses. <i>Fungal Genetics and Biology</i> , 2017, 102, 63-76.	0.9	30
14	A familial study of azoospermic men identifies three novel causative mutations in three new human azoospermia genes. <i>Genetics in Medicine</i> , 2017, 19, 998-1006.	1.1	109
15	Mutations that Allow SIR2 Orthologs to Function in a NAD <sup>+</sup> -Depleted Environment. <i>Cell Reports</i> , 2017, 18, 2310-2319.	2.9	9
16	The crystal structure of Zika virus NS5 reveals conserved drug targets. <i>EMBO Journal</i> , 2017, 36, 919-933.	3.5	107
17	High affinity anchoring of the decoration protein pb10 onto the bacteriophage T5 capsid. <i>Scientific Reports</i> , 2017, 7, 41662.	1.6	21
18	Architecture of the yeast Elongator complex. <i>EMBO Reports</i> , 2017, 18, 264-279.	2.0	75

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19	Function Prediction Using Patches, Pockets and Other Surface Properties. , 2017, , 327-360.		1
20	Crystal structure of a bicupin protein HutD involved in histidine utilization in <i>Pseudomonas</i> . Proteins: Structure, Function and Bioinformatics, 2017, 85, 1580-1588.	1.5	2
21	Allergens involved in the cross-reactivity of <i>Aedes aegypti</i> with other arthropods. Annals of Allergy, Asthma and Immunology, 2017, 118, 710-718.	0.5	14
22	Molecular interactions between tubulin tails and glutamylases reveal determinants of glutamylation patterns. EMBO Reports, 2017, 18, 1013-1026.	2.0	27
23	The molecular mechanism of the type IVa pilus motors. Nature Communications, 2017, 8, 15091.	5.8	108
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25	Non-synonymous single nucleotide polymorphisms of ATG5 destabilize ATG12-ATG5/ATG16L1 complex: An enzyme with E3 like activity of ubiquitin conjugation system. Meta Gene, 2017, 13, 38-47.	0.3	7
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28	Gene duplication and neo-functionalization in the evolutionary and functional divergence of the metazoan copper transporters Ctr1 and Ctr2. Journal of Biological Chemistry, 2017, 292, 11531-11546.	1.6	28
29	Dissecting intrinsic and ligand-induced structural communication in the $\beta$ 3 headpiece of integrins. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 2367-2381.	1.1	13
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33	Molecular Structure of the Human CFTR Ion Channel. Cell, 2017, 169, 85-95.e8.	13.5	421
34	Similarity between the Usher Plug and the Repeating Domain of an Ice Adhesin: Evolution via Surface Reshaping. Israel Journal of Chemistry, 2017, 57, 381-384.	1.0	1
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36	Fourier Analysis of Conservation Patterns in Protein Secondary Structure. Computational and Structural Biotechnology Journal, 2017, 15, 265-270.	1.9	3

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37	Structural Perspectives on Sigma-1 Receptor Function. <i>Advances in Experimental Medicine and Biology</i> , 2017, 964, 5-13.	0.8	14
38	Structural and energetic study of cation-π cation interactions in proteins. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 9849-9861.	1.3	19
39	Suppression and synthetic lethal genetic relationships of <i>GpsB</i> mutations indicate that <i>GpsB</i> mediates protein phosphorylation and penicillin-binding protein interactions in <i>Streptococcus pneumoniae</i> . <i>Molecular Microbiology</i> , 2017, 103, 931-957.	1.2	70
40	Probing the structural dynamics of the CRISPR-Cas9 RNA-guided DNA cleavage system by coarse-grained modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 342-353.	1.5	16
41	Discovery of potential Zika virus RNA polymerase inhibitors by docking-based virtual screening. <i>Computational Biology and Chemistry</i> , 2017, 71, 144-151.	1.1	15
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49	Conserved cytoplasmic domains promote Hrd1 ubiquitin ligase complex formation for ER-associated degradation (ERAD). <i>Journal of Cell Science</i> , 2017, 130, 3322-3335.	1.2	40
50	N-terminomics identifies widespread endoproteolysis and novel methionine excision in a genome-reduced bacterial pathogen. <i>Scientific Reports</i> , 2017, 7, 11063.	1.6	35
51	Dual Specificity Phosphatase Substrate Interaction: A Mechanistic Perspective. , 2017, 7, 1449-1461.		16
52	Use of Single-Cysteine Variants for Trapping Transient States in DNA Mismatch Repair. <i>Methods in Enzymology</i> , 2017, 592, 77-101.	0.4	4
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60	Crystal structure of Sec10, a subunit of the exocyst complex. <i>Scientific Reports</i> , 2017, 7, 40909.	1.6	14
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84	Multispecific Substrate Recognition in a Proton-Dependent Oligopeptide Transporter. <i>Structure</i> , 2018, 26, 467-476.e4.	1.6	67
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#	ARTICLE	IF	CITATIONS
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112	<i>Bacteroides thetaiotaomicron</i> generates diverse $\alpha$ -mannosidase activities through subtle evolution of a distal substrate-binding motif. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 394-404.	1.1	8
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145	The structure of SDS22 provides insights into the mechanism of heterodimer formation with PP1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 817-824.	0.4	5

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