

# The multiple roles of histidine in protein interactions

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Unearthing the Root of Amino Acid Similarity. <i>Journal of Molecular Evolution</i> , 2013, 77, 159-169.	0.8	35
2	In Silico Studies in Exploiting Weak Noncovalent C-H <sup>+</sup> and H <sup>+</sup> Interactions To Achieve Dual Properties: Hyperbasicity and Multiple Dihydrogen Storage Materials with Paracyclophane-Based Carbene Derivatives. <i>Journal of Physical Chemistry C</i> , 2013, 117, 19325-19333.	1.5	9
3	Exploration of the supramolecular interactions involving tris-dipicolinate lanthanide complexes in protein crystals by a combined biostructural, computational and NMR study. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 18235.	1.3	13
4	Theoretical study on the polar hydrogen-H (H-H) interactions between protein side chains. <i>Chemistry Central Journal</i> , 2013, 7, 92.	2.6	36
5	Amino Acid Compositions of 27 Food Fishes and Their Importance in Clinical Nutrition. <i>Journal of Amino Acids</i> , 2014, 2014, 1-7.	5.8	128
6	The structure of H <sup>+</sup> -haemoglobin in complex with a haemoglobin-binding domain from <i>Staphylococcus aureus</i> reveals the elusive H <sup>+</sup> -haemoglobin dimerization interface. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1032-1037.	0.4	6
7	Four Amino Acid Residues Influence the Substrate Chain Length and Regioselectivity of <i>Siganus canaliculatus</i> <sup>4</sup> and <sup>5/6</sup> Desaturases. <i>Lipids</i> , 2014, 49, 357-367.	0.7	30
8	Aromatic ligands for plasmid deoxyribonucleic acid chromatographic analysis and purification: An overview. <i>Journal of Chromatography A</i> , 2014, 1327, 1-13.	1.8	11
9	A novel fluorescence probe for estimation of cysteine/histidine in human blood plasma and recognition of endogenous cysteine in live Hct116 cells. <i>Chemical Communications</i> , 2014, 50, 9899-9902.	2.2	75
10	Application of information theory to a three-body coarse-grained representation of proteins in the PDB: Insights into the structural and evolutionary roles of residues in protein structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3450-3465.	1.5	1
11	Quantitative Understanding of pH- and Salt-Mediated Conformational Folding of Histidine-Containing, H <sup>+</sup> -Hairpin-like Peptides, through Single-Molecule Probing with Protein Nanopores. <i>ACS Applied Materials &amp; Interfaces</i> , 2014, 6, 13242-13256.	4.0	43
12	Exploiting Weak Noncovalent Cation-H Interaction for Designing a Molecular Container for Storage of Methane Molecules with Lithiated Carbene Superbases. <i>Journal of Physical Chemistry C</i> , 2014, 118, 6680-6689.	1.5	12
13	Ion-dynamics in hepatitis C virus p7 helical transmembrane domains - a molecular dynamics simulation study. <i>Biophysical Chemistry</i> , 2014, 192, 33-40.	1.5	17
14	Bh3 induced conformational changes in B <sub>2</sub> X <sub>2</sub> revealed by crystal structure and comparative analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1262-1272.	1.5	35
15	One missense mutation in exon 2 of the PAX5 gene in Iran. <i>Genetics and Molecular Research</i> , 2015, 14, 17768-17775.	0.3	7
16	Overnutrition Determines LPS Regulation of Mycotoxin Induced Neurotoxicity in Neurodegenerative Diseases. <i>International Journal of Molecular Sciences</i> , 2015, 16, 29554-29573.	1.8	37
17	Protein Thermostability Is Owing to Their Preferences to Non-Polar Smaller Volume Amino Acids, Variations in Residual Physico-Chemical Properties and More Salt-Bridges. <i>PLoS ONE</i> , 2015, 10, e0131495.	1.1	61
18	Ultra-high adsorption capacity of zeolitic imidazole framework-67 (ZIF-67) for removal of malachite green from water. <i>Chemosphere</i> , 2015, 139, 624-631.	4.2	355

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25	Anion-π interactions in protein-porphyrin complexes. <i>RSC Advances</i> , 2015, 5, 38361-38372.	1.7	12
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30	Double-peak elution profile of a monoclonal antibody in cation exchange chromatography is caused by histidine-protonation-based charge variants. <i>Journal of Chromatography A</i> , 2015, 1424, 92-101.	1.8	27
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32	Development and Identification of a Novel Anti-HIV-1 Peptide Derived by Modification of the N-Terminal Domain of HIV-1 Integrase. <i>Frontiers in Microbiology</i> , 2016, 7, 845.	1.5	13
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42	Comparative studies on nutrient profiling of two deep sea fish ( <i>Neopinnula orientalis</i> and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Zoology, 2016, 77, 41-48.	0.4	11
43	Copper Ion Binding Site in $\beta$ 2-Amyloid Peptide. <i>Nano Letters</i> , 2016, 16, 6282-6289.	4.5	43
44	Syndromic deafness mutations at Asn 14 differentially alter the open stability of Cx26 hemichannels. <i>Journal of General Physiology</i> , 2016, 148, 25-42.	0.9	28
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46	Reversal of axonal growth defects in an extraocular fibrosis model by engineering the kinesin-microtubule interface. <i>Nature Communications</i> , 2016, 7, 10058.	5.8	26
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57	Combined Utilization of <sup>1</sup> H NMR, IR, and Theoretical Calculations To Elucidate the Conformational Preferences of Some <sup>1</sup> H-Histidine Derivatives. <i>Journal of Physical Chemistry A</i> , 2017, 121, 729-740.	1.1	9
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72	High Susceptibility of Histidine to Charge Solvation Revealed by Cold Ion Spectroscopy. <i>Angewandte Chemie</i> , 2017, 129, 15845-15849.	1.6	1
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74	A novel mechanism of metal gel-shift by histidine-rich Ni <sup>2+</sup> -binding Hpn protein from <i>Helicobacter pylori</i> strain SS1. <i>PLoS ONE</i> , 2017, 12, e0172182.	1.1	7
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89	Synthesis of magnetic metal-organic framework nanocomposite (ZIF-8@SiO <sub>2</sub> @MnFe <sub>2</sub> O <sub>4</sub> ) as a novel adsorbent for selective dye removal from multicomponent systems. <i>Microporous and Mesoporous Materials</i> , 2019, 273, 177-188.	2.2	135
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100	Lateâ€”Stage Functionalization of Histidine in Unprotected Peptides. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 19096-19102.	7.2	47
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129	Comparison of molecularly imprinted plasmonic nanosensor performances for bacteriophage detection. <i>New Journal of Chemistry</i> , 2020, 44, 17654-17663.	1.4	10
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131	Effect of H2A.Z deletion is rescued by compensatory mutations in <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2020, 16, e1009125.	1.5	10
132	Interactions between procyanidin oligomers and the active form of matrix metalloproteinase-7: A theoretical insight. <i>International Journal of Quantum Chemistry</i> , 2020, 120, e26349.	1.0	0
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