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## Solution structure of the cyclic-nucleotide binding homology domain of a KCNH channel

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Journal of Structural Biology, 2014, 186, 68-74.

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8	Insight into the molecular interaction between the cyclic nucleotide-binding homology domain and the eag domain of the hERG channel. <i>FEBS Letters</i> , <b>2014</b> , 588, 2782-8	3.8	7
7	Getting to the heart of hERG K(+) channel gating. <i>Journal of Physiology</i> , <b>2015</b> , 593, 2575-85	3.9	19
6	NMR structural characterization of the N-terminal active domain of the gyrase B subunit from <i>Pseudomonas aeruginosa</i> and its complex with an inhibitor. <i>FEBS Letters</i> , <b>2015</b> , 589, 2683-9	3.8	11
5	Structure of the Cyclic Nucleotide-Binding Homology Domain of the hERG Channel and Its Insight into Type 2 Long QT Syndrome. <i>Scientific Reports</i> , <b>2016</b> , 6, 23712	4.9	6
4	Backbone resonance assignments for the SET domain of human methyltransferase NSD3 in complex with its cofactor. <i>Biomolecular NMR Assignments</i> , <b>2017</b> , 11, 225-229	0.7	2
3	$^1\text{H}$ , $^1\text{N}$ and $^{13}\text{C}$ resonance assignments of the Q61H mutant of human KRAS bound to GDP. <i>Biomolecular NMR Assignments</i> , <b>2021</b> ,	0.7	
2	Secondary Structures of the Transmembrane Domain of SARS-CoV-2 Spike Protein in Detergent Micelles.. <i>International Journal of Molecular Sciences</i> , <b>2022</b> , 23,	6.3	0
1	H, C and N resonance assignments of the first BIR domain of cellular inhibitor of apoptosis protein 1.. <i>Biomolecular NMR Assignments</i> , <b>2022</b> , 1	0.7	