The study of the torsion angles between helical axes in pairs of helices in protein molecules

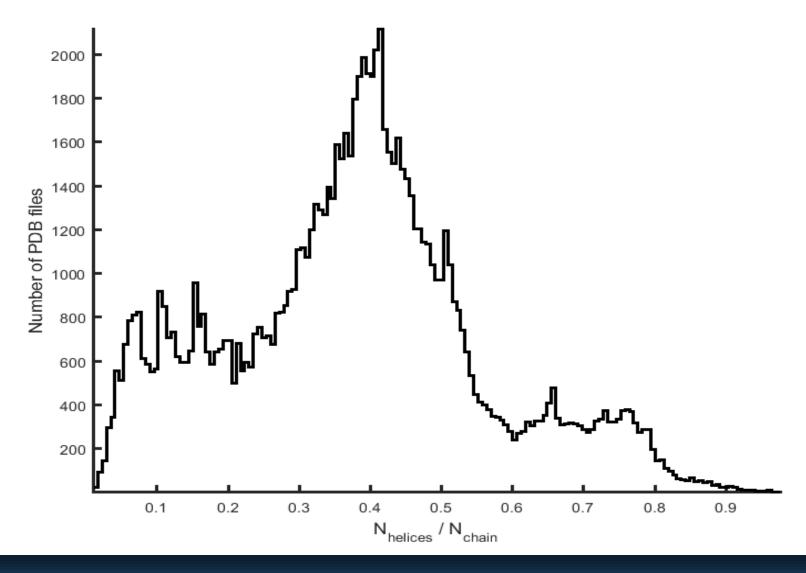
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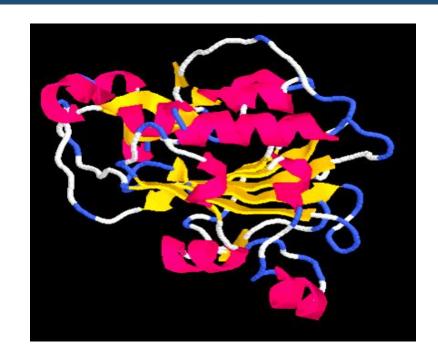
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The study was made with the support from the RFBR: project 16-01-00692-a, project 18-07-01031-a.

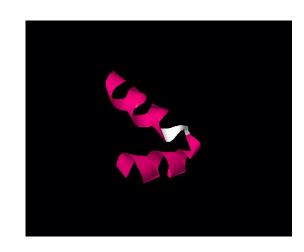
Distribution of the number of proteins in PDB depending on the ratio of amino acids in the helices to the total number of amino acids in the protein



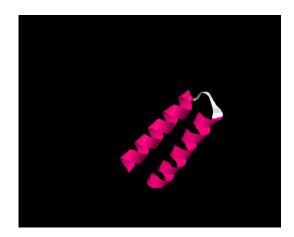


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 α - α -corner



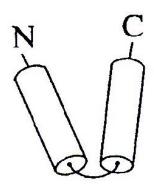
 α - α -hairpins



L- shaped structure



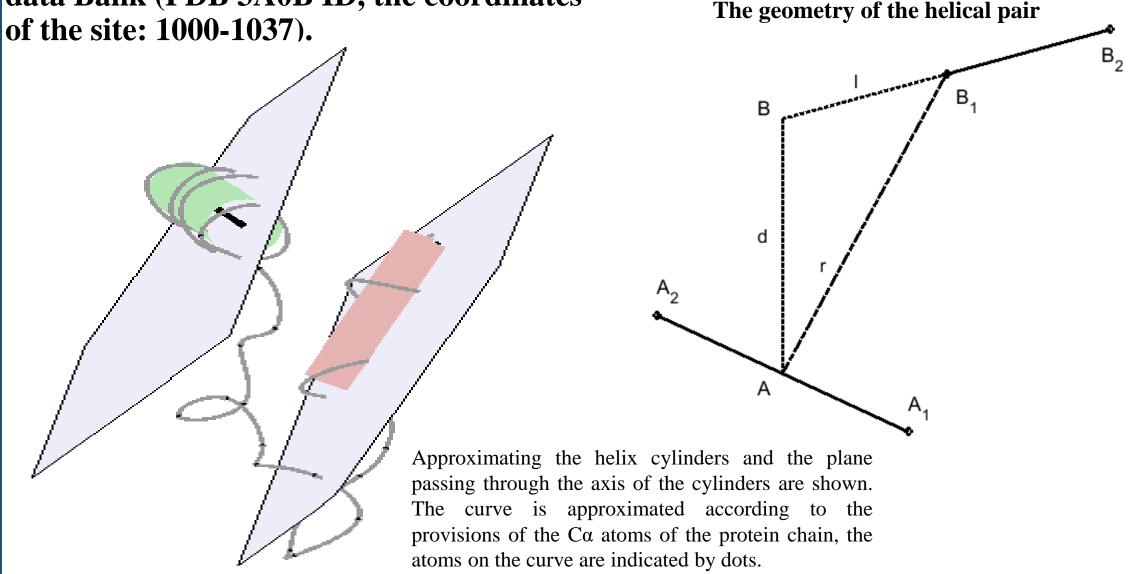
V- shaped structure



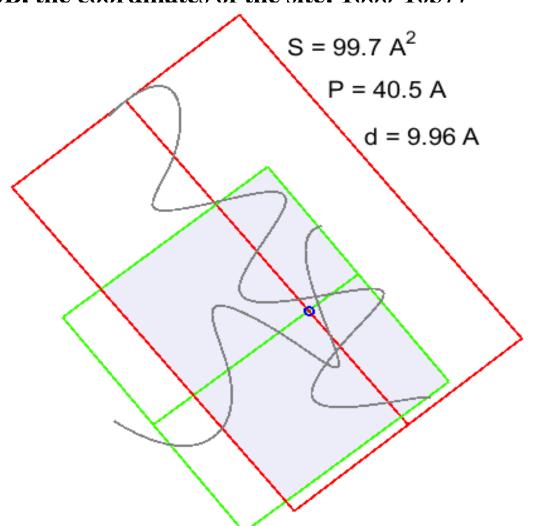
In the present study we delivered two basic tasks:

- select from the protein data bank PDB all structural motifs formed by two helices of any type located in the polypeptide chains one after another and connected by a by connections of varying length and conformation, and create a database for the further studies of such twohelical structures;
- the study of the torsion angles between axes of helices in helical pairs of protein molecules.

An example of the helical pair. A fragment of a protein chain from protein data Bank (PDB 3A0B ID, the coordinates of the site: 1000-1037)

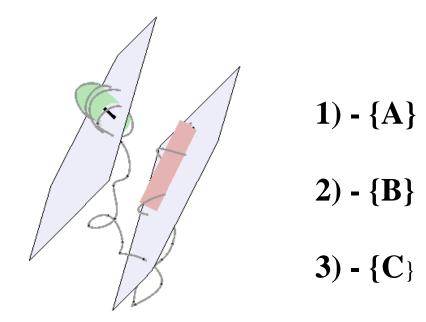


The intersection of the projections of the cylinder of helices of the helical pair. Polygon of helices projections intersection for the helical pair (PDB ID 3A0B, the coordinates of the site: 1000-1037)



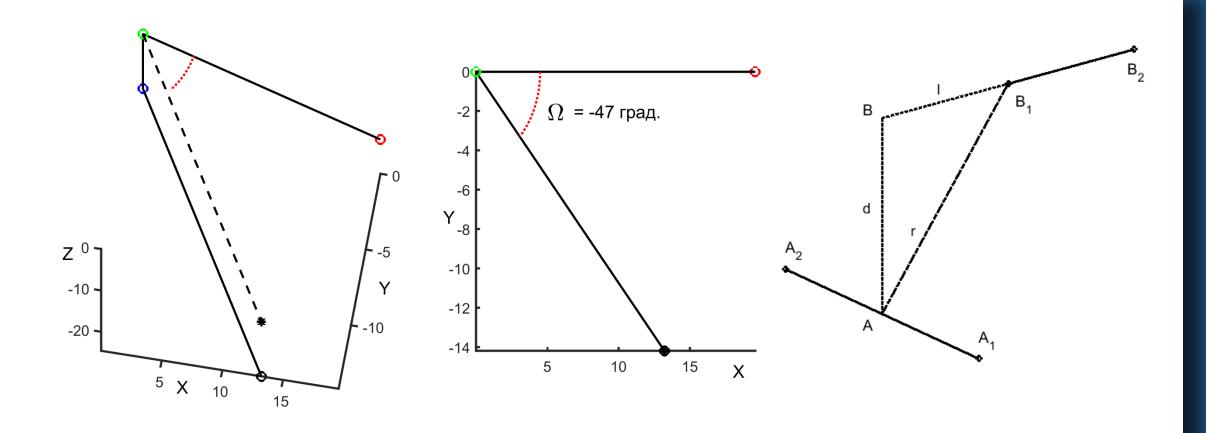
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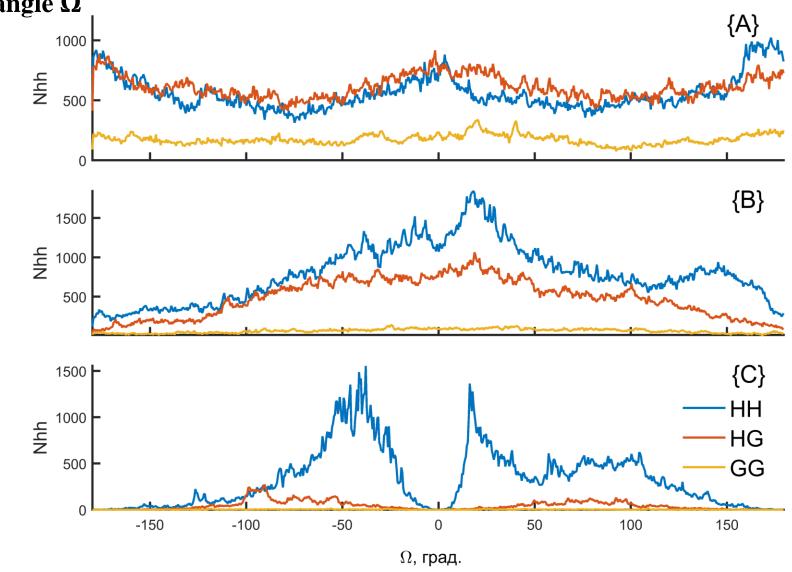
The number of	The number of the	The number of	Number of	Number of	Number of
processed protein	processed of amino	processed amino acid	H-type	G-type	I-type
structures PDB	acid residues	chains	helices	helices	helices
100397	66546491	384666	1952658	750605	2908
			(72.16%)	(27.73%)	(0.1%)

	he sets of helical pairs	Types of helical pairs						
Tl		нн	HG	GG	НІ	GI	II	Number of sets of elements
	{A}	402912	441055	125766	1588	643	0	971964
	{ B }	570830	349024	45513	1677	244	1	967289
	{C}	234000	31719	1598	26	9	0	267352
	The total number of helical pairs by types	1207742 (54.7%)	821798	172877	3291	896	1	2206605

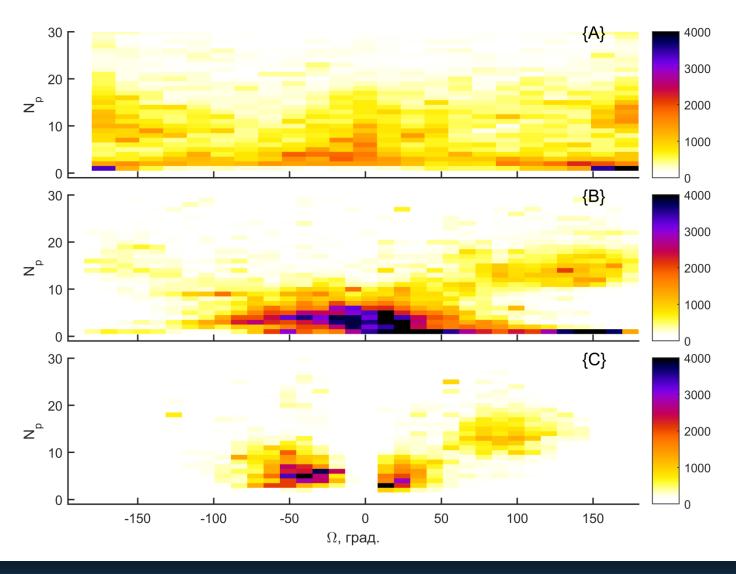


The anticlockwise direction is considered to be a positive angle while the clockwise direction is believed to be a negative angle.

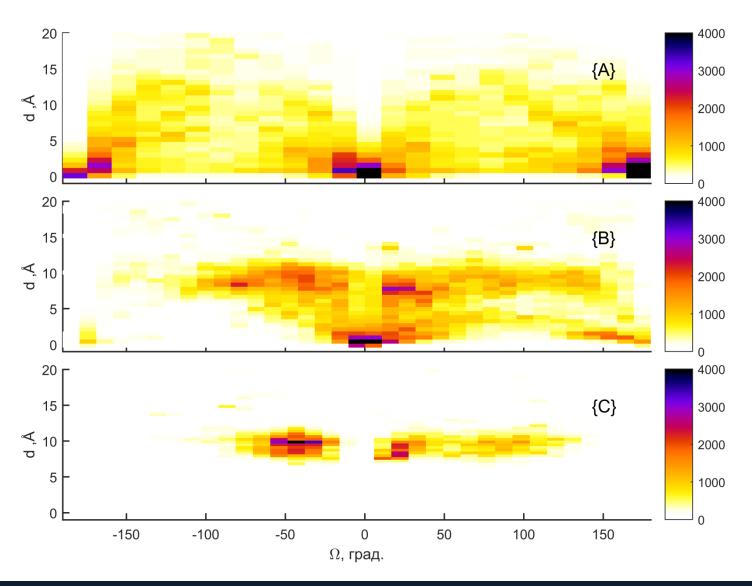
Distribution of different-type structures belonging to different subsets depending on the torsion angle $\boldsymbol{\Omega}$

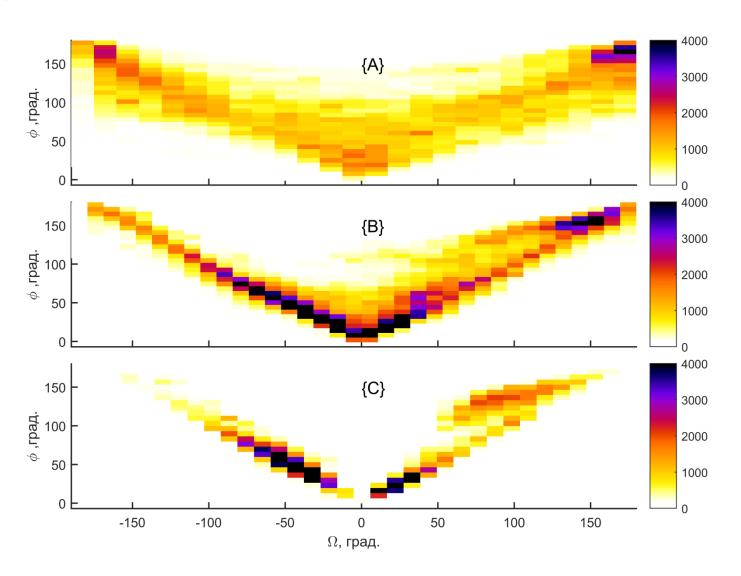


Distribution of helical pairs of HH type belonging to different subsets depending on the torsion angle Ω and the connection length N_p



Distribution of helical pairs of HH type belonging to different subsets depending on the torsion angle Ω and the interplace distance d





In this study, an analysis of distribution of the torsion angles Ω between helical axes in pairs of connected helices found in known proteins has been performed. The database for helical pairs was compiled using the Protein Data Bank taking into account the definite rules suggested earlier. The database was analyzed in order to elaborate its classification and find out novel structural features in helix packing. The database was subdivided into three subsets according to criterion of crossing helix projections on the parallel planes passing through the axes of the helices. It was shown that helical pairs not having crossing projections are distributed along whole range of angles Ω , although there are two maxima at $\Omega =$ 0° and $\Omega = 180^{\circ}$. It is shown that the distribution of all the helical pairs having the crossing helix projections has a maximum at $20^{\circ} < \Omega < 25^{\circ}$. The distribution of only α -helical pairs having crossing axes. projections has three maxima, at -50° < $\Omega < -25^{\circ}$, $20^{\circ} < \Omega < 25^{\circ}$, and $70^{\circ} < \Omega < 110^{\circ}$.

Thank you for your attention!

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