Analysis of helix to coil transitions in human serum albumin

P-02.4-09

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Human serum albumin has quite intriguing distribution of amino acid residues and combinations of hydrophobic and hydrophilic residues (in pentapeptides) among structurally stable (remaining in all 104 analyzed 3D-structures) and structurally instable fragments of its alpha helices (that may turn to random coil at least in one of them). According to the alpha-helical pattern of PentaFOLD algorithm (chemres.bsmu.by), both stable and instable alpha helices are predicted with approximately the same success: 57.5% of helices, 16.4% of beta sheet and 26.1% of random coil vs. 52.28%, 4.6%, and 43.15%, respectively. Unexpectedly, beta-structural pattern of PentaFOLD algorithm predicted 54.3% of residues in structurally stable fragments of alpha helices as beta sheet, while just 29.0% of residues from structurally instable alpha helices, where 44.4% were predicted as random coil. Stable alpha helices are significantly enriched by both amino acid residues and their combinations prone to form beta sheet (34.0% vs. 22.8%, P< 0.05; 38.6% vs. 22.8%, P< 0.05, respectively) relatively to structurally instable alpha helices. Residues from structurally stable fragments of alpha helices show significantly lower average value of surface accessibility calculated by DSSP (https://www3.cmbi.umcn.nl/xssp/) compared to fragments of alpha helices prone to change their conformation to random coil (33.5±5.0% vs. 50.46±4.8%, P< 0.05). Indeed, the usages of strong beta sheet formers are much higher in stable than in structurally instable fragments of alpha helices (Val: 10.6±0.8% vs. 5.9±0.4%; Phe: 7.3±0.6% vs. 4.6±0.3%; Thr: 6.0±0.5% vs. 3.8±0.2%). Alpha-helical hydrophobic buried core of HSA incorporates significant number of residues known to be strong beta-formers. In contrast, fragments of alpha helices on a surface of that protein are protected from alpha to beta transitions by the decreased usage beta-formers, but they are prone to helix to coil transitions.