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ON THE ROLE OF TRYPTOPHAN DERIVED UV FILTERS IN γB HUMAN EYE LENS DYNAMICS

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Derivatives of free and/or bound tryptophan present in the human eye lens act as UV filters preventing UV caused damage in lens and retina. With time and exposition to UV radiation the structures of these filters can change, this is accompanied by changes in the absorption and fluorescence spectra and chemical properties. UV filters may bind to γB-crystallins and cause protein coloration and aggregation; these processes are clinically observed as a cataract – the main cause of blindness.

In aerobic conditions and after UV exposure tryptophan is transformed into kinurenine (Kyn), next derivatives are: 3-hydroksykinurenine (3OHKyn) and 3-hydroksykinurenine glucozyde (3OHKG). Since molecular dynamic simulations (MD) are a powerful tool in getting knowledge about numerous molecular systems important in biology and medicine we prepared calculations for solvated human γB-crystallin and its complex with UV filter molecules. Comparison of protein trajectory obtained in different conditions (with and without UV filter molecules) is can give some insight into cataractogenesis process at a molecular level.

Based on the *ab initio* results (DFT/B3LYP/6-311G(d,p) calculations) we constructed a force field parameters (MOIL and NAMD) for these natural filters and used them to perform MD simulations of γB-crystallin complex with filter molecules. To the best of our knowledge this is the first approach not only to theoretical modelling of isolated UV filters dynamics but also to MD simulations of eye lens proteins in a complex with tryptophan derivatives. These preliminary results provide new data on human γB-crystallin and possible role of natural UV filters in cataract formation.

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