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Anion- π interactions in phycocyanin interfaces: a computational analysis

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We investigated 321 possible anion- π interactions in a data set consisting of different subunit interfaces in 20 phycocyanins PDB structures. We observed that phycocyanobilin tetrapyrrole chromophore is capable of forming anion- π interactions only as an anion. It was found that Tyr is the most common aromatic donor. Although presented in the examined set of interfaces, Trp does not take part in anion- π interactions. Asp-Tyr is the most common anion- π pair, while Glu-His pair does not exist in our data set. Distance examination revealed that anion- π interactions between amino acid residues appear in the range of 3-7 Å, with the average value around 5 Å. The angle between carboxylate and aromatic ring points preference toward higher values, with a peak at 90° and average value around 66° . Interestingly, much less represented anion- π contacts including chromophore show higher values of distance and lower values of this angle. Ab initio calculations revealed that interaction energies lay in the range from +0.3 to -14 kcal mol⁻¹, with generally much higher values for anion- π interaction pairs between amino acid residues compared to the chromophore including interactions. The most common (>50%) anion- π residue in the stabilization protein centers is Phe, while Glu and His are not presented at all. Anion- π interacting residues have high average conservation score of 7.7, which is especially pronounced for anion residues. The highest conservation score is observed for Asp and the lowest for Phe. Anion- π interacting residues show a preference for buried regions. Almost half of the residues involved in anion- π interactions are also part of hotspot regions, but only Asp, Phe, and Tyr. Further, in approximately one-fifth of anion- π interaction pairs, both of the residues come from the same hot-spot region and these are exclusively Asp-Tyr contacts. To conclude, a high percentage of anion- π interacting pairs in stabilization centers, their high presence in hot-spot regions and high conservation score, together with the favorable energy profile, imply that these interactions might have a significant role in the stability of phycocyanin oligomers.

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