Abstract

Tyrosine hydroxylase belongs to the group of hydroxylases of aromatic acids and catalyzes a key step in the biosynthesis of catecholamine neurotransmitters. The tyrosine hydroxylase possesses the homotetrameric structure and contains three structural domains: the N-terminal regulatory domain, the catalytic domain and the C-terminal tetramerization domain. The activity of tyrosine hydroxylase is regulated by phosphorylation and through the regulation of its expression. Phosphorylation at Ser-19 induces binding of the 14-3-3 protein, which affects the structure of the regulatory domain and protects it against both dephosphorylation and degradation. Since the structure of the regulatory domain is still unknown, we decided to perform its structural characterization using NMR techniques. First, the expression and purification protocol of the regulatory domain of tyrosine hydroxylase was optimized. The protein was expressed as a His-tag fusion protein and its purification is composed from two steps: the chelating chromatography and the size-exclusion chromatography. The dynamic light scattering and the ^{1}H nuclear magnetic resonance were used to verify its monodispersity, and hence its suitability for further experiments.