

Structural basis for the tetramerization and oligomerization of BenM, a LysR-type transcriptional regulator

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LysR-type transcriptional regulators (LTTRs) make up one of the largest family of transcription factors in prokaryotes. A general problem in the crystallization of BenM has been solubility difficulties when working with high concentrations of the full-length versions of this family of proteins. Based on the structure determinations of the effector binding domain of BenM (BenM-EBD) crystallized in two different space groups ($P4_322$ and $C222_1$), a general oligomerization scheme is proposed for BenM and other members of the LTTR family. The packing relationships and surface features showed that BenM can form infinite oligomeric arrays in the crystal lattice through its monomer-monomer and dimer-dimer interactions. This property is envisaged as a plausible factor in the significant difficulties encountered when trying to crystallize members of the LTTR family. The oligomerization of dimers to form the biologically important tetramers allows for unsatisfied oligomerization sites, which under the right conditions will favour higher order oligomerization leading to solubility problems. A model for oligomerization formation by BenM and other LTTRs is proposed.

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