

CHAPTER V

CONCLUSION

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This study can be summarized as follows:

1. The present structural analysis on EnvZ domain B (residues 290-450) reveals a novel α/β sandwich motif. This structure also contains a large flexible central loop.
2. EnvZ domain A (residues 223-289) is a homodimeric core region that forms a four-helix bundle. At the buried surface, each helices contributes to form a hydrophobic core, which stabilize the structure.
3. The conserved residues (His-243, Asn-347, and Phe-387) and motifs (G1 and G2 boxes) are exposed to the protein surface. The ATP analogue locates in the close proximity to the conserved Asn-347 and also Phe-387 in the central loop. These active residues are located effectively to enforce phospho-transfer interaction.
4. In the vicinity of surface-exposed His-243, three acidic residues form a patch which may be involved in the recognition of the response regulator, OmpR. The model structure of OmpR shows the complementary basic cluster near the phospho-receiving site (Asp-55). These observations provide a scheme for molecular mechanism between EnvZ and OmpR.