List of Figures

1.1 Codon-anticodon pairing during translation 3
1.2 The active site topology of the two classes of aaRSs 10
1.3 The identity elements of tRNA 12
1.4 The double sieve model 15
1.5 The Editing Model 17
1.6 Schematic representation of the change in the geometry of the Zn-ion after amino acid binding 23
1.7 The editing domain of E.coli ThrRS 24
1.8 Schematic representation of the domain organization of ThrRSs 27
2.1 Picture of SDS-PAGE showing purity of the protein at various steps of purification 36
2.2 Crystals of Pab-NTD and Pab-NTD-L-serine complex 39
4.1 Vectorial representation of phase determination by using the isomorphous phasing replacement method 61
4.2 Harker diagram showing determination of phase in an acentric case 64
4.3 Lack of closure error 67
4.4 Phase circles 112(a) and 317(b) reflections from Horse oxy-hemoglobin, illustrating the difference between most probable and the best phase 70
4.5 Eulerian system of angular rotation 74
4.6 Location of heavy atom sites in the Patterson maps 86
4.7 The MIRAS map and model for Pab-NTD 91
4.8 The Ramachandran plot for Pab-NTD structure obtained using ‘PROCHECK’ 93
4.9 L-serine bound in the active site of Pab-NTD 97
4.10 The Ramachandran plot for Pab-NTD-L-serine complex structure obtained using ‘PROCHECK’ 99
5.1 Structure of Pab-NTD 106
5.2 Crystal structure of Pab-NTD-L-serine complex 109
5.3 Striking structural homology with D-Tyr-tRNA<sub>Tyr</sub> deacylase (DTD) 114
5.4 Structural and sequence comparison of Pab-NTD-L-serine complex and DTD 116
6.1 Crystal soaking experiment 126
6.2 Amino acid-binding studies using Bis-ANS fluorescence 129
6.3 Proposed model for perpetuation of homochirality 132
6.4 Amino acid binding studies on Pab-NTD and its K121M mutant 135
6.5 Amino acid binding studies on Pab-NTD and its F117A mutant 137
6.6 Effect of mutations on D-tyrosine binding 139
6.7 Amino acid binding studies using Bis-ANS fluorescence 140
6.8 Amino acid binding studies on K121M-Pab-NTD using ANS fluorescence 142