6 APPENDIX
6.1 RESEARCH METHODOLOGY: FLOWCHART

Genome of 12 Strains of *Yersinia Pestis* and Comparative analysis

Comparison of Genome properties between all the genomes of Y-Strains

Prediction of Genome Islands Using Island viewer

Genome Islands Prediction & comparison

Sequence based comparison of all the strains of genome islands using clustal

100% similarities within the sequence

100% similarities of the sequence among all the Y-strains

Prediction of the Pathogenic Islands Using GIST

Identifying clusters of functionally related Pathogenic Islands Using Algorithm

Prediction the Functions of PAI – Islands using CDD

Conclusion