# LIST OF FIGURES

<table>
<thead>
<tr>
<th>Figure</th>
<th>Page No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.1 Amyloid plaques and tangles</td>
<td>3</td>
</tr>
<tr>
<td>1.2 AD affected neurons</td>
<td>3</td>
</tr>
<tr>
<td>1.3 Therapeutic target classes and their % probability for drug design</td>
<td>8</td>
</tr>
<tr>
<td>2.1 A SVM algorithm – For achieving maximum separation between the classes</td>
<td>29</td>
</tr>
<tr>
<td>2.2 A SVM algorithm – Distinguishing the classes by dividing with a hyperplane</td>
<td>30</td>
</tr>
<tr>
<td>2.3 A simple neural network</td>
<td>32</td>
</tr>
<tr>
<td>3.1 Healthy neuron and dying neuron</td>
<td>40</td>
</tr>
<tr>
<td>3.2 Chromosome 21 and APP gene</td>
<td>43</td>
</tr>
<tr>
<td>3.3 Chromosome 14 and gene PSEN1</td>
<td>43</td>
</tr>
<tr>
<td>3.4 Chromosome 1 and gene PSEN2</td>
<td>44</td>
</tr>
<tr>
<td>3.5 Chromosome 19 and gene APOE</td>
<td>44</td>
</tr>
<tr>
<td>4.1 ClustalW – multiple sequence analysis of AD proteins</td>
<td>52</td>
</tr>
<tr>
<td>4.2 Major pockets of 1AAP protein-computed with CASTp</td>
<td>57</td>
</tr>
<tr>
<td>4.3 PE of different proteins</td>
<td>62</td>
</tr>
<tr>
<td>4.4 Variation of total energy with pH for 1AAP</td>
<td>64</td>
</tr>
<tr>
<td>4.5 Variation of electrostatic energy with pH for 1AAP</td>
<td>64</td>
</tr>
<tr>
<td>4.6 Variation of protein folding energy with pH for 1AAP</td>
<td>65</td>
</tr>
<tr>
<td>5.1 HMMTOP result for Presenilin 1 protein</td>
<td>78</td>
</tr>
<tr>
<td>6.1 Interaction energy between antisense siRNA strands (complementary to mutated regions on PSEN-1 mRNA) and 1Q8K protein conformers</td>
<td>91</td>
</tr>
<tr>
<td>6.2 Interaction energy between antisense siRNA strands</td>
<td>91</td>
</tr>
</tbody>
</table>
(complementary to mutated regions on PSEN-2 mRNA) and 1Q8K protein conformers

6.3 Interaction energy between antisense siRNA strands complementary to mutated regions on APP mRNA and Argonaute proteins 92

6.4 Interaction energy between antisense siRNA strands complementary to mutated regions on BACE-1 mRNA and Argonaute proteins 94

7.1 Biomoca with the nanopore 98

7.2 Protein residues and their energies (3DXC) 101

7.3 Variation of charge with pH 101

8.1 Drug designing strategy 105

8.2 Alzheimer’s disease pathway 113

8.3 Curcumin (enolic form) 117

8.4 Curcumin (ketonic form) 117

8.5 Three configurations of curcumin 118

9.1 Drug designing strategy 123

9.2 Interaction of a planar ligand in the double helix 125