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   1.1 Cancer
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      1.1.2 Etiology of cancer
      1.1.3 Genetic Mutations Leading To Cancer: “Process of Carcinogenesis”
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      1.1.5 Hallmarks of cancer
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      1.1.7 Diagnosis of cancer
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   2 Protein Tyrosine Kinases: Major Class of Drug Target
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         2.2.1 Chromosomal Translocations
            2.2.1.1 Consequences of Translocations
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4. Materials And Methodology

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         4.1.1a.1 Online Databases
            4.1.1a.1.1 Mitelman Database of Chromosome Aberrations and Gene Fusions in Cancer
            4.1.1a.1.2 Translocation breakpoints in cancer database (TICdb)
            4.1.1a.1.3 UCSC (University of California Santa Cruz) Genome browser
            4.1.1a.1.4 BLAT (BLAST-Like Alignment Tool)
4.1.1a.2  Online Softwares/Tools/Server
4.1.1a.2.1  WebSIDD server
4.1.1a.2.2  DNA base composition analysis Tool
4.1.1a.2.3  RSS (Recombination signal sequences) site prediction tool
4.1.1a.3  Offline Softwares/Tools/Server
4.1.1a.3.1  DiproGB: the dinucleotide properties genome browser

4.1.1b  Methodology For Chromosomal Translocation & Breakpoint Characterization
4.1.1b.1  Data Retrieval
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4.1.2a  Material For In-Silico Mutagenesis and protein stability
4.1.2a.1  Online Softwares/Tools/Server
4.1.2a.1.1  Protein Data Bank (PDB)
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4.1.3a.1.3  YASARA (Yet Another Scientific Artificial Reality Application)
4.1.3a.1.4  FAF Drugs (Free ADME-Tox Filtering Tool)

4.1.3b  Methodology for Virtual Screening by Molecular Docking and MD Simulation
4.1.3b.1 Virtual screening/Molecular Docking

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4.2.1 Collection of Tumor Specimens and Establishment of Primary Lung Cancer Cell Culture

4.2.1.1 Cell Viability/ Dye Exclusion Assay

4.2.1.2 DNA Isolation from Primary Tumour Cultured Cells

PART A

4.2.1.3 Mutation Analysis by Allele Specific Oligonucleotide Polymerase Chain Reaction (ASO– PCR)

4.2.1.3.1 Detection of Amplified PCR product by Agarose Gel Electrophoresis:

4.2.1.3.2 Purification of Amplified PCR Products

PART B

4.2.2 MTT Cell Proliferation Assay

4.2.3 AnnexinV/Propidium Iodide Apoptosis Assay

4.2.4 Dye-Terminator Cycle Sequencing

PART C

4.2.4.1 Purification of Cycle Sequencing Products

4.2.4.2 Separation of Cycle Sequenced Products by Capillary Electrophoresis

5. Result & Discussion

5.1 RESULTS & DISCUSSION OF IN-SILICO ANALYSIS

5.1.1 Result & Discussion: Characterization of the Breakpoints Regions of Major Chromosomal Translocation Leading to Cancer

5.1.2 Result & Discussion: Predicting Protein Stability upon Point Mutations

5.1.3 Result & Discussion: Identification of Potent Lead Molecule through Virtual Screening/Molecular Docking and Molecular Dynamic Simulations

5.1.3.1 EGFR

5.1.3.1.1 Molecular Docking result of EGFR

5.1.3.1.2 Molecular Dynamic Simulation results of EGFR

5.1.3.2 ALK

5.1.3.2.1 Molecular Docking result of ALK

5.1.3.2.2 Molecular Dynamic Simulation results of ALK
ALK

5.1.3.3 BRAF
5.1.3.3.1 Molecular Docking result of BRAF
5.1.3.3.2 Molecular Dynamic Simulation results of BRAF

5.1.3.4 KRAS
5.1.3.4.1 Molecular Docking result of KRAS
5.1.3.4.2 Molecular Dynamic Simulation results of KRAS

5.2 RESULTS & DISCUSSION OF IN-VITRO STUDIES

5.2.1 Result & Discussion of In-Vitro Cell Isolation/Expansion (CFU) & Identification of EGFR Mutation (ASO-PCR)
5.2.2 Result & Discussion of In-Vitro Validation of Selected Compounds against Wild/Mutant Cell type by Biological/Cell-Based Assays (MTT Assay and Annexin V/PI Apoptosis assay)
5.2.3 Result & discussion of Genotypic Analysis of the Amplicons with Capillary Sequencing:

6. Summary & Conclusion

7. References

8. List of Publications and Presentations