Molecular Biology Internship

Developing CRISPR-Cas Systems for More Precise and Efficient Gene Editing
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CRISPR-Cas systems have revolutionized the field of genetic engineering by providing a powerful tool for precise gene editing. The objective of this research is to enhance the accuracy and efficiency of CRISPR-Cas systems to reduce off-target effects and increase their usability in clinical and agricultural applications.

Research Methodology

The research will be structured around three main phases: design optimization, experimental validation, and application testing.

Phase 1: Design Optimization

In this phase, computational models will be developed to predict CRISPR-Cas9 binding efficiency and specificity. Advanced algorithms will be used to design guide RNAs with reduced off-target activity. This involves:

- Utilizing machine learning techniques to analyze genomic data and predict guide RNA efficacy.
- Designing synthetic guide RNAs based on genomic context to minimize unintended mutations.

Phase 2: Experimental Validation

Engineered CRISPR systems will be tested in vitro and in vivo to assess their editing capabilities and specificity. This phase includes:

- Performing in vitro cleavage assays to evaluate guide RNA targeting accuracy.
- Using genetically engineered cell lines and animal models to test the efficiency of the CRISPR modifications.

Phase 3: Application Testing

Successful CRISPR constructs will be applied in more complex biological systems to evaluate their practical utility in real-world scenarios, such as disease models and agricultural enhancements. Activities include:

- Testing gene editing outcomes in disease-specific cell models to observe therapeutic

effects.
- Assessing the impact of edited genes on plant resistance to pests and environmental stress.

Research Approach

The research approach will combine both theoretical and experimental methodologies:

- **Theoretical studies** will involve the use of computational biology to simulate and optimize CRISPR-Cas system designs.
- **Experimental studies** will employ molecular biology techniques, including CRISPR-Cas9 gene editing, next-generation sequencing, and cellular assays to validate the effectiveness of the gene edits.

Unraveling the Complexities of Gene Regulation Mechanisms in Response to Environmental Stresses
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This research aims to understand how genes are regulated in response to environmental stresses, which can provide insights into plant and animal adaptation, resilience, and survival. By studying these mechanisms, we can enhance agricultural productivity and develop strategies to mitigate the effects of climate change.

Research Methodology

The study will employ a multi-tiered approach encompassing data collection, analysis, and functional validation of gene regulatory networks.

Phase 1: Data Collection

Collect comprehensive genomic and transcriptomic data from organisms exposed to various controlled environmental stresses. This phase will include:

- Gathering RNA sequencing data from multiple time points post-stress application to capture dynamic changes in gene expression.
- Utilizing chromatin immunoprecipitation sequencing (ChIP-seq) to identify changes in transcription factor binding sites and histone modifications.

Phase 2: Bioinformatics Analysis

Analyze the collected data to construct models of gene regulatory networks that respond to environmental stresses. This includes:

- Employing machine learning algorithms to correlate specific gene expression patterns with environmental stresses.
- Using network analysis tools to identify key regulatory nodes and pathways involved in stress responses.

Phase 3: Functional Validation

Validate the predicted gene regulatory networks through experimental approaches. Key activities involve:

- Manipulating the expression of key regulatory genes using CRISPR-Cas9 or RNAi technologies in model organisms.
- Assessing phenotypic changes and stress resilience in modified organisms under controlled stress conditions.

Research Approach

This research will integrate both wet-lab and computational approaches:

- **Computational studies** will analyze large datasets to build predictive models and identify potential regulatory elements and interactions.
- **Experimental studies** will focus on molecular genetics techniques such as gene editing, phenotypic assays, and stress application to validate the computational predictions and understand the biological significance of gene regulation under stress.

Identifying Genetic Markers for Complex Diseases Through High-Throughput Sequencing Technologies
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This research aims to identify genetic markers associated with complex diseases by leveraging high-throughput sequencing technologies. Understanding these markers can lead to improved diagnostics, targeted therapies, and personalized treatment plans.

Research Methodology

The project will employ a comprehensive strategy that includes sample collection, sequencing, and data analysis to identify genetic variations linked to disease phenotypes.

Phase 1: Sample Collection and Preparation

Collect DNA samples from a diverse population of individuals, both affected and unaffected by specific complex diseases. This phase involves:

- Establishing collaborations with hospitals and research centers to obtain a wide range of genetic material.
- Preparing samples for sequencing, ensuring high-quality DNA extraction and library preparation.

Phase 2: High-Throughput Sequencing

Perform whole-genome, whole-exome, or targeted sequencing depending on the research focus. This phase includes:

- Utilizing next-generation sequencing (NGS) platforms to obtain detailed genomic data.
- Applying single-cell sequencing technologies to understand cell-to-cell variations within diseased tissues.

Phase 3: Data Analysis and Marker Identification

Analyze the sequencing data using bioinformatics tools to identify genetic markers associated with disease. Activities include:

- Using statistical and computational methods to correlate specific genetic variants with disease phenotypes.
- Employing machine learning techniques to predict disease risk based on genetic profiles.

Research Approach

This project will integrate genomic technologies with computational biology to identify and validate genetic markers:

- **Genomic studies** will focus on sequencing and the technical aspects of handling high-throughput data.
- **Computational studies** will involve data analysis, statistical genetics, and bioinformatics to interpret the vast amounts of data generated and identify meaningful associations with diseases.

Investigating the Roles and Mechanisms of Action of Long Non-Coding RNAs in Gene Regulation
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This research focuses on understanding the complex roles and functional mechanisms of long non-coding RNAs (lncRNAs) in gene regulation. lncRNAs are crucial for various biological processes and their dysregulation is often linked to disease. Unraveling these mechanisms could lead to new therapeutic targets.

Research Methodology

The methodology involves a combination of experimental and computational approaches to dissect the functional roles of lncRNAs in cellular contexts.

Phase 1: lncRNA Identification and Characterization

Identify and catalog lncRNAs expressed under specific biological conditions or in disease states. This phase involves:

- Using RNA-Seq to profile lncRNA expression across different cell types and conditions.
- Characterizing the molecular features of lncRNAs, such as their localization, stability, and secondary structure.

Phase 2: Functional Analysis

Determine the biological functions and mechanisms of action of specific lncRNAs. This includes:

- Employing RNA interference (RNAi) and CRISPR interference (CRISPRi) to knockdown or silence lncRNA expression.
- Conducting rescue experiments to assess the effects of lncRNA manipulation on gene expression and cellular phenotype.

Phase 3: Mechanistic Studies

Explore the molecular mechanisms by which lncRNAs regulate gene expression. Activities involve:

- Using Chromatin Immunoprecipitation Sequencing (ChIP-Seq) to identify interaction sites of lncRNAs with DNA, RNA, and protein complexes.
- Applying RNA pull-down assays to discover interacting proteins and elucidate the role of these interactions in regulatory pathways.

Research Approach

This research will blend experimental biology techniques with computational analysis to provide a comprehensive understanding of lncRNA functions:

- **Experimental approaches** include the use of molecular biology techniques, genetic manipulation tools, and high-throughput sequencing.
- **Computational approaches** involve bioinformatics analysis, such as transcriptome assembly, differential expression analysis, and network modeling to interpret data and predict lncRNA functions.

Mapping the Complete Set of Transcription Factors and Their Binding Sites Across Various Genomes
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This research aims to comprehensively map transcription factors (TFs) and their binding sites across a variety of genomes, enhancing our understanding of regulatory networks in different species. This will aid in discovering new regulatory elements and understanding evolutionary conservation and divergence of gene regulation.

Research Methodology

The study involves a systematic approach to identify and characterize transcription factor binding sites using advanced genomic technologies.

Phase 1: Genome-Wide Identification of TFs

Identify all transcription factors in the genomes of multiple species using bioinformatics tools. This phase involves:

- Conducting in silico analysis of known and predicted transcription factor motifs.
- Using protein sequence databases to annotate transcription factor families across species.

Phase 2: High-Throughput Screening

Use high-throughput techniques like ChIP-seq to map the binding sites of identified transcription factors under various conditions. This includes:

- Performing ChIP-seq experiments to capture TF-DNA interactions across different tissues and developmental stages.
- Integrating ChIP-seq data with RNA-seq data to correlate TF binding with gene expression changes.

Phase 3: Data Integration and Analysis

Analyze the gathered data to construct detailed maps of transcription factor binding sites and to understand their functional implications. Activities involve:

- Employing computational models to predict TF binding specificity and affinity.
- Using systems biology approaches to integrate data and model regulatory networks involving TFs.

Research Approach

This project combines genomic technologies with computational analysis to map transcription factor landscapes:

- **Genomic studies** will focus on employing sequencing technologies and experimental assays to identify TFs and their interactions with the genome.
- **Computational studies** will utilize bioinformatics tools, data integration techniques, and network analysis to interpret the complex data collected and to visualize regulatory networks.

Elucidating the Molecular Basis of Epigenetic Changes and Their Heritability
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This research focuses on understanding the molecular mechanisms underlying epigenetic modifications and how these changes are passed down through generations. Insights gained could revolutionize our understanding of gene regulation, development, and inheritance, and have implications for treating genetic diseases.

Research Methodology

The methodology for this research involves detailed molecular analysis and intergenerational studies to understand the stability and transmission of epigenetic marks.

Phase 1: Characterization of Epigenetic Modifications

Identify and characterize various epigenetic modifications across different cell types and developmental stages. This phase includes:

- Using bisulfite sequencing to map DNA methylation patterns genome-wide.
- Employing ChIP-seq to study histone modifications and their effects on gene expression.

Phase 2: Functional Analysis

Investigate the functional impacts of identified epigenetic modifications on gene regulation and cellular phenotypes. Activities involve:

- Conducting gene expression studies (e.g., RNA-seq) to correlate epigenetic changes with changes in transcript levels.
- Using CRISPR/dCas9 technology to specifically alter epigenetic marks and observe resultant changes in gene activity.

Phase 3: Heritability Studies

Examine the transmission of epigenetic information between generations and its impact on phenotype and disease. This includes:

- Performing cross-generational studies in model organisms to track the inheritance of epigenetic traits.
- Utilizing advanced imaging and sequencing techniques to study epigenetic reprogramming during development.

Research Approach

This research will use a comprehensive approach combining molecular biology, genetics, and bioinformatics:

- **Molecular biology techniques** such as sequencing and chromatin analysis will be used to study epigenetic mechanisms at the DNA and histone levels.
- **Genetic and developmental biology approaches** will help understand the functional consequences of epigenetic modifications and their inheritance patterns.
- **Bioinformatics and computational modeling** will be essential for analyzing large datasets and modeling the complex interactions between epigenetic modifications and gene regulation.

Exploring Gene Expression Patterns in Rare Diseases to Identify Novel Therapeutic Targets
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This research aims to elucidate gene expression patterns in rare diseases, providing insights into disease mechanisms and uncovering potential therapeutic targets. Understanding these patterns could lead to innovative treatments and interventions for conditions that currently have limited options.

Research Methodology

The study will utilize a combination of genomic technologies and bioinformatics analysis to map and understand gene expression in rare diseases.

Phase 1: Patient Sample Collection and RNA Sequencing

Collect tissue samples from patients with rare diseases and perform high-throughput RNA sequencing to capture a broad snapshot of gene expression. This phase involves:

- Gathering patient samples through collaborations with medical institutions and rare disease networks.
- Performing comprehensive RNA-Seq to analyze gene expression profiles in affected tissues compared to healthy controls.

Phase 2: Data Analysis and Differential Expression

Analyze RNA-Seq data to identify genes that are differentially expressed in disease states. This includes:

- Using bioinformatics tools to process and normalize sequencing data.
- Employing statistical methods to identify significantly altered genes that may contribute to disease pathology.

Phase 3: Validation and Functional Studies

Validate the identified gene targets and explore their functional roles in disease progression. Key activities involve:

- Using gene editing technologies, like CRISPR-Cas9, to manipulate the expression of target genes in cell models.
- Conducting functional assays to assess the impact of gene modulation on cellular phenotypes relevant to the disease.

Research Approach

The research approach integrates both experimental and computational strategies:

- **Molecular and cellular biology techniques** will be used to manipulate gene expression and assess its impact on cellular functions and disease phenotypes.
- **Computational and bioinformatics analyses** will handle large-scale data processing and integration to draw meaningful conclusions about gene function and therapeutic potential.

Advancing the Understanding of Genetic Interactions and Network Biology in Multicellular Organisms
+

This research focuses on deepening our understanding of how genetic interactions shape biological networks within multicellular organisms, providing insights into developmental processes, disease mechanisms, and evolution. This complex interplay of genes determines phenotypic outcomes and adaptability.

Research Methodology

The study will utilize a range of genomic, proteomic, and computational techniques to map and analyze the intricate web of genetic interactions in various organisms.

Phase 1: Genomic and Proteomic Data Collection

Collect comprehensive genomic and proteomic data to identify potential genetic interactions. This phase involves:

- Performing high-throughput sequencing and proteomics to gather extensive data on gene and protein expression.
- Using advanced imaging techniques to visualize interactions and cellular locations of proteins.

Phase 2: Bioinformatics and Network Analysis

Analyze the collected data to construct and model genetic and protein interaction networks. This includes:

- Applying machine learning and network analysis tools to identify central nodes and interaction hubs within the networks.
- Integrating data across different biological layers (e.g., transcriptomic, proteomic) to develop a holistic view of cellular functions.

Phase 3: Functional Validation and Phenotypic Characterization

Validate the identified genetic interactions through experimental approaches and characterize their phenotypic manifestations. Key activities involve:

- Using genetic manipulation techniques such as CRISPR to alter identified key interaction nodes.
- Assessing the phenotypic outcomes of these manipulations in model organisms to understand the biological relevance of the interactions.

Research Approach

The research will be conducted using an integrative approach combining molecular biology, genetics, systems biology, and computational modeling:

- **Molecular and genetic techniques** will focus on experimental manipulation of genes and proteins to observe changes in network dynamics and phenotypic outcomes.
- **Systems biology and computational modeling** will be utilized to synthesize data and

model complex biological networks, facilitating understanding of the systemic properties of genetic interactions.

Developing Tools and Methods for Single-Cell Genomics to Understand Cellular Heterogeneity +

This research aims to develop and refine tools and methods for single-cell genomics, enhancing our ability to analyze and understand cellular heterogeneity in various biological contexts. This will improve insights into cellular behavior in development, disease, and tissue regeneration.

Research Methodology

The study will involve the design, optimization, and application of novel single-cell genomic technologies.

Phase 1: Tool Development

Develop innovative tools to capture and analyze single-cell genomic data. This phase involves:

- Creating high-throughput methods for isolating single cells and preparing them for sequencing.
- Enhancing technologies for single-cell RNA-Seq, DNA sequencing, and ATAC-Seq to improve resolution and throughput.

Phase 2: Method Optimization

Optimize these tools for increased efficiency and accuracy in data collection. Activities include:

- Refining bioinformatics pipelines to handle large datasets from single-cell analyses.
- Developing algorithms for better distinguishing between biological signal and technical noise in single-cell data.

Phase 3: Application and Validation

Apply these developed technologies to specific biological studies to validate their effectiveness and gain insights into cellular heterogeneity. This includes:

- Investigating cellular diversity in healthy and diseased tissues to understand cellular roles and dynamics.
- Using single-cell data to map cellular lineage relationships in development and disease progression.

Research Approach

The research will integrate technical development with biological applications:

- **Technical development** involves engineering and bioinformatics, focusing on creating and refining tools for genomic analysis at the single-cell level.

- **Biological application** involves using these tools to conduct detailed studies of cellular heterogeneity, providing insights into biological processes and potential therapeutic targets.

Investigating the Role of Alternative Splicing in Disease and Development
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This research focuses on understanding how alternative splicing contributes to gene regulation in development and disease. By exploring these mechanisms, this study aims to uncover new therapeutic targets and provide insights into developmental biology and pathogenesis.

Research Methodology

The methodology involves a comprehensive approach, utilizing both experimental and computational techniques to analyze alternative splicing events and their biological implications.

Phase 1: Identification of Splicing Events

Identify and catalog alternative splicing events in different tissues, developmental stages, and disease states. This phase involves:

- Collecting RNA samples from diverse biological conditions and disease states.
- Performing high-throughput RNA sequencing to detect alternative splicing events across the transcriptome.

Phase 2: Functional Analysis

Analyze the functional implications of identified splicing events. This includes:

- Using minigene constructs and reporter assays to experimentally validate the impact of specific splicing variants on gene function.
- Applying CRISPR-Cas9 technology to manipulate splicing factors and observe the resultant effects on cell phenotype and function.

Phase 3: Integrative and Computational Studies

Integrate experimental data with computational models to predict and understand the regulatory networks influenced by alternative splicing. Activities involve:

- Developing and utilizing bioinformatics tools to correlate splicing patterns with gene expression data and cellular outcomes.
- Constructing network models to elucidate the interactions between splicing variants and other cellular processes.

Research Approach

The research will employ a multidisciplinary approach, combining molecular biology, genetics, computational biology, and systems biology:

- **Molecular and genetic techniques** will be used for detailed experimental investigations into splicing mechanisms and their effects.
- **Computational and systems biology** approaches will analyze large datasets to model and understand the complex biological systems influenced by alternative splicing.

Other Molecular Biology Research Objectives considered for Internships

1. Decoding the genomic architecture of complex traits to predict phenotypic outcomes.
2. Elucidating the mechanisms of gene silencing and its implications for therapy.
3. Characterizing the genetic basis of adaptation and evolutionary change.
4. Developing computational models to predict regulatory element interactions at a genomic scale.
5. Enhancing the precision of genomic editing tools to target multiple genes simultaneously.
6. Investigating genomic instability and its implications for cancer and aging.
7. Exploring the genetic determinants of cellular metabolism and metabolic disorders.
8. Developing genome-wide CRISPR screens to identify new drug targets.
9. Characterizing the role of gene duplication in evolutionary adaptations and innovations.
10. Elucidating the genetic basis of antibiotic resistance and its spread among bacterial populations.
11. Investigating the regulatory networks involved in plant stress responses.
12. Developing synthetic gene circuits to enhance cellular functions.
13. Exploring the role of transposable elements in shaping genome structure and function.
14. Mapping the spatial organization of the genome in different cell types and conditions.
15. Investigating the influence of chromosomal architecture on gene expression and regulation.
16. Understanding the molecular basis of gene-environment interactions.
17. Exploring the potential of gene therapy in treating genetic disorders.
18. Developing methods to control gene expression using light-sensitive elements.
19. Elucidating the mechanisms of RNA-mediated gene regulation.
20. Investigating the impact of genetic variations on protein-protein interactions.
21. Mapping the genetic pathways involved in the development and progression of autoimmune diseases.
22. Developing novel computational tools for genome annotation and data integration.
23. Exploring the role of gene editing in modulating the immune system for therapy.
24. Investigating genetic adaptations to extreme environments in microbes.
25. Mapping and characterizing the human epigenome across diverse populations.
26. Developing high-throughput technologies for rapid genotyping and phenotyping.
27. Investigating the molecular basis of symbiotic relationships in ecosystems.
28. Elucidating the genetic control of developmental timing and life history traits.
29. Developing gene drive systems to control vector-borne diseases.
30. Characterizing genetic networks that underlie cellular responses to DNA damage.
31. Exploring the use of artificial intelligence in predicting gene expression outcomes.
32. Investigating the role of microRNAs in cancer and other diseases.
33. Developing tools to manipulate the microbiome for health benefits.
34. Characterizing the genetic underpinnings of fertility and reproduction.

35. Exploring therapeutic potentials of gene silencing technologies.
36. Investigating mechanisms of transcriptional noise and its effects on cellular function.
37. Developing new methods for in vivo imaging of gene expression.
38. Investigating the role of genetic factors in aging-related cognitive decline.
39. Elucidating the molecular mechanisms of muscle growth and regeneration.
40. Developing gene therapies for rare and undiagnosed genetic disorders.
41. Exploring the genetic basis of behavioral traits and disorders.
42. Investigating genetic interactions and their role in complex disease phenotypes.
43. Developing technologies to enhance gene therapy delivery and specificity.
44. Mapping the molecular determinants of pathogen virulence and host resistance.
45. Investigating the genetic basis of adaptation to climate change in agricultural species.
46. Elucidating mechanisms of gene regulation during embryonic development.
47. Investigating the role of genetic diversity in ecosystem resilience.
48. Developing methods for precise genetic modifications in non-model organisms.
49. Exploring the impact of genetic mutations on metabolic pathways.
50. Investigating the role of genetic and epigenetic factors in addiction.
51. Characterizing the genetic architecture of psychiatric disorders.
52. Developing genome editing tools for therapeutic modulation of gene activity.
53. Exploring the regulatory complexities of gene expression in hybrid organisms.
54. Investigating the genetic mechanisms of resistance to chemotherapy.
55. Elucidating the role of host genetics in infectious disease susceptibility.
56. Developing computational models to study gene regulation in virtual cells.
57. Investigating the effects of genetic drift on population genetics.
58. Characterizing the role of enhancers and promoters in cancer genomics.
59. Developing novel methods for analyzing genomic data from ancient DNA.
60. Exploring the intersection of genomics and nanotechnology for targeted therapies.
61. Investigating the molecular mechanisms of memory formation and retrieval.
62. Developing gene-based strategies for enhancing photosynthesis and crop yield.
63. Exploring genetic modifications to improve biofuel production.
64. Investigating the role of gene-environment interactions in metabolic syndrome.
65. Characterizing the genetic factors involved in organ development and function.
66. Developing in vitro models to study gene expression in human tissues.
67. Investigating the genetics of plant-pathogen interactions.
68. Developing tools for precise manipulation of mitochondrial DNA.
69. Exploring the use of gene therapy in cardiovascular diseases.
70. Investigating the molecular genetics of sleep and circadian rhythms.
71. Characterizing the influence of genetic factors on immune system function.
72. Developing synthetic biology approaches to bioremediation.
73. Exploring gene therapy options for inherited skin disorders.
74. Investigating the role of genetics in stress response and resilience.
75. Developing methods to enhance the efficiency of gene transfer technologies.
76. Characterizing the role of transcription factors in tissue regeneration.
77. Investigating the genetic basis of sensory disorders.
78. Developing high-resolution techniques for single-gene tracking in live cells.
79. Elucidating the genetic pathways involved in plant immunity and their agricultural applications.

80. Investigating gene expression patterns in response to pharmaceutical treatments.
81. Developing genetic engineering approaches to combat invasive species.
82. Characterizing the role of genetic factors in respiratory diseases.
83. Exploring gene therapy approaches for genetic eye diseases.
84. Developing molecular diagnostics for early detection of genetic disorders.
85. Investigating the molecular genetics of tissue repair and wound healing.
86. Elucidating the role of genetic variations in taste perception and dietary choices.
87. Developing gene-editing tools for correcting mutations in stem cells.
88. Investigating the genetic basis of hormone regulation and its disorders.
89. Exploring the genetic underpinnings of energy balance and obesity.
90. Characterizing gene-environment interactions that lead to neurodevelopmental disorders.
91. Developing genome-wide association studies to uncover genetic markers linked to longevity.
92. Investigating the molecular basis of gene therapy resistance.
93. Developing strategies for the safe integration of gene therapies into the genome.
94. Exploring the genetic foundations of immune system disorders.
95. Characterizing genetic mutations that lead to drug resistance in cancer cells.
96. Developing CRISPR-based diagnostics for rapid genetic testing.
97. Investigating the role of genetics in adaptation to hypoxic environments.
98. Exploring the potential of gene therapies to treat autoimmune diseases.
99. Developing tools to visualize and manipulate genes in their native chromatin context.
100. Characterizing the genetic basis of plant nutrient use efficiency to improve fertilizer usage.
101. Developing targeted gene therapies for neuromuscular diseases.
102. Investigating the role of epigenetic changes in cancer progression.
103. Characterizing the interplay between genetic and metabolic factors in disease.
104. Developing methods for precise gene insertion to avoid off-target effects in gene therapy.
105. Investigating the genetics of aging and related pathologies.

Fee Structure

Note 1: Fee mentioned below is per candidate.
Note 2: Fee of any sort is NON REFUNDABLE once paid. Please cross confirm all the details before proceeding to fee payment

2 Days Total Fee: Rs 1800/-

Reg Fee Rs 540/-

5 Days Total Fee: Rs 3652/-

Reg Fee Rs 1096/-

10 Days Total Fee: Rs 5600/-

Reg Fee Rs 1680/-

15 Days Total Fee: Rs 8842/-

Reg Fee Rs 2653/-

20 Days Total Fee: Rs 13067/-

Reg Fee Rs 3920/-

30 Days Total Fee: Rs 20753/-

Reg Fee Rs 5500/-

45 Days Total Fee: Rs 31624/-

Reg Fee Rs 5500/-

2 Months Total Fee: Rs 39200/-

Reg Fee Rs 5500/-

3 Months Total Fee: Rs 59733/-

Reg Fee Rs 5500/-

4 Months Total Fee: Rs 79333/-

Reg Fee Rs 5500/-

5 Months Total Fee: Rs 99867/-

Reg Fee Rs 5500/-

6 Months Total Fee: Rs 119467/-

Reg Fee Rs 5500/-

7 Months Total Fee: Rs 140000/-

Reg Fee Rs 5500/-

8 Months Total Fee: Rs 159600/-

Reg Fee Rs 5500/-

9 Months Total Fee: Rs 179200/-

Reg Fee Rs 5500/-

10 Months Total Fee: Rs 199733/-

Reg Fee Rs 5500/-

11 Months Total Fee: Rs 219333/-

Reg Fee Rs 5500/-

1 Year Total Fee: Rs 239867/-

Reg Fee Rs 5500/-

Please contact +91-9014935156 for fee payments info or EMI options or Payment via Credit Card or Payment using PDC (Post Dated Cheque).