Chromatin Architecture in Human Disease: Implications for Precision Medicine and Future Gene Therapy Strategies

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Abstract

Researchers would be able to produce an accurate picture of chromatin in disease by combining reported results with new measurements using existing databases. Data mining and the development of new databases will have an effect on how we address chromatin questions in the coming years. The QCBio Collaboratory at UCLA is a unique forum for non-programmers looking for training and collaboration to solve biological problems. Many bioinformatics tools are already available, and more will be developed as new knowledge becomes available. Scientists will continue to be motivated to test the most interesting hypotheses with the right instruments, exposing new insights into cardiac biology. Basic knowledge of how computers work and how to answer problems with big data will continue to inspire scientists to test the most important theories with the right tools, revealing novel insights into cardiac biology.

Heart disease continues to be one of the leading causes of death [1]. The syndrome is described by a dysregulated cardiac myocyte transcriptome, which mimics certain features of a developmentally primitive myocyte [2]. Latest studies have looked at improvements in chromatin organization following cardiac insult to discover pathways behind the transcriptional disarray seen in heart failure. In biology, structure dictates function, so it's useful to think about the different levels of epigenome structural regulation: chemical modifications to DNA sequence; posttranslational modification of histone octamers that make up nucleosomes; accessibility of chromatin fibers made up of DNA wrapped around nucleosomes, chromatin structural proteins, and modifiers; and chromatin compartmentalization [3]. The genome-wide existence of chromatin structural features—that is, chromatin reorganization happens seemingly concurrently (from a developmental or disease perspective) at several distinct locations around the genome—is a recurring finding in the study of gene regulation. Genome-wide high-throughput sequencing-based techniques, which are now commonly available, are needed for precise calculation of the loci where these changes occur. However, these technological advancements have resulted in an influx of vast databases, the biological significance of which can only be deciphered by near cooperation with computer scientists and computational biologists as equal collaborators in the experimental design and data analysis stages of study. Investigations into gene control in the heart.

Initial studies in transcriptomics lay the groundwork for how we learn about gene control in the heart: we now know that pathological perturbation causes thousands of genes to undergo transcriptional changes. Each dataset presented its own set of problems, requiring some ingenuity to make sense of the large data tables that remained inert before a scientist posed a query and tested a hypothesis. In 2009, one lab used array-based techniques to uncover an RNA expression model in which transcription of differentially expressed microRNAs with heart failure normalizes after mechanical unloading, but transcription of differentially expressed mRNAs does not, implying a separate regulatory rubric for non-protein coding RNA species in cardiac disease [4]. These results were critical in propelling cardiac gene regulation research forward; however, they were focused on array-based evidence. Early open source statistical methods for determining differentially expressed genes were developed for microarrays [5] and fine-tuned for RNA-seq approaches to analyze both existing and novel transcripts [6,7,8,9], with essential considerations for multiple testing correction [10, 11]. To that end, the same lab published an RNA-seq analysis in 2010 [12] that used these methods to elucidate transcriptional modifications in a murine Gq transgenic model that causes cardiac pathology.

Notably, low-abundance transcripts were found in this RNA-seq assay that were not detected in a side-by-side microarray analysis of the same samples [12]. Another group used mRNA and microRNA deep sequencing experiments in mice in 2012 to discover that increased PI3K signaling during cardiac hypertrophy is regulated by a reduction in TGF-signaling and miR-21 expression, which results in less fibrosis [13]. The same group then conducted deep mRNA and microRNA sequencing studies in human hearts in early 2014 to figure out how noncoding RNA signatures distinguish failing from nonfailing hearts [14]. Long noncoding RNAs (lncRNAs) are a subset of differentially expressed RNAs in heart failure patients whose expression recovers after mechanical unloading, indicating that noncoding RNA can play a role in shaping the regulatory rationale for disease gene expression regimes [14]. The question of how these transcripts were controlled during disease from a chromatin structural perspective continued during these investigations, and measurements were already being taken.

The Heart's Chromatin as a Goal

Early research on histone deacetylase (HDAC) inhibition resulted in FDA-approved therapies [15], and their use in the heart seems encouraging [16]. However, little is understood about where individual HDAC isoforms are located in the genome and whether this changes during disease progression. Histone marks, on the other hand, have been studied by a number of laboratories (reviewed in [3] and examples described in the next section). Nonetheless, trials looking at phenotypic results appear to show that there is a case to be made for not only casting a broader net to find other chromatin players in heart failure and improving therapeutic modulators of chromatin structure, but also for looking at how chromatin is damaged in disease. Big data and statistical interrogation of datasets are critical for developing a mechanistic interpretation of pathological cardiovascular processes by calculating global chromatin features.

Based on how entrenched chromatin features are before disease, various combinations of chromatin features lead to gene regulation in different ways. For example, atrial fibrillation is linked to mutations in a noncoding area near the human PITX2 locus [17], and chromatin interference between an enhancer from an orthologous region and the mouse Pitx2c promoter was discovered in a 2019 study [18]. Disrupting this relationship by removing the enhancer—or by disrupting an isolated binding site for the chromatin structural protein CTCF within Pitx2c—increases the risk of atrial fibrillation [18]. As a result, we may hypothesize that various degrees of chromatin organization lead to cardiac disease in different ways, with

differing temporal and/or pathological consequences. As a result, we want to understand how and the degree of chromatin organization fits into the framework of global cardiac gene control, with the ultimate goal of developing improved heart failure therapies.

The Cardiac Chromatin Field Advances With New Genomic Tools

When assessed with genomics methods, each stage of chromatin organization shows a vast amount of biological detail. As a result, early research looked at single datasets from a single form of epigenomic assay (for example, ChIP-seq for a certain protein or histone mark) to draw conclusions regarding chromatin in the core. The study of DNA methylation shed light on gene control of failing hearts early on. One group observed DNA methylation dynamics in the promoters of upregulated, but not downregulated, genes in failing human hearts using a methylated DNA immunoprecipitation strategy followed by deep sequencing in 2011 [19]. Our lab investigated DNA methylation dynamics in mouse strains susceptible or immune to isoproterenol-induced heart failure in 2016 and discovered strain-specific methylation trends in the basal, unstressed heart, which predicted the cardiac phenotype after adrenergic stress [20]. These studies condensed massive datasets containing millions of DNA methylation measurements to show that the DNA methylome (in addition to genetic sequence) plays a role in deciding susceptibility to heart failure, and thus provided a basis for investigating DNA methylation modulation as a treatment for heart failure. In 2018, a group found that chemical inhibition of DNA methyltransferases reduces the cardiac hypertrophy caused by pressure overload in mice, implying that global chromatin treatment could be used to treat heart failure, despite the fact that this particular chromatin perturbation did not result in widespread improvements in DNA methylation [21].

Individual studies of polymerase, histone symbol, and transcription factor occupancy in the genome yielded little insight into how transcription in diseased hearts becomes dysregulated after a pathological trigger. RNA polymerase II undergoes transcriptional pause release at a subset of housekeeping genes, and is modulated by pressure overload hypertrophy or de novo recruitment at "specialized genes," according to a 2013 report [22]. After demonstrating that antisense oligo-mediated inhibition of TFIIB transcripts resulted in abolished transcription of cardiac disease genes after pressure overload in a 2015 follow-up analysis from the same lab, TFIIB (a member of the preinitiation complex) was identified as a potential therapeutic target in heart failure [23]. No one has tried this tactic to inhibit heart disease genes from being transcribed yet, but it may be helpful in future research.

H3K27ac (histone 3 lysine 27 acetylation) occupies enhancers in health and disease, according to a 2013 study of cardiac histone marks—post-translational changes that impair nucleosome accessibility. Another research published in 2015 found that when mice are given the HDAC inhibitor trichostatin A, pressure overload-induced H3K9/K14 acetylation is prevented, implying that global chromatin therapy modulates transcriptional readouts to alleviate cardiac pathology [25]. These studies provided a basis for examining regulatory regions in the form of transcription factor binding in cardiac cells and for examining chromatin accessibility—a direct readout of the probability of transcription factor binding—in the heart in both control and pressure overloaded murine hearts.

Cardiovascular transcription factors are difficult to isolate from chromatin, but they can reveal which cardiac enhancers are active at a given developmental or pathological point. Using biotinylated cardiac transcription factor constructs in the HL1 cardiomyocyte cell line and streptavidin-based pulldowns followed by deep sequencing, a cardiac gene regulation lab overcame this barrier in 2011 [26]. This method established a group of active enhancers inhabited by several transcription factors that are not associated with the enhancer-associated protein p300, a newly discovered class of cardiac enhancers [26]. In 2014, the same lab used streptavidin to take down biotinylated GATA4 from mouse hearts, establishing an in vivo knock-in dependent process [27]. This methodology, which was based on their 2011 research, discovered distinct GATA4 binding sites found only in pressure overload hearts—in addition to GATA4 sites found in both banded and developing hearts—and may provide insight into the logic for transcription factor-based pathological gene activation during heart failure [27]. The team used this in vivo biotinylated factor strategy to test occupancy of seven cardiac transcription factors in murine hearts in 2019, and the results indicated that a subset of enhancers co-occupied by multiple cardiac transcription factors that do not have H3K27ac binding (a predictor of active enhancers) exists [28]. Furthermore, this study found that multi-factor bound enhancers had more chromatin accessibility than single-factor bound enhancers, implying that multi-factor bound regions are more likely to be functional in the heart [28]. This lab has faced scientific and philosophical obstacles to investigating abnormal gene expression in the heart as a whole. The team not only devised a novel approach for immunoprecipitating cardiac transcription factors, but they also created in vivo models and incorporated complex datasets downstream of difficult analytical pipelines, allowing the field to accept the challenge of gene regulatory programs during pathology for the first time. To make sense of what is going

on at different levels of chromatin organization in a given disease model, chromatin studies are increasingly integrating several datasets, similar to the example described above.

Integrating Datasets: As Data Becomes Larger, Biological Insights Become More Relevant.

Understanding individual components of chromatin organization in cardiac cells requires a piecemeal approach. However, research has recently benefited from the convergence of a number of large datasets to more powerfully explain the global picture of chromatin organization. The statistical determination of which data points are essential for biological inference is a problem in epigenomics, not the number of data points in a dataset. A ChIP-seq experiment, for example, necessitates the simple processing of millions of reads in order to assess the occupancy of an immunoprecipitated element at thousands of loci. Although a machine can easily quantify this, a mathematical determination of large differences in occupancy necessitates biological replicates and clever methods for processing thousands of data points and performing statistical experiments in a fair amount of time. The difficulty of an experiment needs increasing statistical sophistication to combine datasets so several variables may be immunoprecipitated during a single investigation, including at multiple time points. Furthermore, as orthogonal trials are incorporated into the workflow, data processing gets much more complicated.

In the sense of heart disease, measuring chromatin architecture, as well as other chromatin structure properties, is a more detailed method of examining the complex nucleus during heart failure, especially when used in conjunction with a pathological stimuli that disrupts global chromatin architecture as a positive control for genomic disorganization. In 2017, we demonstrated that pressure overload disrupts chromatin structure in mice, as calculated by high throughput chromatin conformation capture (Hi-C), as well as in a cardiac-specific CTCF depletion model [29]. In the healthy cardiac myocyte, the chromatin structural protein CTCF is essential for mediating stable interaction landscapes: our research found that CTCF depletion had a minor overall impact on genome structure, but was enough to cause pathologic gene activation and heart failure [29]. This research necessitated the development of massive chromatin interaction matrices containing millions of data points, as well as the application of statistical techniques to establish which data points represented true structural features. The findings enabled researchers to determine the regions of the genome physically interact with one another in the three-dimensional sense of the nucleus, which is crucial for understanding gene regulation in living cells. This data was then combined with gene expression and protein

binding data, enabling us to distill billions of measurements into a manageable collection of biologically relevant findings. This heart failure phenotype was replicated using similar molecular methods but a different CTCF depletion technique [30], as were some of the findings regarding improvements in chromatin structure throughout pressure overload.

A Hi-C and DNA methylation analysis published in 2017 found that the nucleus compartmentalizes into active and inactive structural compartments during differentiation, while DNA methylation patterns take longer to form and are formed steadily during development [31]. A 2017 study found two groups of enhancers in three fetal human cardiac cell types and their induced pluripotent cell equivalents, one with H3K4me1 and H3K4me3 deposition in all cell types and the other with cell-specific histone symbol deposition [32]. Since most genetic variation associated with disease in humans exists in non-coding regions and hence may be regulatory in nature, this research may be useful in researching chromatin interactions between distal regulatory regions and gene promoters in the future. One lab reported a 2018 promoter capture Hi-C experiment that demonstrates physical interaction with 2000 disease-related SNPs to hundreds of genes along the genome of human-induced pluripotent stem cell-derived cardiac myocytes [33] to better understand single-nucleotide polymorphisms (SNPs) associated with cardiovascular disease, which are normally localized to non-coding areas. The combination of chromatin structural data with SNP data revealed that the majority of SNP-gene interactions (more than 90%) do not occur with the gene that is nearest to a given SNP [33].

3D chromatin simulation with Hi-C contacts [34], which uses mathematical learning methods to refine 3D positioning of pairwise contacts, is a groundbreaking approach to recovering endogenous structural information from epigenomic studies. Beyond the 2D maps provided by conventional Hi-C studies, this technique contextualizes pairwise interactions into a 3D reconstruction of genomic structure, which can provide clues about chromatin structural control. We collaborated with the Alber lab in 2018 to create 3D models from cardiac myocytes and liver cells, demonstrating distinct chromatin structural strategies that underpin organ-specific gene expression patterns [35]. This form of modeling is useful because it uses pairwise touch data from a population of cells to simulate thousands of structures that will possibly exist inside single cells, and then predicts how chromatin is arranged in a cell population using statistical techniques. To better explain the chromatin structural logic underlying organ-specific transcription, we looked at the relative radial location of cardiac and liver-specific genes inside

the nucleus, as well as interchromosomal chromatin interactions [35]. This method can be readily extended to other organ systems and helps drive hypothesis generation in cardiac biology. Down-regulated genes, for example, can be moved to the nuclear periphery or heterochromatin centers during pathology (as seen in microscopy studies [36]), regions associated with inactivation. Having access to a 3D model of the whole genome allows for direct testing of this phenomenon across all genomes, which is currently difficult to do through microscopy methods.

Cardiac Chromatin Machine Learning

Every year, countless developments and algorithmic advances are made in the field of machine learning. The use of computational mathematics to perform three types of tasks with limited human interference: supervised, unsupervised, and reinforcement learning [37] is a significant advantage of machine learning over manual statistical approaches. In supervised learning, input vectors and their outcomes from a training dataset are applied to new input data to perform classification or regression techniques [37]. For example, using a model developed from clinical data and results from thousands of prior patients, a clinical data vector may be used to determine when a new patient will develop heart failure. Pattern detection can be achieved using unsupervised learning by clustering, density estimation, and/or dimensionality reduction [37]. By using unsupervised clustering methods on datasets from stable and ill individuals, trends suggestive of a pathological condition may be mathematically untangled from a sequence of epigenomic or other broad datasets. Reinforcement learning optimizes an outcome without understanding what it might appear like a priori by using a positive and negative reinforcement scheme [37]. An algorithm learning to beat a master chess player is an example of this.

Some of the most cutting-edge cardiac machine learning research is being conducted using an electrocardiogram, a scientific measurement that cardiologists use on a regular basis (ECG). Using single-lead ECGs from over 53,000 patients, a 2019 study used a deep learning method to identify 12 subsets of cardiac rhythm [38]. The incredible result was that their classifier's F1 value, which measures precision and recall, was higher than the one measured using annotations from board certified cardiologists [38]. This research was notable for its large patient intake, which made for a sufficient training cohort and a separate evaluation cohort. Overall, this machine learning technique could have an effect in the clinic by assisting

healthcare clinicians in prioritizing some types of arrhythmias over others or identifying potentially life-threatening arrhythmias quicker than existing technology.

Until submitting manuscripts to publishers, computational authors also post their findings on preprint repositories, which are online indexes of unfinished research. This allows the public to analyze studies alongside reviewers. OSF, arXiv, bioRxiv, medRxiv, and ChemRxiv, for example, are useful for disseminating experimental study and igniting scientific debate in their respective fields. While the benefits of preprint servers, uploaded manuscripts should be treated with caution because preprints have not yet been evaluated by expert reviewers (as discussed in the cardiovascular context in [39]), even though online discussion of cutting-edge work has sped up the incorporation of new datasets into experimental workflows and fostered more open communication amongst researchers.

A study outlines a mathematical model to estimate biological age using DNA methylation status of cytosines across the genome [40], which is an indicator of the usefulness of machine learning in chromatin. This research discovered that in cancer, "DNA methylation age," or biological age as expected by epigenomic features from the model, accelerates [40]. In other words, in cancer samples, the estimated DNA methylation age is slightly older than the real chronological age [40]. Despite the fact that the original model did not test cardiac theories, a follow-up analysis from 2016 found no connection between epigenetic age and coronary heart disease incidence [41], indicating that coronary heart disease could have other epigenetic markers that predict disease incidence that are independent of DNA methylation-based epigenetic age. Horvath refined his epigenetic aging models in 2019 using evidence from the Framingham Heart Study [42] to estimate lifespan (a device called GrimAge) and age acceleration (AgeAccelGrim), as well as seven DNA methylation-based surrogate biomarkers including smoking pack years [43]. Predicted age acceleration and multiple proxy biomarkers, including nicotine pack years, are predictive of time-to-coronary heart disease in a validation dataset made up of diverse patient cohorts [43], demonstrating the power of statistical learning in assessing cardiovascular health. A 2018 study of genotype and cytosine methylation to predict the 5-year occurrence of coronary heart disease [44] shed light on machine learning's diagnostic potential in the cardiac field.The authors used a random forest method to discover 4 genetic loci and 4 cytosines whose genotype and methylation status together predict coronary heart disease [44]. A random forest approach (a challenge that uses multiple decision trees to refine a selection of candidate predictors that do not actually need to have a linear relationship

[45]) was used in this study. While the model performs well on a broad sample size, it depends on published data [44]. The training and evaluation datasets for this retrospective analysis consisted of 1180 and 524 individuals, respectively. A more powerful potential solution will be to do a longitudinal trial in which thousands of patients are enrolled and their genotype and DNA methylation status are measured to see how this technique can be used to forecast outcomes.

Machine learning strategies require adequate sample size to conduct model training and subsequent processing, which is an elephant in the room in computational biology. Due to overfitting, low n results in bad model output on new datasets. The experiments described above used thousands of patients in their laboratory workflow; but, in fundamental science, this is not always possible. Despite this, during a single sequencing experiment in the cardiac chromatin region, millions of measurements can be made in thousands of cells, and these cells could make up a large enough n to generate training and test datasets for machine learning applications.

During cardiac genomics research, cellular variation in the heart is now being quantitatively deciphered. Adult cardiac myocytes and endothelial cells do not return to a "fetal-like" transcriptional program after myocardial infarction, but fibroblasts and leukocytes do [46]. In 2017, one group used RNA-seq on four FACS-sorted cell types from stable and infarcted hearts and discovered that adult cardiac myocytes and endothelial cells do not revert to a "fetal-like" transcriptional program after my This study looked at cell type heterogeneity in the heart by looking at a sorted, pre-defined subset of cell types, but other cell types, as well as any assessment of cell-to-cell variability, were left out. To counter this, single-cell sequencing methods use sophisticated dimensionality reduction and statistical classification strategies to gain insights into cellular diversity in the heart, though they are not machine learning per se. In 2017, a single-cell RNA-seq experiment from mouse and human left ventricles revealed that heart failure affects various subpopulations of cardiac myocytes, and that long intergenic noncoding RNAs can play a role in the regulatory landscape engendered by pathological processes [47]. For dimensionality reduction, this method used weighted gene correlation network analysis [48] and standard principal component analysis [47]. Since it shows the degree of differential gene expression within a cell type within an individual, a single-cell approach has advantages over bulk sequencing techniques. t-SNE, or t-distributed stochastic neighbor embedding, is a relatively recent machine learning technique that is gaining traction

in the genomics realm to aid in this decision [49]. This nonlinear dimensionality reduction method reduces high-dimensional data to two dimensions, which is useful for data analysis in a variety of fields. The technique's benefit is that it allows for two-dimensional visualization of sample clusters, which means it may be used to visually tease out a transcriptional action inside a subpopulation of cells [50]. In 2018, t-SNE was used as part of a bioinformatics toolkit to identify cytoskeleton-associated protein 4 as a previously unknown activated fibroblast marker in a single-cell RNA-seq analysis in mice [51]. For single-cell experiments, UMAP, or Uniform Manifold Approximation and Projection, is a more effective dimensionality reduction technique since it outperforms t-SNE for larger datasets while maintaining global dataset structure, enabling visual contrast between clusters on a lower dimensional space [52]. UMAP was used in a 2019 analysis to minimize the dimensionality of a single-cell RNA-seq assay measuring dissected cardiogenic regions from three stages of mouse embryonic development with the aim of better understanding mesodermal and neural crest cell subpopulation structures over time [53]. Notably, t-SNE and UMAP can be conveniently applied to transcriptomic data using a number of software tools, including modified versions of Monocle [54], CellRanger [55], and Seurat [56, 57], both of which allow single-cell data analysis available to both dry lab novices and experts. These, as well as other useful computational biology methods, are discussed in.In 2019, one lab used single-cell RNA-seq, ATAC-seq (a high-throughput sequencing measure of chromatin accessibility in the heart), and ChIP-seq of three transcription factors to create a machine learning model that predicts which transcription factors are essential for early fibroblast reprogramming into cardiac myocytes [63]. Another group published single-cell RNA-seq on CD45+ cells from sham and pressure overloaded mouse hearts in 2019 and gained a new understanding of the variety of immune cell types that become triggered during heart disease; it was even more than previously believed [64]. In 2020, a single-nucleus RNA-seq analysis of nearly 300,000 nuclei revealed variations in transcriptional programs between chambers and sexes in the human heart [65]. Another analysis of single-cell and single-nucleus RNA-seq results from the adult human heart showed 5 distinct subpopulations of ventricular and atrial cardiac myocytes, as well as subpopulations of fibroblasts, immune cells, and vascular cells [66]. A single-nucleus and single-cell RNA-seq analysis of fetal gene expression in human fetal tissues (including the heart) discovered 77 cell types, 54 of which are found in only one organ [67]. In addition to traditional cell type markers, this study used unbiased statistical approaches to classify novel cell type markers, which will enable future research into the biological functions of these cells [67]. Importantly, considering the variety of cell types in human cardiac biology, these datasets can be used to further understand the

field of druggable targets. Taken together, single-cell sequencing methods have provided enough evidence for machine learning applications, and research into single cells following pathological stimuli will continue to expose the degree to which gene regulatory environments in different cell types cooperate or compete during disease.

Conclusions and Suggestions for the Future

Using existing databases to combine published data with new measurements will aid researchers in creating a more detailed image of chromatin in disease. The aim of computational biology is to integrate epigenomic datasets in near real time, regardless of the lab where they were collected—similar to a blood pressure, ECG, or troponin examination. Furthermore, epigenome modeling must become complex, accounting for cell-to-cell heterogeneity as well as changes over time caused by natural physiological growth or pathologic stimuli. Probabilistic modeling and deep learning can help with model development while also finding (and quantifying) previously unrecognized emergent properties in chromatin that correlate to cardiac health improvements. A 3D representation of the genome, for example, can show a structural or accessibility function associated with health or disease that can not be characterized solely by epigenomic measurements. Such methods have the potential to advance both biological biology and our understanding of disease.

To promote the creation of more varied professional repertoires, we support incorporating wet and dry lab testing components into training regimens. In the coming years, data mining and the development of new datasets will affect how we answer chromatin questions. Understanding how machines approach problems (in a different way than humans) and how to frame queries computationally can help to provide a common language that will help to complete tasks. Members of the team may not need to be experts in big data, but a collaborative framework is essential for large-scale epigenomic studies to succeed. The QCBio Collaboratory at UCLA is a standout platform for non-programmers seeking training and cooperation to address biological questions [68, 165-191]. Furthermore, the Collaboratory promotes the use of open source resources, which enable lay scientists to access genomics datasets. Many bioinformatics resources now exist and more will be built as new information emerges but basic understanding about how machines function and how to address questions using big data will continue to motivate scientists to test the most important theories with the right tools, revealing novel insights into cardiac biology gene therapy targets.

References

1. Abdelhamid, H. N., M. Dowaidar, M. Hällbrink, and Ü. Langel. 2019. Cell Penetrating Peptides-Hierarchical Porous Zeolitic Imidazolate Frameworks Nanoparticles: An Efficient Gene Delivery Platform. SSRN Electron. J. https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3435895.
2. Abdelhamid, Hani Nasser, Moataz Dowaidar, Mattias Hällbrink, and Ülo Langel. 2020. Gene Delivery Using Cell Penetrating Peptides-Zeolitic Imidazolate Frameworks. Microporous and Mesoporous Materials: The Official Journal of the International Zeolite Association 300 (June): 110173. https://doi.org/10.1016/j.micromeso.2020.110173.
3. Abdelhamid, Hani Nasser, Moataz Dowaidar, and Ülo Langel. 2020. Carbonized Chitosan Encapsulated Hierarchical Porous Zeolitic Imidazolate Frameworks Nanoparticles for Gene Delivery. Microporous and Mesoporous Materials: The Official Journal of the International Zeolite Association 302 (August): 110200. https://doi.org/10.1016/j.micromeso.2020.110200.
4. Ahmad, Almeman, Khalaf Hassan, Rasool Semaab, Moataz Dowaidar, and Al Orainy Mohammad. 2013. The Impact of CYP2C19 Polymorphism on Platelet Reactivity for Guiding Clopidogrel Treatment and Cost Analysis. Journal of the Saudi Heart Association 25 (2): 107. https://doi.org/10.1016/j.jsha.2013.03.005.
5. Algahsham, Abdullah, Ahmad A. A. Settin, Ahmad Ali, and Hisham Ismail. n.d. Association of MTHFR C677T and A1298C Polymorphisms with Hypertension among Saudi Subjects from Qassim Region. International Journal of Health Sciences 6 (1). Accessed June 18, 2021. http://ijhs.org.sa/index.php/journal/article/view/312.
6. Algasham, Abdullah, Hisham Ismail, Moataz Dowaidar, and Ahmad A. Settin. 2011. Methylenetetrahydrofolate Reductase (MTHFR) and Angiotensin Converting Enzyme (ACE) Gene Polymorphisms among Saudi Population from Qassim Region. International Journal of Health Sciences 5 (2 Suppl 1): 3–4. https://www.ncbi.nlm.nih.gov/pubmed/23284552.
7. Alghasham, Abdullah, Ahmad Ali, Hisham Ismail, Moataz Dowaidar, and Ahmad A. Settin. 2012. CYP2J2 -50 G/T and ADRB2 G46A Gene Polymorphisms in Saudi Subjects with Hypertension. Genetic Testing and Molecular Biomarkers 16 (9): 1027–31. https://doi.org/10.1089/gtmb.2012.0006.
8. Alghasham, Abdullah, Ahmad A. Settin, Ahmad Ali, Moataz Dowaidar, and Hisham Ismail. 2012a. Association of MTHFR C677T and A1298C Gene Polymorphisms with Hypertension. International Journal of Health Sciences 6 (1): 3–11. https://doi.org/10.12816/0005968.
9. Moataz Dowaidar. 2012b. Association of MTHFR C677T and A1298C Gene Polymorphisms with Hypertension. International Journal of Health Sciences 6 (1): 3–11. https://doi.org/10.12816/0005968.
10. Ali, Ahmad, Abdullah Alghasham, Hisham Ismail, Moataz Dowaidar, and Ahmad Settin. 2013. ACE I/D and eNOS E298D Gene Polymorphisms in Saudi Subjects with Hypertension. Journal of the Renin-Angiotensin-Aldosterone System: JRAAS 14 (4): 348–53. https://doi.org/10.1177/1470320312459976.
11. Ali, Ahmed A. A., Nahla M. Wassim, Moataz M. Dowaidar, and Ahmed E. Yaseen. 2013. Genetic Polymorphism of CYP2D6 Gene among Egyptian Hypertensive Cases. The Journal of Basic & Applied Zoology 66 (4): 228–33. https://doi.org/10.1016/j.jobaz.2012.12.002.
12. Ali, Ahmed A. A., Nahla M. Wassim, Moataz Dowaidar, and Ahmed E. Yaseen. 2013b. Association of eNOS (E298D) and CYP2J2 (−50G/T) Gene Polymorphisms with Hypertension among Egyptian Cases. The Journal of Basic & Applied Zoology 66 (4): 234–41. https://doi.org/10.1016/j.jobaz.2012.12.001.
13. Moataz Dowaidar. 2013. Association of eNOS (E298D) and CYP2J2 (−50G/T) Gene Polymorphisms with Hypertension among Egyptian Cases. The Journal of Basic & Applied Zoology 66 (4): 234–41. https://doi.org/10.1016/j.jobaz.2012.12.001.
14. Aljarallah, Badr, Ahmed Ali, Moataz Dowaidar, and Ahmad Settin. 2011. Prevalence of α-1-Antitrypsin Gene Mutations in Saudi Arabia. Saudi Journal of Gastroenterology: Official Journal of the Saudi Gastroenterology Association 17 (4): 256–60. https://doi.org/10.4103/1319-3767.82580.
15. Dowaidar, M., J. Regberg, D. A. Dobchev, and T. Lehto. 2017. Refinement of a Quantitative Structure–activity Relationship Model for Prediction of Cell-Penetrating Peptide Based Transfection Systems. International Journal of. https://link.springer.com/content/pdf/10.1007/s10989-016-9542-8.pdf.
16. Dowaidar, Moataz. 2017. In-Silico Design of Peptide-Based Transfection Systems, in-Vitro Validation, and up-Take Pathways Investigation. Department of Neurochemistry, Stockholm University.
17. Moataz Dowaidar. 2018. Chimeric Gene Delivery Vectors : Design, Synthesis, and Mechanisms from Transcriptomics Analysis. Department of Biochemistry and Biophysics, Stockholm University. https://www.diva-portal.org/smash/record.jsf?pid=diva2:1242000.
18. Moataz Dowaidar. Cardiometabolic Conditions Could Be Related to Vitamin D Deficiency. The Genetic Determinants That Affect Vitamin D Pathways May Be Solved with Nanomedicines. https://doi.org/10.31219/osf.io/nqewr.
19. Moataz Dowaidar. Different Insulin Resistance and Inflammation Pathways Are Influenced by Genetic Factors in Metabolic Syndrome. Gene Therapy Enables Early Recognition and Treatment of the Genetic Factors. https://doi.org/10.31219/osf.io/gqwj2.

20. Moataz Dowaidar. Gene Therapy Has Been Shown to Be Valuable for Understanding Complex Disease Pathophysiologies. The Medical Profession as a Whole Will Have to Invest in Specialized Investigations. https://doi.org/10.31219/osf.io/8fg9y.
21. Moataz Dowaidar. Genetic and Epigenetic Discoveries Hold Promising Avenues in Cardiovascular Prevention and Management (CVDs). Key Nucleic Acids Are Being Researched and Developed for Medicinal Use. https://doi.org/10.31219/osf.io/hk7pe.
22. Moataz Dowaidar. Genome Editing Can Now Be Carried out in an Isogenic Setting. It Can Be Effectively Transmitted to Somatic Tissues in Mice, but Not to Humans. Despite These Doubts, CRIS Has Great Potential as a Medical Promise. https://doi.org/10.31219/osf.io/4rn3v.
23. Moataz Dowaidar. Genome-Wide Association Experiments Have Uncovered a Slew of Cardiometabolic Trait-Associated Variants. This Information Can Be Useful in the Implementation of New Diagnostic and Treatment Strategies. https://doi.org/10.31219/osf.io/4vws8.
24. Moataz Dowaidar. Genome-Wide Association Studies (GWAS) Have Revolutionized Our View of Human Health and Disease Genetics and Offered Novel Gene Therapy Targets. https://doi.org/10.31219/osf.io/rvm3z.
25. Moataz Dowaidar. Metabolic Syndrome_ the Presence of Inflammatory Mechanisms in Abdominal Obesity Is Undeniable, Gene Therapy Using Nanoparticles and Adenoviruses Technologies Is Promising. https://doi.org/10.31219/osf.io/2j5xt.
26. Moataz Dowaidar. miRNAs May Be Used as Preventive Agents for Metabolic Diseases in the near Future. Understanding the Interplay between pro-Adipogenic_ and Anti-Ad Pipogenic miRNA' Could Lead to New Biomarkers. https://doi.org/10.31219/osf.io/3dr8c.
27. Moataz Dowaidar. Nanomedicine Has Elegantly Attempted to Cure Multiple Gene Polymorphisms and Mutations in Cardiovascular Diseases Using Gene Therapy Techniques. https://doi.org/10.31219/osf.io/d3x8g.
28. Moataz Dowaidar. Thrombosis Pathways and Therapeutic Strategies. https://doi.org/10.31219/osf.io/57vyz.
29. Moataz Dowaidar. What Genomic Research Has Told Us about the Obesity and Its Possible Gene Therapy Targets. https://doi.org/10.31219/osf.io/ym49s.
30. Moataz Dowaidar. Exosomes Can Make the Use of Circulating miRNA as a Biomarker More Feasible. The Aim of Gene Therapy Should Be to Learn Everything There Is to Know about miRNA Activity. https://doi.org/10.31219/osf.io/edkua.
31. Moataz Dowaidar. Anti-Sense Pathways Have Been Generated Using siRNA. The Liver and Other Often Used Organs Will Now Be Targeted. https://doi.org/10.31219/osf.io/m6xvp.
32. Moataz Dowaidar. CrisPR/CRIS Systems Are Highly Effective and Useful for Genomic Manipulation. Despite This, Cardiac Treatment Remains Difficult due to Existing Genome Editing and Delivery Processes. https://doi.org/10.31219/osf.io/3nwzd.
33. Moataz Dowaidar. Discoveries in Gene-Environment Interactions That Influence CVD, Lipid Traits, Obesity, Diabetes, and Hypertension Appear to Be Able to Influence Gene Therapy. https://doi.org/10.31219/osf.io/cr5af.
34. Moataz Dowaidar. Genome Editing's Potential Target Diseases in the Cardiovascular Field. https://doi.org/10.31219/osf.io/gc23p.
35. Moataz Dowaidar. Key Genetic Factors in the Metabolic Syndrome Predisposition Which May Be a Therapeutic Options by Gene Therapy. https://doi.org/10.31219/osf.io/f38sk.
36. Moataz Dowaidar. miRNA Can Be a Part of Both the Onset and Cure of Coronary Heart Disease. https://doi.org/10.31219/osf.io/teqh8.
37. Moataz Dowaidar. Preclinical Studies and Clinical Trials Have Sparked Interest in Certain Biological Medications for Atherosclerotic Coronary Heart Disease. https://doi.org/10.31219/osf.io/ts8mh.
38. Moataz Dowaidar. Researchers Would Be Able to Develop a Detailed Picture of Chromatin in Disease, Which Would Be Useful for Gene Therapy. https://doi.org/10.31219/osf.io/m9z48.
39. Moataz Dowaidar. The Cardiometabolic-Based Chronic Disease Model Lays the Foundations for Accurate, Evidence-Based Preventive Targeting and Gene Therapy. https://doi.org/10.31219/osf.io/up9z4.
40. Moataz Dowaidar. 2D MOFs Have Unique Features for Biological Applications. They Can Be Utilized for Gene Therapy, Bioimaging, Biosensing, Photodynamic Therapy, and Tissue Engineering. https://doi.org/10.31219/osf.io/4q9ct.
41. Moataz Dowaidar. 3D Bioprinting for Enhanced Vascularization, and Gene Editing to Provide a More Favorable Immunological Response Are Just Some of the Potential Uses of Carbon Materials. https://doi.org/10.31219/osf.io/v2xy8.
42. Moataz Dowaidar. Anderson–Fabry Disease Can Be a Target for Gene Therapy. https://doi.org/10.31219/osf.io/tcgka.
43. Moataz Dowaidar. Antisense Oligonucleotides (ASOs) and CRISPR Systems Are Promising Gene Therapy Treatments for Alzheimer's Disease. https://doi.org/10.31219/osf.io/ws796.
44. Moataz Dowaidar. Any Alteration in PPAR Genomic Sequence, Splicing Pattern, or PTM Is Likely to Cause Major Alterations in Its Function. In Personalized Medicine, Such Data Becomes More Significant in Gene Therapy Design. https://doi.org/10.31219/osf.io/y8n79.

45. Moataz Dowaidar. Applying Genome-Wide Association Technology to Brain Diseases Enables the Discovery of lncRNas Targets for Gene Therapy. https://doi.org/10.31219/osf.io/hm4eu.
46. Moataz Dowaidar. Autophagy and Proteostasis Adjustment Role in Normal Brain Function and Neurodegenerative Disorders. https://doi.org/10.31219/osf.io/m4yra.
47. Moataz Dowaidar. Basal Ganglia-Cerebellar and Brainstem-Cerebellar Circuits May Interact Improperly with Dystonia. Linking Network Disruptions to Cell Failure Will Enable Understanding Pathophysiology and Designing Gene Therapy Methods. https://doi.org/10.31219/osf.io/8w35s.
48. Moataz Dowaidar. Blood Products Are Used to Treat a Multitude of Diseases, so the Blood Transfusion System Needs to Be Enhanced. CRISPR/Cas9 Has Made It Viable to Make HLA Class I-Deleted Blood Products to Avoid Rejection. https://doi.org/10.31219/osf.io/egr3n.
49. Moataz Dowaidar. Calixarenes (CAs) Are Promising in Biomedicine, Biosensing, Bioimaging and Gene Delivery Systems. https://doi.org/10.31219/osf.io/n9vjy.
50. Moataz Dowaidar. CAR T Cell Research Has Quickly Advanced from the Bench to the Clinic and Back. The Results of the Trials Have Revealed New Mechanisms. https://doi.org/10.31219/osf.io/f9wm7.
51. Moataz Dowaidar. CAR T-Cell Treatment Remains Clinically Challenging. Therapeutic Strategies May Be Designed to Cut off Immunotherapy Utilizing Safety Switches. https://doi.org/10.31219/osf.io/s7x4y.
52. Moataz Dowaidar. Central Nervous System Gene Therapy Has Entered a New Development Paradigm. New Techniques Are Being Employed for a Wide Range of Illness Indications and Pathways. https://doi.org/10.31219/osf.io/j49wz.
53. Moataz Dowaidar. Chronic Obstructive Pulmonary Condition (COPD) Is a Prevalent, Preventable, and Curable Illness with Persistent Respiratory Symptoms and Airflow Limitation. https://doi.org/10.31219/osf.io/vkdut.
54. Moataz Dowaidar. CircRNAs Have the Potential to Aid in the Diagnosis and Treatment of Lipid Diseases. https://doi.org/10.31219/osf.io/y3hp4.
55. Moataz Dowaidar. Clinical Symptoms, Underlying Pathogenesis, and the Prospect of Tailored Therapies Have All Benefited from Genetic Discoveries in Parkinson's Disease. https://doi.org/10.31219/osf.io/pdzqb.
56. Moataz Dowaidar. Code Distribution of siRNA for Cancer Genes such as p53 and Bcl2 Family Genes Has Demonstrated Efficacy in Killing Cancer Cells. Nanoparticles Can Produce a Surface Where Numerous Drugs May Be Coupled, Allowing Combinatory Treatment. https://doi.org/10.31219/osf.io/hvcse.
57. Moataz Dowaidar. Cognitive Deficiencies Pathophysiology Are Mainly an Unknown Area. Curing the Neurological Conditions Could Be an Objective for Gene Therapy. https://doi.org/10.31219/osf.io/23xf8.
58. Moataz Dowaidar. CRISPR-Based Gene Editing Is Presently Being Tried in Many Clinical Trials. https://doi.org/10.31219/osf.io/qbngx.
59. Moataz Dowaidar. CRISPR–Cas9 Gene Editing as a Tool for Developing Immunotherapy for Cancer. https://doi.org/10.31219/osf.io/dvr4t.
60. Moataz Dowaidar. CRISPR/Cas System Research Has Advanced Significantly in Biological sciences.There Are Still Many Challenges to Effective Delivery before Efficient Gene Editing May Be Achieved. https://doi.org/10.31219/osf.io/mc26v.
61. Moataz Dowaidar. CRISPR/Cas9 Genome Editing Technology Applications in Biological and Biomedical Fields. https://doi.org/10.31219/osf.io/ctqbe.
62. Moataz Dowaidar. Critical Limb Ischemia Potential Gene Therapy Strategies. https://doi.org/10.31219/osf.io/aqcpt.
63. Moataz Dowaidar. Deep Learning Algorithms for scRNAseq Analysis Have Yielded Positive Results, but There Are Still More Promising Ways That Need to Be Developed for Regenerative Medicine. https://doi.org/10.31219/osf.io/dh2pt.
64. Moataz Dowaidar. Depression May Be Epigenetically Controlled by miRNAs Making It a Diagnostic or Gene Therapy Target. https://doi.org/10.31219/osf.io/fw65m.
65. Moataz Dowaidar. Dermatophytes: Role of Host Genetics in the Development of Illness. https://doi.org/10.31219/osf.io/mf3bu.
66. Moataz Dowaidar. Developments in Biomedical Technology Will Increase the Importance of mRNA in Treating Brain Tumors, as Well as Other Malignancies. https://doi.org/10.31219/osf.io/tvj5x.
67. Moataz Dowaidar. Downstream Processing of Virus, Virus-like Particles and Nanoparticulate Inclusion Bodies to Be Used as Gene Delivery Vehicles for Human Gene Therapy Applications. https://doi.org/10.31219/osf.io/exa3q.
68. Moataz Dowaidar. Dravet Syndrome Is a Severe Developmental and Epileptic Encephalopathy. Fenfluramine and Gene Therapy Are Promising. https://doi.org/10.31219/osf.io/zvq8y.
69. Moataz Dowaidar. Exosomes' Function in Cardiovascular Protection and Neovascularization Implies That They Might Be Used to Treat Ischemia and Atherosclerotic Cardiovascular Diseases. https://doi.org/10.31219/osf.io/2h8c7.
70. Moataz Dowaidar. Ferropsis Cell Death Can Cause Complications That May Be Difficult to Detect and Quantify: Autophagy Role and Possible Therapeutics. https://doi.org/10.31219/osf.io/zd2jg.
71. Moataz Dowaidar. Following the Discovery of Anti-MDA5 Ab, the Clinical Understanding of Dermatomyositis Has Been Improved. https://doi.org/10.31219/osf.io/j2t5f.

72. Moataz Dowaidar. For the Treatment of Cystic Fibrosis, RNA Medicines, Gene Transfer Therapies, and Gene Editing Treatments Have Potential. https://doi.org/10.31219/osf.io/6afzm.
73. Moataz Dowaidar. Frontotemporal Dementia Is a Complex Disorder with a Wide Spectrum of Clinical Symptoms. Personalized Medicine and Gene Therapy Are Promising Strategies for Treatment. https://doi.org/10.31219/osf.io/gh4x7.
74. Moataz Dowaidar. G6PD Deficiency Is a Common Genetic Trait That Can Protect Heterozygotes from Dying from Malaria. https://doi.org/10.31219/osf.io/g2kza.
75. Moataz Dowaidar. Gastric Cancer Is the World's Second-Largest Death Cause. Peptides Can Be Used to Deliver Radiation or Other Fatal Chemicals to Tumors. https://doi.org/10.31219/osf.io/eu5mj.
76. Moataz Dowaidar. Gene Doping May Be Possible for Lifestyle Enhancement. https://doi.org/10.31219/osf.io/8xkm5.
77. Moataz Dowaidar. Gene Expression Assays Gather Evidence That They Can Provide Useful Therapeutic Information in Young Women. https://doi.org/10.31219/osf.io/d372s.
78. Moataz Dowaidar. Gene Therapy and Genome-Editing Treatments That Can Protect Patients from Coronary Artery Disease Are under Investigation. https://doi.org/10.31219/osf.io/xqgf8.
79. Moataz Dowaidar. Gene Therapy Approaches for Hemophilia A and B. https://doi.org/10.31219/osf.io/ufc4g.
80. Moataz Dowaidar. Gene Therapy for the Central Nervous System Has Been Initiated. This Expansion Will Require Some Degree of Simplicity in Delivery Processes. https://doi.org/10.31219/osf.io/hdy5q.
81. Moataz Dowaidar. Gene Therapy for the Treatment of Spinal Muscular Atrophy. https://doi.org/10.31219/osf.io/kpz5f.
82. Moataz Dowaidar. Gene Therapy May Benefit Inherited Ichthyoses with Concurrent Fungal Infections and Severe Ich Thyroidoses. https://doi.org/10.31219/osf.io/zxmun.
83. Moataz Dowaidar. Gene Therapy May Target APOE for Alzheimer's Disease. https://doi.org/10.31219/osf.io/3y52k.
84. Moataz Dowaidar. Gene Therapy Promises Accurate, Targeted Administration and Overcoming Drug Resistance in Diverse Cancer Cells. https://doi.org/10.31219/osf.io/j34n6.
85. Moataz Dowaidar. Gene Therapy Targeting FVIII, FIX for Haemophilia Treatment. https://doi.org/10.31219/osf.io/qcbwp.
86. Moataz Dowaidar. Gene Therapy Targeting PRMT5 May Be Useful in Immunotherapy. https://doi.org/10.31219/osf.io/gkw8j.
87. Moataz Dowaidar. Gene Therapy Using Extracellular Vesicles Loaded with miRNA Derived from Bone Marrow Mesenchymal Stem Cells Is a Cell-Free Medication Delivery Method Used in a Variety of Diseases. https://doi.org/10.31219/osf.io/3znvw.
88. Moataz Dowaidar. Genetic Engineered MSCs Are Attractive Possibilities for Regenerative Stem-Cell Therapy to Treat Several Liver Diseases. https://doi.org/10.31219/osf.io/4cfrd.
89. Moataz Dowaidar. Genetic Variants Shared between Alzheimer's Disease and Parkinson's Disease Have Been Discovered in Blood and Brain Samples. Somatic Mosaicism Might Function as an Accelerator. https://doi.org/10.31219/osf.io/tr58n.
90. Moataz Dowaidar. Genome-Wide Association Studies Promise to Discover Novel Indicators of Hypertension. Endothelin-Related SNPs Are Currently in Clinical Trials. https://doi.org/10.31219/osf.io/2n4wa.
91. Moataz Dowaidar. Gingival and Intraventricular Haemorrhages Are Severe Newborn Diseases Causing Damage to White Matter and Neurological Dysfunction in Surviving Newborns Who Can Benefit from Gene Therapy. https://doi.org/10.31219/osf.io/qb84p.
92. Moataz Dowaidar. Glioblastoma Therapeutic Approaches Were Established Utilizing Contemporary Discoveries in Delivering Medicines to the Brain as Smart Nanoparticles for Focused Therapy. https://doi.org/10.31219/osf.io/db4f6.
93. Moataz Dowaidar. Haemophilia Gene Therapy Is in Clinical Studies, Making Continuous Safety and Efficacy Testing a Key Emphasis. https://doi.org/10.31219/osf.io/sa8ny.
94. Moataz Dowaidar. Hematopoietic Stem Cell Transplantation and Gene Therapy Are the Sole Treatments for Sickle Cell Disease and Other Hemoglobinopathies. https://doi.org/10.31219/osf.io/v8xqc.
95. Moataz Dowaidar. Huntington's Disease Gene Therapy and Nanomedicines May Be Available Shortly. https://doi.org/10.31219/osf.io/rxvgd.
96. Moataz Dowaidar. Hybrid Gene Therapy Designed to Fully Understand the Underlying Molecular Cancer Process May Be a Feasible Option. https://doi.org/10.31219/osf.io/ajyfd.
97. Moataz Dowaidar. Hydrogels Are Promising Considering Their Incredible Capacity to Modify, Encapsulate and Co-Deliver Medicinal Compounds, Cells, Biomolecules, and Nanomaterials. https://doi.org/10.31219/osf.io/px3qy.
98. Moataz Dowaidar. Immune Evasion Is Linked to Histone Variation Malfunction. Gene Therapy Could Provide Tools for Targeting Histone Variant Deposition as a Critical Part of Its Pharmacology. https://doi.org/10.31219/osf.io/kjm76.
99. Moataz Dowaidar. Implementing the Human Artificial Chromosome Gene Therapy Platform Remains Challenging, but Continuous Animal Model Research Will Advance the Platform Closer to Clinical Trials. https://doi.org/10.31219/osf.io/a53f7.

100. Moataz Dowaidar. Inflammatory Breast Cancer Remains the Most Aggressive Form of Breast Cancer. A Multimodality Therapeutic Plan Has Shown Improved Survival Results. https://doi.org/10.31219/osf.io/cr935.
101. Moataz Dowaidar. Inherited Immunohematological and Metabolic Diseases Have the Potential to Improve Significantly, or Be Cured, Using Haematopoietic Stem Cell Transplantation Gene Therapy. https://doi.org/10.31219/osf.io/ukbnm.
102. Moataz Dowaidar. Insulin and IGF-1 Receptors Mutations Can Lead to Targets for Gene Therapy in Diabetes, Obesity, and Metabolic Syndrome. https://doi.org/10.31219/osf.io/s86x5.
103. Moataz Dowaidar. Integrating High-Throughput Genetics and Neuroimaging Technologies Promises Greater Information on Neurobiological Anomalies in Neurodegenerative Diseases. https://doi.org/10.31219/osf.io/hpgyz.
104. Moataz Dowaidar. Intravitreal and Subretinal Injections Currently Deliver Most Gene Therapy, Including siRNA for Eye Illnesses. Non-Viral Vectors May Provide Targeting. https://doi.org/10.31219/osf.io/rjkhy.
105. Moataz Dowaidar. LncRNA Regulating Reprogramming Glucose Metabolism Has Become One of the Most Tempting Antineoplastic Targets for Gene Therapy. https://doi.org/10.31219/osf.io/hqma5.
106. Moataz Dowaidar. lncRNAs Are Upregulated and Downregulated in OS Cells. Angiogenesis, Metastasis, Cell Signaling, Autophagy, and Death Are among Biological Processes That RNAs Play a Role in. https://doi.org/10.31219/osf.io/48n7q.
107. Moataz Dowaidar. Magnetic Nanoparticles Are Widely Used in Drug Delivery, Imaging, Diagnosis, and Targeting. It Has Promises for the Treatment of Inflammatory Disorders such as Rheumatoid Arthritis. https://doi.org/10.31219/osf.io/p2gme.
108. Moataz Dowaidar. Many miRNAs Participate in Inflammatory Regulation and Bone Metabolism. Overexpression of miR21 and miR155 Releases Proinflammatory Cytokines. https://doi.org/10.31219/osf.io/2wuvp.
109. Moataz Dowaidar. MiR490's Diagnostic Capacity Was Demonstrated in Various Cancer Kinds and Diseases, Adding to Its Clinical Value. https://doi.org/10.31219/osf.io/wysre.
110. Moataz Dowaidar. miRNAs Have an Impact on Xeno-Infectious Diseases by Influencing Host And/or Infection Factors. https://doi.org/10.31219/osf.io/7qewx.
111. Moataz Dowaidar. Mutations in MED12 Lead to Mental Retardation, Including Opitz–Kaveggia Syndrome, Ohdo Syndrome, Lujan–Fryns Syndrome, and Psychosis. It's a Target for Gene Therapy. https://doi.org/10.31219/osf.io/cyns8.
112. Moataz Dowaidar. Nanocarriers Can Be Used to Control the Activity of Genome Editing in a Spatiotemporal Way by Using Stimulusresponsive Nanocarriers. https://doi.org/10.31219/osf.io/nua89.
113. Moataz Dowaidar. Nanomaterials Were Formed into Various Shapes, with Functionalization Aimed at Various Internalization Processes. Their Nanoscale Size Allows Drugs to Reach Cells or Extracellular Environments. https://doi.org/10.31219/osf.io/p2ajv.
114. Moataz Dowaidar. Nanomedicine Is Offering Promising Strategies for Tumor Blockade Treatment. https://doi.org/10.31219/osf.io/yzxuq.
115. Moataz Dowaidar. Network Medicine Might Lead to New Treatments for Dyslipidemia. It Will Be a Challenging Method to Implement in a Clinical Context. https://doi.org/10.31219/osf.io/nksbw.
116. Moataz Dowaidar. Neuroinflammation Caused by Activated Microglia and Astrocytes Can Contribute to the Progression of Pathogenic Damage to Substantia Nigra Neurons, Playing a Role in Parkinson's Disease Progression. https://doi.org/10.31219/osf.io/ac896.
117. Moataz Dowaidar. Neurologists Rarely Perform Genetic Testing for Parkinson's Disease. Evidence Suggests That Many Patients with Major Genetic Variants Go Undiagnosed. https://doi.org/10.31219/osf.io/ykpb2.
118. Moataz Dowaidar. Neuronal Intranuclear Hyaline Inclusion Disease Is a Neurodegenerative Condition Which Can Be a Target for Gene Therapy. https://doi.org/10.31219/osf.io/upgqd.
119. Moataz Dowaidar. New Therapies Aim at Restoring the Molecular, Morphological, and Functional Integrity of Parkinson's Specific Brain Circuits. https://doi.org/10.31219/osf.io/dvyxc.
120. Moataz Dowaidar. Not All lncMIRHGs Are 'Junk Transcripts,'. LncM IRHG Loci May Make Both Functional miRNAs and lncRNAs, Which Can Work Together or Separately. https://doi.org/10.31219/osf.io/a567w.
121. Moataz Dowaidar. Nrf2 Signaling Pathways Are Part of a Wider Network of Signaling Pathways Regulating Thymoquinone Therapeutic Actions Which Need Innovative Formulations and Delivery Methods. https://doi.org/10.31219/osf.io/u2fa7.
122. Moataz Dowaidar. Omics Should Be Integrated with Genomics to Uncover Molecular Networks and Tissue and Single-Cell Epigenetic Changes. With These Findings, Targeted Pseudoexfoliation Syndrome and Glaucoma Gene Therapy Procedures May Be Viable. https://doi.org/10.31219/osf.io/48fj5.
123. Moataz Dowaidar. Ophthalmic Gene and Cell Therapies. https://doi.org/10.31219/osf.io/n84m9.
124. Moataz Dowaidar. P21 Is a Flexible, Multi-Functional Protein. It Governs Various Tumor Cell Activities, Including Autophagy. p21 Is a Possible Radiotherapy Target. https://doi.org/10.31219/osf.io/ydkca.
125. Moataz Dowaidar. Parkinson's Disease Simulating Complexity via Improving the Identification of Significant Genetic Alterations and Environmental Contaminants Should Be a Priority. https://doi.org/10.31219/osf.io/pmcu9.

126. Moataz Dowaidar. Patient-Specific Microphysiology Systems Are Likely to Become a Crucial Aspect of Translational Research and Precision Medicine. https://doi.org/10.31219/osf.io/bc8fr.
127. Moataz Dowaidar. Patients with PMD Who Are Thoroughly Screened by Genomic Medicine Have a Considerable Chance of Benefiting Greatly from Whole-Genome Sequencing. https://doi.org/10.31219/osf.io/dajft.
128. Moataz Dowaidar. Polydopamine Nanoparticles' Activity and Long-Term Stability Should Be Fully Studied for Gene Therapy Applications. https://doi.org/10.31219/osf.io/x4nej.
129. Moataz Dowaidar. Potential Therapeutics for Primary Mitochondrial Disorders. https://doi.org/10.31219/osf.io/6pz5k.
130. Moataz Dowaidar. Potentials of Medicinal Nanostructured Diamond Particles and Coatings. https://doi.org/10.31219/osf.io/h68xz.
131. Moataz Dowaidar. Preclinical Investigations Revealed Possibilities for Salmonella Tumor Treatment. Bacteria Can Also Be Coupled to Nanomaterials Enabling Drug-Loading, Photocatalytic And/or Magnetic Properties, Using the Bacteria's Net Negative Charge. https://doi.org/10.31219/osf.io/embqk.
132. Moataz Dowaidar. Research into P2X Purinergic Receptor Function in Tumor Growth Has Made Substantial Progress with Potential Gene Therapy Targeting. https://doi.org/10.31219/osf.io/r34fs.
133. Moataz Dowaidar. RNA Therapies Hold Great Promise for Treating Cancer. High-Throughput Screening Techniques Have Facilitated the Development of RNA Treatments. https://doi.org/10.31219/osf.io/9vxrb.
134. Moataz Dowaidar. RNAi Treatment Has Been Shown to Successfully Modify Human-Related Target Gene Expression, Including Cancer. It Has the Capacity to Control Non-Standard Oncogenes, such as Oncogenic lncRNAs. https://doi.org/10.31219/osf.io/bwqep.
135. Moataz Dowaidar. RNAs Hold a Lot of Potential When It Comes to Druggable Molecular Targets. https://doi.org/10.31219/osf.io/2dtxg.
136. Moataz Dowaidar. Shadow Enhancers' Objective Seems to Be to Establish Robust Growth Patterns Independent of Genetic or Environmental Stress. https://doi.org/10.31219/osf.io/qfnkp.
137. Moataz Dowaidar. Sickle Cell Disease Hematopoietic Stem Cell Gene Therapy with Globin Gene Addition Is Promising. https://doi.org/10.31219/osf.io/j5fkb.
138. Moataz Dowaidar. Single-Gene Mutations in mtDNA-Associated Proteins Are Unlikely to Be the Main Cause of Sporadic Parkinson's Disease. Cumulative Genetic Variation in Numerous Genes May Be Important in Neurodegeneration and PD Risk. https://doi.org/10.31219/osf.io/89qte.
139. Moataz Dowaidar. Small Nuclear Ribonucleoproteins (snRNPs) Based Gene Therapy. https://doi.org/10.31219/osf.io/c43r9.
140. Moataz Dowaidar. Studying the Pathologic Mechanisms of Osteoporosis and the Bone Microenvironment May Help Researchers Better Know the Etiology of Rheumatoid Arthritis, Periodontitis, and Multiple Myeloma, as Well as Other Inflammatory and Autoimmune Disorders. https://doi.org/10.31219/osf.io/t3z6y.
141. Moataz Dowaidar. Suicide Gene Therapy May Be Effective in the Treatment of Malignant Glioma. https://doi.org/10.31219/osf.io/vdkst.
142. Moataz Dowaidar. Synuclein Is a Protein That Is Expressed in Brain Tissue. The Specific Missense Mutation (SNCA) Found in a Family with Parkinson's Disease Is the Cause. Other Diseases Include Alzheimer's Disease and REM Sleep Behavior Disorder. https://doi.org/10.31219/osf.io/bs8rc.
143. Moataz Dowaidar. Systems Biology Is a Method for Analyzing Massive Amounts of Multidimensional Data Generated by Omics Technologies. Cross-Validation of the Various Technological Platforms Is Critical. https://doi.org/10.31219/osf.io/p8vkd.
144. Moataz Dowaidar. Targeting Mitochondria and Especially Taz Gene Mutation Induces CL May Give Novel Therapeutic Alternatives for Treating Barth Syndrome. https://doi.org/10.31219/osf.io/unfpy.
145. Moataz Dowaidar. The Ability to Combine Multiple mRNA Antigens Targeting Multiple Pathogens Simultaneously, and the Robust Immune Responses Are Confirmed in Several Clinical Studies. https://doi.org/10.31219/osf.io/6qksx.
146. Moataz Dowaidar. The Cubic Polyhedral Oligomeric Silsesquioxanes Based Hybrid Materials Have a Wide Variety of Applications, Including Drug Administration, Gene Therapy, Biological Imaging, and Bone Regeneration. https://doi.org/10.31219/osf.io/9peq8.
147. Moataz Dowaidar. The Development of Tissue Replacement Therapies and Drug Discovery Was a Critical Milestone in Advancing Regenerative Medicine. https://doi.org/10.31219/osf.io/w9bsm.
148. Moataz Dowaidar. The Epidemic of COVID-19 Prompted Widespread Use of mRNA Vaccinations. https://doi.org/10.31219/osf.io/jqws5.
149. Moataz Dowaidar. The Most Useful and Commonly Available Acute Rejection Surveillance Strategies Are Routine Monitoring of Myocardial Function and Donor-Specific Anti-HLA Abs Monitoring. https://doi.org/10.31219/osf.io/ebw68.
150. Moataz Dowaidar. The Protease MBTPS2 Is an Important Regulator of Several Cellular Processes, Especially in Health and Sickness. https://doi.org/10.31219/osf.io/qyn6h.

151. Moataz Dowaidar. The Sigma 1 Receptor (S1R) Is a Potential Therapeutic Target for the Treatment of Huntington's Disease. https://doi.org/10.31219/osf.io/mcefx.
152. Moataz Dowaidar. The Use of a Network Medicine Approach Might Result in Innovative Strategies for Lowering Coronary Heart Disease and CV Risks. https://doi.org/10.31219/osf.io/eakg8.
153. Moataz Dowaidar. The Vasoconstrictor Endothelin System Involvement in Chronic Kidney Diseases Pathogenesis Is Now the Most Often Employed Treatment Method. https://doi.org/10.31219/osf.io/cnkqy.
154. Moataz Dowaidar. The VPS35-D620N Mutation Is Associated with Parkinson's Disease and Can Be a Target for Gene Therapy. https://doi.org/10.31219/osf.io/83sxr.
155. Moataz Dowaidar. Therapeutics Including Gene Therapy for Osteoarthritis as a Concept. https://doi.org/10.31219/osf.io/7zsqy.
156. Moataz Dowaidar. Tissue Hypoxia Has Been Established as a Master Regulator for Alternative Splicing, with Substantial Clinical Consequences and Possibilities for Gene Therapy Targeting. https://doi.org/10.31219/osf.io/5pbw4.
157. Moataz Dowaidar. To Rectify Alzheimer's Disease Etiology, Excessive Mitochondrial Division Might Be Stopped or Mitophagy Might Be Promoted. https://doi.org/10.31219/osf.io/6kdxw.
158. Moataz Dowaidar. Transcriptomics Is a Rapidly Growing Field That Generates New Data That May Be Used on Its Own or in Combination with Existing Clinical Data for Development of New Therapeutics, Including Gene Therapy. https://doi.org/10.31219/osf.io/kfr6a.
159. Moataz Dowaidar. Tumor Microenvironment Has Clinical Significance in Terms of Prognosis and Therapy Prediction. https://doi.org/10.31219/osf.io/4dz8q.
160. Moataz Dowaidar. Using AAV as a Gene Delivery Vector in the Neural System Is Effective in Several Animals, such as Nonhuman Primates. https://doi.org/10.31219/osf.io/ut4fa.
161. Moataz Dowaidar. Using Pre-Existing Datasets to Combine Published Information with New Metrics Would Help Researchers Construct a Broader Picture of Chromatin in Disease. https://doi.org/10.31219/osf.io/gsqv5.
162. Moataz Dowaidar. Virus-like Particles Are Good Nanocarriers for Liquid Biopsy Probes, Imaging Contrast Agents, and Anticancer Medications. https://doi.org/10.31219/osf.io/xbtka.
163. Moataz Dowaidar. ZEB1 Controls the Expression of ICAM1, Promoting Monocyte-Macrophage Adhesion and Hence the Formation of Atherosclerotic Lesions. https://doi.org/10.31219/osf.io/kzjqg.
164. Moataz Dowaidar. Gene Therapy Development and Legislation. https://doi.org/10.31219/osf.io/mwb2n.
165. Moataz Dowaidar. Next-Generation Sequencing Is Now Utilized to Identify Genetic Abnormalities and Develop Gene Therapy. https://doi.org/10.31219/osf.io/em7xp.
166. Moataz Dowaidar. Nucleic Acid Designs, Artificial Intelligence for Screening Nanomaterials, and Enhanced Characterization Methods Are Needed to Make Nanomedicine More Successful. https://doi.org/10.31219/osf.io/2w5aq.
167. Moataz Dowaidar. Potential Strategies for Cancer Gene Therapy. https://doi.org/10.31219/osf.io/atcqz.
168. Moataz Dowaidar. Quantitative Groups Will Be Critical to the Success of Future Gene Therapy Programs. https://doi.org/10.31219/osf.io/v97ht.
169. Moataz Dowaidar. The Treatment of Major Human Illnesses with Recombinant Adeno-Associated Virus (rAAV) Has Shown Tremendous Promises. https://doi.org/10.31219/osf.io/uwa4e.
170. Moataz Dowaidar. Carbon Nanotubes Have Enormous Potential in Gene Therapy. https://doi.org/10.31219/osf.io/9bcxk.
171. Moataz Dowaidar. Charge-Alteration-Based Approaches Can Address the Evolving Needs of Nucleic Acid-Based Gene Therapy, Charge Reversal Techniques Are Also Promising. https://doi.org/10.31219/osf.io/zwq5h.
172. Moataz Dowaidar. Chromosome X, the Most Explored Genome-Editing Chromosome, Presents Possibilities for Hemophilia A Treatments. https://doi.org/10.31219/osf.io/6vsdz.
173. Moataz Dowaidar. Clinical Investigations Show That siRNA May Be Used to Treat a Variety of Disorders, Including Cancer. https://doi.org/10.31219/osf.io/fcsgq.
174. Moataz Dowaidar. Cyclodextrins as Potential Gene Therapy Vectors. https://doi.org/10.31219/osf.io/zhtsc.
175. Moataz Dowaidar. Development of Specialized Carriers Capable of Delivering Effective RNAi and siRNA Gene Therapy. https://doi.org/10.31219/osf.io/3ykwm.
176. Moataz Dowaidar. Gene Therapy Can Target Mutations such as BRAF, Which Have Been Shown to Make Tumors More Susceptible to Autophagy Suppression. https://doi.org/10.31219/osf.io/3gwra.
177. Moataz Dowaidar. Gene Therapy Vectors Should Enable CRISPR Systems to Accumulate at Disease Sites and Successfully Penetrate Nuclei. https://doi.org/10.31219/osf.io/xzmnc.
178. Moataz Dowaidar. Nanoformulations Can Be Utilized to Deliver Effective siRNA to Tumor Cells to Decrease Gene Expression. https://doi.org/10.31219/osf.io/zvukc.
179. Moataz Dowaidar. Neuronal Ceroid Lipofuscinosis Therapeutics. https://doi.org/10.31219/osf.io/75vcp.
180. Moataz Dowaidar. Nonviral Gene Delivery Vectors for Transfection of the CAR Gene for CAR-T Cell Therapy. https://doi.org/10.31219/osf.io/ckxh5.
181. Moataz Dowaidar. Potential HIV Gene Therapy Strategies. https://doi.org/10.31219/osf.io/e5hm2.

182. Moataz Dowaidar. Research on Cell Sources for Brain Cell Replacement Methods Has Gained Major Importance. Cell and Gene Therapy Are Potentially Intriguing New Domains of Regenerative Medicine. https://doi.org/10.31219/osf.io/g835b.
183. Moataz Dowaidar. RNAi-Based Gene Therapy Provides a Wide Variety of Applications. Safe, Biodegradable Nano Delivery Vectors Are Still Needed. https://doi.org/10.31219/osf.io/s2zhn.
184. Moataz Dowaidar. Strategies for Treating Multiple Sclerosis with Gene Therapy. https://doi.org/10.31219/osf.io/sycn6.
185. Moataz Dowaidar. The Combination of Unique Biomolecules and Nanoparticles Has Shown Successful Gene Therapy Treatment Approaches for Non-Small Cell Lung Cancer Treatment. https://doi.org/10.31219/osf.io/yeq5z.
186. Moataz Dowaidar. Understanding Why the Same Gene Delivery Vector Behaves Differently in Different Cell Types Is Essential for Developing More Adaptable Transfection Systems. https://doi.org/10.31219/osf.io/6q8af.
187. Moataz Dowaidar. AAV9 Is Considered the Most Efficient AAV Serotype Targeting Blood-Brain Barriers. To Enhance Effective Gene Therapy for CNS Illnesses, Testing Novel Vectors with More Efficient Crossing Capabilities Is Vital. https://doi.org/10.31219/osf.io/7bf5s.
188. Moataz Dowaidar. Artificial miRNAs Are Potential Gene Therapy Tools, Especially for Incurable Monogenic Disorders. https://doi.org/10.31219/osf.io/d5rnm.
189. Moataz Dowaidar. Breakthroughs in mRNA Modification and Nanoparticle-Based Delivery Vehicles Facilitate Gene Therapy Strategies. https://doi.org/10.31219/osf.io/ky7dt.
190. Moataz Dowaidar. CRISPR/Cas9-Mediated Genome Editing Has Demonstrated Significant Promise for Genetic Correction in Autologous Hematopoietic Stem/progenitor Cells (HSPCs) and Induced Pluripotent Stem Cells (iPSCs). https://doi.org/10.31219/osf.io/xk54r.
191. Moataz Dowaidar. Gene Therapy Vectors for Targeting the Heart. https://doi.org/10.31219/osf.io/gcbhf.
192. Moataz Dowaidar. Liposomes Can Minimize Cardiotoxicity, Address Drug Resistance, and Improve Overall Drug Release Profiles in Breast Cancer. https://doi.org/10.31219/osf.io/tn56d.
193. Moataz Dowaidar. Liposomes with Cerasome-Forming Lipids as Gene Therapy Vectors. https://doi.org/10.31219/osf.io/zjn6v.
194. Moataz Dowaidar. Nanomaterials Combine Multiple Therapeutic Approaches for Cancer Cell Multidrug Resistance, Ferroptotic Cell Death Is Promising in Various Cancers. https://doi.org/10.31219/osf.io/7bg9t.
195. Moataz Dowaidar. Nanomedicines for Enhanced Permeability and Retention (EPR)-Stratified Patients Have the Potential to Improve Treatment Outcomes. https://doi.org/10.31219/osf.io/xrcb2.
196. Moataz Dowaidar. RNA-Based Gene Therapy for Manipulating the Neuroinflammatory Cascade Closely Linked to Neurodegeneration Can Help Reduce Disease Development. https://doi.org/10.31219/osf.io/2hswv.
197. Moataz Dowaidar. Targeted Chemical Nucleases Have a Wide Range of Untapped Applications in Biological Fields, Including Gene Therapy. https://doi.org/10.31219/osf.io/6bexs.
198. Moataz Dowaidar. Bacterial Nanoparticles Can Deliver Proteins, Medications, Enzymes, and Genes to Diagnose and Cure Numerous Illnesses. https://doi.org/10.31219/osf.io/7gyna.
199. Moataz Dowaidar. Exosomal miRNA Diagnostic and Gene Therapy Tools. https://doi.org/10.31219/osf.io/aknrc.
200. Moataz Dowaidar. Gene Modification Research Has Potential, from Diagnostic to Therapeutic Levels. The Most Promising Metabolic Pathways Include the TGF-1 Signaling System, Inflammation and Protein Transport. https://doi.org/10.31219/osf.io/5ert4.
201. Moataz Dowaidar. Gene Therapy Using MnO2 Nanoparticles. https://doi.org/10.31219/osf.io/xmwjs.
202. Moataz Dowaidar. Gene-Regulatory Elements May Change the Amount, Timing, or Location of Gene Expression, Cis-Regulation Therapy Platforms Might Become a Gene Therapy to Treat Many Genetic Diseases. https://doi.org/10.31219/osf.io/xc5a2.
203. Moataz Dowaidar. Hemophilia Therapeutics. https://doi.org/10.31219/osf.io/gu74x.
204. Moataz Dowaidar. Mesenchymal Stem Cells Strategies in Cancer Immunotherapy. https://doi.org/10.31219/osf.io/dkv6w.
205. Moataz Dowaidar. Nanomaterials Can Inhibit Planktonic and Biofilm Bacteria and Can Be Used as Topical Therapy for Mouth and Wound-Related Infections. https://doi.org/10.31219/osf.io/aqd2e.
206. Moataz Dowaidar. New Technologies to Improve CAR T Cell Generation and Biomanufacturing Will Lead to Safer, More Therapeutically Effective Cells. https://doi.org/10.31219/osf.io/un8gp.
207. Moataz Dowaidar. Ocular Gene Therapy Strategies. https://doi.org/10.31219/osf.io/7en3k.
208. Moataz Dowaidar. Peripheral Nerve Injury Therapeutics, Including Electrical Stimulation, Stem Cell Treatments, and Synthetic Neural Scaffolds, Have Shown Promising Preclinical and Even Clinical Results with Potential Regenerative Treatment. https://doi.org/10.31219/osf.io/m8cs9.
209. Moataz Dowaidar. Photothermal and Photodynamic Photoactivation of Nanomaterials-Based Prodrugs Are Two Key Methods for NIR Light-Mediated Photoactivation. https://doi.org/10.31219/osf.io/2bh3r.
210. Moataz Dowaidar. Quantum Dots Have the Potential to Be Used in Gene Therapy. https://doi.org/10.31219/osf.io/bdeg6.

211. Moataz Dowaidar. Sickle Cell Disease Has Emerged as a Public Health Concern. Some Drugs May Conflict with Curative Therapies, yet They May Be Useful as a Bridge to HSCT and Gene Therapy. https://doi.org/10.31219/osf.io/6kufh.
212. Moataz Dowaidar. Stimulator of Interferon Genes (STING)-Activating Nanoparticles Can Be Employed as a Tool for Controlled Immune Activation. https://doi.org/10.31219/osf.io/2ez7a.
213. Moataz Dowaidar. CRISPR/Cas9 Has Introduced New Gene Therapy Possibilities for Muscular Dystrophies. https://doi.org/10.31219/osf.io/ug8v4.
214. Moataz Dowaidar. Degradable Branched Polycationic Systems Are Promising Gene Therapy Vectors. https://doi.org/10.31219/osf.io/utypf.
215. Moataz Dowaidar. Developing Nanotechnology Platforms for Peptide-Based Combinatory Cancer Gene Therapy Will Likely Have a Significant Influence on the Development of Personalized Cancer Medicines. https://doi.org/10.31219/osf.io/zbrkj.
216. Moataz Dowaidar. Exosomes May Prevent Cardiac Attacks, Heart Failure, and Cardiomyopathy. https://doi.org/10.31219/osf.io/agm3k.
217. Moataz Dowaidar. 2021gr. Exosomes Potential Therapeutics. https://doi.org/10.31219/osf.io/mhwt3.
218. Moataz Dowaidar. Gene Therapy Using miRNA Treatment Suppresses the Expression of Bone-Forming Defective Genes and Raises the Expression of Genes That Become Dormant during Bone Building. https://doi.org/10.31219/osf.io/tcka3.
219. Moataz Dowaidar. Genome-Editing Is Promising for Producing Therapeutically Relevant Animal Models for Possible Therapies for Rare Human Diseases. https://doi.org/10.31219/osf.io/dehr9.
220. Moataz Dowaidar. Human Corneal Endothelial Cells Grafts to Replace Cadaveric Donor Corneas. https://doi.org/10.31219/osf.io/p9x7e.
221. Moataz Dowaidar. Hybrid Nanotechnology and Peptide Nucleic Acid Could Improve the Effectiveness of Gene Therapy by Increasing Its Cell Permeability. https://doi.org/10.31219/osf.io/d8wzt.
222. Moataz Dowaidar. In Prenatal Stem Cell Transplantation and in Utero Gene Therapy, a Wide Spectrum of Genetic Diseases Can Be Diagnosed and Treated before Birth. https://doi.org/10.31219/osf.io/sa3vz.
223. Moataz Dowaidar. Magnetic Iron Oxide Nanoparticles Have Potential on Gene Therapy Effectiveness and Biocompatibility. https://doi.org/10.31219/osf.io/f3hm4.
224. Moataz Dowaidar. Neurotrophin Gene Therapy May Be Able to Treat Individuals with Noise-Induced Hearing Loss or Neural Presbyacusis. https://doi.org/10.31219/osf.io/spkxh.
225. Moataz Dowaidar. Plant Viral Nanoparticles Can Be Used in Biological Systems for Loading and Transporting Cargo. https://doi.org/10.31219/osf.io/txdka.
226. Moataz Dowaidar. Polydopamine May Be Easily Functionalized with a Range of Nanomaterials for Synergistic Cancer Therapy, in Addition to Its Exceptional Photothermal Effects. https://doi.org/10.31219/osf.io/cq942.
227. Moataz Dowaidar. Tumor-Targeted Drug Delivery Systems for Anticancer Therapies Can Selectively Provide an Appropriate Cytotoxic Payload to Cancer Cells, Reducing the Side Effects of Chemo. https://doi.org/10.31219/osf.io/683nj.
228. Dowaidar, Moataz, Hani Nasser Abdelhamid, Mattias Hällbrink, Krista Freimann, Kaido Kurrikoff, Xiaodong Zou, and Ülo Langel. 2017. Magnetic Nanoparticle Assisted Self-Assembly of Cell Penetrating Peptides-Oligonucleotides Complexes for Gene Delivery. Scientific Reports 7 (1): 9159. https://doi.org/10.1038/s41598-017-09803-z.
229. Dowaidar, Moataz, Hani Nasser Abdelhamid, Mattias Hällbrink, Ülo Langel, and Xiaodong Zou. 2018. Supplemental Material for Chitosan Enhances Gene Delivery of Oligonucleotide Complexes with Magnetic Nanoparticles–cell-Penetrating Peptide. SAGE Journals. https://doi.org/10.25384/SAGE.7105436.V1.
230. Dowaidar, Moataz, Hani Nasser Abdelhamid, Mattias Hällbrink, Xiaodong Zou, and Ülo Langel. 2017. Graphene Oxide Nanosheets in Complex with Cell Penetrating Peptides for Oligonucleotides Delivery General Subjects. Biochimica et Biophysica Acta, General Subjects. https://pubag.nal.usda.gov/catalog/5734174.
231. Moataz Dowaidar. 2017. Graphene Oxide Nanosheets in Complex with Cell Penetrating Peptides for Oligonucleotides Delivery. Biochimica et Biophysica Acta, General Subjects 1861 (9): 2334–41. https://doi.org/10.1016/j.bbagen.2017.07.002.
232. Dowaidar, Moataz, and Moataz Dowaidar. 2018. Chimeric Gene Delivery Vectors : Design, Synthesis, and Mechanisms from Transcriptomics Analysis.
233. Moataz Dowaidar. Addiction Biology Research on miRNAs, and Their Role in the Pathophysiology of Addiction Is Enabling Gene Therapy Opportunities. https://doi.org/10.31219/osf.io/z5wyt.
234. Moataz Dowaidar. Aptamers Targeting Vascular Endothelial Growth Factor Molecular Regulation as Potential Therapists. https://doi.org/10.31219/osf.io/a8qpr.
235. Moataz Dowaidar. Arrhythmogenic Cardiomyopathy Is a Set of Hereditary Cardiac Muscle Disorders Where Various Etiologies Converge. Most ACM Patients Do Not Have a Genetic Diagnosis. https://doi.org/10.31219/osf.io/pztv3.

236. Moataz Dowaidar. Autophagy, Immunological Response, and Inflammation All Rely on the TRIM Family Proteins. TRIM-Based Therapeutics for Inflammatory Illnesses Including Diabetes and Diabetic Comorbidities Are Promising. https://doi.org/10.31219/osf.io/y4g6e.
237. Moataz Dowaidar. Biogenic Particles Can Be Multiantigenic, Immunostimulative and Activate Innate Immunity While Suppressing Tumor Development. https://doi.org/10.31219/osf.io/q2kby.
238. Moataz Dowaidar. Biological Medications for Interventional Pain Have a Lot of Clinical Data behind Them. It Is Fair to Assume They Will Replace Steroid-Based Interventional Techniques, Providing Patients with Longer Relief. https://doi.org/10.31219/osf.io/4y5fm.
239. Moataz Dowaidar. Carbon Nanofibers Assist in the Manufacture of Prosthetic Joints, Promote Tissue, Organ, Nerve Regeneration and Development, and Improve Anticancer Therapy Impact and Chemosensitization for a Range of Tumor Types. https://doi.org/10.31219/osf.io/z3ucn.
240. Moataz Dowaidar. Emerging Therapy Options May Help Patients with RAG Deficiency, Especially Those with Severe Immune Dysregulation. https://doi.org/10.31219/osf.io/v5tjg.
241. Moataz Dowaidar. Exosomes as Promising Gene Therapy Tools Still Need to Be Researched and Manufactured More Efficiently. https://doi.org/10.31219/osf.io/nw4z7.
242. Moataz Dowaidar. Focus on Exosomes Could Help Make the Use of Circulating miRNA as Biomarkers More Practical. A Detailed Understanding of miRNA Behavior Should Be a Subject of Gene Therapy. https://doi.org/10.31219/osf.io/uan6x.
243. Moataz Dowaidar. Gene-Free Viral-like Particles (VLPs) Offer a Safer Alternative to Inactivating or Weakening Viral Strains for Traditional Vaccines. VLP-Based Vaccinations without Adjuvants Have Been Found to Promote Humoral and Cellular Immunity. https://doi.org/10.31219/osf.io/9dvut.
244. Moataz Dowaidar. Given the Importance of mTOR Signaling in a Number of Illnesses, It Looks Suitable to Use miR 99 Family Members as a Therapeutic Intervention to Deal with These Illnesses by Using Gene Therapy Tools. https://doi.org/10.31219/osf.io/8cwgh.
245. Moataz Dowaidar. HMGB1 Has Sparked a Lot of Attention as a Model DAMP Molecule Involved in Inflammation, Inflammatory Diseases, and Cancer. https://doi.org/10.31219/osf.io/5qx36.
246. Moataz Dowaidar. Nucleic Acid Nanocarriers Can Be Programmable, Spatially Adjustable and Biocompatible, Minimizing Systemic Toxicity and Improving Pharmacodynamics. https://doi.org/10.31219/osf.io/wr237.
247. Moataz Dowaidar. Osteoporosis Is a Prominent Source of Morbidity and Mortality in the Elderly, Particularly in Postmenopausal Women. Long Noncoding RNAs (lncRNAs) Have Been Found to Be Important Regulators and Possible Gene Therapy Targets. https://doi.org/10.31219/osf.io/ghfpt.
248. Moataz Dowaidar. Polycomb Genes Role in Cancer Pathophysiology Is Offering Targets for Therapeutics Including Gene Therapy. https://doi.org/10.31219/osf.io/sfvej.
249. Moataz Dowaidar. RNA Sequencing and Microarray Analysis Are Helpful Techniques to Detect Obesity-Related lncRNAs. LncRNA Can Alter Cholesterol Metabolism and Can Be a Target for Gene Therapy. https://doi.org/10.31219/osf.io/3fb6w.
250. Moataz Dowaidar. Sepsis-Associated Acute Kidney Damage Is a Disease That Affects the Patient's Quality of Life. It Should Be a Target for Gene Therapy. https://doi.org/10.31219/osf.io/49k7q.
251. Moataz Dowaidar. The Gene Expression Profiling Gives an in-Depth Insight of Breast Cancer Heterogeneity, Better than a Single Protein or Gene Expression. It Is Time to Include It in the Daily Routine. https://doi.org/10.31219/osf.io/xhyd7.
252. Moataz Dowaidar. The Nanomedicine System Has Successfully Inhibited Tumor Neovascularization Using Gene Silencing, Chemotherapy, Photothermal Therapy, and Other Therapies. https://doi.org/10.31219/osf.io/rk2bf.
253. Moataz Dowaidar. The Therapeutic Application of a Nucleic Acid Sequence to Patients' Diseased Organs Is Currently Available. https://doi.org/10.31219/osf.io/pqsbf.
254. Moataz Dowaidar. Triple-Negative Breast Cancer, Which Lacks the Expression of Hormone Receptors and HER2, Has a Worse Prognosis. Massive Parallel Sequencing Is Capable of Reliably Breaking down the Intra-Tumor and Inter-Tumor Heterogeneity. https://doi.org/10.31219/osf.io/pvk7u.
255. Dowaidar, Moataz, H. A. Ismail, A. A. Alghasham, M. M. Dowaidar, and A. A. Settin. 2011. Polymorophisms in MTHF and Ace Genes and the Association with Hypertension among Saudi Population from Qassim Region. Egyptian Journal of Biochemistry and Molecular Biology 29 (1). https://doi.org/10.4314/ejbmb.v29i1.67382.
256. Dowaidar, Moataz, Hani Nasser Abdelhamid, Mattias Hällbrink, Ülo Langel, and Xiaodong Zou. 2018. Chitosan Enhances Gene Delivery of Oligonucleotide Complexes with Magnetic Nanoparticles-Cell-Penetrating Peptide. Journal of Biomaterials Applications 33 (3): 392–401. https://doi.org/10.1177/0885328218796623.
257. Dowaidar, Moataz, and Ahmad Settin. 2010. Risk of Myocardial Infarction Related to Factor V Leiden Mutation: A Meta-Analysis. Genetic Testing and Molecular Biomarkers 14 (4): 493–98. https://doi.org/10.1089/gtmb.2010.0017.
258. Gestin, Maxime, Moataz Dowaidar, and Ülo Langel. 2017. Uptake Mechanism of Cell-Penetrating Peptides. Advances in Experimental Medicine and Biology 1030: 255–64. https://doi.org/10.1007/978-3-319-66095-0_11.

259. Ismail, H. A., A. A. Alghasham, M. M. Dowaidar, and A. A. Settin. 2011. Polymorophisms in MTHF and Ace Genes and the Association with Hypertension among Saudi Population from Qassim Region. Egyptian Journal of Biochemistry and Molecular Biology 29 (1). https://doi.org/10.4314/ejbmb.v29i1.67382.
260. Settin, Ahmad A., Abdullah Algasham, Moataz Dowaidar, and Hisham Ismail. 2009. Methylene Tetrahydrofolate Reductase and Angiotensin Converting Enzyme Gene Polymorphisms Related to Overweight/obesity among Saudi Subjects from Qassim Region. Disease Markers 27 (2): 97–102. https://doi.org/10.3233/DMA-2009-0660.
261. Settin, Ahmad A., Abdullah Alghasham, Ahmad Ali, Moataz Dowaidar, and Hisham Ismail. 2012. Frequency of Thrombophilic Genetic Polymorphisms among Saudi Subjects Compared with Other Populations. Hematology 17 (3): 176–82. https://doi.org/10.1179/102453312X13376952196575.
262. Settin, Ahmad, Ibrahem S. Abu-Saif, Rizk El-Baz, Moataz Dowaidar, Rabab Abu-Al Kasim, and Shaimaa Shabana. 2007a. Diagnosis of Sex Chromosome Disorders and Prenatal Diagnosis of Down Syndrome Using Interphase Fluorescent In-Situ Hyperidization Technique. International Journal of Health Sciences 1 (2): 203–9. https://www.ncbi.nlm.nih.gov/pubmed/21475429.
263. Settin, Ahmad, Abdullah Algasham, Moataz Dowaidar, and Hisham Ismail. 2011. Methylene Tetrahydrofolate Reductase (MTHFR) and Angiotensinogen Converting Enzyme (ACE) Gene Polymorphisms Related to Overweight and Obesity among Saudi Patients in Al Qassim. International Journal of Health Sciences 5 (2 Suppl 1): 24–25. https://www.ncbi.nlm.nih.gov/pubmed/23284565.
264. Settin, Ahmad, Hala Almarsafawy, Ahmad Alhussieny, and Moataz Dowaidar. 2008a. Dysmorphic Features, Consanguinity and Cytogenetic Pattern of Congenital Heart Diseases: A Pilot Study from Mansoura Locality, Egypt. International Journal of Health Sciences 2 (2): 101–11. https://www.ncbi.nlm.nih.gov/pubmed/21475491.
265. Settin, Ahmad, Moataz Dowaidar, Rizk El-Baz, Ayman Abd-Al-Samad, Ibrahim El-Sayed, and Mahmoud Nasr. 2008. Frequency of Factor V Leiden Mutation in Egyptian Cases with Myocardial Infarction. Hematology 13 (3): 170–74. https://doi.org/10.1179/102453308X316158.
266. Venit, Tomas, Moataz Dowaidar, Maxime Gestin, Syed Raza Mahmood, Ülo Langel, and Piergiorgio Percipalle. 2020. Transcriptional Profiling Reveals Ribosome Biogenesis, Microtubule Dynamics and Expression of Specific lncRNAs to Be Part of a Common Response to Cell-Penetrating Peptides. Biomolecules 10 (11): 1567. https://doi.org/10.3390/biom10111567.
267. Dowaidar, M. Cell-Penetrating Peptides Uptake Pathways and Role in Drug Deliverywith Potentials for Gene Therapy and Vaccine Development . Preprints.org 2023, 2023070889. https://doi.org/10.20944/preprints202307.0889.v1