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Education Silent Abstracts

E-2000

Non-canonical Base Pairs in Self-assembling DNA Crystals. WILLIAM BERNFELD[1] and Simon Vecchioni[2]. [1]King School and [2]New York University. Email: williambernfeld1122004@gmail.com

The scientific community has long recognized the four naturally-occurring nucleobases as the universal genetic language. However, this four-base model has recently been turned on its head with the development of "hachimoji" nucleic acids, which use up to eight bases. Four new synthetic components have been incorporated into a variety of sequences. These sequences, in turn, have been used to encode basic information and to construct a wide variety of crystals and nanocages. In this investigation, we furthered our understanding of hachimoji DNA by using the Python-based Hierarchical ENvironment for Integrated Xtallography (PHENIX), the Crystallographic Object-Oriented Toolkit (COOT), and ChimeraX to simulate a base pair between cytosine and 5-methyl isocytosine. This virtual base pair is situated at the center of a DNA strand derived from a previously-designed sequence, developed roughly 11 years prior. This pairing is considered degenerate because its components do not normally form hydrogen bonds. However, it shows coherence within the digitized sequence, and therefore suggests that the pair can exist in the real world. Should future research reveal further evidence of its existence, this development has tremendous implications for the biochemical sciences, e.g., molecular computing, genetics, and immunology. Because the new base pair may be capable of encoding peptides using non-proteinogenic amino acids, our findings may be used for the development of new, unique proteins. These molecules, encoded using hachimoji nucleic acids containing the cytosine-5-methyl-isocytosine base pair, may prove effective in the treatment of genetic and/or metabolic illnesses such as diabetes, anemia, and cancer.

E-2001

Differences Between Glial Cells in the Brain and in the Gut. S. L. MCDERMOTT[1,2], M. Scavuzzo[2],and P. Tesar[2]. [1]Shaker Heights High School, 15911 Aldersyde Drive, Shaker Heights, OH, 44106 and [2]Case Western Reserve University, 11100 Euclid Ave, Cleveland, OH, 44106. Email: slmcdermott10@gmail.com

Glial cells are the supporting cells of the enteric and the central nervous systems. Traditionally, glia had been thought of as a type of biological glue that hold the neurons together; however, now these cells are recognized as complex contributors of the nervous system. The molecular differences between glia of the enteric nervous system and the central nervous system are largely unknown. However, knowing these potential similarities and differences may inform our understanding of glia in both systems. Previously, we used single nuclei RNA-sequencing of mouse brain and gut tissue to discover genes expressed. Here, we employed quantitative PCR on glial cDNA from the enteric and central nervous system to measure the abundance of transcripts found to be enriched in gut glia or brain glia that had been cultured in vitro. We identified differences in gene expression between enteric glia and central nervous system cells, including in the expression of members of the cadherin and the phosphodiesterase families. These differences may yield insights into the functions of each of these cell types.

E-2002

Progress of Peptide Inhibitors' Abilities to Prevent the Protein Complex Formation of PD-1 and PD-L1 for the Immune System to Recognize and Defend Against Cancer Cell Invasion. S. NIKKU, R. Carter, and A. Haymond. Center for Applied Proteomics and Molecular Medicine, 10920 George Mason Cir, Manassas, VA 20109. Email: sirincollge@gmail.com

Cancer cells exploit immune checkpoint pathways by upregulating proteins such as PD-L1 to avoid T-cell detection. PD-L1 binds to PD-1 on the surface of T-cells resulting in deactivated T-cells that do not attack the cancer cell. Current antibody treatment targeting PD-1/PD-L1 interaction causes autoimmune side effects as a result of their long half-lives. The goal of this research was to identify a peptide inhibitor that would block the interaction between PD-1 and PD-L1 with high affinity

and potency while also causing fewer side effects. A set of preliminary PD-1/PD-L1 inhibitors were examined to identify the optimal inhibitor of PD-1/PD-L 1 interaction. Circular dichroism (CD) was utilized to investigate the structure of two peptide inhibitors and of PD-1 and PD-L1 proteins created in the lab. After comparing CD outputs from batches of both proteins, graphical analysis verified the proteins folded correctly. AlphaScreening determined whether a protein-protein interaction such as PD-1 and PD-L1 was blocked by a peptide inhibitor. From this, the concentration of the inhibitor which prevented 50% of PD-1/PD-L1 binding was calculated (IC50). By determining the IC50 value for each inhibitor, they were then compared to determine which inhibitor was the most effective. When one of the best preliminary inhibitors was tested alongside an optimized version of the inhibitor, the IC50 value indicated that more of the optimized peptide was needed to achieve the same inhibition as the preliminary inhibitor. This indicated that the optimization of preliminary inhibitors needed to be repeated thus providing direction for further research.