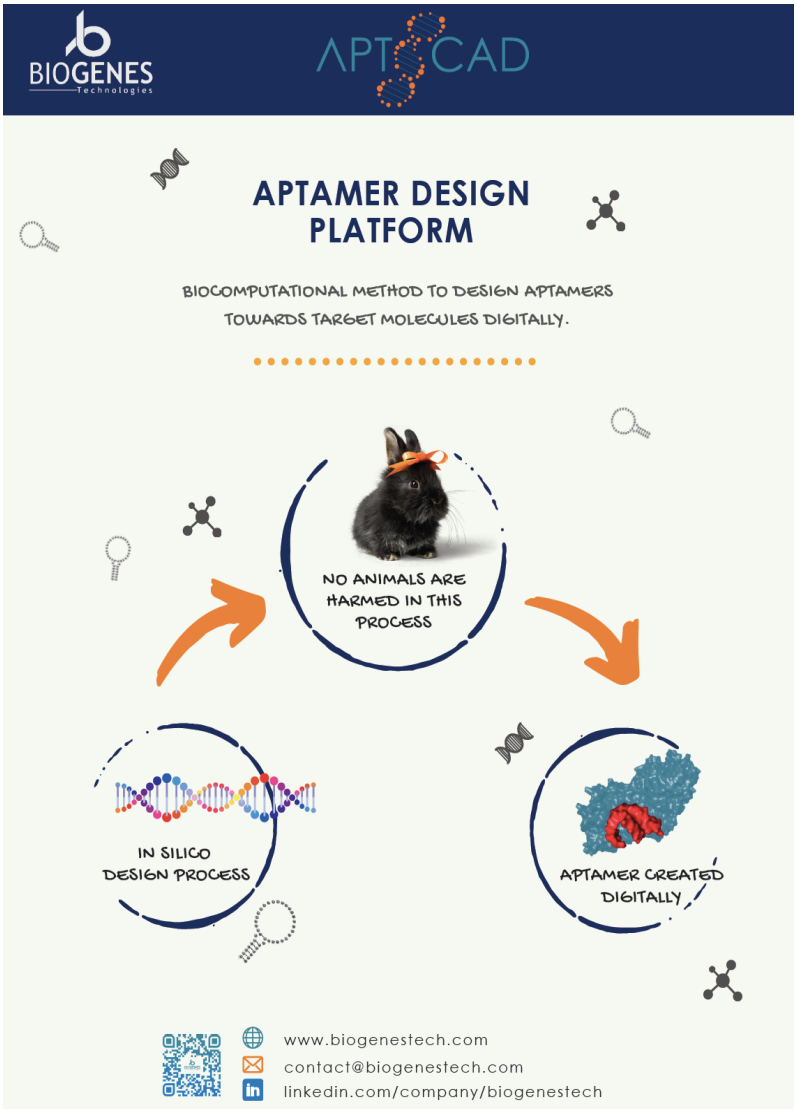
TECHNOLOGY DESCRIPTION
APTAMER COMPUTER AIDED DESIGN

APTCAD or Aptamer Computer Aided Design is BIOGENES' proprietary technology platform used for the *in silico* design of synthetic antibodies, known as 'aptamers' to substitute the use of animal-derived antibodies. Aptamers are ligands constructed from oligonucleotide sequences of 30-100mers in length that can designed to bind specifically to target molecules such as proteins, peptides, hormones & other small molecules. Aptamers works by natural of folding the oligonucleotide sequences into 3D structure to bind to target molecules via hydrogen bonding and surface charges. The design of aptamers using APTCAD platform involves several steps described below.

Quick description silico aptamer design at link here:
https://youtu.be/-k6Y9cGxr00?si=QwFkqhkwNzDmHzIE



a) TARGET MOLECULE IDENTIFICATION & SELECTION

The specific target molecule (proteins, peptides, hormones & other small molecules) that needs to be detected is identified and selected from Protein Database and Uniprot. Once identified, the digital coordinates of the target molecule is downloaded into APTCAD for the next step. In the event that target molecules especially proteins are not available in the Protein Database, software such as Alphafold is utilized to predict folding structure of the protein targets from the protein amino acid sequences. PDBQT file of the protein will then be generated and used for docking on APTCAD platform.

b.) APTAMER SEQUENCE SELECTION AND VISUALISATION IN 2D & 3D

Random tRNA sequence that act as starter sequence of the aptamer was retrieved from tRNA database. This sequence is then folded and visualised the folding via APTCAD. The stability, in form of ΔG, of the sequence can also be known from APTCAD. Only sequence with higher stability will be chosen for further analysis. After the sequence has passed the selection, the PDB file of the aptamer sequence was then retrieved from APTCAD.

c.) APTAMER CANDIDATES' PREPARATION

The aptamer file was first converted from RNA to DNA then prepped for docking using the next stage of APTCAD. All rotating bonds was set to 0 prior to retrieving PDBQT of the aptamer file.

d.) IN SILICO DOCKING

Docking of the aptamer candidates to the target molecule is done using APTCAD. Pre-prepared PDBQT of aptamer and protein file are used here. After docking, the binding affinity can be observed based on the minimum binding energy in form of kcal/mol in order from highest binding affinity to lowest. Output files can also be used in PyMol to visualise the location of the aptamer binding to the protein. Long aptamer sequence can be selected and then truncated into shorter sequence by going through same order of the designing process.

Optionally, further analysis can be done with Molecular Dynamics (MD). MD simulations provide insights into the structural stability, binding interactions, and conformational flexibility of aptamer-target complexes. By simulating the movement of atoms over time, MD helps to understand how aptamers adapt to their target molecules, optimizing their binding affinity and specificity. This computational approach allows for the refinement of aptamer sequences by predicting the most stable configurations and identifying potential structural modifications that enhance performance.

Once the process is completed, the aptamer candidates are synthesized and folded in buffer for the next stage of wet lab validation.

BIOGENES Technologies

Biogenes Technologies Sdn. Bhd. is a Malaysian company that focuses on the development and commercialisation of aptamer-based rapid test solutions for sectors such as healthcare, food production, food safety and environmental monitoring.