FORM 6-K
SECURITIES AND EXCHANGE COMMISSION

Washington, D.C. 20549

Report of Foreign Private Issuer

Pursuant to rule 13a-16 or 15d-16 of the Securities Exchange Act of 1934
for the month of October 2004

Compugen Ltd.
(Translation of registrant's name in English)

72 Pinchas Rosen Street, Tel-Aviv 69512, Israel
(Address of principal executive offices)

Indicate by check mark whether the registrant files or will file annual reports under cover Form 20-F or Form 40-F.

Form 20-F X Form 40-F ___

On October 27th, 2004 Compugen Ltd. (the "Registrant") issued a Press Release, filed as Exhibit 1 to this Report on Form 6-K, which is hereby incorporated by reference herein.

SIGNATURE

Pursuant to the requirements of the Securities Exchange Act of 1934, the Registrant has duly caused this report to be signed on its behalf by the undersigned, thereunto duly authorized.

Compugen Ltd.
(Registrant)
By: /s/ Mor Amitai
Title: President & CEO
Date: October 27th, 2004

Exhibit 1

Compugen and Tel Aviv University Announce Unique Predictive Method for Identifying Alternative Splicing in the Human Genome

- New method does not require EST or microarray data -
- Hundreds of novel proteins found to date -

Tel Aviv, Israel – October 27, 2004 – Compugen Ltd. (NASDAQ: CGEN) and Tel Aviv University announced today the development of a new method for identifying alternative splicing without the need for either EST (Expressed Sequence Tag) data or microarray experimentation. Hundreds of novel predicted proteins discovered to date using this new predictive method are currently undergoing initial assessment for possible addition to Compugen's growing therapeutic and diagnostic pipeline, and for licensing. The work, which was published in Genome Research (Volume 14, Pages 1617-1623), was a collaborative effort between Compugen's scientists and Professors Ron Shamir and Gil Ast from Tel Aviv University.

The novel method announced today is based on a computer-learning model incorporating algorithms reflecting Compugen's deeper understanding of the process of alternative splicing. Currently, the two most common methods for identifying alternative splicing rely on the mining of substantial experimental data, either EST libraries or microarray results. It is well accepted that these methods cannot detect a substantial fraction of splice variants in the human genome. This is due to the fact that ESTs – the main source of information for alternative splicing prediction – are biased towards under-representation of splice variants with low expression levels; and large-scale microarray-based methods cannot sample all possible combinations of tissues, developmental stages, and conditions.
In contrast, Compugen's method, which is based on comparative genomics, can accurately predict alternative splicing based solely on human and mouse genomic DNA.

Using the model developed by Compugen's scientists in collaboration with Professors Shamir and Ast, Compugen to date has discovered over 300 novel predicted splice variants. As this was only an initial application of the computer-learning model, hundreds more novel splice variants are expected to emerge from future applications.

"This development is another example of the unique research that is done at Compugen, relying on proprietary predictive modeling and experimental validation, rather than high-throughput experimental approaches. The early use of this splice variant model has already increased our collection of potential therapeutic proteins and diagnostic markers beyond that which was possible with our industry leading EST-based LEADS predictive model," said Mor Amitai, Ph.D., President and Chief Executive Officer of Compugen Ltd. "Therefore, we expect this development to allow us to substantially narrow the knowledge gap between the human genome and proteome by providing a much fuller picture of splice variants. Together with our other understandings of important biological phenomena, such as antisense and RNA editing, this

capability is enabling us to continuously improve our computational platforms and discovery engines, which provide the foundation for our drug and diagnostic product programs."

"The development of this exciting computational method is the fruit of a collaborative research project performed at Tel Aviv University and Compugen," said Isaac T. Kohlberg, Chief Executive Officer of Ramot at Tel Aviv University Ltd., the technology transfer company of Tel Aviv University. "This is an example of a unique collaboration between the university and industry, which benefits basic science as well as product-driven research, and eventually the lives of patients worldwide."

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About Compugen
Compugen, a genomics-based drug and diagnostic discovery company, increases the probability of successful development of novel drug and diagnostic products by incorporating ideas and methods from mathematics, computer science, and physics into biology, chemistry and medicine. This unique capability results in powerful predictive models and discovery engines, which are both advancing the understanding of important biological phenomena and enabling the discovery of numerous potential therapeutic products and diagnostic markers. The Company has an early stage in-house pipeline consisting of selected therapeutic protein candidates discovered by the Company; additional discoveries have been out-licensed for development. Among Compugen's customers and partners are leading pharmaceutical and diagnostic companies, such as Abbott Laboratories, Diagnostic Products Corporation, Novartis, and Pfizer. Compugen has established a small-molecule drug discovery subsidiary – Keddem Bioscience, and an agricultural biotechnology subsidiary – Evogene. For additional information, please visit Compugen's corporate Website at www.cgen.com.

About Ramot at Tel Aviv University Ltd.
Ramot, the technology transfer company of Tel Aviv University (TAU), seeks to strengthen the relationship between TAU's research community and the business community, and to expedite the transfer of promising new technologies from the university to the market place. Ramot identifies emerging technologies ripe for commercial development, establishes patent positions, structures research and license agreements and forms R&D collaborations, joint ventures and start up companies.

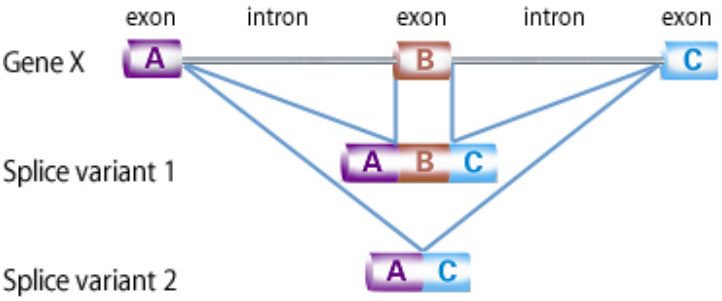
This press release contains "forward-looking statements" within the meaning of the Private Securities Litigation Reform Act of 1995. These statements include words like "may," "expects," "believes," and "intends," and describe opinions about future events. These forward-looking statements involve known and unknown risks and uncertainties that may cause the actual results, performance or achievements of Compugen to be materially different from any future results, performance or achievements expressed or implied by such forward-looking statements. Some of these risks are: changes in relationships with collaborators; the impact of competitive products and technological changes; risks relating to the development of new products; the ability to implement technological improvements; the ability of Compugen to obtain and retain customers. These and other factors are identified and more fully explained under the heading "Risk Factors" in Compugen's annual reports filed on form 20F that are filed with the Securities and Exchange Commission.

Notes to Editors:

About Alternative Splicing

Alternative splicing is the differential joining of exons in the same gene to produce two or more splice variants. It has been recently estimated to occur in at least 50% of human genes. Although discovered in 1980, alternative splicing was considered rare until just a few years ago. As early as 1997, Compugen used advanced mathematical modeling to accurately predict that alternative splicing is the rule rather than the exception in humans, and that proteins vastly outnumber genes. Protein isoforms derived from the same gene often possess different biological functions, which is significant for target identification and drug discovery.

A Schematic Representation of Alternative Splicing in Gene X



Alternative splicing is one of the major contributing factors to the diversity of the proteome and the transcriptome, which is defined as the complete collection of RNA molecules derived from a genome. A transcriptome in a cell is dynamic and is changed both spatially and temporally. While different tissues or cell types in an organism have the same genome (except for somatic mutations), their transcriptomes could be vastly different. The analysis of the dynamic and transitive nature of the transcriptome requires unique technologies and computational considerations.