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 April 2011

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 April 27, 2011, 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: Ms. Dikla Czaczkes Axselbrad
Title: Chief Financial Officer
Date: April 27, 2011

Compugen Discloses Splice Variant Based Program to Discover Superior Oncology Drug Targets for mAb Therapy

To date four protein splice variants have been identified and predicted to have potential advantages as oncology targets compared with the known proteins

Other Compugen target discovery programs are based on new members of protein families, expression analysis and functionality prediction

Tel Aviv, Israel, April 27, 2011 --- Compugen Ltd. (NASDAQ: CGEN) announced today that it is utilizing its proprietary *in silico* human transcriptome and proteome and additional computational systems to discover splice variants of known drug targets of high industry interest and of other known proteins with potential to become cancer targets for mAb therapy. This program has resulted so far in the discovery of four novel splice variant proteins predicted to be superior oncology targets compared with the previously known proteins. These four splice variants have entered Compugen's Pipeline Program and are at various stages of validation.

Compugen's proprietary *in silico* transcriptome and proteome infrastructure is the result of its decade-long research and modeling of various biological phenomena, including alternative splicing, resulting in a rich, comprehensive, and broadly applicable discovery infrastructure consisting of all genes and their respective splice variants and resulting proteins. In this program, Compugen is utilizing this proprietary knowledge database, together with additional discovery systems and tools, to discover novel splice variants that can serve as superior mAb targets.

Dr. Zurit Levine, Compugen's VP of R&D, stated, "We first selected a list of known proteins and drug targets that meet industry therapeutic criteria. Challenging traditional experimental discovery methods, we then utilized our *in silico* predictive human transcriptome and proteome, and additional proprietary discovery tools, to systematically discover previously unknown splice variants, which, although expressed by the same genes as the known proteins, have a unique epitope within their extracellular region which would allow the development of specific mAbs. Next, we tested their predicted expression, function and certain other properties compared with the known proteins. For example, several of these candidate targets exhibited a potential unique expression pattern, while others exhibited a potential superiority in their functional or structural characteristics. To date, this process has resulted in four candidate targets with predicted superiority compared with the existing proteins."

Dr. Levine continued, "Including this splice variant program, we are now discovering potential targets for monoclonal antibodies and other therapeutic approaches through the use of four distinct but mutually supporting programs. The other three target discovery programs are based on sophisticated expression analysis utilizing our unique MED Platform and its new field extension modules, new protein family members, and, at an earlier stage of capability development, functional prediction. With respect to mAb therapy, these four approaches facilitate discovery of candidate targets applicable for various mAb technologies, such as antibody-drug conjugates (ADCs), and enhanced antibody dependent cell mediated cytotoxicity (enhanced ADCC)."

Dr. Anat Cohen-Dayag, president & CEO of Compugen, added, "This is an excellent example of how we can utilize our proprietary predictive biology infrastructure on a 'market-need' driven basis to quickly identify *in silico* discoveries in areas of high industry interest that have eluded traditional experimentally based approaches. It took more than a decade of pioneering the understanding of key life processes at the molecular level, such as alternative splicing, to create the core of this infrastructure, but it is now proving to be a valuable and unique resource for systematic therapeutic and diagnostic product candidate discovery."

About Alternative Splicing

mRNA transcripts are produced from the genome by a process of transcription and splicing, in which the exons of the gene are derived from the genome and connected to create the resulting transcript. Alternative splicing is a phenomena that occurs when various different exon combinations are possible, thus resulting in multiple mRNA transcripts originating from the same gene. These different mRNA transcripts are translated into multiple possible protein isoforms which may have similar or different functions. The combinatorial nature of alternative splicing enables the genome to produce numerous transcripts from a relatively small number of genes, allowing a more varied proteome.

For more than a decade, Compugen has been a pioneer and continues to be a world leader in understanding the alternative splicing of genes and predicting the resulting combination of exons leading to the formation of splice variants that are probable to occur in nature. One of Compugen's first breakthroughs in the deeper understanding of biological phenomena at the molecular level was its prediction regarding the high prevalence of alternative splicing. This prediction, that alternative splicing is the norm rather than the exception, was later confirmed by the Human Genome Project and following works, which resulted in the understanding that fewer genes exist in the human genome than previously believed.

About Compugen

Compugen is a leading drug and diagnostic discovery company providing novel product candidates addressing important unmet therapeutic and diagnostic needs to pharmaceutical, biotech and diagnostic companies under milestone and royalty bearing or other revenue sharing agreements. Unlike traditional high throughput trial and error experimental based discovery, Compugen's discovery efforts consist of *in silico* (by computer) hypothesis-driven product candidate prediction and selection followed by *in vitro* and *in vivo* experimental validation. Compugen' unique *in silico* prediction and selection capabilities are based on a broad and continuously growing infrastructure of proprietary scientific understandings and predictive platforms, algorithms, machine learning systems and other computational biology tools. Industry collaborations may be entered into before product candidate discovery is undertaken pursuant to "discovery on demand" type arrangements, or with respect to existing product candidates, can be initiated prior to, or at the proof of concept stage, or after selected preclinical activities have been undertaken by Compugen. In 2002, Compugen established an affiliate, Evogene Ltd. (www.evogene.com) (TASE:EVGN.TA), to utilize certain of the Company's *in silico* predictive discovery capabilities in agricultural biotechnology. For additional information, please visit Compugen's corporate website at www.cgen.com.

This press release may contain "forward-looking statements" within the meaning of the Private Securities Litigation Reform Act of 1995. These statements include words such as "may", "expects", "anticipates", "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; and the ability to implement technological improvements. These and other factors are identified and more fully explained under the heading "Risk Factors" in Compugen's annual reports filed with the Securities and Exchange Commission.

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