Team cracks the atomic structure of a major cancer drug target

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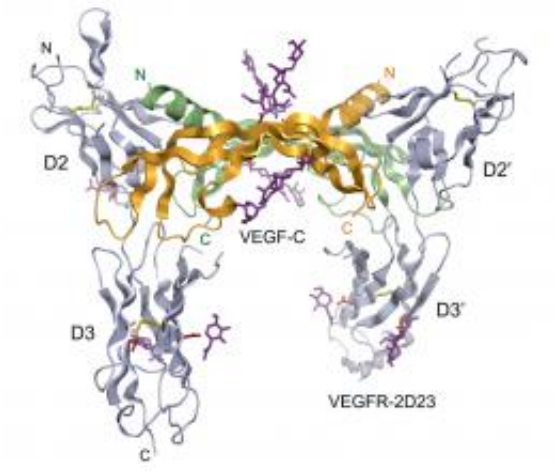

The crystal structure of the complex between the VEGF-C growth factor and the VEGFR2 receptor. The VEGF-C polypeptide chains are colored in yellow and green and the receptor chains are colored in light blue. The sugar moieties are in purple.

(PhysOrg.com) -- Researchers at the University of Helsinki, Finland, and the Paul Scherrer Institute (PSI) in Villigen, Switzerland, have determined the crystal structure of the ligand binding domain of a vascular endothelial growth factor (VEGF) receptor in complex with one of its ligands (VEGF-C).

Cancer cells require access to blood and lymph vessels for invasive growth and metastasis. By releasing VEGFs, cancer cells stimulate the

surrounding blood vessels to invade the cancerous tumor mass. Blocking this process is a new strategy to inhibit tumor growth.

VEGFs and their receptors have been identified as major targets for drug development in cancer therapy and the VEGF receptor that the groups analyzed is currently the most important target of such drugs. The Finnish group discovered the VEGF-C growth factor in 1996 and found that it is involved in lymphatic vessel growth, cancer metastasis and, more recently, also in blood vessel growth in cancer.

The collaborative work published in *PNAS* by the two research teams provides significant new insights into VEGF receptor function. It was also made possible by the long-standing interest and collaborative research of the binational team and the availability of excellent crystallography beamlines at the Swiss Synchrotron Light Source located at PSI, and supported by the European Union.

More information: V-M Leppänen, A Prota, M Jeltsch, A Anisimov, N Kalkkinen, T Strandin, H Lankinen, A Goldman, K Ballmer-Hofer and K Alitalo, Structural determinants of growth factor binding and specificity by VEGF-Receptor 2. Proc. Natl. Acad. Sci. USA

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