MY CANCER GENOME

June 2013 Volume 1, Issue 2

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New Disease Content

Acute Myeloid Leukemia

HER2 in Breast Cancer

PR in Breast Cancer

Updated Genes on MCG

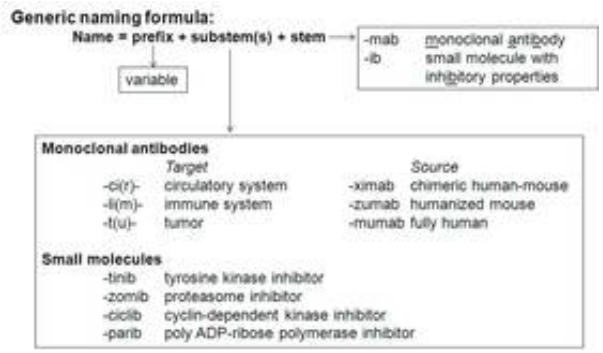
NRAS in Lung Cancer

RET in Lung Cancer

Articles of Interest

Awad MM et al. Acquired resistance to crizotinib from a mutation in CD74-ROS1. N. Engl. J. Med. 2013 Epub Jun 1

My Cancer Genome Feature: Table of Anti-cancer Agents



As anti-cancer agents move through the development lifecycle, they are sequentially assigned a development name, a generic name, and a trade name. Keeping up to date with these names can be a challenge, and a regularly updated anticancer agent list provides a resource for clinicians for this task. Starting in October 2012, we have expanded our molecular medicine content to include our targeted therapeutics list.

Generic names and trade names are assigned by two different processes. After a drug has been assigned an IND number by the FDA and entered clinical trials, an application is submitted to the United States Adopted Name (USAN) Council to obtain the generic name. The generic names follow specific nomenclature guidelines. In general, after phase III trials are completed, the trade name is obtained as part of the FDA approval process. Classification and naming of targeted therapeutics is described in our overview of targeted therapies for cancer page on My Cancer Genome.

Our targeted therapeutics list has been divided into six tables of anticancer agents: kinase inhibitors, therapeutic antibodies, immunotherapies, chemotherapies, hormonal agents and other agents. The tables provide information on the class or sub-class, drug target, development name, generic name, trade name and other information for each agent. The table is updated regularly from recent publications, the USAN monthly listings of adopted names, and ASCO notifications of trade names for newly approved anti-cancer drugs.

Contributor Highlight: Recent Content Updates on MCG

David B. Solit, M.D.

Shaw AT et al. Crizotinib versus chemotherapy in advanced ALK-positive lung cancer. N. Engl. J. Med. 2013 Epub Jun 1

Newsletter Archive

May 2013 MCG Newsletter

Contact Us

mycancergenome@vanderbilt.edu

www.mycancergenome.org

Associate Attending Physician, Memorial Sloan-Kettering Cancer Center

Bladder Cancer Section Editor and Melanoma Consulting Editor, MyCancerGenome.org

Dr. Solit is the Section editor for the bladder cancer section and a consulting editor for the melanoma section of MyCancerGenome.org. New content in the bladder cancer and *TSC1* mutation pages include updates from Dr. Solit's study entitled " Genome sequencing identifies a basis for everolimus sensitivity". This pivotal study identified a *TSC1* mutation in a patient's tumor tissue after the patient demonstrated a 3-year remission on everolimus in an advanced bladder cancer trial. This study and similar studies provide the rationale for the new NCI Initiatives for Exceptional Responders and the NCI-MATCH trial - see article below.

Oliver Gautschi, M.D.

Senior Consultant, Cantonal Hospital Luzern; Assistant Professor, Universtity of Bern; President, SAKK Lung Cancer Group and ETOP Study Coordinator

Lung Cancer Contributor, MyCancerGenome.org

Dr. Gautschi is a contributor for the lung cancer section of MyCancerGenome.org. Recently, the *HER2* Exon 20 Insertion in Lung Cancer and the *RET* Fusions in Lung Cancer pages in the lung cancer section have been updated with information from two of Dr. Gautschi's studies. In the first study, a retrospective analysis in collaboration with French investigators of 65 NSCLC patients, outcomes on several targeted therapies including anti-HER2 agents were correlated with *HER2* mutation status. In the second study, Dr. Gautschi et al. reported a first patient with lung adenocarcinoma harboring KIF5B-RET who responded to the multi-targeted tyrosine kinase inhibitor vandetanib. Previously, Dr. Gautschi reported on a first patient with BRAF V600E lung adenocarcinoma responding to vemurafenib.

Contributor Highlight: Molecular Medicine - Drug Table

Christine M. Lovly, M.D., Ph.D.

Instructor of Medicine, Division of Hematology and Oncology; Vanderbilt University

Deputy Editor, MyCancerGenome.org

Dr. Lovly has been involved with the planning, design and content of MyCancerGenome.org since its inception in 2010. In addition to her contributions to the molecular medicine section, she is the section editor of the lung cancer and melanoma sections, as well as a contributor to the inflammatory myofibroblastic tumor (IMT) section. Dr. Lovly recently presented on potentially actionable kinase fusions in IMT at ASCO 2013 - Abstract 10513. In addition to reporting on 14 *ALK* fusions in a 30-

sample tumor tissue cohort, the study also identified novel *ROS1* and *PDGFRβ* fusions in this rare cancer type. Dr. Lovly is also a recent recipient of a Damon Runyon Clinical Investigator Award.

Jonathan L. Aston, Pharm.D.

Clinical Pharmacist, Medical Oncology; Vanderbilt University

Molecular Medicine Contributor, MyCancerGenome.org

Dr. Aston recently joined the MyCancerGenome.org contributor team in 2013 and is a contributor to the molecular medicine section, with a particular emphasis on the list of anticancer agents. Dr. Aston is a graduate of Lipscomb University and the University Illinois Chicago College for Pharmacy, and has been a Clinical Oncology Pharmacist at Vanderbilt since 2008.

Trial Design Highlight: NCI Exceptional Responders Initiative and MATCH (Molecular Analysis for Therapy Choice) Initiative

At the American Association for Cancer Research (AACR) annual meeting in April 2013, the National Cancer Institute (NCI) announced two new initiatives for genetically informed cancer medicine. In the NCI Exceptional Responders initiative, 100 to 200 exceptional responders will be identified (defined as patients demonstrating at least a 6-month response in a clinical trial where only 1-10% of patients demonstrated a response in the cancer type, and the drug was not approved in that indication). This initiative could provide the rationale for renewed drug development or the basis for developing novel predictive assays.

In the NCI-MATCH (Molecular Analysis for Therapy Choice) clinical trial, 3000 patients will be screened to enroll 800-1000 participants. Enrollment is expected to start by mid-2014. One quarter of enrolled patients will have rare cancers, while 75% will have common cancers including breast, lung, colon or prostate cancer. Whole genome sequencing will be performed on available tissue from enrolled patients to identify 100 actionable mutations. A potential bank of drugs that have completed safety and toxicity trials but have been terminated or have not been approved will be matched to the patients with actionable mutations.