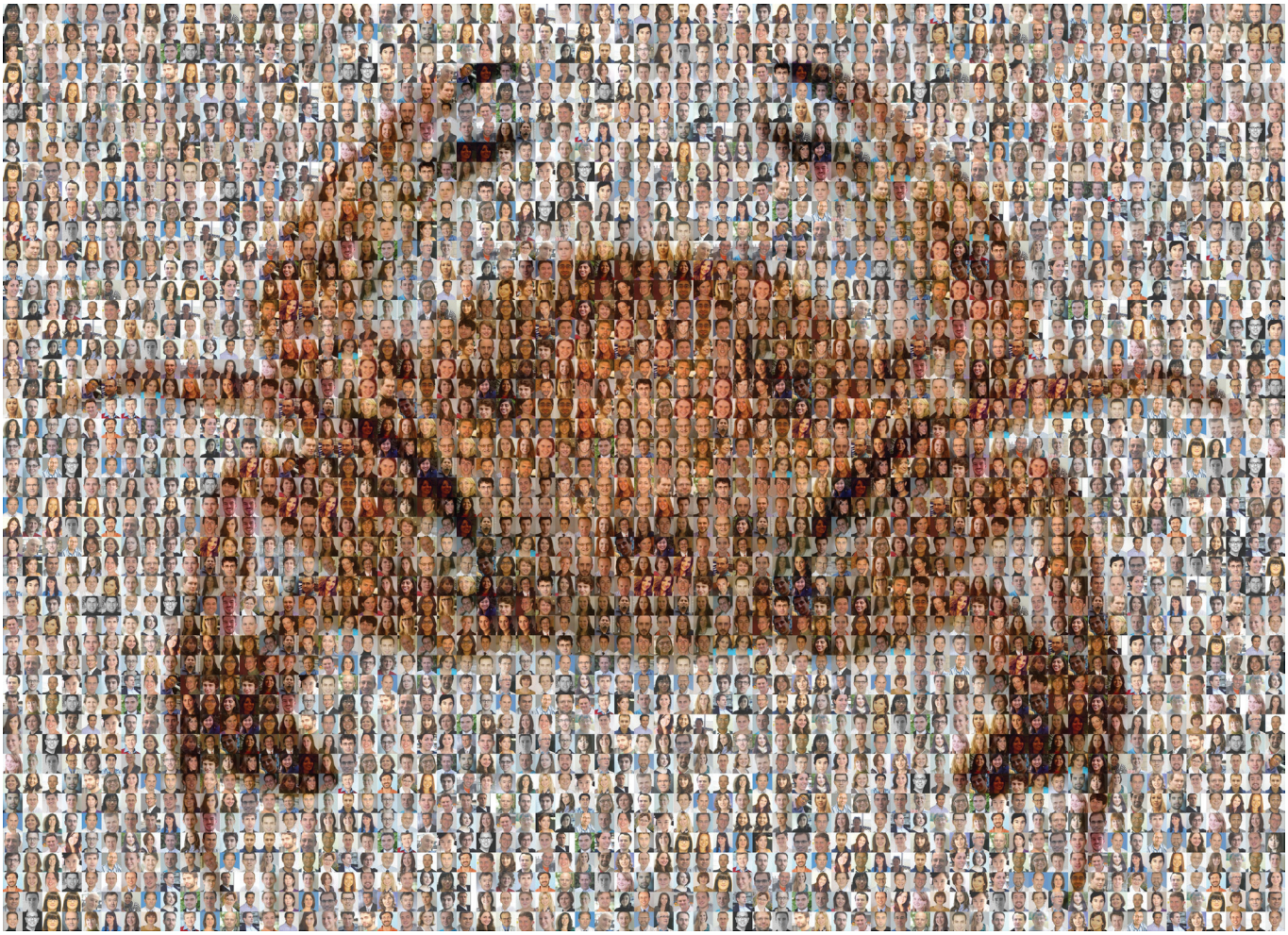
University of Zurich[UZH] | ETH zürich

SCOOPED

ISSUE 2 06/2015

The Cancer Biology PhD Program Newsletter



Dear Readers,

This is the second issue of SCOOPED, the biannual Cancer Biology PhD program newsletter.

So far, contribution to the newsletter has been fantastic and we would like to thank everybody involved for making the effort. However, the success of this newsletter will always depend on your assistance, ideas and feedback. We therefore encourage you to contact us when:

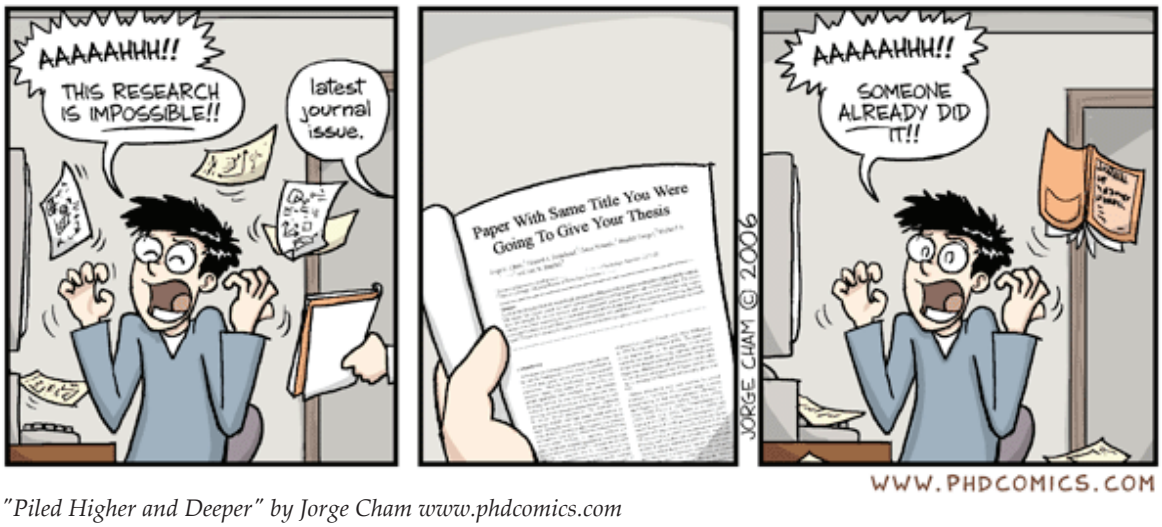
- **you publish a paper you would like to share with the cancer research community in our «Research Highlights» section**
- **you develop an exceptional technique other labs could profit from, which you would like to explain in more detail**
- **you go to a conference and would like to write a brief report about the highlights of the meeting**
- **you have some other type of information you would like to communicate**
- **you want to give us some general feedback**

In addition we are looking for motivated people who are interested in joining the newsletter team. Please contact us if you would like to contribute to the next issue of SCOOPED by collecting information, conducting interviews or writing articles:

CancerBioNews@gmail.com

We hope you enjoy reading this issue :)

Mara Hartung, Corina Schmid, Michael Flori and Hannah Parker



"Piled Higher and Deeper" by Jorge Cham www.phdcomics.com

Recent Publications by CB PhD Students

Melanie Ruf - Group Prof. Dr. Holger Moch

We discovered that the frequent CD70 expression in clear cell renal cell carcinoma is directly driven by HIF as a consequence of inactivated Von Hippel-Lindau protein. Furthermore, CD27+ lymphocytes preferentially infiltrate CD70-expressing tumors, which is linked to high soluble CD27 levels observed in the sera of patients. CD27 could thus present a new diagnostic serum marker.

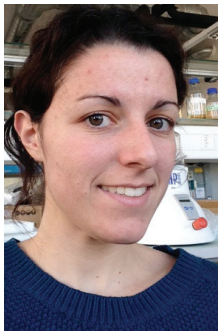
pVHL/HIF-regulated CD70 expression is associated with infiltration of CD27+ lymphocytes and increased serum levels of soluble CD27 in clear cell renal cell carcinoma

Ruf M, Mittmann C, Nowicka AM, Hartmann A, Hermanns T, Poyet C, van den Broek M, Sulser T, Moch H, Schraml P

Abstract:
Purpose: CD70, a member of the TNF ligand superfamily, has been shown frequently overexpressed in clear cell renal cell carcinoma (ccRCC). The mechanisms of CD70's upregulation and its role in ccRCC are unknown. Experimental Design: CD70 expression was immunohistochemically analyzed in 667 RCCs and RCC metastases. Von Hippel–Lindau gene (VHL) mutations, expression patterns of VHL protein (pVHL), hypoxia-inducible factor (HIF) α, and several HIF targets were studied in tissues and cell lines and correlated with CD70 overexpression. Gene promoter analysis was performed to confirm CD70 as HIF target gene. Consecutive tissue sections were immunostained to reveal the relation between CD70-expressing RCCs and tumor-infiltrating lymphocytes positive for the CD70 receptor (CD27). CD70-mediated release of soluble CD27 in RCC was assessed by coculture experiments and sera analysis of patients with RCC. Results: Elevated CD70 expression was seen in 80% of primary tumors and metastases of ccRCC and correlated with dysregulation of the pVHL/HIF pathway. In vitro analyses demonstrated that CD70 upregulation is driven by HIF. Furthermore, CD27+ lymphocytes preferentially infiltrate CD70-expressing ccRCCs. CD70-dependent release of soluble CD27 in cocultures may explain the high CD27 levels observed in sera of patients with CD70-expressing ccRCC. The combination of lymphocyte infiltration and CD70 expression in RCC was associated with worse patient outcome.
Conclusion: Our findings demonstrate that in ccRCC, CD70 expression is regulated by HIF as a consequence of pVHL inactivation. Increased serum levels of CD27 suggest the existence of CD70-expressing ccRCC, thus representing a potential serum marker for patients suffering from this disease.

Read full article here
Clin Cancer Res. 2015 Feb 15;21(4):889-98

Laura Surace - Group Prof. Dr. Maries van den Broek



Our work sheds new light on the role of the complement system in cancer. Anaphylatoxins (C3a and C5a) are potent pro-inflammatory mediators produced when complement is activated. We could demonstrate that stimulation of tumor-specific immunity, in particular activation of CD8+ T cells and dendritic cells, depends on the intratumoral generation of C3a and C5a upon radiotherapy. Our findings demonstrate that anaphylatoxins are crucial to the therapeutic efficacy of the treatment.

Complement is a central mediator of Radiotherapy-induced tumor-specific immunity and clinical response

Surace L, Lysenko V, Fontana AO, Cecconi V, Janssen H, Bicvic A, Okoniewski M, Pruschy M, Dummer R, Neefjes J, Knuth A, Gupta A, van den Broek M

Abstract:
Radiotherapy induces DNA damage and cell death, but recent data suggest that concomitant immune stimulation is an integral part of the therapeutic action of ionizing radiation. It is poorly understood how radiotherapy supports tumor-specific immunity. Here we report that radiotherapy induced tumor cell death and transiently activated complement both in murine and human tumors. The local production of pro-inflammatory anaphylatoxins C3a and C5a was crucial to the tumor response to radiotherapy and concomitant stimulation of tumor-specific immunity. Dexamethasone, a drug frequently given during radiotherapy, limited complement activation and the anti-tumor effects of the immune system. Overall, our findings indicate that anaphylatoxins are key players in radiotherapy-induced tumor-specific immunity and the ensuing clinical responses.

Read full article here
Immunity. 2015 Apr 21;42(4):767-777

Recent Publications by CB PhD Students

Daniel Zingg - Group Prof. Dr. Lukas Sommer

In this study, we demonstrate the relevance of EZH2-mediated epigenetic gene repression for melanoma. By taking advantage of a murine melanoma model, we highlight that Ezh2 function is essential for malignant melanoma progression in vivo. Furthermore, we uncover that EZH2 facilitates the processes of melanoma growth and metastasis by controlling functionally distinct tumor suppressors.

The epigenetic modifier EZH2 controls melanoma growth and metastasis through silencing of distinct tumour suppressors
Zingg D, Debbache J, Schaefer SM, Tuncer E, Frommel SC, Cheng P, Arenas-Ramirez N, Haeusel J, Zhang Y, Bonalli M, McCabe MT, Creasy CL, Levesque MP, Boyman O, Santoro R, Shakhova O, Dummer R, Sommer L

Abstract:
Increased activity of the epigenetic modifier EZH2 has been associated with different cancers. However, evidence for a functional role of EZH2 in tumorigenesis in vivo remains poor, in particular in metastasizing solid cancers. Here we reveal central roles of EZH2 in promoting growth and metastasis of cutaneous melanoma. In a melanoma mouse model, conditional Ezh2 ablation as much as treatment with the preclinical EZH2 inhibitor GSK503 stabilizes the disease through inhibition of growth and virtually abolishes metastases formation without affecting normal melanocyte biology. Comparably, in human melanoma cells, EZH2 inactivation impairs proliferation and invasiveness, accompanied by re-expression of tumour suppressors connected to increased patient survival. These EZH2 target genes suppress either melanoma growth or metastasis in vivo, revealing the dual function of EZH2 in promoting tumour progression. Thus, EZH2-mediated epigenetic repression is highly relevant especially during advanced melanoma progression, which makes EZH2 a promising target for novel melanoma therapies.

Read full article here
Nat Commun. 2015 Jan 22;6:6051

Call for Papers

We would like to continue the section «Research Highlights» in the next issue of SCOOPED. The idea is to briefly highlight work that you have published as first author during your PhD in order to provide others with an overview of the research topics of the PhD program.

If you would like to share your recent publication with the cancer research community using this platform, please send the abstract and concise summary/significance (no more than 300 characters) of your work to:

CancerBioNews@gmail.com

Data mining the Cancer Genome Atlas

by Phil Cheng, Group Prof. Dr. Dummer

The Cancer Genome Atlas (TCGA)[1] is a large multicenter collaboration to characterize over 30 cancer types with genomic, transcriptomic, epigenomic and clinical data that is made publically available for every clinician and researcher to explore and analyze. To date, there are 10,000 cases in 33 tumor types available, with 20 cancer types having more than 200 cases (Table 1). The data are centralized at the TCGA data portal and can be downloaded for academic use.

The data types available are somatic mutations, copy number, gene expression, miRNA expression, DNA methylation, reverse protein phase array (RPPA), and clinical information. Access to the raw sequencing files from the exome sequencing, RNA sequencing (RNAseq), microRNA sequencing (miRNAseq), and copy number data require authorization from the Cancer Genomics Hub (CGHub). All the processed and annotated data are publically available and downloadable at the data portal. The analytical pipelines for each data type are available in a text file that is included in the download. By providing a standard method for raw data processing and annotation, it allows for reproducibility in downstream analysis.

Although the data is freely available, to analyze and interpret the data requires some bioinformatics expertise. Many webtools have been created to help biologists and clinicians to explore and analyze all this data. Of note, cBioportal [2] and the UCSC Cancer browser [3] are two of the best webtools to explore the TCGA data. Our lab has also created a webtool with the purpose of correlating gene expression with patient survival. Thus far we have generated the tool for 5 cancer types and will be continuing to add more for all TCGA cancers. The tool is located on the URPP cancer webpage at http://www.cancer.uzh.ch/research/Three/webtool.html.

The tool allows the user to select a gene and define the percentile of patients they want to compare for survival in the left toolbar (Figure 1). We take an unbiased approach in selecting the top and bottom percentiles for comparison. For instance, if the user selects 10% the tool will compare the top 10% patients expressing the gene of interest versus the bottom 10%. For some of the cancers, the data for overall survival and progression free survival are available and can easily be looked at with changing the survival time option in the left toolbar. The user can see the distribution of gene expression in the dot plot in the bottom of the left toolbar.

Table 1:

Cancer Types	Cases
Acute Myeloid Leukemia [LAML]	200
Bladder Urothelial Carcinoma [BLCA]	412
Brain Lower Grade Glioma [LGG]	516
Breast invasive carcinoma [BRCA]	1098
Cervical squamous cell carcinoma and endocervical adenocarcinoma [CESC]	308
Colon adenocarcinoma [COAD]	461
Glioblastoma multiforme [GBM]	528
Head and Neck squamous cell carcinoma [HNSC]	528
Kidney renal clear cell carcinoma [KIRC]	536
Kidney renal papillary cell carcinoma [KIRP]	291
Liver hepatocellular carcinoma [LIHC]	377
Lung adenocarcinoma [LUAD]	521
Lung squamous cell carcinoma [LUSC]	504
Ovarian serous cystadenocarcinoma [OV]	586
Prostate adenocarcinoma [PRAD]	498
Sarcoma [SARC]	261
Skin Cutaneous Melanoma [SKCM]	470
Stomach adenocarcinoma [STAD]	443
Thyroid carcinoma [THCA]	507
Uterine Corpus Endometrial Carcinoma [UCEC]	548

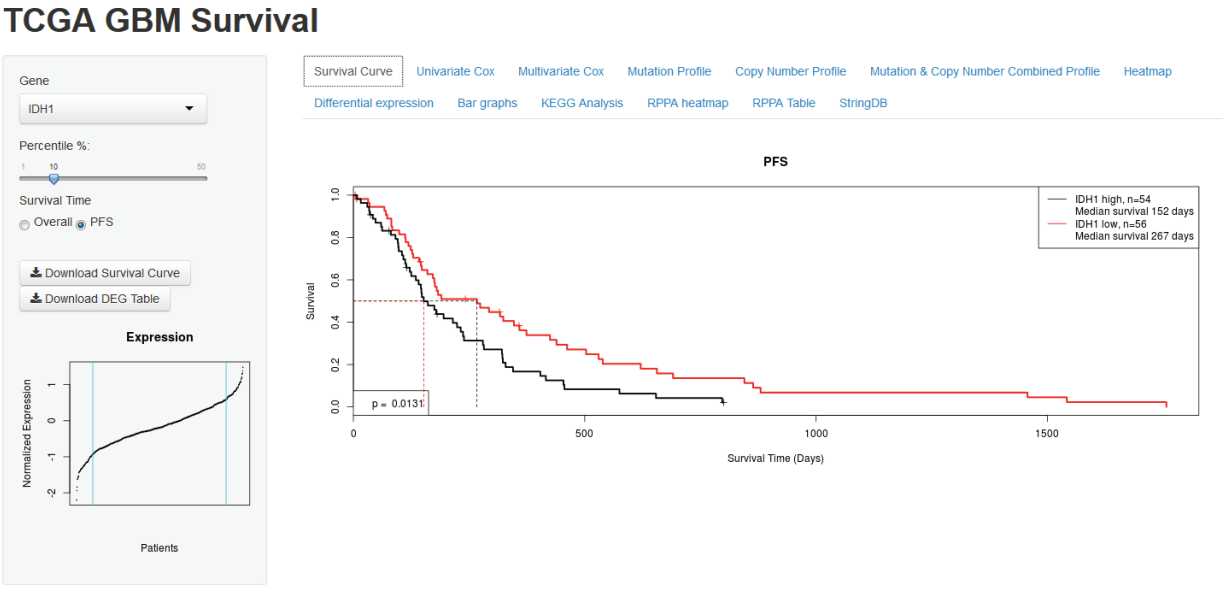


Figure 1: Survival module of the webtool. On the left toolbar, the gene of interest is displayed with the percentile of patients selected. Overall or progression free survival (PFS) can be chosen for the Kaplan-meier plot. The dot plot shows the distribution of gene expression across all the patients and the light blue bars shows the cohorts of patients selected by percentile. The main area of the webtool shows the Kaplan-Meier plot based on the gene of interest and percentile of patients with the p-value calculated by the log-rank test.

The tool has many modules for analysis of these two patient cohorts. The first is Survival Curve. Kaplan-meier analysis is performed on the two patient cohorts and the p-value is calculated from the log-rank test. Univariate and multivariate Cox regression analysis is also performed to determine the risk of high or low gene expression. In the mutation profile, copy number profile and combined profile modules, the most common genes with mutations and copy number alterations for the cancer are displayed in an Oncoprint-like graphic for the two patient cohorts (Figure 2). For downstream analysis, differential gene expression and pathway analysis are performed on the two patient cohorts. The heatmap and gene table for differentially expression genes are displayed and pathway analysis using the KEGG and StringDB databases are performed. Differential protein analysis is performed using the RPPA data and the heatmap with the gene table are also generated. Finally, the bar graphs module looks at the distribution of patients between the two cohorts based on clinical characteristics like age and gender (Figure 3).

In summary, this tool allows for easy access to the TCGA data with a focus on survival analysis. The user can input their gene of interest and choose the percentile they want to compare and instantly retrieve a wealth of information and analysis about this gene in terms of survival, mutation profile, differential gene expression and differential protein expression. We are slowly adding analysis modules and if you have any suggestions please feel free to email phil.cheng@usz.ch.

1. Weinstein JN, Collisson EA, Mills GB, Shaw KR, Ozenberger BA, Ellrott K, Shmulevich I, Sander C, Stuart JM, Network CGAR: The Cancer Genome Atlas Pan-Cancer analysis project. Nat Genet 2013, 45:1113-1120.

2. Cerami E, Gao J, Dogrusoz U, Gross BE, Sumer SO, Aksoy BA, Jacobsen A, Byrne CJ, Heuer ML, Larsson E, et al: The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. Cancer Discov 2012, 2:401-404.

3. Goldman M, Craft B, Swatloski T, Cline M, Morozova O, Diekhans M, Haussler D, Zhu J: The UCSC Cancer Genomics Browser: update 2015. Nucleic Acids Res 2015, 43:D812-817.

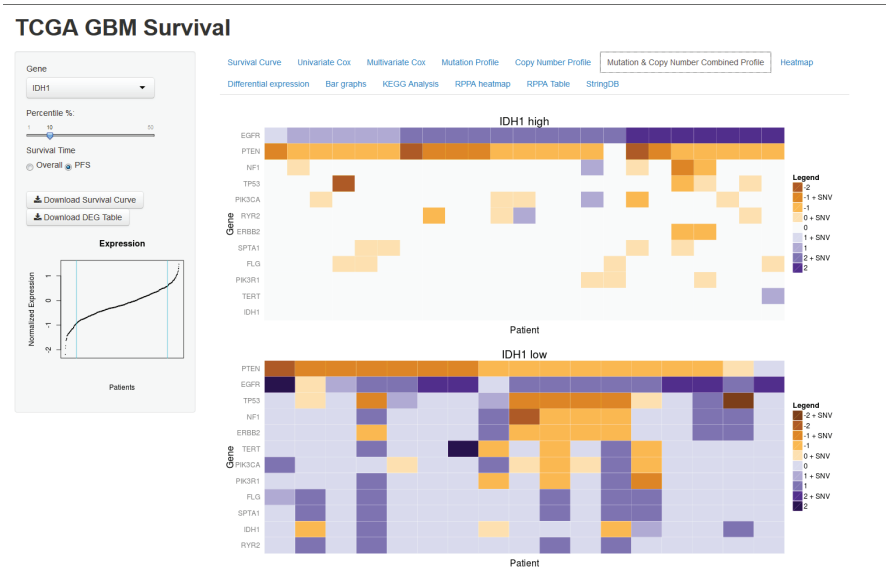


Figure 2: Combined mutation and copy number profile. In the main area of the webtool, Oncoprint-like graphics for IDH1 high and IDH1 low are displayed. Each column represents one patient and each row represents one gene. The blocks are color coded for copy number loss or gain and mutation.

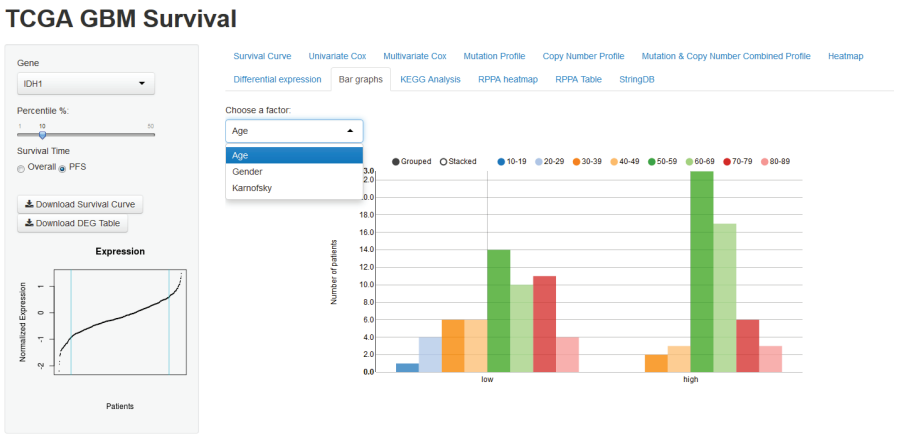


Figure 3; Bar graphs for clinical characteristics. In the main area of the webtool, bar graphs display the various clinical characteristics between the IDH1 high and IDH1 low groups. Here the user can select to look at age, gender and Karnofsky score.

Whatever became of...

...Isabelle Arnold - Postdoctoral Fellow, John Radcliffe Hospital, Oxford, UK

In which group of the CNZ did you obtain your PhD and how did you proceed afterwards?
I completed my Ph.D in 2010 in the lab of Prof. Anne Müller as part of the first promotion of CNZ students. After graduating, I stayed another 6 months in the lab to finish my ongoing work. In 2011, I successfully applied for an SNSF early post-doc mobility fellowship and joined the lab of Prof. Fiona Powrie at the University of Oxford in England.
Could you give us a short description of your current position, including daily responsibilities?
For the last four years, I have been working within the Translational Gastro-enterology Unit (TGU) of the John Radcliffe Hospital in Oxford. This lab has the particularity of bringing together fundamental scientists and medical researchers to study the pathogenesis of intestinal diseases at multiple levels. My project typically focuses on fundamental aspects of mucosal immunology, mostly involving animal experiments, but I also had the opportunity to work on collaborative projects with pharmaceutical companies and patient samples.
Besides the bench work, I supervise the progress and experimental design of PhD students' projects, write project proposals and contribute to the academic life through the active participation at multiple meetings and seminars.
Why did you choose this position?
During my Ph.D, I came to dive into the fascinating world of gastrointestinal immunology and it is very naturally that I decided to explore this field in more depth by joining a large and reputable group working in the field. The idea of doing a post-doc abroad to gain international experience and exposure to a multi-faceted approach to my work was also a key consideration to my choice.
Where did you apply for your current position and what did the application process look like?
Like most of the time in academia, opportunities come along with professional encounters and support from your supervisor. I first met Fiona Powrie during a conference. After visiting her lab in Oxford and meeting the people working there, she very nicely offered me to join her group as a post-doc.
Are you happy with your current position and to whom would you recommend it?
If you enjoy academic research and plan to stay in this career path, joining a well-established international research group abroad is an amazing experience, both for your personal and scientific development. The daily contact with young researchers from different nationalities and backgrounds offers a unique opportunity to broaden scientific knowledge and is, in my view, a key element for scientific creativity.
What are your plans for the future?
My medium term goal would be to lead my own research group in an academic institution, but I'm still evaluating possible options regarding the setting and location.

...David Fischer - Research Scientist Analytical Chemistry, Evolva AG, Reinach, CH

In which group of the CNZ did you obtain your PhD and how did you proceed afterwards?
I was working at the Functional Genomics Center in collaboration with Giancarlo Marra's lab. Main focus of the thesis was technology development (Mass spectrometry, metabolomics) with application in colorectal cancer. While I was writing my thesis, I was looking for job opportunities in these technology fields.
Could you give us a short description of your current position, including daily responsibilities?
I am still a scientist and the work is flexible and creativity-driven. There are two major differences I see compared to my PhD thesis: 1) I am working together in a team where everybody works for the same goal. Every week our team discusses the next steps and experiments. 2) This goal is clearly formulated, e.g. to produce a certain amount of a compound that we would like to produce by yeast fermentation. As a research scientist in analytical chemistry I am responsible for the analysis of fermentation products, mainly for the target compound we like to produce. This involves method development, routine analysis of samples and data processing/interpretation.
Why did you choose this position?
I always liked the analytical part of biological experiments. In this job I work together with biologists and am involved in discussing biology problems. But I am responsible for the analytics.
Where did you apply for your current position and what did the application process look like?
I found the application through "jobs.ch". Evolva requests to fill out a standardized online-form. After applying there, I was invited for a first interview with the analytical chemistry team. After this first round I was invited to a second interview where I had to give a presentation to all scientists in Evolva.
Are you happy with your current position and to whom would you recommend it?
I am here since 1 year and I still like it. There are some routine parts of the job, but still I would say it is mainly a research job where you are constantly thinking about (applied) scientific problems. Therefore I would recommend it to everybody who always liked to work in a lab, but wants to work more target- and team-oriented. You should be aware that working in such a small company in the biotechnology field is not the safest job and requires some flexibility.
What are your plans for the future?
I have no plan yet to leave my current job. I like to work practically and within a technology-driven environment. Maybe for the far future I can also see myself in a more administrative role, but for the moment I like it the way it is.

Whatever became of...

...Martin Steger - Postdoctoral Fellow, Max-Planck-Institute of Biochemistry, Munich, GER

In which group of the CNZ did you obtain your PhD and how did you proceed afterwards?
I graduated in the group of Prof. Alessandro Sartori at the IMCR (University of Zurich) in late 2012 and after a short postdoctoral stay (3 months) I decided to relax a little and went traveling etc. for 4 months. In the meantime I was looking for jobs, preferentially in the industry (science related) or for postdoc positions with a more technical focus (mass spectrometry). I applied (all blind applications) for positions in several labs with leading expertize in mass spec and finally got accepted in the lab of Prof. Matthias Mann at the Max-Planck-Institute of Biochemistry in Munich. I started my postdoc in June 2013 with a Max-Planck fellowship and obtained the Swiss National Science Foundation Early Postdoc Mobility fellowship later in 2013.
Could you give us a short description of your current position, including daily responsibilities?
Currently I am involved in various projects of biomedical relevance (often in collaboration with pharmaceutical companies) in which mass spectrometry-based proteomics is applied. I have to deal with many different things including chromatography, mass spectrometry and bioinformatics but also all kind of cell biology and biochemistry. I have also a lot of internal meetings and teleconferences with my collaborators and quite some freedom in leading projects.
Why did you choose this position?
As I mentioned earlier, I chose this position because I wanted to change research focus. During my PhD I was mostly doing cell biology and a bit of biochemistry. I liked my work but at the same time I could not imagine to do the same things during my postdoc. Now my research focus is much more oriented on technical aspects of protein mass spectrometry.
Where did you apply for your current position and what did the application process look like?
I personally contacted my current supervisor and applied for a position. I was then invited for a one day interview in which I had to give a talk and then I was interviewed by ~10 persons (project leaders, postdocs and PhD students) all day long. Shortly after, I was offered the position.
Are you happy with your current position and to whom would you recommend it?
I am very happy with the current position because I can manage my time the way I like it and I have lots of freedom in leading my projects. The Max-Planck-Institute is a fantastic place for science with many possibilities for career development. I would recommend my position to both PhDs who want to pursue an academic career and those who are interested in joining a company after their postdoctoral experience.
What are your plans for the future?
If possible I will try to stay here at the MPIB for another 2-3 years. Depending on the possibilities and on the publication record I will then decide whether or not it makes senses to follow an academic career. I am very much open on where to go; ideally I would prefer to be around the Alps though.

New CNZ Members 2015

January
Prof. Dr. Burkhard Ludewig - Institute of Immunobiology, Cantonal Hospital St. Gallen
Prof. Dr. Damien Weber - Center for Proton Therapy, Paul Scherrer Institut
Prof. Dr. Lorenza Penengo - Institute of Molecular Cancer Research, UZH

February
Prof. Dr. Matthias Altmeyer - Institute of Veterinary Biochemistry and Molecular Biology, UZH

March
PD Dr. Raffaela Santoro - Institute of Veterinary Biochemistry and Molecular Biology, UZH
Prof. Dr. Markus Rudin - Institute for Biomedical Engineering, ETH and UZH

April
Prof. Dr. Christoph Driessen - Cantonal Hospital St. Gallen

Prof. Dr. Matthias Altmeyer

Institute of Veterinary Biochemistry and Molecular Biology

Can you give us a brief overview of your career?
I studied Biology at the University of Konstanz in southern Germany. From there I moved further south to Zurich in 2007 to pursue a Ph.D. in Molecular Biology within the MLS Program of the Life Science Zurich Graduate School. In 2010 I headed north to Copenhagen, Denmark, for my postdoctoral studies with Prof. Jiri Bartek and Prof. Jiri Lukas – first at the Danish Cancer Society and later at the Novo Nordisk Foundation Center for Protein Research at the University of Copenhagen.
When did you move to Zurich?
I moved back to Zurich in October 2014.
When did you join the Cancer Network Zurich and why?
I joined the Cancer Network Zurich shortly after, in February 2015. The CNZ is a vital platform to connect researchers and clinicians who share the common goal to better understand how cancer develops and how we can improve prevention, diagnosis and therapy. Such interdisciplinary scientific exchange holds great promises, and I look very much forward to sharing know-how and ideas with other CNZ members.
How many people are currently working in your lab?
We are currently a group of five: two Ph.D. students, one research technician, a master student, and me.
What is the main focus of your research?
Research in my lab is focused on how mammalian cells maintain a stable genome, and how the underlying molecular mechanisms are subverted in cancer. Cells have developed a fantastic molecular choreography to coordinate a multitude of DNA transactions in space and time. With the help of quantitative cell imaging and high-content microscopy we aim to understand the principles of this choreography, and how it is altered in cancer cells. In particular, we study how chromatin modifications such as phosphorylation, ubiquitylation and poly(ADP-ribosyl)ation are regulated in response to genotoxic stress and how they facilitate the repair of DNA lesions.
What was your most memorable lab experience?
I am always amazed when a research project, born from a simple and often naïve idea, suddenly reaches the level when all the different bits and pieces fall into place and everyone in the lab starts to contribute and help develop the project further. The experience of such dynamics in a team of dedicated scientists is among the best lab memories I have.
What is the motivation that keeps you going?
The fact that in research there is always the chance to find something new, something unexpected, something exciting. Having the possibility to explore, as part of an imaginative and motivated team, is a great privilege.
Which advice would you give a fresh PhD student?
Stay fresh in your mind, keep yourself motivated, and enjoy the quest.
What is the last book you have read?
The Art of Travel by Alain de Botton.

PD Dr. Raffaella Santoro

Institute of Veterinary Biochemistry and Molecular Biology

Can you give us a brief overview of your career?
I studied Chemistry at the University of Rome, La Sapienza, where I have also performed my PhD work. I then moved to Germany for a postdoc (2 years in Jena and 9 years in Heidelberg at the German Cancer Research Center). Since my PhD, I have been working on epigenetics that is still the main focus of my research.
When did you move to Zurich?
I moved to the University of Zurich, at the Institute of Veterinary Biochemistry and Molecular Biology, in October 2009.
When did you join the Cancer Network Zurich and why?
March 2015. To progress in the development of effective therapy and early diagnosis of cancer it is essential to establish an active crosstalk between basic and clinical research and CNZ represents an important platform to facilitate communication between clinicians and research scientists. That is why I joined CNZ.
How many people are currently working in your lab?
7 PhD students, 2 Master students and 1 research technician
What is the main focus of your research?
An important aim of my research is the molecular understanding of epigenetic dis-regulation that is a hallmark of cancer cells.
What was your most memorable lab experience?
Actually many, here you are the most recent. Apart from the curiosity, we all work in basic research with the idea that maybe one day our results will be useful for the fight against cancer. Last year we found out that all the work done over the years to understand the basics of epigenetic regulation turned out to be informative for early detection of aggressive prostate cancer and thus helpful in preoperative therapy decision-making for prostate cancer patients. I think this is a good and instructive example of bridging together basic research with clinical investigation.
What is the motivation that keeps you going?
Curiosity, learning every day new things, keeping myself updated for new technologies and the firm belief that the knowledge of basic molecular mechanisms will be one day instrumental for therapy and diagnosis of cancer.
Which advice would you give a fresh PhD student?
I always say to my fresh PhD students that, particularly at the beginning, they need help from the others being in the lab since longer time. They have not to be too proud to ask. In six months, the others will also start to ask his/her advices. It makes things running faster, increases communication skills and team work and obviously establish a nice and collaborative atmosphere in the lab that is so necessary for a good work.
What is the last book you have read?
I have just finished Edge of Eternity by Ken Follett and re-reading The Count of Monte Cristo by Alexandre Dumas.

CNZ Retreat 2015

by Daniela Engler-Anders

Dear CNZ Members,

From April 12 - 14 2015, the 6th CNZ retreat took place in Emmetten with a total of 136 participants joining the event. We had an outstanding scientific program, with interesting and fruitful discussions and a beautiful location with perfect weather. The Cancer Biology Mini Symposium organised by the PhD students was also part of our program. Fran Balkwil, Mohamed Bentires-Alj, Steve Jackson and Timm Schroeder made sure that we had great scientific input from the cancer community outside of the CNZ. Furthermore, the URPP Translation Cancer Research with presentations from Burkhard Becher, Mitch Levesque, Maries van den Broek and Evelyn Lattmann, completed this outstanding program. During both evenings, we had our poster sessions and, since the posters were of such great quality, it was difficult for the poster session committee to decide on the poster prizes. We had 4 poster prize winners this time: Daniel Zingg, Julia Aguade-Gorgorio, Maryna Levikova and Gabriele Manzella. The winner of the prize for the best talk was Corina Schmid.

We would like to thank all participants for making it such a great retreat!

Poster and Talk Price Winners: Julia Aguade-Gorgorio, Maryna Levikova, Daniel Zingg, Gabriele Manzella, Corina Schmid

We thank our supporters:

krebsforschung schweiz
recherche suisse contre le cancer
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Roche

NOVARTIS

New CB PhD Student Representatives

Sabine Urban and Chiara Giorgi introduce themselves as the new PhD Student Representatives...

Where do you come from?
Sabine I am from Germany and was born and raised in Jülich - a small town near the border to Belgium and Holland.
Chiara I come from the Italian city of Pisa, most famous for its Leaning Tower.

Where did you do your masters?
Sabine I did my masters in the student city of Münster in Germany and in Edinburgh.
Chiara I studied Biotechnology and Molecular/Cellular biology at the University of Pisa.

In which lab are you doing your PhD?
Sabine At the moment I work in the lab of Anne Müller at the IMCR (UZH) on Irchel.
Chiara I am currently working on Ewing sarcoma in the laboratory of Beat Schäfer, at the University Childrens' Hospital of Zürich.

Why did you choose to become a student representative and what will your tasks be as the new representative?
Sabine When I chose my place for a PhD I wanted to join a graduate school because I hoped to find exactly what I found at the Cancer Biology PhD graduate school. A mixed group of young and motivated PhD students who love to talk about their work and discuss it but also want to build up a social network. By this it was easy to get connected. And knowing people makes life easier at work if you need help or support. Because I had such a great benefit I really like to keep up the tradition of social and network events. By this also the younger generation of PhD students will profit from all the opportunities as I did and still do. Together, we want to carry on organising the social and network events. We are the contact persons for any concern and we are open to discuss suggestions and ideas concerning the PhD program.
Chiara The Cancer Biology PhD program offered me and all students the chance to meet and create a network. Already during the round of interviews that I had in September 2012, I liked the atmosphere of unity that characterised the program. Besides the interviews, thanks to the variety of events organised, I also had the chance to meet my future colleagues and friends. As I really like organising events and since I wanted to be more involved in this program, I decided to candidate-myself as student representative together with Sabine Urban. Our tasks will be to take part actively in steering committee meetings to propose the students' point of view and to organise social events.

Left: Chiara **Right**: Sabine

What is your favourite dish?
Sabine In this point I am a bit British. I love teatime, especially with cake.
Chiara I like cooking and experimenting in the kitchen.

Where is your favourite place in Switzerland?
Sabine This country has too many fantastic places to mention just one. In Zürich I love to be at the lake and the river to walk and relax.
Chiara I love spending the early mornings during the weekend riding my bike along the lake of Zürich.

Tell us one interesting fact about yourself.
Sabine I like fencing and climbing.
Chiara I like playing volleyball in a team here in Zürich.

Impressum

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