## Biomedical Neuenheim Campus

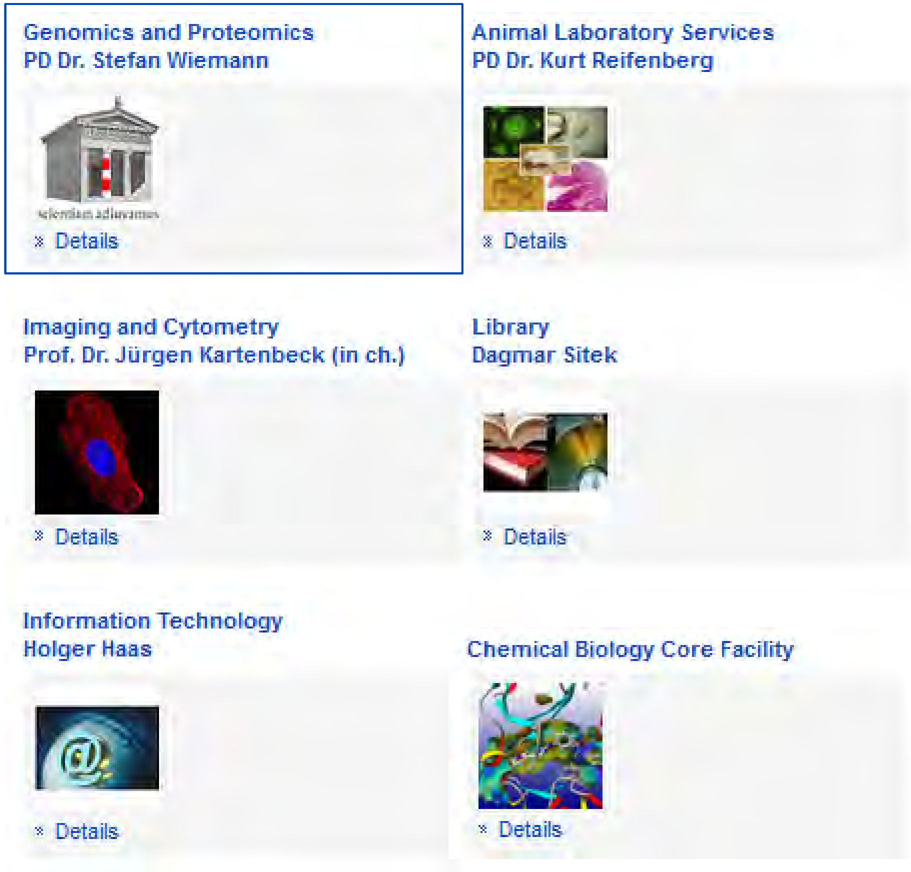
# German Cancer Research Center (DKFZ) Heidelberg

## Genomics and Proteomics Core Facility

**Stefan Wiemann**

GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION

# Core Facilities at DKFZ



Genomics and Proteomics
PD Dr. Stefan Wiemann

» Details

Animal Laboratory Services
PD Dr. Kurt Reifenberg

» Details

Imaging and Cytometry
Prof. Dr. Jürgen Kartenbeck (in ch.)

» Details

Library
Dagmar Sitek

» Details

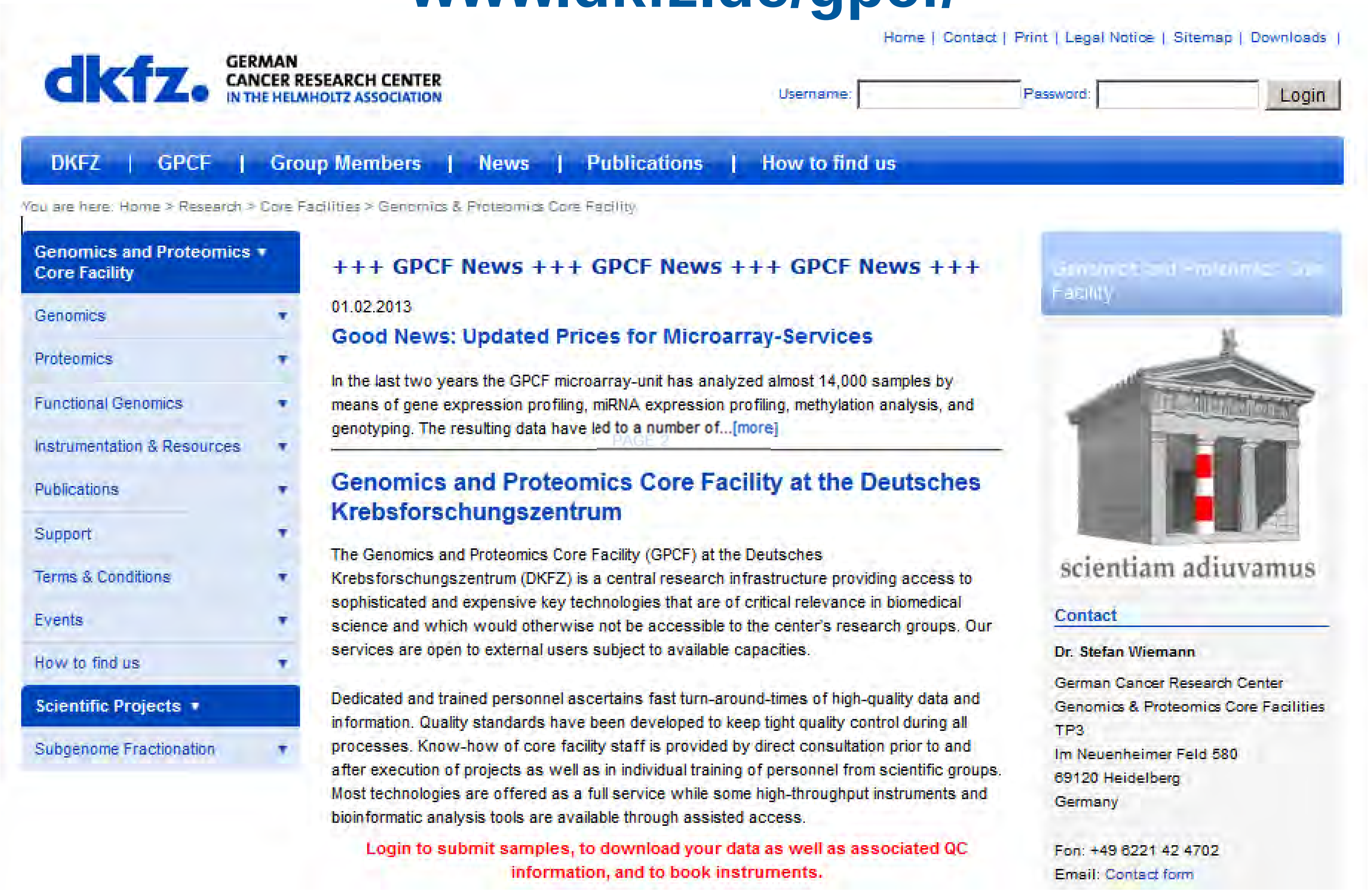
Information Technology
Holger Haas

» Details

Chemical Biology Core Facility

» Details

# www.dkfz.de/gpcf/



+++ GPCF News +++ GPCF News +++ GPCF News +++

01.02.2013

**Good News: Updated Prices for Microarray-Services**

In the last two years the GPCF microarray-unit has analyzed almost 14,000 samples by means of gene expression profiling, miRNA expression profiling, methylation analysis, and genotyping. The resulting data have led to a number of...[more]

**Genomics and Proteomics Core Facility at the Deutsches Krebsforschungszentrum**

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**Login to submit samples, to download your data as well as associated QC information, and to book instruments.**

**Contact**

Dr. Stefan Wiemann

German Cancer Research Center
Genomics & Proteomics Core Facilities
TP3
Im Neuenheimer Feld 580
69120 Heidelberg
Germany

Fon: +49 6221 42 4702
Email: Contact form

# Genomics and Proteomics Core Facility

## Objectives

- Provide **access to state-of-the-art technologies**
  - Mostly high-throughput / large scale / complex methods
  - Simple access to expensive infrastructure
  - For technologies requested in several groups at the DKFZ
- Have **skilled and dedicated personnel**
  - Reproducible data and high quality information
  - Shortest possible turn-around times
  - Advice and education to customers

- „first come first served“ access

# Genomics and Proteomics Core Facility

## Units

### Genomics

**Sequencing**
Dr. Stefan Wolf

**Microarray Unit**
Dr. Melanie Bewerunge-Hudler

**Bioinformatics**
Karl-Heinz Glatting

### Proteomics

**Quantitative Proteomics**
Dr. Martina Schnölzer

**Phospho-Proteomics**
Prof. Wolf-Dieter Lehmann

**NMR**
Dr. Karel Klika

**Protein Protein Interaction Analysis**
Dr. Frank Schwarz

### Functional Genomics

**Monoclonal Antibodies**
Claudia Tessmer
Prof. Hanswalter Zentgraf

**Isogenic Cell Lines**
Dr. Rainer Will

# Genomics and Proteomics Core Facility

- Genomics
  - **Microarray Unit**

**Services**

- mRNA Expression Profiling (human, mouse, rat, multiple species…….)
- miRNA Profiling (human, mouse, rat)
- Genotyping (human)
- Methylation Analysis (human)

> 5,000 gene/miRNA expression
> 3,800 genotyping
> 3,700 methylation

**Specials**

- Profiling on formalin-fixed tissue (FFPE)
- Small sample protocol
- Central support for analysis software: Ingenuity, Metacore, Chipster
- Access to Roche Light Cycler 480 Real Time PCR-System
- Courses and training (qPCR, Chipster, ArrayExpress)

Dr. Melanie Bewerunge-Hudler

# Genomics and Proteomics Core Facility

- Genomics
  - **Epigenome Profiling**

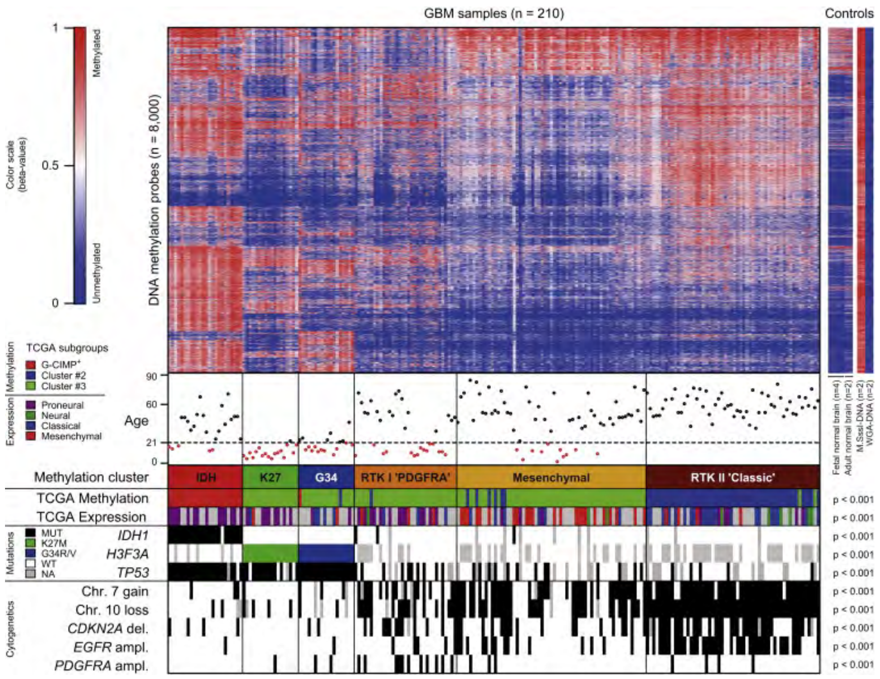
450k Methylation arrays

Cancer Cell
Article

Cell PRESS

**Hotspot Mutations in *H3F3A* and *IDH1* Define Distinct Epigenetic and Biological Subgroups of Glioblastoma**

Dominik Sturm,[1,42] Hendrik Witt,[1,7,42] Volker Hovestadt,[2,42] Dong-Anh Khuong-Quang,[11,42] David T.W. Jones,[1] Carolin Konermann,[3] Elke Pfaff,[1] Martje Tönjes,[2] Martin Sill,[4] Sebastian Bender,[1] Marcel Kool,[1] Marc Zapatka,[2] Natalia Becker,[4] Manuela Zucknick,[4] Thomas Hielscher,[4] Xiao-Yang Liu,[11] Adam M. Fontebasso,[12] Marina Ryzhova,[13] Steffen Albrecht,[14] Karine Jacob,[11] Marietta Wolter,[15] Martin Ebinger,[16] Martin U. Schuhmann,[17] Timothy van Meter,[18] Michael C. Frühwald,[19] Holger Hauch,[20] Arnulf Pekrun,[21] Bernhard Radlwimmer,[2] Tim Niehues,[22] Gregor von Komorowski,[23] Matthias Dürken,[23] Andreas E. Kulozik,[7] Jenny Madden,[24] Andrew Donson,[24] Nicholas K. Foreman,[24] Rachid Drissi,[25] Maryam Fouladi,[25] Wolfram Scheurlen,[26] Andreas von Deimling,[5,9] Camelia Monoranu,[27] Wolfgang Roggendorf,[27] Christel Herold-Mende,[8] Andreas Unterberg,[8] Christof M. Kramm,[28] Jörg Felsberg,[15] Christian Hartmann,[29] Benedikt Wiestler,[10] Wolfgang Wick,[10] Till Milde,[6,7] Olaf Witt,[6,7] Anders M. Lindroth,[3] Jeremy Schwartzentruber,[30] Damien Faury,[11] Adam Fleming,[11] Magdalena Zakrzewska,[31] Pawel P. Liberski,[31] Krzysztof Zakrzewski,[32] Peter Hauser,[33] Miklos Garami,[33] Almos Klekner,[34] Laszlo Bognar,[34] Sorana Morrissy,[35] Florence Cavalli,[35] Michael D. Taylor,[35] Peter van Sluis,[36] Jan Koster,[36] Rogier Versteeg,[36] Richard Volckmann,[36] Tom Mikkelsen,[37] Kenneth Aldape,[38] Guido Reifenberger,[15] V. Peter Collins,[39] Jacek Majewski,[40] Andrey Korshunov,[5] Peter Lichter,[2] Christoph Plass,[3,41,*] Nada Jabado,[11,41,*] and Stefan M. Pfister[1,7,41,*]



Sturm *Cancer Cell* 2012

Aim:
develop the technology as a tool for patient stratification (in Glioblastoma)

Dr. Melanie Bewerunge-Hudler

# Genomics and Proteomics Core Facility

- Genomics
  - **Sequencing**

HiSeq2000

- **Genome Sequencing** – „Single nucleotide variants“ (SNV), larger in/dels, rearrangements
- **Exome sequencing** – subgenome enrichment (e.g., all exons), SNV analysis
- **ChIP-seq** – transcription factor binding sites
- **Bisulfite Sequencing** – methyl-C analysis („epigenetics“)
- **mRNA-seq** – „digital gene expression profiling“, splice varients, mutations, allele-specific expression
- **miRNA-seq** – quantitative analysis of miRNA expression and detection of „new“ miRNAs
- **tRNA-seq** – quantitative analysis of tRNAs

Dr. Stephan Wolf

# Genomics and Proteomics Core Facility

- Genomics
  - **Sequencing**

International Cancer Genome Consortium

Deutsches Konsortium für Translationale Krebsforschung

**in-house projects**

↓

**clinical projects**

dkfz.

2,900 samples
(~ 1,000 lanes WGS, ~ 400 lanes bisulfite-seq, ~ 220 lanes exome-seq, ~ 190 lanes ChIP-seq, ~ 250 lanes m/miRNA-seq)

NCT POP Personalized Oncology Program

hipo dkfz.

Dr. Stephan Wolf

**Infrastructure: 14x Illumina HiSeq 2000/2500, 2x Illumina MiSeq, 1x Roche 454**

# Genomics and Proteomics Core Facility

- Genomics
  - **Sequencing**

whole-genome sequencing

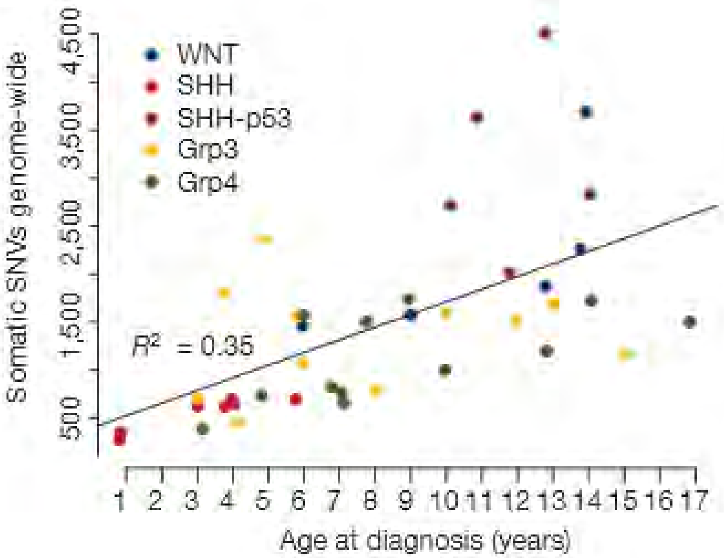
LETTER

nature

doi:10.1038/nature11284

## Dissecting the genomic complexity underlying medulloblastoma

David T. W. Jones[1]*, Natalie Jäger[2]*, Marcel Kool[1], Thomas Zichner[3], Barbara Hutter[2], Marc Sultan[4], Yoon-Jae Cho[5], Trevor J. Pugh[6], Volker Hovestadt[7], Adrian M. Stütz[3], Tobias Rausch[3], Hans-Jörg Warnatz[4], Marina Ryzhova[8], Sebastian Bender[1], Dominik Sturm[1], Sabrina Pleier[1], Huriye Cin[1], Elke Pfaff[1], Laura Sieber[1], Andrea Wittmann[1], Marc Remke[1], Hendrik Witt[1,9], Sonja Hutter[1], Theophilos Tzaridis[1], Joachim Weischenfeldt[3], Benjamin Raeder[3], Meryem Avci[4], Vyacheslav Amstislavskiy[4], Marc Zapatka[7], Ursula D. Weber[7], Qi Wang[2], Bärbel Lasitschka[10], Cynthia C. Bartholomae[11], Manfred Schmidt[11], Christof von Kalle[11], Volker Ast[12], Chris Lawerenz[12], Jürgen Eils[12], Rolf Kabbe[2], Vladimir Benes[13], Peter van Sluis[14], Jan Koster[14], Richard Volckmann[14], David Shih[15], Matthew J. Betts[16], Robert B. Russell[16], Simona Coco[17], Gian Paolo Tonini[17], Ulrich Schüller[18], Volkmar Hans[19], Norbert Graf[20], Yoo-Jin Kim[21], Camelia Monoranu[22], Wolfgang Roggendorf[22], Andreas Unterberg[23], Christel Herold-Mende[23], Till Milde[9,24], Andreas E. Kulozik[9], Andreas von Deimling[25,26], Olaf Witt[9,24], Eberhard Maass[27], Jochen Rössler[28], Martin Ebinger[29], Martin U. Schuhmann[30], Michael C. Frühwald[31], Martin Hasselblatt[32], Nada Jabado[33], Stefan Rutkowski[34], André O. von Bueren[34], Dan Williamson[35], Steven C. Clifford[35], Martin G. McCabe[36,37], V. Peter Collins[37], Stephan Wolf[10], Stefan Wiemann[10,38], Hans Lehrach[4], Benedikt Brors[2], Wolfram Scheurlen[39], Jörg Felsberg[40], Guido Reifenberger[40], Paul A. Northcott[15], Michael D. Taylor[41], Matthew Meyerson[6,42], Scott L. Pomeroy[6,43], Marie-Laure Yaspo[4], Jan O. Korbel[3], Andrey Korshunov[25,26], Roland Eils[2,44,45]*, Stefan M. Pfister[1,9]* & Peter Lichter[7]*



International Cancer Genome Consortium

ICGC PedBrain Tumor

Jones, Jäger *Nature* 2012

Dr. Stephan Wolf

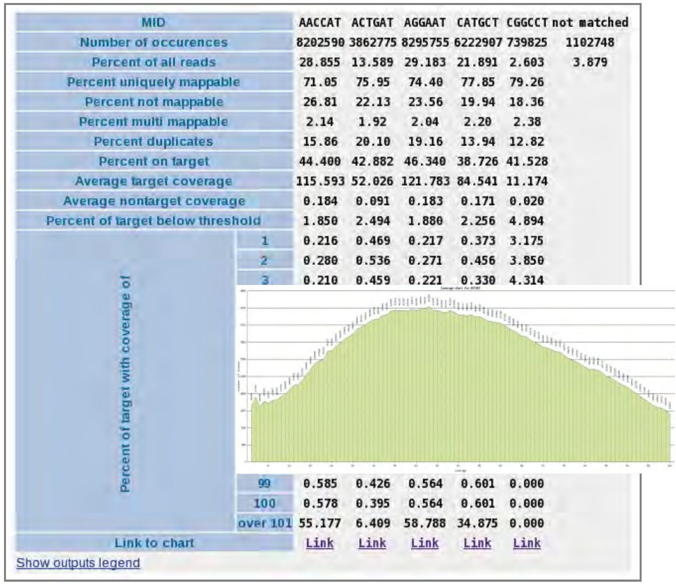
# Genomics and Proteomics Core Facility

- Biointormatics
  - **Sequencing**

**NGS analysis pipelines:**

- ***OnTarget*** (subgenomic enrichment, e.g., exome-seq)
- ***PeakDetector*** (peak detection for ChIP-Seq)
- ***ChiPeAn*** (peak analysis for ChIP-Seq)
- ***sRNAMapper*** (read mapper for sRNA-Seq)
- ***ncRNAAnnotator*** (annotation of sRNA mappings)
- ***CompaRNA*** (comparison of annotated sRNA mappings)
- ***SplicingCompass*** (alternative splicing)
- ***Contaminator*** (analysis of unmapped reads)

OnTarget Output

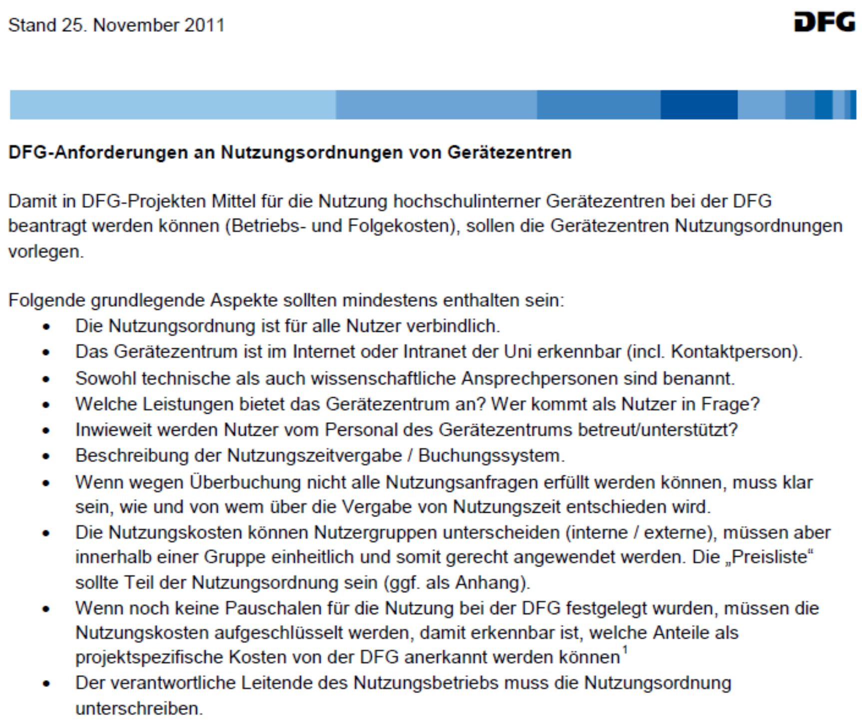


| MID | | AACCAT | ACTGAT | AGGAAT | CATGCT | CGGCCT | not matched |
|---|---|---|---|---|---|---|---|
| Number of occurences | | 8202590 | 3862775 | 8295755 | 6222907 | 739825 | 1102748 |
| Percent of all reads | | 28.855 | 13.589 | 29.183 | 21.891 | 2.603 | 3.879 |
| Percent uniquely mappable | | 71.05 | 75.95 | 74.40 | 77.85 | 79.26 | |
| Percent not mappable | | 26.81 | 22.13 | 23.56 | 19.94 | 18.36 | |
| Percent multi mappable | | 2.14 | 1.92 | 2.04 | 2.20 | 2.38 | |
| Percent duplicates | | 15.86 | 20.10 | 19.16 | 13.94 | 12.82 | |
| Percent on target | | 44.400 | 42.882 | 46.340 | 38.726 | 41.528 | |
| Average target coverage | | 115.593 | 52.026 | 121.783 | 84.541 | 11.174 | |
| Average nontarget coverage | | 0.184 | 0.091 | 0.183 | 0.171 | 0.020 | |
| Percent of target below threshold | | 1.850 | 2.494 | 1.880 | 2.256 | 4.894 | |
| Percent of target with coverage of | 1 | 0.216 | 0.469 | 0.217 | 0.373 | 3.175 | |
| | 2 | 0.280 | 0.536 | 0.271 | 0.456 | 3.850 | |
| | 3 | 0.210 | 0.459 | 0.221 | 0.330 | 4.314 | |
| | 99 | 0.585 | 0.426 | 0.564 | 0.601 | 0.000 | |
| | 100 | 0.578 | 0.395 | 0.564 | 0.601 | 0.000 | |
| | over 101 | 55.177 | 6.409 | 58.788 | 34.875 | 0.000 | |
| Link to chart | | Link | Link | Link | Link | Link | |

Show outputs legend

Karl-Heinz Glatting

# Requirements for Research Infrastructures



Stand 25. November 2011

DFG

**DFG-Anforderungen an Nutzungsordnungen von Gerätezentren**

Damit in DFG-Projekten Mittel für die Nutzung hochschulinterner Gerätezentren bei der DFG beantragt werden können (Betriebs- und Folgekosten), sollen die Gerätezentren Nutzungsordnungen vorlegen.

Folgende grundlegende Aspekte sollten mindestens enthalten sein:

- Die Nutzungsordnung ist für alle Nutzer verbindlich.
- Das Gerätezentrum ist im Internet oder Intranet der Uni erkennbar (incl. Kontaktperson).
- Sowohl technische als auch wissenschaftliche Ansprechpersonen sind benannt.
- Welche Leistungen bietet das Gerätezentrum an? Wer kommt als Nutzer in Frage?
- Inwieweit werden Nutzer vom Personal des Gerätezentrums betreut/unterstützt?
- Beschreibung der Nutzungszeitvergabe / Buchungssystem.
- Wenn wegen Überbuchung nicht alle Nutzungsanfragen erfüllt werden können, muss klar sein, wie und von wem über die Vergabe von Nutzungszeit entschieden wird.
- Die Nutzungskosten können Nutzergruppen unterscheiden (interne / externe), müssen aber innerhalb einer Gruppe einheitlich und somit gerecht angewendet werden. Die „Preisliste“ sollte Teil der Nutzungsordnung sein (ggf. als Anhang).
- Wenn noch keine Pauschalen für die Nutzung bei der DFG festgelegt wurden, müssen die Nutzungskosten aufgeschlüsselt werden, damit erkennbar ist, welche Anteile als projektspezifische Kosten von der DFG anerkannt werden können[1]
- Der verantwortliche Leitende des Nutzungsbetriebs muss die Nutzungsordnung unterschreiben.

http://www.dfg.de/foerderung/programme/infrastruktur/wgi/stellungnahmen_informationen/index.html
http://www.dfg.de/download/pdf/foerderung/programme/wgi/basic_requirements_research_infrastructures.pdf

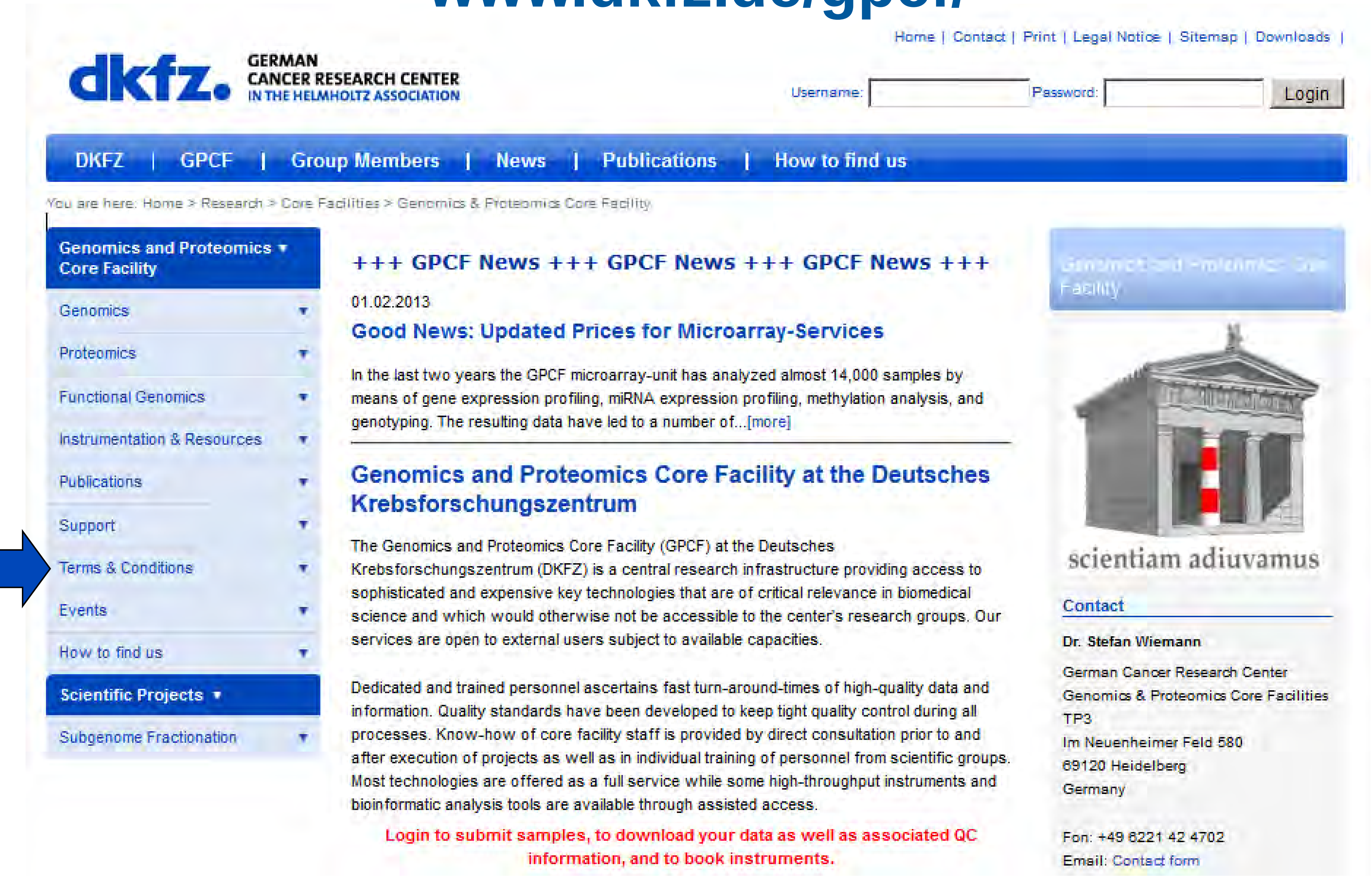
EUROPEAN SCIENCE FOUNDATION
SETTING SCIENCE AGENDAS FOR EUROPE

EUROHORCs
EUROPEAN HEADS OF RESEARCH COUNCILS

## Basic Requirements for Research Infrastructures in Europe

http://www.esf.org/activities/mo-fora/research-infrastructures.html

# www.dkfz.de/gpcf/



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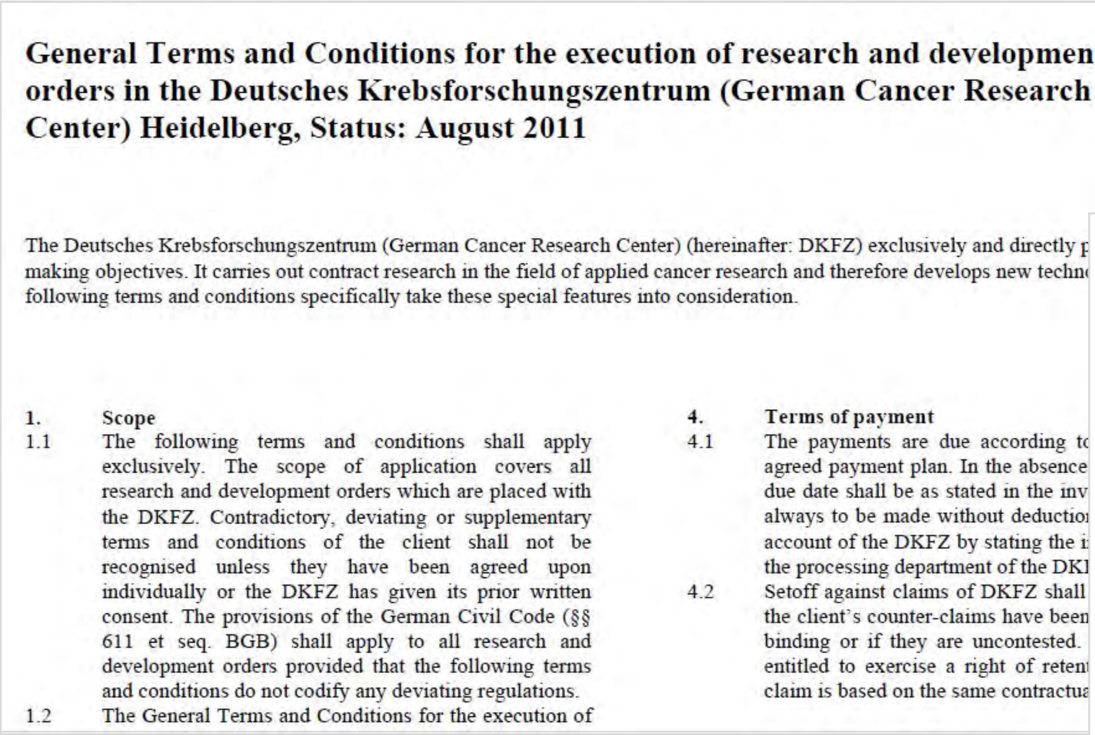
Fon: +49 6221 42 4702
Email: Contact form

# Access to the GPCF Research Infrastructure



## General Terms and Conditions for the execution of research and development orders in the Deutsches Krebsforschungszentrum (German Cancer Research Center) Heidelberg, Status: August 2011

The Deutsches Krebsforschungszentrum (German Cancer Research Center) (hereinafter: DKFZ) exclusively and directly p
making objectives. It carries out contract research in the field of applied cancer research and therefore develops new techn
following terms and conditions specifically take these special features into consideration.

**1. Scope**

1.1 The following terms and conditions shall apply exclusively. The scope of application covers all research and development orders which are placed with the DKFZ. Contradictory, deviating or supplementary terms and conditions of the client shall not be recognised unless they have been agreed upon individually or the DKFZ has given its prior written consent. The provisions of the German Civil Code (§§ 611 et seq. BGB) shall apply to all research and development orders provided that the following terms and conditions do not codify any deviating regulations.

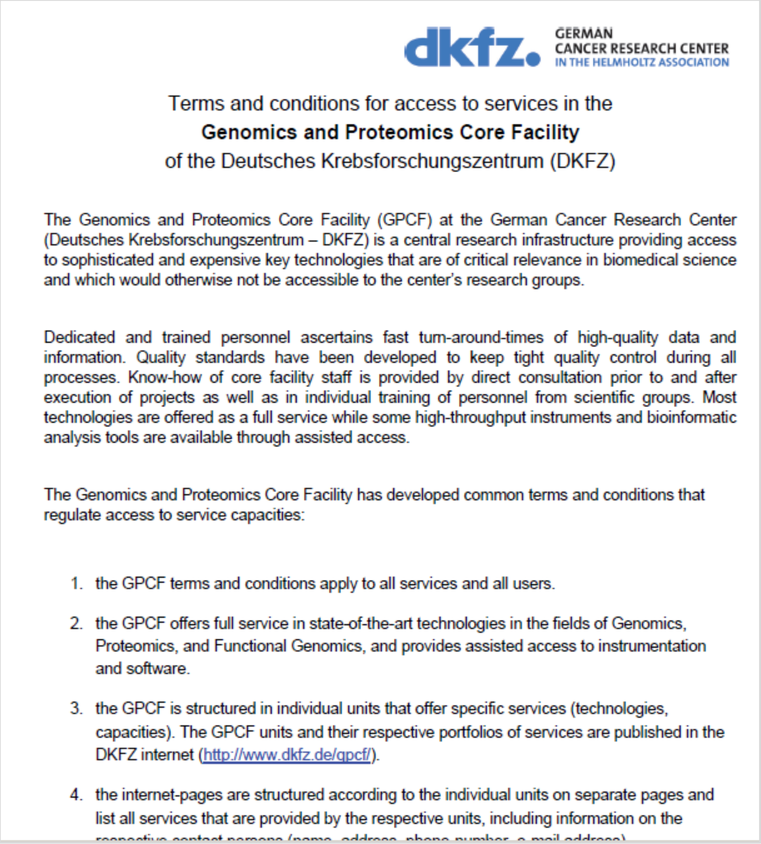
1.2 The General Terms and Conditions for the execution of

**4. Terms of payment**

4.1 The payments are due according to
agreed payment plan. In the absence
due date shall be as stated in the inv
always to be made without deductio
account of the DKFZ by stating the i
the processing department of the DK

4.2 Setoff against claims of DKFZ shall
the client's counter-claims have been
binding or if they are uncontested.
entitled to exercise a right of reten
claim is based on the same contractu

the „AGB" of the GPCF/DKFZ



dkfz. GERMAN CANCER RESEARCH CENTER IN THE HELMHOLTZ ASSOCIATION

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The Genomics and Proteomics Core Facility has developed common terms and conditions that regulate access to service capacities:

1. the GPCF terms and conditions apply to all services and all users.
2. the GPCF offers full service in state-of-the-art technologies in the fields of Genomics, Proteomics, and Functional Genomics, and provides assisted access to instrumentation and software.
3. the GPCF is structured in individual units that offer specific services (technologies, capacities). The GPCF units and their respective portfolios of services are published in the DKFZ internet (http://www.dkfz.de/gpcf/).
4. the internet-pages are structured according to the individual units on separate pages and list all services that are provided by the respective units, including information on the

http://www.dkfz.de/gpcf/terms_and_conditions.html

special terms of the GPCF