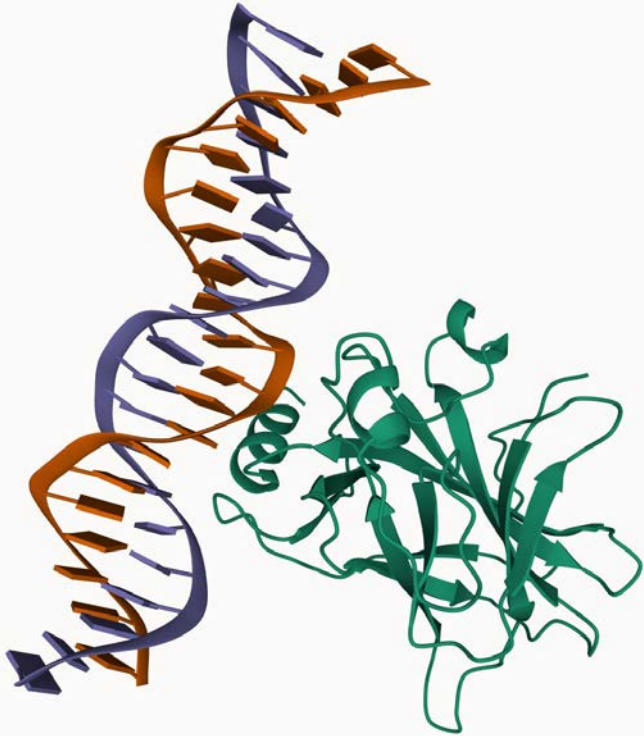


Breakout Session 1: Track B

**NCI CRDC Cloud Transfer of TP53 Website
and Database**

Mr. William Longabaugh
Senior Software Engineer, Institute for Systems Biology



NCI CRDC Cloud Transfer of *TP53* Website and Database

William Longabaugh

Senior Software Engineer, Institute for Systems Biology

Jan 17 2024

Funding

- We received funds from *“FY2021 Request for ODSS Funds to Catalyze Migration to and Usage of the Cloud via the STRIDES Initiative (HVD 21)”*
- Google cloud credits were provided to us to support cloud operations underlying our migration of the IARC WHO TP53 database (now retired) to become part of the ISB-CGC Cloud Resource, a component of the Cancer Research Data Commons (CRDC)
- Additionally, the credits covered cloud operation costs of our development, test, and production tier Google cloud projects until September 2023

Thank you to the Office of Data Science Strategy

The *TP53* Database: Aim and Scope

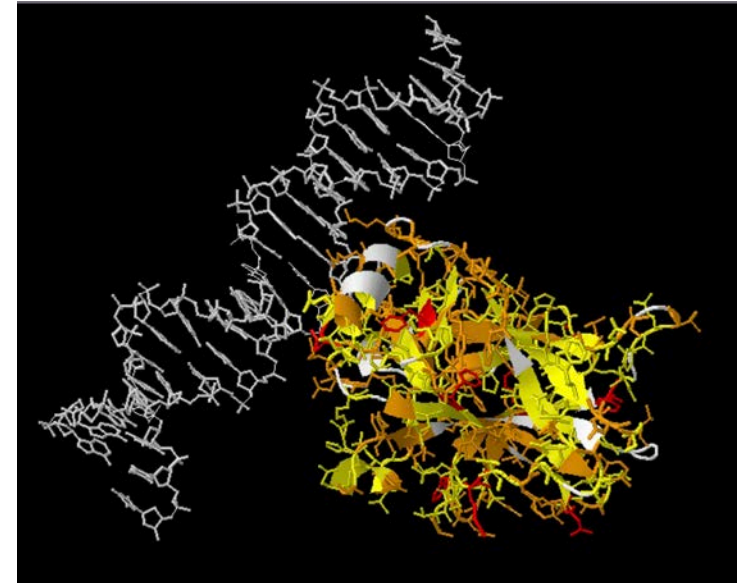
Database compiles *TP53* variant data from 1989

Currently holds information on 24,547 *TP53* variants

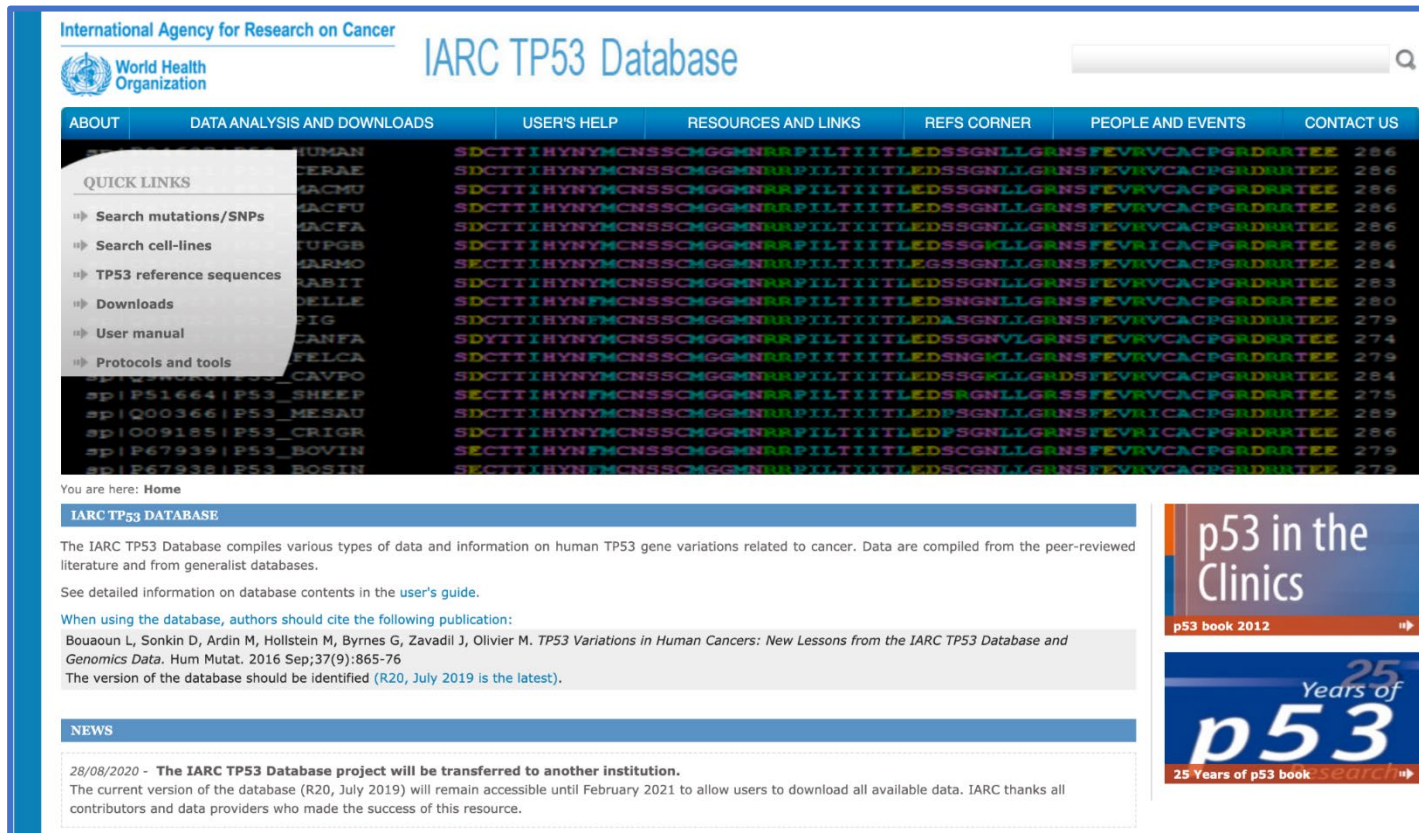
Database includes:

- *TP53* **functional** and **structural** data
- *TP53* **tumor** variants in sporadic cancer
- *TP53* **germline** variants in cancer patients, families with cancers
- *TP53* gene status in human **cell-lines**
- **Mouse models** with engineered *p53*
- **Experimentally-induced** *TP53* variants

Holds information on *TP53* variants for a broad range of scientists and clinicians who work in different research areas



IARC TP53 Database



International Agency for Research on Cancer
World Health Organization

IARC TP53 Database

ABOUT DATA ANALYSIS AND DOWNLOADS USER'S HELP RESOURCES AND LINKS REFS CORNER PEOPLE AND EVENTS CONTACT US

QUICK LINKS

- Search mutations/SNPs
- Search cell-lines
- TP53 reference sequences
- Downloads
- User manual
- Protocols and tools

SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D S S G N L L G R N S F E V R V C A C P G R D R A T E E 286
SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D S S G N L L G R N S F E V R V C A C P G R D R A T E E 286
SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D S S G N L L G R N S F E V R V C A C P G R D R A T E E 286
SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D S S G N L L G R N S F E V R V C A C P G R D R A T E E 286
SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D S S G N L L G R N S F E V R V C A C P G R D R A T E E 286
SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D S S G K L L G R N S F E V R I C A C P G R D R A T E E 286
S E C T T I H Y N Y M C N S S C M G G M N R R P I L T I I T L E G S S G N L L G R N S F E V R V C A C P G R D R A T E E 284
SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D S S G N L L G R N S F E V R V C A C P G R D R A T E E 283
SDCTT I H Y N F M C N S S C M G G M N R R P I L T I I T L E D S N G N L L G R N S F E V R V C A C P G R D R A T E E 280
SDCTT I H Y N F M C N S S C M G G M N R R P I L T I I T L E D A S G N L L G R N S F E V R V C A C P G R D R A T E E 279
S D Y T T I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D S S G N V L G R N S F E V R V C A C P G R D R A T E E 274
SDCTT I H Y N F M C N S S C M G G M N R R P I I T I T L E D S N G K L L G R N S F E V R V C A C P G R D R A T E E 279
SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D S S G K L L G R D S F E V R V C A C P G R D R A T E E 284
S E C T T I H Y N F M C N S S C M G G M N R R P I L T I I T L E D S A G N L L G R S S F E V R V C A C P G R D R A T E E 275
SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D P S G N L L G R N S F E V R I C A C P G R D R A T E E 289
SDCTT I H Y N Y M C N S S C M G G M N R R P I L T I I T L E D P S G N L L G R N S F E V R I C A C P G R D R A T E E 286
S E C T T I H Y N F M C N S S C M G G M N R R P I L T I I T L E D S C G N L L G R N S F E V R V C A C P G R D R A T E E 279
S E C T T I H Y N F M C N S S C M G G M N R R P I L T I I T L E D S C G N L L G R N S F E V R V C A C P G R D R A T E E 279

You are here: [Home](#)

IARC TP53 DATABASE

The IARC TP53 Database compiles various types of data and information on human TP53 gene variations related to cancer. Data are compiled from the peer-reviewed literature and from generalist databases.

See detailed information on database contents in the [user's guide](#).

When using the database, authors should cite the following publication:
Bouaoun L, Sonkin D, Ardin M, Hollstein M, Byrnes G, Zavadil J, Olivier M. *TP53 Variations in Human Cancers: New Lessons from the IARC TP53 Database and Genomics Data*. *Hum Mutat*. 2016 Sep;37(9):865-76
The version of the database should be identified (R20, July 2019 is the latest).

NEWS

28/08/2020 - **The IARC TP53 Database project will be transferred to another institution.**
The current version of the database (R20, July 2019) will remain accessible until February 2021 to allow users to download all available data. IARC thanks all contributors and data providers who made the success of this resource.

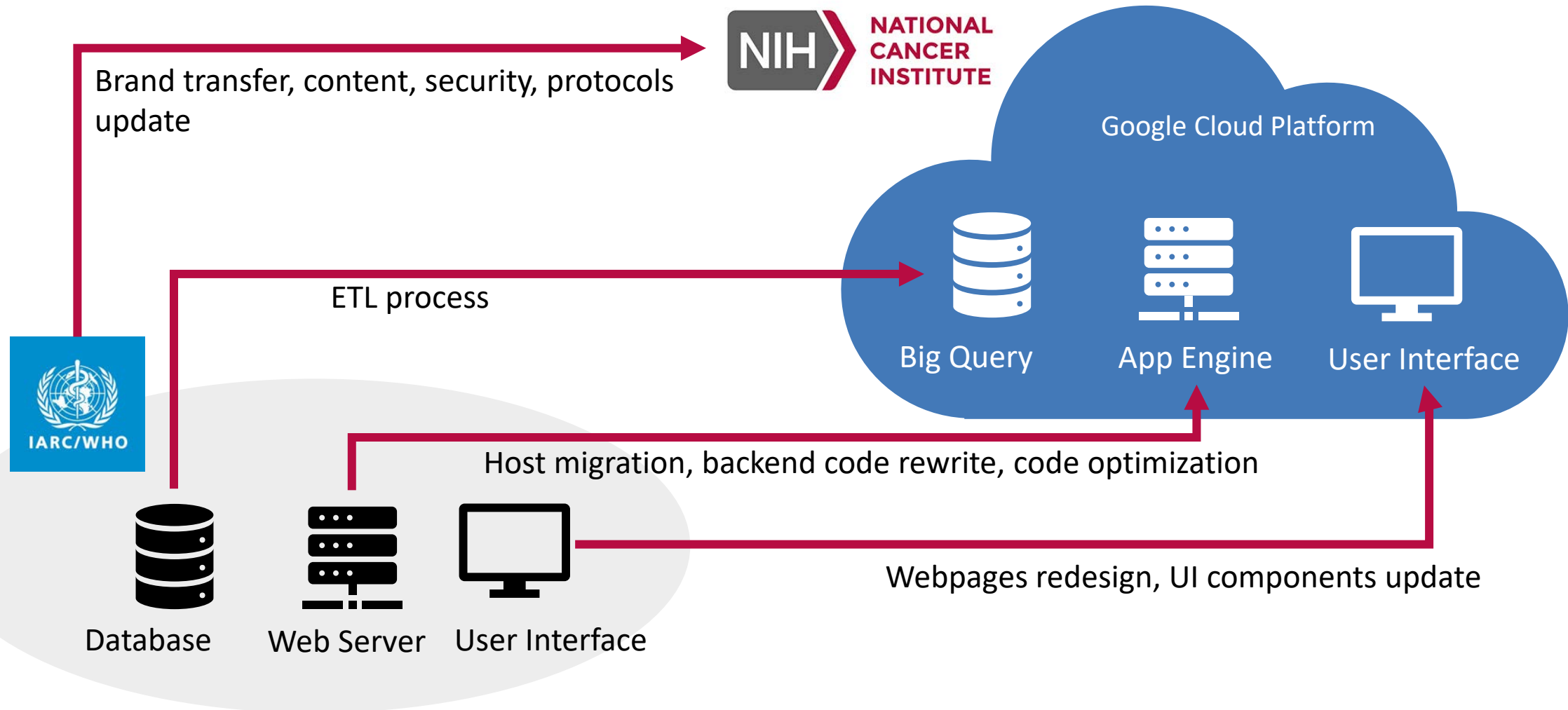
p53 in the Clinics
p53 book 2012

25 Years of p53
25 Years of p53 book search

The original **TP53 database** was initiated in 1991, further developed and maintained by WHO's **International Agency for Research on Cancer** until 2021.

IARC TP53 Database Website in 2020

Transfer of Website and Database into the Cloud



Transfer of Website and Database into the Clouds: Mitelman Database

- The **Mitelman Database** was part of CGAP (Cancer Genome Anatomy Project, NCI)
- That website was retired on 2019
- ISB-CGC was responsible for transferring all web components to the Google Cloud Platform
- The application has been further developed for advanced queries and additional features

<https://mitelmandatabase.isb-cgc.org>



All data is publicly available in BigQuery.

The image displays a Google Cloud BigQuery interface. On the left, the Explorer pane shows a project named "mitelman-db" with various resources like "AuthorReference", "Cytobands_hg38", "Cytobands_hg19", "Cytobands_hg22", "Cytobands_hg24", "Cytobands_hg25", "Cytobands_hg26", "Cytobands_hg27", "Cytobands_hg28", "Cytobands_hg29", "Cytobands_hg30", "Cytobands_hg31", "Cytobands_hg32", "Cytobands_hg33", "Cytobands_hg34", "Cytobands_hg35", "Cytobands_hg36", "Cytobands_hg37", "Cytobands_hg38", "Cytobands_hg39", "Cytobands_hg40", "Cytobands_hg41", "Cytobands_hg42", "Cytobands_hg43", "Cytobands_hg44", "Cytobands_hg45", "Cytobands_hg46", "Cytobands_hg47", "Cytobands_hg48", "Cytobands_hg49", "Cytobands_hg50", "Cytobands_hg51", "Cytobands_hg52", "Cytobands_hg53", "Cytobands_hg54", "Cytobands_hg55", "Cytobands_hg56", "Cytobands_hg57", "Cytobands_hg58", "Cytobands_hg59", "Cytobands_hg60", "Cytobands_hg61", "Cytobands_hg62", "Cytobands_hg63", "Cytobands_hg64", "Cytobands_hg65", "Cytobands_hg66", "Cytobands_hg67", "Cytobands_hg68", "Cytobands_hg69", "Cytobands_hg70", "Cytobands_hg71", "Cytobands_hg72", "Cytobands_hg73", "Cytobands_hg74", "Cytobands_hg75", "Cytobands_hg76", "Cytobands_hg77", "Cytobands_hg78", "Cytobands_hg79", "Cytobands_hg80", "Cytobands_hg81", "Cytobands_hg82", "Cytobands_hg83", "Cytobands_hg84", "Cytobands_hg85", "Cytobands_hg86", "Cytobands_hg87", "Cytobands_hg88", "Cytobands_hg89", "Cytobands_hg90", "Cytobands_hg91", "Cytobands_hg92", "Cytobands_hg93", "Cytobands_hg94", "Cytobands_hg95", "Cytobands_hg96", "Cytobands_hg97", "Cytobands_hg98", "Cytobands_hg99", "Cytobands_hg100". The main pane shows a notebook titled "Mitelman_Cytogenetics_Subsets.ipynb" with a code cell containing SQL queries. The notebook content includes a title, author, creation date, URL, and purpose. It also contains a section titled "Cytogenetics and Data Subsets in the Mitelman Database" with a list of examples of unique subsets of the Mitelman Database that may be useful in Cytogenetics research. The notebook content is as follows:

```
1 SELECT DISTINCT
2   c.RefNo,
3   c.CaseNo,
4   c.InNo,
5   Reference.Abbreviation,
6   Reference.Journal,
7   KoderT.Benaming AS Morph,
8   KoderT.Benaming AS Topo,
9   c.KaryShort,
10  c.KaryLong
11 FROM
12   mitelman-db-prod.Cytogenetics AS c,
13   mitelman-db-prod.Reference AS r,
14   mitelman-db-prod.Cytogenetics AS cyto
15 LEFT JOIN mitelman-db-prod.KoderT AS k
16 ON
17   (Cytogen_Top = KoderT_Top AND k.InNo = c.InNo)
18 LEFT JOIN mitelman-db-prod.KoderT AS k2
19 ON
20   (Cytogen_Top = KoderT_Top AND k2.InNo = c.InNo)
21 LEFT JOIN mitelman-db-prod.KaryB1 AS kb1
22 ON kb1.InNo = c.InNo
23 Cytogen_RefNo = c.RefNo
24 AND Cytogen_CaseNo = c.CaseNo
25 AND c.RefNo = Reference.RefNo
26 AND c.RefNo = KaryB1.RefNo
27 AND c.CaseNo = KaryB1.CaseNo
28 AND c.InNo = KaryB1.InNo
29 AND c.KaryB1 = KaryB1.KaryB1
```

Cytogenetics and Data Subsets in the Mitelman Database

Check out other notebooks as our [Community Notebooks Repository!](#)

Title: Cytogenetics and Data Subsets in the Mitelman Database
Author: Jacob Wilson
Created: 2023-08-21
URL: https://github.com/ISB-CGC/Community-Notebooks/blob/master/MitelmanDB/Mitelman_Cytogenetics_Subsets.ipynb
Purpose: Demonstrate examples of unique subsets of the Mitelman Database that may be useful in Cytogenetics research.

In this notebook, we will explore multiple methods for subsetting the Mitelman dataset into groupings that are relevant to Cytogenetics research. The goal of this exercise is to show how the Mitelman Database can be used in BigQuery to perform research on various groupings of cytogenetic abnormalities. In the following examples, we will:

utilize CytoConverter coordinates to:

- target specific gene loci and groups of genes
- compare to microarray copy number data

The image shows a search result table and a cytogenetics visualization. The table is titled "Cases Cytogenetics Search Result" and has columns for Morphology, Topography, Karyotype, Case No, Reference, and View Case. The table contains several rows of search results. The visualization is a cytogenetics plot showing the frequency of cytogenetic abnormalities across chromosomes. The plot is titled "1 Extra Copy" and "Loss of 1 Copy" and shows the frequency of abnormalities for each chromosome. The plot is a bar chart with the x-axis representing chromosomes and the y-axis representing frequency. The bars are colored green for "1 Extra Copy" and red for "Loss of 1 Copy". The plot shows a high frequency of abnormalities for chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, X, Y.

Transfer of Website and Database into the Clouds: The *TP53* Database

<https://tp53.isb-cgc.org>

The screenshot shows the homepage of the TP53 Database. At the top, there is a navigation bar with links for 'The TP53 Database', 'About', 'User Manual', 'Other Resources', 'Events', and 'Release Notes'. Below the navigation bar, a blue banner contains the text: 'The TP53 Database compiles various types of data and information from the literature and generalist databases on human TP53 gene variations related to cancer. The database is hosted by the National Cancer Institute (NCI) of the United States. The content reflects the R20, July 2019 version'. A light purple announcement box below the banner reads: '[ANNOUNCEMENT] Direct Sequencing by Sanger protocol has been updated. A polymorphic site has been detected in P-326 primer (17-7579619-G-T) with an allele frequency of 2,76% in individuals of African/African American ancestry (gnomAD v2.1.1). 1/3/24'. The main content area features six data categories, each with a green header and a plus icon: 'Functional / Structural Data', 'Tumor Variants', 'Germline Variants', 'Cell Lines', 'Mouse Models', and 'Experimentally Induced Variants'. Each category has a brief description of the data available.

- The TP53 Database of NCI was launched in 2021 with all of its web components operating under **Google Cloud Platform**.
- All web queries are directly run in **BigQuery**.

The *TP53* Database of NCI

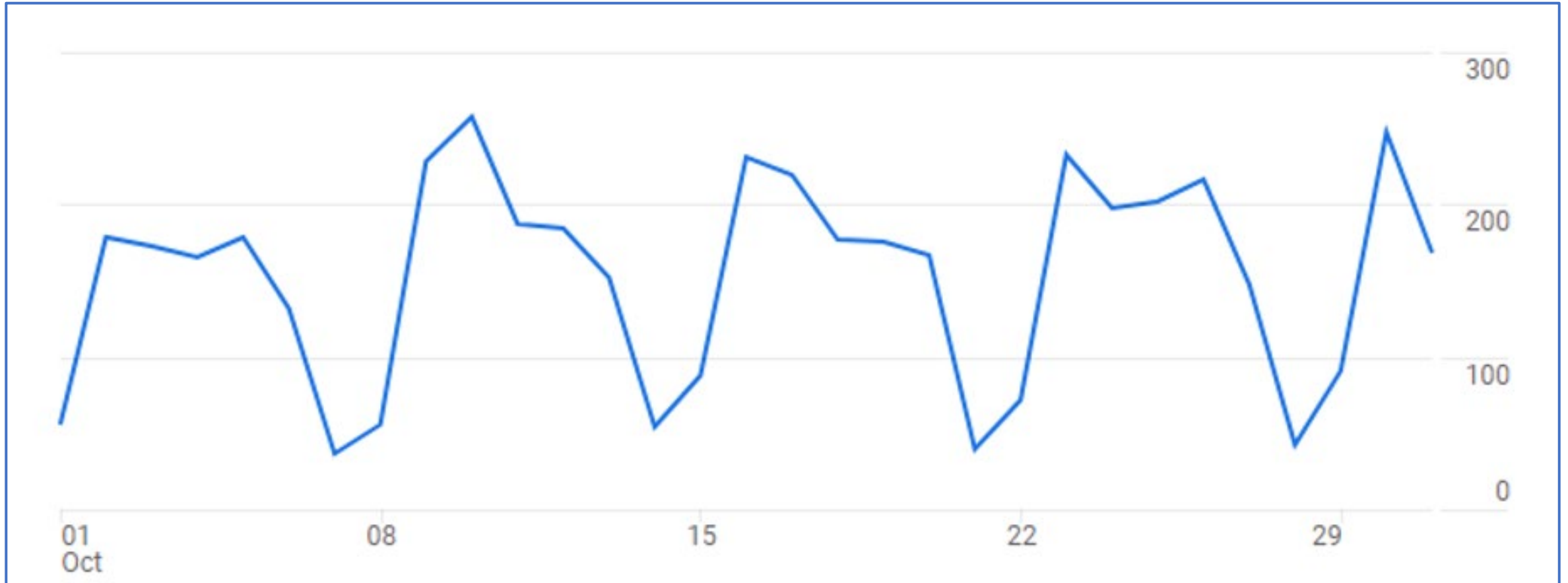
Application is now

- Faster to search or run analyses
- Easier to navigate
- Secure
- Shares the same development, deployment, hosting, testing, and security framework with other ISB-CGC components

The image displays four overlapping screenshots of the TP53 Database interface:

- Top Left:** Search Functional / Structural Data: by Gene Variants. Shows search criteria (cDNA, Protein, Genomic) and a list of protein descriptions.
- Top Center:** Search Results: Functional / Structural Data. A table with columns for Genomic, Description, cDNA, Proteins, Exon, TA, LOP, GVSD, Somatic, Germline, CellLine, KOSG, Validated, and Director. It lists various TP53 variants.
- Top Right:** Statistics on Functional/Structural Data: Variant Distributions. Features a bar chart for Allele Frequency Distribution (N = 10,263) and a pie chart for Variant Types.
- Bottom Right:** 3D Structures Analysis. Includes a 3D Viewer showing a DNA double helix and protein structure, and a section on Structural Impacts of Variants with a list of publications.

TP53 Database Usage



Future Development:

Easy Access to *TP53* dataset in BigQuery

- The current BigQuery tables are not yet public (*cf.* Mitelman Database)
- The current data tables are too complex
 - The data is extracted from 70 tables, which have over 500 columns all together
 - Need to optimize the data by trimming fields that are not related to *TP53* variants
 - Need to remove extraneous columns that were never exposed
- Making the data in BigQuery public will make it easily accessible to any researcher or clinician
- The field of the data analysis can then be easily expanded with arbitrary queries

Future Development: Linking *TP53* variant data with GDC case data

With TP53 now part of the CRDC, we can use the data to inform analyses of CRDC data

The screenshot shows the 'The TP53 Database' search results for 'Functional / Structural Data'. The table includes columns for variant details (Genomic Variant, cDNA, Protein, Exon, Effect, TA Class, DNE / LOF Class, Align-GVGD Class, Somatic Count, Germline Count, CellLine Count, TCGA GDC GENE Count, GDC Case Count, Validated SNP, ClinVar, COSMIC, dbSNP, gnomAD, SpliceAI DS_AG, DS_AL, DS_DG, DS_DL) and a red box highlights the 'GDC Case Count' column.

Genomic Variant	cDNA	Protein	Exon	Effect	TA Class	DNE / LOF Class	Align-GVGD Class	Somatic Count	Germline Count	CellLine Count	TCGA GDC GENE Count	GDC Case Count	Validated SNP	ClinVar	COSMIC	dbSNP	gnomAD	SpliceAI DS_AG	DS_AL	DS_DG	DS_DL
p.T337P	c.1123A>G	p.T337P	11-exon	missense	functional	ncDNE_ncLOF	C0	0	0	0	1	485	no		1658794	774269719	17-7572990-T-G	0.02	0.06	0	0
p.S378P	c.1132T>C	p.S378P	11-exon	missense	functional	ncDNE_ncLOF	C0	0	0	0	0	297	no			80184030	17-7572977-A-G	0.02	0.06	0	0.01
p.R175H	c.524G>A	p.R175H	5-exon	missense	non-functional	DNE_LOF	C25	1216	59	79	1000	182	no	12374	10648	28934578	17-7578406-G-T	0	0	0.01	0
p.R273C	c.817C>T	p.R273C	8-exon	missense	non-functional	DNE_LOF	C65	707	27	59	655	144	no	4394	10659	121913343	17-757121-G-A	0.06	0	0.01	0
p.R249Q	c.743G>A	p.R249Q	7-exon	missense	non-functional	DNE_LOF	C35	937	48	116	651	126	no	12366	10662	11540055	17-7577338-G-T	0	0	0	0
p.R273H	c.818G>A	p.R273H	8-exon	missense	non-functional	DNE_LOF	C25	858	51	83	635	114	no	12366	10660	28934576	17-757120-G-T	0.01	0.02	0	0
p.R248W	c.742C>T	p.R248W	7-exon	missense	non-functional	DNE_LOF	C65	739	49	56	528	95	no	12347	10656	121912651	17-757539-G-A	0.01	0	0.01	0
p.R282W	c.844C>T	p.R282W	8-exon	missense	non-functional	DNE_LOF	C65	581	36	31	502	93	no	12364	10704	28934574	17-7577094-G-A	0.01	0.01	0.01	0
p.R213*	c.527C>T	p.R213*	6-exon	nonsense	NA	ncDNE_LOF	NA	329	19	25	430	79	no	43960	6503387	397516436	17-7578212-G-A	0	0.37	0	0.47
p.Y220C	c.859A>G	p.Y220C	6-exon	missense	non-functional	DNE_LOF	C65	402	17	26	329	72	no	12719	10758	121912686	17-7578190-T-C	0	0.03	0.13	0.04

Prototype: TP53 variant search results with GDC case info

The screenshot shows a 'Summary' page for a patient. It includes a 'FILES' section with 63 files and an 'ANNOTATIONS' section with 1 annotation. The clinical data is organized into tabs: Demographic, Diagnoses / Treatments (1), Family Histories (0), Exposures (1), and Follow-Ups (0). The patient's vital status is 'Dead'.

Case ID	Project	Project Name	Disease Type	Program	Primary Site	Images
	TCGA-GBM	Glioblastoma Multiforme	Gliomas	TCGA	Brain	(2)

Clinical Summary:

Demographic	Diagnoses / Treatments (1)	Family Histories (0)	Exposures (1)	Follow-Ups (0)
UID				
Ethnicity				
Gender				
Race				
Days To Birth				
Days To Death				
Vital Status				

Genomic Data Common case page

ISB-CGC



Elaine Lee

William Longabaugh

Boris Aguilar

Lauren Hagen

Lauren Wolfe

Mi Tian

Suzanne Paquette

Ilya Shmulevich

GENERAL DYNAMICS
Information Technology

David Pot

Danna Huffman

Deena Bleich

Fabian Seidl

Jacob Wilson

Poojitha Gundluru

Prema Venkatesan

Owais Shahzada

DCEG

Division of Cancer Epidemiology &
Genetics at the National Cancer Institute

Kelvin de Andrade

Sharon Savage

Original Team and IARC

Monica Hollstein

Curt C. Harris

Pierre Hainaut

Magali Olivier

Lucile Alteyrac

Jiri Zavadil

Plus...

Elise Tookmanian, Chimene Kesserwan, James Manfredi, Jessica Hatton, Jennifer Loukissas, Lei Zhou, Megan Frone, Christian Kratz, David Malkin, Pierre Hainaut

<https://tp53.isb-cgc.org/>