



**СБМ**

НАУЧНО-ИССЛЕДОВАТЕЛЬСКИЙ ИНСТИТУТ  
СИСТЕМНОЙ БИОЛОГИИ И МЕДИЦИНЫ  
РОСПОТРЕБНАДЗОРА

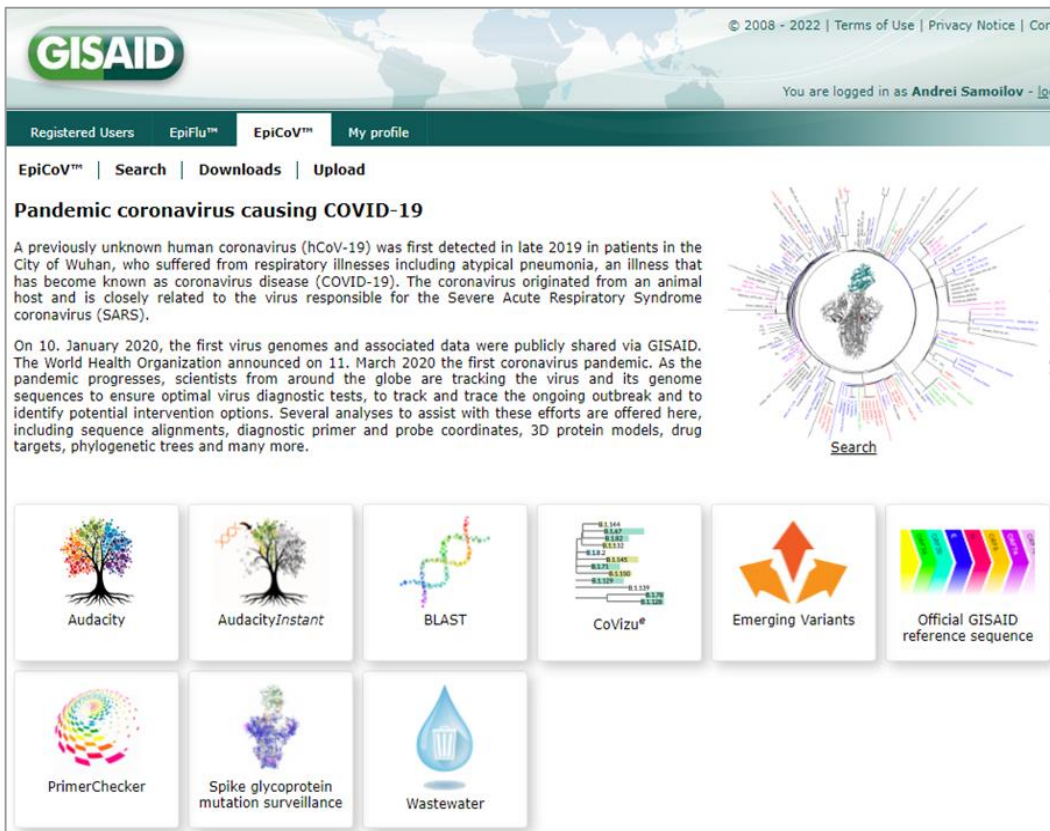
# КЛАССИФИКАЦИЯ SARS-CoV-2

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# АНАЛИЗ И КЛАССИФИКАЦИЯ ПОСЛЕДОВАТЕЛЬНОСТЕЙ SARS-CoV-2

- Много разных способов анализа
- Несколько методов классификации
- Всё доступно в интернете и не требует установки

# GISAID – КРУПНЕЙШАЯ БАЗА ГЕНОМОВ SARS-CoV-2



The screenshot shows the GISAID website interface. At the top, there is a navigation bar with the GISAID logo and user information: "© 2008 - 2022 | Terms of Use | Privacy Notice | Cont" and "You are logged in as Andrei Samoilov - log". Below the navigation bar, there are tabs for "Registered Users", "EpiFlu™", "EpiCoV™", and "My profile". The main content area is titled "EpiCoV™ | Search | Downloads | Upload" and features a section for "Pandemic coronavirus causing COVID-19". This section includes a paragraph describing the virus's discovery in late 2019 in Wuhan and its classification as COVID-19. Below the text, there is a circular phylogenetic tree visualization of the virus genome. At the bottom of the page, there is a grid of nine tool icons: Audacity, AudacityInstant, BLAST, CoVizu®, Emerging Variants, Official GISAID reference sequence, PrimerChecker, Spike glycoprotein mutation surveillance, and Wastewater.

- ❑ Большое количество аналитики
- ❑ Более 15 млн геномов со всего мира!
- ❑ Большое количество способов анализа

# ОФИЦИАЛЬНАЯ ИНФОРМАЦИЯ ОТ ВОЗ

## Currently circulating variants of concern (VOCs) as of 15 March 2023

Note: To better reflect the current variant landscape, which is dominated by Omicron descendant lineages, WHO updated its tracking system and working definitions of VOCs and VOIs on 15 March 2023.

15 March 2023

Updated working definitions and primary actions for SARS-CoV-2 variants

## Currently circulating variants of interest (VOIs) as of 15 March 2023

Pango lineage	Nextstrain clade	Genetic features	Earliest documented samples	Date of designation and risk assessments
XBB 1.5	23A	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1.  XBB + S:F486P	05-01-2022	11-Jan-2023  XBB 1.5 Rapid Risk Assessment, 11 January 2023  XBB 1.5 Updated Rapid Risk Assessment, 25 January 2023  XBB 1.5 Updated Risk Assessment, 24 February 2023

## Currently circulating VUMs (as of 15 March 2023)

Pango lineage	Nextstrain clade	Genetic features	Earliest documented samples	Date of designation and risk assessments
BQ.1	22E	BA.5 + S:R346T, S:K444T, S:N460K	07-02-2022	21-Sep-2022
BA.2.75	22D	BA.2 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:D339H, S:G446S, S:N460K, S:Q493R reversion	31-12-2021	06-Jul-2022
CH.1.1	22D	BA.2.75 + S:L452R, S:F486S	27-07-2022	08-Feb-2023

## Греческие буквы

варианты (классификация ВОЗ)

## VOC

Variant of Concern (Alpha, Beta, Gamma, Delta, Omicron)

## VOI

Variant of Interest

## VUM

Variant under Monitoring

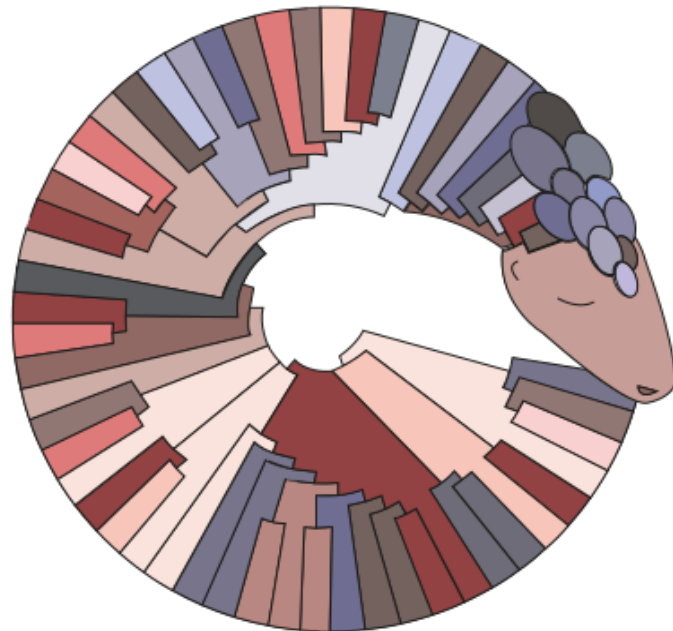
<https://www.who.int/activities/tracking-SARS-CoV-2-variants>

# PANGOLIN – БЫСТРЫЙ СПОСОБ КЛАССИФИКАЦИИ

- Детальная классификация последовательностей
- Быстрый
- Пользуются все!

<https://cov-lineages.org/resources/pangolin.html>

<https://pangolin.cog-uk.io/>



# PANGOLIN – НЕИДЕАЛЬНЫЙ СПОСОБ КЛАССИФИКАЦИИ

- ❑ Непрозрачный алгоритм классификации
- ❑ Редкие, но невообразимо тупые ошибки
- ❑ Не основан на филогенетике
- ❑ Авторы тоже люди



# КАКОЙ РЕЗУЛЬТАТ ВЫДЕТ PANGOLIN

## Lineage List

This is a list of active lineages which have been seen in the last year. A complete list of lineages can be found on [the PANGO designation GitHub](#) and a JSON file containing the equivalent data from this page for the full set of lineages can be downloaded in JSON format [here](#).

All Fields Search for lineage...

Lineage	Most common countries	Earliest date	# designated	# assigned	Description	WHO Name
A	United States of America 32.0%, United_Arab_Emirates 11.0%, China 9.0%, Germany 7.0%, Canada 4.0%	2019-12-30	1697	2682	One of the two original haplotypes of the pandemic (A and B). Many sequences originating from China and many global exports; including to South East Asia Japan South Korea Australia the USA and Europe represented in this lineage	
B	United States of America 38.0%, United Kingdom 16.0%, China 7.0%, Mexico 6.0%, Germany 5.0%	2019-12-24	4001	9704	One of the two original haplotypes of the pandemic (and first to be discovered)	
B.1	United States of America 46.0%, Turkey 11.0%, United Kingdom 6.0%, Canada 4.0%, France 3.0%	2020-01-01	46228	117729	A large European lineage the origin of which roughly corresponds to the Northern Italian outbreak early in 2020.	

AY.122 = B.1.617.2.122

BA.1 = B.1.1.529.1

~~X~~BB.1.5 = BJ.1 + BM.1.1.1

BJ.1 = BA.2.10.1.1 = B.1.1.529.2.10.1.1

BM.1.1.1 = BA.2.75.3.1.1.1 =  
B.1.1.529.2.75.3.1.1.1

[https://cov-lineages.org/lineage\\_list.html](https://cov-lineages.org/lineage_list.html)

[https://github.com/cov-lineages/pango-designation/blob/master/lineage\\_notes.txt](https://github.com/cov-lineages/pango-designation/blob/master/lineage_notes.txt)

# ОШИБКИ КЛАССИФИКАТОРА PANGOLIN

## Virus detail

**Virus name:** hCoV-19/pangolin/Guangxi/P2V **2017**  
**Accession ID:** EPI\_ISL\_410542  
**Type:** betacoronavirus  
**Clade:** S  
**Pango Lineage:** **AY.43.6** (Pango v.4.1.2 PLEARN-v1.14)

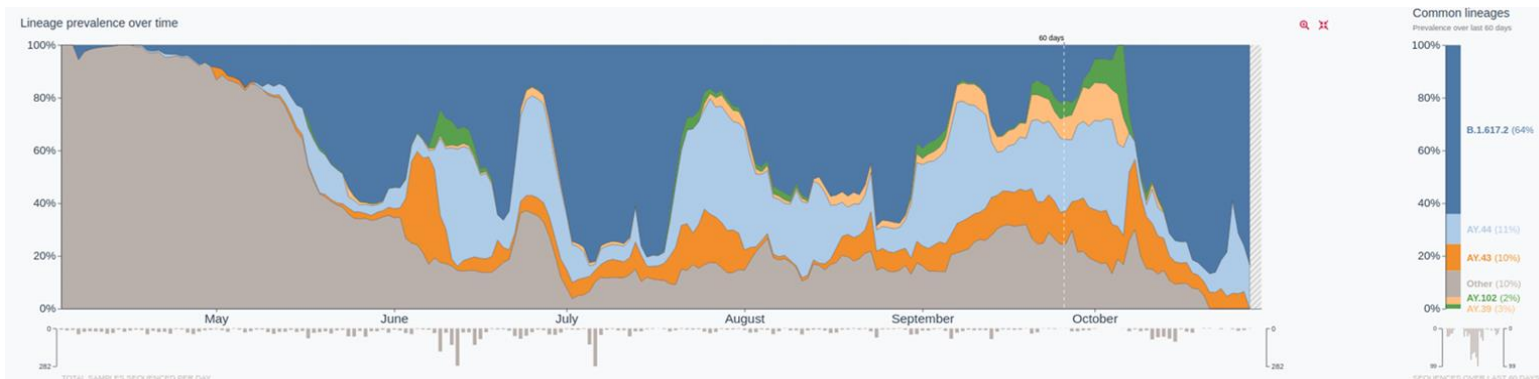
## Virus detail

**Virus name:** hCoV-19/pangolin/Guangxi/P3B **2017**  
**Accession ID:** EPI\_ISL\_410543  
**Type:** betacoronavirus  
**Clade:** S  
**Pango Lineage:** **BA.1** (Pango v.4.1.2 PLEARN-v1.14)

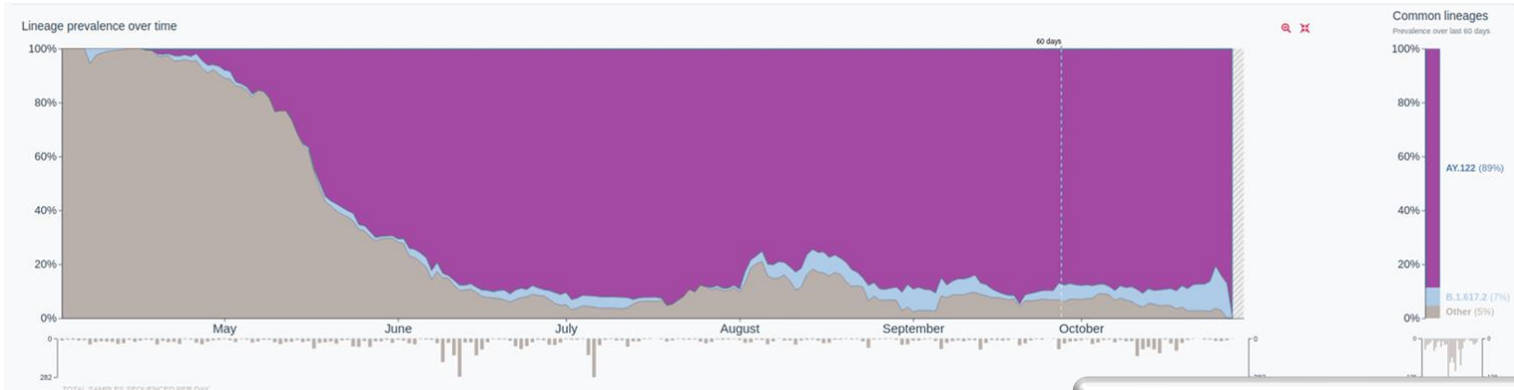


# КАК МЕНЯЕТСЯ РЕЗУЛЬТАТ ПРИ ОБНОВЛЕНИИ КЛАССИФИКАТОРА RANGOLIN

24.11.21



26.11.21



# NEXTCLADE – ФИЛОГЕНЕТИЧЕСКИЙ АНАЛИЗ И КЛАССИФИКАЦИЯ

## Nextclade v1.14.0

Clade assignment, mutation calling, and sequence quality checks

### Selected pathogen

**SARS-CoV-2**

Reference: Wuhan-Hu-1/2019 (genbank: MN908947)

Updated: 2022-03-14 12:00 (UTC)

Change

[Recent dataset updates](#)

[Customize dataset files](#)

### Provide sequence data

[File](#) [Link](#) [Text](#)

Drag & Drop a file here

or



Select a file

Run automatically

[Load example](#)


Run

- ☐ Большое количество аналитики
- ☐ Красивые картинки



a standardized, open-source database of COVID-19 resources and epidemiology data

## Variants

enabled by data from 

Explore SARS-CoV-2 lineage, variant, and mutation situation reports

 Search PANGO lineage

Try: Omicron >> BA.2 >> BA.1 >> BA.11 >> Delta >>

 Select location

Try: USA >> U.K. >> New York >> San Diego >>

- Визуализация данных GISAID
- Распространённость вариантов в отдельных странах, статистика по отдельным линиям
- Анализ частоты мутаций в различных линиях
- И многое другое