INVIVYD

Developing mAb therapies to keep pace with rapidly evolving viral threats

World Vaccine Congress Washington 2026

CAUTIONARY NOTE REGARDING FORWARD-LOOKING STATEMENTS

This presentation contains forward-looking statements within the meaning of the U.S. Private Securities Litigation Reform Act of 1995. Statements in this presentation that are not statements of historical fact are forward-looking statements. Words such as “may,” “will,” “should,” “expect,” “plan,” “anticipate,” “seek,” “could,” “intend,” “target,” “aim,” “project,” “designed to,” “estimate,” “believe,” “predict,” “potential” or “continue” or the negative of these terms or other similar expressions are intended to identify forward-looking statements, though not all forward-looking statements contain these identifying words. Forward-looking statements may include statements concerning, among other things, plans related to Invivyd’s research and development activities; the future of the infectious disease landscape; expectations and hypotheses about SARS-CoV-2 and measles evolution; predictive trends in spike Receptor Binding Domain (RBD) polymorph data; beliefs about the stability of the epitope targeted by pemivibart and VYD2311; expectations regarding pemivibart and VYD2311 neutralization activity; expectations about Invivyd antibody development programs and the potential to develop effective treatment and protection options for vulnerable people; the potential to develop monoclonal antibody (mAb) therapies that keep pace with rapidly evolving viral threats; and related scientific concepts, strategies, research and discovery efforts, or other statements that are not historical fact. The plans, intentions or expectations described in or implied by the forward-looking statements may not be achieved, and you should not place undue reliance on any forward-looking statements. These forward-looking statements involve risks and uncertainties that could cause actual results to differ materially from the results described in or implied by the forward-looking statements, including, without limitation: the timing, progress and results of the company’s discovery, preclinical and clinical development activities; whether or not any preclinical candidate identified by the company is determined to be suitable for clinical development; variability of results in models and methods used to predict neutralization activity against SARS-CoV-2 variants; potential variability in neutralizing activity of product candidates tested in different assays, such as pseudovirus assays and authentic assays; the risk that results of nonclinical studies may not be predictive of future results, and interim data are subject to further analysis; the predictability of clinical success of product candidates based on neutralizing activity in nonclinical studies; reliance on third parties with respect to virus assay creation and product candidate testing; whether mutations that have been historically explored by the SARS-CoV-2 virus dominate in the future; whether the epitopes that pemivibart and VYD2311 target remain structurally intact; and whether the company’s product candidates are able to demonstrate and sustain neutralizing activity against major SARS-CoV-2 variants, particularly in the face of viral evolution. Other factors that may cause actual results to differ materially from those expressed or implied in the forward-looking statements in this presentation are described under the heading “Risk Factors” in Invivyd’s Annual Report on Form 10-K for the year ended December 31, 2025 filed with the Securities and Exchange Commission (SEC), and in the company’s other filings with the SEC, and in the company’s future reports to be filed with the SEC and available at www.sec.gov. Forward-looking statements contained in this press release are made as of this date, and Invivyd undertakes no duty to update such information whether as a result of new information, future events or otherwise, except as required under applicable law.

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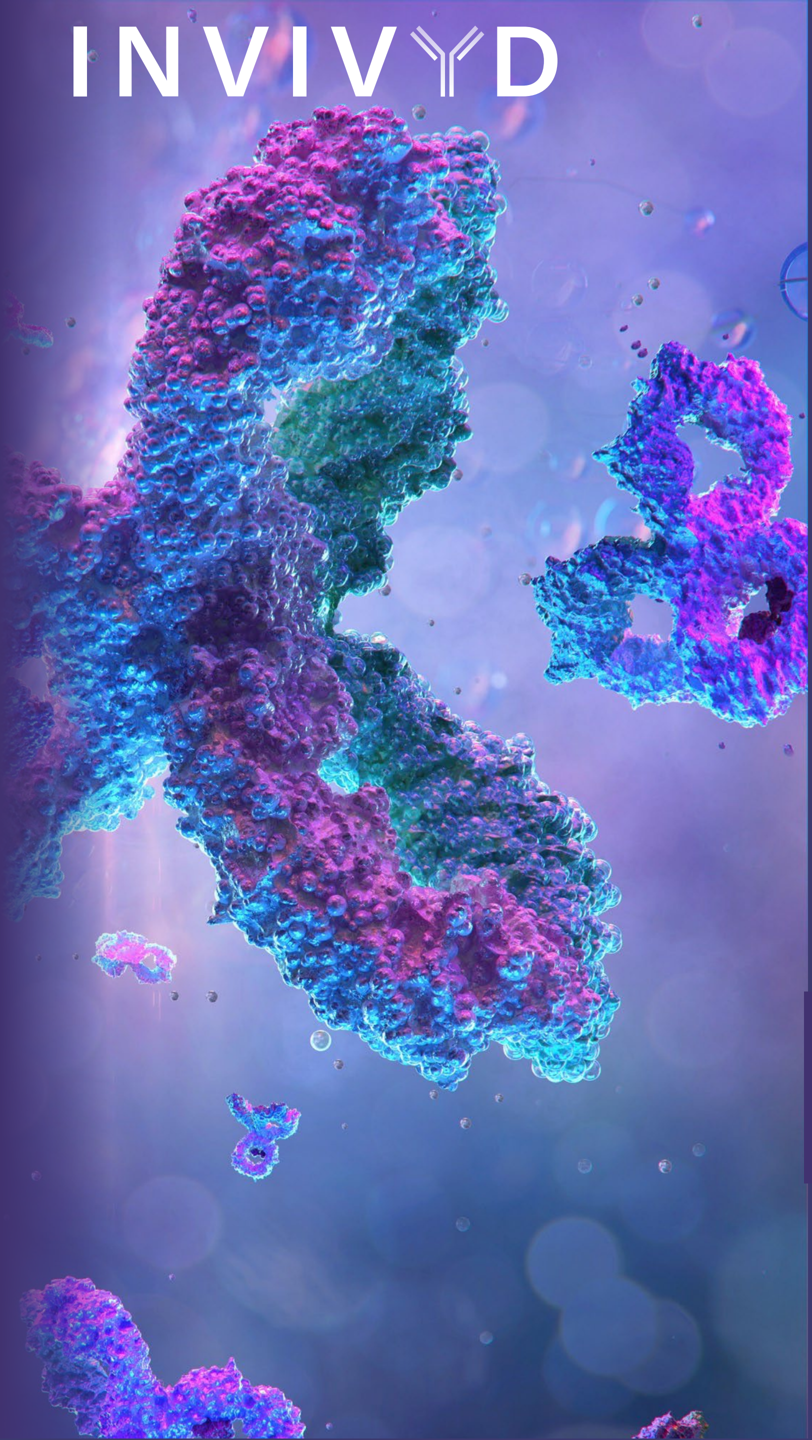
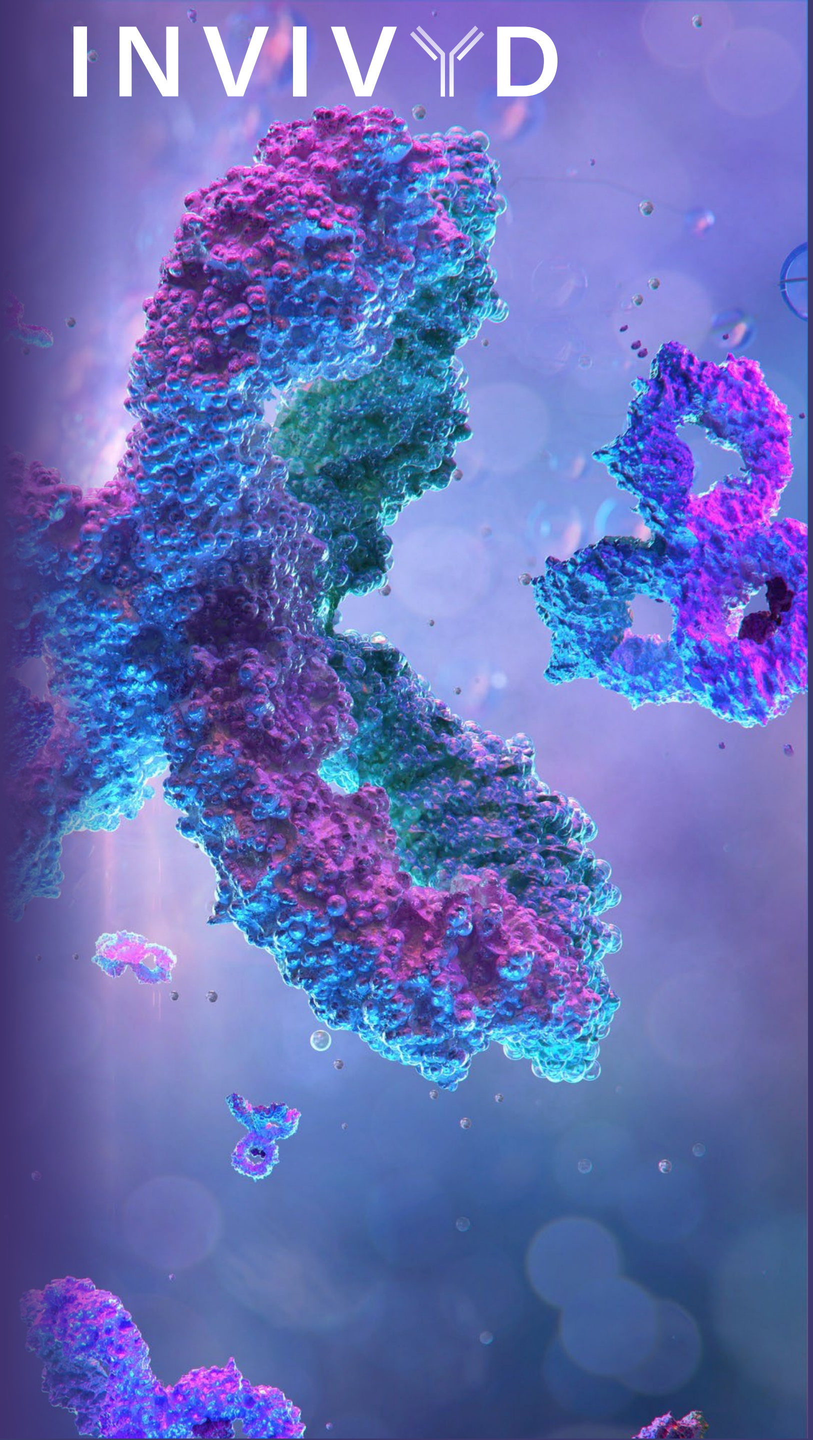
WHY MONOCLONAL ANTIBODIES (MABS) AT WVC?



A lack of choice is driving a growing gap in protection against the threat of infectious disease

Even the best vaccines have not fully contained the public health burden of any pathogens except smallpox

Invivyd is committed to developing effective treatments and protection for a growing population of vulnerable people



KEY CHALLENGES TO BROAD MAB USAGE DO NOT DIFFER FROM THOSE FACED BY VACCINES

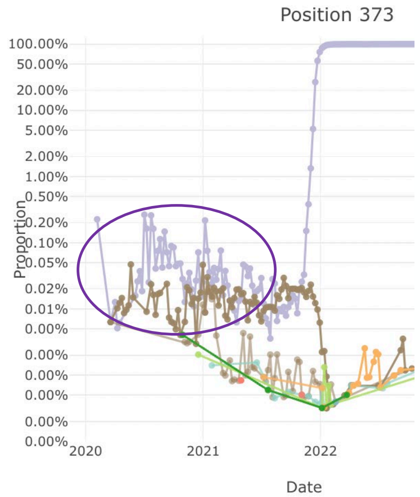
SCALE

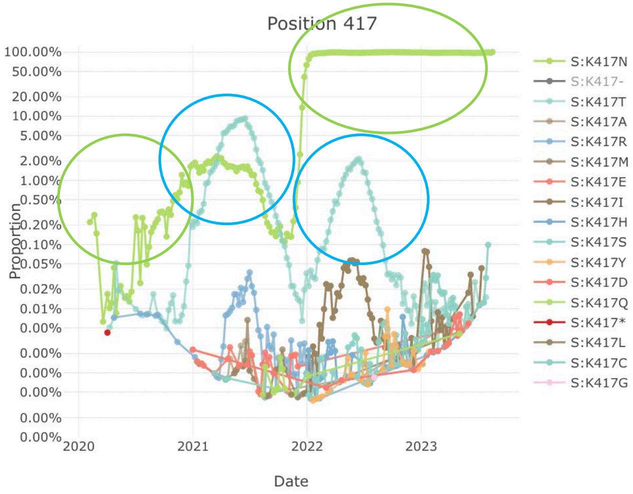
ACCESS

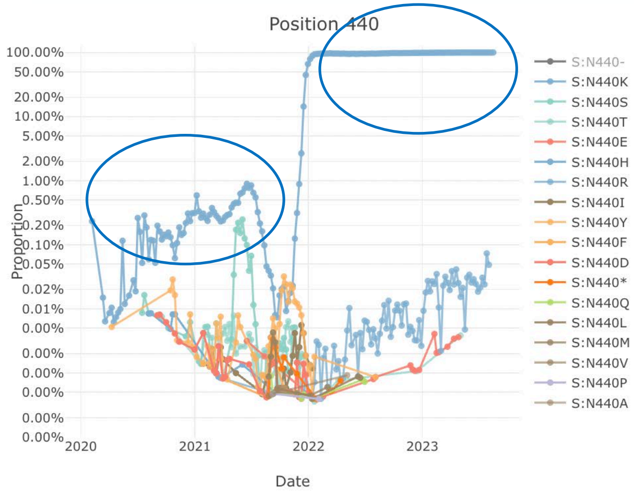
PATHOGEN STRAIN VARIATION

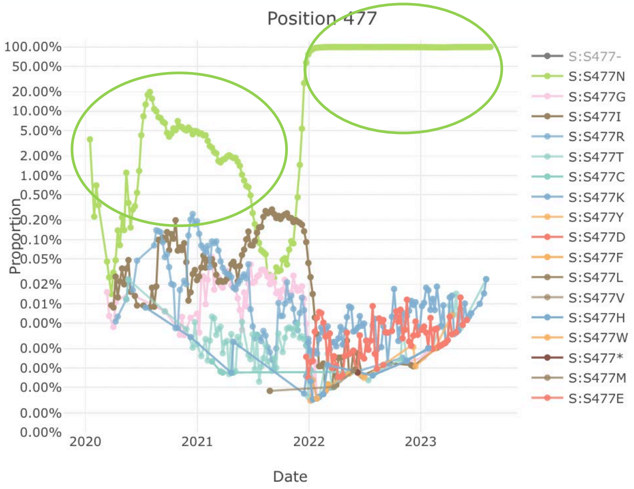
Predictive trends in Spike RBD polymorph data

Mutations that are ‘explored’ by the virus are more likely to dominate in the future









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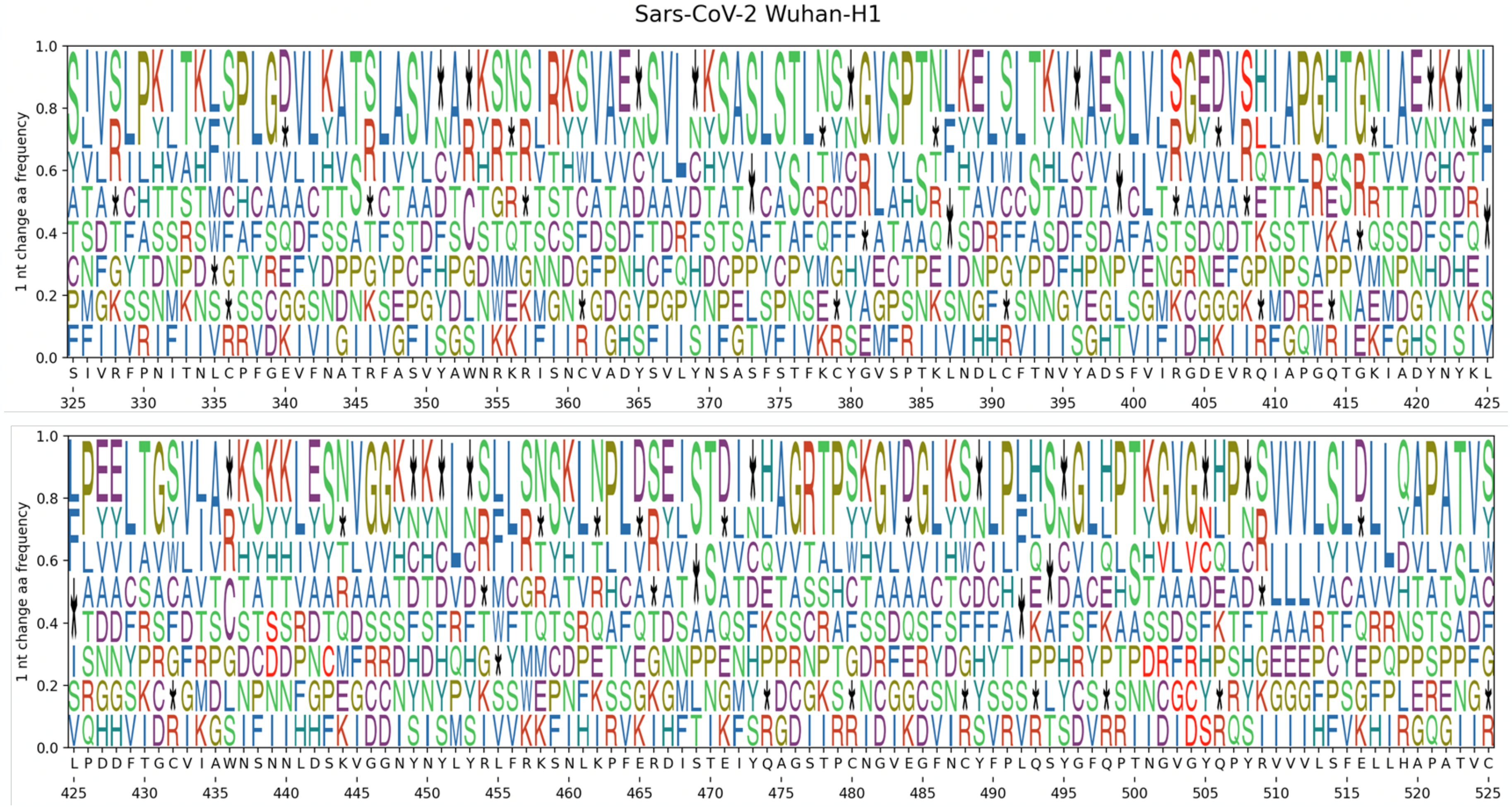
Mutagenic space within 1 nt change from Wuhan-H1



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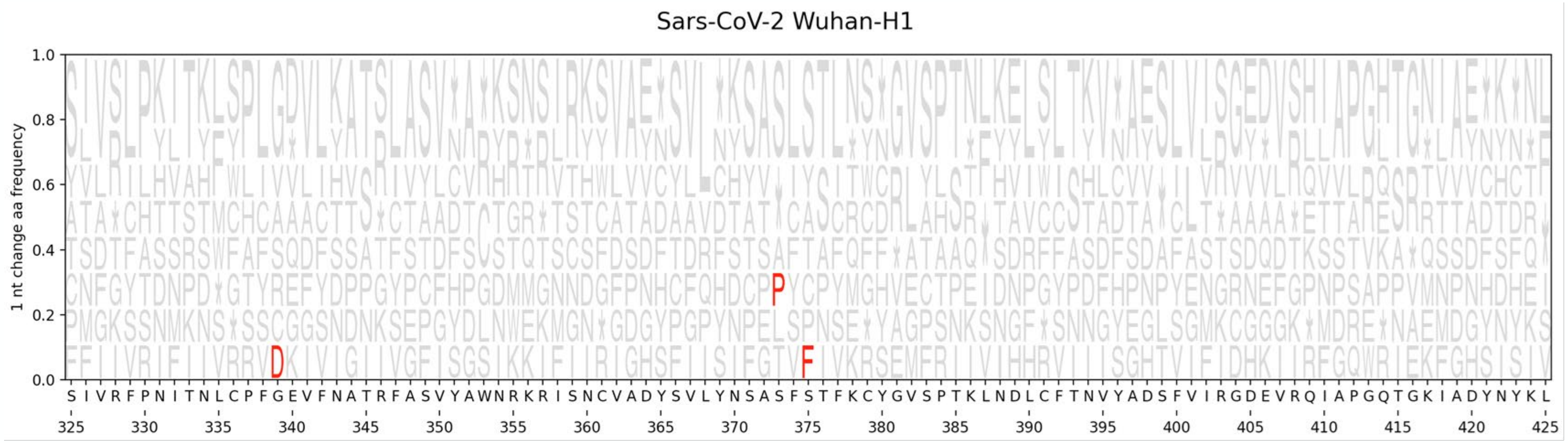
AA changes resulting from single nucleotide changes observed in circulating variant 2 years after Wuhan-H1emergence



The only RBD mutation in Omicron BA.1 not accessible with a single nucleotide mutation is S371L.

Although BA2 & BA5 have S371F which is accessible by a single nucleotide mutation.

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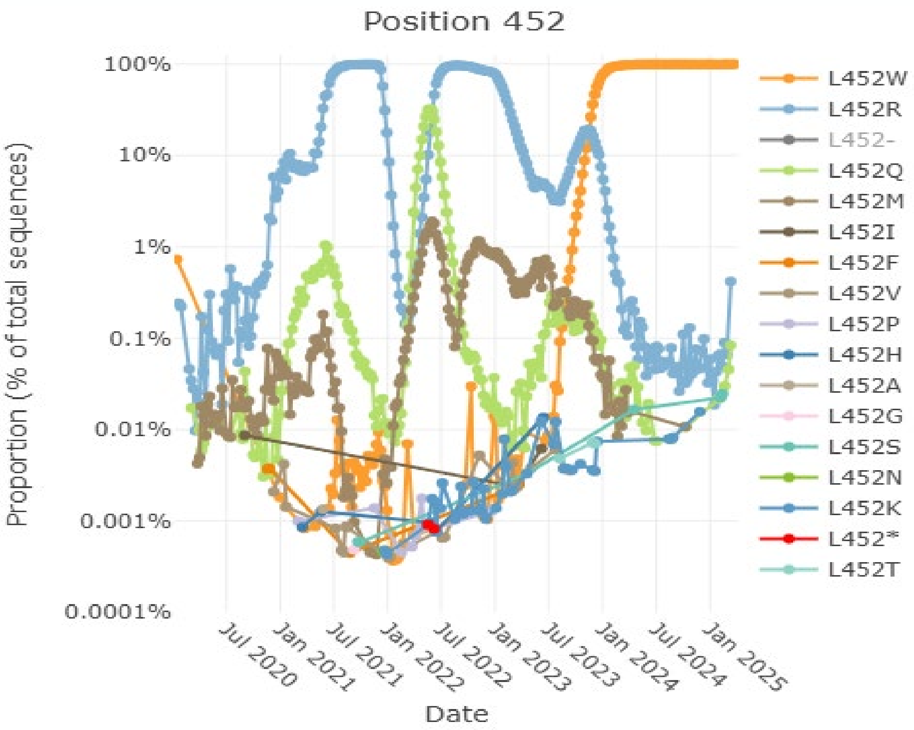
The defining mutations of LP.8.1 emerged from single nucleotide changes

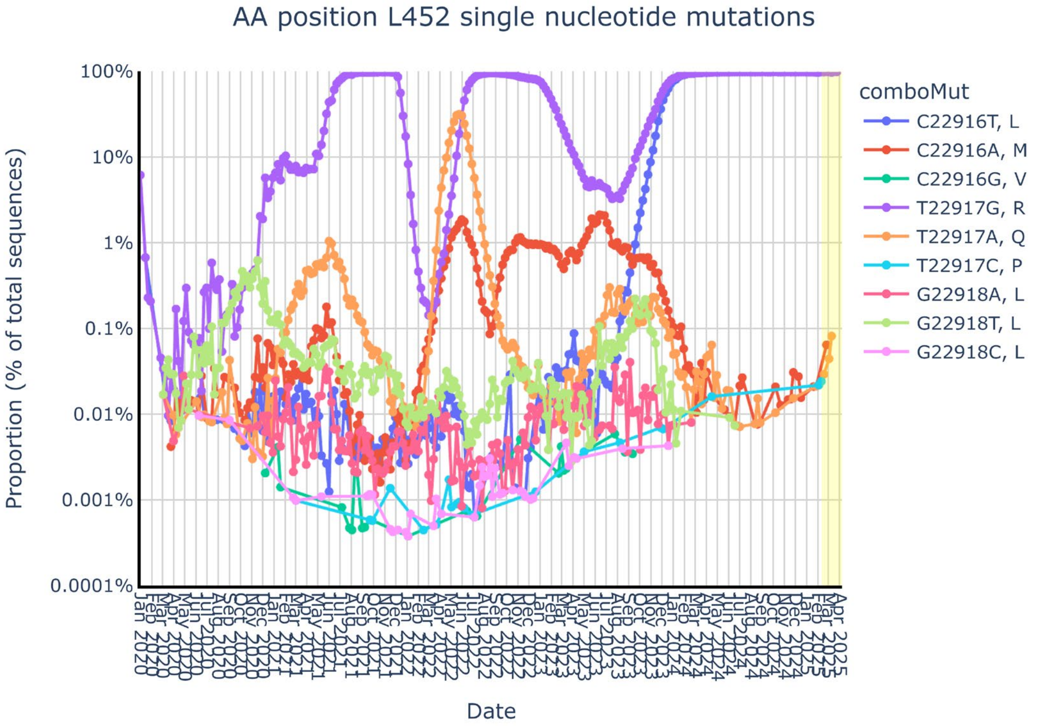
LP.8.1 is differentiated from its KP.1.1 parent at 4 positions in the spike protein

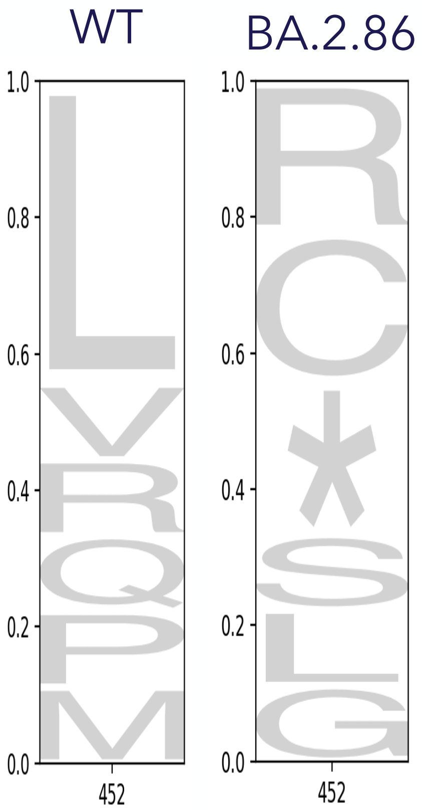
	KP.1.1		**LP.8.1 (KP.1.1.3.8.1)**	
S position (genome position)	amino acid	codon	amino acid	codon
186 (22118-22120)	F	TTC	L	TTA
190 (22130-22132)	R	AGG	S	AGT
445 (22895-22897)	H	CAT	R	CGT
493 (23039-23041)	Q	CAA	E	GAA

All four of the defining mutations of LP.8.1 were accessed from a single nucleotide change compared to the parent KP.1.1 variant.

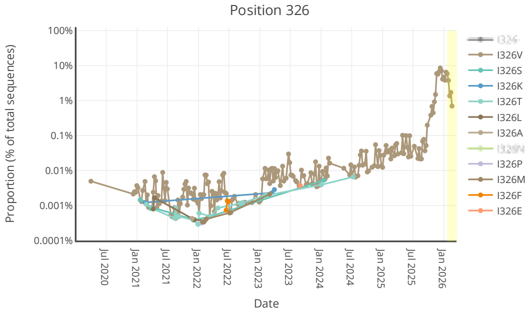
Polymorphs at the amino acid and nucleotide level

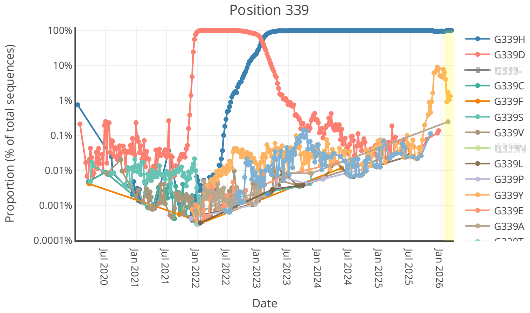


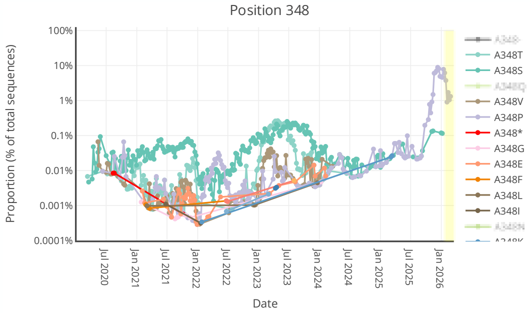




BA.3.2 RBD AMINO ACID POLYMORPH GRAPHS


Position 326


Position 339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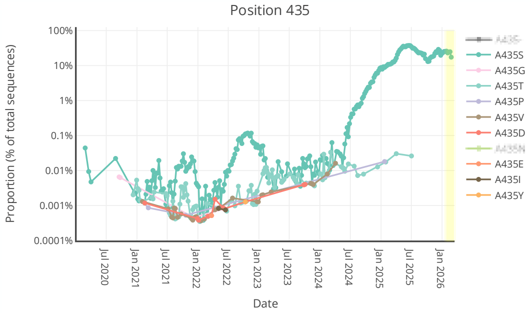
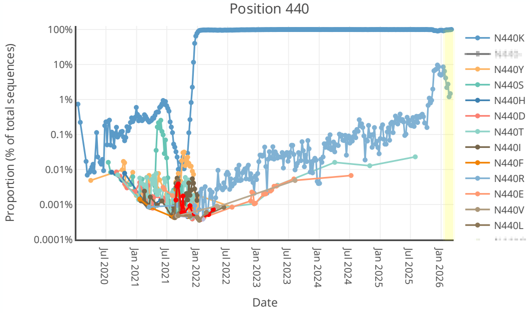
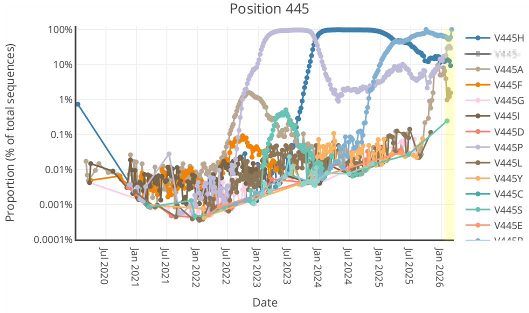
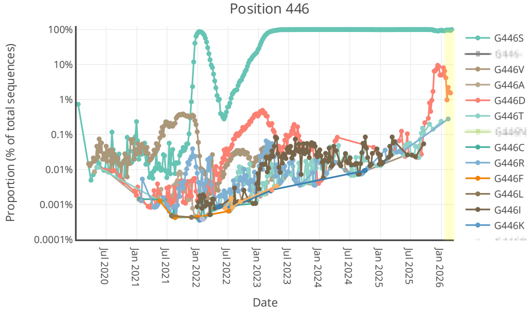
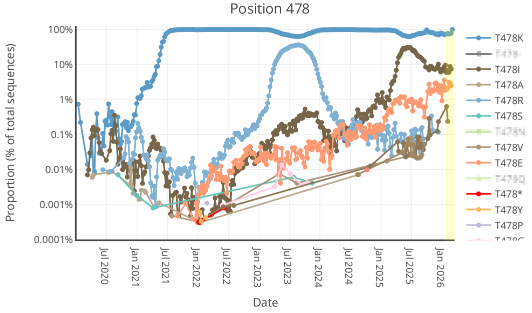
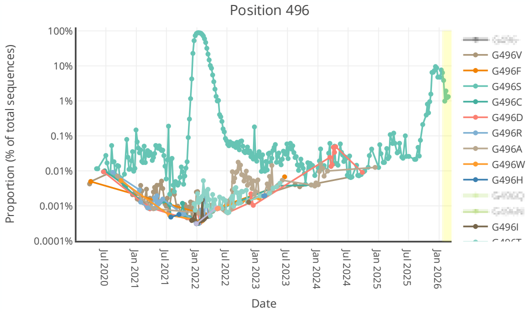

Position 435

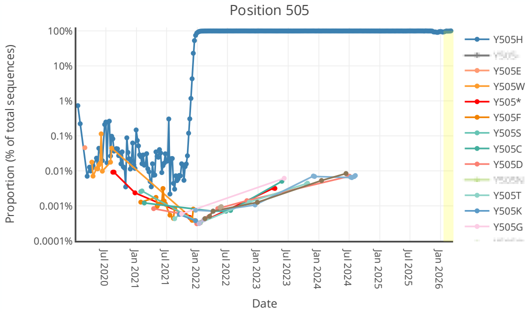

Position 440

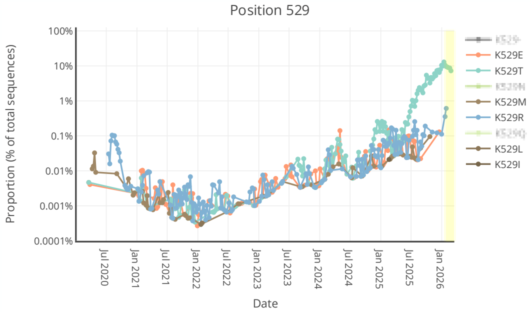

Position 445


Position 446

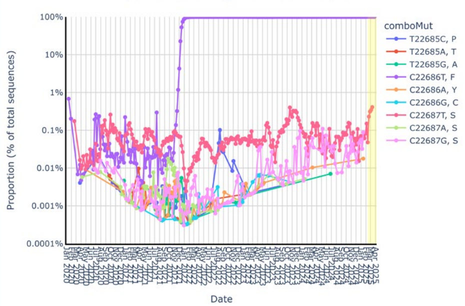

Position 478

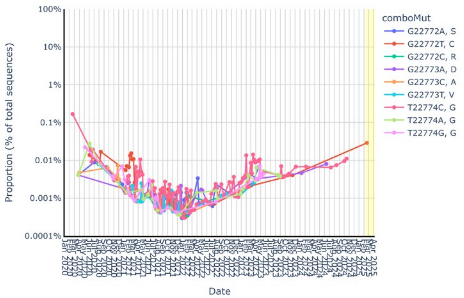

Position 496

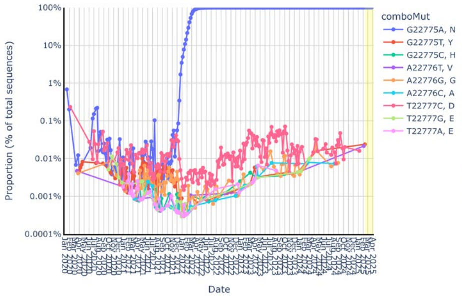

Position 505

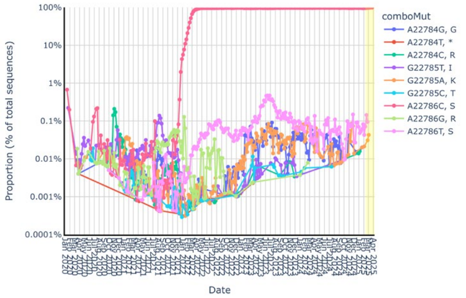

Position 529

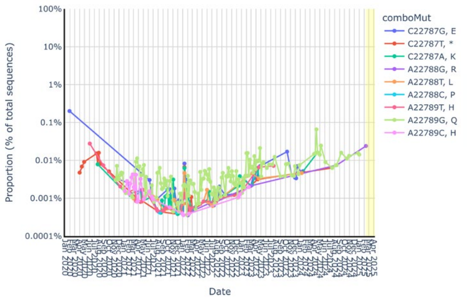
Single nucleotide polymorph graphs: pemivibart epitope

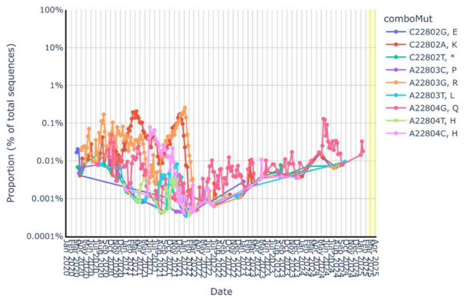

AA position S375 single nucleotide mutations

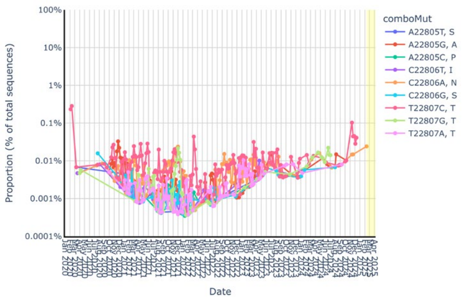

AA position G404 single nucleotide mutations

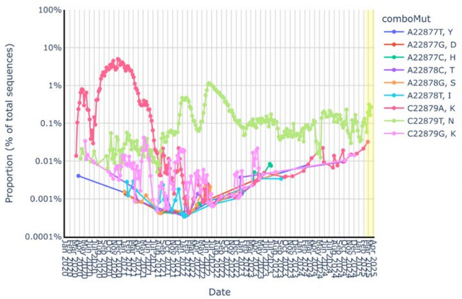

AA position D405 single nucleotide mutations

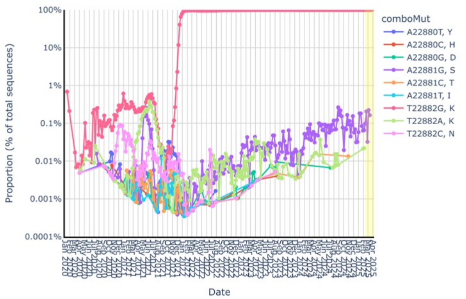

AA position R408 single nucleotide mutations

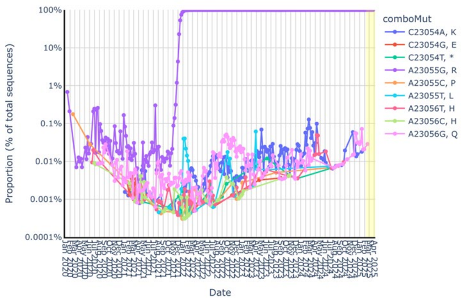

AA position Q409 single nucleotide mutations

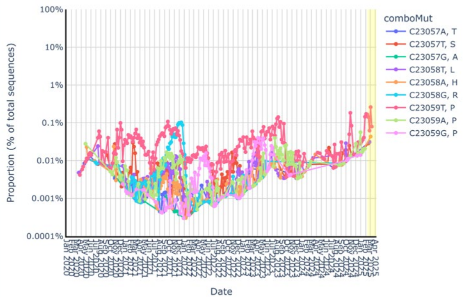

AA position Q414 single nucleotide mutations

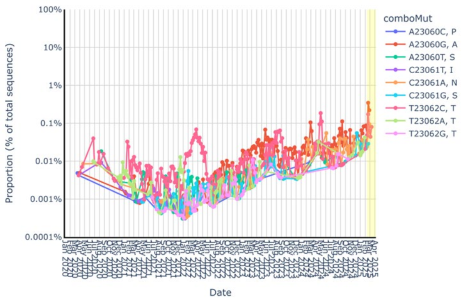

AA position T415 single nucleotide mutations

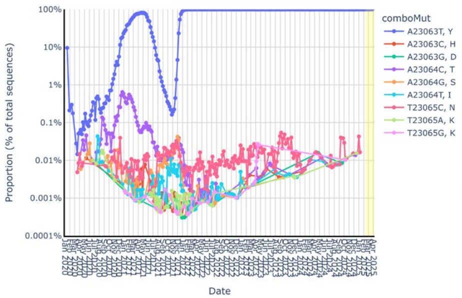

AA position N439 single nucleotide mutations

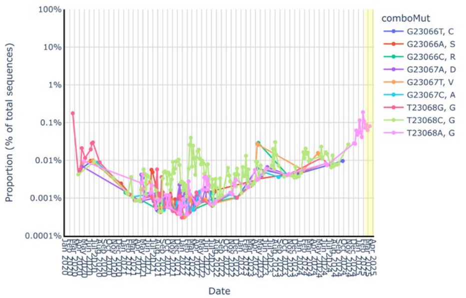

AA position N440 single nucleotide mutations

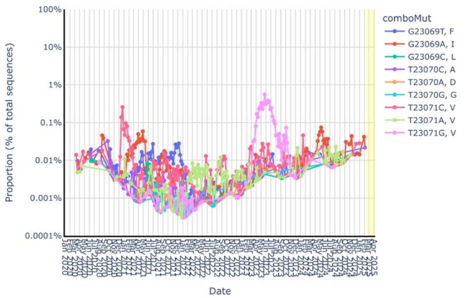

AA position Q498 single nucleotide mutations

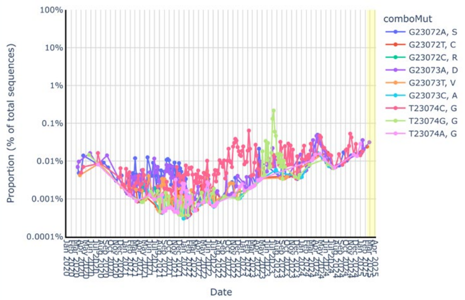

AA position P499 single nucleotide mutations

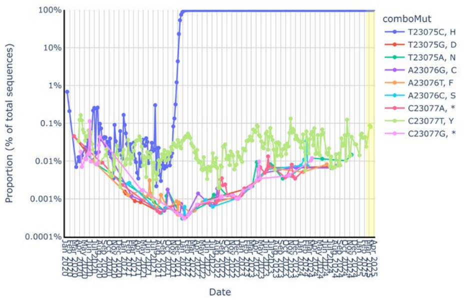

AA position T500 single nucleotide mutations


AA position N501 single nucleotide mutations


AA position G502 single nucleotide mutations


AA position V503 single nucleotide mutations


AA position G504 single nucleotide mutations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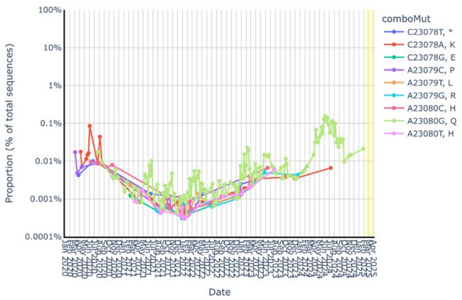
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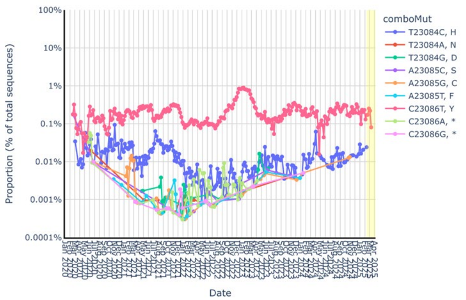
AA position Y508 single nucleotide mutations

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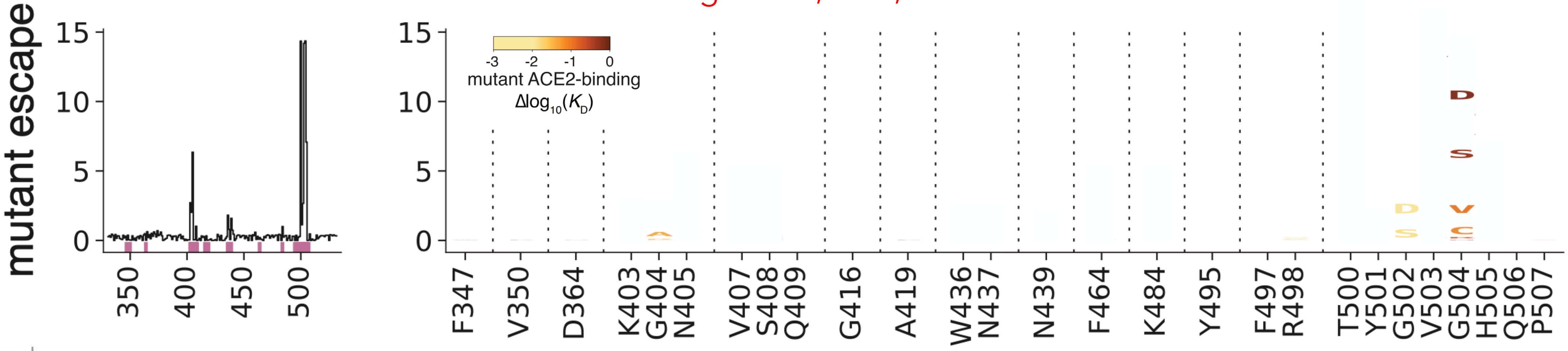
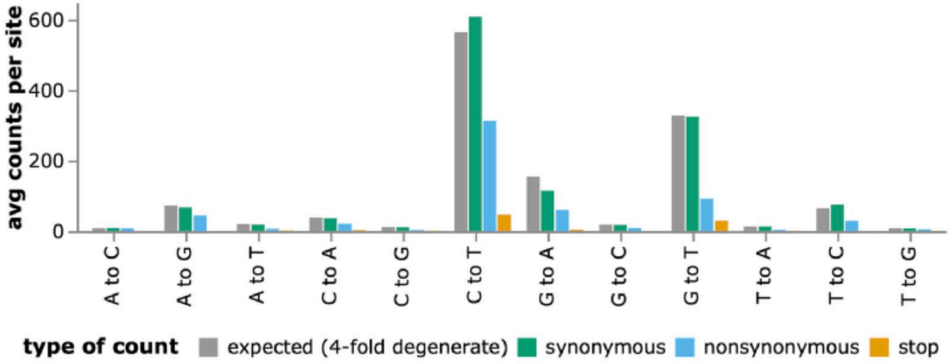
Further filtering based on single nucleotide substitution bias in SARS-CoV-2

Pemivibart DMS Escape Determinants in the BA.2.86 Background

-- mutations accessible from a single C>T, G>T, or G>A nucleotide mutation --





Bloom et al., *Virus Evolution*, Volume 9, Issue 2, 2023, vead055, https://doi.org/10.1093/ve/vead055

SARS-CoV-2 heavily favors C>T and G>T nucleotide mutations, which enables further filtering of evolutionary complexity, and finer focusing of discovery efforts.

SARS-COV-2 Spike Receptor Binding Domain (RBD) Residue Plasticity Index (RPI)

Poll sequence data for weekly mutation proportions

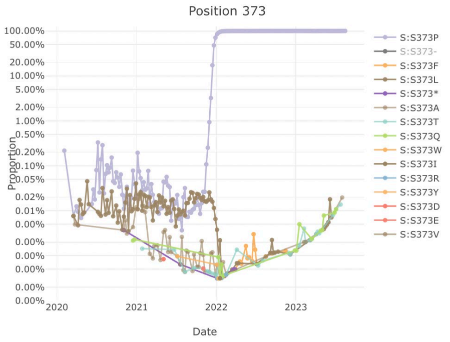
For all mutations, populate missing dates with proportion = 0

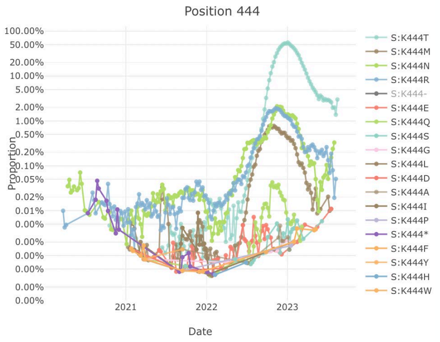
Calculate the absolute rate of change for each mutation

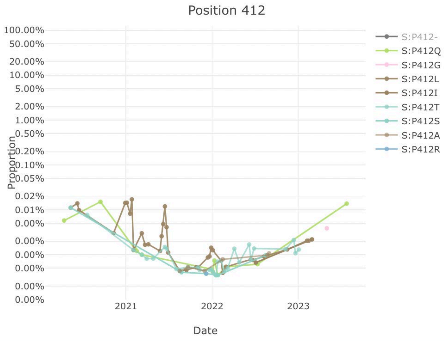
Isolate date range & sum rate of change for all mutations at each position

Complete non-mutating positions as a rate of change = 0

Calculate RPI as the positional rate of change



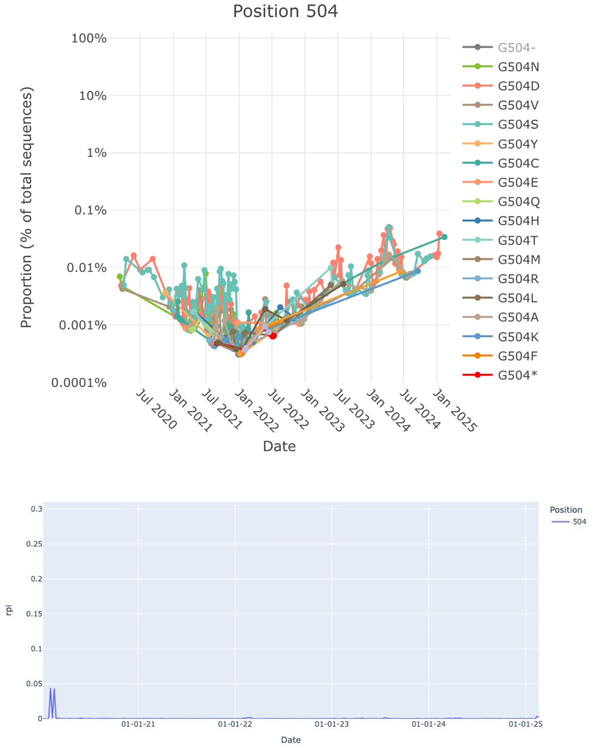




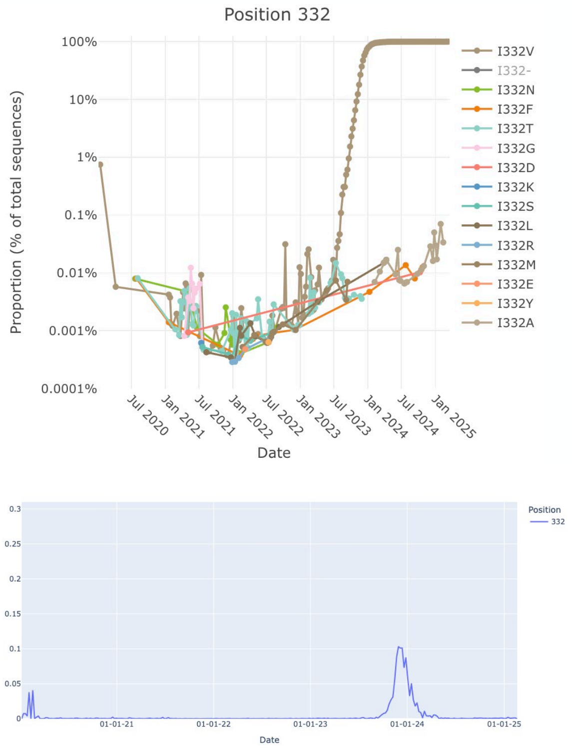
- The RPI is based on the polymorph graphs
- It shows which mutations, and by extension which positions, are changing the most over time

RPI measurements of Spike RBD residues

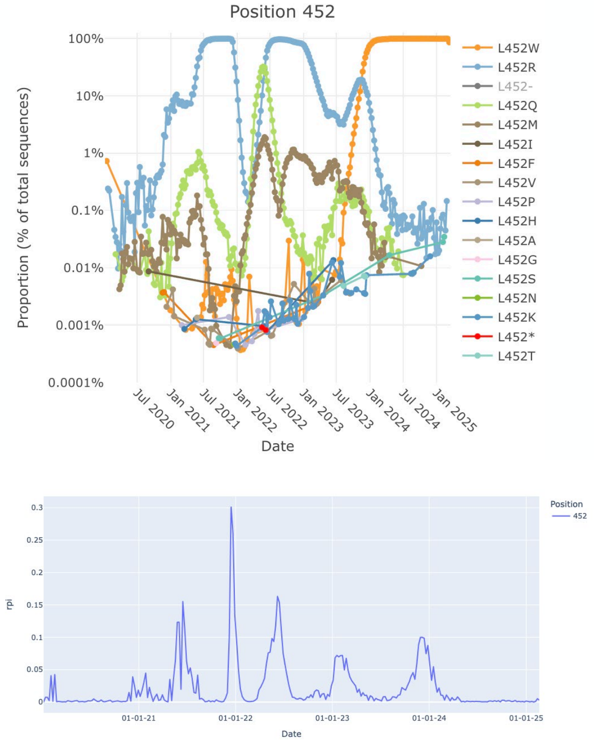
Position 504 RPI



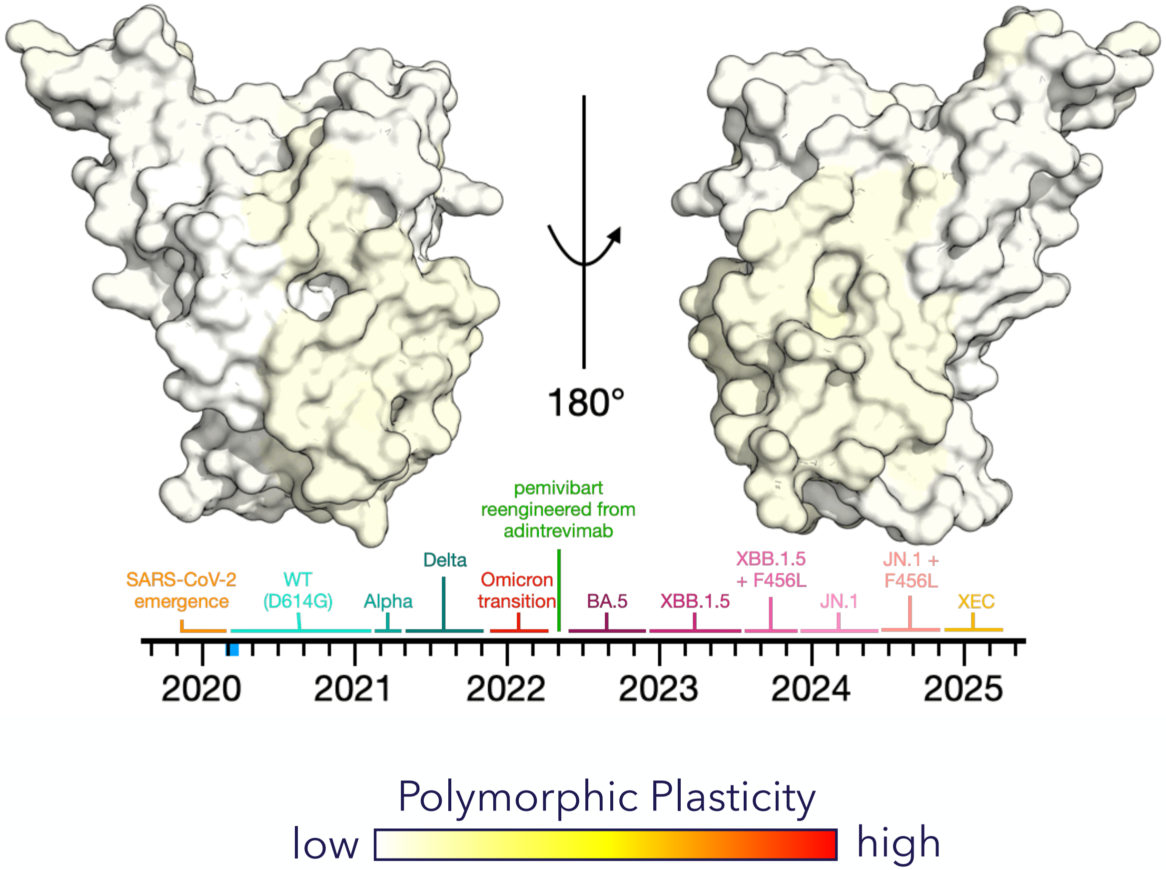
Position 332 RPI



Position 452 RPI



The monthly RBD RPI shows evolutionary hotspots as they emerge



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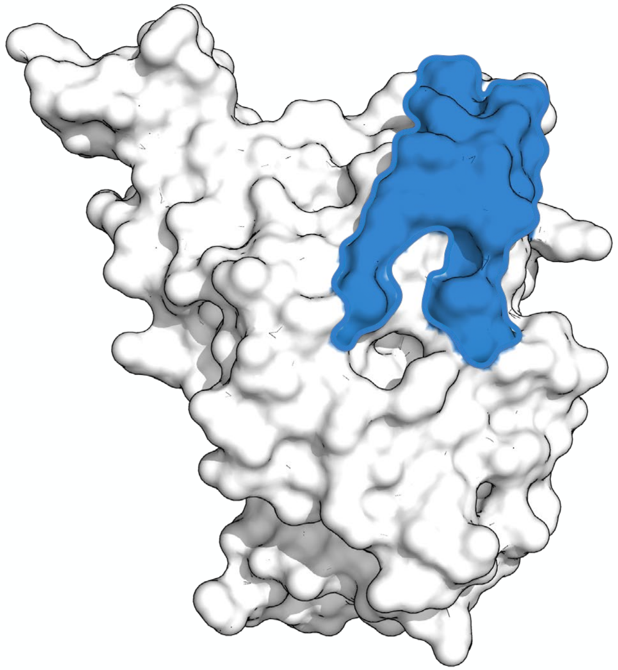
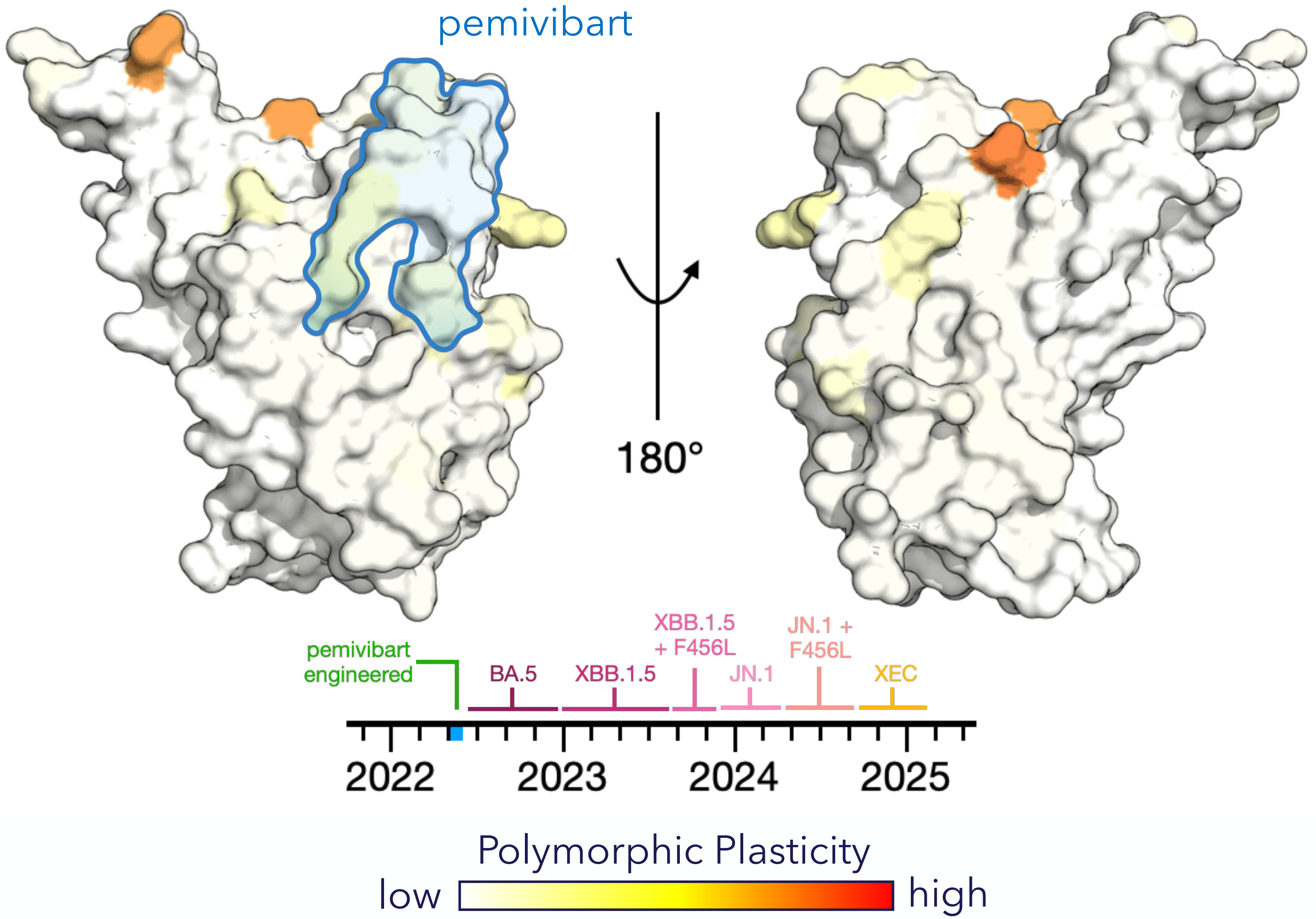
Pemivibart epitope RPI has remained **Stable** in the post-omicron era





Pemivibart epitope derived from 5 Å residue cloud as modeled bound to the BA.5 RBD.

-Data through Sept 2025

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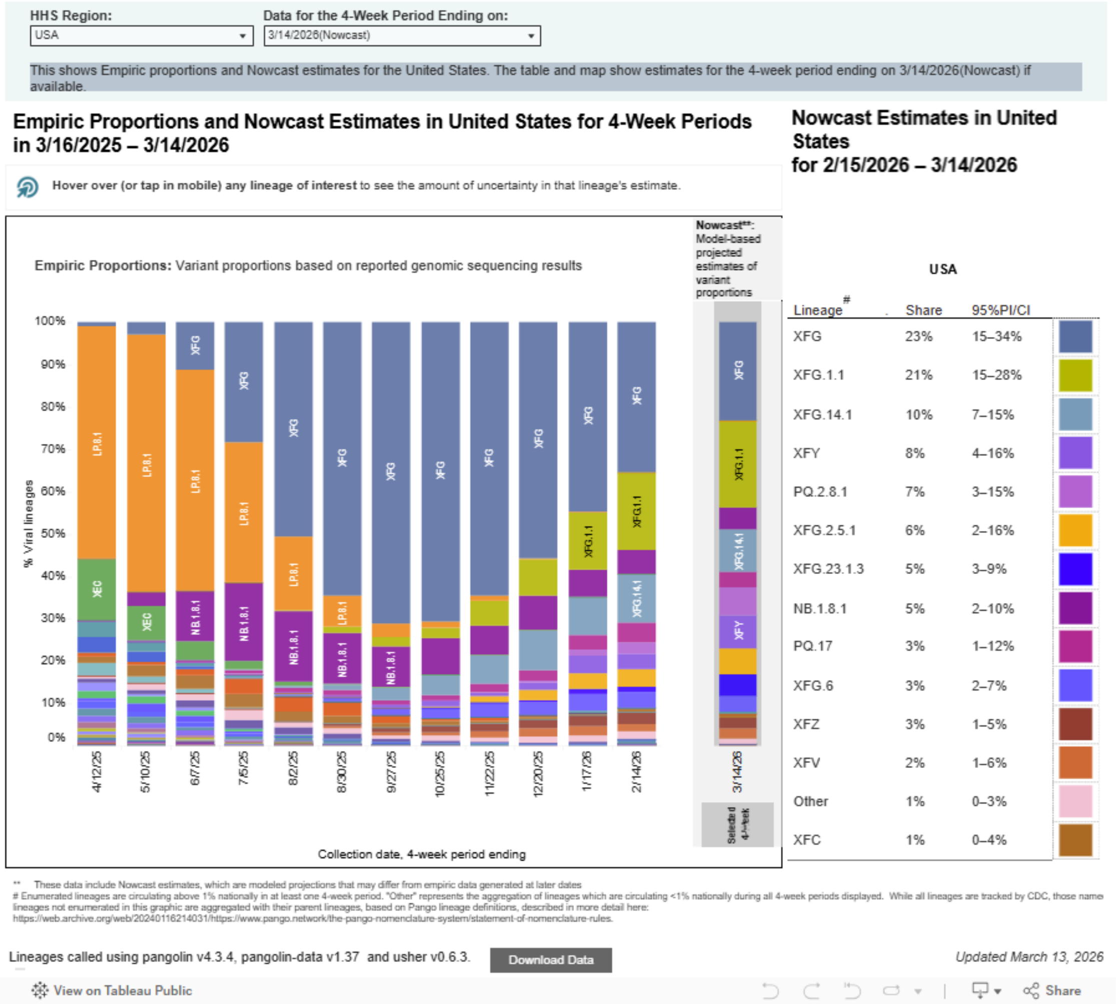
CDC COVID DATA TRACKER THROUGH MARCH 13TH SHOWS XFG IN DOMINANT POSITION



HHS Region: USA

Data for the 4-Week Period Ending on: 3/14/2026(Nowcast)

This shows Empiric proportions and Nowcast estimates for the United States. The table and map show estimates for the 4-week period ending on 3/14/2026(Nowcast) if available.

Empiric Proportions and Nowcast Estimates in United States for 4-Week Periods in 3/16/2025 – 3/14/2026

Hover over (or tap in mobile) any lineage of interest to see the amount of uncertainty in that lineage's estimate.

Empiric Proportions: Variant proportions based on reported genomic sequencing results

Nowcast:** Model-based projected estimates of variant proportions

Nowcast Estimates in United States for 2/15/2026 – 3/14/2026

USA

Lineage#	Share	95%PI/CI	
XFG	23%	15–34%	■
XFG.1.1	21%	15–28%	■
XFG.14.1	10%	7–15%	■
XFY	8%	4–16%	■
PQ.2.8.1	7%	3–15%	■
XFG.2.5.1	6%	2–16%	■
XFG.23.1.3	5%	3–9%	■
NB.1.8.1	5%	2–10%	■
PQ.17	3%	1–12%	■
XFG.6	3%	2–7%	■
XFZ	3%	1–5%	■
XFV	2%	1–6%	■
Other	1%	0–3%	■
XFC	1%	0–4%	■

** These data include Nowcast estimates, which are modeled projections that may differ from empiric data generated at later dates

Enumerated lineages are circulating above 1% nationally in at least one 4-week period. "Other" represents the aggregation of lineages which are circulating <1% nationally during all 4-week periods displayed. While all lineages are tracked by CDC, those name lineages not enumerated in this graphic are aggregated with their parent lineages, based on Pango lineage definitions, described in more detail here: https://web.archive.org/web/20240116214031/https://www.pango.network/the-pango-nomenclature-system/statement-of-nomenclature-rules.

Lineages called using pangolin v4.3.4, pangolin-data v1.37 and usher v0.6.3.

Updated March 13, 2026

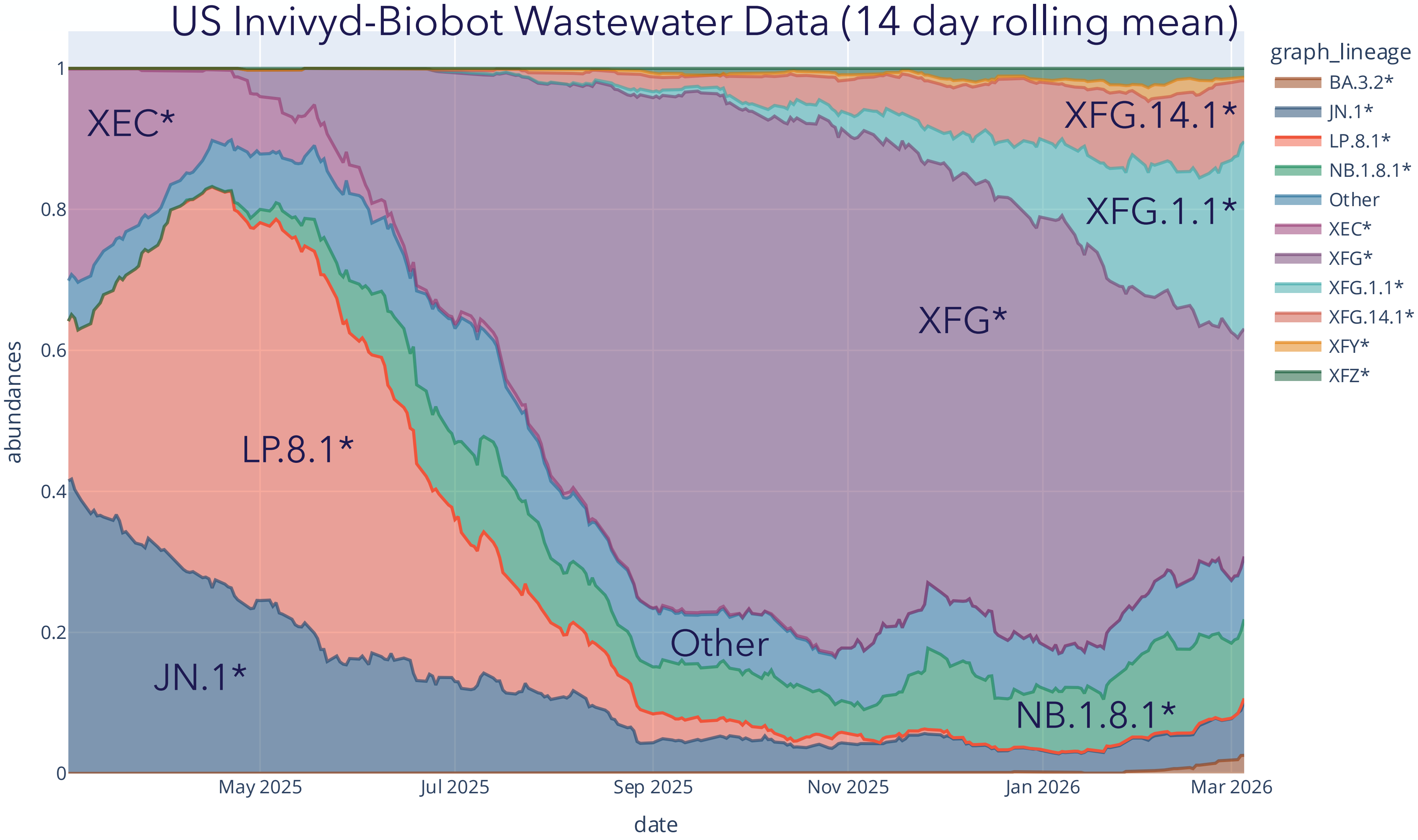
- XFG at 23%
- XFG.1.1 at 21%
- XFG.14.1 at 10%

- CDC nowcast reports which SARS-COV-2 variants were present in the US over a given period of time
- The average IC50 for that time period then becomes the average IC50 against the variants present *weighted* by their relative proportion

- Accessed 3/17/26: https://www.cdc.gov/covid/php/variants/variants-and-genomic-surveillance.html

INVIVYD

INTERNAL ANALYSIS CONFIRMS THAT XFG* IS THE LIKELY LEADING VARIANT CLADE IN US BASED ON BIOBOT WASTEWATER DATA

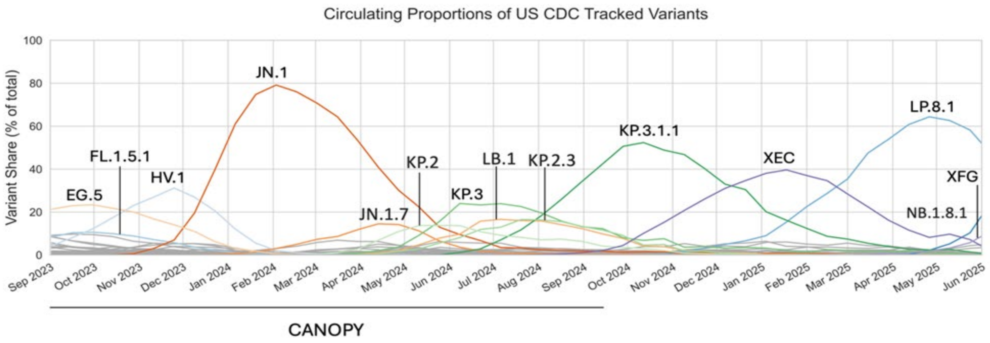

US Invivyd-Biobot Wastewater Data (14 day rolling mean)

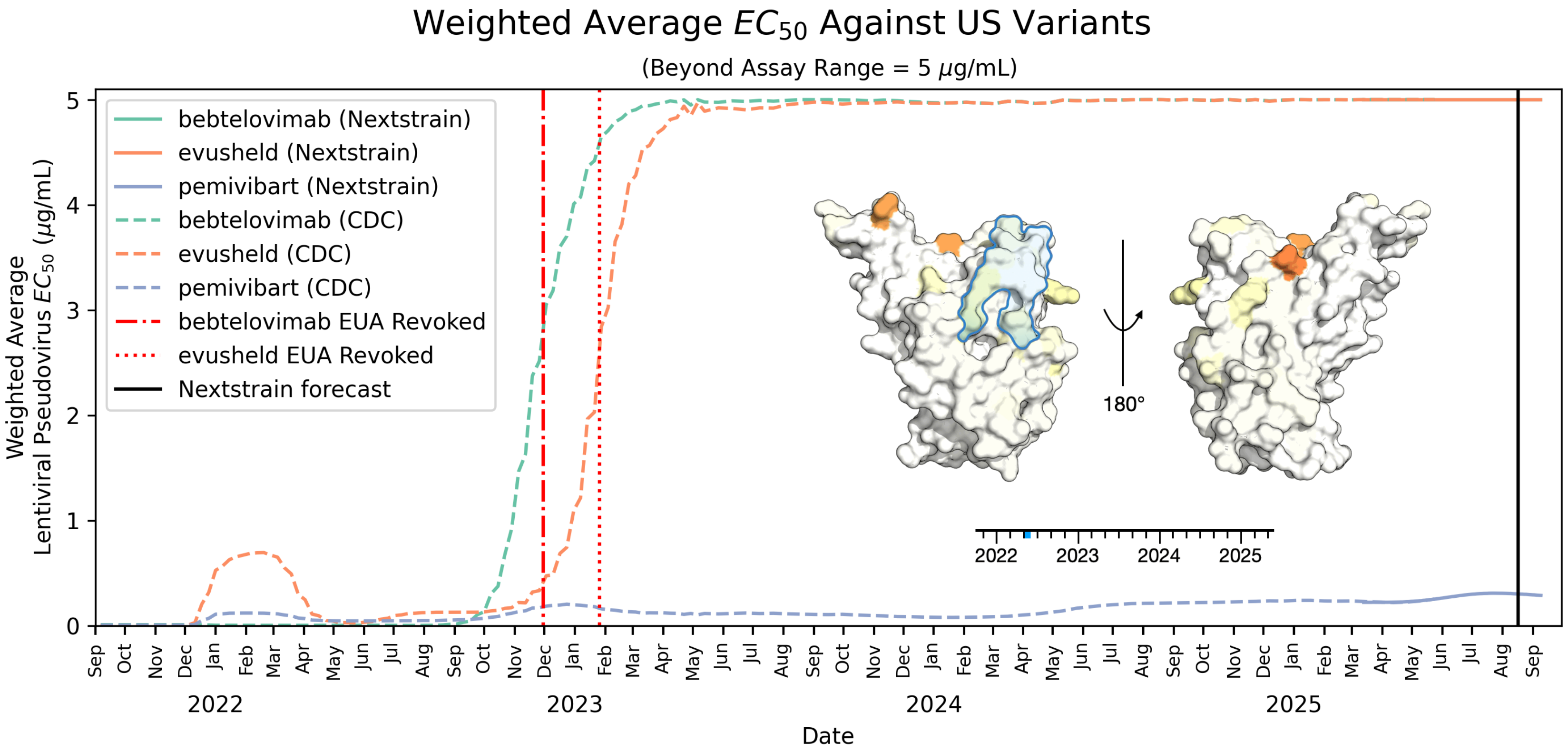
On a national scale, for samples collected as of March 5th, 2026:

- ⬇ XFG.14.1* is decreasing (currently ~8.6%)
- ⬇ XFZ* is decreasing (currently ~1.3%)
- ⬇ NB.1.8.1* is decreasing (currently ~11.2%)
- ⬇ Other is decreasing (currently ~8.9%)
- ⬇ XFG* is decreasing (currently ~32.3%)
- ⬆ BA.3.2* is increasing (currently ~2.6%)

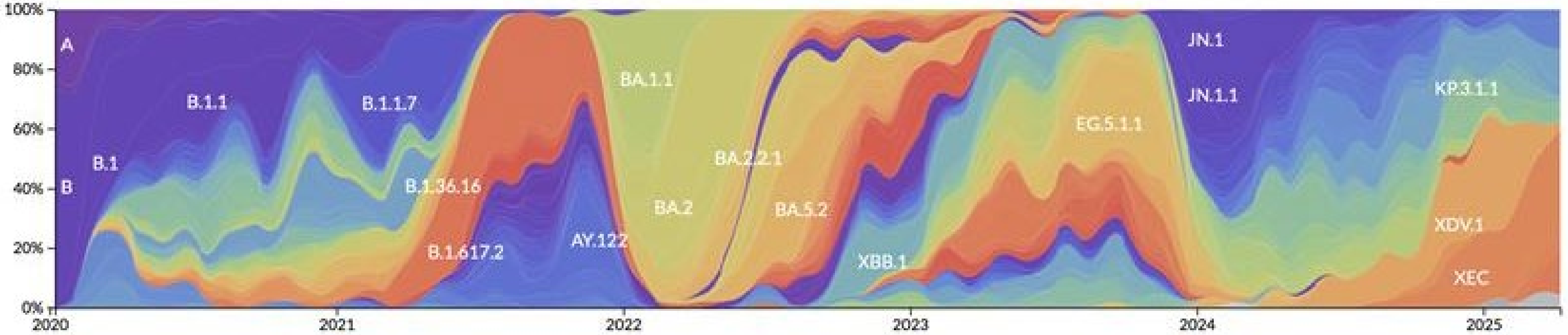
INVIVYD

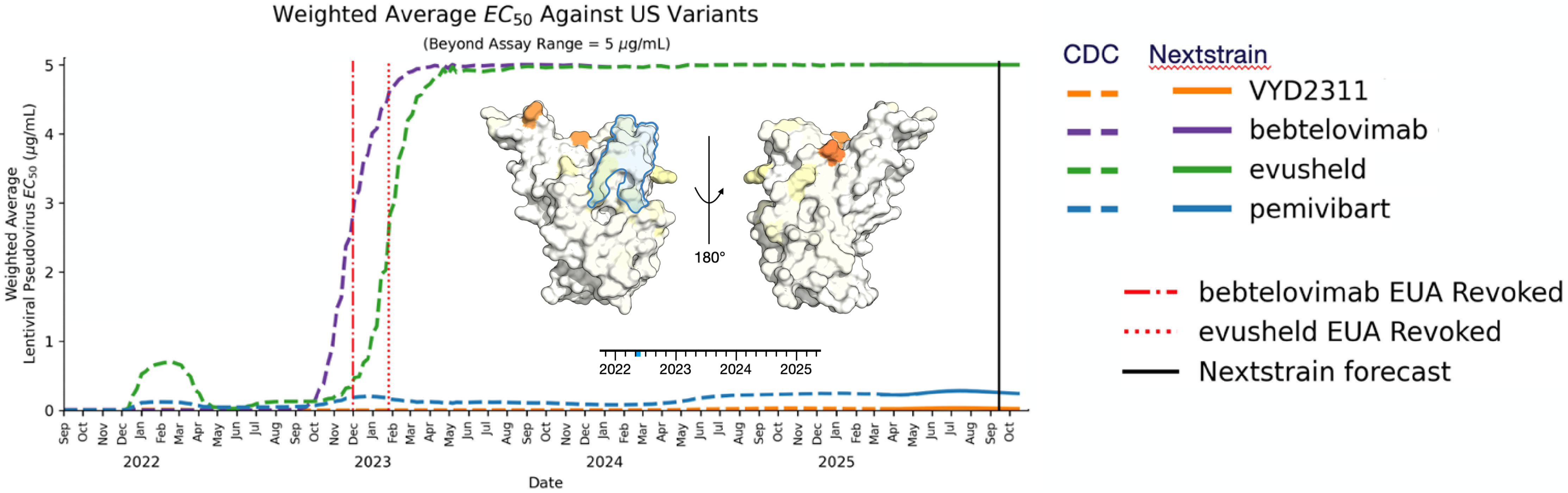
Pemivibart epitope and neutralization potency have remained stable





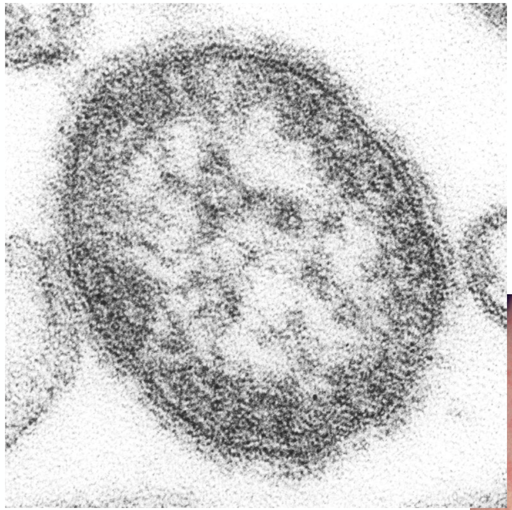
Pemivibart and VYD2311 epitope and neutralization potency have remained stable



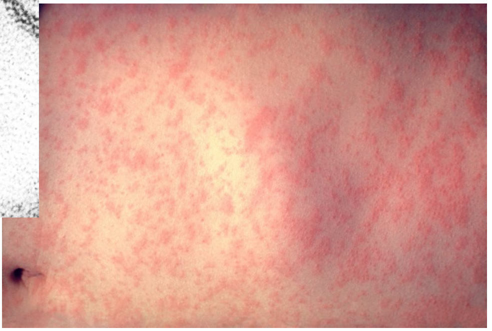


MEASLES VIRUS BACKGROUND

- The Measles Virus (MeV) is an RNA *Morbillivirus*
  - There are 24 strains of MeV divided into 8 clades: A-H
- Transmission occurs through respiratory droplets and is highly infectious
  - Symptoms include fever, coughing, malaise, and a rash
  - Complications occur in ~30% of cases requiring hospitalization
  - ~2/1000 children infected results in death
- Vaccination is the primary form of preventing Measles
  - The first Measles vaccine was introduced in 1963
  - Introduction of the MMR vaccine in 1971 reduced Measles cases by >99%
    - MMR-II was approved in 1978 for children 12 months and older [Measles, Mumps and Rubella Virus Vaccine Live | FDA]
- There are few treatments for Measles
  - IVIg/IMIg is an expensive option reserved for the most at risk patients
- Less than 220 cases per year were reported in the USA between 1997 and 2013
  - In 2025 there were 2285 confirmed cases of Measles in the USA
  - As of March 16 2026, there have been 1487 confirmed cases of Measles reported in the USA in 24 states
  - [Measles Cases and Outbreaks | Measles (Rubeola) | CDC]

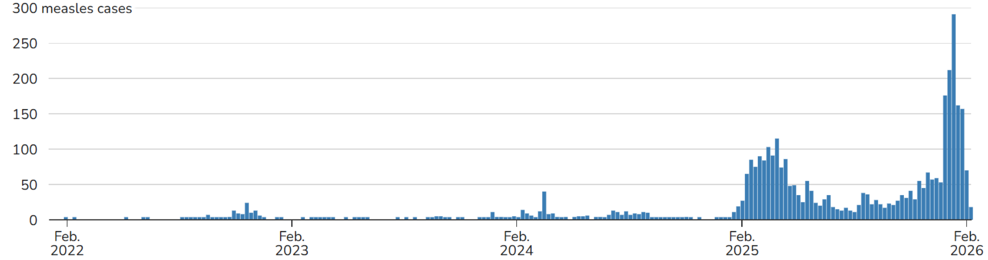


[Measles]

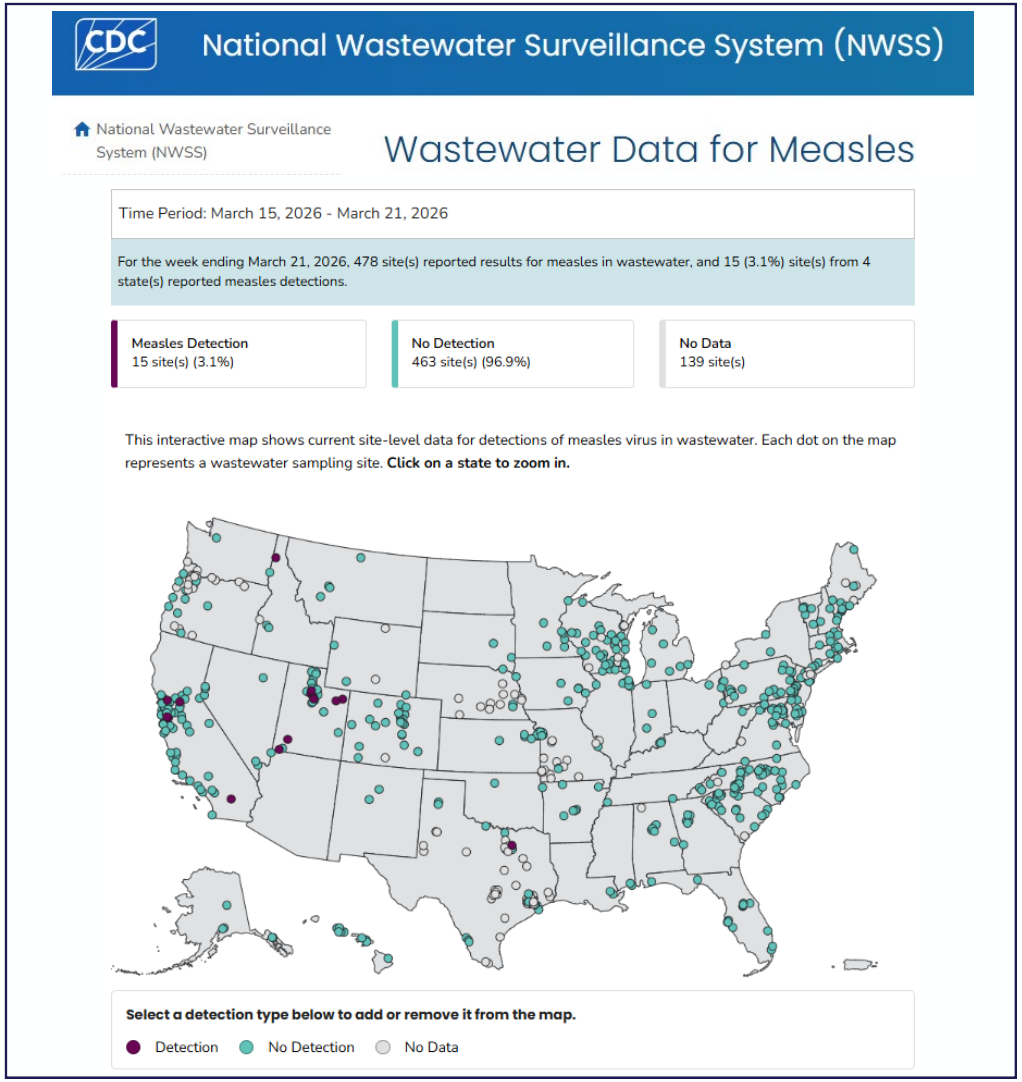


Weekly measles cases by rash onset date

2023–2026* (as of February 12, 2026)



MEASLES VIRUS WASTEWATER SURVEILLANCE



CDC National Wastewater Surveillance System (NWSS)

National Wastewater Surveillance System (NWSS)

Wastewater Data for Measles

Time Period: March 15, 2026 - March 21, 2026

For the week ending March 21, 2026, 478 site(s) reported results for measles in wastewater, and 15 (3.1%) site(s) from 4 state(s) reported measles detections.

Measles Detection	No Detection	No Data
15 site(s) (3.1%)	463 site(s) (96.9%)	139 site(s)

This interactive map shows current site-level data for detections of measles virus in wastewater. Each dot on the map represents a wastewater sampling site. **Click on a state to zoom in.**

Select a detection type below to add or remove it from the map.

● Detection ● No Detection ○ No Data

Biobot

- Quantitative measurement, but no genotyping
- ddPCR for non-vaccine strain H gene

- New methods for complete genome sequencing from wastewater are now being explored.

Integrating measles wastewater and clinical whole-genome sequencing enables high-resolution tracking of virus evolution and transmission

Sipho Gwala[1#], Joshua I. Levy[2#], Victor Mabasa[1], Kathleen Subramoney[1,6], Nkosenhle L. Ndlovu[1], Chris Kent[3], Maryam Ahmadi Jeshvaghane[2], Praneeth Gangavarapu[2], Menzi Sikakane[1], Natasha Singh[1], Mantshali Motloung[1], Lethabo Monametsi[1], Lebohang Rabotapi[1], Emmanuel Phalane[1], Mokgaetji Macheke[1], Fiona Els[1,4,5], Chenoa Sankar[1], Tshepo Motsamai[1], Sibonginkosi Maposa[1], Nishi Prabdial-Sing[1,6], Joshua Quick[3], Kristian G. Andersen[2], Kerrigan McCarthy[1,6], Mukhlid Yousif[1,6*]

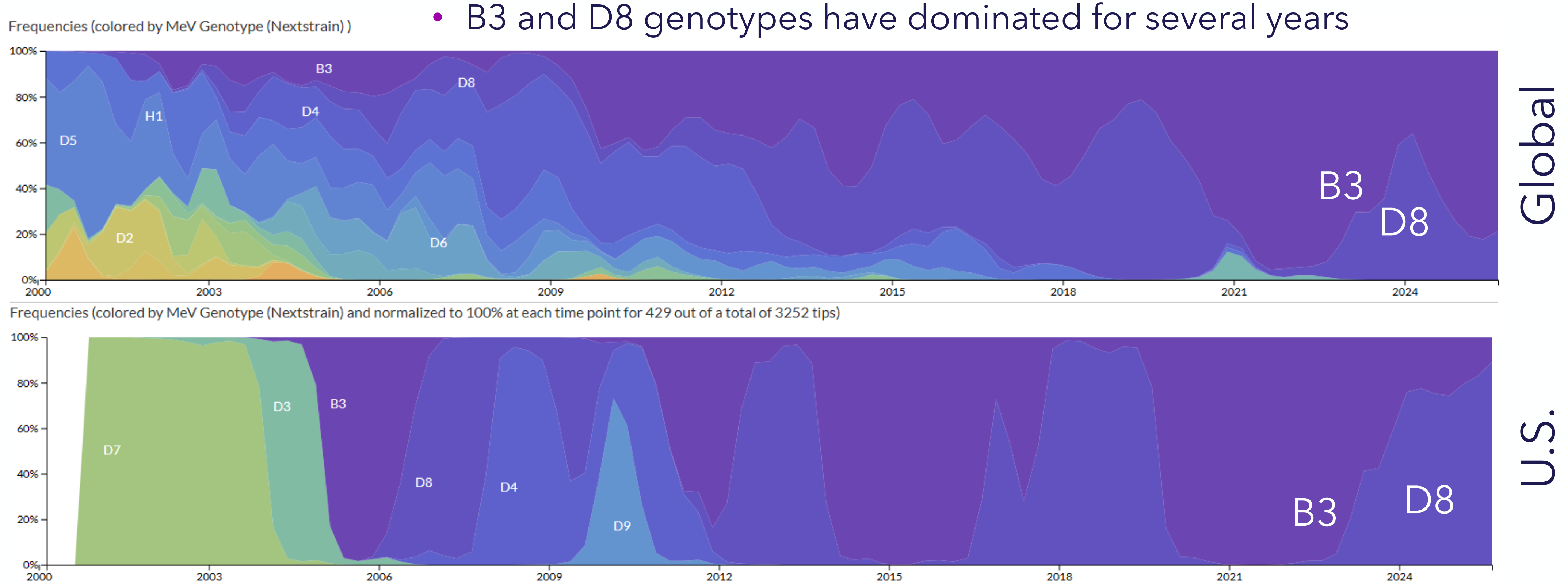
[1] Centre for Vaccines & Immunology, National Institute for Communicable Diseases, A Division of the National Health Laboratory Service, Johannesburg, South Africa.

CURRENT MEASLES VIRUS VARIANTS

FUSION (F) CONSERVATION

Pathoplexus

- B3 and D8 genotypes have dominated for several years



Current outbreak in South Carolina

- 139 complete F sequences from the past 6 months, all of genotype D8
- 125 (90%) are identical
- 14 carry a single amino acid change
  - T95A (x3) L197S (x1) H297Y (x1) D472N (x1) G541R (x8)

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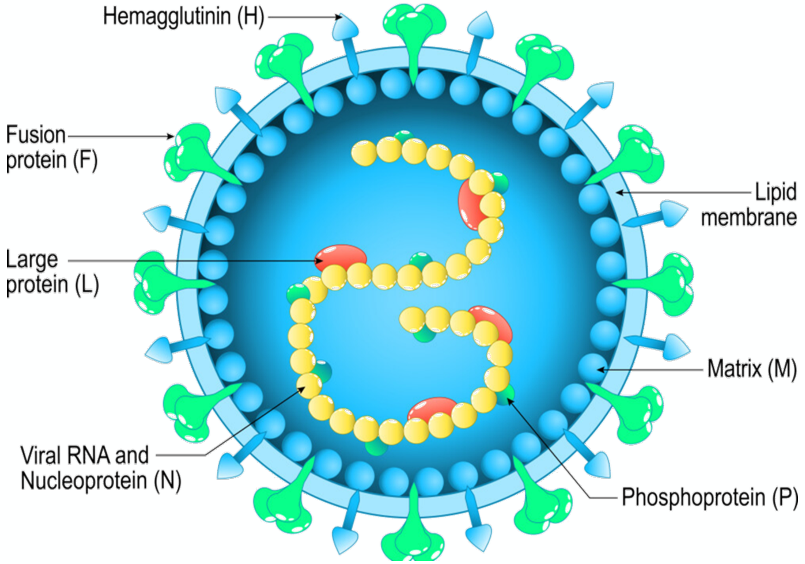
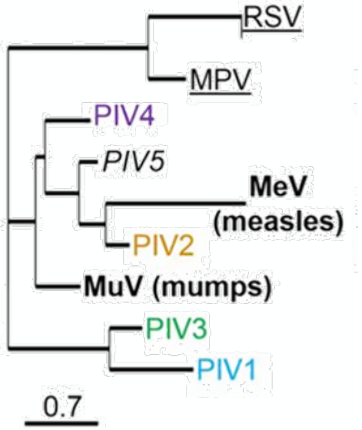
*based on N450 sequences (https://nextstrain.org/measles/N450)

MEASLES VIRUS SURFACE PROTEINS

- Like PIV and MuV, the MeV genome encodes for two surface proteins: Fusion (F) and Hemagglutinin (H)
  - The F-protein is the trimeric fusion protein responsible for viral membrane fusion
  - The H-protein is responsible for cell adhesion
- Antibodies isolated from vaccinated individuals show anti F- and H-protein antibodies that are neutralizing
- Measles can utilize multiple receptors for cell entry including CD150 (SLAM), CD46, and Nectin-4
- MeV-H and MeV-F co-localize on the viral surface and are known to interact
- The MeV-H protein is responsible for receptor binding. When it binds to a receptor MeV-H undergoes a conformational change that triggers the MeV-F protein that is responsible for viral fusion

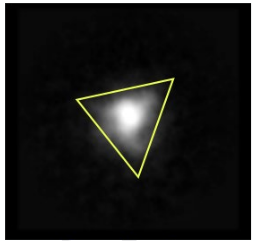




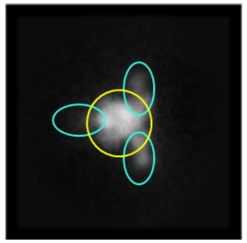
F-protein phylogenetic tree
PNAS

THE MEV-F PROTEIN

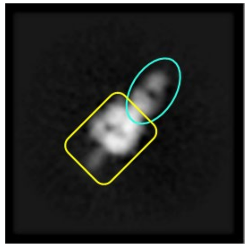
- MeV-F is responsible for viral-cell fusion in measles
- It is a trimeric protein similar to RSV-F, with a pre-fusion and post-fusion conformation
- The MeV-F0 protein is cleaved by Furin (**red arrow**) into F2 and F1
  - There is a conserved fusion peptide in F1
- To produce a stable pre-fusion trimer, four cysteines were introduced in the stem region
- We produced several MeV-F variants internally at Invivyd in HEK293 cells
  - This preserves the native glycosylation structures
  - These include the Edmonston, B3, and D8 variants
- These proteins were stable and shown to be folded correctly through binding studies and imaging



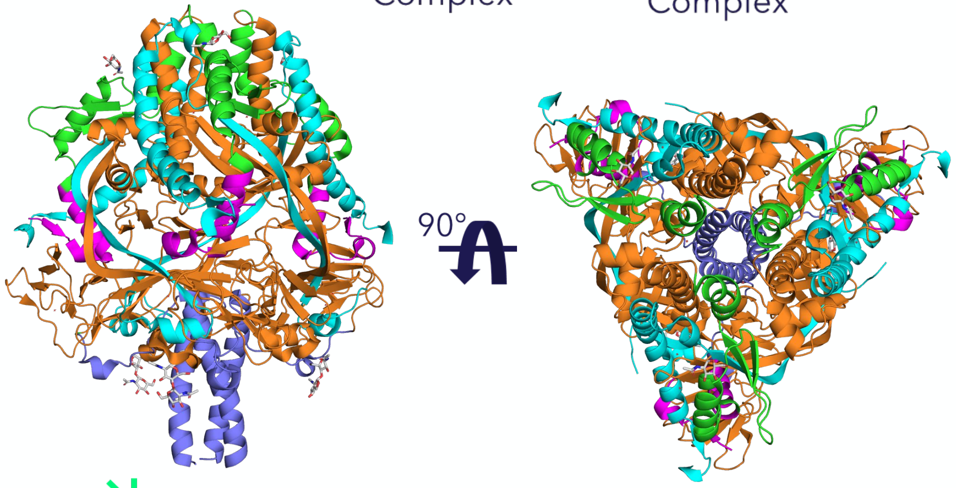
Pre-Fusion
No FAB

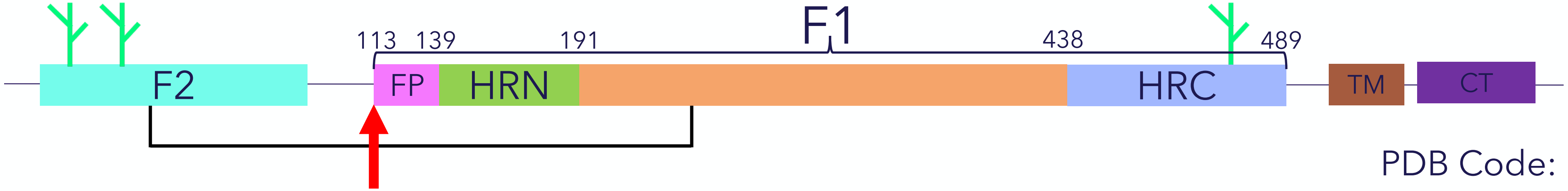


3:1
FAB:Pre-fusion
Complex



1:1
FAB:Pre-fusion
Complex



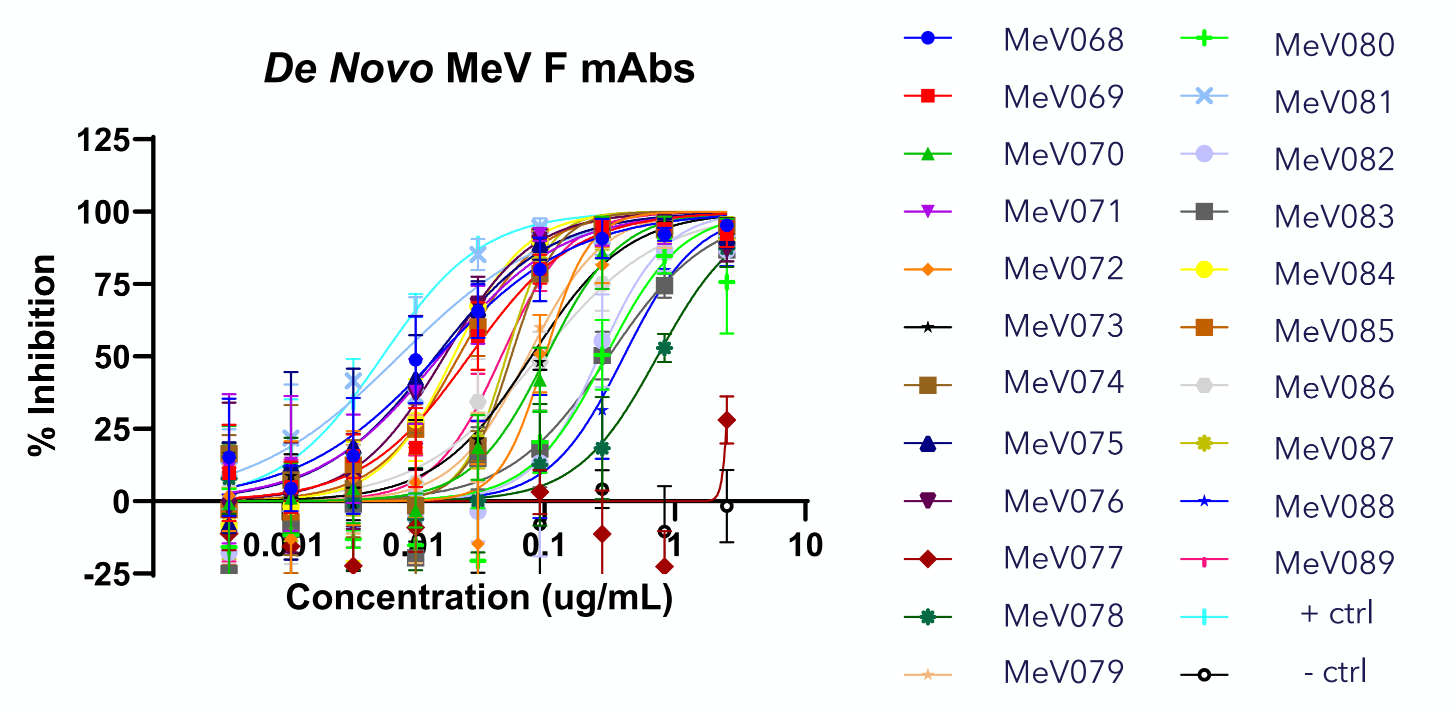


PDB Code: 5YXW

INVIVYD

MEASLES *DE NOVO* DISCOVERY – NEUTRALIZATION ASSAYS

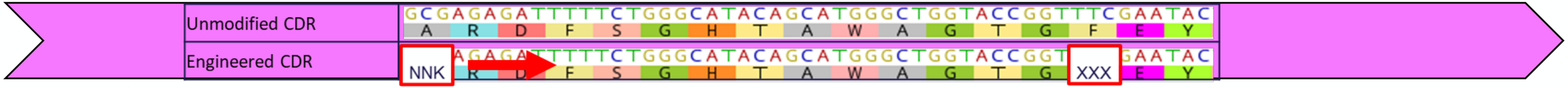
- Invivyd *De Novo* B Cell discovery begins with human donor PBMC's, often convalesced from or vaccinated to the target pathogen
- Biospecimen are prepared and enriched for antibody producing B cells with binding activity to the viral antigens
- Antibody sequences are isolated from the enriched B cells and cloned into yeast cells
- IgG antibodies are produced and purified from yeast cells for characterization and antibody engineering



- B cells with confirmed binding activity were selected for pseudovirus neutralization assay (PVNA) screening
- 21 novel neutralizing antibodies identified
- Antibodies exhibit a range of activity and sequence diversity presenting a variety of antibody engineering starting points
- 7 best neutralizing antibodies selected for mammalian antibody expression
- B Cell-derived antibody IC_{50} Values range from 1.2-735.8 ng/mL

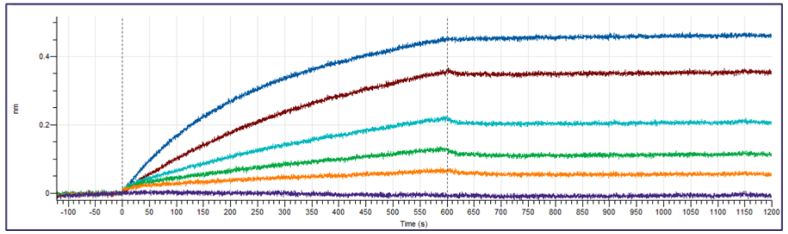
INVIVYD

HIT TO LEAD LIBRARY OF RANDOM AND SITE-DIRECTED MUTATIONS

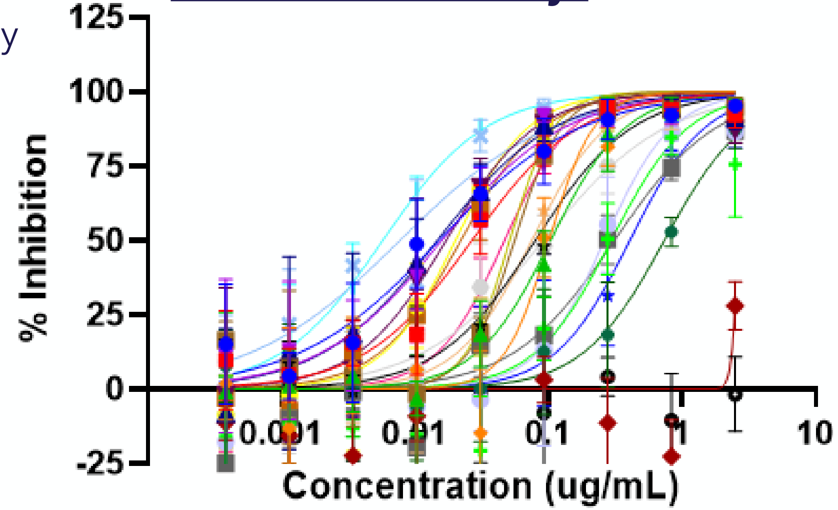


- Top hits from high throughput yeast progress to mammalian expression for screening in a suite of functional and biophysical assays:
  - **Pseudoviral neutralization assays**
    - Evaluating CD46 and CD150 pseudoviral entry
  - **Authentic virus neutralization assays**
  - **HIC and B$_{22}$**: For assessment of self-association
  - **Thermal stability (T$_M$)**: For assessment of stability
    - Also measures aggregation temperature (T$_{agg}$)
  - **Dynamic Light Scattering (DLS)**: For the assessment of aggregation and polydispersity
  - **Binding kinetics**: To ascertain K_D (affinity), k_d ("off-rate'), and k_a ("on-rate")

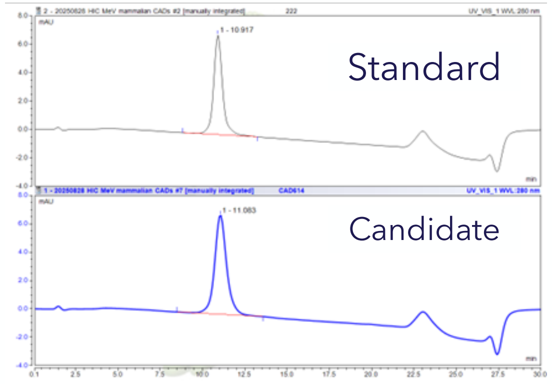
Binding Kinetics



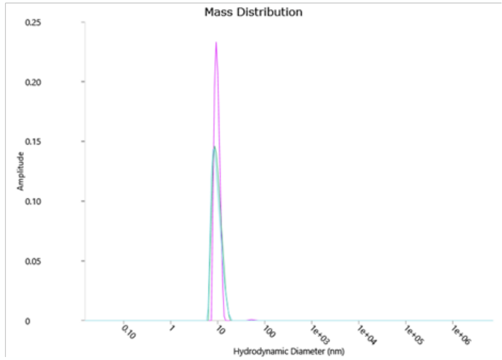
Neutralization Assays



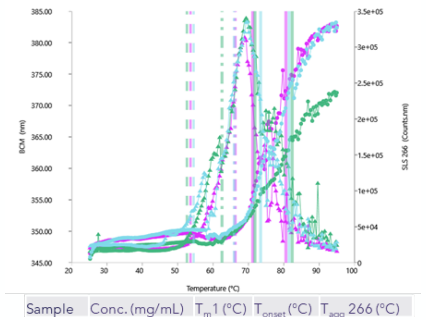
HIC:



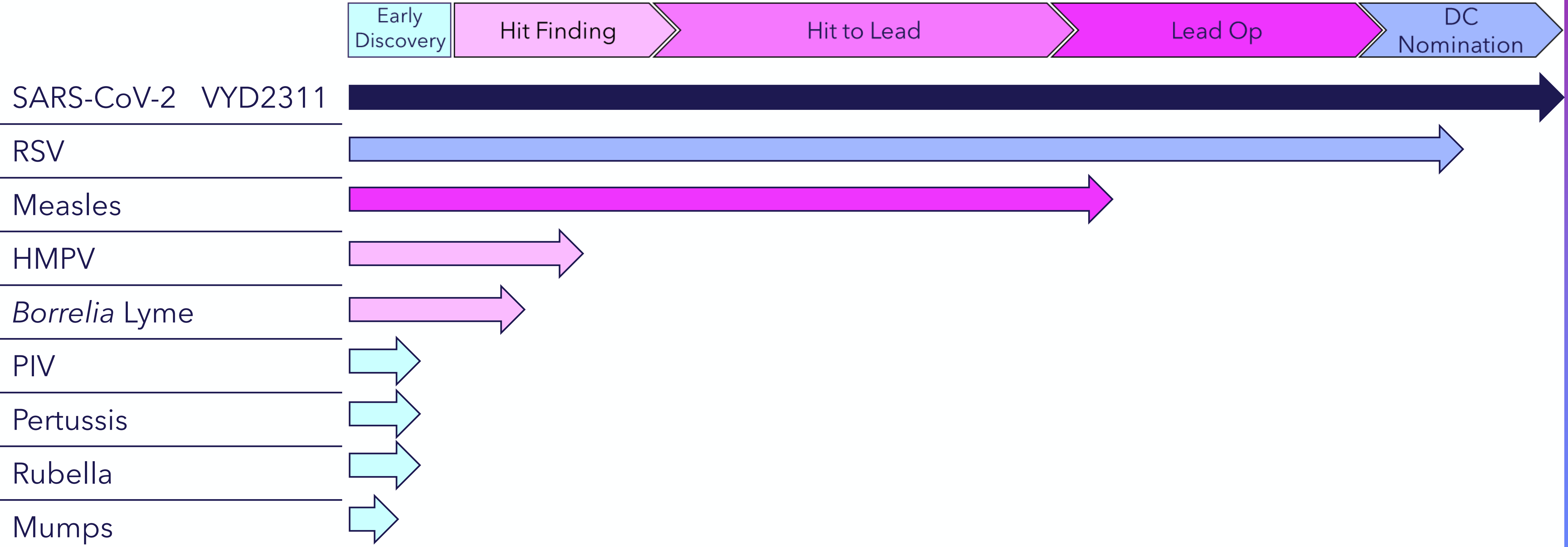
DLS:



T$_m$:



INVIVYD ANTIBODY DEVELOPMENT PROGRAMS



Early Discovery
Hit Finding
Hit to Lead
Lead Op
DC Nomination

SARS-CoV-2 VYD2311
RSV
Measles
HMPV
Borrelia Lyme
PIV
Pertussis
Rubella
Mumps

ACKNOWLEDGEMENTS

- Tyler Starr Lab at University of Utah

- Ian Wilson Lab at Scripps Research
- Kristian Andersen Lab at Scripps Research

Scripps

- Invivyd Variant Monitoring
- Invivyd Antibody Discovery
- Invivyd Virology