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Updates on Epidemiology of COVID-19 and SARS-CoV-2 Genomics

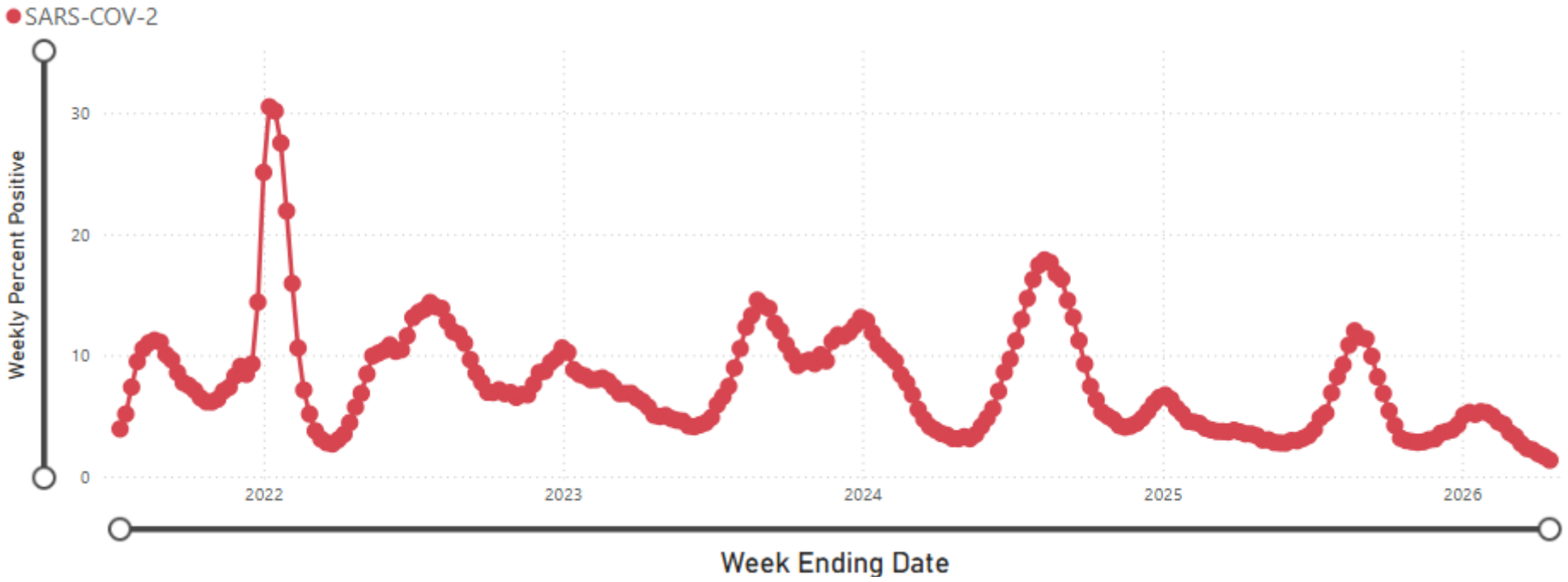
Natalie J. Thornburg, PhD

Centers for Disease Control and Prevention

May 28, 2026

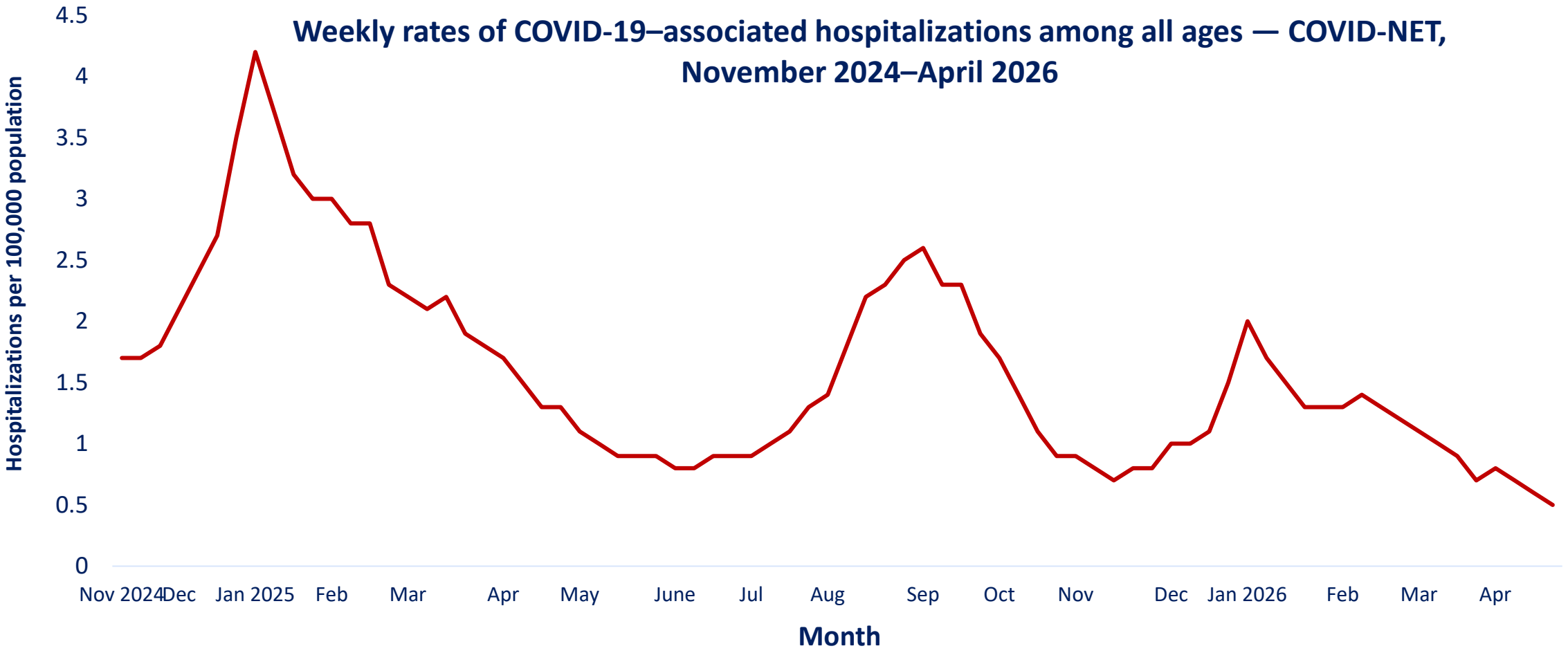
Epidemiologic update

National SARS-CoV-2 weekly % positivity: 2021-2026



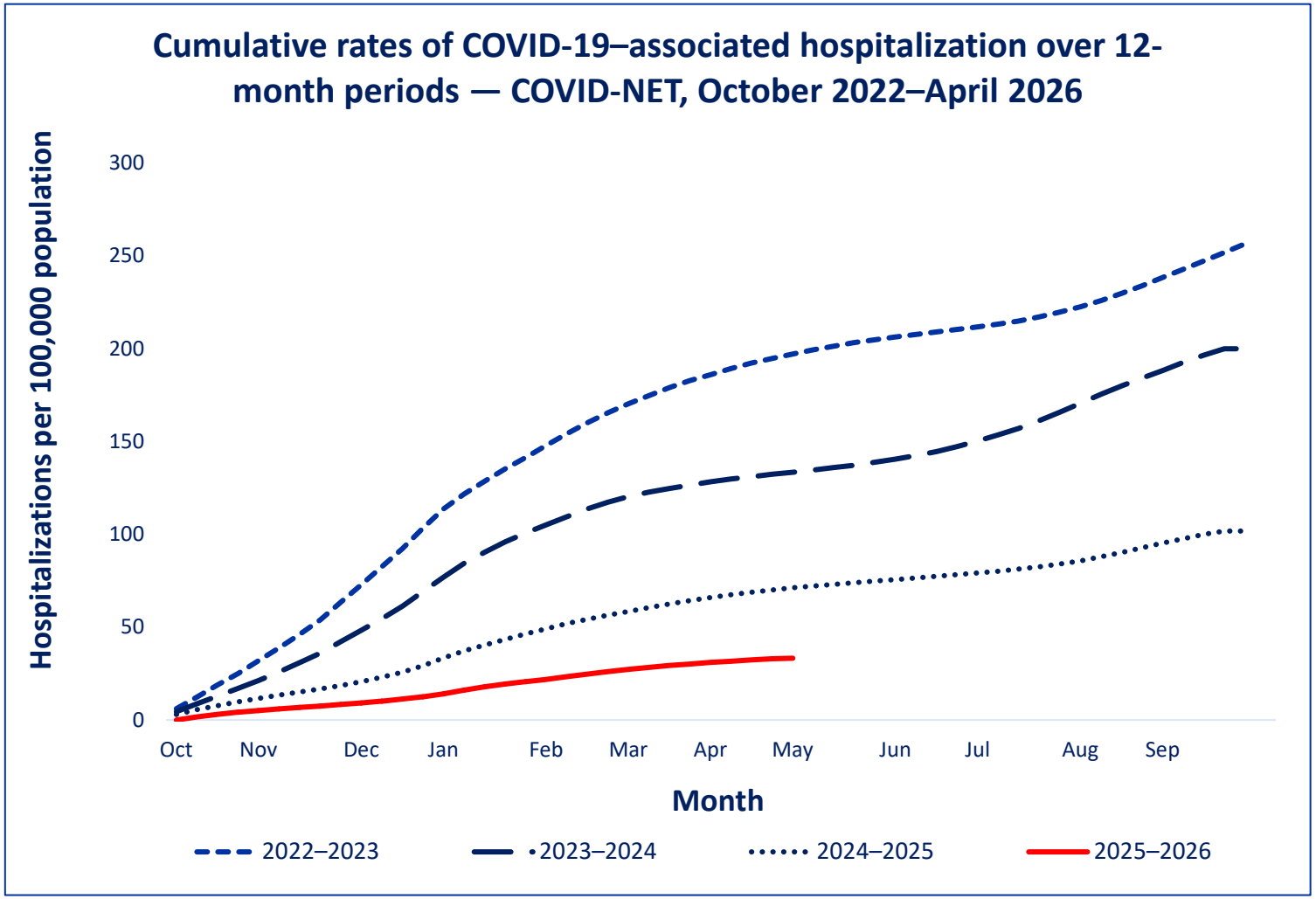
Source: Interactive Dashboard | The National Respiratory and Enteric Virus Surveillance system (NREVSS) | CDC As of April 30, 2026

Overall weekly rates of COVID-19–associated hospitalizations continue to peak in both winter and summer periods.



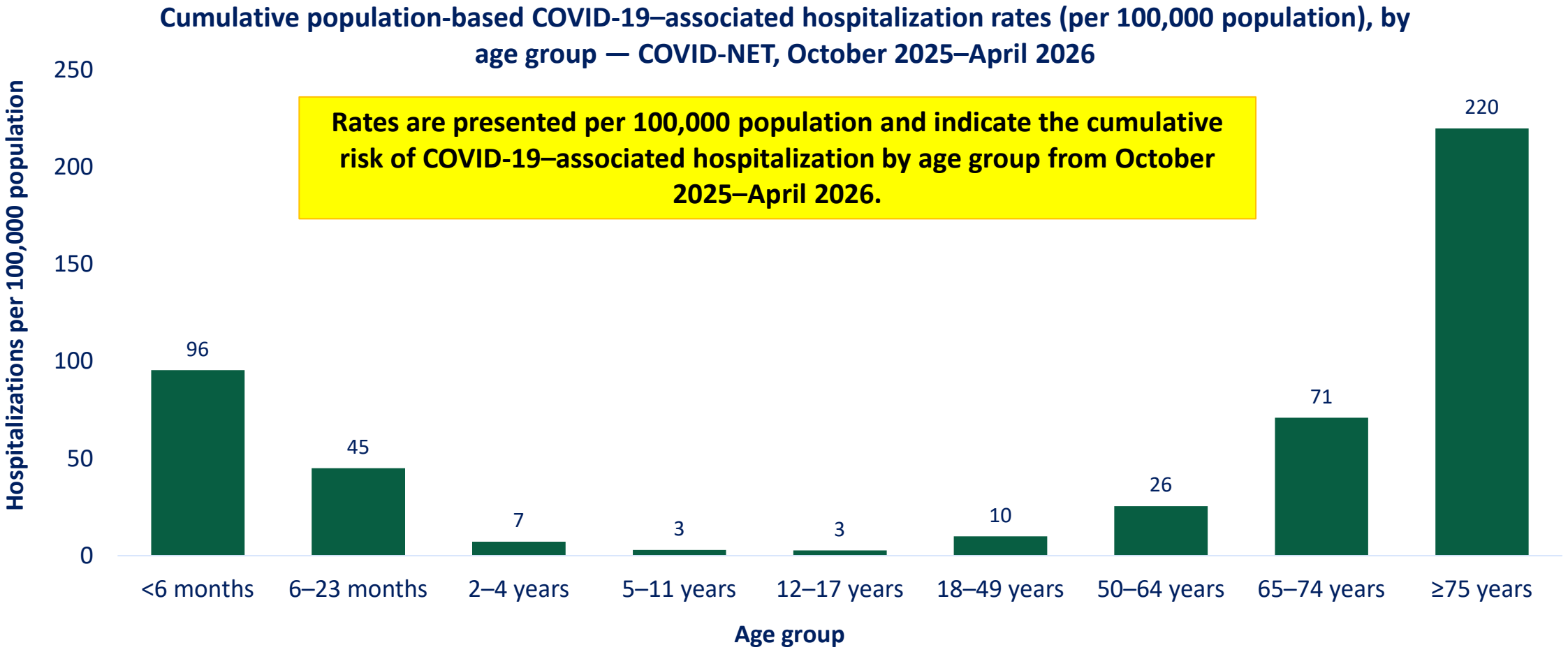
COVID-NET: COVID-19-Associated Hospitalization Surveillance Network.

Cumulative rates of COVID-19 associated hospitalization during 2025–2026 are lower than prior seasons.



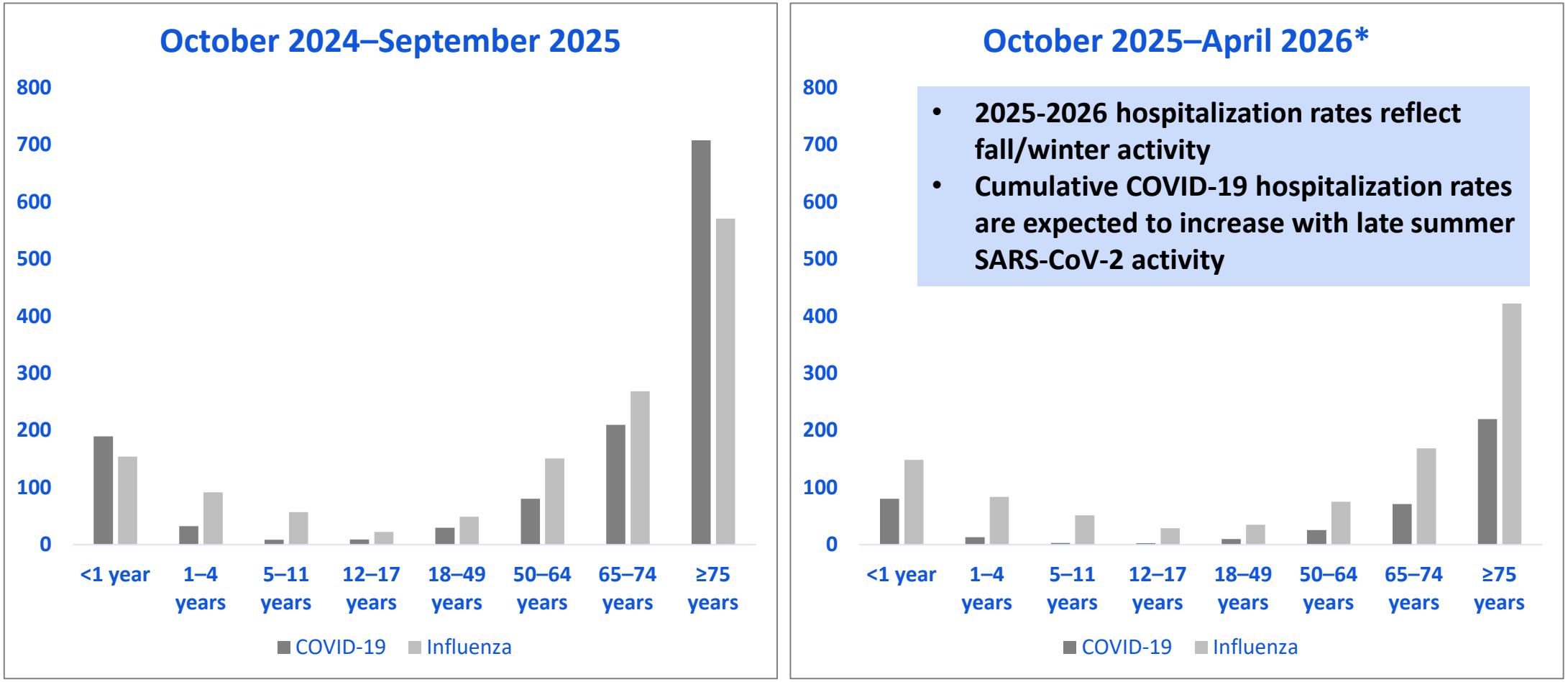
COVID-NET: COVID-19-Associated Hospitalization Surveillance Network

Rates of COVID-19–associated hospitalization remain highest among the youngest and oldest age groups.



COVID-NET: COVID-19-Associated Hospitalization Surveillance Network.
Cumulative rates are the sum of total hospitalizations over the surveillance period (October–April) divided by the total population of the catchment area.

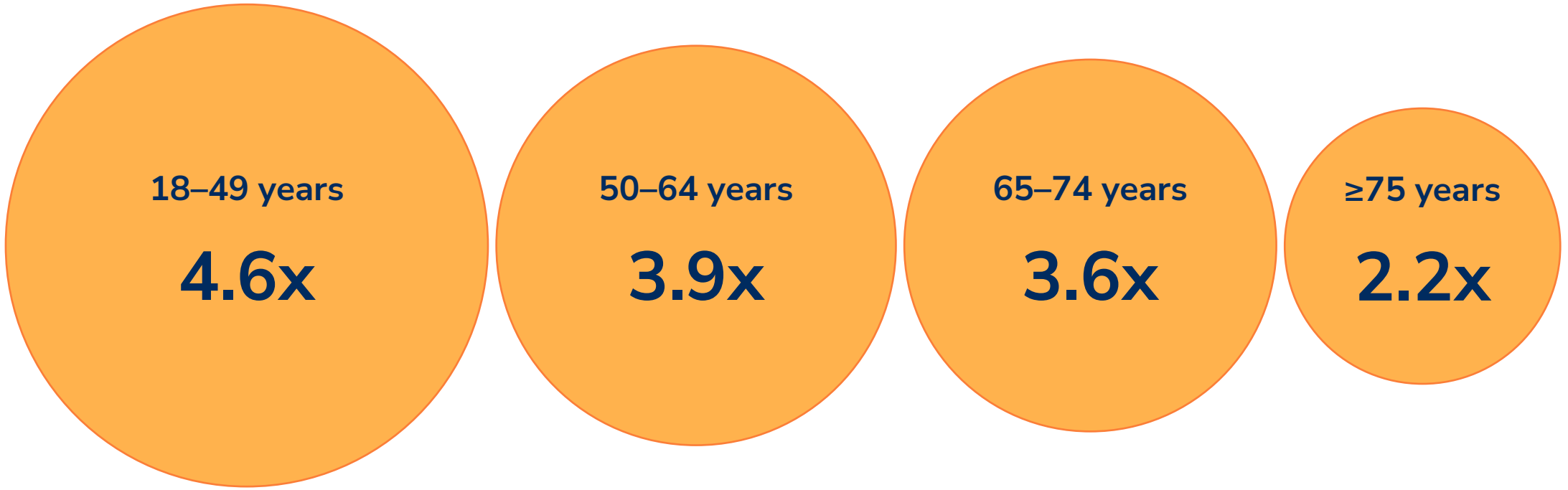
Cumulative rates of COVID-19 hospitalization were in line with those for influenza among infants aged <1 year and adults 65-74 years and ≥75 years during the 2024–2025 surveillance period



* Data for the 2025–2026 surveillance period are presented through April; reporting will continue through September 2026. During the 2024–2025 surveillance period, hospitalizations occurring during May–September accounted for 30% of all 2024–2025 hospitalizations.

Adults with ≥1 underlying medical conditions* are at increased risk for COVID-19 hospitalization compared to those no conditions, regardless of age group.

Risk† for hospitalization among adults with underlying medical conditions who get COVID-19 compared to adults with no condition(s), by age group



Data from Hamid, et al: https://doi.org/10.1016/j.amepre.2025.108227.

* Limited to the underlying conditions examined in the analysis among community-dwelling adults, 2022–2023 (asthma, chronic obstructive pulmonary disease [COPD], coronary artery disease, chronic kidney disease, diabetes mellitus, history of stroke, nonsevere obesity [BMI=30–39 kg/m²], severe obesity (BMI≥40 kg/m²), and current smoking).

† Rate ratios adjusted for sex and race and ethnicity.

More than 40% of children and adolescents and 76% of infants hospitalized due to COVID-19 had no underlying medical conditions

- **Among children and adolescents ages 6 months–17 years hospitalized due to COVID-19, 41% had no underlying medical conditions.[*]**
  - Some conditions increased the risk for severe in-hospital outcomes[‡] due to COVID-19: chronic lung disease, cardiovascular disease, diabetes, and neurologic disorders, including cerebral palsy
- **Among infants ages <6 months hospitalized due to COVID-19, 76% had no underlying medical conditions.[†]**

[*] Hospitalization for COVID-19 and Risk Factors for Severe Disease Among Children: 2022–2024: https://doi.org/10.1542/peds.2025-072788.

[†] COVID-19–Associated Hospitalizations and Maternal Vaccination Among Infants Aged <6 Months — COVID-NET, 12 States, October 2022–April 2024: http://dx.doi.org/10.15585/mmwr.mm7338a1.

[‡] Defined as intensive care unit admission, mechanical ventilation, extracorporeal membrane oxygenation, or in-hospital death.

Among adults, age is the strongest risk factor for COVID-19 hospitalization; chronic conditions increase risk.

- **In a recently published study of adults,[*] age was the strongest risk factor for being hospitalized due to COVID-19.**
- **Most chronic health conditions were associated with increased risk of being hospitalized.**
  - Chronic kidney disease, diabetes, history of stroke, severe obesity,[†] coronary artery disease, chronic obstructive pulmonary disease (COPD), current or former smoker, and asthma

Age group	Hospitalization rate per 100,000 population (with 95% uncertainty interval), adults with no conditions[‡]	Hospitalization rate per 100,000 population (with 95% uncertainty interval), adults with ≥1 condition[‡]
≥75 years	**583 (414–825)**	1,299 (1,053–1,626)
65–74 years	144 (102–207)	**531 (443–646)**
50–64 years	55 (36–85)	226 (177–291)
18–49 years	18 (13–27)	88 (66–117)

[*] Chronic Conditions as Risk Factors for COVID-19–Associated Hospitalization Among Adults, 2020–2023. https://doi.org/10.1016/j.amepre.2025.108227.

[†] Severe obesity is defined as body mass index (BMI) ≥40 kg/m²

[‡] Refers to the conditions examined in the analysis.

Summary: COVID-19–associated hospitalizations

- **Overall and age group-specific weekly rates of COVID-19–associated hospitalizations continue to peak in both summer and winter.**

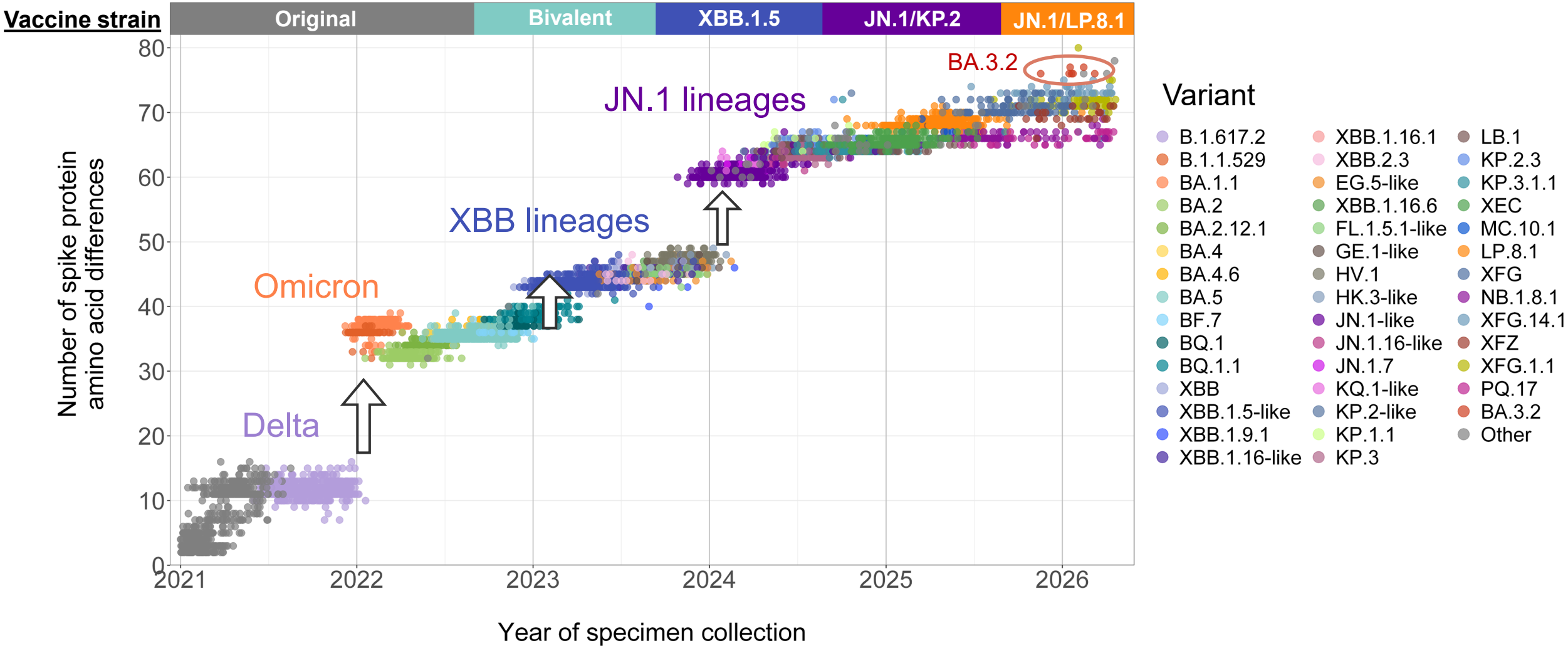
- **Rates of COVID-19–associated hospitalization remain highest among the youngest (<6 months) and oldest (≥65 years) age groups.**
  - COVID-19–associated hospitalizations in these age groups are in line with influenza-associated hospitalization rates.

- **Among adults, older age is the strongest risk factor for COVID-19 hospitalization.**
  - Chronic conditions increase risk for COVID-19 hospitalization.

Genomics update

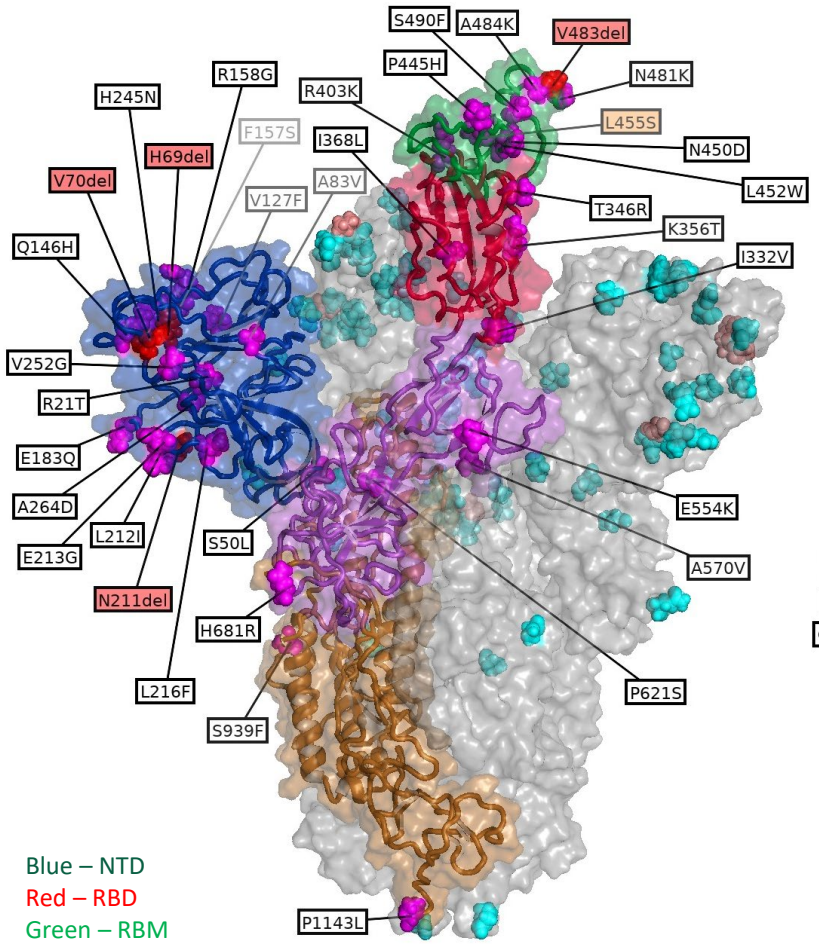
Subsampled SARS-CoV-2 sequences by lineage, date of specimen collection, and number of spike protein amino acid differences relative to Wuhan-Hu-1 reference

United States, January 1, 2021–April 21, 2026

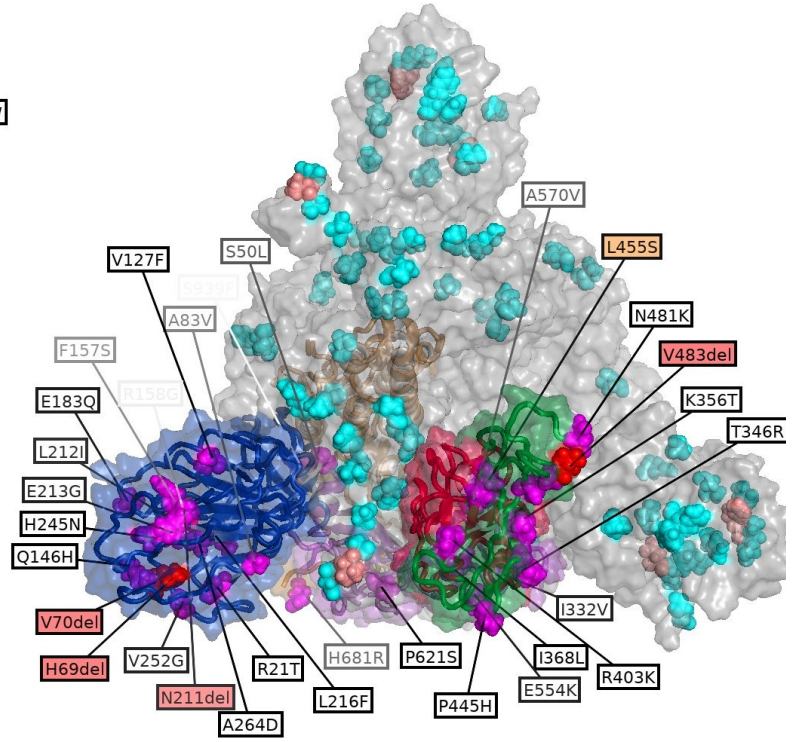


Sequences were subsampled (~100 per month) for analysis from an initial dataset of >1 million sequences spanning January 1, 2021–April 21, 2026. Only lineages circulating at >5% prevalence nationally during at least one 4-week period are displayed. Sequences are reported to CDC through the National SARS-CoV-2 Strain Surveillance program, contract laboratories, public health laboratories, and other U.S. institutions. Lineages were ordered by date of first appearance on CDC's SARS-CoV-2 variant proportions dashboard (https://www.cdc.gov/covid/php/variants/variants-and-genomic-surveillance.html). Lineages with identical spike receptor binding domain amino acid sequences (residues 332 to 527) were grouped with a representative lineage and denoted as "representative lineage-like." Vaccine availability for a given composition was defined by the estimated date of earliest possible administration.

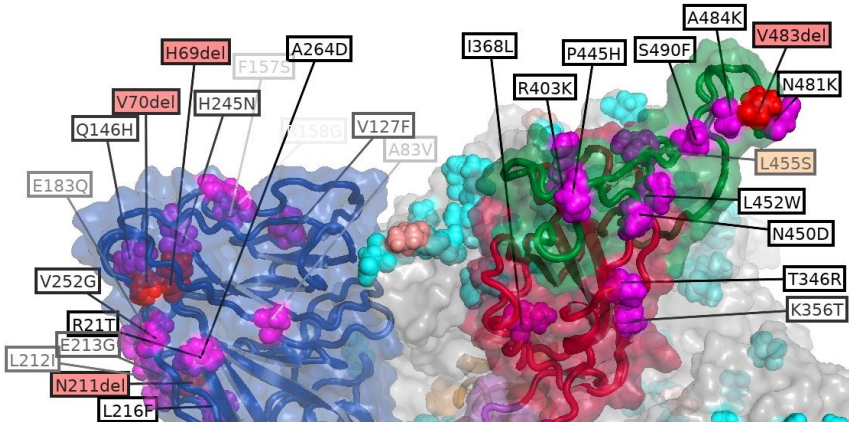
In summer 2024, the composition of COVID-19 vaccines updated from XBB.1.5 to KP.2/JN.1 spike



Blue – NTD
Red – RBD
Green – RBM
Purple – S1
Gold – FCS
Brown – S2

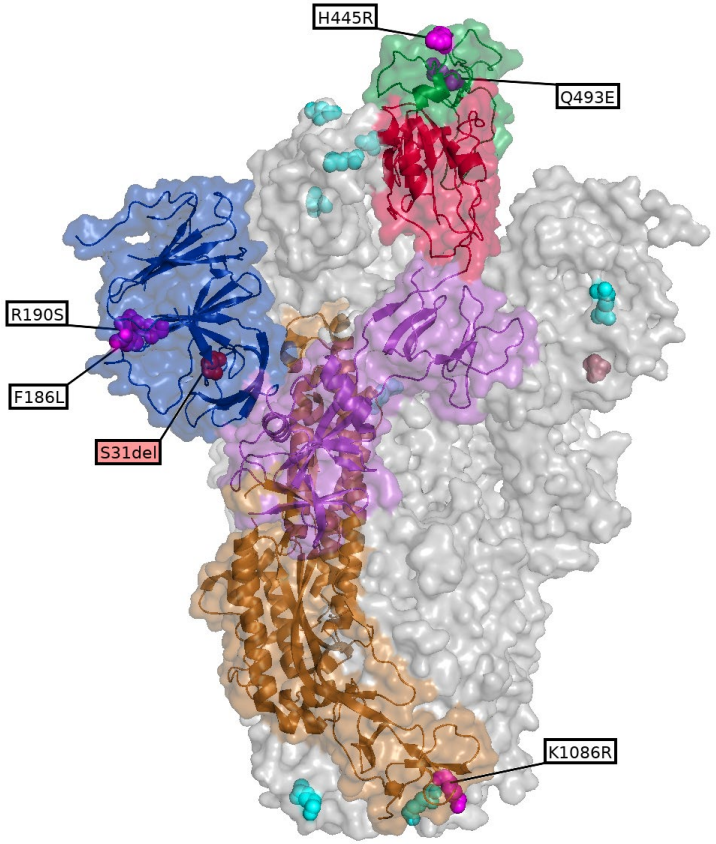


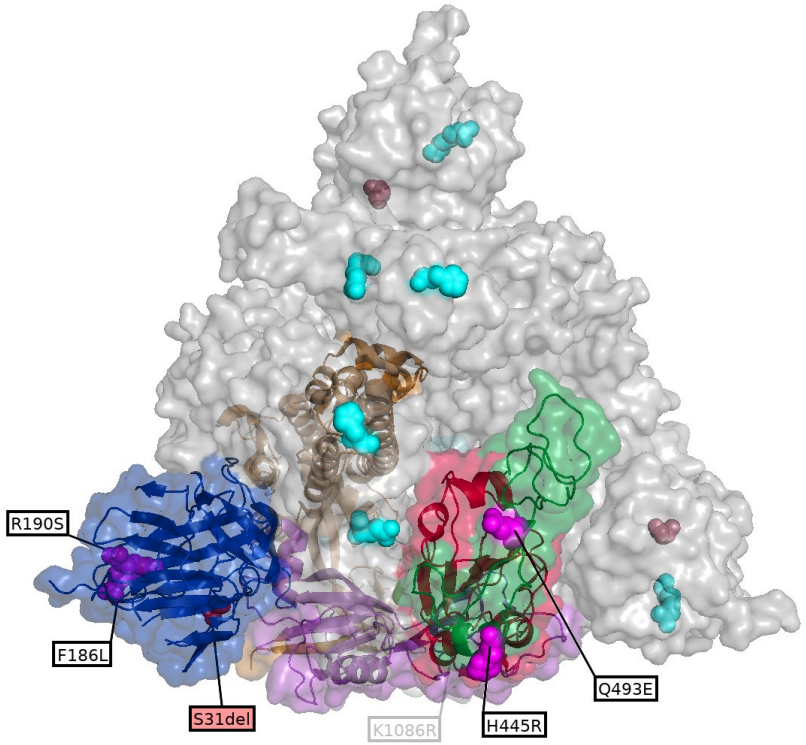
Red sphere – deletions in one chain (labeled)
Magenta sphere – substitutions in one chain (labeled)
Raspberry sphere – deletions in rest 2 chains
Cyan sphere – substitutions in rest 2 chains

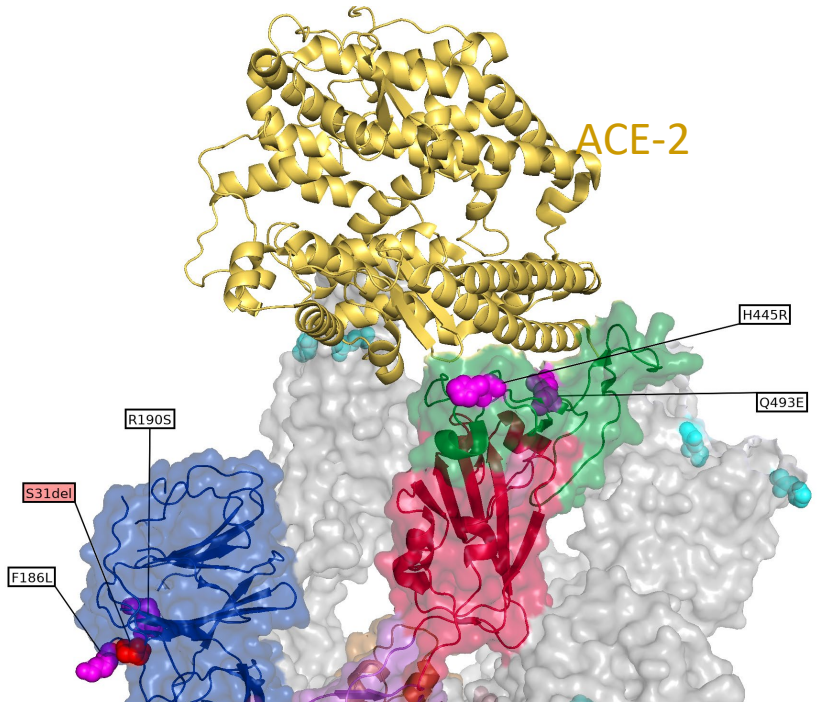


Schrodinger homology model of JN.1, starting with 7YR2 (BA.2.75)

In summer 2025, the composition of COVID-19 vaccines updated from KP.2/JN.1 to LP.8.1/JN.1 spike







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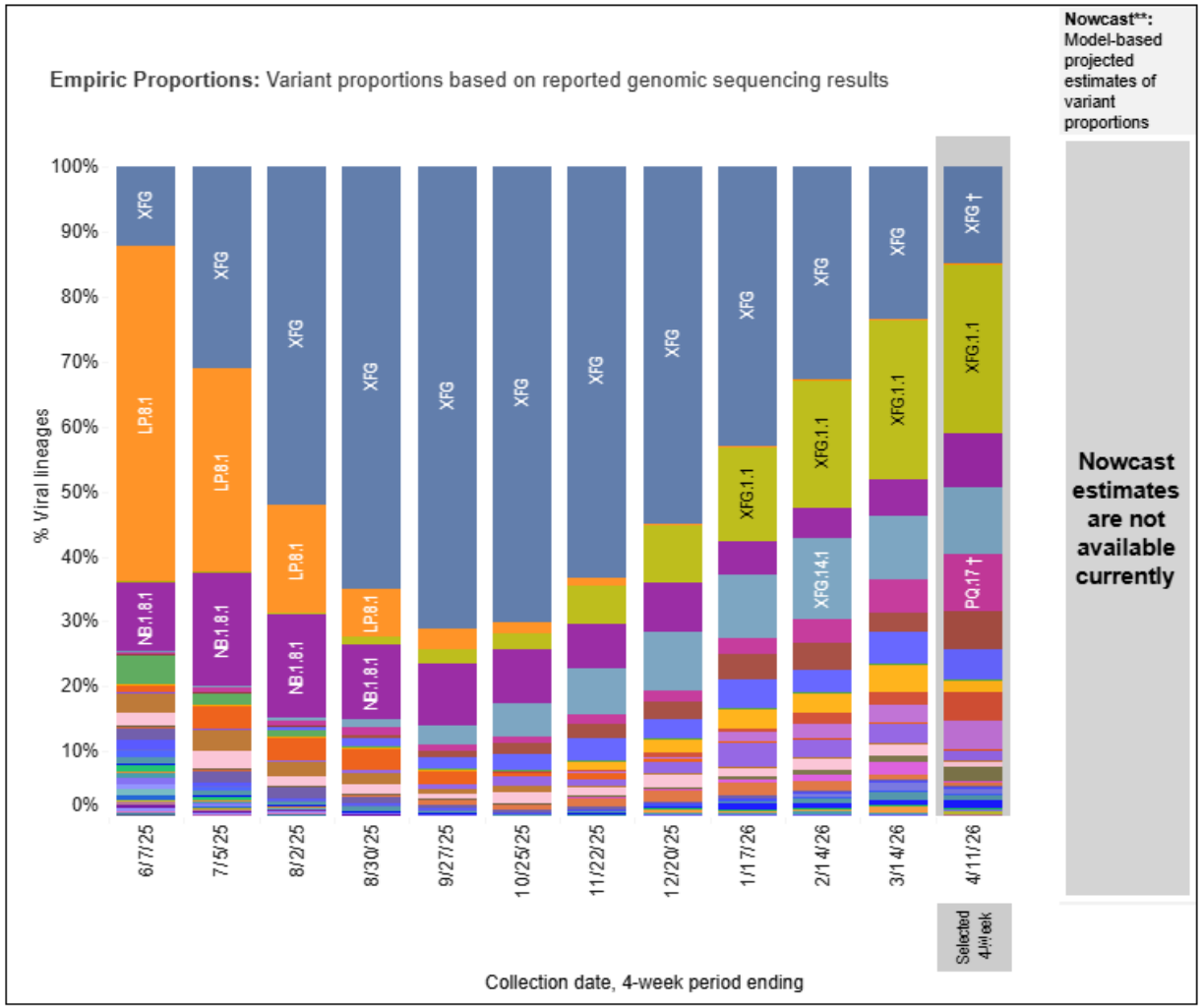
Structure of JN.1 (PDB ID: 8Y5J)

Red sphere – deletions in one chain (labeled)
Magenta sphere – substitutions in one chain (labeled)
Raspberry sphere – deletions in rest 2 chains
Cyan sphere – substitutions in rest 2 chains

Structure of JN.1 in complex with ACE-2 (PDB ID: 8YZE)

Most viruses circulating above 1% prevalence are JN.1 lineages



USA

Lineage#		Share	95%PI/CI
XFG.1.1		26%	22–31%
XFG	†	15%	11–19%
XFG.14.1	†	10%	7–14%
PQ.17	†	9%	6–13%
NB.1.8.1	†	8%	6–12%
XFZ	†	6%	4–9%
XFG.6	†	5%	3–8%
BA.3.2	†	4%	3–7%
PQ.2.8.1	†	4%	3–7%
XFG.10.4	†	2%	1–5%
XFG.2.5.1	†	2%	1–4%
XFY	†	2%	1–4%
LF.7	†	1%	0–3%
XFG.23.1.3	†	1%	0–3%
Other	†	1%	0–3%
RV.1	†	1%	0–3%
MC.1	†	1%	0–2%
XFV	†	1%	0–2%

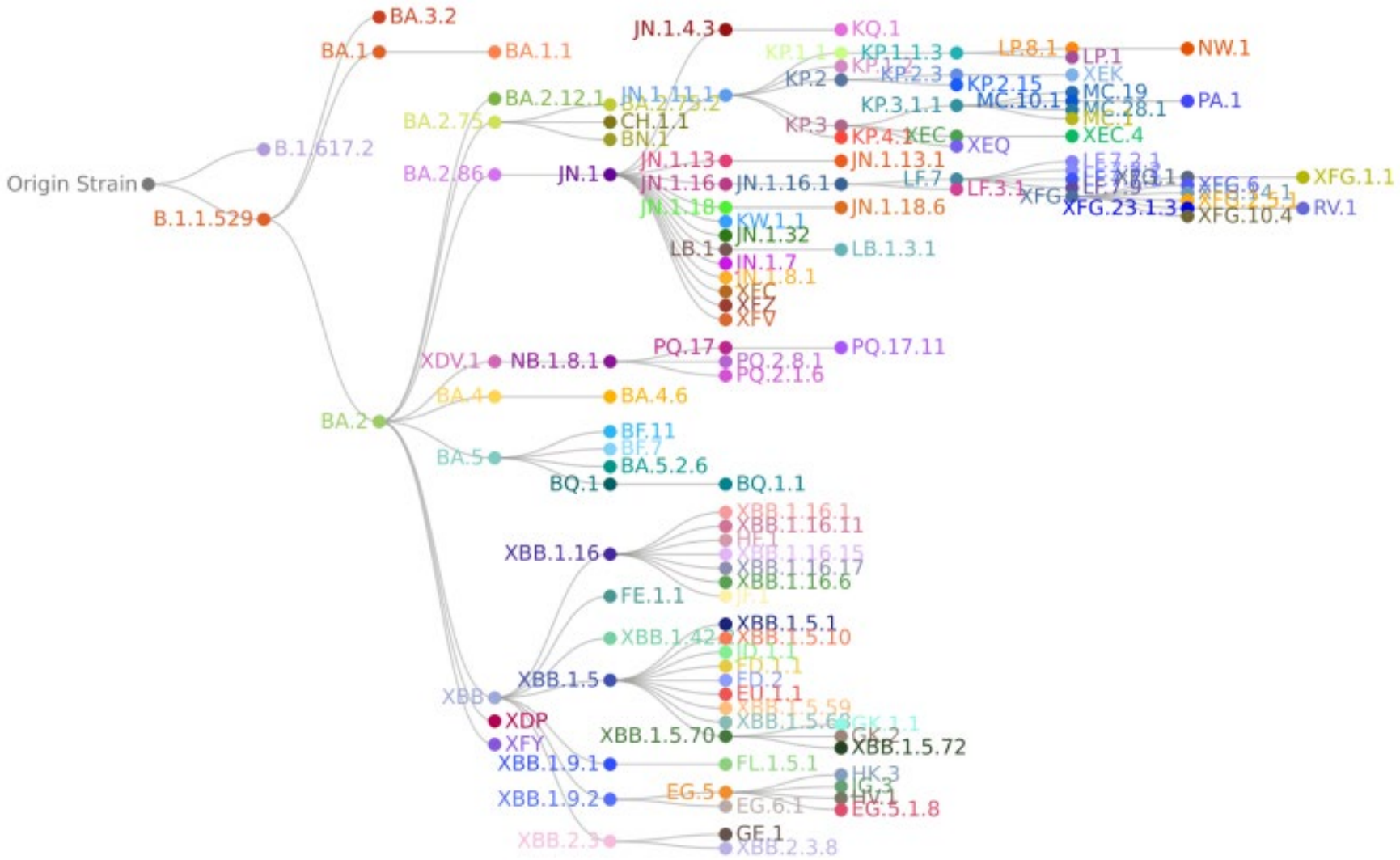
** These data include Nowcast estimates, which are modeled projections that may differ from empiric data generated at later dates
† Estimates are less reliable based on one or more violations of NCHS data presentation standards for proportions: https://www.cdc.gov/nchs/data/series/sr_02/sr02_175.pdf
# 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 v4.4, pangolin-data v1.38 and usher v0.6.3. Download Data

Updated May 8, 2026

https://www.cdc.gov/covid/php/variants/variants-and-genomic-surveillance.html

Most viruses circulating above 1% prevalence are JN.1 lineages



https://www.cdc.gov/covid/php/variants/variants-and-genomic-surveillance.html

Key changes in circulating SARS-CoV-2 spike proteins* relative to LP.8.1†

	N-terminal domain								*Receptor-binding domain*													*FCS*		*S2*		
	22	**31**	**59**	**96**	**182**	**184**	**186**	**190**	**346**	**435**	**441**	**444**	**445**	**452**	**478**	**487**	**493**	**529**	**572**	**604**	**677**	**679**	**1086**	**1104**	**1264**
LP.8.1 Reference†	T	-	F	E	K	G	L	S	T	A	L	K	R	W	K	N	E	K	T	T	Q	K	R	L	V
LF.7	N	P			R		F					R	H				Q						K	V	
NB.1.8.1	N	S	S			S	F	R	R	S			H		I								K	V	
PQ.2.8.1	N	S	S			S	F	R	R	S			P		I								K	V	
PQ.17	N	S	S			S	F	R	R	S			H		T								K	V	
XFG	N	P			R		F					R				D			I				K	V	
XFG.1.1	N	P		D	R		F					R	P	R		D			I				K	V	
XFG.6	N	P			R		F				I	R				D			I				K	V	
XFG.14.1	N	P			R		F					R				D		T	I	I			K	V	L
XFY	N	P			R		F					R				D			I		H		K	V	
XFZ	N	P			R		F								E							R	K		L

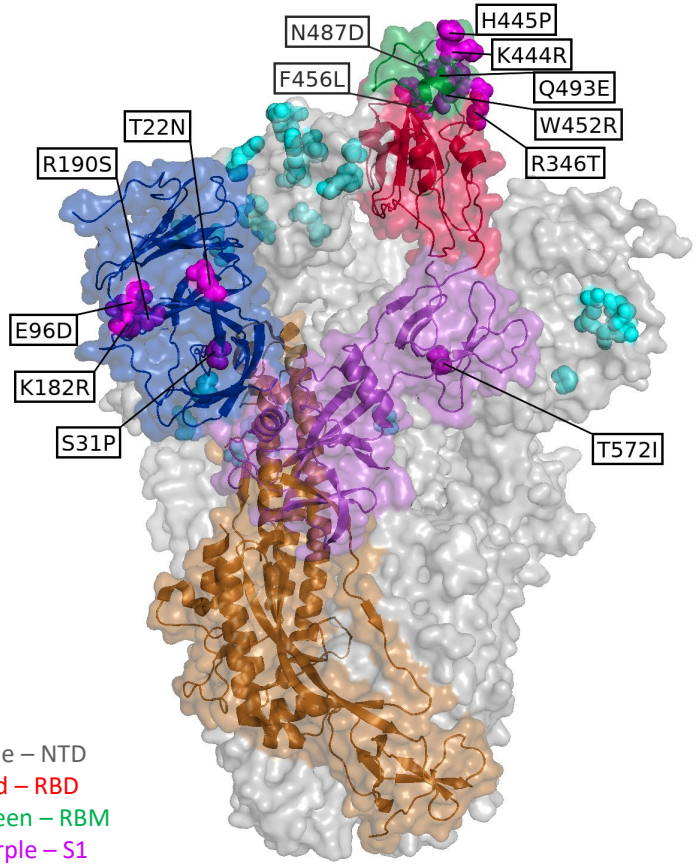
FCS = furin cleavage site.

***** Lineages or lineage groups with ≥1% prevalence in at least one recent 4-week period and substitutions present in ≥50% of sequences belonging to a lineage were included.

† The LP.8.1 spike protein sequence was used as a reference because of its inclusion in updated mRNA-based 2025–2026 COVID-19 vaccines.

Bold indicates increasing or stable in proportion in recent 4-week periods.

XFG.1.1, the current most prevalent lineage, has 13 spike substitutions in comparison to JN.1



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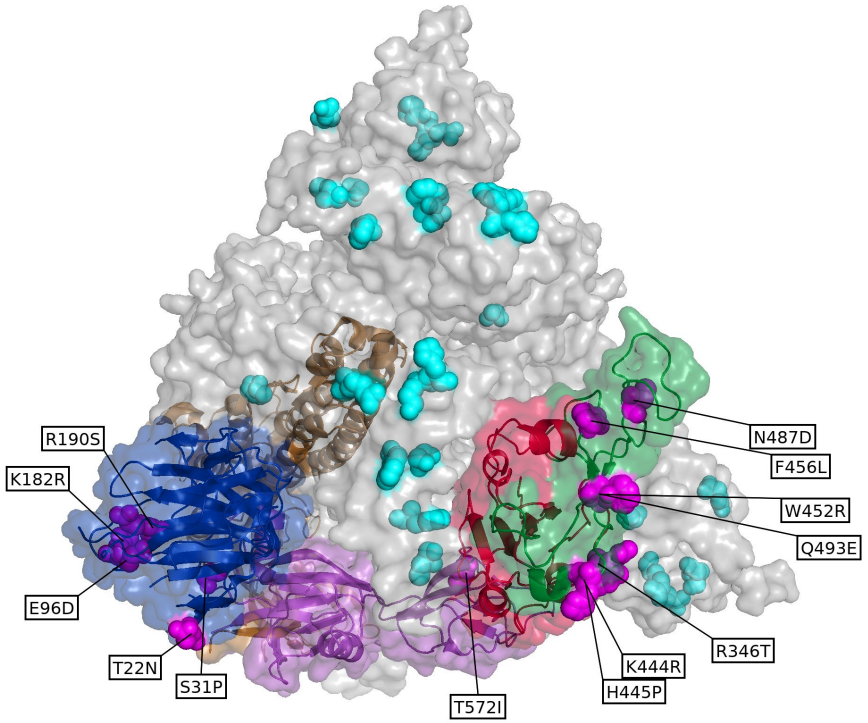
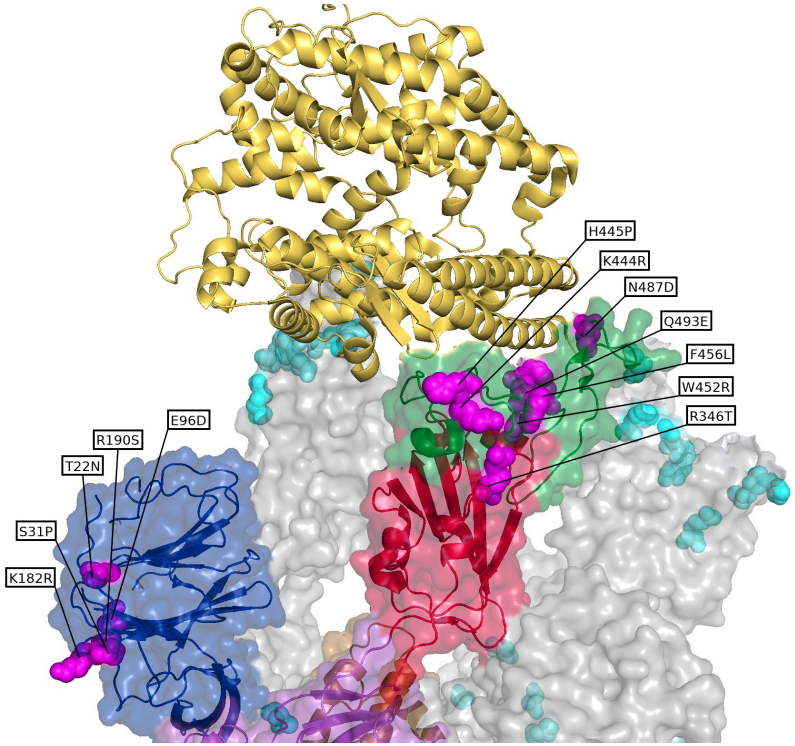
Magenta sphere – substitutions in one chain (labeled)
Cyan sphere – substitutions in rest 2 chains



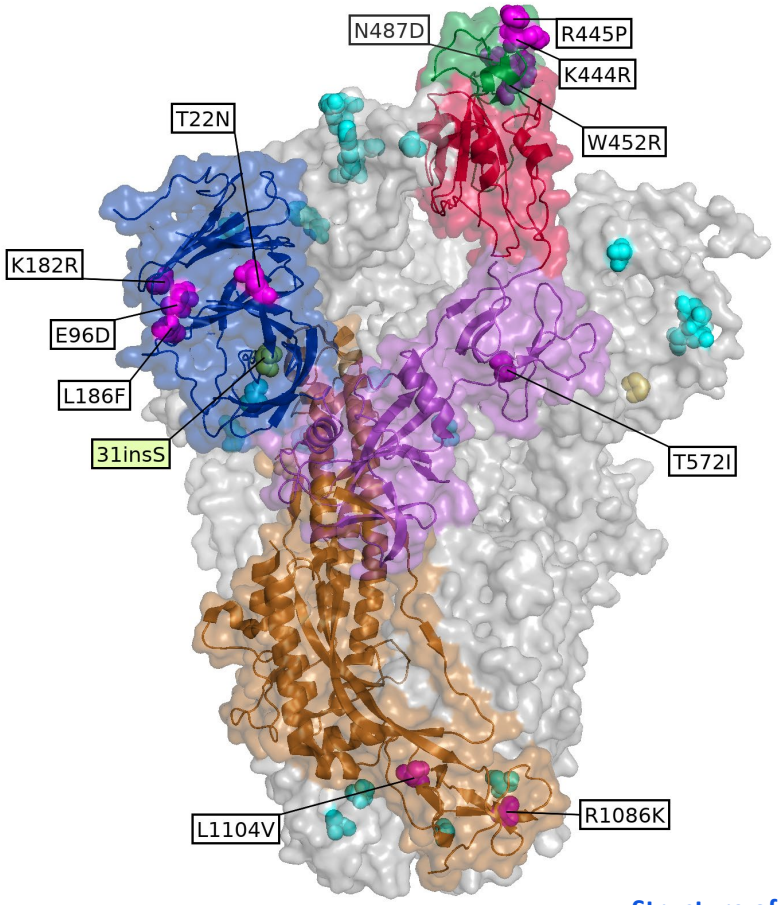
Structure of JN.1 (PDB ID: 8Y5J)

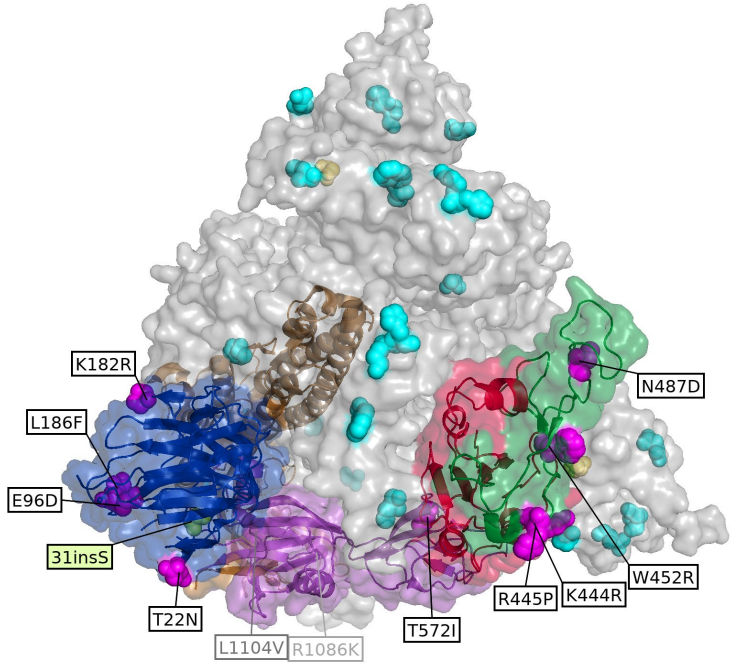


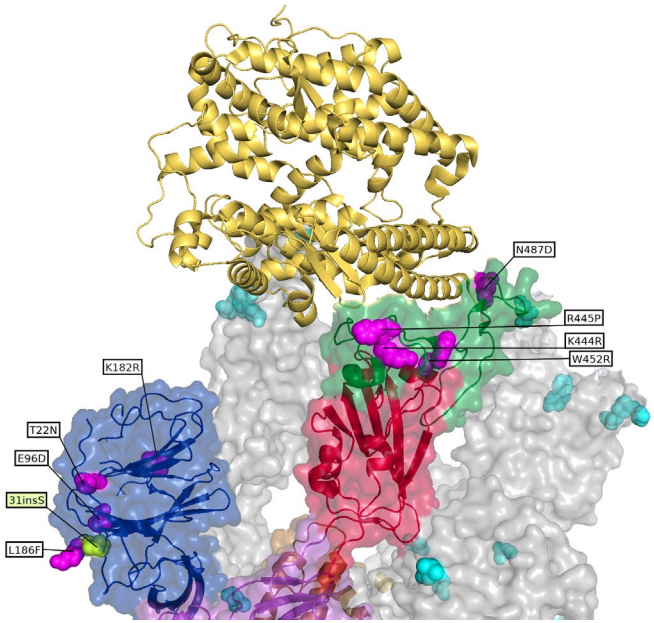
Structure of JN.1 in complex with ACE-2 (PDB ID: 8YZE)

XFG.1.1, the current most prevalent lineage, has 12 spike substitutions in comparison to LP.8.1

Limon sphere – insertions in one chain (labeled)
Magenta sphere – substitutions in one chain (labeled)
Cyan sphere – substitutions in rest 2 chains
Yellow-orange sphere – insertions in rest 2 chains







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Structure of JN.1 (PDB ID: 8Y5J)

Structure of JN.1 in complex with ACE-2 (PDB ID: 8YZE)

NB.1.8.1, a lineage growing in the US, has 12 spike substitutions in comparison to LP.8.1

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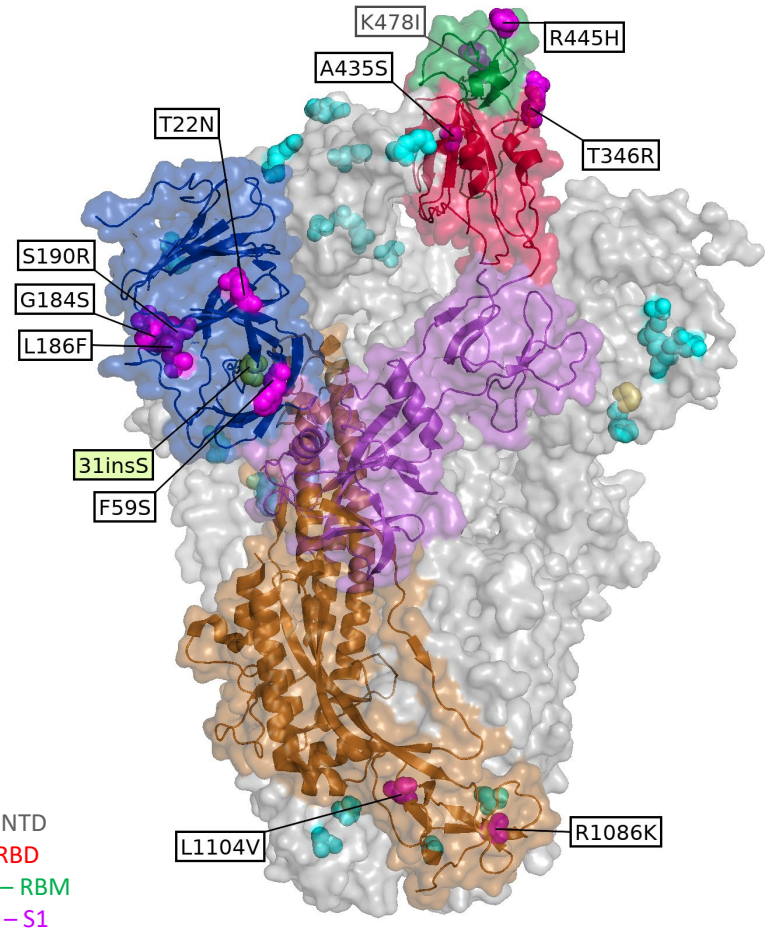

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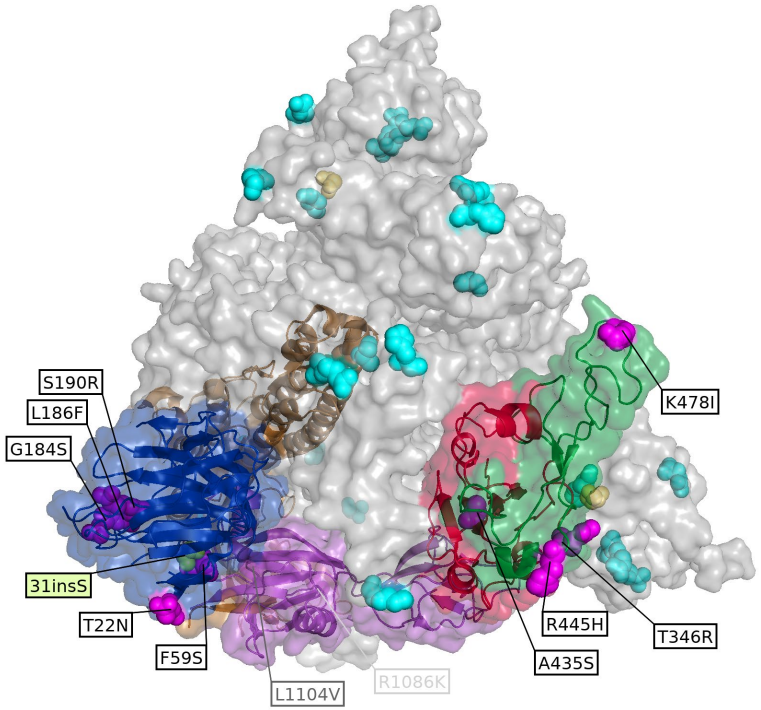
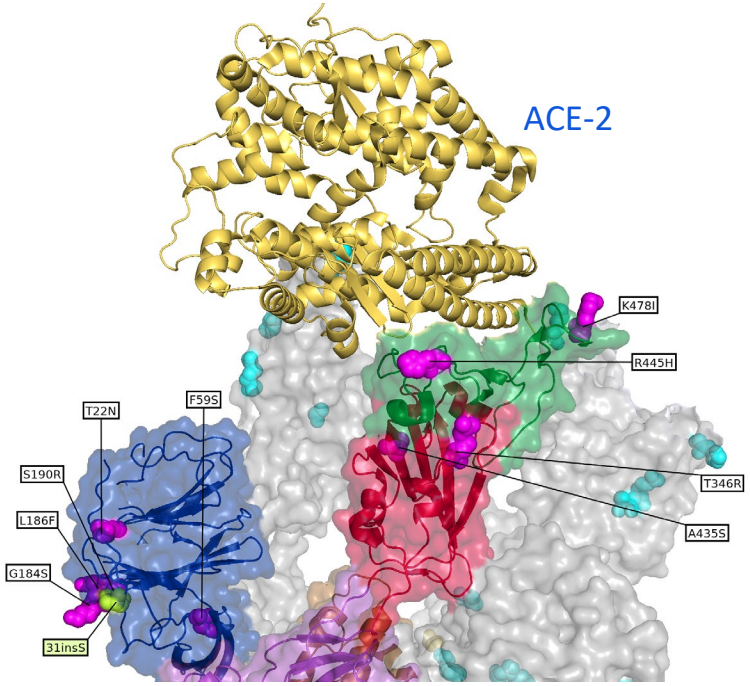
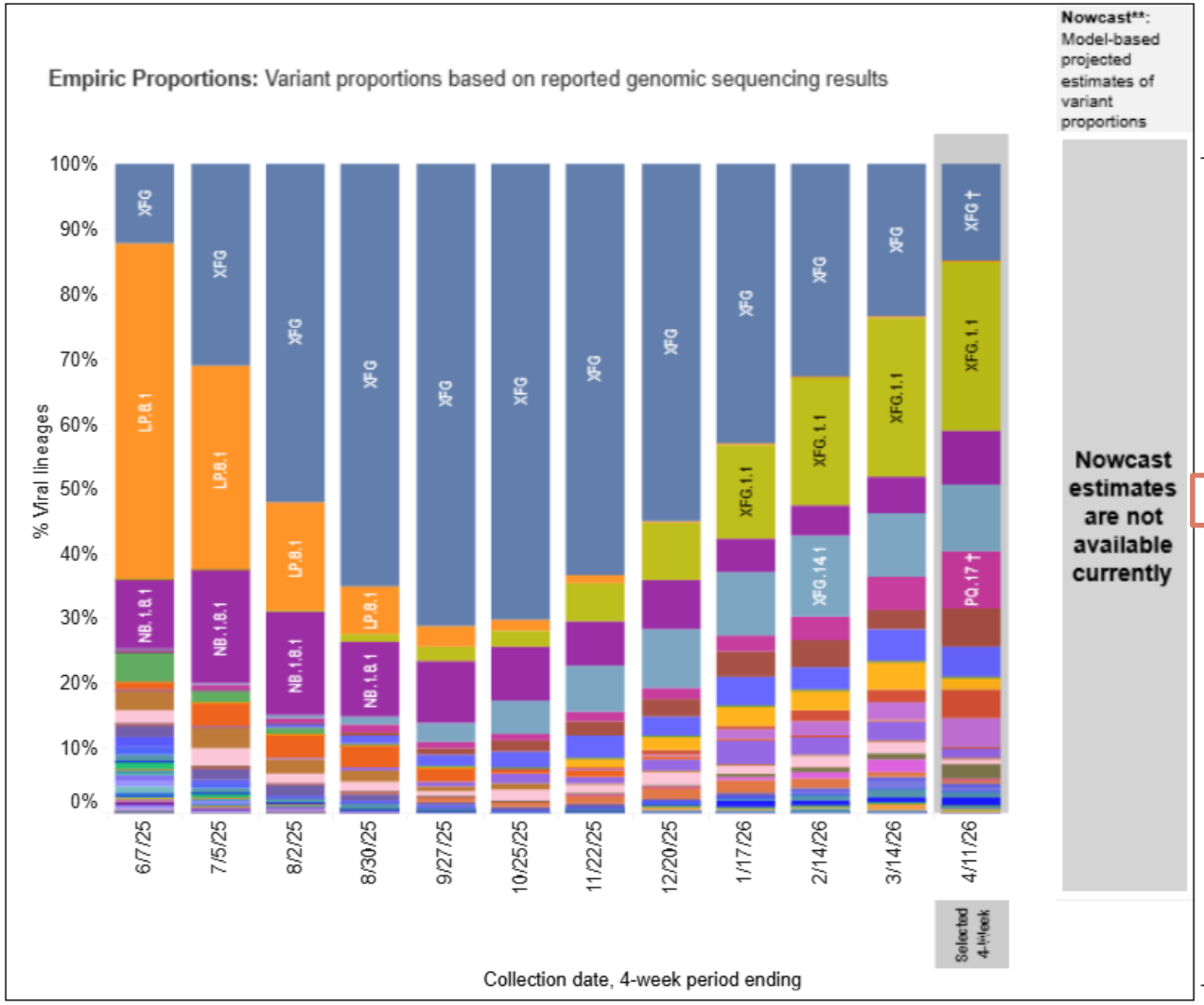
Structure of JN.1 (PDB ID: 8Y5J)





Structure of JN.1 in complex with ACE-2 (PDB ID: 8YZE)

BA.3.2 prevalence in national genomic surveillance



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PQ.2.8.1	†	4%	3–7%
XFG.10.4	†	2%	1–5%
XFG.2.5.1	†	2%	1–4%
XFY	†	2%	1–4%
LF.7	†	1%	0–3%
XFG.23.1.3	†	1%	0–3%
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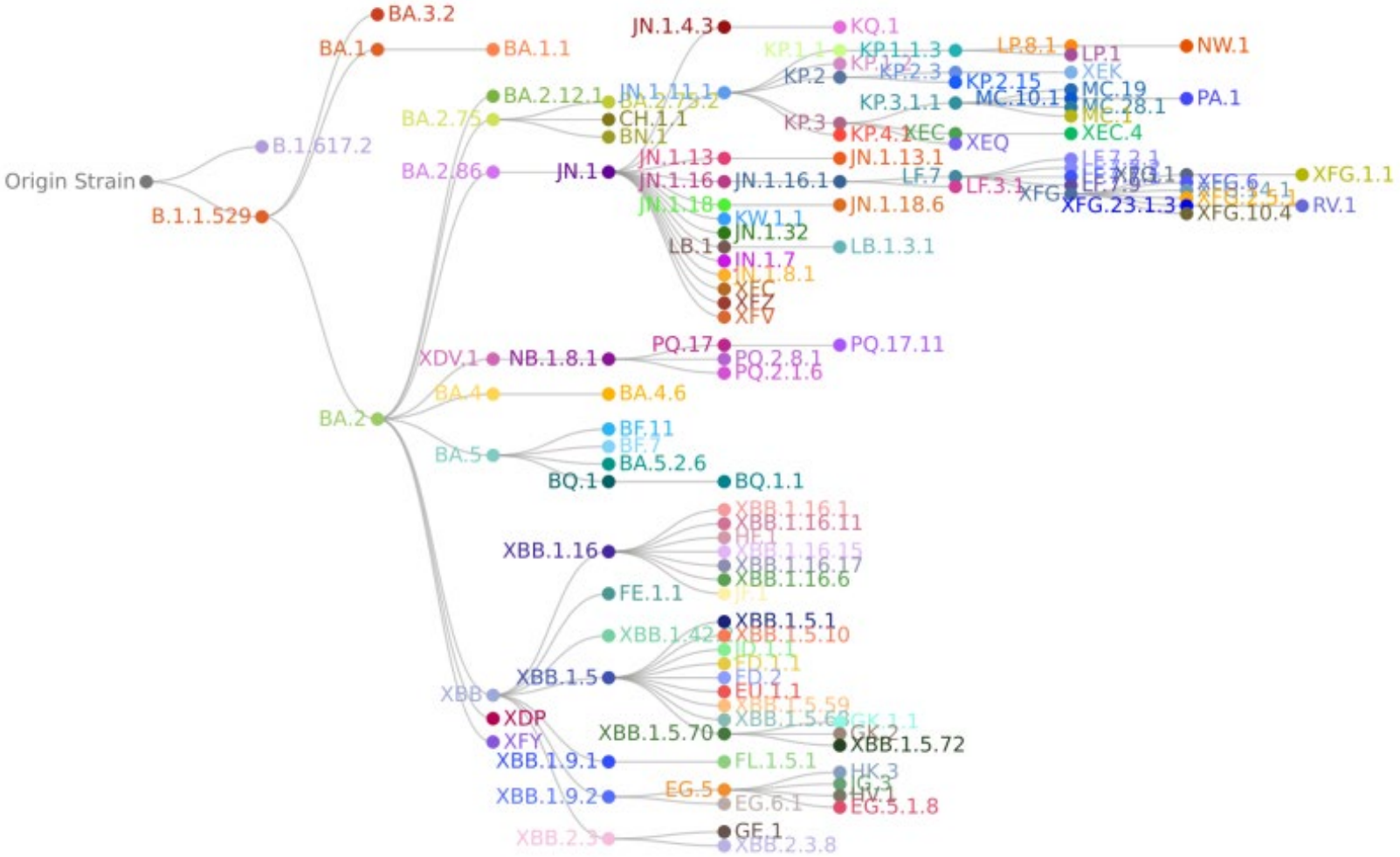
MC.1	†	1%	0–2%
XFV	†	1%	0–2%

https://www.cdc.gov/covid/php/variants/variants-and-genomic-surveillance.html

Most viruses circulating above 1% prevalence are JN.1 lineages, but BA.3.2 is not descended from JN.1



https://www.cdc.gov/covid/php/variants/variants-and-genomic-surveillance.html

Situational report on BA.3.2

- The divergent SARS-CoV-2 variant BA.3.2 was first detected in a respiratory sample collected November 2024 in South Africa
- BA.3.2 contains 58 substitutions, 5 amino acid insertions, and 13 amino acid deletions (76 total differences) compared to LP.8.1

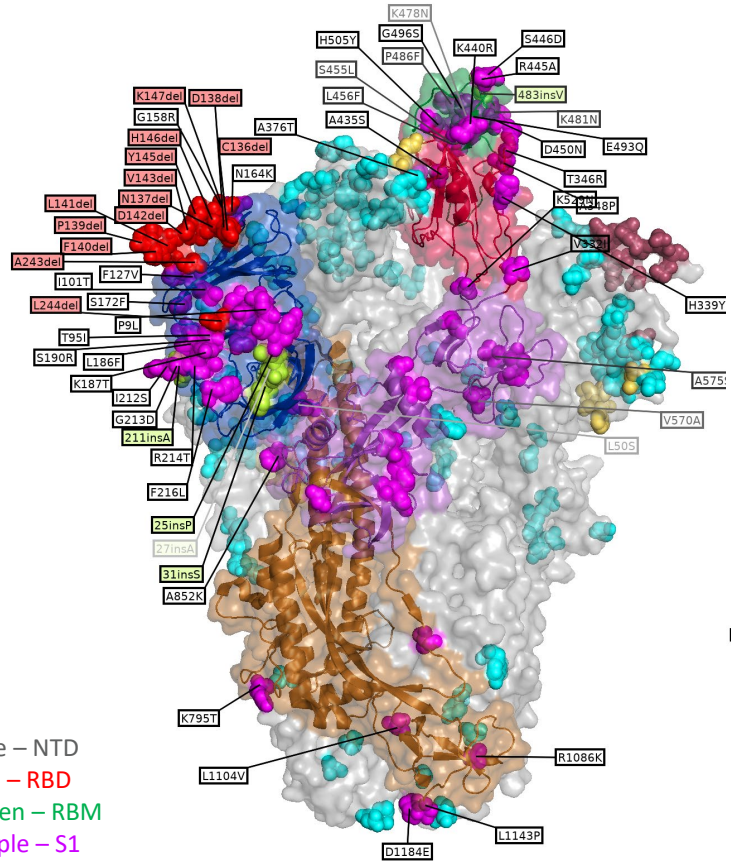
		S1 (14-685)																																			
		NTD (14-305)																																			
Position (Wuhan-hu-1 coordinates)	9	19	24	25	26	27	31	50	67	95	101	127	136	137	138	139	140	141	142	143	145	146	147	158	164	172	186	187	190	213	216	243	244	245	251	264	326
LP.8.1 (Reference)	P	I	-	-	-	S	-	L	A	T	I	F	C	N	D	P	F	L	D	V	Y	H	K	G	N	S	L	K	S	G	F	A	L	N	P	D	I
BA.3.2.1	L	T	L	P	L	A	S	S	V	I	T	V	-	-	-	-	-	-	-	-	-	-	-	R	K	F	F	T	R	V	L	-	-	H	S	A	V
BA.3.2.2	L	T	L	P	L	A	S	S	V	I	T	V	-	-	-	-	-	-	-	-	-	-	-	R	K	F	F	T	R	V	L	-	-	H	S	A	V

	S1 (14-685)																																S2 (686-1273)								
	RBD (332-527)																																							
Position (Wuhan-hu-1 coordinates)	332	339	346	348	356	376	435	440	445	446	450	455	456	478	481	483	486	493	496	505	529	540	570	575	583	621	625	641	642	654	679	681	688	704	795	852	1086	1104	1143	1162	1184
LP.8.1 (Reference)	V	H	T	A	T	A	A	K	R	S	D	S	L	K	K	-	P	E	G	H	K	K	V	A	E	S	H	N	V	E	K	R	A	S	K	A	R	L	L	P	D
BA.3.2.1	I	Y	R	P	K	T	S	R	A	D	N	L	F	N	N	V	F	Q	S	Y	N	D	A		D	P	R	K	G	K	R		D	L	T	K	K	V	P	R	E
BA.3.2.2	I	Y	R	P		T	S	R	A	D	N	L	F	N	N	V	F	Q	S	Y	N	D	A	S	D	P	R	K	G	K	R	H	D	L	T	K	K	V	P		E

Alignment of spike protein sequences from LP.8.1, BA.3.2.1, and BA.3.2.2. Gray shading indicates deletions and green shading indicates sites that differ between BA.3.2.1 and BA.3.2.2.

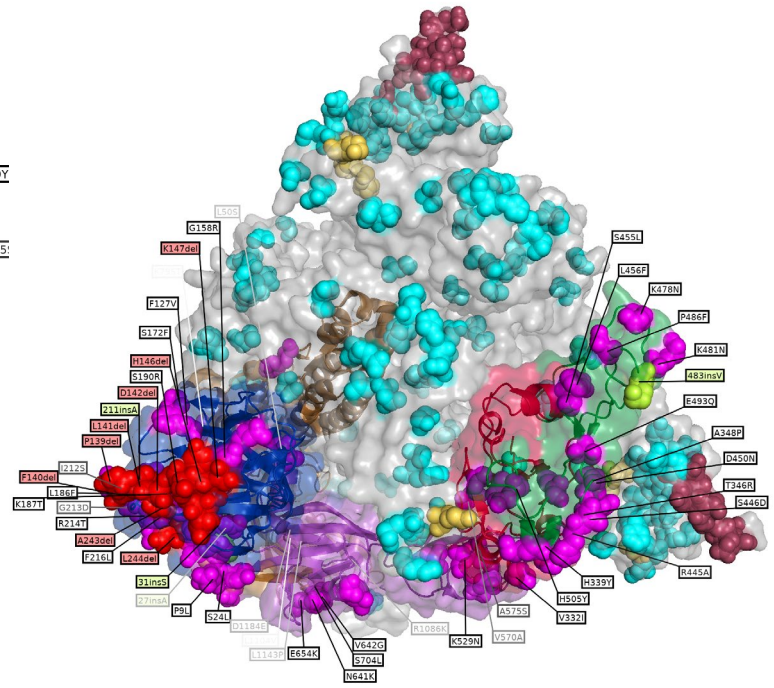
RE.2, the most common BA.3.2 sublineage, has many substitutions in comparison to LP.8.1

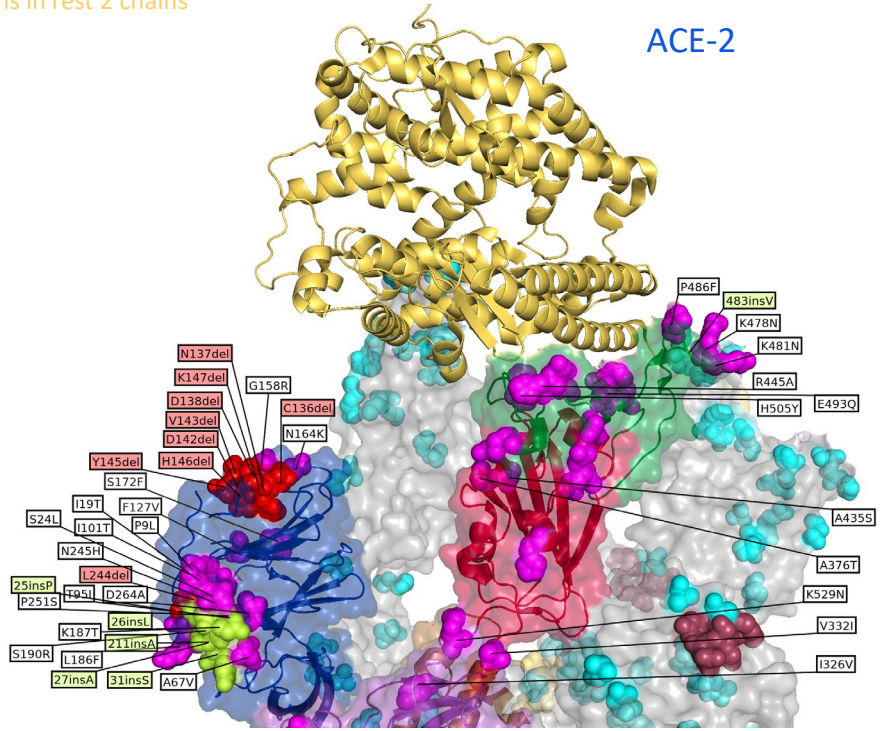
Red sphere – deletions in one chain (labeled)
Limon sphere – insertions in one chain (labeled)
Magenta sphere – substitutions in one chain (labeled)
Raspberry sphere – deletions in rest 2 chains
Cyan sphere – substitutions in rest 2 chains
Yellow-orange sphere – insertions in rest 2 chains



Blue – NTD
Red – RBD
Green – RBM
Purple – S1
Gold – FCS
Brown – S2

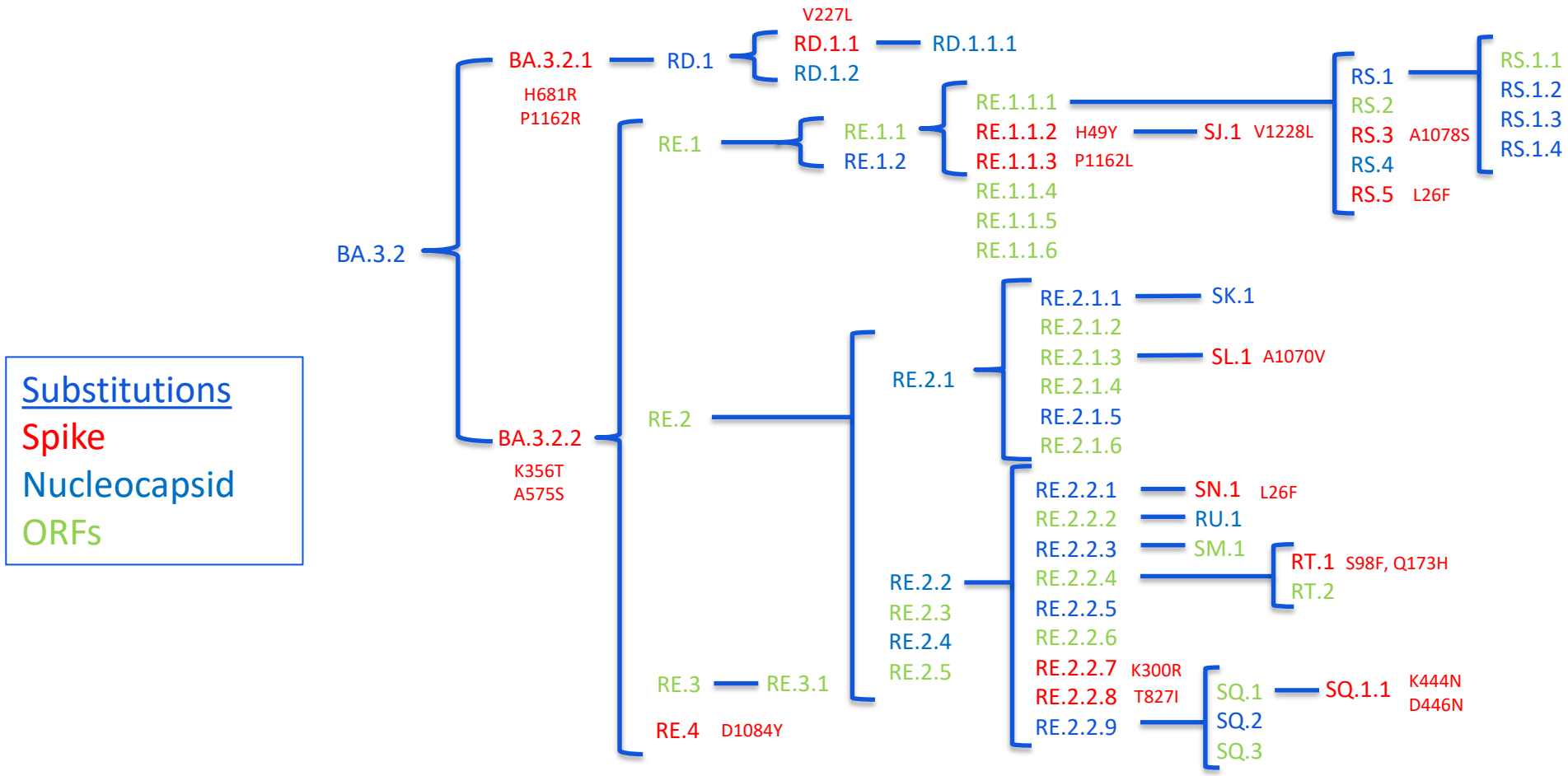
Structure of JN.1 (PDB ID: 8Y5J)





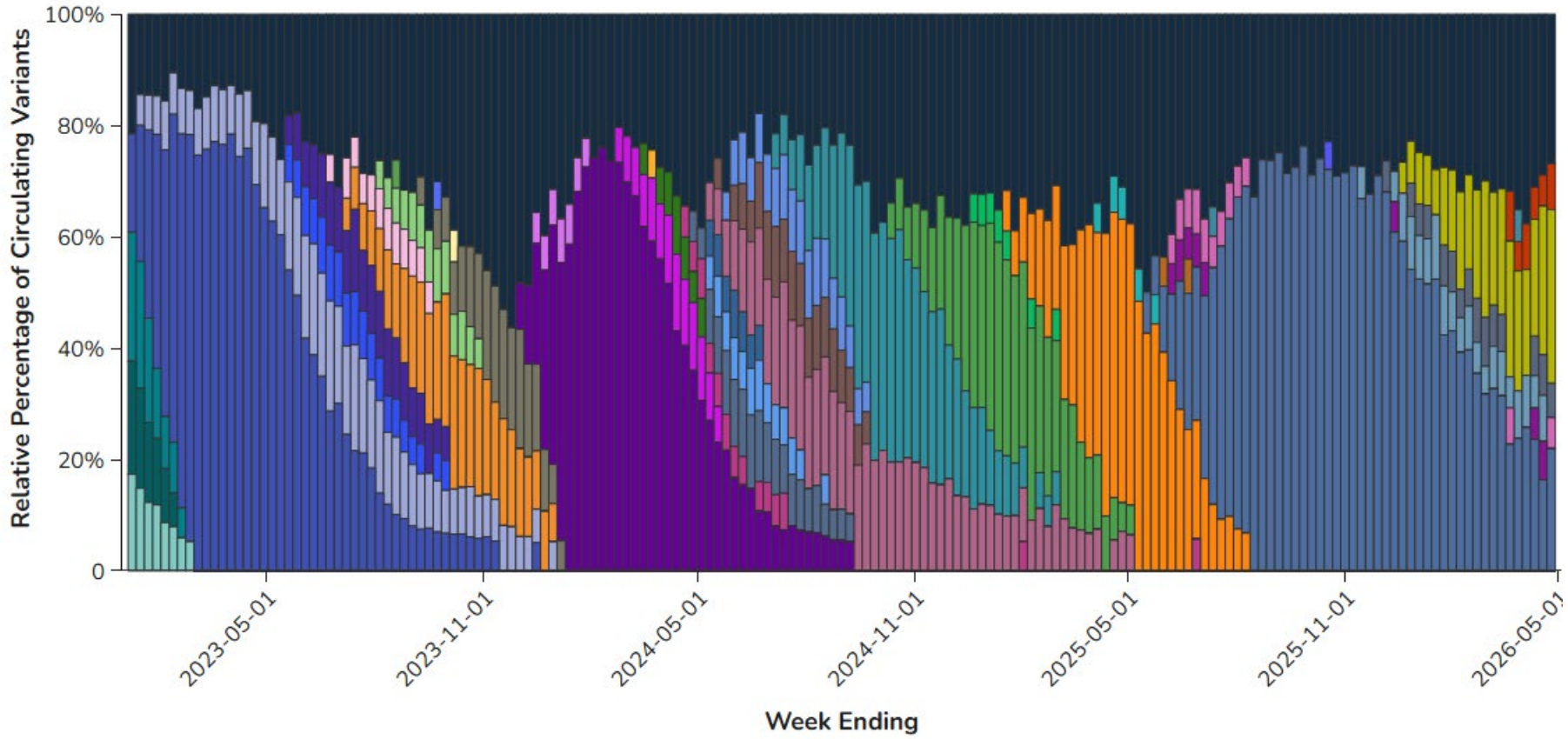
Structure of JN.1 in complex with ACE-2 (PDB ID: 8YZE)

BA.3.2 sublineages have continued to diversify



Color indicates mutation category as assigned by a priority order of spike, nucleocapsid, and then ORF mutations. Lineages may contain mutations in more than one category.

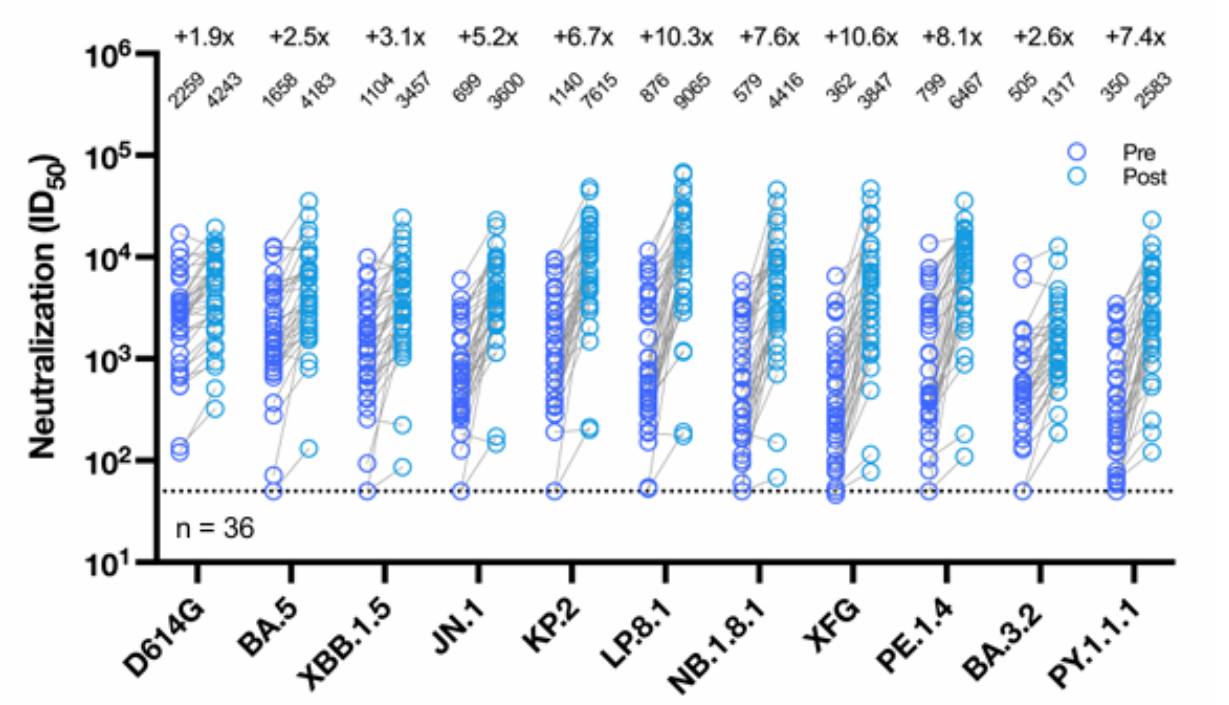
BA.3.2 detections and prevalence in US wastewater surveillance

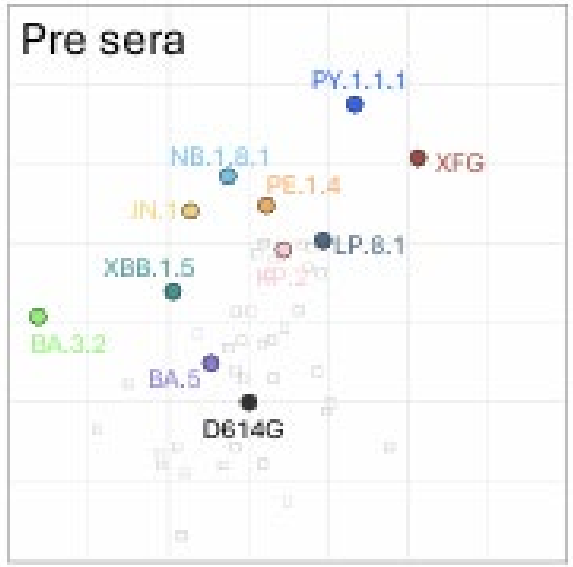


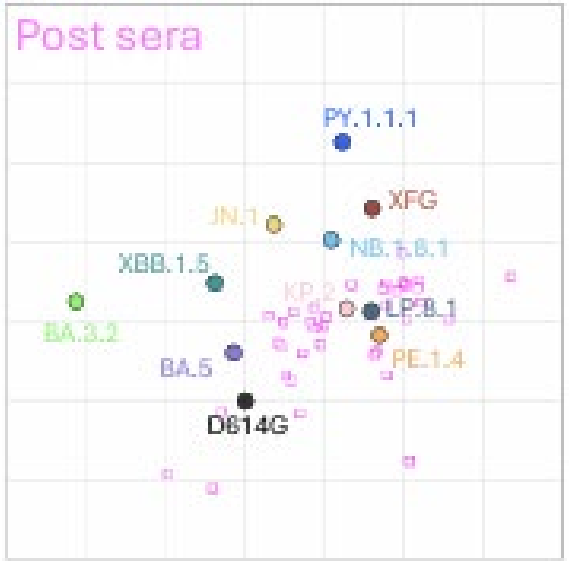
- There have been BA.3.2 detections in 36 states or territories.

https://www.cdc.gov/wastewater/respiratory-viruses/covid-19-variants.html

Vaccination with LP.8.1 formulation boosted neutralizing antibodies against all tested viruses







[LP.8.1-directed COVID-19 mRNA vaccines durably boost neutralizing antibodies and mitigate ancestral immune imprinting]

Genomics conclusions

- Most lineages that are currently circulating are descended from JN.1
- Circulating JN.1 lineages have similar spike proteins with 8-13 spike substitutions in comparison to last year's vaccine formulations
  - The most prevalent lineages are XFG* and NB.1.8.1
- A minority of detected viruses are BA.3.2 descendants, which are phylogenetically distinct from other circulating viruses
  - BA.3.2 was first detected in November 2024
  - It has increased in proportion globally, though very slowly
  - BA.3.2 sublineages have continued to diversify

Overall conclusions

- SARS-CoV-2 circulation has continued to peak in late summer / fall and winter
- Rates of COVID-19–associated hospitalization remain highest among the youngest (<6 months) and oldest (≥65 years) age groups
  - COVID-19–associated hospitalizations in these age groups are in line with influenza-associated hospitalization rates
- Most circulating viruses continue to be JN.1 descendants, which emerged in fall 2023
  - Current circulating JN.1 descendant viruses have very similar or identical spike sequences
- A minority of detected viruses are BA.3.2

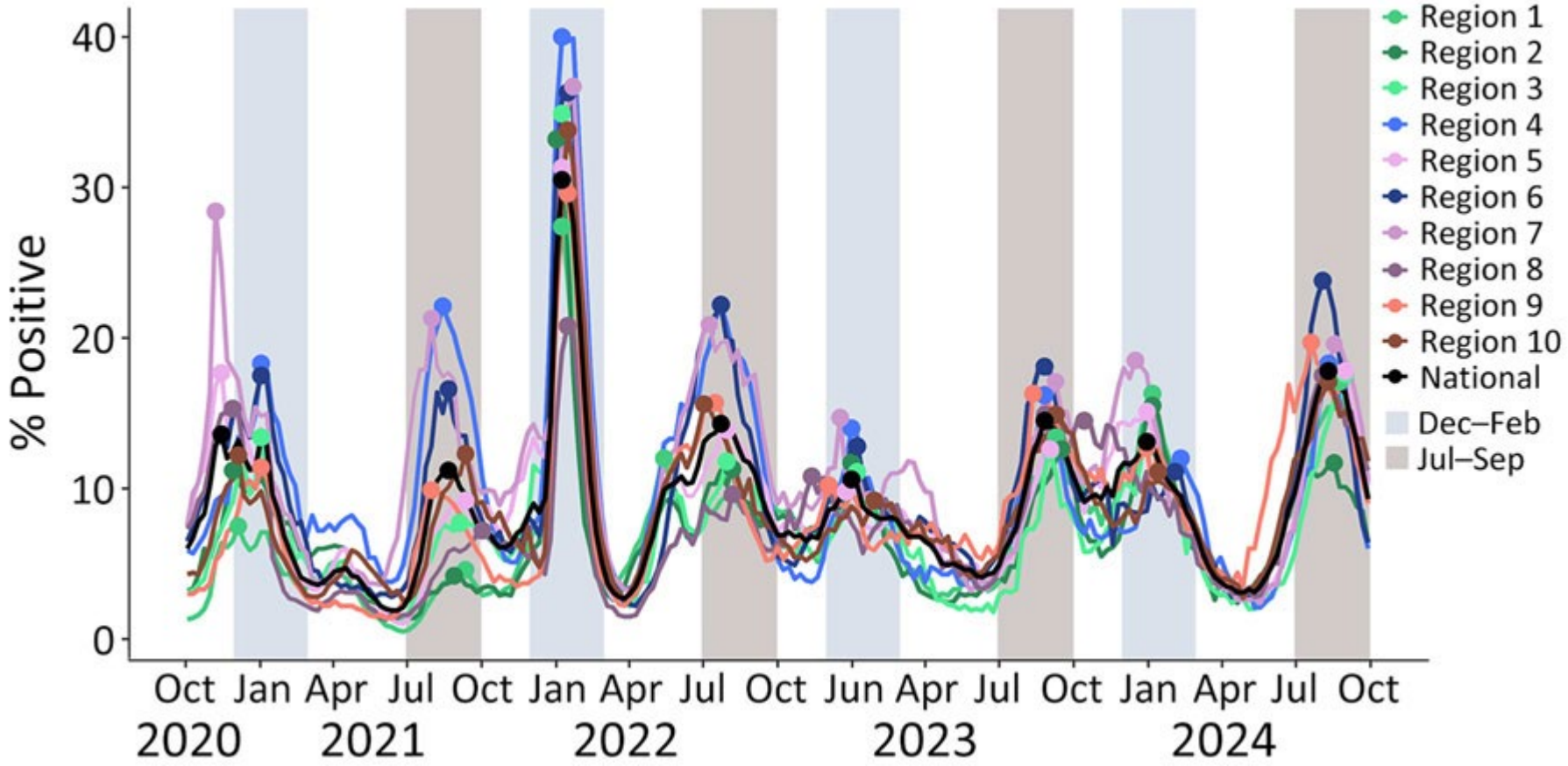
Acknowledgements

- The National Respiratory and Enteric Virus Surveillance System
- Respiratory Virus Hospitalization Surveillance Network (RESP-NET)
- SARS-CoV-2 Variant and Genomic Surveillance System
- SARS-CoV-2 Assessment of Viral Evolution (SAVE) Network

For more information, contact CDC
1-800-CDC-INFO (232-4636)
TTY: 1-888-232-6348 cdc.gov

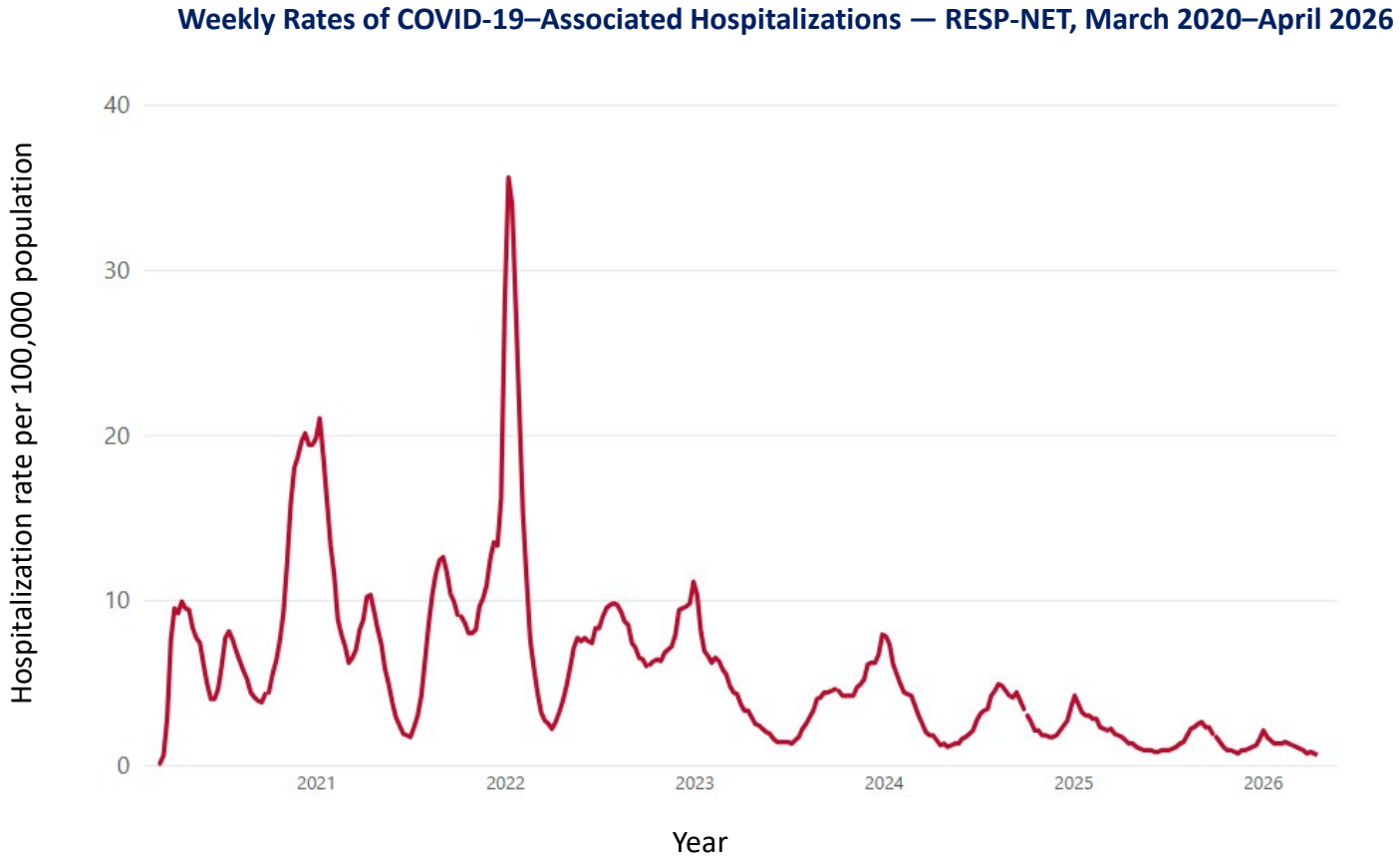
Extra slides

COVID-19 peaks in late summer (July-September) and winter (December-February)



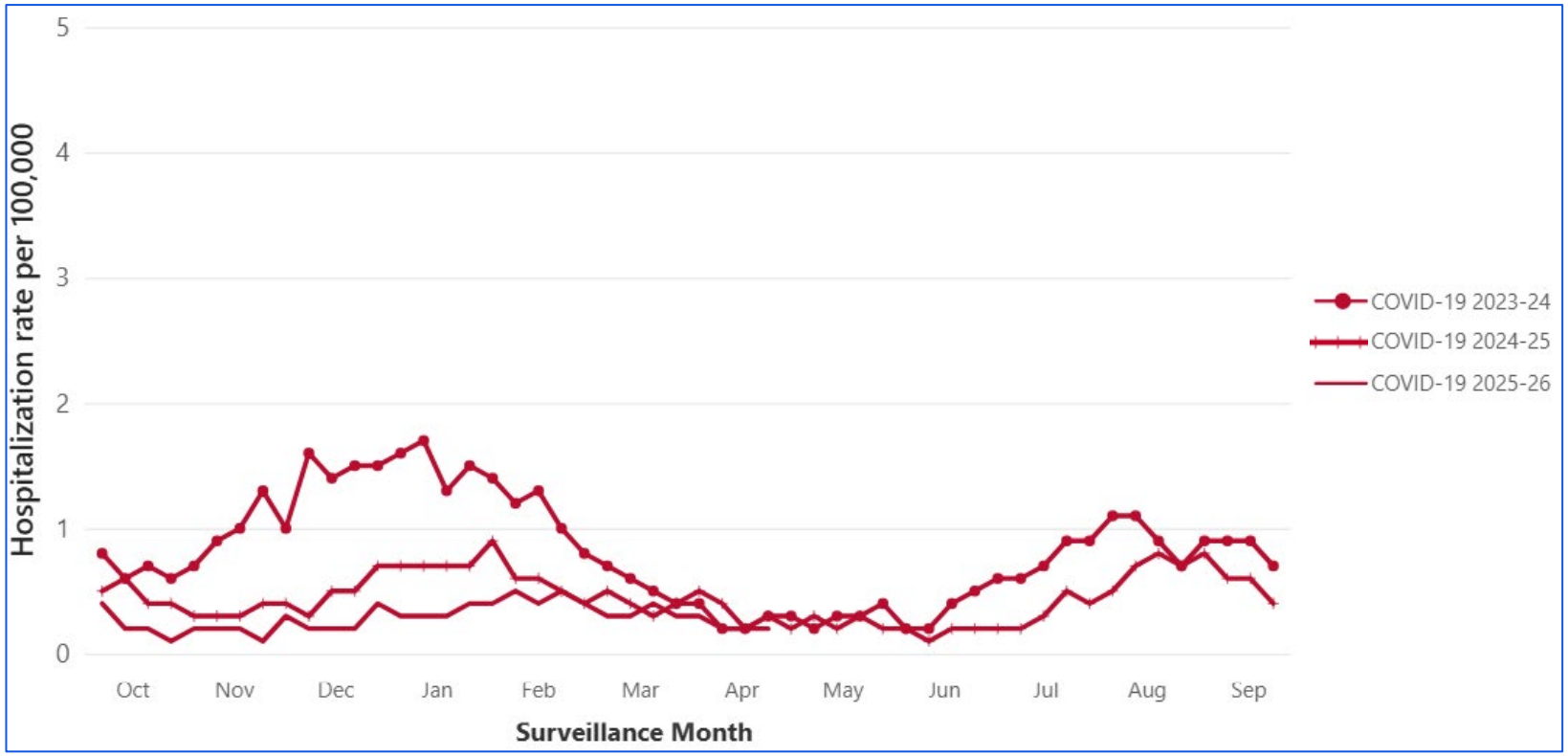
Rose E, Paden CR, Cook PW, Ma KC, Winn A, Castro J, et al. Estimated COVID-19 Periodicity and Correlation with SARS-CoV-2 Spike Protein S1 Antigenic Diversity, United States. Emerg Infect Dis. 2025;31(8):1573-1579. https://doi.org/10.3201/eid3108.250451

COVID-19 hospitalization rates have had both winter and summer peaks.



Rates for COVID-19 are laboratory-confirmed. Data source: https://www.cdc.gov/resp-net/dashboard/
Note that rates are not adjusted for testing or limited to admissions where the respiratory infection is the likely primary reason for admission.

Rates of COVID-19 hospitalizations among children aged 0-17 years remain similar or lower to prior seasons



COVID-NET

COVID-19-associated deaths have been undercounted

- Numerous published studies of excess mortality measure how COVID-19–associated deaths were undercounted during the pandemic*
- Mandated reporting of cases and deaths from public health jurisdictions ended in May 2023†

* Estimating excess mortality due to the COVID-19 pandemic: a systematic analysis of COVID-19-related mortality, 2020–21. 10.1016/S0140-6736(21)02796-3
Monthly excess mortality across counties in the United States during the COVID-19 pandemic, March 2020 to February 2022. 10.1126/sciadv.adf9742
Excess natural-cause mortality in US counties and its association with reported COVID-19 deaths doi.org/10.1073/pnas.2313661121

† COVID-19 Surveillance After Expiration of the Public Health Emergency Declaration — United States, May 11, 2023. https://www.cdc.gov/mmwr/volumes/72/wr/mm7219e1.htm

COVID-19–associated deaths have been undercounted

- People hospitalized for other conditions secondary to COVID-19 (e.g., stroke or heart attack) may not get tested, get accurate results, or be diagnosed with COVID-19

- COVID-19-associated deaths that occur outside a hospital are more likely not to be listed on a death certificate

Modeled Estimates of COVID-19–Associated Deaths, October 2024–September 2025, Show the Highest Mortality Burden in Older Adults*

Age group	Reported Deaths†	Estimated Deaths	Uncertainty Interval (UI)§	Estimated Mortality Rate per 100,000 (UI)
0–4 years	102	180	140-220	1.0 (0.8-1.2)
5–17 years	36	290	210-390	0.5 (0.4-0.7)
18–49 years	716	2,200	1,800-2,700	1.6 (1.3-1.9)
50–64 years	2,134	7,000	5,800-8,600	11.2 (9.3-13.8)
≥65 years	22,609	43,500	35,800-51,600	73.4 (60.4-87.1)
TOTAL	25,597	53,200	44,700-63,600	15.9 (13.3-19.0)

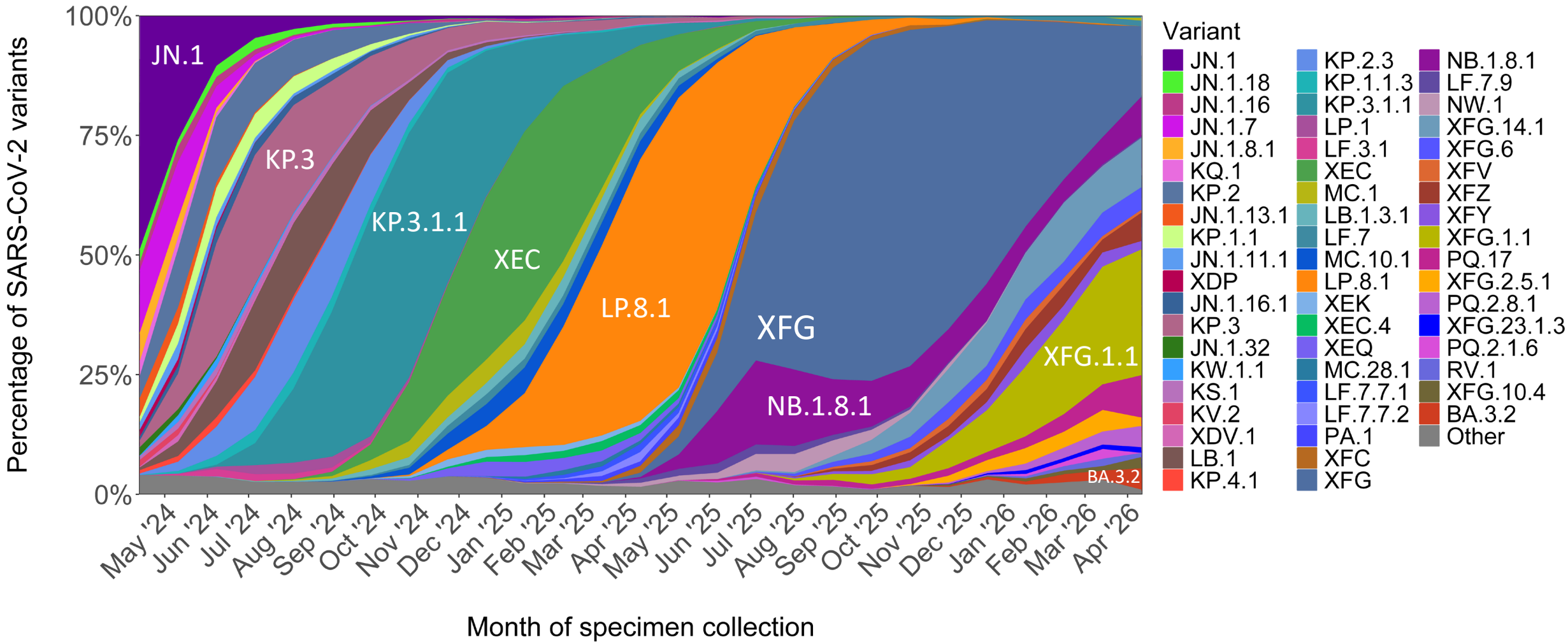
* The National Vital Statistics Surveillance (NVSS) is a comprehensive system that collects and disseminates U.S. vital statistics data. Estimated deaths are derived using published methods (Source: https://jamanetwork.com/journals/jamainternalmedicine/fullarticle/2843383).

† Reported deaths for 2024-2025 include provisional NVSS data for 2025.

§ Uncertainty intervals capture the most credible range of values for the distribution of estimates.

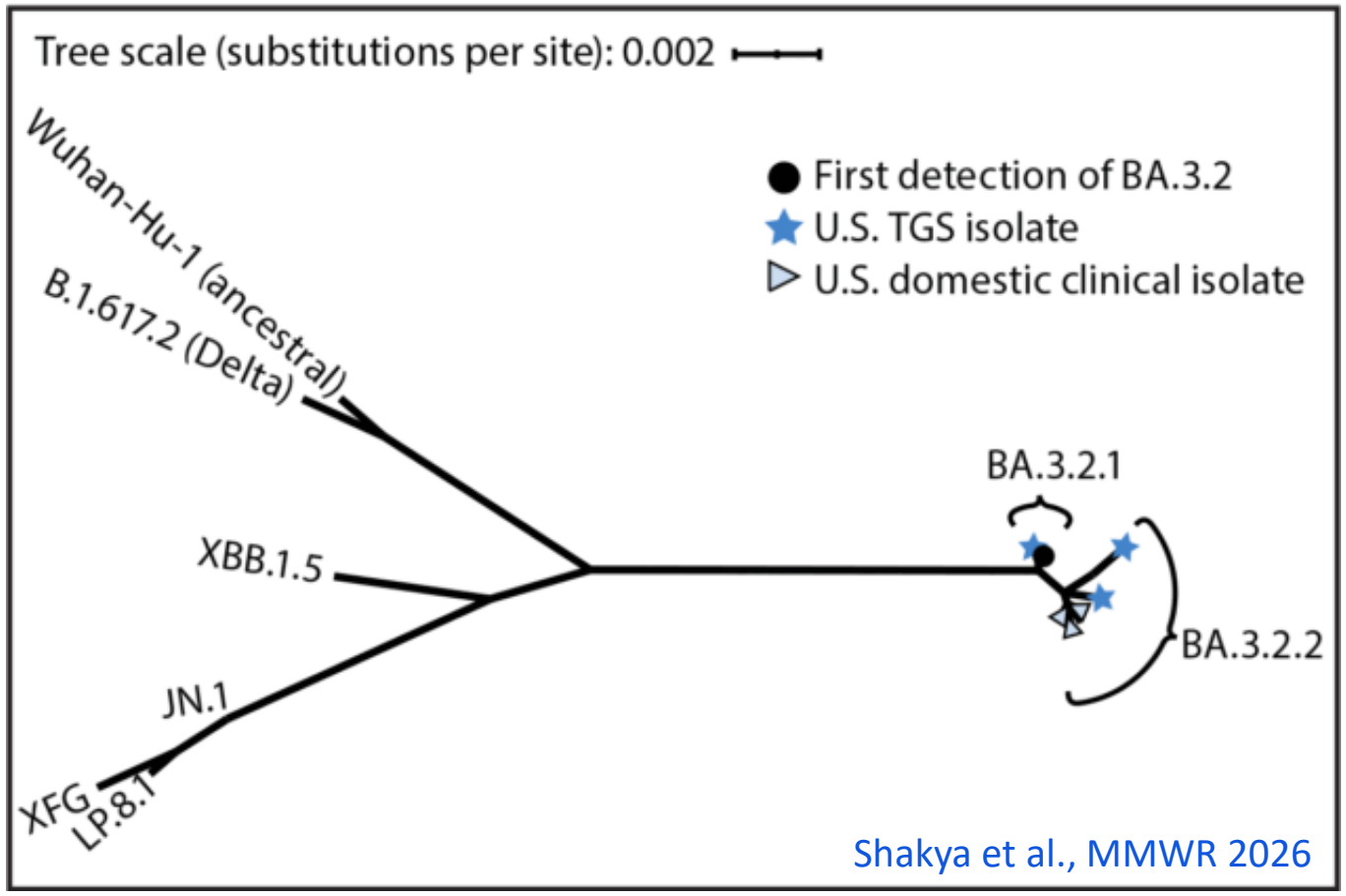
SARS-CoV-2 Variant Proportion Estimates: JN.1 Lineages and BA.3.2

United States, April 13, 2024–April 11, 2026



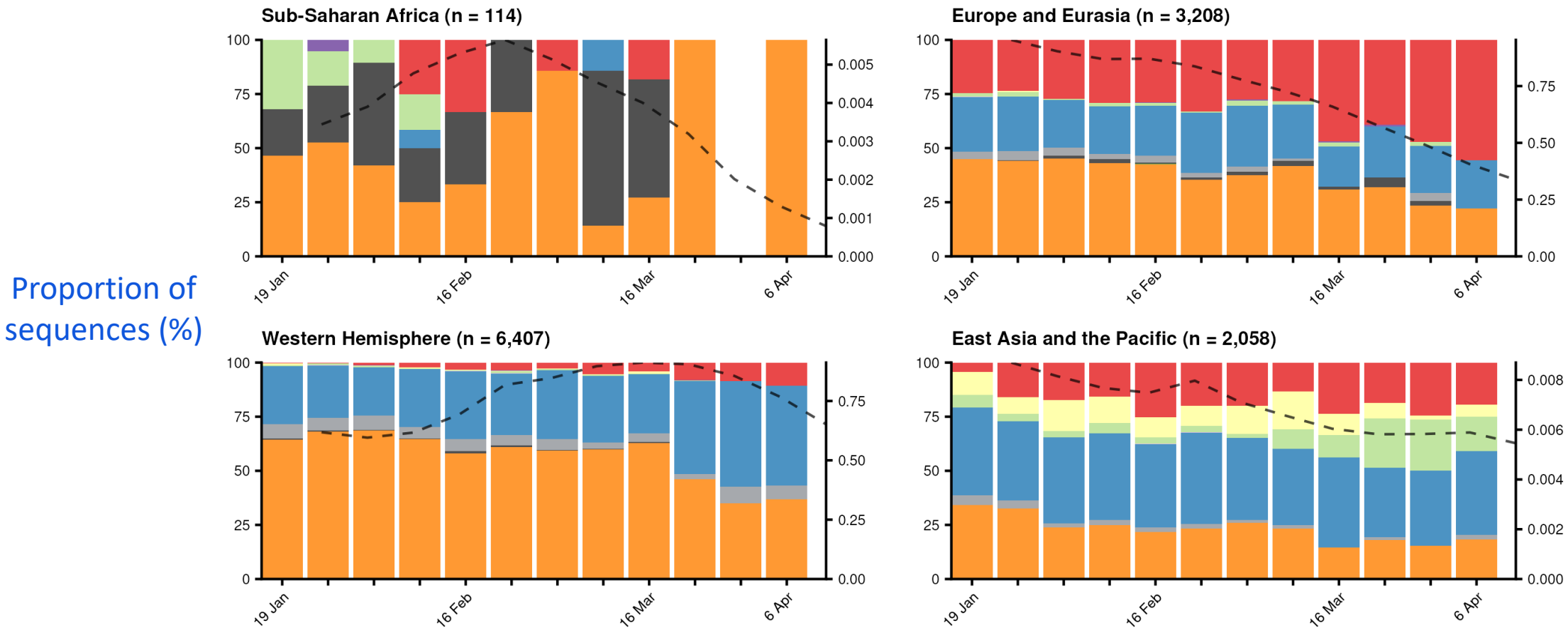
"Other" represents aggregated lineages circulating at <1% prevalence nationally during all 4-week periods displayed.
Lineages were ordered by date of first appearance on CDC's SARS-CoV-2 variant proportions dashboard (https://www.cdc.gov/covid/php/variants/variants-and-genomic-surveillance.html).

Phylogenetic tree of the SARS-CoV-2 spike glycoprotein gene from selected U.S. and global BA.3.2 isolates and reference strains



Spike gene regions from 16 BA.3.2 isolates and representative historical SARS-CoV-2 lineages were aligned using MAFFT, and an unrooted maximum likelihood tree was inferred using PhyML. U.S. BA.3.2 isolates comprise the first three detections in nasal swabs from international travelers (from Japan, Kenya, and the Netherlands) participating in the Traveler's Genomic Surveillance program and the first three U.S. clinical detections.

Trends in BA.3.2 global circulation patterns



Data as of May 1, 2026

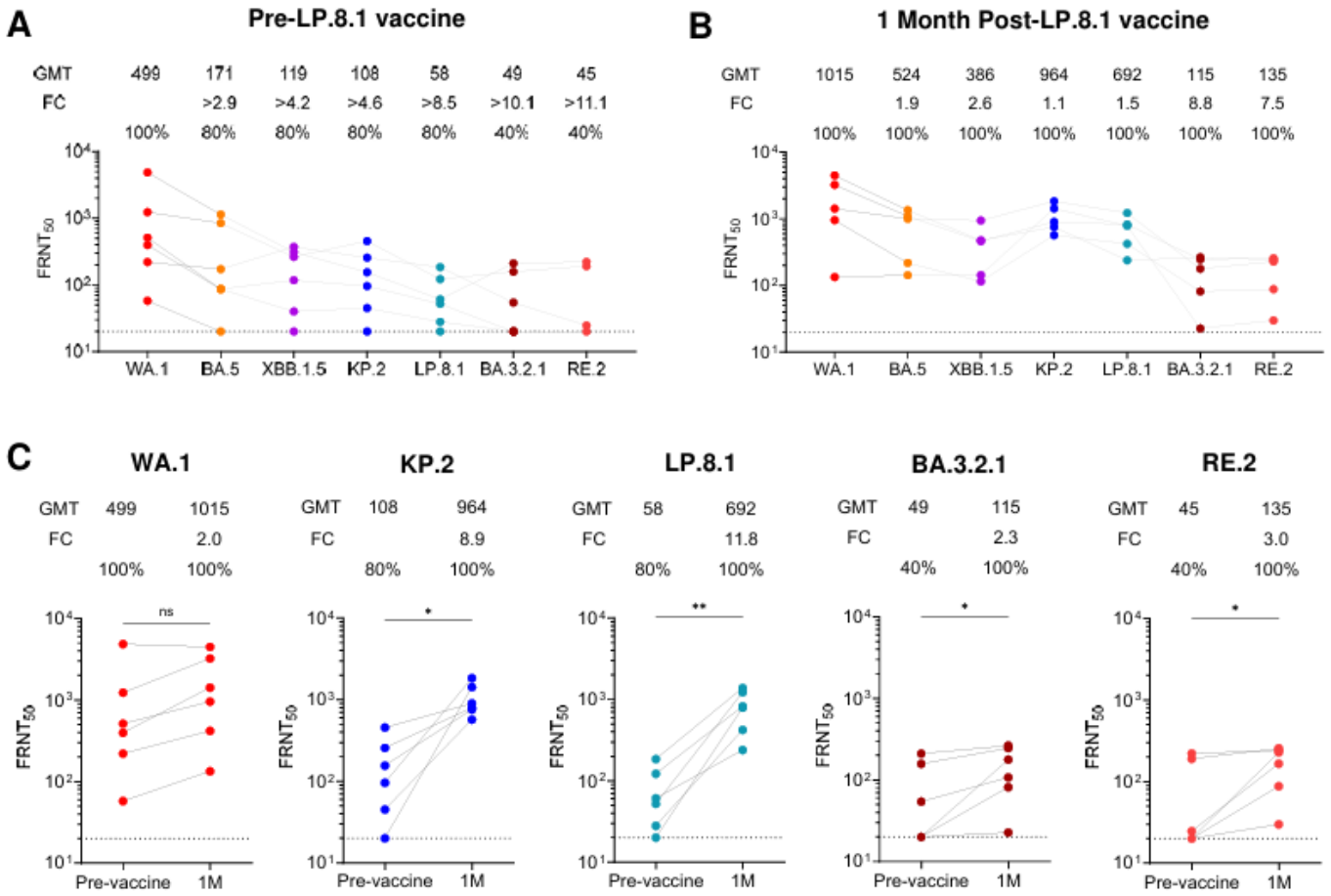
Proportions of sequences by lineage were calculated using data from public sequence repositories, including GISAID and NCBI Genbank.

Preliminary assessment of age distribution of patients with BA.3.2 vs other SARS-CoV-2 lineage infections

Limitations: sequences are not necessarily from representative sampling, age data is missing for a large proportion of sequences, and data are insufficient for assessing changes in severity

Data from countries with age metadata and at least 10 BA.3.2 detections (n=9) were obtained from GISAID/NCBI. The analytic period spanned September 1, 2025 to March 31, 2026.

Vaccination with LP.8.1 formulation boosts neutralization titers to ancestral, JN.1, and BA.3.2 viruses



[Immunological imprinting shapes the cross-reactive antibody responses to the KP.2 and LP.8.1 vaccine doses]