

TABLE 6. Annual reported cases of notifiable diseases and rates, by race*,†,§, United States, excluding U.S. Territories and Non-U.S. Residents, 2022

(Accessible Version: <https://wonder.cdc.gov/nndss/static/2022/annual/2022-table6.html>)

Disease	American Indian or Alaska Native		Asian or Pacific Islander		Black or African American		White		Other or Multi-Race¶	Race not stated	Total
	No.	Rate	No.	Rate	No.	Rate	No.	Rate			
Total	80	1.60	270	1.15	1,019	2.11	8,938	3.48	778	1,521	12,606
Confirmed	64	1.28	224	0.95	841	1.74	7,074	2.76	685	1,281	10,169
Probable	16	0.32	46	0.20	178	0.37	1,864	0.73	93	240	2,437
Cyclosporiasis	13	0.30	102	0.46	154	0.35	2,162	0.91	193	467	3,091
Dengue virus infections ¶¶											
Dengue	1	0.02	159	0.68	37	0.08	996	0.39	150	111	1,454
Dengue-like illness	—	—	6	0.03	3	0.01	21	0.01	2	1	33
Severe dengue	—	—	8	0.03	2	0.00	23	0.01	7	3	43
Diphtheria	5	5	5	5	5	5	5	5	5	5	1
Ehrlichiosis and Anaplasmosis											
<i>Anaplasma phagocytophilum</i> infection	27	0.61	39	0.18	29	0.06	4,598	1.86	110	848	5,651
<i>Ehrlichia chaffeensis</i> infection	5	0.11	23	0.10	29	0.06	1,296	0.52	77	139	1,569
<i>Ehrlichia ewingii</i> infection	—	—	—	—	—	—	23	0.01	1	1	25
Undetermined ehrlichiosis/anaplasmosis	—	—	—	—	3	0.01	79	0.03	4	9	95
Giardiasis	74	1.91	390	1.95	838	2.27	7,414	3.62	1,187	3,916	13,819
Gonorrhea	9,964	199.19	9,835	41.89	249,067	516.48	186,593	72.72	52,589	139,962	648,010
<i>Haemophilus influenzae</i> , invasive disease											
All ages, all serotypes	83	1.66	89	0.38	763	1.58	3,569	1.39	198	634	5,336
Age <5 years											
Serotype b	5	5	5	5	5	5	5	5	5	5	17
Non-b serotype	16	3.98	2	0.15	27	0.79	67	0.50	9	19	140
Nontypeable	6	1.49	9	0.66	38	1.12	150	1.12	13	38	254
Unknown serotype	2	0.04	8	0.03	45	0.09	141	0.05	23	54	273
Hansen's disease	—	—	13	0.06	6	0.01	21	0.01	5	17	62
Hantavirus infection, non-hantavirus pulmonary syndrome ***	—	—	—	—	—	—	—	—	—	—	—
Hantavirus pulmonary syndrome	5	5	5	5	5	5	5	5	5	5	11
Hemolytic uremic syndrome post-diarrheal	6	0.13	16	0.07	14	0.03	244	0.10	20	12	312
Hepatitis, Viral Disease †††											
Hepatitis A	27	0.54	101	0.43	347	0.72	1,484	0.58	147	158	2,264
Hepatitis B											
Acute	11	0.22	60	0.26	424	0.88	1,376	0.54	113	142	2,126
Perinatal infection	5	—	5	—	5	—	5	—	5	5	13
Hepatitis C											
Acute	82	1.84	80	0.35	711	1.49	3,788	1.52	396	571	5,628
Confirmed	66	1.48	71	0.31	630	1.32	3,211	1.28	349	521	4,848
Probable	16	0.36	9	0.04	81	0.17	577	0.23	47	50	780
Perinatal infection	4	NC	4	NC	11	NC	113	NC	18	47	197
Human immunodeficiency virus diagnoses	217	4.34	879	3.74	14,582	30.24	9,110	3.55	12,875	—	37,663
Influenza-associated pediatric mortality	1	0.07	4	0.08	23	0.18	72	0.14	2	14	116
Invasive pneumococcal disease §§§											
All ages	485	15.42	271	1.97	2,950	7.41	11,541	5.98	751	2,364	18,362
Confirmed	484	15.39	267	1.94	2,879	7.24	11,291	5.85	735	2,260	17,916
Probable	1	0.03	4	0.03	71	0.18	250	0.13	16	104	446
Age <5 years	28	0.75	45	0.30	235	0.56	582	0.28	57	170	1,117
Confirmed	28	9.29	44	4.92	228	7.62	557	5.15	55	166	1,078
Probable	—	—	1	0.11	7	0.23	25	0.23	2	4	39

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Disease	American Indian or Alaska Native		Asian or Pacific Islander		Black or African American		White		Other or Multi-Race¶	Race not stated	Total
	No.	Rate	No.	Rate	No.	Rate	No.	Rate	No.	No.	No.
Legionellosis	29	0.58	114	0.49	1,558	3.23	4,804	1.87	468	539	7,512
Leptospirosis	—	—	3	0.02	4	0.01	37	0.02	5	13	62
Listeriosis ¶¶¶¶											
Total	5	0.10	66	0.28	89	0.18	610	0.24	71	122	963
Confirmed	5	0.10	61	0.26	83	0.17	572	0.22	65	116	902
Probable	—	—	5	0.02	6	0.01	38	0.01	6	6	61
Lyme disease ****											
Total	146	2.92	467	2.07	630	1.31	32,520	12.70	1,063	27,602	62,428
Confirmed	2	0.04	15	0.07	16	0.03	1,587	0.62	55	391	2,066
Probable	144	2.88	452	2.01	614	1.27	30,933	12.08	1,008	27,211	60,362
Malaria	—	—	53	0.23	1,344	2.87	204	0.08	131	200	1,932
Measles ****											
Total	—	—	7	0.03	93	0.19	14	0.01	1	6	121
Indigenous	—	—	5	0.02	74	0.15	12	0.00	1	6	98
Imported	—	—	2	0.01	19	0.04	2	0.00	—	—	23
Meningococcal disease											
All serogroups	4	0.08	5	0.02	92	0.19	162	0.06	19	30	312
Serogroups ACWY	4	0.08	2	0.01	60	0.12	77	0.03	15	10	168
Serogroup B	—	—	1	0.00	5	0.01	39	0.02	—	2	47
Other serogroups	—	—	1	0.00	5	0.01	12	0.00	1	1	20
Unknown serogroup	—	—	1	0.00	22	0.05	34	0.01	3	17	77
Mpox §§§§	282	5.64	856	3.65	9,829	20.38	13,268	5.17	2,648	2,938	29,821
Mumps	2	0.04	24	0.10	31	0.06	225	0.09	18	86	386
Novel Influenza A virus infections	S	S	S	S	S	S	S	S	S	S	12
Pertussis	17	0.34	81	0.34	188	0.39	1,949	0.76	162	647	3,044
Plague ¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Poliomyelitis, paralytic	S	S	S	S	S	S	S	S	S	S	1
Poliovirus infection, nonparalytic	—	—	—	—	—	—	—	—	—	—	—
Psittacosis	S	S	S	S	S	S	S	S	S	S	7
Q fever											
Total	1	0.02	7	0.03	9	0.02	121	0.05	21	35	194
Acute	1	0.02	6	0.03	9	0.02	103	0.04	20	32	171
Chronic	—	—	1	0.00	—	—	18	0.01	1	3	23
Rabies											
Human	—	—	—	—	—	—	—	—	—	—	—
Rubella	S	S	S	S	S	S	S	S	S	S	7
Rubella, congenital syndrome	—	—	—	—	—	—	—	—	—	—	—
Salmonella Paratyphi infection *****	—	—	55	0.23	4	0.01	35	0.01	24	12	130
Salmonella Typhi infection ****	6	0.12	201	0.86	24	0.05	80	0.03	76	55	442
Salmonellosis (excluding S. Typhi infection and S. Paratyphi infection) §§§§§	473	9.46	1,979	8.43	4,841	10.04	37,054	14.44	4,323	7,459	56,129
Severe acute respiratory syndrome-associated coronavirus disease	—	—	—	—	—	—	—	—	—	—	—
Shiga toxin-producing Escherichia coli (STEC)	109	2.18	507	2.16	879	1.82	11,278	4.40	1,538	2,095	16,406
Shigellosis	130	2.60	607	2.59	2,060	4.27	7,596	2.96	1,833	2,518	14,744
Smallpox	—	—	—	—	—	—	—	—	—	—	—
Spotted fever rickettsiosis											
Total	42	0.86	14	0.06	41	0.09	978	0.38	40	177	1,292
Confirmed	1	0.02	2	0.01	1	0.00	36	0.01	3	4	47
Probable	41	0.84	12	0.05	40	0.08	942	0.37	37	173	1,245

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Disease	American Indian or Alaska Native		Asian or Pacific Islander		Black or African American		White		Other or Multi-Race¶	Race not stated	Total
	No.	Rate	No.	Rate	No.	Rate	No.	Rate	No.	No.	No.
Streptococcal toxic shock syndrome	4	0.14	10	0.08	41	0.12	259	0.16	7	12	333
Syphilis											
Total, all stages ¶¶¶¶¶¶	5,447	108.89	4,231	18.02	65,540	135.91	91,784	35.77	22,093	18,128	207,223
Congenital *****	181	433.53	67	23.87	1,144	180.26	1,868	66.94	254	241	3,755
Primary and secondary	1,756	35.10	1,239	5.28	18,979	39.36	27,393	10.68	5,705	3,938	59,010
Tetanus	—	—	—	—	—	—	23	0.01	1	2	26
Toxic shock syndrome (other than Streptococcal)	—	—	—	—	1	0.00	14	0.01	2	14	31
Trichinellosis	S	S	S	S	S	S	S	S	S	S	9
Tuberculosis	139	2.78	2,893	12.32	1,380	2.86	3,390	1.32	276	253	8,331
Tularemia	6	0.12	3	0.01	3	0.01	128	0.05	10	17	167
Vancomycin-intermediate <i>Staphylococcus aureus</i>	—	—	—	—	18	0.04	48	0.02	1	15	82
Vancomycin-resistant <i>Staphylococcus aureus</i> †††††	S	S	S	S	S	S	S	S	S	S	2
Varicella morbidity	45	1.16	213	1.10	334	0.83	2,447	1.14	288	1,021	4,348
Varicella mortality	U	U	U	U	U	U	U	U	U	U	U
Vibriosis											
Total	17	0.34	137	0.59	272	0.57	2,007	0.80	174	431	3,038
Confirmed	9	0.18	56	0.24	81	0.17	1,042	0.41	95	191	1,474
Probable	8	0.16	81	0.35	191	0.40	965	0.38	79	240	1,564
Viral hemorrhagic fevers											
Chapare virus §§§§§§	—	—	—	—	—	—	—	—	—	—	—
Crimean-Congo hemorrhagic fever virus ¶¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Ebola virus ¶¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Guanarito virus ¶¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Junin virus ¶¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Lassa virus ¶¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Lujo virus ¶¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Machupo virus ¶¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Marburg virus ¶¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Sabia virus ¶¶¶¶¶¶	—	—	—	—	—	—	—	—	—	—	—
Yellow fever	—	—	—	—	—	—	—	—	—	—	—
Zika virus											
Zika virus disease, congenital *****	S	S	S	S	S	S	S	S	S	S	1
Zika virus disease, non-congenital	S	S	S	S	S	S	S	S	S	S	5
Zika virus infection, congenital *****	—	—	—	—	—	—	—	—	—	—	—
Zika virus infection, non-congenital	S	S	S	S	S	S	S	S	S	S	2

—: No reported cases — The reporting jurisdiction did not submit any cases to CDC.

NC: Not Calculated — There is insufficient data available to support this statistic.

U: Unavailable — The data are unavailable.

S: Suppressed

* Conditions with <25 cases reported in the year were not broken down by race.

† Race data were collected using current Office of Management and Budget (OMB) standards for race/ethnicity data and were mapped to bridged race categories.

§ Any variation of disease incidence by race or ethnicity does not reflect biological differences but reflects systemic, cultural, behavioral, and social factors including structural racism.

¶ Includes individuals reported as other race or multiple races.

** Note that *Candida auris* colonization/screening cases are not included in this table. Additionally, there may be case count discrepancies of *Candida auris* clinical cases reported by the NNDSS and the CDC's Mycotic Diseases Branch due to differences in data sources, reporting and aggregation methods. Please refer to the Mycotic Diseases Branch's [Tracking C. auris | Candida auris \(C. auris\) | CDC for Candida auris case data reported by jurisdictions](#). These data are submitted to the CDC separately of NNDSS by jurisdictions and are published by location of the facility.

Please also see [Note #8](#).

†† Beginning in January 2022, only confirmed cases are published to align with the approved CSTE position statement 21-ID-06, whereas in previous years, all case classification statuses were published. This change may cause a decrease in published case counts when compared to previous years.

§§ Of the reporting areas that submitted 2022 aggregate COVID-19 data to CDC, three did not submit probable cases. American Samoa, New York (excluding New York City), and U.S. Virgin Islands did not collect probable cases.

¶¶ Counts include confirmed and probable dengue cases.

*** Case counts may include Old World hantavirus infections, such as Seoul virus.

††† Chronic hepatitis B and chronic hepatitis C data are not included in NNDSS tables but reported case counts are included in the annual Viral Hepatitis Surveillance Report, 2022, published online by CDC's Division of Viral Hepatitis, available at

<https://www.cdc.gov/hepatitis/statistics/SurveillanceRpts.htm>.

§§§ Counts include drug resistant and susceptible cases of Invasive Pneumococcal Disease. This condition was previously named *Streptococcus pneumoniae* invasive disease and cases were reported to CDC using different event codes to specify whether the cases were drug resistant or in a defined age group, such as <5 years.

¶¶¶ Before 2019, probable cases were not reported, and cases in neonates ≤60 days of age were counted as one case in a mother-infant pair. Beginning in 2019, confirmed and probable cases are being reported, and maternal and neonatal cases are being counted separately.

**** For surveillance reporting purposes, jurisdictions are grouped into high- and low-incidence categories. Confirmed cases are only reported from low-incidence jurisdictions; however, probable cases are reported from both high- and low-incidence jurisdictions. For more information on jurisdiction classifications, visit <https://www.cdc.gov/lyme>. Currently, high-incidence jurisdictions include Connecticut, Delaware, Maine, Maryland, Massachusetts, Minnesota, New Hampshire, New Jersey, New York (excluding New York City), New York City, Pennsylvania, Rhode Island, Vermont, Virginia, West Virginia, Wisconsin, and the District of Columbia.

†††† Measles is considered imported if the disease was acquired outside of the United States and is considered indigenous if the disease was acquired anywhere within the United States or it is not known where the disease was acquired.

§§§§ CSTE adopted Mpox as a nationally notifiable condition on June 23, 2022 and beginning August 1, 2022 confirmed and probable cases are published to align with the CSTE position statement 22-ID-10. Case classifications for cases reported prior to August 1, 2022 should not have been retroactively changed based on the case definition in the CSTE position statement 22-ID-10.

¶¶¶¶ Beginning in 2020, confirmed and probable plague cases began to be combined and published.

***** Beginning in January 2019, cases began to be reported as *Salmonella* Paratyphi infection. In 2018, cases were reported as paratyphoid fever. Prior to 2018, cases of paratyphoid fever were considered salmonellosis.

††††† Beginning in January 2019, cases began to be reported as *Salmonella* Typhi infection. In previous years, cases were reported as typhoid fever.

§§§§§ Beginning in January 2019, cases began to be reported as salmonellosis (excluding *Salmonella* Typhi infection and *Salmonella* Paratyphi infection). In 2018, cases were reported as salmonellosis (excluding paratyphoid fever and typhoid fever). Prior to 2018, cases of paratyphoid fever were considered salmonellosis.

¶¶¶¶¶ Includes the following categories: primary; secondary; early non-primary non-secondary (includes cases previously reported as early latent); unknown duration or late (includes cases previously reported as late latent syphilis and cases previously reported as late syphilis with clinical manifestations) and congenital syphilis.

***** Congenital syphilis cases are usually assigned to the mother's state of residence at the time of delivery. Data for congenital syphilis are aggregated by the infant's year of birth.

†††††† Vancomycin-resistant *Staphylococcus aureus* cases reported in this table may not have been verified by CDC. CDC verified 0 vancomycin-resistant *Staphylococcus aureus* cases in 2022.

§§§§§§ Beginning in January 2022, Chapare virus was added as a nationally notifiable condition, and confirmed and suspect cases combined are published to align with the approved CSTE position statement 21-ID-04.

¶¶¶¶¶¶ Beginning in January 2022, confirmed and suspect cases combined are published to align with the approved CSTE position statement 21-ID-04, whereas in previous years, only confirmed cases were published.

***** Data reported to ArboNET using the national surveillance case definition for congenital Zika virus infection (CSTE Position Statement 16-ID-01).

Notes:

1. These are **annual** cases of selected infectious national notifiable diseases from the National Notifiable Diseases Surveillance System (NNDSS). NNDSS data reported by the 50 states, New York City, the District of Columbia, and the U.S. territories are collated and published. Cases are reported by state health departments to CDC weekly. Because source datasets may be updated as additional information is received, statistics in publications based on that source data may differ from what is presented in these tables. Source datasets for the 2022 annual tables were officially closed on March 29, 2024.
2. The list of national notifiable Infectious diseases and conditions for 2022 and their national surveillance case definitions are available by navigating to the [Surveillance Case Definitions | CDC](#) web page, selecting "2022" for the notifiable condition list year, checking "Infectious" conditions, and clicking "Get Notifiable List by Year". Publication criteria for the finalized 2022 data are available at https://wonder.cdc.gov/nndss/documents/NNDSS_Publication_Criteria_2022.pdf. See also [Guide to Interpreting Provisional and Finalized NNDSS Data](#).
3. Population estimates for incidence rates are July 1st, 2022 postcensal estimates of the resident population of the United States for July 1, 2020, to July 1, 2022, by year, county, single year of age (range: 0 to 85+ years), bridged-race (American Indian or Alaska Native, Asian or Pacific Islander, Black or African American, White), Hispanic ethnicity (Hispanic or Latino, not Hispanic or Latino), and sex (Female, Male), prepared under a collaborative arrangement with the U.S. Census Bureau and the National Cancer Institute (NCI). The "Vintage 2022" population estimates for years 2020-2022 were released March 2024 by the National Cancer Institute at <https://seer.cancer.gov/popdata/>. For more information, see <https://seer.cancer.gov/popdata/singleages.html> Population estimates for territories are the 2022 mid-year estimates from the U.S. Census Bureau International Data Base, accessed on May 02, 2024, at https://www.census.gov/data-tools/demo/idb/#/country?YR_ANIM=2022. The choice of population denominators for incidence is based on the availability of population data at the time of publication preparation.
4. Annual tables for 2016 and later years are available on [CDC WONDER](#).
5. Annual summary reports from 1993–2015 are available as published in the [Morbidity and Mortality Weekly Report](#).
6. NNDSS annual tables since 1952 are available at [CDC Stacks](#). To find them, search for "NNDSS" under Collections. Once in NNDSS Collections, navigate to the "Genre" box on the left-hand side and select "Annual Reports".
7. For most conditions, national incidence rates are calculated as the number of reported cases for each infectious disease or condition divided by the U.S. resident population for the specified demographic population or the total U.S. resident population, multiplied by 100,000. When a national notifiable infectious condition is associated with a specific age restriction, the same restriction was applied to the population in the denominator of the incidence rate calculation. In addition, population data from reporting jurisdictions in which the disease or condition was not reportable or not available were excluded from the denominator of the incidence rate calculations.

Age restrictions in the numerator and denominator are applied for the following childhood conditions:

Zika virus disease, congenital (age restriction in numerator and denominator is <1 year)

Zika virus infection, congenital (age restriction in numerator and denominator is <1 year)

Haemophilus influenzae, invasive disease <5 years (age restriction in numerator and denominator is <5 years)

Invasive pneumococcal disease <5 years (age restriction in numerator and denominator is <5 years)

Influenza associated pediatric mortality (age restriction in numerator and denominator is <18 years)

Infant botulism (age restriction in numerator and denominator is <1 year)

Congenital rubella syndrome (age restriction in numerator and denominator is <1 year)
Perinatal hepatitis B infection (age restriction is ≤24 months)
Perinatal hepatitis C infection (age restriction is ≤36 months).

Data for congenital syphilis are aggregated by the infant's year of birth. The rate for congenital syphilis is based upon the number of reported cases per 100,000 live births, using natality data for 2022 (National Center for Health Statistics [Natality 2022](#), as compiled from data provided by the Vital Statistics Cooperative Program). Congenital syphilis cases are usually assigned to the mother's state of residence at the time of delivery. The mother's race and ethnicity are used for race- and ethnicity-specific rates of congenital syphilis cases.

8. Surveillance data reported by other CDC programs might vary from data reported in these tables because of differences in 1) the date used to aggregate the data, 2) the timing of reports, 3) the source of the data, 4) surveillance case definitions, and 5) policies regarding case jurisdiction (i.e., which jurisdiction should submit the case notification to CDC).
9. Disease data presented in the 2022 tables reflect impacts of the COVID-19 pandemic, such as changes in exposure-related behavior, healthcare-seeking behavior, disease reporting, and public health investigations.

Suggested Citation:

- Centers for Disease Control and Prevention. National Notifiable Diseases Surveillance System, 2022 Annual Tables of Infectious Disease Data. Atlanta, GA. CDC Office of Public Health Data, Surveillance, and Technology, 2024. Available at: <https://www.cdc.gov/nndss/data-statistics/infectious-tables/index.html>.

Acknowledgment:

- CDC acknowledges the local, state, and territorial health departments that collected the data from a range of case ascertainment sources (e.g., healthcare providers, hospitals, laboratories) and reported these data to CDC's National Notifiable Diseases Surveillance System.

National Notifiable Diseases Surveillance System

Provided by [CDC WONDER](#)