

Nationally Notifiable Infectious Diseases and Conditions, United States: Annual Tables

TABLE 7. Annual reported cases of notifiable diseases and rates, by ethnicity*,†,‡,§,¶, United States, excluding U.S. Territories and Non-U.S. Residents, 2023

Disease	Hispanic or Latino		Non-Hispanic/Latino		Ethnicity not stated	Total
	No.	Rate	No.	Rate		
Anthrax	—	—	—	—	—	—
Arboviral diseases						
Chikungunya virus disease	31	0.05	78	0.03	41	150
Eastern equine encephalitis virus disease						
Neuroinvasive	S	S	S	S	S	7
Non-neuroinvasive	—	—	—	—	—	—
Jamestown Canyon virus disease						
Neuroinvasive	S	S	S	S	S	20
Non-neuroinvasive	S	S	S	S	S	7
La Crosse virus disease						
Neuroinvasive	1	0.00	27	0.01	6	34
Non-neuroinvasive	S	S	S	S	S	1
Powassan virus disease						
Neuroinvasive	—	—	43	0.02	4	47
Non-neuroinvasive	S	S	S	S	S	2
St. Louis encephalitis virus disease						
Neuroinvasive	S	S	S	S	S	14
Non-neuroinvasive	S	S	S	S	S	7
West Nile virus disease						
Neuroinvasive	234	0.36	1,309	0.49	248	1,791
Non-neuroinvasive	70	0.11	613	0.23	156	839
Western equine encephalitis virus disease						
Neuroinvasive	—	—	—	—	—	—
Non-neuroinvasive	—	—	—	—	—	—
Babesiosis						
Confirmed	231	0.40	1,910	0.83	975	3,116
Probable	17	0.03	265	0.12	188	470
Total	248	0.42	2,175	0.94	1,163	3,586
Botulism						
Foodborne	S	S	S	S	S	17
Infant	40	3.99	92	3.48	42	174
Other (wound & unspecified)	S	S	S	S	S	14
Total	42	0.06	114	0.04	49	205
Brucellosis	90	0.14	41	0.02	14	145
Campylobacteriosis	11,922	18.28	53,016	19.66	16,609	81,547
<i>Candida auris</i>						
Clinical#	323	0.55	2,109	0.85	768	3,200
Screening**	291	0.45	2,919	1.08	1,156	4,366
Carbapenemase-producing organisms (CPO), total††, ‡‡	522	1.12	4,524	1.97	1,864	6,910
Chancroid	S	S	S	S	S	4
<i>Chlamydia trachomatis</i> infection	252,833	387.72	792,108	293.69	603,503	1,648,444
Cholera	S	S	S	S	S	19
Coccidioidomycosis§§						
Confirmed	3,868	14.13	8,812	7.74	8,005	20,685
Probable	31	0.11	192	0.17	104	327
Total	3,899	14.24	9,004	7.91	8,109	21,012
Coronavirus Disease 2019 (COVID-19)						

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Disease	Hispanic or Latino		Non-Hispanic/Latino		Ethnicity not stated	Total
	No.	Rate	No.	Rate	No.	No.
Confirmed	710,897	1177.09	3,033,866	1339.51	1,151,488	4,896,251
Probable¶¶	362,563	600.32	1,514,389	668.63	597,219	2,474,171
Total	1,073,460	1777.41	4,548,255	2008.14	1,748,707	7,370,422
Cryptosporidiosis						
Confirmed	1,388	2.13	7,098	2.63	2,098	10,584
Probable	275	0.42	2,110	0.78	341	2,726
Total	1,663	2.55	9,208	3.41	2,439	13,310
Cyclosporiasis	696	1.11	2,633	1.05	1,134	4,463
Dengue virus infections##						
Dengue	1,011	1.55	674	0.25	259	1,944
Dengue-like illness	S	S	S	S	S	23
Severe dengue	30	0.05	17	0.01	6	53
Diphtheria	S	S	S	S	S	2
Ehrlichiosis and Anaplasmosis						
<i>Anaplasma phagocytophilum</i> infection	138	0.22	4,628	1.78	2,513	7,279
<i>Ehrlichia chaffeensis</i> infection	62	0.10	1,465	0.56	380	1,907
<i>Ehrlichia ewingii</i> infection	—	—	22	0.01	4	26
Undetermined ehrlichiosis/anaplasmosis	—	—	76	0.03	13	89
Giardiasis	2,180	4.52	9,304	4.27	4,694	16,178
Gonorrhea***	83,521	128.08	350,010	129.78	167,731	601,262
<i>Haemophilus influenzae</i> , invasive disease						
Age <5 years						
Non-b serotype	25	0.50	94	0.70	20	139
Nontypeable	55	1.10	155	1.15	45	255
Serotype b	2	0.04	20	0.15	12	34
Unknown serotype	37	0.74	153	1.13	38	228
All ages, all serotypes	594	0.91	5,167	1.92	1,066	6,827
Hansen's disease	11	0.02	48	0.02	29	88
Hantavirus infection, non-hantavirus pulmonary syndrome†††	S	S	S	S	S	1
Hantavirus pulmonary syndrome	3	0.00	20	0.01	3	26
Hemolytic uremic syndrome post-diarrheal	36	0.06	218	0.09	22	276
Hepatitis, Viral Disease†††						
Hepatitis A, acute	488	0.75	1,006	0.37	149	1,643
Hepatitis B, acute	337	0.52	1,586	0.59	289	2,212
Hepatitis B, perinatal infection	S	—	S	—	S	7
Hepatitis C, acute						
Confirmed	738	1.18	3,318	1.26	908	4,964
Probable	46	0.07	441	0.17	87	574
Total	784	1.25	3,759	1.42	995	5,538
Hepatitis C, perinatal infection	10	NC	157	NC	68	235
Human immunodeficiency virus diagnoses	13,035	19.99	25,815	9.57	—	38,850
Influenza-associated pediatric mortality	34	0.18	94	0.18	14	142
Invasive pneumococcal disease						
Age <5 years						
Confirmed	183	5.04	795	6.99	136	1,114
Probable	5	0.14	59	0.52	3	67
Total	188	5.18	854	7.51	139	1,181
All ages						

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Disease	Hispanic or Latino		Non-Hispanic/Latino		Ethnicity not stated	Total
	No.	Rate	No.	Rate	No.	No.
Confirmed	1,745	4.06	15,330	7.36	3,476	20,551
Probable	52	0.12	419	0.20	129	600
Total§§§	1,797	4.18	15,749	7.56	3,605	21,151
Legionellosis	707	1.08	6,267	2.32	1,127	8,101
Leptospirosis	6	0.01	59	0.03	29	94
Listeriosis¶¶¶						
Confirmed	147	0.23	691	0.26	96	934
Probable	18	0.03	34	0.01	12	64
Total	165	0.25	725	0.27	108	998
Lyme disease####						
Confirmed	88	0.14	2,377	0.89	1,065	3,530
Probable	1,602	2.46	32,655	12.17	51,681	85,938
Total	1,690	2.60	35,032	13.05	52,746	89,468
Malaria	264	0.40	1,847	0.68	495	2,606
Measles****						
Imported	—	—	16	0.01	6	22
Indigenous	3	0.00	34	0.01	5	42
Total	3	0.00	50	0.02	11	64
Melioidosis++++	S	S	S	S	S	6
Meningococcal disease						
All serogroups	91	0.14	323	0.12	24	438
Other serogroups	11	0.02	22	0.01	—	33
Serogroup B	7	0.01	35	0.01	2	44
Serogroups ACWY	52	0.08	196	0.07	12	260
Unknown serogroup	21	0.03	70	0.03	10	101
Mpox	512	0.79	1,074	0.40	144	1,730
Mumps	87	0.13	266	0.10	80	433
Novel Influenza A virus infections	S	S	S	S	S	3
Pertussis	923	1.42	4,720	1.75	1,420	7,063
Plague+++	S	S	S	S	S	2
Poliomyelitis, paralytic	—	—	—	—	—	—
Poliovirus infection, nonparalytic	—	—	—	—	—	—
Psittacosis	S	S	S	S	S	1
Q fever						
Acute	34	0.05	112	0.04	35	181
Chronic	4	0.01	24	0.01	10	38
Total	38	0.06	136	0.05	45	219
Rabies						
Human	—	—	—	—	—	—
Rubella	S	S	S	S	S	11
Rubella, congenital syndrome	S	S	S	S	S	1
Salmonella Paratyphi infection§§§§	13	0.02	136	0.05	32	181
Salmonella Typhi infection¶¶¶¶	73	0.11	378	0.14	84	535
Salmonellosis (excluding <i>S. Typhi</i> infection and <i>S. Paratyphi</i> infection)#####	10,999	16.87	39,404	14.61	10,531	60,934
Severe acute respiratory syndrome-associated coronavirus disease	—	—	—	—	—	—
Shiga toxin-producing <i>Escherichia coli</i> (STEC)	3,985	6.11	11,853	4.39	3,006	18,844
Shigellosis	5,231	8.02	11,999	4.45	4,539	21,769
Smallpox	—	—	—	—	—	—

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Disease	Hispanic or Latino		Non-Hispanic/Latino		Ethnicity not stated	Total
	No.	Rate	No.	Rate	No.	No.
Spotted fever rickettsiosis						
Confirmed	6	0.01	40	0.01	10	56
Probable	32	0.05	807	0.30	309	1,148
Total	38	0.06	847	0.32	319	1,204
Streptococcal toxic shock syndrome	96	0.34	728	0.39	67	891
Syphilis						
Congenital*****	1,172	116.78	2,529	95.61	181	3,882
Primary and secondary	10,997	16.86	37,416	13.87	4,575	52,988
Total++++	55,606	85.27	130,972	48.56	22,541	209,119
Tetanus	S	S	S	S	S	18
Toxic shock syndrome (other than Streptococcal)	3	0.01	22	0.01	14	39
Trichinellosis	S	S	S	S	S	1
Tuberculosis	3,546	5.44	6,043	2.24	44	9,633
Tularemia	12	0.02	152	0.06	32	196
Vancomycin-intermediate <i>Staphylococcus aureus</i>	3	0.01	46	0.02	10	59
Vancomycin-resistant <i>Staphylococcus aureus</i> ++++	S	S	S	S	S	1
Varicella morbidity§§§§§	2,415	4.22	3,158	1.42	1,323	6,896
Varicella mortality	U	U	U	U	U	U
Vibriosis						
Confirmed	181	0.28	1,091	0.41	270	1,542
Probable	274	0.42	1,192	0.45	414	1,880
Total	455	0.70	2,283	0.86	684	3,422
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¶¶¶¶¶	—	—	—	—	—	—
Zika virus disease, non-congenital	S	S	S	S	S	6
Zika virus infection, congenital¶¶¶¶¶	—	—	—	—	—	—
Zika virus infection, non-congenital	S	S	S	S	S	1

—: 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 ethnicity.

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

‡ Delaware was unable to provide race and ethnicity data for COVID-19 cases; therefore, these cases have been categorized as 'Race not stated' and 'Ethnicity not stated' in Tables 6 and 7.

§ Delaware identified an issue that prevented the correct assignment of ethnicity values within their surveillance system for certain conditions included in the 2023 NNDSS annual tables. As a result, case counts for chronic hepatitis B virus infection, *Haemophilus influenzae*, varicella morbidity, and invasive pneumococcal disease were re-assigned to 'Ethnicity not stated' in Table 7.¶ Connecticut identified an issue that prevented the correct assignment of ethnicity values in case notifications to the CDC for the 2023 NNDSS annual tables, specifically affecting case counts for sexually transmitted diseases, including chancroid, *chlamydia trachomatis* infection, gonorrhea, and all stages of syphilis, which were re-assigned to 'Ethnicity not stated' in Table 7.# Beginning in 2023, only confirmed cases of *Candida auris* clinical are published to align with CSTE position statement 22-ID-05, whereas in previous years, confirmed and probable case classification statuses were published. 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 2023, *Candida auris* screening was added as a nationally notifiable condition, and confirmed cases are published to align with the approved CSTE position statement 22-ID-05.Additionally, there may be case count discrepancies of *Candida auris* screening 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 2023, cases began to be reported as carbapenemase-producing organisms, clinical or carbapenemase-producing organisms, screening. In previous years, only carbapenemase-producing carbapenem-resistant *Enterobacteriaceae* (CP-CRE) cases were reported.

‡ CPO total is the sum of CP-CRE cases reported in MMWR year 2023, CPO, clinical cases, and CPO, screening cases.

§§ For coccidioidomycosis surveillance reporting purposes, jurisdictions are grouped into high- and low-incidence categories. Probable cases are only reported from low-incidence jurisdictions, while confirmed cases are reported from both high- and low-incidence jurisdictions.

††† Of the reporting areas that submitted 2023 aggregate COVID-19 data to CDC, four did not submit probable cases. American Samoa, Commonwealth of Northern Mariana Islands, New York (excluding New York City), and U.S. Virgin Islands did not collect probable cases.

Counts include confirmed and probable dengue cases.

*** Beginning in 2023, confirmed and probable cases of gonorrhea are published to align with the approved CSTE position statement 22-ID-03, 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.

††† 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, 2023, published online by CDC's Division of Viral Hepatitis, available at <https://www.cdc.gov/hepatitis/php/statistics-surveillance/>.

§§§ 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 Lyme 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.

†††† Beginning in 2023, melioidosis was added as a nationally notifiable condition, and confirmed and probable cases are published to align with the approved CSTE position statement 22-ID-08.

†††† 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.

***** 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.

††††† Includes the following categories: primary; secondary; early non-primary non-secondary; unknown duration or late; and congenital syphilis.

††††† 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 2023.

§§§§§ Beginning in 2023, varicella mortality will have an age restriction of <50 years applied to the numerator (i.e., case counts).

†††††† 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 2023 annual tables were officially closed on November 7, 2024.

2. The list of national notifiable infectious diseases and conditions for 2023 and their national surveillance case definitions are available by navigating to the [Surveillance Case Definitions | CDC](#) web page, selecting "2023" for the notifiable condition list year, checking "Infectious" conditions, and clicking "Get Notifiable List by Year". Publication criteria for the finalized 2023 data are available at <https://www.cdc.gov/nndss/infectious-disease/notice-to-data-users.html>. See also [Guide to Interpreting Provisional and Finalized NNDSS Data](#).

3. Population estimates for incidence rates are July 1st, 2023 postcensal estimates of the resident population of the United States for July 1, 2020, to July 1, 2023, 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 2023" population estimates for years 2020–2023 were released February 2025 by the National Cancer Institute at <https://seer.cancer.gov/popdata/>. For more information, see <https://seer.cancer.gov/popdata/singleages.html>. 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's NNDSS Annual Summary Data Query](#).

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 "Resource Type Specific" section on the left-hand side and select "Annual Reports" (1952–2015) or "Annual Tables" (2016–present).

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 in numerator is ≤24 months; however, rates will not be calculated due to population estimates not being available for the specific sub-population required to align with the defined age restriction criteria)

Perinatal hepatitis C infection (age restriction in numerator is ≤36 months; however, rates will not be calculated due to population estimates not being available for the specific sub-population required to align with the defined age restriction criteria).

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 2023 (National Center for Health Statistics [Natality 2023](#), 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).

Suggested Citation:

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