

TABLE 6. Annual reported cases of notifiable diseases and rates, by race*,†,§, United States, excluding U.S. Territories and Non-U.S. Residents, 2020

Data from some reporting areas may be incomplete due to the coronavirus disease 2019 (COVID-19) pandemic or due to post-reconciliation data updates that could not be confirmed or included in the final data set. Please see Note #9 and Note #10, respectively.

(Accessible Version: <https://wonder.cdc.gov/nndss/static/2020/annual/2020-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	No.	No.	No.
Total	54	1.10	84	0.37	581	1.23	5,265	2.06	438	1,226	7,648
Confirmed	40	0.82	65	0.29	457	0.97	3,957	1.55	356	986	5,861
Probable	14	0.29	19	0.08	124	0.26	1,308	0.51	82	240	1,787
Cyclosporiasis	19	0.45	20	0.09	95	0.22	1,843	0.80	143	569	2,689
Dengue virus infections §§											
Dengue	—	—	25	0.11	17	0.04	263	0.10	55	81	441
Dengue-like illness	S	S	S	S	S	S	S	S	S	S	9
Severe dengue	—	—	—	—	—	—	—	—	—	—	—
Diphtheria	S	S	S	S	S	S	S	S	S	S	1
Ehrlichiosis and Anaplasmosis											
<i>Anaplasma phagocytophilum</i> infection	10	0.23	16	0.08	18	0.04	2,386	0.97	156	1,051	3,637
<i>Ehrlichia chaffeensis</i> infection	1	0.02	15	0.07	36	0.08	838	0.34	56	232	1,178
<i>Ehrlichia ewingii</i> infection	S	S	S	S	S	S	S	S	S	S	21
Undetermined ehrlichiosis/anaplasmosis	—	—	—	—	2	0.00	37	0.02	1	10	50
Giardiasis	74	1.96	193	1.01	568	1.59	5,214	2.61	1,116	2,288	9,453
Gonorrhea	8,923	182.12	7,398	33.01	274,869	582.58	186,552	73.16	42,432	157,577	677,751
<i>Haemophilus influenzae</i> , invasive disease											
All ages, all serotypes	36	0.73	30	0.13	470	1.00	1,905	0.75	132	423	2,996
Age <5 years											
Serotype b	S	S	S	S	S	S	S	S	S	S	15
Non-b serotype	4	0.97	—	—	15	0.44	41	0.29	2	14	76
Nontypeable	3	0.72	—	—	23	0.67	53	0.38	7	18	104
Unknown serotype	2	0.04	2	0.01	20	0.04	73	0.03	8	16	121
Hansen's disease	—	—	16	0.08	3	0.01	30	0.01	6	13	68
Hantavirus infection, non-hantavirus pulmonary syndrome ¶¶	S	S	S	S	S	S	S	S	S	S	2
Hantavirus pulmonary syndrome	S	S	S	S	S	S	S	S	S	S	14
Hemolytic uremic syndrome post-diarrheal	2	0.04	5	0.02	7	0.01	124	0.05	12	17	167
Hepatitis, Viral Disease ***											
Hepatitis A	60	1.22	96	0.43	703	1.49	8,022	3.15	302	763	9,946
Hepatitis B											
Acute	10	0.20	52	0.23	317	0.68	1,485	0.59	110	181	2,155
Perinatal infection	S	S	S	S	S	S	S	S	S	S	10
Hepatitis C											
Acute	66	1.52	89	0.41	553	1.20	4,261	1.72	331	725	6,025
Confirmed	51	1.18	78	0.36	473	1.02	3,290	1.33	291	615	4,798
Probable	15	0.35	11	0.05	80	0.17	971	0.39	40	110	1,227
Perinatal infection	—	—	3	0.40	5	0.27	109	1.48	11	37	165
Human immunodeficiency virus diagnoses	164	3.35	571	2.55	11,011	23.34	6,653	2.61	6,608	—	25,007
Influenza-associated pediatric mortality	5	0.35	14	0.28	32	0.26	98	0.18	1	21	171
Invasive pneumococcal disease †††											
All ages	265	8.66	160	1.23	1,884	4.85	6,931	3.63	476	2,230	11,946
Confirmed	252	8.24	160	1.23	1,863	4.80	6,813	3.56	464	2,166	11,718
Probable	13	0.42	—	—	21	0.05	118	0.06	12	64	228
Age <5 years	12	0.33	14	0.10	103	0.25	294	0.14	31	107	561
Confirmed	11	3.56	14	1.54	101	3.37	276	2.44	30	104	536
Probable	1	0.32	—	—	2	0.07	18	0.16	1	3	25

TABLE 6. Annual reported cases of notifiable diseases and rates, by race*,†,§, United States, excluding U.S. Territories and Non-U.S. Residents, 2020

Data from some reporting areas may be incomplete due to the coronavirus disease 2019 (COVID-19) pandemic or due to post-reconciliation data updates that could not be confirmed or included in the final data set. Please see Note #9 and Note #10, respectively.

(Accessible Version: <https://wonder.cdc.gov/nndss/static/2020/annual/2020-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	No.	No.	No.
Legionellosis §§§	22	0.45	87	0.39	1,297	2.75	3,970	1.56	444	490	6,310
Leptospirosis	—	—	4	0.02	2	0.01	28	0.01	8	9	51
Listeriosis ¶¶¶¶											
Total	6	0.12	56	0.25	61	0.13	499	0.20	76	82	780
Confirmed	6	0.12	53	0.24	58	0.12	488	0.19	71	78	754
Probable	—	—	3	0.01	3	0.01	11	0.00	5	4	26
Lyme disease											
Total	22	0.45	132	0.61	167	0.35	9,785	3.84	325	7,569	18,000
Confirmed	11	0.22	73	0.34	96	0.20	6,528	2.56	218	5,197	12,123
Probable	11	0.22	59	0.27	71	0.15	3,257	1.28	107	2,372	5,877
Malaria	—	—	22	0.10	371	0.79	80	0.03	57	73	603
Measles ****											
Total	S	S	S	S	S	S	S	S	S	S	12
Indigenous	S	S	S	S	S	S	S	S	S	S	6
Imported	S	S	S	S	S	S	S	S	S	S	6
Meningococcal disease											
All serogroups	3	0.06	2	0.01	57	0.12	126	0.05	16	38	242
Serogroups ACWY	1	0.02	1	0.00	20	0.04	44	0.02	8	6	80
Serogroup B	1	0.02	—	—	6	0.01	23	0.01	2	8	40
Other serogroups	—	—	—	—	4	0.01	11	0.00	—	1	16
Unknown serogroup	1	0.02	1	0.00	27	0.06	48	0.02	6	23	106
Mumps	3	0.06	55	0.25	40	0.08	323	0.13	30	243	694
Novel Influenza A virus infections	—	—	—	—	—	—	—	—	—	—	—
Pertussis	37	0.76	110	0.49	299	0.63	3,924	1.54	270	1,484	6,124
Plague ****	S	S	S	S	S	S	S	S	S	S	9
Poliomyelitis, paralytic	—	—	—	—	—	—	—	—	—	—	—
Poliovirus infection, nonparalytic	—	—	—	—	—	—	—	—	—	—	—
Psittacosis	S	S	S	S	S	S	S	S	S	S	8
Q fever											
Total	—	—	4	0.02	3	0.01	80	0.03	16	17	120
Acute	—	—	3	0.01	2	0.00	59	0.02	13	13	90
Chronic	—	—	1	0.00	1	0.00	21	0.01	3	4	30
Rabies											
Human	—	—	—	—	—	—	—	—	—	—	—
Rubella	S	S	S	S	S	S	S	S	S	S	6
Rubella, congenital syndrome	—	—	—	—	—	—	—	—	—	—	—
Salmonella Paratyphi infection §§§§	1	0.02	35	0.16	4	0.01	15	0.01	11	9	75
Salmonella Typhi infection ¶¶¶¶	1	0.02	89	0.40	9	0.02	25	0.01	45	13	182
Salmonellosis (excluding S. Typhi infection and S. Paratyphi infection) *****	338	6.90	1,079	4.81	4,079	8.65	28,331	11.11	3,923	7,692	45,442
Severe acute respiratory syndrome-associated coronavirus disease	—	—	—	—	—	—	—	—	—	—	—
Shiga toxin-producing <i>Escherichia coli</i> (STEC)	82	1.67	269	1.20	540	1.14	6,693	2.62	945	1,393	9,922
Shigellosis	94	1.92	255	1.14	1,749	3.71	4,652	1.82	1,002	1,356	9,108
Smallpox	—	—	—	—	—	—	—	—	—	—	—
Spotted fever rickettsiosis											
Total	45	0.94	8	0.04	30	0.06	812	0.32	26	254	1,175
Confirmed	2	0.04	—	—	2	0.00	39	0.02	2	19	64
Probable	43	0.90	8	0.04	28	0.06	773	0.30	24	235	1,111

TABLE 6. Annual reported cases of notifiable diseases and rates, by race*,†,§, United States, excluding U.S. Territories and Non-U.S. Residents, 2020

Data from some reporting areas may be incomplete due to the coronavirus disease 2019 (COVID-19) pandemic or due to post-reconciliation data updates that could not be confirmed or included in the final data set. Please see Note #9 and Note #10, respectively.

(Accessible Version: <https://wonder.cdc.gov/nndss/static/2020/annual/2020-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	No.	No.	No.
Streptococcal toxic shock syndrome	2	0.07	3	0.03	24	0.07	162	0.10	9	24	224
Syphilis											
Total, all stages ****	2,067	42.19	3,080	13.74	44,871	95.10	59,236	23.23	12,154	12,525	133,933
Congenital §§§§§	63	150.90	34	12.11	765	120.54	1,034	37.06	94	158	2,148
Primary and secondary	712	14.53	1,029	4.59	14,180	30.05	19,039	7.47	3,467	3,227	41,654
Tetanus	S	S	S	S	S	S	S	S	S	S	17
Toxic shock syndrome (other than Streptococcal)	S	S	S	S	S	S	S	S	S	S	24
Trichinellosis	—	—	—	—	—	—	—	—	—	—	—
Tuberculosis	93	1.90	2,590	11.56	1,456	3.09	2,772	1.09	161	102	7,174
Tularemia	18	0.37	2	0.01	4	0.01	87	0.03	8	31	150
Vancomycin-intermediate <i>Staphylococcus aureus</i>	—	—	1	0.01	8	0.02	24	0.01	6	6	45
Vancomycin-resistant <i>Staphylococcus aureus</i> ¶¶¶¶¶	S	S	S	S	S	S	S	S	S	S	1
Varicella morbidity	22	0.57	199	1.02	238	0.58	1,462	0.68	229	777	2,927
Varicella mortality	U	U	U	U	U	U	U	U	U	U	U
Vibriosis											
Total	9	0.19	85	0.38	165	0.35	1,131	0.45	162	300	1,852
Confirmed	6	0.12	46	0.21	82	0.17	714	0.29	109	176	1,133
Probable	3	0.06	39	0.18	83	0.18	417	0.17	53	124	719
Viral hemorrhagic fevers											
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	S	S	S	S	S	4
Zika virus infection, congenital *****	—	—	—	—	—	—	—	—	—	—	—
Zika virus infection, non-congenital	S	S	S	S	S	S	S	S	S	S	19

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

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.

** *Candida auris* colonization/screening cases are not included in this table. These data are available on the Mycotic Diseases Branch's Tracking *Candida auris* page (<https://www.cdc.gov/fungal/candida-auris/tracking-c-auris.html>)

†† Please see Note #11.

§§ 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, 2020, 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.

§§§ In 2020, the CSTE case definition changed such that cases diagnosed by PCR were classified as confirmed, whereas previously those cases were classified as suspect and did not meet the publication/print criteria.

¶¶¶ 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.

**** 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 2020, confirmed and probable plague cases are being combined and published. In 2019, only confirmed plague cases were 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 2020.

***** 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 2020 annual tables were officially closed on September 27, 2022.
2. The list of national notifiable Infectious diseases and conditions for 2020 and their national surveillance case definitions are available by navigating to the [Surveillance Case Definitions | CDC](#) web page, selecting "2020" for the notifiable condition list year, checking "Infectious" conditions, and clicking "Get Notifiable List by Year". This list incorporates the Council of State and Territorial Epidemiologists (CSTE) position statements approved in 2019 by CSTE for national surveillance that were implemented in January 2020. Revised case definitions were implemented for the following conditions: plague, legionellosis, acute hepatitis C, spotted fever rickettsiosis, and pertussis. In addition, CSTE adopted the first coronavirus disease 2019 (COVID-19) national surveillance case definition on April 5, 2020, and they approved a revision to the COVID-19 national surveillance case definition, effective August 5, 2020. Publication criteria for the finalized 2020 data are available at https://wonder.cdc.gov/nndss/documents/2020_NNDSS_Publication_Criteria_03162022.pdf. See also [Guide to Interpreting Provisional and Finalized NNDSS Data](#).
3. Population estimates for incidence rates are July 1st, 2020, estimates obtained from the National Center for Health Statistics (NCHS) postcensal estimates of the resident population of the United States for April 1, 2010, to July 1, 2020, by year, county, single year of age (range: 0 to 85 years), bridged-race (white, black or African American, American Indian or Alaska Native, Asian, or Pacific Islander), Hispanic ethnicity (not Hispanic or Latino, Hispanic or Latino), and sex (Vintage 2020), prepared under a collaborative arrangement with the U.S. Census Bureau. Population estimates for states released September 21, 2021, are available at https://www.cdc.gov/nchs/nvss/bridged_race/data_documentation.htm. Population estimates for territories are the 2020 mid-year estimates from the U.S. Census Bureau International Data Base, accessed on March 15, 2022, 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](#) (once in CDC Stacks, select "Annual Reports" in the "Genre" box to the left).
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, denominator is <24 months)
- Perinatal hepatitis C infection (age restriction in numerator is ≤36 months, denominator 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 2020 (National Center for Health Statistics [Natality 2020](#), 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. The following reporting areas may have incomplete data, due to technical or programmatic challenges while reconciling data during the COVID-19 pandemic: California, Guam, and Minnesota.

10. The following reporting areas may have incomplete data due to updates made to their data after the 2020 reconciliation period ended and there was not sufficient time before publication of the annual tables to confirm the updated counts: Idaho, Kansas, Maryland, Vermont, and Virgin Islands.
11. Of the reporting areas that submitted 2020 aggregate COVID-19 data to CDC, three did not submit probable cases. New York (excluding New York City) and Utah did not collect probable cases. U.S. Virgin Islands collected probable cases, but did not report them to CDC.
12. Disease data presented in the 2020 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, 2020 Annual Tables of Infectious Disease Data. Atlanta, GA. CDC Division of Health Informatics and Surveillance, 2023. 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](#)