TABLE 7. Annual reported cases of notifiable diseases and rates, by ethnicity*,[†], 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.

Eastern equine encephalitic virus disease S	Disease		Hispanic or Latino		ı- ′Latino	Ethnicity not stated	Total
Arboviral diseases Image: Comment of the		No.	Rate	No.	Rate	No.	No.
Chikungunya virus disease	Anthrax	S	S	S	S	S	1
Eastern equine encephalitis virus disease	Arboviral diseases						
Neuroinvasive	Chikungunya virus disease	5	0.01	15	0.01	17	37
Non-neuroliviaskive S	Eastern equine encephalitis virus disease						
Jamestown Canyon virus disease	Neuroinvasive	S	S	S	S	S	13
Neuroinvasive	Non-neuroinvasive	_	_	_	_	_	_
Non-neuroinvasive	Jamestown Canyon virus disease						
La Crosse virus disease	Neuroinvasive	S	S	S	S	S	10
Neuroinvasive 6 0.01 47 0.02 31 1 Non-neuroinvasive 5	Non-neuroinvasive	S	S	S	S	S	3
Non-neuroinvasive S S S S C Powssan virus disease I	La Crosse virus disease						
Neuroinvasive	Neuroinvasive	6	0.01	47	0.02	31	84
Neuroinvasive	Non-neuroinvasive	S	S	S	S	S	4
Non-neuroinvasive S	Powassan virus disease						
St. Louis encephalitis virus disease Image: Continuation of the probability of the prob	Neuroinvasive	S	S	S	S	S	19
Neuroinvasive S <	Non-neuroinvasive	S	S	S	S	S	,
Neuroinvasive S <	St. Louis encephalitis virus disease						
West Nile virus disease Image: Control of the control of	Neuroinvasive	S	S	S	S	S	14
Neuroinvasive 114 0.19 3.45 0.13 3.99 5.55 Non-neuroinvasive 19 0.03 102 0.04 5.11 1.11 Western equine encephalitis virus disease 10 10 10 10 10 Non-neuroinvasive 10 10 10 10 10 10 Babesiosis 10 10 10 10 10 10 10 Total 10 10 10 10 10 10 10 1	Non-neuroinvasive	S	S	S	S	S	2
Non-neuroinvasive 19 0.03 102 0.04 51 11	West Nile virus disease						
Western equine encephalitis virus disease Image: Composition of the properties o	Neuroinvasive	114	0.19	345	0.13	99	558
Neuroinvasive	Non-neuroinvasive	19	0.03	102	0.04	51	172
Neuroinvasive	Western equine encephalitis virus disease						
Babesiosis Image: Confirmed of the probable of the pro		_	_	_	_	_	_
Babesiosis Image: Confirmed of the probable of the pro	Non-neuroinvasive	_	_	_	_	_	_
Total 83 0.15 965 0.42 772 1,83 Confirmed 74 0.13 865 0.38 692 1,66 Probable 9 0.02 100 0.04 80 11 Botulism 9 0.02 100 0.04 46 11 Total 39 0.06 104 0.04 46 11 Foodborne 1 5 5 5 5 1 Infant 29 2.99 82 2.97 35 1 Other (wound & unspecified) 9 0.01 17 0.01 9 1 Brucellosis 37 0.06 31 0.01 19 2 Gampylobacteriosis 6,240 10.18 29,425 10.97 16,099 51,76 Carbapenemase-producing carbapenem-resistant Enterobacteriaceae 8 0.16 837 0.34 92 1,88 Chalamydia trachomatis infection 188,936							
Confirmed 74 0.13 865 0.38 692 1,65 Probable 9 0.02 100 0.04 80 18 Botulism 9 0.02 100 0.04 40 18 Total 39 0.06 104 0.04 46 18 Foodborne \$		83	0.15	965	0.42	772	1,820
Probable 9 0.02 100 0.04 80 11 Botulism							1,631
Botulism Image: Continue of the contin							189
Total 39 0.06 104 0.04 46 11 Foodborne S S S S S S S Infant 29 2.99 82 2.97 35 14 Other (wound & unspecified) 9 0.01 17 0.01 9 3 Brucellosis 37 0.06 31 0.01 19 3 Campylobacteriosis 6,240 10.18 29,425 10.97 16,099 51,76 Candida auris, clinical § 20 0.04 140 0.06 95 22 Carbapenemase-producing carbapenem-resistant Enterobacteriaceae 86 0.16 837 0.34 925 1,88 Chancroid ————————————————————————————————————			0.02		0.0 .		
Foodborne		39	0.06	104	0.04	46	189
Infant				_			8
Other (wound & unspecified) 9 0.01 17 0.01 9 3 Brucellosis 37 0.06 31 0.01 19 3 Campylobacteriosis 6,240 10.18 29,425 10.97 16,099 51,70 Candida auris, clinical § 20 0.04 140 0.06 95 25 Carbapenemase-producing carbapenem-resistant Enterobacteriaceae 86 0.16 837 0.34 925 1,86 Chancroid — <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>146</td>							146
Brucellosis 37 0.06 31 0.01 19 38 Campylobacteriosis 6,240 10.18 29,425 10.97 16,099 51,76 Candida auris, clinical [§] 20 0.04 140 0.06 95 25 Carbapenemase-producing carbapenem-resistant Enterobacteriaceae 86 0.16 837 0.34 925 1,86 Chancroid — </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>35</td>							35
Campylobacteriosis 6,240 10.18 29,425 10.97 16,099 51,70 Candida auris, clinical § 20 0.04 140 0.06 95 25 Carbapenemase-producing carbapenem-resistant Enterobacteriaceae 86 0.16 837 0.34 925 1,8 Chancroid —	•						87
Candida auris, clinical § 20 0.04 140 0.06 95 25 Carbapenemase-producing carbapenem-resistant Enterobacteriaceae 86 0.16 837 0.34 925 1,86 Chancroid — <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>							
Carbapenemase-producing carbapenem-resistant Enterobacteriaceae 86 0.16 837 0.34 925 1,84 Chancroid −							255
Enterobacteriaceae	·	20	0.0 1	1.10	0.00		25.
Chancroid —		86	0.16	837	0.34	925	1,848
Chlamydia trachomatis infection 188,936 308.15 762,201 284.22 628,700 1,579,83 Cholera S		_	_	_	_	_	_
Cholera S S S S S Coccidioidomycosis 2,663 10.18 5,400 4.73 11,157 19,23 Coronavirus Disease 2019 (COVID-19) ————————————————————————————————————		188.936	308.15	762.201	284.22	628.700	1,579,837
Coccidioidomycosis 2,663 10.18 5,400 4.73 11,157 19,22 Coronavirus Disease 2019 (COVID-19)							1
Coronavirus Disease 2019 (COVID-19) 4,233,166 6,904.20 10,493,416 3,912.95 6,423,149 21,149,73 Confirmed 3,983,486 6,496.98 9,362,160 3,491.11 5,833,710 19,179,33 Probable ¶ 249,680 407.22 1,131,256 421.84 589,439 1,970,33 Cryptosporidiosis 572 0.93 5,088 1.90 1,988 7,64 Confirmed 458 0.75 3,831 1.43 1,572 5,88							19,220
Total 4,233,166 6,904.20 10,493,416 3,912.95 6,423,149 21,149,73 Confirmed 3,983,486 6,496,98 9,362,160 3,491.11 5,833,710 19,179,33 Probable ¶ 249,680 407.22 1,131,256 421.84 589,439 1,970,33 Cryptosporidiosis 572 0.93 5,088 1.90 1,988 7,64 Confirmed 458 0.75 3,831 1.43 1,572 5,88	-	_,565		2, .30		,	-,
Confirmed 3,983,486 6,496.98 9,362,160 3,491.11 5,833,710 19,179,35 Probable ¶ 249,680 407.22 1,131,256 421.84 589,439 1,970,33 Cryptosporidiosis 572 0.93 5,088 1.90 1,988 7,64 Confirmed 458 0.75 3,831 1.43 1,572 5,88		4,233.166	6,904.20	10,493.416	3,912.95	6.423.149	21,149.731
Probable ¶ 249,680 407.22 1,131,256 421.84 589,439 1,970,33 Cryptosporidiosis 572 0.93 5,088 1.90 1,988 7,64 Confirmed 458 0.75 3,831 1.43 1,572 5,88							
Cryptosporidiosis 572 0.93 5,088 1.90 1,988 7,64 Confirmed 458 0.75 3,831 1.43 1,572 5,86							
Total 572 0.93 5,088 1.90 1,988 7,64 Confirmed 458 0.75 3,831 1.43 1,572 5,86		245,000	+07.22	1,131,230	721.04	JUJ-139	.,,,,,,,,
Confirmed 458 0.75 3,831 1.43 1,572 5,80		F73	0.03	E 000	1.00	1 000	7640
Uropanio	Probable	114	0.75	1,257	0.47	416	1,787

TABLE 7. Annual reported cases of notifiable diseases and rates, by ethnicity*,[†], 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.

	Hispanic or Latino		Non- Hispanic/Latino		Ethnicity not stated	Total
Disease	No.	Rate	No.	Rate	No.	No.
Cyclosporiasis	194	0.33	1,688	0.70	807	2,689
Dengue virus infections **						
Dengue	183	0.30	168	0.06	90	441
Dengue-like illness	S	S	S	S	S	9
Severe dengue	_	_	_	_	_	_
Diphtheria	S	S	S	S	S	1
Ehrlichiosis and Anaplasmosis						
Anaplasma phagocytophilum infection	51	0.09	2,128	0.82	1,458	3,637
Ehrlichia chaffeensis infection	23	0.04	867	0.33	288	1,178
Ehrlichia ewingii infection	S	S	S	S	S	21
Undetermined ehrlichiosis/anaplasmosis	2	0.00	38	0.01	10	50
Giardiasis	650	1.44	5,108	2.40	3,695	9,453
Gonorrhea	73,313	119.57	400,347	149.29	204,091	677,751
Haemophilus influenzae, invasive disease					·	
All ages, all serotypes	225	0.37	2,073	0.77	698	2,996
Age <5 years			, , ,			,
Serotype b	S	S	S	S	S	15
Non-b serotype	3	0.06	56	0.39	17	76
Nontypeable	20	0.40	54	0.38	30	104
Unknown serotype	27	0.04	69	0.03	25	121
Hansen's disease	5	0.01	45	0.02	18	68
Hantavirus infection, non-hantavirus pulmonary syndrome ^{††}	S	S	S	S	S	2
	S	S		S	S	14
Hantavirus pulmonary syndrome			S		27	167
Hemolytic uremic syndrome post-diarrheal	18	0.03	122	0.05	27	107
Hepatitis, Viral Disease ^{§§}						
Hepatitis A	386	0.63	8,031	2.99	1,529	9,946
Hepatitis B						
Acute	155	0.25	1,624	0.61	376	2,155
Perinatal infection	S	S	S	S	S	10
Hepatitis C						
Acute	485	0.83	4,302	1.65	1,238	6,025
Confirmed	415	0.71	3,390	1.30	993	4,798
Probable	70	0.12	912	0.35	245	1,227
Perinatal infection	7	0.29	95	1.22	63	165
Human immunodeficiency virus diagnoses	6,141	10.02	18,866	7.04	_	25,007
Influenza-associated pediatric mortality	32	0.17	118	0.22	21	171
Invasive pneumococcal disease ¶¶						
All ages	836	2.09	7,953	3.86	3,157	11,946
Confirmed	816	2.04	7,820	3.80	3,082	11,718
Probable	20	0.05	133	0.06	75	228
Age <5 years	77	0.18	357	0.16	127	561
Confirmed	76	2.13	339	2.83	121	536
Probable	1	0.03	18	0.15	6	25
Legionellosis ***	440	0.72	4,578	1.71	1,292	6,310
Leptospirosis	3	0.01	29	0.01	19	51
Listeriosis ***						
Total	99	0.16	551	0.21	130	780
Confirmed	92	0.15	538	0.20	124	754
Probable	7	0.13	13	0.20	6	26
Lyme disease	,	3.51	.5	5.55		
Total	370	0.60	8,742	3.28	8,888	18,000
Confirmed	247	0.40		2.13	6,189	12,123

TABLE 7. Annual reported cases of notifiable diseases and rates, by ethnicity*,[†], 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.

	Hispanic or Latino		Non- Hispanic/Latino		Ethnicity not stated	Total
Disease	No.	Rate	No.	Rate	No.	No.
Probable	123	0.20	3,055	1.14	2,699	5,877
Malaria	6	0.01	437	0.16	160	603
Measles §§§						
Total	S	S	S	S	S	12
Indigenous	S	S	S	S	S	6
Imported	S	S	S	S	S	6
Meningococcal disease						
All serogroups	44	0.07	156	0.06	42	242
Serogroups ACWY	23	0.04	48	0.02	9	80
Serogroup B	3	0.00	28	0.01	9	40
Other serogroups	3	0.00	11	0.00	2	16
Unknown serogroup	15	0.02	69	0.03	22	106
Mumps	101	0.16	334	0.12	259	694
Novel Influenza A virus infections	_	_	_	_	_	_
Pertussis	861	1.40	3,639	1.36	1,624	6,124
Plague ¶¶¶	S	S	S	S	S	9
Poliomyelitis, paralytic	_	_	_	_	_	_
Poliovirus infection, nonparalytic	_	_	_	_	_	
Psittacosis	S	S	S	S	S	8
Q fever						
Total	15	0.02	73	0.03	32	120
Acute	12	0.02	52	0.02	26	90
Chronic	3	0.00	21	0.01	6	30
Rabies						
Human	_	_	_	_	_	
Rubella	S	S	S	S	S	6
Rubella, congenital syndrome	_	_	_	_	_	_
Salmonella Paratyphi infection ****	2	0.00	53	0.02	20	75
Salmonella Typhi infection ****	21	0.03	119	0.04	42	182
Salmonellosis (excluding <i>S.</i> Typhi infection and <i>S.</i> Paratyphi		0.03		0.01	12	102
infection) §§§§§	6,263	10.21	27,175	10.13	12,004	45,442
Severe acute respiratory syndrome-associated coronavirus disease	_	_	_	_	_	_
Shiga toxin-producing <i>Escherichia coli</i> (STEC)	1,367	2.23	6,316	2.36	2,239	9,922
Shigellosis	2,087	3.40	4,947	1.84	2,074	9,108
Smallpox	_	_	_		_	
Spotted fever rickettsiosis						
Total	26	0.04	841	0.32	308	1,175
Confirmed	5	0.01	44	0.02	15	64
Probable	21	0.03	797	0.30	293	1,111
Streptococcal toxic shock syndrome	20	0.08	161	0.09	43	224
Syphilis						
Total, all stages ¶¶¶¶	32,942	53.73	88,656	33.06	12,335	133,933
Congenital *****	637	69.64	1,395	48.24	116	2,148
Primary and secondary	8,421	13.73	29,718	11.08	3,515	41,654
Tetanus	S	S	S	S	S	17
Toxic shock syndrome (other than Streptococcal)	S	S	S	S	S	24
Trichinellosis						
Tuberculosis	2,133	3.48	5,030	1.88	11	7,174
Tularemia	4	0.01	106	0.04	40	150
Vancomycin-intermediate Staphylococcus aureus	4	0.01	36	0.02	5	45
Vancomycin-resistant <i>Staphylococcus aureus</i> *****	S	S	S	S	S	1

TABLE 7. Annual reported cases of notifiable diseases and rates, by ethnicity*,[†], 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.

		Hispanic or Latino		ı- 'Latino	Ethnicity not stated	Total
Disease	No.	Rate	No.	Rate	No.	No.
Varicella morbidity	531	0.96	1,665	0.74	731	2,927
Varicella mortality	U	U	U	U	U	U
Vibriosis						
Total	199	0.33	1,168	0.44	485	1,852
Confirmed	110	0.18	740	0.28	283	1,133
Probable	89	0.15	428	0.16	202	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	4
Zika virus infection, congenital ^{§§§§§}	_	_	_	_	_	_
Zika virus infection, non-congenital	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 ethnicity.
- † 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.
- § 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).

- 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 \leq 36 months, denominator is \leq 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.