



PulseNet 2.0 Reference Guide



Overview of Allele Databases and Genotyping Tools

The tables below show the current allele schemes and genotyping tools used within each organism database in PulseNet 2.0.

Coming soon: *C. botulinum*, *Cronobacter*, *Yersinia*

	<i>Escherichia</i>	<i>Salmonella</i>	<i>Listeria</i>	<i>Campylobacter</i>	<i>Vibrio</i>
Year WGS Database Online	2019	2019	2019	2019	2024
wgMLST Loci	34,453	25,365	4,804	6,651	40,260
cgMLST Loci	2,513 (Enterobase)	3,002 (Enterobase)	1,748 (Pasteur)	1,343 (Oxford) (jejuni/coli)	2,443 (<i>cholerae</i>); 2254 (para.)
MLST	Achtman	Achtman	BIGSdb-Pasteur	PubMLST	PubMLST
Genotyping Tools used in PulseNet 2.0	SerotypeFinder (KMA), AMRFinder, VirulenceFinder, PlasmidFinder	SeqSero2/ANI, AMRFinder, PlasmidFinder	AMRFinder, PlasmidFinder, Lineage/ANI	AMRFinder, PlasmidFinder	AMRFinder, Serogroup/toxin finder for <i>V. cholerae</i>
Surveillance Species	coli and Shigella	enterica, bongori	monocytogenes	coli, fetus, jejuni, lari, upsaliensis	cholerae, parahaemolyticus, vulnificus
NCBI PulseNet Bioproject	PRJNA218110	PRJNA230403	PRJNA212117	PRJNA239251	PRJNA266293

Genotyping Tools

SerotypeFinder (KMA):	Predicts serotypes in total or partial sequenced isolates of <i>E. coli</i>
AMRFinderplus:	Identifies acquired antibiotic resistance genes
VirulenceFinder:	Identifies acquired virulence genes
PlasmidFinder:	Identifies plasmids in total or partial sequenced isolates of bacteria
SeqSero2:	Predicts the <i>Salmonella</i> serotype of either the pre-assembled or raw read sequence data GitHub - denglab/SeqSero2: SeqSero2
ANI (Average Nucleotide Identity):	Uses a calculation for species identification

Contact Us

	www.cdc.gov/pulsenet
	PulseNet@cdc.gov
	1600 Clifton Rd NE Atlanta, GA, 30329