

Table 2. Distribution of *tet* resistance genes among Gram-negative bacteria Modified April 20, 2021

Originally modified from MMBR 2001; 65:232-260 with permission from ASM Journals [n=88 genera]

Efflux		Ribosomal Protection and/or Efflux and/or Enzymatic	
One Gene n=13	Two or More Genes n=9	One Gene n=14	Two or More Genes n=52
<i>Aggregatibacter</i> <i>tet</i> (B)	<i>Bordetella</i> <i>tet</i> (A)(C)(31) ^p	<i>Acidaminococcus</i> ^b <i>tet</i> (W)	<i>Acinetobacter</i> <i>tet</i> (A)(B)(C)(D) ^{ac} (G)(H)(L)(M)(O) ^{ac} (W) ^{ac} (X)(Y) ^z (39)
<i>Agrobacterium</i> <i>tet</i> (30)	<i>Mannheimia</i> <i>tet</i> (B)(G)(H)(L)	<i>Capnocytophaga</i> <i>tet</i> (Q)	<i>Aggregatibacter</i> ^{1.am} <i>tet</i> (B)(H)(L)(O)
<i>Alteromonas</i> <i>tet</i> (D)	<i>Moraxella</i> <i>tet</i> (B)(H)	<i>Comamonas</i> <i>tet</i> (X) ^u	<i>Aeromonas</i> <i>tet</i> (A)(B)(C)(D)(E)(G)(H)(L) ^{ab} (M)(O) ⁿ (T) ⁿ (Y)(31)(34)
<i>Bibersteinia</i> <i>tet</i> (H)	<i>Ochrobactrum</i> <i>tet</i> (A)(B) ^y (G)(L)	<i>Delftia</i> <i>tet</i> (X) ^u	<i>Anaerovibrio</i> ^b <i>tet</i> (O)(Q)
<i>Chlamydia</i> <i>tet</i> (C)	<i>Plesiomonas</i> <i>tet</i> (A)(B)(D)	<i>Eikenella</i> <i>tet</i> (M)	<i>Alcaligenes</i> <i>tet</i> (A)(E)(M) ^{aa} (30) ^{aa} (39) ^k (M) ^{aa}
<i>Erwinia</i> <i>tet</i> (B)	<i>Burkholderia</i> <i>tet</i> (D) ⁿ (O) ⁿ (64) ^{al}	<i>Epilithonimonas</i> <i>tet</i> (X)	<i>Bacteroides</i> ^b <i>tet</i> (M)(Q)(W)(X)(36)
<i>Gillamella</i> <i>tet</i> (H)	<i>Halomonas</i> <i>tet</i> (C)(D)(G)	<i>Hafnia</i> <i>tet</i> (M) ^j	<i>Brevundimonas</i> <i>tet</i> (B) ⁿ (D) ⁿ (G)(O) ⁿ (T) ⁿ (W) ⁿ (39) ^k
<i>Francisella</i> <i>tet</i> (C)	<i>Variovorax</i> <i>tet</i> (A)(L)	<i>Kingella</i> <i>tet</i> (M)	<i>Burkholderia</i> <i>tet</i> (D) ⁿ (O) ⁿ (64) ^{aj} (X) ^{an}
<i>Histophilus</i> ^e <i>tet</i> (H)	<i>Yersinia</i> <i>tet</i> (B)(D)	<i>Legionella</i> <i>tet</i> (56)	<i>Butyrivibrio</i> <i>tet</i> (O)(W)
<i>Laribacter</i> <i>tet</i> (A)		<i>Spingobacterium</i> <i>tet</i> (X) ^c	<i>Campylobacter</i> <i>tet</i> (O)(44) ^o
<i>Treponema</i> ^a <i>tet</i> (B)		<i>Wautersiella</i> <i>tet</i> (X) ^z	<i>Chryseobacterium</i> <i>tet</i> (A)(D) ^l (T) ^l (W) ^l (X) ^{an}
<i>Empedobacter</i> <i>tet</i> (X) ^{an}		<i>Ralstonia</i> <i>tet</i> (M)	<i>Citrobacter</i> <i>tet</i> (A)(B)(C)(D)(E)(L)(M)(O)(S)(W) ^j
<i>Picirickettsia</i> <i>tet</i> (31) ^{an}		<i>Dialister</i> <i>tet</i> (M) ^{ah}	<i>Edwardsiella</i> <i>tet</i> (A)(D)(M)
		<i>Raoultella</i> <i>tet</i> (X) ^{an}	<i>Enterobacter</i> <i>tet</i> (A)(B)(C)(D)(E)(G) ^j (L)(M)(39) ^k (X) ^u
			<i>Escherichia</i> (A)(B)(C)(D)(E)(G)(J)(L)(M)(W) ^j (Y)(X) ^u (32)(34) ^{ao}
			<i>Elizabethkingia</i> <i>tet</i> (W)(X) ^{an}
			<i>Flavobacterium</i> <i>tet</i> (A)(E)(L)(M)
			<i>Fusobacterium</i> ^b <i>tet</i> (G)(L)(M)(O)(Q)(W)
			<i>Gallibacterium</i> <i>tet</i> (B)(H)(K)(L)(31)(Y)(M) ^{ao}

<i>Haemophilus</i>	<i>tet</i> (B)(K)(M)
<i>Klebsiella</i>	<i>tet</i> (A)(B)(C)(D)(E) ^{aa} (L) ^{ab} (M)(S)(W) ^j (X) ^u
<i>Kurthia</i>	<i>tet</i> (L)(M)
<i>Lawsonia</i> ^f	<i>tet</i> (M)(W) ^f
<i>Megasphaera</i>	<i>tet</i> (O)(W)
<i>Mitsuokella</i>	<i>tet</i> (Q)(W)
<i>Morganella</i>	<i>tet</i> (A) ^{aa} (D)(J)(L)(M) ^{aa}
<i>Myroides</i>	<i>tet</i> (L)(X) ^{ab}
<i>Neisseria</i>	<i>tet</i> (B)(M)(O)(Q)(W)
<i>Pantoea</i>	<i>tet</i> (B)(M)
<i>Pasteurella</i>	<i>tet</i> (B)(D)(H)(G)(L)(M)(O) ^l
<i>Photobacterium</i>	<i>tet</i> (B)(D)(M)(Y)
<i>Porphyromonas</i> ^b	<i>tet</i> (Q)(W)
<i>Prevotella</i> ^b	<i>tet</i> (M)(Q)(W)
<i>Proteus</i>	<i>tet</i> (A)(B)(C)(E)(H)(G)(L)(J)(M) ^j (X)
<i>Providencia</i>	<i>tet</i> (B)(E)(G)(H)(J)(M) ^j (39) ^k (57) ^y
<i>Pseudoalteromonas</i>	<i>tet</i> (B) ^l (M) ^m
<i>Pseudomonas</i>	<i>tet</i> (A)(B)(C)(D) ⁿ (E)(G)(K)(L)(M)(O) ⁿ (T) ⁿ (W) ⁿ (X)(Y)(34)(39) ^x (42) ^h
<i>Psychrobacter</i>	<i>tet</i> (H) ⁱ (M) ^g (O)(39) ^x
<i>Rahnella</i>	<i>tet</i> (A)(L)(M)
<i>Rhizobium</i> ⁿ	<i>tet</i> (A) ^w (B)(D)(M)(O)(T)(W) ^w
<i>Riemerella</i>	<i>tet</i> (A)(B)(M)(O)(Q) ^{ad} (X) ^s
<i>Roseobacter</i>	<i>tet</i> (B)(C)(E)(G)(X) ^{ai}
<i>Salmonella</i>	<i>tet</i> (A)(B)(C)(D)(G)(L)(M)(X)(Y)
<i>Selenomonas</i> ^b	<i>tet</i> (M)(Q)(W)
<i>Serratia</i>	<i>tet</i> (A)(B)(C)(E)(M)(S) ^{ab} (X) ^w (34)(41)

Shewanella *tet(B)ⁿ(D)(G)(M)(O)ⁿ(T)ⁿ(W)ⁿ*
Shigella *tet(A)(B)(C)(D)(M)^j*
Sphingobacterium tet(X)^{an}
Stenotrophomonas tet(B)(H)^{ac}(M)ⁿ(O)ⁿ(T)ⁿ(35)(39)^k(X)^{an}
Subdolgranulum^b *tet(Q)(W)*
Veillonella^b *tet(A)(L)(M)(Q)(S)(W)*
Vibrio *tet(A)(B)(C)(D)(E)(G)(K)^l(L)(M)(X)(Y)(34)(35)*

Carrying Mosaic genes^d n=4

Campylobacter tet(O/32/O)^{af}
Megasphaera tet(O/W), tet(O/W/O)^q
Riemerella tet(O/W/32/O)^{ad}

Blue: new since last update

Some genera not listed that are found in Pathogen Detection Microbial Browser for Identification of Genetic and Genomic Elements (MicroBIGG-E)[<https://www.ncbi.nlm.nih.gov/pathogens/microbigge/>] Because they have only been determined by WGS because it is not clear if the host is resistant to the gene they may carry and thus unknown if they are functional

Stanton & Humphrey, 2003, Appl Environ Microbiol, 69:3874 ; van Hoek *et al.*, 2008 52:248; Dang *et al.*, Microb Ecol. 2007 doi:10.1007/s00248-007-9271-9; Akinbowale *et al.*, J App Micro. 103:2016 ; Dang *et al.*, J App Micro 103:2580 ; Fan *et al.*, 2007 Mol Cell Probes 21:245 ; Stine *et al.* 2007, Int J Antimicrob Agents 29 :348 ; Gordon *et al.*, 2008 JAC, 62: 65-71; Lau *et al.*, 2008, JAC 61:3

¹*Actinobacillus actinomycetemcomitans* is now *Aggregatibacter actinomycetemcomitans*;

^a*T. denticola* anaerobic but not all species in genus are anaerobes; ^bAnaerobic genus; ^cFirst aerobic species identified with *tet(X)*;

^d Mosaic ribosomal protection genes have been found in two anaerobic genera (*Clostridium*, *Lactobacillus* [Gram-positive] and *Megasphaera* [Gram-negative]) (Levy, *et al.*, 2005, AAC 43:1523); ^e formally *Haemophilus*; ^f obligate intercellular bacteria from whole genome not clear if isolate is Tc^r; ^g Rahman *et al.*, JAC 62:627, 2008; ^h Brown *et al.* AAC 52:4518, 2008;

ⁱ Petrova Gorlenko, Mindlin, FEMS Micro Lett. 296:190, 2009; ^j Srinivasan *et al.*, Microb Ecol 55:184, 2008;

^k Adelowo & Fagade. Let App Microbiol 2009, 48:167-172;

^l Millan *et al.*, AAC 53:3399, 2009; ^m Nonaka *et al.*, 2007, 4:355; ⁿ Popwska *et al.*, AAC, 2012, 56:1434;

^o Abril, Broadard, Perreten. AAC, 2010, 54:3052; ^p Kadlec *et al.*, ICAAC 2012 C1-679; ^q Stanton *et al.*, 2004 Appl Environ Microb 70:3754-57; GenBank YP_594556; ^r Chen *et al.* Avian Path. 39:333, 2010; ^s Leski *et al.*, Intern J Antimicrob Agents 42:83, 2013;

^v Ghosh & LaPara, ISME 1:191, 2007; ^w Sullivan, Gentry, Karthikeyan. J App Micro. 115:774, 2013;

^x Roberts *et al.*, J. Antimicrob. Chemother. 70:619, 2015; ^y Huang, Zhang, Wang, J Food Protect 78:1581, 2015 name changed to *tet(57)*;

^z Kyselkova *et al.* Front Microbiol. 6:536, 2015 doi: 10.3389/fmicob.2015.00536; ^{aa} Adesoji *et al.*, Annals of Clinical Microb & Antimicrob 14:35, 2015; ^{ab} Li *et al.*, J. Food Sci 81:M1489, 2016; ^{ac} Gao *et al.*, Water Reserach 2012; 46:235; ^{ac} Dang *et al.*, Microb Ecol. 55:237, 2008;

^{ad} Zhu *et al.* Frontiers Microb 10.3390/fmicb.2018.00585, 2018; ^{ac} Zhao *et al.* Frontiers Microb 10.3389/fmicb.2018.00549, 2018;

^{af} **Lopes, Strachan, Ramjee *et al.*, Emerg Infect Dis 2019; 25:1320-1329 doi:<https://doi.org/10.3201/eid2507.18a572>;**

^{ah} Rocas, Siqueira Anaerobe 2012, 18:576 <http://dx.doi.org/10.1016/j.anaerobe.2012.10.001>

^{ai} **Liu, Zhai, Song *et al.* JAC 2020 75:1428-1431 doi:10.1093/jac/dkaa037;**

^{aj} **Somprasong, Hall, Webb *et al.*, AAC 2021 65:e01767-20 <https://doi.org/10.1128/AAC.01767-20>**

^{ak} **Van Driessche, Vanneste, Bogaerts *et al.*, Emerg Infect Dis 2020 26: April DOI: <https://doi.org/10.3201/eid2604.19062>**

^{al} **Somprasong, Hall, Webb *et al.*, AAC 2021 65:e01767-20 <https://doi.org/10.1128/AAC.01767-20>**

^{am} *Aggregatibacter was Actinobacillus* ;

^{an} **Zhang, Dong, Shen *et al.*, Nature communications 2020 11:4648 <https://doi.org/10.1038/s41467-020-18475-9>**

^{an} **Furlan, Stehling, J Global Antimicrob Res 2019 16:181-182 <https://doi.org/10.1016/j.jgar.2019.01.026>;**

^{ao} **Driessche, Vanneste, Bogaerts *et al.*, 2020 Emerging Infect dis 26 https://wwwnc.cdc.gov/eid/article/26/4/19-0962_article**

Some groups have used alleles numbers for *tet(X)*. We do not recommend this because many of the alleles are 95-99% aa identical and the same genes has previously been listed as *tet(X)* in GenBank. So there are the same genes with two different names which is confusing. We would recommend that everyone uses just *tet(X)* and Tet(X) in the future. Some genera not listed that is found in Pathogen Detection Microbial Browser for Identification of Genetic and Genomic Elements (MicroBIGG-E)[<https://www.ncbi.nlm.nih.gov/pathogens/microbigge/>] Because they have only been determined by WGS because it is not clear if the host is resistant to the gene they may carry and thus unknown if they are functional