

Table 2. Distribution of *tet* resistance genes among Gram-negative bacteria Modified **Feb. 1, 2024**

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) <sup>p</sup>	<i>Acidaminococcus</i> <sup>b</sup>	<i>tet</i> (W) <i>Acinetobacter</i> <i>tet</i> (A)(B)(C)(D) <sup>ac</sup> (G)(H)(L)(M)(O) <sup>ac</sup> (W) <sup>ac</sup> (X)(Y) <sup>z</sup> (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> <sup>1,am</sup> <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) <sup>u</sup> <i>Aeromonas</i> <i>tet</i> (A)(B)(C)(D)(E)(G)(H)(L) <sup>ab</sup> (M)(O) <sup>n</sup> (T) <sup>n</sup> (Y)(31)(34)
<i>Bibersteinia</i>	<i>tet</i> (H)	<i>Ochrobactrum</i>	<i>tet</i> (A)(B) <sup>y</sup> (G)(L)	<i>Delftia</i>	<i>tet</i> (X) <sup>u</sup> <i>Anaerovibrio</i> <sup>b</sup> <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) <sup>aa</sup> (30) <sup>aa</sup> (39) <sup>k</sup> (M) <sup>aa</sup>
<i>Erwinia</i>	<i>tet</i> (B)	<i>Burkholderia</i>	<i>tet</i> (D) <sup>n</sup> (O) <sup>n</sup> (64) <sup>al</sup>	<i>Epilithonimonas</i>	<i>tet</i> (X) <i>Bacteroides</i> <sup>b</sup> <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) <sup>j</sup> <i>Brevundimonas</i> <i>tet</i> (B) <sup>n</sup> (D) <sup>n</sup> (G)(O) <sup>n</sup> (T) <sup>n</sup> (W) <sup>n</sup> (39) <sup>k</sup>
<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) <sup>n</sup> (O) <sup>n</sup> (64) <sup>aj</sup> (X) <sup>an</sup>
<i>Histophilus</i> <sup>e</sup>	<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) <sup>c</sup> <i>Campylobacter</i> <i>tet</i> (O)(44) <sup>o</sup>
<i>Treponema</i> <sup>a</sup>	<i>tet</i> (B)			<i>Wautersiella</i>	<i>tet</i> (X) <sup>z</sup> <i>Chryseobacterium</i> <i>tet</i> (A)(D) <sup>t</sup> (T) <sup>t</sup> (W) <sup>t</sup> (X) <sup>an</sup>
<i>Empedobacter</i>	<i>tet</i> (X) <sup>an</sup>			<i>Ralstonia</i>	<i>tet</i> (M) <i>Citrobacter</i> <i>tet</i> (A)(B)(C)(D)(E)(L)(M)(O)(S)(W) <sup>j</sup>
<i>Picirickettsia</i>	<i>tet</i> (31) <sup>an</sup>			<i>Dialister</i>	<i>tet</i> (M) <sup>ah</sup> <i>Edwardsiella</i> <i>tet</i> (A)(D)(M)
				<i>Raoultella</i>	<i>tet</i> (X) <sup>an</sup> <i>Enterobacter</i> <i>tet</i> (A)(B)(C)(D)(E)(G) <sup>j</sup> (L)(M)(39) <sup>k</sup> (X) <sup>u</sup>
					<i>Escherichia</i> (A)(B)(C)(D)(E)(G)(J)(L)(M)(W) <sup>j</sup> (Y)(X) <sup>u</sup> (32)(34) <sup>ao</sup>
					<i>Elizabethkingia</i> <i>tet</i> (W)(X) <sup>an</sup>
					<i>Flavobacterium</i> <i>tet</i> (A)(E)(L)(M)
					<i>Fusobacterium</i> <sup>b</sup> <i>tet</i> (G)(L)(M)(O)(Q)(W)
					<i>Gallibacterium</i> <i>tet</i> (B)(H)(K)(L)(31)(Y)(M) <sup>ao</sup>

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

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

**Carrying Mosaic genes<sup>d</sup> n=4**

*Campylobacter* tet(O/32/O)<sup>af</sup>  
*Megasphaera* tet(O/W), tet(O/W/O)<sup>q</sup>  
*Riemerella* tet(O/W/32/O)<sup>ad</sup>

Blue: new since last update

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

**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

<sup>l</sup>*Actinobacillus actinomycetemcomitans* is now *Aggregatibacter actinomycetemcomitans*;

<sup>a</sup>*T. denticola* anaerobic but not all species in genus are anaerobes; <sup>b</sup>Anaerobic genus; <sup>c</sup>First aerobic species identified with *tet(X)*;

<sup>d</sup> 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); <sup>e</sup> formally *Haemophilus*; <sup>f</sup> oblicagtate intercelluarle bacteria from whole genome not clear if

isolate is Tc<sup>r</sup>; <sup>g</sup> Rahman et al., JAC 62:627, 2008; <sup>h</sup> Brown et al AAC 52:4518, 2008; <sup>i</sup> Petrova Gorlenko, Mindlin, FEMS Micro Lett. 296:190, 2009; <sup>j</sup> Srinivasan et al., Microb Ecol 55:184, 2008; <sup>k</sup> Adelowo & Fagade. Let App Microbiol 2009, 48:167-172;

<sup>l</sup> Millan et al., AAC 53:3399, 2009; <sup>m</sup> Nonaka et al, 2007, 4:355; <sup>n</sup> Popwska et al, AAC, 2012, 56:1434;

<sup>o</sup> Abril, Broadard, Perreten. AAC, 2010, 54:3052; <sup>p</sup> Kadlec et al., ICAAC 2012 C1-679; <sup>q</sup> Stanton et al., 2004 Appl Environ Microb 70:3754-57;

<sup>r</sup> GenBank YP\_594556; <sup>s</sup> Chen et al. Avian Path. 39:333, 2010; <sup>u</sup> Leski et al., Intern J Antimicrob Agents 42:83, 2013;

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

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

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

<sup>ad</sup> Zhu et al. Frontiers Microb 10.3390/fmicb.2018.00585, 2018; <sup>ae</sup> Zhao et al. Frontiers Microb 10.3389/fmicb.2018.00549, 2018;

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

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

<sup>ai</sup> Liu, Zhai, Song et al. JAC 2020 75:1428-1431 doi:10.1093/jac/dkaa037;

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

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

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

<sup>am</sup> *Aggregatibacter* was *Actinobacillus* ; <sup>an</sup> Zhang, Dong, Shen et al., Nature communications 2020 11:4648 <https://doi.org/10.1038/s41467-020-18475-9>

<sup>an</sup> Furlan, Stehling, J Global Antimicrob Res 2019 16:181-182 <https://doi.org/10.1016/j.gar.2019.01.026>;

<sup>ao</sup> Driessche, Vanneste, Bogaerts et al., 2020 Emerging Infect dis 26 [https://wwwnc.cdc.gov/eid/article/26/4/19-0962\\_article](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**