

Table 1. rRNA Methylase Genes Modified **May 4, 2022**

Most genes, except noted, confer resistance to macrolides, lincosamides and streptogramin B

Originally modified from AAC 1999 43:2823-30 with permission from ASM Journals

Class	Protein name	Gene name	Gene(s) included	% homology		Plasmid Transposon	GenBank number *
				DNA	aa		
rRNA METHYLASES							
A	Erm(A)	<i>erm(A)</i>	<i>erm(A)</i> <i>erm(TR)</i>	83%	81%	Tn554	X03216 AF002716
B	Erm(B)	<i>erm(B)</i>	<i>erm(AM)</i> <i>erm(AM)</i> <i>erm(AM)</i> <i>erm(B)</i> <i>erm(B)</i> <i>erm(B)</i> <i>erm(B)</i> <i>erm(B)</i> <i>erm(AMR)</i> <i>erm(BC)</i> <i>erm(P), erm(BP)</i> <i>erm(IP)</i>	98%-100%	98%-100%	Tn1545 pAMβ-1 pAM77 Tn917 pAD2 pTE44 pSE20 pIP1527 pIP402 pIP501	X52632 Y00116 K00551 M36722 M11180 NC_003528 AJ294530 AF242872, AF368302 AF406971, AF299292 U35228 U86375 M19270 U18931 X72021

			<i>erm</i> (Z), <i>erm</i> (BZ1), <i>erm</i> (BZ2)			Tn5398	AF109075
			<i>erm</i>			pLEM3	U48430, X82819
			<i>erm</i> (2)			pBT233, pMD101	X64695, X66468
			<i>erm</i> (80)			pTE80	AF080450
C	Erm(C)	<i>erm</i> (C)	<i>erm</i> (C)	99%-100%	98%-100%	pE194	V01278
			<i>erm</i> (C)			pT48	M19652
			<i>erm</i> (C)			pE5	M17990
			<i>erm</i> (C)			pJR5	L04687
			<i>erm</i> (C)			pA22	X54338
			<i>erm</i> (C)			pSES6	X82668
							X82665, X82667
			<i>erm</i> (C)			pSES5	Y09001
			<i>erm</i> (C)			pSES4a	Y09002
			<i>erm</i> (C)			pSES21	Y09003
			<i>erm</i> (C)			J3356::pOX7	U36911
			<i>erm</i> (IM)			pIM13	M13761
			<i>erm</i> (M)			pNE131	M12730
			<i>erm</i> (M)			pPV141	U82607
			<i>erm</i> (M)			pPV42	AF019140
D	Erm(D)	<i>erm</i> (D)	<i>erm</i> (D)	97%-99	97%-99%	pBD90	M29832
			<i>erm</i> (J)			pBA423	L08389
			<i>erm</i> (K)				M77505
E	Erm(E)	<i>erm</i> (E)	<i>erm</i> (E)	99%	96%	pUC31, pIJ43	X51891
			<i>erm</i> (E2)				M11200
F	Erm(F)	<i>erm</i> (F)	<i>erm</i> (F)	98%-100%	97%-100%	pBF4	M14730

			<i>erm(F)</i>			Tn4351	M17124
			<i>erm(FS)</i>			pBI106, Tn4551	M17808
			<i>erm(FU)</i>			Chromosome	M62487
G	Erm(G)	<i>erm(G)</i>	<i>erm(G)</i>	99%	99%	pBD370	M15332
			<i>erm(G)</i>			Tn7853	L42817
H	Erm(H)	<i>erm(H)</i>	<i>car(B)</i>			pOJ159	M16503
I	Erm(I)	<i>erm(I)</i>	<i>mdm(A)</i>				Hara & Hutchinson ^h
N	Erm(N)	<i>erm(N)</i>	<i>tlr(D)</i>				X97721
O	Erm(O)	<i>erm(O)</i>	<i>lrm</i>	84%	84%	pLST391	M74717
			<i>srm(A)</i>				AJ223970
Q	Erm(Q)	<i>erm(Q)</i>	<i>erm(Q)</i>			Chromosome	L22689
R	Erm(R)	<i>erm(R)</i>	<i>erm(A)</i>				M11276
			<i>erm(R)</i>				AY623658
S	Erm(S)	<i>erm(S)</i>	<i>erm(SF)</i>	100%	100%	pET23	M19269
			<i>tlr(A)</i>				P45439
T	Erm(T)	<i>erm(T)</i>	<i>erm(GT)</i>	85%-99%	85%-100%	pGT633	M64090
						Chromosome	AY894138
						p121BS	AF310974
			<i>erm(LF)</i>			pLME3000	AJ488494
U	Erm(U)	<i>erm(U)</i>	<i>lmr(B)</i>			Chromosome	NG_047843
V	Erm(V)	<i>erm(V)</i>	<i>erm(SV)</i>				U59450
W	Erm(W)	<i>erm(W)</i>	<i>myr(B)</i>				D14532

X	Erm(X)	<i>erm(X)</i>	<i>erm(CD), erm(A)</i> <i>erm(Y)</i>	99%-100%	99%-100%	pNG2 Tn5432 pAP2	M36726, X51472 U21300 NC_005206
Y	Erm(Y)	<i>erm(Y)</i>	<i>erm(GM)</i>			pMS97	AB014481
Z	Erm(Z)	<i>erm(Z)</i>	<i>srm(D)</i>				AM709783
30	Erm(30)	<i>erm(30)</i>	<i>pikR1</i>			Chromosome	AF079138
31	Erm(31)	<i>erm(31)</i>	<i>pikR2</i>			Chromosome	AF079138
32	Erm(32)	<i>erm(32)</i>	<i>tlr(B)</i>			Chromosome	AJ009971
33	Erm(33)	<i>erm(33)^a</i>				pSCFS1	AJ313523 AJ579365
34	Erm(34)	<i>erm(34)</i>					AY234334
35	Erm(35)	<i>erm(35)</i>					AF319779
36	Erm(36)	<i>erm(36)</i>	<i>erm(MT)</i>				AF462611
37	Erm(37)	<i>erm(37)</i>				Chromosome ^b	Z74025
38	Erm(38)	<i>erm(38)</i>				Chromosome ^c	AY154657
39	Erm(39)	<i>erm(39)</i>				Chromosome ^c	AY487229
40	Erm(40)	<i>erm(40)</i>				Chromosome ^c	AY570506
41	Erm(41)	<i>erm(41)</i>				Chromosome ^c	EU177504
42	Erm(42)	<i>erm(42)</i>	<i>erm(MI)</i>		99%	Chromosome pPDP9106b	FR734406 AB601890
43	Erm(43)	<i>erm(43)</i>				Chromosome	HE650138
44	Erm(44)	<i>erm(44)</i>			81%	Chromosome, prophage	HG796218, LN623525 KJ728534, LK392593.1, KJ72853
44	Erm(44) _v	<i>erm(44)_v^c</i>					KACC16562
45	Erm(45)	<i>erm(45)</i>				Chromosome, genomic island	CEJ95855
46	Erm(46)	<i>erm(46)</i>				pREm46	KM679362

47	Erm(47)	<i>erm</i> (47)			Chromosome	KU612222
48	Erm(48)	<i>erm</i> (48) ^f			Plasmid	LT223129
49	Erm(49)	<i>erm</i> (49) ^j			Chromosome	MWVR01000009.1 [34385-35299]
50	Erm(50)	<i>erm</i> (50)			pTZC1	LC473083
51	Erm(51)	<i>erm</i> (51)			pRErm51	MN928789
52	Erm(52)	<i>erm</i> (52) ^l			Chromosome	MW269959.1
53	Erm(53)	<i>erm</i> (53) ^m			Chromosome	TN085784.1
54	Erm(54)	<i>erm</i>(54)^o			Plasmid	ULG10102
55	Erm(55)	<i>erm</i>(55)^p			Plasmid	

S-adenyosylmethionine rRNA methyltransferase ⁿ

Phenicol, lincosamides, oxazolidinones, pleuromutlins, streptogramin A

<i>cfr</i> ^d	<i>cfr</i>				pSCFS3, pSWCF36 Chromosome, Tn649	AJ879565, AM408573
<i>cfr</i> (B) ^d	<i>cfr</i> (B)	99%-100%	99%-100%		Chromosome Plasmid	KM359438, KM359439 KR610408
<i>cfr</i> (C) ^g	<i>cfr</i> (C)				Chromosome, Plasmid	CCL89685, ENZ41453 KX686749
<i>cfr</i> (D) ⁱ	<i>cfr</i> (D)				Plasmid	CP044327
<i>cfr</i> (E)	<i>cfr</i> (E) ^k				Chromosome	WP_10511968658, AJ879565

Blue changes since last update ND= not done;

Genera that may carry MLS genes found by WGS and unknown if the genes are expressed are not listed in the current table

^a Hybrid between *erm*(A) and *erm*(C) < 80% aa identity with either gene; ^b Innate methylase from the chromosome of *Mycobacterium tuberculosis* named Rv1988 in *M. tuberculosis* H37Rv and MT2042 in *M. tuberculosis* CDC155; ^c Innate methylase from the chromosome of other *Mycobacterium* sp.; ^d Confers resistance to lincosamides, oxazolidinones, streptogramin A, phenicol & pleuromutilins [PhLOPS_A] but not macrolides; ^e Confers resistance to

macrolides, lincosamides but not streptogramins Strauss, Hu, Coates, Perreten AAC 61:e01655-16, 2017; ^f Wipf et al., AAC e00066-17, 2017; ^g Tang et al. manuscript in preparation; ^h Hara, Hutchison, J Antibiotics 977, 1990 https://www.jstage.jst.go.jp/article/antibiotics1968/43/8/43_8_977/_pdf; ⁱ **Guerin et al., JAC 2020 doi:10.1093/jac/dkaa125**; ^j Martinez et al., AEM 2018 e02888-17; ^k Stojkovic et al., 2019. AAC2019 doi 10.1128/AAC.01074-19; ^l Imwattana et la. bioRxiv doi: <https://doi.org/10.1101/2020.11.12.379040>; ^m Greninger, Addetia, Starr et al., CID 2020: 71 DOI: 10:1093/cid/ciz1060; ⁿ **Schwarz et al., 2021. CMR doi: 10.1128/CMR.00188-20 review on mobile oxazolidinone genes; ^o Kruger, Ji, Hanke et al. JAC accepted; ^p Alexander, Brown-Elliott, Wallace Jr. in preparation**

* Not all GenBank# are provided just some represented ones.