

# Complete Genome Sequence Analysis of *Kribbella* sp. CA-293567 and Identification of the Kribbellichelins A & B and Sandramycin Biosynthetic Gene Clusters

Marina Sánchez-Hidalgo\*, María Jesús García, Ignacio González, Daniel Oves-Costales, Olga Genilloud

Fundación MEDINA, Avenida del Conocimiento 34, PTS Health Sciences Technology Park, 18016 Granada, Spain

\* Correspondence: marina.sanchez@medinaandalucia.es (M.S-H.), +34958993965

**Table S1.** Publicly available genomes from *Kribbella* strains used in this study. The genome accession codes and number of antiSMASH predicted regions are indicated.

Strain	GenBank accession	Assembly code	WGS accession	Assembly Level	Number of contigs	Size	GC content	Number of antiSMASH predicted regions
<i>Kribbella flavida</i> DSM 17836	GCA_000024345.1	ASM2434v1	CP001736.1	Complete	1	7,579,488	70.5	12
<i>Kribbella catacumbae</i> DSM 19601	GCA_000372465.1	ASM37246v1	AQUZ000000000.1	Contig	152	9,627,810	67.5	17
<i>Kribbella</i> sp. AU-6-A	GCA_001984195.1	ASM198419v1	MTQN000000000.1	Contig	12	8,101,914	69.5	12
<i>Kribbella monticola</i> NEAU-SW521	GCA_003261635.1	ASM326163v1	QFXK000000000.1	Contig	92	8,028,932	67.8	12
<i>Kribbella</i> sp. VKM Ac-2569	GCA_004216905.1	ASM421690v1	SGXJ000000000.1	Contig	13	8,427,108	68	7
<i>Kribbella soli</i> VKM Ac-2540	GCA_004217145.1	ASM421714v1	SHKR000000000.1	Contig	22	8,637,800	67.5	9
<i>Kribbella speibonae</i> SK5	GCA_004331335.1	ASM433133v1	SIJY000000000.1	Contig	21	8,874,969	68.6	9
<i>Kribbella soli</i> KCTC 29219	GCA_004331345.1	ASM433134v1	SIJZ000000000.1	Contig	10	8,785,001	68	9
<i>Kribbella speibonae</i> YM55	GCA_004331375.1	ASM433137v1	SJKC000000000.1	Contig	17	9,285,392	68.6	9
<i>Kribbella sindirgiensis</i> DSM 27082	GCA_004331435.1	ASM433143v1	SJKA000000000.1	Contig	54	8,891,727	68.5	8
<i>Kribbella pittospori</i> NRRL B-24813	GCA_004331465.1	ASM433146v1	SJKB000000000.1	Contig	70	9,491,812	68.1	12
<i>Kribbella capetownensis</i> YM53	GCA_004331485.1	ASM433148v1	SJKD000000000.1	Contig	31	8,831,527	68	9
<i>Kribbella</i> sp. VKM Ac-2500	GCA_004340265.1	ASM434026v1	SLVW000000000.1	Contig	82	9,277,683	68	9
<i>Kribbella</i> sp. VKM Ac-2572	GCA_004342025.1	ASM434202v1	SLWN000000000.1	Contig	45	9,146,758	68	10
<i>Kribbella</i> sp. VKM Ac-2538	GCA_004342085.1	ASM434208v1	SLWM000000000.1	Contig	73	9,192,871	68	8
<i>Kribbella</i> sp. VKM Ac-2568	GCA_004345365.1	ASM434536v1	SLVF000000000.1	Contig	41	8,875,416	68	10
<i>Kribbella</i> sp. VKM Ac-2541	GCA_004345665.1	ASM434566v1	SLWR000000000.1	Contig	33	8,102,898	67.5	13
<i>Kribbella albertanoniae</i> JCM 30547	GCA_004348455.1	ASM434845v1	SMKA000000000.1	Contig	593	9,727,339	67.4	25
<i>Kribbella turkmenica</i> 16K104	GCA_004348725.1	ASM434872v1	SMKR000000000.1	Contig	351	7,447,142	69.4	10
<i>Kribbella antibiotica</i> JCM 13523	GCA_004349055.1	ASM434905v1	SMKX000000000.1	Contig	348	9,279,240	67	33
<i>Kribbella</i> sp. VKM Ac-2527	GCA_004361855.1	ASM436185v1	SNWQ000000000.1	Contig	98	9,457,695	67.5	12
<i>Kribbella</i> sp. VKM Ac-2571	GCA_004362255.1	ASM436225v1	SNWS000000000.1	Contig	50	8,494,871	68	8
<i>Kribbella</i> sp. VKM Ac-2575	GCA_004365175.1	ASM436517v1	SOCE000000000.1	Contig	9	8,032,448	68	13
<i>Kribbella</i> sp. VKM Ac-2573	GCA_004365355.1	ASM436535v1	SODP000000000.1	Contig	15	8,365,383	68	8
<i>Kribbella</i> sp. VKM Ac-2570	GCA_004365875.1	ASM436587v1	SODF000000000.1	Contig	12	8,322,687	67.5	9
<i>Kribbella</i> sp. VKM Ac-2566	GCA_004366005.1	ASM436600v1	SODT000000000.1	Contig	25	8,670,423	68	8
<i>Kribbella</i> sp. VKMAc-2574	GCA_004366075.1	ASM436607v1	SODU000000000.1	Contig	14	8,387,673	68	7
<i>Kribbella jiaozeonensis</i> NEAU-THZ27	GCA_005233875.1	ASM523387v1	SZPZ000000000.1	Contig	12	8,659,701	68	10
<i>Kribbella jejuensis</i> DSM 17305	GCA_006715085.1	ASM671508v1	VFMM000000000.1	Contig	4	7,505,702	68.5	9
<i>Kribbella amoyensis</i> DSM 24683	GCA_007828865.1	ASM782886v1	VIVK000000000.1	Contig	8	8,120,218	70	9
<i>Kribbella shirazensis</i> DSM 45490	GCA_011761605.1	ASM1176160v1	JAASRO010000001.1	Contig	1	8,596,726	69	7
<i>Kribbella sandramycini</i> ATCC 39419	GCA_013131805.1	ASM1313180v1	JABJRC000000000.1	Contig	34	8,105,579	69.1	19
<i>Kribbella italica</i> DSM 28967	GCA_014205135.1	ASM1420513v1	JACHMY000000000.1	Contig	1	8,885,108	69.5	14
<i>Kribbella solani</i> DSM 17294	GCA_014205295.1	ASM1420529v1	JACHNF000000000.1	Contig	2	7,851,691	68	11
<i>Kribbella sandramycini</i> DSM 15626	GCA_014207795.1	ASM1420779v1	JACHKF010000001.1	Contig	1	8,120,153	69	20
<i>Kribbella qitaiheensis</i> SPB151	GCA_014217565.1	ASM1421756v1	CP043661.1	Complete	1	8,156,807	67	12
<i>Kribbella aluminosa</i> DSM 18824	GCA_017876295.1	ASM1787629v1	JAGINT000000000.1	Contig	2	8,936,317	68.5	11
<i>Kribbella</i> sp. b6_HoplandSoilSeptJan	GCA_021154635.1	ASM2115463v1	JAJKIE000000000.1	Contig	425	4,085,102	68	4
<i>Kribbella</i> sp. CA-293567				Complete	1	7,611,196	68.6	19

**Table S2.** *Kribbella* sp. CA-293567 genome statistics.

Characteristic	Value	% of Total
Genome size (bp)	7,611,196	
DNA G+C content (bp)		68.6
Number of replicons	1	
Extrachromosomal elements	0	
Total genes	7,057	100
Protein-coding genes	6982	98.93
Genes with function prediction	3197	45.3

**Table S3.** ORFs present in the kribbellichelins A-B BGC.

ORF	Length of encoded protein (AA)	Closest BLAST homolog [Strain] Ref	Identity (%)	Similarity (%)
<i>krb1</i>	352	Hypothetical protein [ <i>Kribbella catacumbae</i> ] WP_020384918.1	71	79
<i>krb2</i>	275	Undecaprenyl-diphosphate phosphatase [ <i>Streptomyces</i> sp. SID13031] WP_164593903.1	95	98
<i>krb3</i>	356	LLM class F420-dependent oxidoreductase [ <i>Kribbella catacumbae</i> ] WP_026162457.1	95	97
<i>krb4</i>	313	Aldo/keto reductase [ <i>Kribbella</i> sp. VKM Ac-2568] WP_132297909.1	99	100
<i>krb5</i>	61	DUF5703 family protein [ <i>Kribbella qitaiheensis</i> ] WP_185445878.1	100	100
<i>krb6</i>	405	Major facilitator superfamily MFS_1 [ <i>Kribbella flavida</i> DSM 17836] ADB32869.1	76	85
<i>krb7</i>	295	LysR family transcriptional regulator [ <i>Kribbella</i> sp. VKM Ac-2568] WP_132297890.1	83	89
<i>krb8</i>	252	SDR family oxidoreductase [ <i>Acrocarpospora macrocephala</i> ] WP_155361669.1	69	82
<i>krb9</i>	443	M20/M25/M40 family metallo-hydrolase [ <i>Streptomyces</i> sp. SID13031] WP_164593881.1	95	97
<i>krb10</i>	1051	S8 family serine peptidase [ <i>Streptomyces</i> sp. SID13031] WP_164593874.1	93	96
<i>krb11</i>	260	Hypothetical protein [ <i>Amycolatopsis keratiniphila</i> ] WP_043848172.1	52	63
<i>krb12</i>	133	Hypothetical protein [ <i>Amycolatopsis alba</i> ] WP_020634912.1	60	76
<i>krb13</i>	263	Class I SAM-dependent methyltransferase [ <i>Kribbella</i> sp. VKM Ac-2575] WP_133979490.1	92	94
<i>krb14</i>	417	ABC transporter substrate-binding protein [ <i>Kribbella speibonae</i> ] WP_131462990.1	83	91
<i>krb15</i>	348	Iron chelate uptake ABC transporter family permease subunit [ <i>Kribbella antibiotica</i> ] WP_132168665.1	93	97
<i>krb16</i>	369	Iron chelate uptake ABC transporter family permease subunit [ <i>Kribbella speibonae</i> ] WP_202875736.1	90	93
<i>krb17</i>	294	ABC transporter ATP-binding protein [ <i>Streptomyces</i> sp. SID13031] WP_164596070.1	95	97
<i>krb18</i>	2463	Non-ribosomal peptide synthetase [ <i>Streptomyces</i> sp. SID13031] WP_164596008.1	84	89
<i>krb19</i>	616	Siderophore-interacting protein [ <i>Streptomyces</i> sp. SID13031] NEA32353.1	88	93
<i>krb20</i>	83	Phosphopantetheine-binding protein [ <i>Streptomyces</i> sp. SID13031] WP_164596006.1	93	96
<i>krb21</i>	285	Class I SAM-dependent methyltransferase [ <i>Streptomyces</i> sp. SID13031] WP_164596005.1	95	97
<i>krb22</i>	581	ABC transporter ATP-binding protein [ <i>Streptomyces</i> sp. SID13031] NEA32350.1	92	95
<i>krb23</i>	556	ABC transporter ATP-binding protein/permease [ <i>Kribbella italica</i> ] WP_202893055.1	90	93
<i>krb24</i>	3107	Amino acid adenylation domain-containing protein [ <i>Streptomyces</i> sp. SID13031] WP_239062464.1	85	90
<i>krb25</i>	406	FAD-dependent monooxygenase [ <i>Streptomyces</i> sp. SID13031] WP_164596002.1	92	96
<i>krb26</i>	541	AMP-binding protein [ <i>Kribbella albertanoniae</i> ] WP_132402990.1	96	98
<i>krb27</i>	232	4'-phosphopantetheinyl transferase superfamily protein [ <i>Streptomyces</i> sp. SID13031] WP_164596000.1	89	92
<i>krb28</i>	273	Alpha/beta hydrolase [ <i>Kribbella albertanoniae</i> ] WP_132402993.1	89	92
<i>krb29</i>	248	4-hydroxy-tetrahydroadipicinate reductase [ <i>Streptomyces</i> sp. SID13031] WP_164595998.1	90	95
<i>krb30</i>	137	Aspartate 1-decarboxylase [ <i>Streptomyces</i> sp. SID13031] WP_164595997.1	97	99
<i>krb31</i>	80	MbtH family NRPS accessory protein [ <i>Kribbella albertanoniae</i> ] WP_132403002.1	97	98
<i>krb32</i>	490	FAD-dependent tricarballoylate dehydrogenase TcuA [ <i>Kribbella albertanoniae</i> ] WP_132403005.1	94	96
<i>krb33</i>	546	Alpha/beta hydrolase [ <i>Kribbella flavida</i> ] WP_041289211.1	88	93
<i>krb34</i>	242	MerR family transcriptional regulator [ <i>Kribbella albertanoniae</i> ] WP_132405175.1	83	89
<i>krb35</i>	156	Nuclear transport factor 2 family protein [ <i>Streptomyces phaeochromogenes</i> ] WP_055611607.1	78	88
<i>krb36</i>	206	TetR/AcrR family transcriptional regulator [ <i>Kibdelosporangium persicum</i> ] WP_173131860.1	78	88
<i>krb37</i>	400	Pimeloyl-ACP methyl ester carboxylesterase [ <i>Kribbella</i> sp. VKM Ac-2571] TDO68387.1	91	95
<i>krb38</i>	431	Epoxide hydrolase [ <i>Kribbella</i> sp. VKM Ac-2571] WP_133782690.1	89	93
<i>krb39</i>	220	DUF998 domain-containing protein [ <i>Kribbella turkmenica</i> ] WP_132321484.1	77	87
<i>krb40</i>	112	Hypothetical protein [ <i>Kribbella flavida</i> ] WP_012919172.1	81	91
<i>krb41</i>	181	Hypothetical protein [ <i>Kribbella amoyensis</i> ] WP_145806086.1	72	79

**Table S4.** ORFs present in the sandramycin BGC from *Kribbella* sp. CA-293567. A comparison with the ORFs present in the *sdm* and *tio* BGCs is shown.

ORF	Length of encoded protein (AA)	Closest BLAST homolog [Strain] Ref	Identity (%)	Similarity (%)	<i>K. sandramycini</i> homologous gene	Identity (%)	Similarity (%)	Thiocoralline homologous gene	Identity (%)	Similarity (%)
<i>san1</i>	144	VOC family protein [ <i>Kribbella qitaiheensis</i> ] WP_185445859.1	81	92	<i>sdm1</i>	73.4	81.1	<i>tioX</i>	56.7	70.1
<i>san2</i>	355	Ornithine cyclodeaminase family protein [ <i>Kribbella qitaiheensis</i> ] WP_185445860.1	90	94	<i>sdm2</i>	84.6	92.4			
<i>san3</i>	526	AMP-binding protein [ <i>Kribbella qitaiheensis</i> ] WP_185445861.1	84	91	<i>sdm3</i>	83.7	89.5	<i>tioJ</i>	63.5	78.2
<i>san4</i>	582	Non-ribosomal peptide synthetase [ <i>Kribbella qitaiheensis</i> ] WP_185445862.1	83	90	<i>sdm4</i>	81.3	88	<i>tioK</i>	61.5	74.4
<i>san5</i>	398	Cytochrome P450 [ <i>Amycolatopsis</i> sp. MtRt-6] WP_206792488.1	88	94	<i>sdm5</i>	85.7	91.7	<i>tioI</i>	65.2	77.4
<i>san6</i>	257	Thioesterase [ <i>Kribbella qitaiheensis</i> ] QNE17028.1	77	86	<i>sdm6</i>	74.7	79.4	<i>tioQ</i>	48.6	62.4
<i>san7</i>	248	NAD(P)-dependent dehydrogenase [ <i>Kribbella sandramycini</i> ] MBB6569689.1	78	89	<i>sdm7</i>	78	89	<i>tioH</i>	58.7	71.6
<i>san8</i>	409	Pyridoxal phosphate-dependent aminotransferase [ <i>Amycolatopsis bullii</i> ] WP_191307014.1	87	92	<i>sdm8</i>	86.6	91.4	<i>tioG</i>	61.8	74.5
<i>san9</i>	239	Tryptophan 2,3-dioxygenase family protein [ <i>Kribbella qitaiheensis</i> ] WP_185445866.1	87	93	<i>sdm9</i>	86.4	95	<i>tioF</i>	58.8	71.6
<i>san10</i>	168	DNA-binding response OmpR family regulator [ <i>Kribbella sandramycini</i> ] MBB6569686.1	90	94	<i>sdm10</i>	90	94			
<i>san11</i>	3635	Amino acid adenylation domain-containing protein [ <i>Kribbella qitaiheensis</i> ] QNE17032.1	76	85	<i>sdm11</i>	74.7	83.8			
<i>san12</i>	3090	Non-ribosomal peptide synthetase [ <i>Kribbella qitaiheensis</i> ] WP_185445868.1	77	85	<i>sdm12</i>	73.1	82.9			
<i>san13</i>	73	Mbth family NRPS accessory protein [ <i>Amycolatopsis</i> sp. MtRt-6] WP_206792493.1	85	91	<i>sdm13</i>	68.5	82.2	<i>tioT</i>	70.4	84.5
<i>san14</i>	145	Hypothetical protein [ <i>Rhodococcus marinonascens</i> ] WP_245813747.1	65	76	<i>sdm14</i>	65.8	76			
<i>san15</i>	233	TetR family transcriptional regulator [ <i>Streptomyces</i> sp. SID13031] WP_164593841.1	83	88	-	-	-			
<i>san16</i>	321	ABC transporter ATP-binding protein [ <i>Kribbella qitaiheensis</i> ] WP_185445870.1	87	92	<i>sdm15</i>	78.3	88.2			
<i>san17</i>	283	ABC transporter permease [ <i>Kribbella qitaiheensis</i> ] WP_185445871.1	83	88	<i>sdm16</i>	79.7	88.6			
<i>san18</i>	228	HNH endonuclease family protein [ <i>Streptomyces</i> sp. SID13031] WP_164593685.1	90	94	<i>sdm17</i>	71.5	78.5			
<i>san19</i>	475	Aminopeptidase P family protein [ <i>Kribbella catacumbae</i> ] WP_020390480.1	81	86	-	-	-			