



Dr. Cathrin Spröer

Leibniz-Institut DSMZ GmbH · Inhoffenstraße 7 B · 38124 Braunschweig

Dr. David Baltrus
The University of Arizona
School of Plant Sciences
P.O. Box 210036
Forbes Building, 303
Tucson, Arizona USA 85721-0036

Inhoffenstraße 7 B
38124 Braunschweig
GERMANY

Tel.: +49(0)531 26 16-0
Fax: +49(0)531 26 16-418
E-mail: contact@dsmz.de
Internet: www.dsmz.de

U S A

Ihr Zeichen/Your ref.

Your order dated
17.01.2018

Unser Zeichen/Our ref.

Luteibacter sp strain 433 (ID 18-203)
Luteibacter sp strain 1164 (ID 18-204)

+49 (0)531-2616-

Datum/Date

101 15.05.2018
ckc@dsmz.de

Dear Dr. Baltrus,

we have performed the DNA-DNA hybridization of *Luteibacter sp* strain 433 (ID 18-203) against *Luteibacter sp* strain 1164 (ID 18-204).

We got the following results:

% DNA-DNA similarity (in 2 X SSC + 10% formamide at 69°C)

	<i>Luteibacter sp</i> strain 433 (ID 18-203)
<i>Luteibacter sp</i> strain 1164 (ID 18-204)	31.8 (25.4)

(Values in parentheses are results of measurements in duplicate)

Luteibacter sp strain 433 (ID 18-203) does not belong to the species *Luteibacter sp* strain 1164 (ID 18-204) when the recommendations of a threshold value of 70 % DNA-DNA similarity for the definition of bacterial species by the *ad hoc* committee (Wayne *et al.*, 1987) are considered.



Sincerely yours,

A handwritten signature in black ink, appearing to read "Cathrin Spröer".

Dr. Cathrin Spröer

Wayne, L. G., Brenner, D. J., Colwell, R. R., Grimont, P. A. D., Kandler, O., Krichevsky, M. I., Moore, L. H., Moore, W. E. C., Murray, R. G. E., Stackebrandt, E., Starr, M. P. & Trüper, H. G. (1987). Report of the ad hoc committee on reconciliation of approaches to bacterial systematics. *Int J Syst Bacteriol* 37, 463-464.

Spectroscopic DNA-DNA hybridization

Material and Methods:

DNAs of the genus *Vitellibacter* were prepared according to a modified method of Marmur's procedure (Roalkvam *et al.*).

Cells of the genus *Roseivirga* were disrupted by using a Constant Systems TS 0.75 KW (IUL Instruments, Germany). DNA in the crude lysate was purified by chromatography on hydroxyapatite as described by Cashion *et al.* (1977).

DNA-DNA hybridization was carried out as described by De Ley *et al.* (1970) under consideration of the modifications described by Huss *et al.* (1983) using a model Cary 100 Bio UV/VIS-spectrophotometer equipped with a Peltier-thermostatted 6x6 multicell changer and a temperature controller with *in-situ* temperature probe (Varian).

References

Marmur, J. (1961). A Procedure for the Isolation of Deoxyribonucleic Acid from Micro-organisms *J Mol Biol* **3**, 208-218.

Roalkvam, I, Drønen, K., Stokke, R., Daae, F.L., Dahle, H., & Stehen, I.H. (2015). Physiological and genomic characterization of *Arcobacter anaerophilus* IR-1 reveals new metabolic features in Epsilonproteobacteria, *Front.Microbiol* Volume **6**, Article 987

Cashion, P., Hodler-Franklin, M. A., McCully, J. & Franklin, M. (1977). A rapid method for base ratio determination of bacterial DNA. *Anal Biochem* **81**, 461-466.

De Ley, J., Cattoir, H. & Reynaerts, A. (1970). The quantitative measurement of DNA hybridization from renaturation rates. *Eur J Biochem* **12**, 133-142.

Huss, V. A. R., Festl, H. & Schleifer, K. H. (1983). Studies on the spectrophotometric determination of DNA hybridization from renaturation rates. *Syst Appl Microbiol* **4**, 184-192.

Leibniz-Institut
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Mikroorganismen und Zellkulturen GmbH



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Datum/Date

231
identification@dsMZ.de

2018-06-20

DSMZ-IDENTIFICATION SERVICE

Dear Dr. Baltrus,

We now have completed the analyses for your strain

Luteibacter sp. 9143 – ID 18-203

Result of the analysis of the respiratory quinones: Ubiquinone 8 (Q8).

Should the data supplied be used in a publication the following acknowledgement should be included in the "Materials and Methods", "Analysis of respiratory quinones were carried out by the Identification Service and Dr. Brian Tindall, DSMZ, Braunschweig, Germany."

Where work has been carried out on cell material or strains supplied by the customer, DSMZ makes no guarantee concerning the authenticity of the material/strain supplied.

Leibniz-Institut DSMZ-Deutsche Sammlung von
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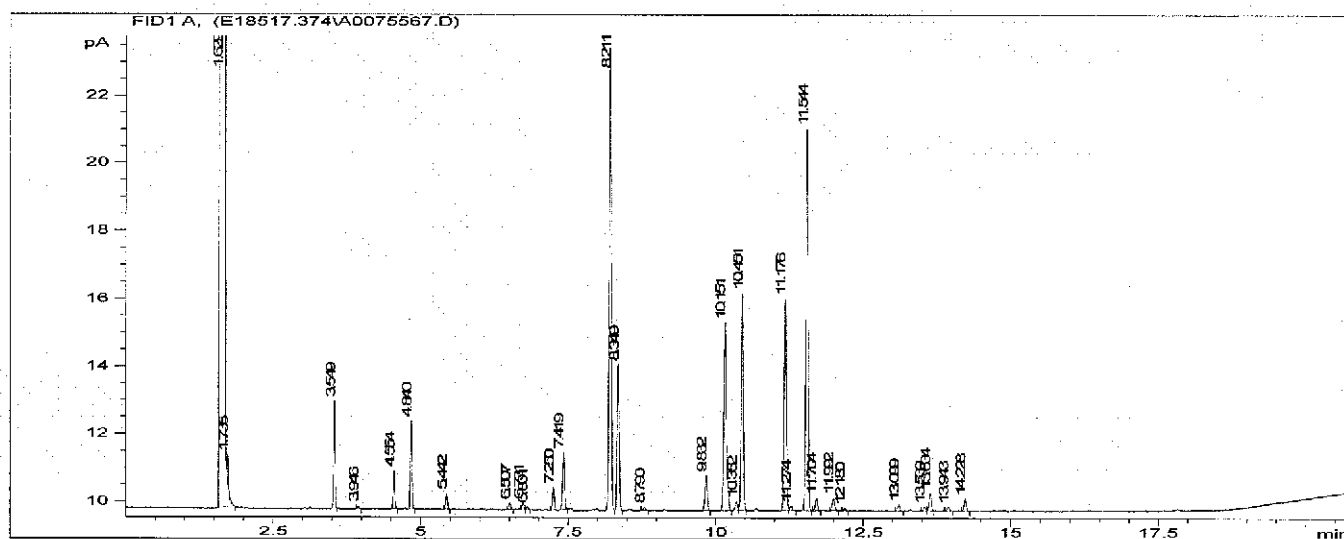
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 Created: 5/17/2018 11:27:08 AM
 Sample ID: UN-V-18-203-9143-ARIZONA(15mg ZM)

RT	Response	Ar/Ht	RFact	ECL	Peak Name	Percent	Comment1	Comment2
1.629	3.629E+8	0.025	----	7.015	SOLVENT PEAK	----	< min rt	
1.735	2205	0.021	----	7.226		----	< min rt	
3.549	10474	0.025	1.162	10.606	11:0 ISO	4.14	ECL deviates 0.000	Reference -0.005
3.946	344	0.028	----	11.136		----		
4.554	4373	0.031	1.090	11.799	unknown 11.799	1.62	ECL deviates 0.000	
4.840	9958	0.030	1.075	12.090	11:0 ISO 3OH	3.64	ECL deviates 0.001	
5.442	1815	0.031	1.050	12.613	13:0 ISO	0.65	ECL deviates -0.001	Reference -0.005
6.507	866	0.034	1.015	13.456	12:0 3OH	0.30	ECL deviates 0.002	
6.731	900	0.033	1.009	13.619	14:0 ISO	0.31	ECL deviates 0.000	Reference -0.004
6.801	403	0.033	----	13.671		----		
7.250	2986	0.036	0.995	13.999	14:0	1.01	ECL deviates -0.001	Reference -0.005
7.419	7787	0.037	0.992	14.110	13:0 ISO 3OH	2.63	ECL deviates 0.001	
8.211	65054	0.038	0.976	14.624	15:0 ISO	21.60	ECL deviates 0.001	Reference -0.003
8.349	20730	0.039	0.973	14.714	15:0 ANTEISO	6.86	ECL deviates 0.001	Reference -0.004
8.790	450	0.034	0.965	15.000	15:0	0.15	ECL deviates 0.000	Reference -0.004
9.832	5263	0.039	0.949	15.626	16:0 ISO	1.70	ECL deviates -0.001	Reference -0.005
10.151	33469	0.046	0.945	15.818	Sum In Feature 3	10.76	ECL deviates -0.004	16:1 w7c/15 iso 2OH
10.352	1410	0.040	----	15.939		----		
10.451	33574	0.041	0.941	15.998	16:0	10.75	ECL deviates -0.002	Reference -0.006
11.176	33743	0.041	0.932	16.418	ISO 17:1 w9c	10.71	ECL deviates 0.002	
11.274	846	0.045	0.931	16.474	Sum In Feature 4	0.27	ECL deviates -0.002	17:1 ISO I/ANTEI B
11.544	60234	0.042	0.928	16.631	17:0 ISO	19.03	ECL deviates 0.001	Reference -0.004
11.704	2013	0.043	0.926	16.723	17:0 ANTEISO	0.63	ECL deviates 0.000	Reference -0.004
11.992	2097	0.046	0.923	16.890	17:0 CYCLO	0.66	ECL deviates 0.002	Reference -0.003
12.180	432	0.036	0.921	16.998	17:0	0.14	ECL deviates -0.002	Reference -0.006
13.099	1135	0.045	0.913	17.520	16:0 3OH	0.35	ECL deviates 0.001	
13.539	731	0.044	0.909	17.770	18:1 w9c	0.23	ECL deviates 0.001	
13.634	3056	0.044	0.908	17.824	18:1 w7c	0.94	ECL deviates 0.001	
13.943	795	0.045	0.905	17.999	18:0	0.24	ECL deviates -0.001	Reference -0.006
14.228	2182	0.046	0.903	18.162	17:0 ISO 3OH	0.67	ECL deviates 0.001	Reference -0.004
----	33469	----	----	----	Summed Feature 3	10.76	16:1 w7c/15 iso 2OH	15:0 ISO 2OH/16:1w7c
----	846	----	----	----	Summed Feature 4	0.27	17:1 ISO I/ANTEI B	17:1 ANTEISO B/I

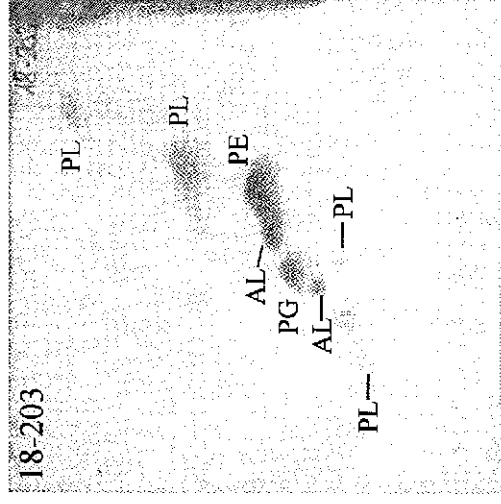
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 Total Response: 307119
 Percent Named: 99.30%

Reference ECL Shift: 0.005 Number Reference Peaks: 15
 Total Named: 304962
 Total Amount: 293793

*** No Matches found in TSBA40



DSMZ Identification Services polar lipid report



AL = Aminolipid

PL = Phospholipid

PG = Phosphatidylglycerol

PE = Phosphatidylethanolamine