A Gram-staining-positive, coccoid, halotolerant bacterial strain, designated SV-16T, was isolated from marine sediment and subjected to a polyphasic taxonomic study. The strain exhibited phenotypic properties that included chemotaxonomic characteristics consistent with its classification in the genus Salinicoccus. Growth occurred at temperatures in the range 25–37 °C (optimum 30 °C), at pH 7.0–11.0 (optimum pH 8.0) and at NaCl concentrations of up to 25.0 % (optimum 15.0 %). The highest level of 16S rRNA gene sequence similarity was with Salinicoccus carnicancri CrmT (98.6 %) followed by Salinicoccus halodurans W24T (96.6 %). The predominant polar lipids were diphasatidylglycerol, phosphatidylinostitol and phosphatidylglycerol. The major cellular fatty acids were iso-C15 : 0, anteiso-C15 : 0, iso-C17 : 0 and anteiso-C17 : 0. The draft genome of strain SV-16T consisted of 2 591 284 bp with a DNA G+C content of 48.7 mol%. On the basis of the phenotypic characteristics and genotypic distinctiveness of strain SV-16T, it should be classified within a novel species of the genus Salinicoccus, for which the name Salinicoccus sediminis sp. nov. is proposed. The type strain is SV-16T (=MTCC 11832T =DSM 28797T).

The genus Salinicoccus belonging to the family Staphylococcaceae was first proposed by Ventosa et al. (1990) as an aerobic, Gram-staining-positive, coccoid and moderately halophilic bacterium isolated from a solar saltern. At the time of writing, there are 15 species (www.bacterio.net/salinicoccus.html) in the genus Salinicoccus: Salinicoccus roseus (Ventosa et al., 1990), Salinicoccus hispanicus (Marquez et al., 1990; Ventosa et al., 1992), Salinicoccus alkaliphilus (Zhang et al., 2002), Salinicoccus salsiaticae (França et al., 2006), Salinicoccus jeotgali (Aslam et al., 2007), Salinicoccus luteus (Zhang et al., 2007), Salinicoccus carnicancri (Chen et al., 2007), Salinicoccus kumingensis (Chen et al., 2007), Salinicoccus iranensis (Amoozegar et al., 2008), Salinicoccus halodurans (Wang et al., 2008), Salinicoccus albus (Chen et al., 2009), Salinicoccus carnicancri (Jung et al., 2010), Salinicoccus sesuvii (Kämpfer et al., 2011), Salinicoccus qingdaonensis (Qu et al., 2012) and Salinicoccus halitifaciens (Ramana et al., 2013). Among the species of the genus Salinicoccus, six species were isolated from the salt-related environment, i.e. salt mines (S. albus and S. kumingensis), a soda lake (S. alkaliophilus), saline soil (S. halodurans), seawater (S. qingdaonensis) and a solar saltern (S. roseus). Whereas, three species were isolated from fermented seafood (S. carnicancri and S. jeotgali) and fermented shrimp paste (S. siamensis). The remaining species of the genus Salinicoccus were isolated from textile industry wastewater (S. iranensis), dessert soil (S. luteus) and the rhizosphere of Sesuvium portulacastrum (S. sesuvii). In this study, a novel halotolerant, cream-pigmented bacterial strain, SV-16T, which was isolated from marine sediment, is described along with its genomic features.

Strain SV-16T was isolated from marine sediment samples (sample pH 7.8) collected from Sothavilai, Kanyakumari.
strains *S. carnicancri* incubated at 30 °C as well as on tryptic soy agar (TSA; pH 7.3; HiMedia) and incubated at 30 °C for 1 week. Colonies were purified and subculturing was performed on ZMA and TSA at 30 °C for 24 h and the bacterial isolate was maintained as a glycerol stock at −70 °C. For the polyphasic taxonomic study, strain SV-16T was compared in parallel with reference strains *S. carnicancri* JCM 15796T, obtained from the Japan Collection of Microorganisms (JCM), Japan, and *S. halodurans* DSM 19336T, obtained from German Collection of Microorganisms and Cell Cultures (DSMZ), Germany.

Colonial morphology was examined by studying the growth of the strain on TSA at 30 °C for 24 h. Cell morphology was investigated by means of light microscopy (Zeiss) at ×1000. Motility was checked using the method described by Skerman (1967). The Gram reaction was determined using a Gram-staining kit (HiMedia) according to the manufacturer’s instructions. Growth at different temperatures (10, 12, 20, 25, 30, 37 and 42 °C) and NaCl concentrations (0, 2.0, 5.0, 7.0, 10.0, 12.0, 15.0, 18.0, 20.0, 22.0, 25.0 and 27.0 %, w/v) was studied as described by Cowan & Steel (1965). Growth at pH 5.0, 6.0, 7.0, 8.0, 9.0, 10.0 and 12.0 was checked using the biological buffers Na2HPO4/NaH2PO4 and Na2CO3/NaHCO3 for pH below 8 and Na2HPO4/NaOH for pH above 8. All biochemical and physiological studies were carried out at pH 8.0. The following characteristics were determined as described by Cowan & Steel (1965): hydrolysis of gelatin, casein and starch; Voges–Proskauer, methyl red, catalase and oxidase (oxidation of tetramethyl-p-phenylenediamine dihydrochloride; Sigma) activities; growth on Simmons’ citrate and MacConkey agar; production of H2S and indole; reduction of nitrate. Acid production from various carbohydrates was tested as described by Claus & Berkeley (1986). The sensitivity of the strain to various antibiotics was tested using antibiotic-susceptibility discs (HiMedia) on TSA. For enzyme activities, VITEK 2-GP cards were used in triplicate using 36-hour-old culture, incubated at 30 °C as per the instructions of the manufacturer.

For cellular fatty acid analysis, the strains were grown on TSA medium at 30 °C for 36 h; fatty acids were saponified, methylated and extracted using the standard protocol of MIDI (Sherlock Microbial Identification System, version 6.0). The fatty acids were analysed by GC (Hewlett Packard 7890) and identified by using the TSBA50 database of the Microbial Identification System as described by Sasser (1990) and Pandey *et al.* (2002). Ice-dried cells for other chemotaxonomic analyses were prepared following growth of the strains in tryptic soy broth (HiMedia, India) with 10 % NaCl for 4 days at 30 °C. The peptidoglycan structure was determined by using a hydrolysate of purified cell walls, according to the method of Schleifer (1985). The diagnostic amino acids were separated by two-dimensional ascending TLC as described by Schleifer & Kandler (1972), with the modification that TLC on cellulose sheets (Merck 5577) was used instead of paper chromatography. Polar lipids were extracted and analysed by using the methods described by Minnikin *et al.* (1984). Total lipids were detected and identified by spraying with 10 % molybdatephosphoric acid (v/v) in 95 % ethanol. Menaquinones were extracted from 200 mg dry cell mass with a 10 % aqueous solution of 0.3 % (w/v) NaCl in methanol and petroleum ether (60–80 °C boiling point) at a ratio of 1 : 1. The upper phase was collected and dried in a Turbo Vap LV evaporator (Zymark). The residue was dissolved in 100 μl acetone. The extract was developed on a TLC plate (Merck 20 × 20 cm Silica gel 60 F254) using petroleum ether (boiling point 60–80 °C) and diethyl ether (85 : 15, v/v). Purified menaquinones were dissolved in 2-propanol and analysed by reverse-phase TLC according to the protocol of Collins & Jones (1980).

Genomic DNA extraction, amplification and sequencing of the 16S rRNA gene were performed as described previously by Mayilraj *et al.* (2006). To determine the phylogenetic relationships of strain SV-16T, the 16S rRNA gene sequence consisting of 1453 bp was compared with those of type strains of species of recognized genera and identification of phylogenetic neighbours and the calculation of pairwise 16S rRNA gene sequence similarities were achieved using the EzTaxon-e server (Kim *et al.*, 2012) and sequences were aligned using MEGA version 6.0 (Tamura *et al.*, 2013). Phylogenetic trees were reconstructed using the neighbour-joining as well as maximum-parsimony and maximum-likelihood algorithms. Bootstrap analysis was performed to assess the confidence limits of the branching. Evolutionary analyses were carried out in MEGA6. The neighbour-joining tree was reconstructed using standard parameters of CLUSTAL W alignment with a gap-opening penalty of 15 and a gap-extension penalty of 6.66 for both pairwise and multiple alignments. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) was shown next to the branches. The tree was drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the maximum composite likelihood model (effective nucleotide substitution model with rate uniformity, pattern homogeneity, rate variation among sites, pattern heterogeneity between lineages, rate variation and pattern heterogeneity) and are in the units of base substitutions per site. The optimal tree with the sum of branch length = 0.31474296 was retrieved. The analysis involved 16 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 1299 positions in the final dataset.

DNA–DNA hybridization was carried out between strains SV-16T and *S. carnicancri* CrmT using the membrane filter method (Tourova & Antonov, 1987) as described by Reddy *et al.* (2003) except that the probe labelling for DNA–DNA hybridization was performed by using the
Table 1. Differential characteristics of strain SV-16T and the type strains of closely related species

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Growth at 12 °C</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Growth with NaCl 25 % (w/v)</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Citrate utilization</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Acid production from: Glucose</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Maltose</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Sorbitol</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Trehalose</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Sucrose</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Enzyme activity using VITEK 2-GP cards</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>β-Glucuronidase</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Pyrolidonyl-arylamidase</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>β-Glucuronidase</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Tyrosine arylamidase</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>48.7</td>
<td>47.8</td>
<td>45.8</td>
</tr>
</tbody>
</table>

nonradioactive Biotin DecaLabel DNA Labelling kit (Thermo Scientific); hybridized DNA was visualized using the Biotin Chromogenic Detection kit (Thermo Scientific) and the level of DNA–DNA relatedness was quantified by measuring the intensity of the spots by using the densitometry software of a gel documentation system (Alpha Imager). Digital DNA–DNA hybridization (DDDH) was also performed between strains SV-16T and S. carnicancri CrmT. This technique is used for in silico analysis to estimate overall similarity between the genomes of two organisms. It uses high-scoring segment pairs (HSPs) or maximally unique matches (MUMs) for analysis (Auch et al., 2010; Meier-Kolthoff et al., 2013).

The draft genome of SV-16T was sequenced at Genotypic (Bengaluru, India; http://www.genotypic.co.in). Library preparation was performed at Genotypic Technology’s Genomics facility following the NEXTFlex DNA library preparation as per the manufacturer’s instructions (Bioo Scientific). Approximately 3 µg of genomic DNA was sonicated (Covaris) to obtain 500 to 700 bp fragment sizes. The size distribution was checked by running an aliquot of the sample on an Agilent HS DNA Chip. The resulting fragmented DNA was cleaned up using a HighPrep PCR clean up system (MagBio) as described by the manufacturer. Fragmented DNA was subjected to a series of enzymatic reactions that repair frayed ends, phosphorylate the fragments, add a single nucleotide A overhang and ligate adaptors using the NEXTFlex DNA Sequencing kit (Bioo Scientific) following the protocol as described by the manufacturer. Sample clean-up was done using HighPrep PCR beads (MagBio). After ligation cleanup, approximately 500–800 bp fragments were size-selected on 2 % low melting agarose gel and cleaned using a MinElute column (Qiagen). PCR (10 cycles) amplification of adaptor-ligated fragments was done and cleaned up using HighPrep PCR clean-up beads. The libraries prepared were quantified using a Qubit fluorometer (Life Technologies) and validated for quality by running an aliquot on a High Sensitivity Bio analyser Chip (Agilent).

Sequencing was done using Illumina Miseq paired-end technology (2 × 300) and produced a total of 6 528 742 paired-end reads (insert size 598 bp) of 300 bp. We used the NGS QC Toolkit v2.3 to filter the data for high-quality (HQ) vector- and adaptor-free reads for genome assembly (cut-off read length for HQ, 80%; cut-off quality score, 20). A total of 4 434 816 HQ vector-filtered reads were used for assembly with MaSuRCA (Zimin et al., 2013) genome assembler version 2.3.2. The draft genome was annotated with the help of the Rapid Annotations using Subsystems Technology (RAST) server (Aziz et al., 2008).

Analysis of the whole genome sequence of a newly isolated strain allows the calculation of average nucleotide identity (ANI) scores, providing global comparisons of the novel strain with previously isolated strains whose genome sequences are deposited in databases. These ANI scores will probably serve as the next-generation gold standard for species delineation (Kim et al., 2014).

Differential phenotypic properties are shown in detail in Table 1 and also in the species description. Growth was observed at temperatures in the range 25–37 °C (optimum 30 °C), at pH 7.0–11.0 (optimum pH 8.0), but not at pH 5.0, and with between 0 and 25 % NaCl, confirming strain SV-16T to be a halotolerant bacterium. Strain SV-differed from closely related reference strains by at least twelve characteristic features like growth at 12 °C, citrate utilization, growth with 25 % NaCl (w/v), acid production from glucose, maltose, galactose, sorbitol, trehalose and sucrose, and enzyme activity using VITEK 2-GP cards of β-glucuronidase, L-pyrolidonyl-arylamidase and tyrosine arylamidase. The cells of strain SV-16T were sensitive to the following antibiotics (µg per disc): ampicillin (10), chloramphenicol (30), ciprofloxacin (5), erythromycin (10), furazolidone (50), gentamicin (10), nalidixic acid (30), neomycin (30), oleandomycin (15), rifampicin (5),...
spectinomycin (100), streptomycin (10), sulphadiazine (300), sulphamethizole (300) and tetracycline (30), and resistant to the following antibiotics: cephaloridine (30), cloxacillin (5), colistin (10), novobiocin (30), penicillin (10 IU), sulphafurazole (100), tobramycin (10) and trimethoprim (25).

Most of the chemotaxonomic properties of strain SV-16T (presented in the species description) were typical of members of the genus *Salinicoccus*. The major fatty acids (anteiso-C₁₅ : ₀, iso-C₁₅ : ₀, iso-C₁₇ : ₀ and anteiso-C₁₇ : ₀) detected in the novel strain (presented in the species description) were consistently found in members of the genus *Salinicoccus*. The fatty acid compositions of the reference strains analysed were qualitatively similar, but varied quantitatively from those of the novel strain (Table 2).

The predominant polar lipids were diphosphatidylglycerol, phosphatidylinositol and phosphatidylglycerol, along with one unknown glycolipid and three unknown phospholipids (Fig. S1, available in the online Supplementary Material). The major menaquinone detected for strain SV-16T was MK-6. The diagnostic cell wall diamino acid was L-lysine and the inter-peptide bridge consisted of L-Lys–D-Gly.

The DNA G+C content of strain SV-16T was calculated as 48.7 mol% (based on whole genome data), which falls within the defined range (45.7–54.5 mol%) accepted for the members of the genus *Salinicoccus*. The almost complete sequence (1453 bases) of the 16S rRNA gene of strain SV-16T was determined and was compared with those of closely related taxa retrieved from the GenBank database. The phylogenetic tree (Fig. 1) reconstructed using the neighbour-joining method suggested that this strain is a member of the genus *Salinicoccus*. Almost the same pattern was obtained using other algorithms like maximum-parsimony and maximum-likelihood. Pairwise

### Table 2. Percentage of total cellular fatty acids from strain SV-16ᵀ and the type strains of closely related species

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>C₁₂ : ₀</td>
<td>2.3</td>
<td>1.5</td>
<td>1.8</td>
</tr>
<tr>
<td>iso-C₁₄ : ₀</td>
<td>1.1</td>
<td>0.8</td>
<td>1.0</td>
</tr>
<tr>
<td>iso-C₁₅ : ₀</td>
<td>23.9</td>
<td>27.4</td>
<td>20.0</td>
</tr>
<tr>
<td>anteiso-C₁₅ : ₀</td>
<td>27.4</td>
<td>27.5</td>
<td>35.5</td>
</tr>
<tr>
<td>C₁₆ : ₀₇c alcohols</td>
<td>2.0</td>
<td>2.4</td>
<td>2.2</td>
</tr>
<tr>
<td>iso-C₁₆ : ₀</td>
<td>4.1</td>
<td>3.5</td>
<td>3.5</td>
</tr>
<tr>
<td>C₁₆ : ₁₁c</td>
<td>0.9</td>
<td>0.54</td>
<td>1.0</td>
</tr>
<tr>
<td>C₁₆ : ₀</td>
<td>1.4</td>
<td>1.0</td>
<td>1.0</td>
</tr>
<tr>
<td>C₁₇ : ₀₉₁₀c</td>
<td>4.1</td>
<td>5.6</td>
<td>4.1</td>
</tr>
<tr>
<td>anteiso-C₁₇ : ₀</td>
<td>11.2</td>
<td>10.2</td>
<td>12.0</td>
</tr>
<tr>
<td>iso-C₁₇ : ₀</td>
<td>9.9</td>
<td>9.7</td>
<td>7.2</td>
</tr>
<tr>
<td>iso-C₁₉ : ₀</td>
<td>4.2</td>
<td>3.3</td>
<td>3.2</td>
</tr>
<tr>
<td>anteiso-C₁₉ : ₀</td>
<td>1.4</td>
<td>1.1</td>
<td>1.4</td>
</tr>
<tr>
<td>C₁₈ : ₀</td>
<td>0.8</td>
<td>0.8</td>
<td>0.54</td>
</tr>
<tr>
<td>C₂₀ : ₀</td>
<td>1.1</td>
<td>0.54</td>
<td>0.52</td>
</tr>
<tr>
<td>Summed feature 4*</td>
<td>1.7</td>
<td>2.8</td>
<td>3.2</td>
</tr>
</tbody>
</table>

*Summed features represent groups of two or three fatty acids that could not be separated by GC with the MIDI system. Summed feature 4 contained iso-C₁₇ : ₁₁ and/or anteiso-C₁₇ : ₁₁.

*Salinicoccus salsiraiae* RH₁ᵀ (DQ333949)
*Salinicoccus siamensis* PN₁-2ᵀ (AB258358)
*Salinicoccus jeotgali* S₂R₅₃-₅ᵀ (DQ471329)
*Salinicoccus roseus* DSM 5₃₅₁ᵀ (X945559)
*Salinicoccus iranensis* QW₀ᵀ (DQ986633)
*Salinicoccus sesuvii* CC-SPL₁₅-₂ᵀ (FR669114)
*Salinicoccus halodurans* W₂₄ᵀ (DQ986633)
*Salinicoccus sediminis* SV-₁₆ᵀ (KF701618)
*Salinicoccus carnicancri* Crmᵀ (FJ82049)
*Salinicoccus qingdaonensis* ZXM₂₂₃ᵀ (FJ436724)
*Salinicoccus kunmingensis* YIM Y₁₅ᵀ (DQ837380)
'Salinicoccus kekensis' K1₆₄ (GU363531)
*Salinicoccus alkaliphilus* T₈ᵀ (AF275710)
*Salinicoccus albus* YIM-Y₂₁ᵀ (EF177692)
*Bacillus altitudinis* 4₁KF₂bᵀ (AJ831842)

**Fig. 1.** Neighbour-joining tree based on 16S rRNA gene sequences, showing the phylogenetic relationship between strain SV-₁₆ᵀ and other related members of the genus *Salinicoccus*. *Bacillus altitudinis* 4₁KF₂bᵀ (AJ831842) was used as an outgroup. Bootstrap values (expressed as percentages of 100 replications) greater than 70 % are given at nodes. Filled circles indicate that the corresponding nodes were also recovered in the tree generated with the maximum-parsimony and maximum-likelihood algorithms. Bar 0.1 % sequence variation.
sequence analysis revealed that the highest sequence similarity was with S. carnicancri Crm\(^T\) (98.6 %) followed by S. halodurans W24\(^T\) (96.6 %); the remaining species with validly published names showed less than 95.0 % similarity.

The DNA–DNA reassociation values between strain SV-16\(^T\) and the moderately related strain S. carnicancri Crm\(^T\) using the membrane filter method of Tourova & Antonov (1987) was 51.60 ± 0.6 %. The DDH method, using the genomes of strain SV-16\(^T\) and S. carnicancri Crm\(^T\), revealed a value of 51.30 ± 2.65 %. The overall genomic relatedness of SV-16\(^T\) with respect to the other related species may not be high because, as Stackebrandt & Goebel (1994), Stackebrandt & Ebers (2006) and Kim et al. (2014) observed, strains with less than 98.6 % 16S rRNA gene sequence similarity have DNA–DNA relatedness values below 70 %, where this value is considered as the ‘gold standard’ for bacterial species definition (Wayne et al., 1987), which makes it unnecessary to perform DNA–DNA hybridization, hence DNA–DNA hybridization was therefore not executed for the other species. The draft genome of strain SV-16\(^T\) consisted of 2 591 284 bp with a DNA G+C content of 48.71 mol%, 2592 predicted CDSs, 92 RNAs and 385 subsystems. The ANI of the genome sequence of strain SV-16\(^T\) against the species of the genus Salinicoccus for which genome sequences are publicly available ranged from 92.98 to 93.07 % (with strain S. carnicancri JCM 15796\(^T\)). These ANI values are also considerably lower than the 95 to 96 % threshold used to identify isolates as belonging to the same bacterial species (Goris et al., 2007; Richter & Rosselló-Móra, 2009). Based on the differential phenotypic and genotypic characteristic features of strain SV-16\(^T\) in comparison with closely related species, it is concluded that strain SV-16\(^T\) represents a novel taxon for which the name *Salinicoccus sediminis* sp. nov. is proposed.

**Description of Salinicoccus sediminis sp. nov.**


Cells are aerobic, Gram-staining-positive, motile cocci. Colonies are circular, convex, smooth and pigmented creamish-yellow. Catalase and oxidase are produced. Negative for H\(_2\)S, indole and urease production, and methyl red and Voges–Proskauer tests. No growth occurs on MacConkey agar or Simmons’ citrate agar. Growth occurs at temperatures of up to 25–37 °C (optimum 30 °C), at pH 7.0–11.0 (optimum pH 8.0) and at NaCl concentrations of up to 25 % (optimum 15 %). Nitrate is reduced to nitrite. Hydrolyses casein, gelatin and starch. Cell wall contains lysine as the diagnostic diamino acid. The predominant polar lipids are diphosphatidylglycerol, phosphatidylinositol and phosphatidylglycerol along with one unknown glycolipid and three unknown phospholipids. The major isoprenoid quinone is MK-6. The major cellular fatty acids are iso-C\(_{15}:0\), anteiso-C\(_{15}:0\), iso-C\(_{17}:0\) and anteiso C\(_{17}:0\).

The type strain, SV-16\(^T\) (=MTCC 11832\(^T\)=DSM 28797\(^T\)), was isolated from marine sediment at a depth of 12.5 m, collected from Sothavilai, Kanyakumari, Bay of Bengal coast, India. The DNA G+C content of the type strain is 48.7 mol%.

**Acknowledgements**

We wish to express our gratitude to Dr Citarasu and Mr Velmurugan for their excellent assistance during the sample collection. We also thank Mr Malik Singh for his technical assistance. This work is supported by the project ‘Expansion and modernization of Microbial Type Culture Collection and Gene Bank (MTCC)’ jointly supported by Council of Scientific and Industrial Research (CSIR) grant no. BSC0402 and Department of Biotechnology (DBT) Govt. of India grant no. BT/PR7368/INF/22/177/2012. This is IMTECH communication number 055/2014.

**References**


Salinicoccus sediminis sp. nov., from marine sediment


