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June 2025



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Diatom Biosilica: Synthesis, Characteristics, Modification, and Application

A. GolubevaM. Kulikovskiy

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Microbial Communities and Biogeochemical Processes in High-Altitude Cascade Lakes of Central Caucasus (Lake Klukhor)

A. S. SavvichevV. V. KadnikovN. V. Pimenov

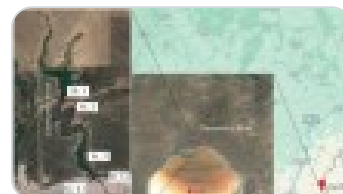
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Role of Microorganisms in the Hydrocarbon Balance in the Highly Productive System of the Chernavka Salt River (Elton Region)

T. A. KanapatskiyI. A. NemirovskayaN. V. Pimenov

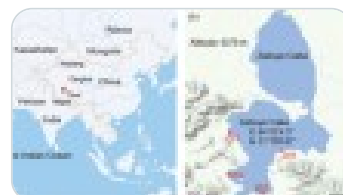
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Archaeal Communities within the Alkaline-Soda Zabuye Lake in the Qinghai-Tibet Plateau

Yujie TaoRui HanPeixia Zhang

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***Desulfosporosinus shakirovi* sp. nov., a Sulfate-Reducing Bacterium Capable of Degrading Petroleum Hydrocarbons**

A. I. EskovaYa. V. RyzhmanovaV. A. Shcherbakova

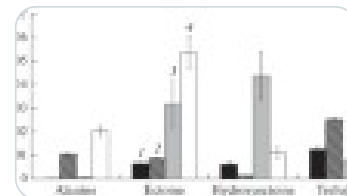
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Adaptation to Growth at Low Temperature of Psychrotrophic Bacteria Isolated from Soil of the Northern Perm Krai

L. N. Anan'inaA. A. GorbunovO. V. Yastrebova

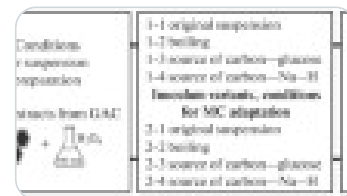
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Formation of Biofilms by Groundwater Microorganisms on Granular Activated Carbon

Z. N. LitvinenkoL. M. Kondratyeva

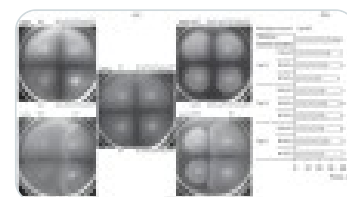
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Bacteria of the Genus *Azospirillum* Form Biofilms with *Enterobacter cloacae* K7 in the Root System of Wheat Seedlings

A. V. Shelud'koD. I. MokeevL. Yu. Matora

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Towards the Regulatory Network of Methanotrophs Based on Available Gene Expression Profiles

T. S. SokolovaS. K. KolmykovI. R. Akberdin

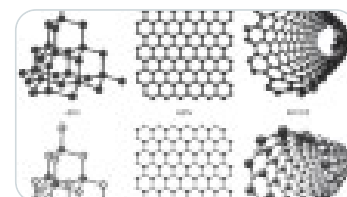
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Comparative Analysis of the Effect of Nanoparticles with Different Composition on Escherichia coli Cells

E. A. ObratsovaS. TerekhovE. V. Sorokina

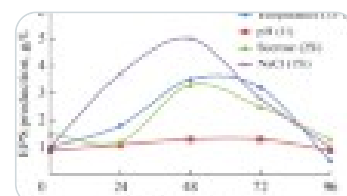
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Exopolysaccharide Production by *Bacillus* sp. NIOTSM16 from Arabian Sea Seamounts: Characterization and Optimization

H. MurugesanS. ShobananDh. Gopal

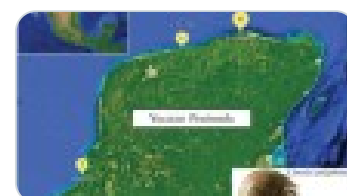
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Gut Microbiota Composition of American Horseshoe Crabs (*Limulus polyphemus*) from Yucatan Peninsula

J. G. Nic-MatosC. A. Puch-HauJ. J. Sandoval-Gio

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The Whole Genome Sequencing Analysis of a Halophilic *Streptomyces* sp. C11-1

P. GuanW. MaP. Qin

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BacTFid—A Simple, Efficient Bacterial Transcription Factor Identifier and Classifier

P. VychykA. DigrisY. Nikolaichik

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A screenshot of the BacTFid software interface. The interface displays a table of identified transcription factors. The table has columns for 'Transcription Factor Name', 'Accession Number', 'Length', 'Score', and 'Description'. The table lists several transcription factors, including 'BacTFid_1', 'BacTFid_2', 'BacTFid_3', 'BacTFid_4', 'BacTFid_5', 'BacTFid_6', 'BacTFid_7', 'BacTFid_8', 'BacTFid_9', 'BacTFid_10', 'BacTFid_11', 'BacTFid_12', 'BacTFid_13', 'BacTFid_14', 'BacTFid_15', 'BacTFid_16', 'BacTFid_17', 'BacTFid_18', 'BacTFid_19', 'BacTFid_20', 'BacTFid_21', 'BacTFid_22', 'BacTFid_23', 'BacTFid_24', 'BacTFid_25', 'BacTFid_26', 'BacTFid_27', 'BacTFid_28', 'BacTFid_29', 'BacTFid_30', 'BacTFid_31', 'BacTFid_32', 'BacTFid_33', 'BacTFid_34', 'BacTFid_35', 'BacTFid_36', 'BacTFid_37', 'BacTFid_38', 'BacTFid_39', 'BacTFid_40', 'BacTFid_41', 'BacTFid_42', 'BacTFid_43', 'BacTFid_44', 'BacTFid_45', 'BacTFid_46', 'BacTFid_47', 'BacTFid_48', 'BacTFid_49', 'BacTFid_50', 'BacTFid_51', 'BacTFid_52', 'BacTFid_53', 'BacTFid_54', 'BacTFid_55', 'BacTFid_56', 'BacTFid_57', 'BacTFid_58', 'BacTFid_59', 'BacTFid_60', 'BacTFid_61', 'BacTFid_62', 'BacTFid_63', 'BacTFid_64', 'BacTFid_65', 'BacTFid_66', 'BacTFid_67', 'BacTFid_68', 'BacTFid_69', 'BacTFid_70', 'BacTFid_71', 'BacTFid_72', 'BacTFid_73', 'BacTFid_74', 'BacTFid_75', 'BacTFid_76', 'BacTFid_77', 'BacTFid_78', 'BacTFid_79', 'BacTFid_80', 'BacTFid_81', 'BacTFid_82', 'BacTFid_83', 'BacTFid_84', 'BacTFid_85', 'BacTFid_86', 'BacTFid_87', 'BacTFid_88', 'BacTFid_89', 'BacTFid_90', 'BacTFid_91', 'BacTFid_92', 'BacTFid_93', 'BacTFid_94', 'BacTFid_95', 'BacTFid_96', 'BacTFid_97', 'BacTFid_98', 'BacTFid_99', 'BacTFid_100'. The table also includes a 'Description' column for each transcription factor.