



Henkel AG & Co. KGaA  
Attn. Dr. Christian Degering  
Henkelstr. 67  
40589 Düsseldorf

Madrid, 29 November 2022

Dear Dr. Degering,

The Institute of Catalysis and Petrochemistry (ICP-CSIC) is fully committed to the United Nations Convention on Biological Diversity and the associated Nagoya Protocol, which regulates the balanced and fair sharing of the benefits arising from the use of genetic resources. The following sequences are foreseen to be transferred to Henkel:

1.

Name	FE_Lip9
Location origin (Country)	Seongsan-ri, Jeju Island, South Korea (33.38°N 126.53°E) Note: the sequence was identified by homology screen in the MarRef - Marine Metagenomics Database, a manually curated marine microbial reference genome database that contains completely sequenced genomes ( <a href="https://mmp2.sfb.uit.no/marref/">https://mmp2.sfb.uit.no/marref/</a> ). This protein is similar to one isolated from a strain isolated from the marine sponge in the seawater in front of Seongsan-ri, Jeju Island, South Korea (E-value of 8,56E-137 with WP_034624255.1_MMP06016472 MULTISPECIES: esterase [Bacillus] [mmp_id=MMP06016472] [mmp_db=marref]). Sample was collected 2011-11 ( <a href="https://www.ebi.ac.uk/biosamples/samples/SAMN06016472">https://www.ebi.ac.uk/biosamples/samples/SAMN06016472</a> ), so that before the Nagoya Protocol entered into force on 12 October 2014
Date of sampling	November 2011
Date of discovery	July 2021

Protein sequence:

MKVMFVKKRSLQILIALALVIGSMAFIQPKVKAAEHNPPVVMVHGIGGASYNFFSIKSY-  
LATQGWDRNQLY AIDFIDKTGNRRNNGPRLSRFVKDVL DKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTIGGANGLVS  
SRALPGTDPNQKILYTSVYSSADLIVVNSLSRLIGARNVLIHGVGHIGLLTSSQVKGYIKEGLNGGGQNTN

2.

Name	FE_ID9
Location origin (Country)	Byfjorden, Bergen, Norway (60.397093N; 5.301293E) ID9 (original name EstLip_NODE_494_length_56501_cov_3.272419_27) was isolated from the microbial assemblages from bone surface and the bone-eating worm <i>Osedax mucofloris</i> (BioProject ID PRJNA606180), collected at Byfjorden, Bergen, Norway (60.397093N; 5.301293E). The samples were collected from 01.2017 to 11.12.2017 in Norway, in the frame of the EraNet project ProBone. Norway was among the first when ratifying the Nagoya protocol so that Nagoya protocol applies; all documentation (including pictures) that shows where the samples were taken can be made available upon request.
Date of sampling	Sampling done from 01.2017 to 11.12.2017
Date of discovery	July 2021

Protein sequence:

MTNLSKPIPMPREYPILPPDMNYIYFENAHLFPFEPEKRDYSPVNAWWLSECAFLVYCHPG-  
FARMAMALVGFDFHFFQKGTCEMVSWNKDSIIVAFRGTEMKSLSAFHELRTDLNTAPVDFDKGSKVHKGFLKGLQEIWEGEE  
GLKLFLETLSAEAPSRSMWICGHS LGGALAALCFARLEKASGLYIYG-  
APRIGDGEFVRICDNRPVWRVEHGRDPIPLVPPDVPALNFNFKDMGKLIYIDYRGEILFERPLVTVEEEKSKVLLNISQQRKRRESLS

VEGFKGVLDKDRAKTLINGINEHIMQSRVEWKEYFDSLDKGIGLKIKDHMPYYCAKLWNILIEGL

3.

Name	FE_Polur1
Location origin (Country)	Rothamsted, UK (Latitude, longitude: 51.8138, -0.3783) The sequence was identified by homology screen in the NCBI's database; it corresponds to the uncharacterized protein WP_127927389.1 from the genome of <i>Pseudomonas</i> sp. RU47. The genome of this strain, sequenced at the JGI, was released 2021-01-04. The strain was isolated from soil sample at Rothamsted, UK in 2007 (BioSample: SAMN07173783), before the Nagoya Protocol entered into force on 12 October 2014
Date of sampling	Sampling done on 18.03.2002
Date of discovery	July 2021

Protein sequence:

MGVYDYKNFGTADSKALFSDAMAITLYSYHNLNNGFAAGYQHNGFGLGLPATLVTALLGGTD-SQGVIPGIPWNPDESEKLALDAVKQAGWTPITASQLGYDGKTDARGTFFGEKAGYT-TAQVEILGKYDAQGHLELGIARFGTSGPRENLILDSIGDVINDLLAAFGPKDYAK-NYVGEAFGNLLNDVVAFKANGLSGKDVLSVSHSLGGLAVNS-MADLSGGKWGGFFADSNIYASPTQSSTDKVLNVGYENDPVFRALDGSTFTGASVGVHDAP-KESATDNIVSFNDHYASTAWNLLPYSILNIPTWISHLPTAYGDGMNRVIDSKFYDLTSRD-STIIVANLSDPARANTWVQDLNRNAETHKGSTFIIGSDANDLIQGGSGNDYLEGRAG-NDTFRDSGGYNVILGGQGSNTLDLQSAVKNFDFANDGAGNLYVRDANGGISITRDIGSIVT-KEPGFLWGLFKDDVTHSVTASGLKVGNNVTAYESSVKSAGADTLKAHSGGDWLFGLD-GNDHLIGGAGNDVFGGAGNDLMESGGGADTFLFNGAFGQDRVVGYSND-~~K~~LVFLGVQGVLP AEDFRAHAATVGGQDTVLTFGNDSVTLVGVSLNSLSAEGVVIA

Name	FE_Lip5lid
Location origin (Country)	Seongsan-ri, Jeju Island, South Korea (33.38°N 126.53°E) Note: the native sequence (FE_Lip5) was identified by homology screen in the MarRef - Marine Metagenomics Database, a manually curated marine microbial reference genome database that contains completely sequenced genomes ( <a href="https://mmp2.sfb.uit.no/marref/">https://mmp2.sfb.uit.no/marref/</a> ). This protein is similar to one isolated from a strain isolated from the seawater in Trondheimsfjord (Norway), front of Seongsan-ri, Jeju Island, South Korea (E-value of 2,53E-11 with WP_075743487.1_MMP03339750 MULTISPECIES: lipase [Actinoalloteichus] [mmp_id=MMP03339750] [mmp_db=marref])). Sample was collected in 2005 ( <a href="https://www.ebi.ac.uk/biosamples/samples/SAMN03339750">https://www.ebi.ac.uk/biosamples/samples/SAMN03339750</a> ), so that before the Nagoya Protocol entered into force on 12 October 2014. The FE_Lip5lid is a mutant of FE_Lip5, designed by a collaboration CSIC-BSC.
Date of sampling	2005
Date of discovery	July 2021

Protein sequence:

MAHHHHHHVGTGSNDDDDKSPDPMTVSALDHRVTGYQLDHAYWLGKAAKLAYSGLGEEIRAE-TARWGFDRFRFLHVVRDLPVPLDDTQAYLAASDHMIILAFRGTNSFRSAITDIVFTTPVAPG-PADRGLVHLGFDQALATVLPVLCQGIKELRTNDQSIWLTGHSLGGALAMLAATLY-FEDPNLTPDGVYTFGQPRTCDPRLAHAYDEALEGRTRFRVNNNDIVPQLPPEPVFRHV-KAARYFDRTGALHEQLSLWGGIADKVGGHTEDELLLPGSALDKDHPMDRYLENIEKNL

ICP-CSIC, confirms that the genetic sequences, enzymes, named above that are handed over to Henkel within the collaboration project FUTUREZYME (EU Horizon 2020 project 101000327, FNR-16-2020)



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have been accessed in accordance with applicable access and benefit sharing (ABS) regulation, incl. the Nagoya protocol, EU ABD regulation 511/2014 and potentially other regulatory requirements.

With the best regards,  
Prof Manuel Ferrer

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