

Natural biocide cocktails: Combinatorial antibiotic effects of prodigiosin and biosurfactants

Jennifer Hage-Hülsmann, Alexander Grünberger, Stephan Thies, Beatrix Santiago-Schübel, Andreas Sebastian Klein, Jörg Pietruszka, Dennis Binder, Fabienne Hilgers, Andreas Domröse, Thomas Drepper, Dietrich Kohlheyer, Karl-Erich Jaeger, Anita Loeschcke

Description	Max score	Total score	Query cover	E-value	Identity	Similarity
rhamnosyltransferase [<i>Dickeya dianthicola</i>] WP_024106541.1	539	539	98%	0.0	60%	75%
rhamnosyltransferase subunit B [<i>Pseudomonas aeruginosa</i> PAO1] NP_252168.1	220	220	91%	4e-68	31%	50%

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NP_252168.1      1  MHALIATGSGAGDVPEFPIGLARLAKLRGHNVSICLTPVFRDAVEQHGIAFVFLSDELTVRRTMGDFRLWDPKTSFGVLWQATAGMIEPVVBYVSA
WP_024106541.1  1  MRVFLSLTGSAGDVYPIIRFGEAERKNGGLDVIYCTPFYEQTKRERGMSTFVGSSEDLKLVNSQRZWHQOSEKEMVKEHNAQQOQADAVV
WP_021016571.1  1  MKIFLALGSGAGDVYPIAIGESLITQAGYDVIYCTNPFPEKTALEERHEHFEIVGANEVYLAVNSKRZWHKRYATKEECHMMQQOQLYDAENS

NP_252168.1      96  QRHDDIVVVGSLWALGRTAHERKYGIPYLSAQVSPSTLMSAHLPPVHPKFNVPQMPFLAMRKLWRCLEKFLDRTCAPPETNAVRKVGLETPVK
WP_024106541.1  96  RVDKSSVITLSLWAFSAKMLSEKKGCCVFPVRSPTLMSAYETAHRRYTAQLSHPFRIRREVLGLTERVITDRSEAPLNOFRVSLGLP-KEH
WP_021016571.1  96  VTDSSSILLTSLWAFSAKMLSEKKGCCVFPVRSPTLMSAYETAHRRYTAQLSHPFRIRREVLGLTERVITDRSEAPLNOFRVSLGLP-KEH

NP_252168.1      191  RIFQWVHSP-QGVVCLFPFAWFAFPQODWFOPLHMGFFLEFGSIPGTFLDDELRQRFIDQGSRLVFLQGSTEHLQGFYVMALRALERLQVGRGI
WP_024106541.1  190  RVLPSVHRFDAAALLCFPEWESPLPDWFDHVRQVGFPLNML--DNGQDDLAQET-ARRRZVIEFMPSNALSARRSLAI---SFLVKKRQRCY
WP_021016571.1  190  RLLPSWZHKRDSNVIICFPDPWFAAPQPDWRHKKQVGFPLNML--ARRQDDLDCEFNASNKVIEFMPSNALSARRSLAI---EFLVKKRRCY

NP_252168.1      285  FLTGACQE-PLRGLPNHVLQRAYAPLGLALTESCAGLVHDCGICGAMSLATAAGVPOVLLWPCAHDQFDNAERLVRHCCGMRRCVPLRQELRGAFWR
WP_024106541.1  279  QCLIVCKPFYHELADDFQVRAEGHTNLGQYLHRCALTIHGGGIGTMAQSFACITPQDVLPSAFDQFDNARRVTAKCGEWHFES-DIDKLDKRR
WP_021016571.1  280  QCLIVCKPFYHELADDFQVRAEGHTNLGQYLHRCALTIHGGGIGTMAQSFACITPQDVLPSAFDQFDNARRVTAKCGEWHFES-DIDKLDKRR

NP_252168.1      379  LLEDPAMAAACRRRPMELSPHSTACGKAAQVVER-----CHRECDARWLKAAS
WP_024106541.1  373  LLSADFLAEHCQRTRQQFPSEDAVGSHTVDTVREKVARHMAKVDSEHAVIHPD-
WP_021016571.1  374  TLFDRSAAQHCQYLRNDFANQAVYQQLVAIVEAQLNENTPMV-----

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S5 Fig. Sequence alignment of *Serratia* sp. ATCC 39006 putative glycosyltransferase with two putative homologs. The putative glycosyltransferase from *Serratia* sp. ATCC 39006 (NCBI RefSeq WP_021016571.1) was identified by BLASTP similarity search using the known rhamnosyl transferase RhIB from *Pseudomonas aeruginosa* (NCBI RefSeq NP_252168.1) to search for similar sequences within the NCBI protein sequences database limited to *Serratia* sp. ATCC 39006 (Genome at NCBI Genbank Masterentry NZ_AWXH0000000.1). The sequence of the putative glycosyltransferase from *Serratia* sp. ATCC 39006 was then subjected to NCBI protein sequences database similarity search with BLASTP and yielded the best scoring hit with the sequence of a putative rhamnosyltransferase from *Dickeya dianthicola*. Result table of BLASTP pairwise alignment of the *Serratia* sp. ATCC 39006 glycosyltransferase with the two homologous proteins and Clustal Omega (Sievers *et al.* (2011), doi:10.1038/msb.2011.75) multiple sequence alignment of all three proteins are shown.