

ЭКСПЕРИМЕНТАЛЬНЫЕ СТАТЬИ

***PALUDISPHAERA MUCOSA* SP. NOV., НОВЫЙ ПЛАНКТОМИЦЕТ СЕМЕЙСТВА *ISOSPHAERACEAE* ИЗ БОРЕАЛЬНОГО НИЗИННОГО БОЛОТА**

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Таблица S1. Гликозил-гидролазы штамма Pla2^T, проанализированные в работе

Обозначение	Подсемейство	Длина	Ближайший гомолог	Аминокислотная последовательность
Pla2_03346	GH10a	401	<i>Paludisphaera soli</i> , WP_165250526.1, 73%	MPSRPLVSRRRIGLRGWWRPAFALLTAAAMGSDGPGPGAHPGDSGV PMGIEAVDPEAGTLWQAARGRLLIGAAVSSRQFDDAGLAALIAEQFDC LTAENEFKPMSLQPRPNQFRFEAADRIVEFARRHGMKVVGHTLCWHS QSPRWLFAGDDGKPLPRDEALKNLEAHVAAVVGRYRGRVLGWDVVN EAIGDAPNAHLRDTPALRAIGGDYIVKAFQFARAADPDAELYNDYGN EAPAKLEKTLRLVRELKAAGVRLDAVGIQSHFVLGDTDATDRLKRAV EALAAEGVKVAVTELDVDVLPRRGRGADVAAAREQGGADPYTEGLPAE VAEAQARFYARIFRVAVDHPGVVARVTFWGTHTDGTSWLNFYPAGRRT NHPLLWDRKLKPAFEAVLKLLNTP
Pla2_05951	GH10a	406	<i>Paludisphaera soli</i> , WP_165250526.1, 72%	MHAHPRTSRPFSPRAWSPLAFAVLSAAAVATARAGWGGPAAAPPSG AGGPAAVATALPEGETLRQAAKGRFLIGAAVSSRQLGDPKMADLIARQ FDSLTAADNEFKPISLQPRPGQFRFDAADRIIEFAQAHGMKVVGHTLCW HSQSPRWLFEGEDGKPLPRDEALRNKKAHIDAVAGHFRRKVVGWDVV NEAISDRPGEYLRDTPARRAIGDDYVVKAFEFAREADPDAELYNDYG DEEPGKLEKTLRLVRELKAAGARLDAVGIQAHFVLKDADSPDQLERAI GALAAAGVKVVVTELDVDVLPRRVRGADVAARERGAADPYTEGLPP DVAEAQARFYERIFRAVLKHPGVATRVTFWGTHTDGTSWLNFFPAGRR TNHPLLFDGRGHQPKPAFGAVLGVLSPP
Pla2_04228	GH10b	496	<i>Paludisphaera rhizosphaerae</i> , WP_165063590.1, 84%	MGVLKFRLPSNEIAGKLASQRRVYTTGLDRTPGRLGLDFRNGLMTCTS DSSESGRLFTPWPIAGFGSPVVGATLGERAAPYVLALCLARGKLNDV RNQSADWTQLGLRTESTLDDLMRTSRAAFVRAALLADDPDASYAAQ ESLEASSLAGAQLTETYLAQVLQNRLAVAGRLSTNLGCVLSGDPDKAA GSATWPSTFNTAQTAASWKDVAPSEGKHRWDLLDAQVAWARKHHL NVEGGPLIEFRAACLPDWIWLWDGDVDTISSFVADYVRQVVTRYRGK VPIWHVAHRPAGHDVLGLGEEDQIRITARALQVARQADPAAQLCLGID RPWMEWMSSSRFQLGPLHLCDYLIRSDVGISSVALEIAPGYSNPGSDGR DLFEFSRLLDLYSLNVLPLNVTLVAPSAATPDPNADANVKVEVWQWP APPTASQAQEWAAARWTS LAVAKPFVRAVNWLQPSDGITHLYPHGGLH RPDGSPKAAVARLRTIRGDLLA

Pla2_02372	GH27a	519	<i>Acidobacteriota</i> bacterium, MBI3680388.1, 60%	MQDRTRRSAAAVALAFLGVLAPADARSQEPGRSNLWTPPATLAPRL NGPAVYGVVRPGREVIHRIACTGERPIAFAVEGLTEGLTFDAAAGVIRGK APSREGRHPLKITARNRHGEASRSLALAVGPTIALTPPMGFNDWYTWA DRITQKDMLAATAKAMIDSGLADHGYYVNVDDCWMVKPGSADPDRL GDSADPAAAIRPNRRFPDMKGLADSVHALGLKAGLYSSPGPLTCAGFA GSFGHEAADAEEFAAWGFDLKYDWCSEQVAVGPGLEKHQKPYRL MGELLAQQRDIVLNLCCQYGVADVWTWGASVGGQSWRTTGDLGLEP GSRLPGFYAIGLSNAKHAEHAGPGRWNPDIYILIGIVGDAGDFTRPPRK APLTVEEQYSYMSLWCLMAAPLFYSGDVTRMDEQTLNVLGNDELIAI DQDELGRQARVVRRTDDELVLAKPLADGGGLAVGLFNLSESTVAAS WPELGVDGARTIRDCWRRRDLGSSDARCESKLARHSVAVVRVPRGG
Pla2_03258	GH27e	445	<i>Abditibacteriota</i> bacterium, BCM93998.1, 59%	MRFRRSIAWLPLVLAAPPAATPARAERPPAERPYLGWSSWSLQATESP GYGKAFLTAENVKRQSDAMAARLQAHGFLRINVDSGWRGGWDEHGR PTPDLERFPQGVVDVADHVHAHGQKFGIYYVPGVDDDLLALDPPIGT SYTVRQIVHTPRRLAHAWKGGHAIDFAKPGAKEYVRSIADRFAAWGV DFLKFDGVTGSDVDDPSIDARDDVAAWSESLLATGRPIWLTVSWKLD MRHADFWRGRADAVRVTQDVESYDALLTHWRPQILRAFPAARDFGPT SGRGKGWNDLDSLLVGNGAMSGLTPDERRSAMTLWAVACSPLYAGD DLTKLDDLGLELLTNDEVIAVQQAGFPAALIRDDGRGGQVWSSANAG GKVVALFNLAEEERTISIPSLGLPSSVAARDLWARRDLPAASDRVEA DLAPHACRLLRLAPEPPR
Pla2_05968	GH32b	708	<i>Planctomyces</i> sp. SH-PL62, AMV40679.1, 76%	MLATMVLVGLLAGAPAAQDAKRPDVPIADFEGPDYGGWKATGEAFG PAPARGTLPQMTVEGYLGQGLVNSFRGGDDATGELASPPFRIEREHL NFLIGGGGWAGETCLDLLVDGKVVRSATGPNRDPGGTERLRWAAWD VKDLQGGKDATLRVVDRRKGGWGHVNVQIVQTDAPKLPVRATRAIA LKDRYLLIPVKTGAPKVRKILGERGETLRDFDVELAPGEADFFAFSDL AAHRGSTVTVRVDELEDPTALGRIQQSAFLPGAAEAYKEKHRPQLHFT SRVGWLNDPNGLVWQDGEYHLFYQHNPFGWAWGNMHWGHAVSPD LVHWKEAGIALYPHEYGDWAFSGSAVVDVKNTGGFQKGDKPPIVAAY TSTGRGECIVYSNDGGRTMTEYEGNPVVKHEGRDPRLLWHEPSKRWW MAVYDEGKNPDRQSIDFYTSPDLKAWTFGSRLDGGFFECPDFELAVDG DPSNKLWVVYAADGKYKLGKFDGKTFEVVSQPEKLVFRHGNFYAAQ TFSDEPKGRRIQIGWANGVTFPGSPFNQQMSLPTLTLRMTKDGPRIFA

				EPVAELKSLRAGAREFSKTTLEPGAKNPLEGATSGDLYEIELAFRPNGA ESVELDLRGTPLVYDVKRQDVVCKQVRTFVPQVDGLVTLHVFDVDRGSI EVFANGGRTAISVADLADDANHSLGIAAKGGAVGLERLVVYPLRSSW
Pla2_05839	GH32b	620	<i>Capsulimonas corticalis</i> , BDI30740.1, 71%	MPLSTLALGLSLLSACAQPPASAPDVVIGEFEEAAAHAPWEASGTAFGS GPALGAKAADLEIAGVRGDGVASSEFAGDGPVGTLTSPPFQVERRFIAF VIGGGSFERDTCLDLVVDGKVVRSATGANSDLLRPCSWDVTPFLGREA RVRVVDRASGDWGHVNVVDHVVTDRPERPPVVAQPLYRENHRPRFH FTARQWTVDRNLNPGMREEGWLNGLVYYDGEYHLFAQRWNKCW IHAVSRDLVRWTELEPAFWEEALDVGVSQSGTCVVDYANSSGLSPDPAT PPMVAFWTRNDNRSHGIAFSLDHGRTWKYGPRNPVLVKPERDPMVFR HKPTQKWVMIMYGEDKYHVLTSNLLDWKDEKRPIANSFECPDFFEL AVAGDPATRKWALIRGDGRYSLGSFDGSEFREETAQFESDGGPNFYAT QTWGNVETGDGRRIQAAMRGGAYPDMPPFNQQVTFPRELTLRPTPAG LRLFREPVEIATLHRDERKFEARILQAGERLALDEPGDALHIKMDVAV PEGATLTLRIRGVPLVLGRRSIACKSGPQAVAGDLEAVEVLIDRTSIEAF ANHGEASTSTCFLPAGDEVAFEAAAGGPATIRALS VFRLEGIWDGRAAK
Pla2_05993	GH32(?)	740	<i>Planctomyces</i> sp. SH- PL62, AMV40650.1, 84%	MTTRRGLARSASWLVLFLGLSVPTLAAEWELRDKTLVVAAPANLGQ QGGSALTQQPGGGFDVVFGEAPGRWMAGSEFFRRTQTDQSAAAA ETGDAKTLVQVAVAYKGRRVSIYRDARPYAEYDMASEPVAFTSSSSVA LLGLRHLEMMGGPTFRGEIEDARIYPLALDAGALSKLKPDQPSDPAPLA WWTFFDDGKVDDRMGAFFPARLMGAATVRDGRHLHDGGFAMIGKGIG AARTRETDWPTYHVSALPREGLARPYDANGCIYWKGYHLMYIYQD PKLPKGGHCWGHAVSTDLDVDTFLPPALVPQREDRDVGIFSGNAFLD KNGVPTLCWFGVEAGVCVATAADDDLVWKKHPKNPIIPMPRPGEPG HGVYTVWDPYLWLEGDDYICLLGGNKL PNGKDTLYTMKSKDLVSWA PVGPFDDHPDLSWTTEGEDCSCPDFFKIGGKRALLCISHKVGGRIYIGRY ENDRFFPEKHVRMNWPGGQFFAPESLLDDKGRRIIWA WVTDPRTLPTQ QATGSGVQSLPRVIDLDVEGNLTIKPVPELERLRNPRRSADMSVGSEV AVATFDGAPIRGDAMELALSVEPGSAEEVAVAVRCTPDDSEKTVIRYR PGAKTLAIDSSKSTRRDDVVYTNGPLDTGGLLRGSDYKNPRNVFEAPL ELKPGEPLRLRIFLDGPMLEVFANDRQCLTQQVFPESEKARMVKVSAQ GGPVIFNGIEAWDPAKFDKKGAN

Pla2_03686	GH36A	685	<i>Aquisphaera</i> sp. JC669, WP_165226234.1, 58%	MKSLRRRLAAVIFLGASLAPTPATAEEPTAEEFATARTWIDSRFTARAE PRPPFSFTYGDERSSELLPTWRKDYAEQPIDAARTERAMRFTDPRTDLR VECTATVYRDFFPAVDWVVKFTNAGTDDTPILSAVLPLDAMVVACGQG MPGVLFHSRGSKARIDDFEPLRTVLASDEIWSGSSFGGRSSDGVLPFFK LVGRAAGASIDVGWSGDWSAEFRVFFRGQAVARIGQRTFHAKLRPGE SIRTPSIVVHFWDKKDPERGGNLHRRFLRKHFTPTVAGQPVDPPIAASP HATIGFEKTTEANMLRQIANVARHGVGFDYWWIDAGWYTCGDNWAR YVGNVDPDPARFPSGLKPVADAAHAAGMRFLWNEPERVMPGTWLH KNHPEWLIAPPEGMPADLQYQRNDGFHLLDLGNPEALAWSIEHYSKMI AATGIECFRNDFNMYPGFYWNAAEPADRVGLREARYVTGLYRLF DAL RGRHPGLMIDDCASGGRRIDVEMLRALVLTRSDYLWDPVGQQAHTF GLARWIPITGIGAASVDVYSRRSGLGNHFTLAADYDSQEPVAWDAIRA TVAEYRALKPYYEGDFHPLGAYSVAEDAWMAWQFDRPEQGDGLVQA FRRKACEVDASIYKLRGLEPDAEYEVVNRDAADRTVRSGRSLRDEGFK VTIAEKPGAAVYSYRKVGR
Pla2_05159	GH36A	877	<i>Thermoguttaceae</i> bacterium, MCR4411221.1, 59%	MLTSVLVRPRRILFAAAAALAVGIPATAGVVAPAPEEMARLRRWVAE HLDGPDASAPFSFRYAGRPSAGLLKTWEKAHESRELDPTRSERVATYT DRATGLVVRCTAIVYKDFPTVEWTVVFRNGGAAETPILEDVQGLDGIW TGGGGAAVLHHARGSICTAGDYEPFATPLAPGTSSRFSGSAGRPSGDD WPYFNLQQGDAGLIVAVGWPAQWAGTFAAEADGVIRIRAGQEGVHAK LLPGEEIRTPLMALQFWNGDRARSQNVWRRWMTAHGMTRPSGAPPPP QFVASSSRA YGEMVHADEGKQLMFIDRYLEEGIKLDAWWMDAGWYV QEQQGWPQVGTWEVDAKRFPRLRAVSDHAHARGRLRTIVWFEPERVAP GTWL YENHSEWLLPRHAPGTAESPGLRSWSSASIGVDPVVIANLSDEPR ELGAIHVAPRGMTFHPGPDGEFCVVRWTAPEAGDV AIRAAFRAADPK ATTDVHVLLAGKPIFEDRVGEKGREPSCDRSLTVARGDAIDFVVGP GG NGHGF DSTSLTATLATTSGATHDAALEFAVDRNPGSAWSYGWLKPGA TPDASTFTPFD RKGRPGEDASKLLNLGSPAAREWLT DHVDRTLAEQGV DLYRQDFNIDPLPFWRAADAPDRRGVTENHHVVG YLAYWDELIRRRP GLLIDSCASGGRRNDLETMRRAVPLWRTDYAFQAIADQGMTYGLSPW LPYFGSGTTAARDASYMGAGFSAVDPYAFWSNATPSISCGVDVRERGI DYKTLRTL VGRWRELSRFYYDDFYALTPYSLATDAWIAWQYNAPERR

				EGAVQAFRRQDAPEARIRLKLHGLDADAVYALSTLDATEPREAAGRDL MATGLEVDIPARPAAAVVFYRRRD
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