

20160928_PR76177_Seq list.txt
SEQUENCE LISTING

<110> INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)

<120> Bacterial strains with an inactivated peptidoglycan O-acetyltransferase
oatA for treating and preventing gastrointestinal inflammation

<130> PR76177

<160> 10

<170> BiSSAP 1.3.6

<210> 1

<211> 1980

<212> DNA

<213> Lactobacillus casei

<220>

<223> nucleic sequence coding for LCABL_15730 of Lbcasei BL23

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gaatttgacc gcaatcatcg aattgatttt aaaagttttt ttattcgacg atttaaacgc	240
ctatatcctg ggtaattac cgtcctcttt gggacagcag cctatatcac gttattctcg	300
caaaacttgc tgcataactt gcacatgatg gtattgacca atttacttta tgtgtacaat	360
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cgattgttaa gtaatccttt gttcagctat atcggcagtc gtagttatgg cttgtatttg	960

20160928_PR76177_Seq list.txt

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gacaagtcta atggatcatc tgattggttc tataacgaca tggttcatat gaatccgaat 1920
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<210> 2

<211> 659

<212> PRT

<213> Lactobacillus casei

<220>

<223> amino acid sequence of LCABL_15730 of Lb casei BL23

<400> 2

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20 25 30
Pro Glu Leu Phe Arg Gly Gly Tyr Leu Gly Val Pro Ile Phe Met Val
35 40 45
Val Ser Gly Tyr Leu Ile Thr Asp Gly Leu Leu Ile Glu Phe Asp Arg
50 55 60

20160928_PR76177_Seq list.txt

Asn	His	Arg	Ile	Asp	Phe	Lys	Ser	Phe	Phe	Ile	Arg	Arg	Phe	Lys	Arg
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Leu	Tyr	Pro	Gly	Leu	Ile	Thr	Val	Leu	Phe	Gly	Thr	Ala	Ala	Tyr	Ile
				85					90					95	
Thr	Leu	Phe	Ser	Gln	Asn	Leu	Leu	His	Asn	Leu	His	Met	Met	Val	Leu
			100					105					110		
Thr	Asn	Leu	Leu	Tyr	Val	Tyr	Asn	Trp	Trp	Gln	Ile	Leu	Asn	Gly	Gln
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Ser	Tyr	Phe	Ala	Arg	Tyr	Ala	Asn	Gly	Glu	Ser	Pro	Phe	Thr	His	Leu
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Trp	Thr	Leu	Ser	Ile	Glu	Gly	Gln	Tyr	Tyr	Leu	Ile	Trp	Pro	Phe	Leu
145					150					155					160
Val	Leu	Ala	Leu	Leu	Leu	Val	Lys	Ser	Arg	His	Gln	Ile	Ala	Asn	
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Ile	Val	Leu	Ile	Leu	Ala	Ala	Ala	Ser	Gly	Ala	Trp	Met	Ala	Ile	Leu
			180					185					190		
Tyr	Met	Met	Thr	Ile	Ala	His	Val	Gln	Pro	Ala	Ala	Phe	Asp	Pro	Ser
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Arg	Leu	Tyr	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Phe	Ser	Ile	Leu	Phe	Gly
	210					215					220				
Ala	Ala	Leu	Ala	Phe	Ile	Trp	Pro	Ser	Gly	Arg	Leu	Ser	Gln	His	Leu
225					230					235					240
Gly	Lys	Lys	Trp	Val	Ile	Gly	Leu	Asp	Leu	Leu	Gly	Thr	Ala	Ser	Phe
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Leu	Gly	Leu	Leu	Val	Met	Val	Phe	Thr	Ile	Asp	Ala	Gln	Ser	Ser	Phe
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Leu	Tyr	Glu	Gly	Gly	Met	Val	Leu	Phe	Ser	Ile	Val	Thr	Thr	Ile	Leu
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Val	Ala	Val	Val	Ala	His	Pro	Ala	Ala	His	Phe	Asp	Arg	Leu	Leu	Ser
	290					295					300				
Asn	Pro	Leu	Phe	Ser	Tyr	Ile	Gly	Ser	Arg	Ser	Tyr	Gly	Leu	Tyr	Leu
305					310					315					320
Tyr	Gln	Phe	Pro	Val	Met	Ile	Phe	Trp	Glu	Asn	Arg	Phe	Arg	Asn	Ile
				325					330					335	
Ala	Asp	His	Pro	Val	Leu	Tyr	Pro	Val	Ile	Glu	Val	Val	Leu	Ile	Val
			340					345					350		
Val	Ile	Thr	Glu	Leu	Ser	Tyr	Arg	Phe	Ile	Glu	Gln	Pro	Ala	Ala	His
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Phe	Asn	Tyr	His	Lys	Thr	Trp	Ala	Phe	Leu	Lys	Gly	Leu	Ala	Asn	Pro
	370					375					380				
Lys	Val	Arg	Met	Gly	Lys	Thr	Arg	Trp	Val	Ser	Tyr	Val	Ala	Leu	Ile
385					390					395					400
Ile	Leu	Ala	Ile	Gly	Ser	Val	Gly	Leu	Ala	Lys	Ala	Pro	Ser	Val	Lys
				405					410					415	
Ala	Glu	Gly	Asp	Asn	Ser	Pro	Leu	Ala	Gln	Gln	Leu	Lys	Lys	Arg	Gly
			420					425					430		
Val	Ser	Thr	Lys	Glu	Lys	Glu	Lys	Arg	Leu	Ala	Ala	Met	Arg	Ser	Ser
		435					440					445			
Ile	Ala	Ala	Gln	Lys	Lys	Ala	Asp	Lys	Asn	Lys	Ala	Ala	Glu	Glu	Ser
	450					455					460				
Ser	Ser	Lys	Ala	Leu	Glu	Ala	Lys	Tyr	Ala	Ser	Gln	Ala	Lys	Thr	His
465					470					475					480
Pro	Val	Asn	Arg	Glu	Tyr	Glu	Gln	Tyr	Gly	Leu	Thr	Gln	Ile	Gln	Leu
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20160928_PR76177_Seq list.txt

Gln	Gln	Ala	Gln	Asp	Ile	Gly	Leu	Thr	Ala	Ile	Gly	Asp	Ser	Val	Met
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		515				520						525			
Asp	Ala	Ala	Val	Ser	Arg	Gln	Met	Ile	Asn	Ser	Ile	Asp	Leu	Val	Arg
	530					535					540				
Ser	Tyr	Ala	Asp	Arg	Gly	Val	Leu	Gly	Asn	Ile	Val	Leu	Ile	Gly	Leu
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Gly	Thr	Asn	Gly	Pro	Phe	Ser	Asp	Asp	Gln	Leu	Ala	Gln	Met	Met	Gln
				565					570						575
Ala	Ile	Gly	Pro	Asp	Arg	Gln	Val	Phe	Trp	Ile	Asn	Val	Arg	Val	Pro
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Thr	Arg	Ala	Trp	Gln	Asn	Asp	Val	Asn	Ser	Lys	Leu	Ala	Ala	Ala	Gln
	595						600					605			
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<211> 366

<212> PRT

<213> Artificial Sequence

<220>

<223> COG1835 domain found in the acetyltransferases

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Pro	Glu	Leu	Phe	Arg	Gly	Gly	Tyr	Leu	Gly	Val	Pro	Ile	Phe	Met	Val
	35					40					45				
Val	Ser	Gly	Tyr	Leu	Ile	Thr	Asp	Gly	Leu	Leu	Ile	Glu	Phe	Asp	Arg
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Asn	His	Arg	Ile	Asp	Phe	Lys	Ser	Phe	Phe	Ile	Arg	Arg	Phe	Lys	Arg
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Leu	Tyr	Pro	Gly	Leu	Ile	Thr	Val	Leu	Phe	Gly	Thr	Ala	Ala	Tyr	Ile
			85						90					95	
Thr	Leu	Phe	Ser	Gln	Asn	Leu	Leu	His	Asn	Leu	His	Met	Met	Val	Leu
			100					105						110	
Thr	Asn	Leu	Leu	Tyr	Val	Tyr	Asn	Trp	Trp	Gln	Ile	Leu	Asn	Gly	Gln
			115				120							125	
Ser	Tyr	Phe	Ala	Arg	Tyr	Ala	Asn	Gly	Glu	Ser	Pro	Phe	Thr	His	Leu
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Trp	Thr	Leu	Ser	Ile	Glu	Gly	Gln	Tyr	Tyr	Leu	Ile	Trp	Pro	Phe	Leu
145					150					155					160
Val	Leu	Ala	Leu	Leu	Leu	Leu	Val	Lys	Ser	Arg	His	Gln	Ile	Ala	Asn

20160928_PR76177_Seq list.txt

				165					170					175					
Ile	Val	Leu	Ile	Leu	Ala	Ala	Ala	Ser	Gly	Ala	Trp	Met	Ala	Ile	Leu				
				180					185					190					
Tyr	Met	Met	Thr	Ile	Ala	His	Val	Gln	Pro	Ala	Ala	Phe	Asp	Pro	Ser				
		195					200					205							
Arg	Leu	Tyr	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Phe	Ser	Ile	Leu	Phe	Gly				
	210					215					220								
Ala	Ala	Leu	Ala	Phe	Ile	Trp	Pro	Ser	Gly	Arg	Leu	Ser	Gln	His	Leu				
225					230					235					240				
Gly	Lys	Lys	Trp	Val	Ile	Gly	Leu	Asp	Leu	Leu	Gly	Thr	Ala	Ser	Phe				
				245				250						255					
Leu	Gly	Leu	Leu	Val	Met	Val	Phe	Thr	Ile	Asp	Ala	Gln	Ser	Ser	Phe				
		260					265					270							
Leu	Tyr	Glu	Gly	Gly	Met	Val	Leu	Phe	Ser	Ile	Val	Thr	Thr	Ile	Leu				
	275					280					285								
Val	Ala	Val	Val	Ala	His	Pro	Ala	Ala	His	Phe	Asp	Arg	Leu	Leu	Ser				
	290				295					300									
Asn	Pro	Leu	Phe	Ser	Tyr	Ile	Gly	Ser	Arg	Ser	Tyr	Gly	Leu	Tyr	Leu				
305				310					315						320				
Tyr	Gln	Phe	Pro	Val	Met	Ile	Phe	Trp	Glu	Asn	Arg	Phe	Arg	Asn	Ile				
				325				330						335					
Ala	Asp	His	Pro	Val	Leu	Tyr	Pro	Val	Ile	Glu	Val	Val	Leu	Ile	Val				
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Val	Ile	Thr	Glu	Leu	Ser	Tyr	Arg	Phe	Ile	Glu	Gln	Pro	Ala						
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<210> 4

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> SGNH hydrolases domain (cd01840)

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Gln	Met	Ile	Asn	Ser	Ile	Asp	Leu	Val	Arg	Ser	Tyr	Ala	Asp	Arg	Gly				
	35					40					45								
Val	Leu	Gly	Asn	Ile	Val	Leu	Ile	Gly	Leu	Gly	Thr	Asn	Gly	Pro	Phe				
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Ser	Asp	Asp	Gln	Leu	Ala	Gln	Met	Met	Gln	Ala	Ile	Gly	Pro	Asp	Arg				
65				70					75					80					
Gln	Val	Phe	Trp	Ile	Asn	Val	Arg	Val	Pro	Thr	Arg	Ala	Trp	Gln	Asn				
				85				90						95					
Asp	Val	Asn	Ser	Lys	Leu	Ala	Ala	Ala	Gln	Lys	Gln	Tyr	Lys	Asn	Leu				
		100				105							110						
Thr	Val	Ile	Asp	Trp	Tyr	Asp	Lys	Ser	Asn	Gly	His	Pro	Asp	Trp	Phe				
	115					120						125							
Tyr	Asn	Asp	Met	Val	His	Met	Asn	Pro	Asn	Gly	Asn	Pro	Gln	Tyr	Ala				
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<220>
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<210> 7
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<400> 7
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<210> 8
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<220>
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20160928_PR76177_Seq list.txt

<210> 9
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<212> DNA
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<220>
<223> primer

<400> 9
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<210> 10
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<223> primer

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