

## SEQUENCE LISTING

&lt;110&gt; DSM IP Assets B.V.

&lt;120&gt; NOVEL PREBIOTICS

&lt;130&gt; 26233WO

&lt;160&gt; 5

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 2542

&lt;212&gt; DNA

<213> *Penicillium chrysogenum*

&lt;400&gt; 1

agctgaagaa	tagatgaatt	tctatgttgc	gaataatagt	agtttccaat	actacaaatt	60
tggagagtca	ttaagtacta	aaatgtttgg	atatccccac	ctagcgtggg	gattgggtca	120
gtgctatttg	acccgatcgc	gtcgcaaatg	caaccgcgac	ggatcggagt	ccggtcttcg	180
cggctcgtatt	cagacatcta	gcggggccat	caatagcgcg	tggtaacgca	tgacactgcg	240
tggcgctcgca	tgtctgattc	agtggttcgc	ttcagttctt	caacgttgcg	gtcaatgaga	300
ttgtggtaac	gcagtcagca	tacagatcct	gtgaagctaa	accagcagag	ccagtgggac	360
cagtgggacc	agtggatacc	ttccactccc	cagggctctgc	attttccggg	gaaaccgacg	420
taagccaagg	aactcaaaaat	tggtatgtac	tatctatcct	ctaccggtca	atacatacta	480
tgtgttattg	gattttccctc	tatcaaatcg	aatagactgc	atagattgca	gtcctttcct	540
ttcgtcagat	tatccagatt	atccagatca	gtcccgaag	tgaaactgaa	tccaatcttc	600
gatataaata	gctccttggt	cctccaaaaa	aacaagagtc	atcatctcag	ttagctgttt	660
ccacacttcc	tctttcactc	aaaagcccgc	tttttcagggt	caatttttagt	ggactaaactt	720
cacgatgcta	tcttcattga	tgtatttggc	acgtgagtg	tccatcttgc	gcgctatctc	780
cttatgtgcc	atcctcgccg	tggcaactcc	tgcggcgagc	gcaagcgtca	cagcaaagca	840
cacgctggcc	acaaatggaa	aggggtgtt	tccacagtac	cgaattgttg	ccttggcaag	900
tctgggaaat	ggtgttctcc	tggcctcata	tgatgggcgc	ccagatggag	gagattcgcc	960
atccccaaat	tcaattctac	aacgacgcag	tacggacggt	gggaagactt	ggggcaaccc	1020
aacatatatt	gcgcgaggtc	aaccagcgtc	gtcgacactc	caacagtacg	gctttagtga	1080
cccaagctac	gtggctcgact	ccggtactgg	aaaggtcttt	aattttccatg	tcttctcgaa	1140
gaaccagga	tttctcaata	gcgaaattgg	aatgacgac	accgacttaa	acatagttag	1200
cgtgaagtc	tccgtttcga	ctgatggagg	acttagctgg	accactgatc	cagaccatga	1260
atcctctttg	cctcccgttg	catctgccga	cgttggtgca	ccgccactca	ttacgaaagc	1320
aatcaagccc	gtgggtagta	cttccaacgg	ggtagccaac	gtcggtgga	ttactgggat	1380
gtttgcctca	tccggagagg	ggattcaact	caaatacggc	aaacacgccc	ggcgctgggt	1440
tcaacaattc	cttgggaaaag	tcatccaatc	agacggttca	aaggtctcgc	aagcctacag	1500
tgtctacagt	gacgacgggtg	gcgctatatg	gaagatgggg	aaagtcattg	gcactgggat	1560
ggatgagaac	aaagttgtgg	agctatcaaa	cggcaacttg	atgcttaact	cacgcccagag	1620
cgatggtagc	ggatatcgaa	aggtggcaac	ctcaaccgat	ggtggtgaaa	cttgggtcaac	1680
accagcaagc	gaaacccaac	tccctgaccc	aggaaataac	ggagcaatta	ccaggatgta	1740
tcctgatgcg	gcacatgggt	cggccaatgc	caagatcctc	ctgtttacca	atgcaaacag	1800
taaaacaagc	cgaagcaatg	gtacaatccg	ctattcctgt	gacgacggaa	agacctggtc	1860
ttctggcgca	gtgttccagt	ctggctcgat	gtcctattcc	actgtcaccg	cactcggcga	1920
tgacaggttc	ggaatathtt	acgaggggga	tagcaacgac	ctcgtctaca	ttgaagtttc	1980
caaggathtt	attgggggtt	cctgctgata	aaactcccat	tggcagtggt	ctctacttgg	2040
gaacttgggt	tttacattgt	acctaaggtc	atgtgtacat	gtatgtacta	cagcgtcatc	2100
tcaaatattc	ttttgggaaa	ggacctgaca	atggcggcag	catgatggat	tttgggtctc	2160
ggccatttat	tgacgatggc	acacgatagc	tatcgaaact	actggtagct	attgcgaatg	2220
ttcagtacag	gtggcggttg	ttcctctagt	cacgcctgga	tgaaatcaga	ccgttatagt	2280
gacaccttcc	tatgacacta	tattctgtat	tgtgaaccca	atattttccat	ggtagtagtt	2340

```

tcaggtgaca gcaagggcaa aaattcttat tgctcaaaag taacattgca tgtagagatc 2400
ccatagtcaa ggtggcggtt gagagattta taggtggtaa aatcatgcta tttttaggct 2460
taggaacaat gctcgcaaga cgaacgaacg atgtagtagg ttggattaga gccagtaag 2520
aatggaattc ctatcacaag ca 2542

```

```

<210> 2
<211> 1224
<212> DNA
<213> Penicillium chrysogenum

```

```

<220>
<221> CDS
<222> (1)..(1224)

```

```

<400> 2
atg cta tct tca ttg atg tat ttg gca cgt gag tgc tcc atc ttg cgc 48
Met Leu Ser Ser Leu Met Tyr Leu Ala Arg Glu Cys Ser Ile Leu Arg
1 5 10 15
gct atc tcc tta tgt gcc atc ctc gcc gtg gca act cct gcg gcg agc 96
Ala Ile Ser Leu Cys Ala Ile Leu Ala Val Ala Thr Pro Ala Ala Ser
20 25 30
gca agc gtc aca gca aag cac acg ctg gcc aca aat gga aag ggg ctg 144
Ala Ser Val Thr Ala Lys His Thr Leu Ala Thr Asn Gly Lys Gly Leu
35 40 45
ttt cca cag tac cga att gtt gcc ttg gca agt ctg gga aat ggt gtt 192
Phe Pro Gln Tyr Arg Ile Val Ala Leu Ala Ser Leu Gly Asn Gly Val
50 55 60
ctc ctg gcc tca tat gat ggg cgc cca gat gga gga gat tcg cca tcc 240
Leu Leu Ala Ser Tyr Asp Gly Arg Pro Asp Gly Asp Ser Pro Ser
65 70 75 80
cca aat tca att cta caa cga cgc agt acg gac ggt ggg aag act tgg 288
Pro Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Lys Thr Trp
85 90 95
ggc aac cca aca tat att gcg cga ggt caa cca gcg tcg tcg aca ctc 336
Gly Asn Pro Thr Tyr Ile Ala Arg Gly Gln Pro Ala Ser Ser Thr Leu
100 105 110
caa cag tac ggc ttt agt gac cca agc tac gtg gtc gac tcc ggt act 384
Gln Gln Tyr Gly Phe Ser Asp Pro Ser Tyr Val Val Asp Ser Gly Thr
115 120 125
gga aag gtc ttt aat ttc cat gtc ttc tcg aag aac cag gga ttt ctc 432
Gly Lys Val Phe Asn Phe His Val Phe Ser Lys Asn Gln Gly Phe Leu
130 135 140
aat agc gaa att gga aat gac gac acc gac tta aac ata gtc agc gct 480
Asn Ser Glu Ile Gly Asn Asp Asp Thr Asp Leu Asn Ile Val Ser Ala
145 150 155 160
gaa gtc tcc gtt tcg act gat gga gga ctt agc tgg acc act gat cca 528
Glu Val Ser Val Ser Thr Asp Gly Gly Leu Ser Trp Thr Thr Asp Pro
165 170 175
gac cat gaa tcc tct ttg cct ccc gtt gca tct gcc gac gtt gcc aac 576
Asp His Glu Ser Ser Leu Pro Pro Val Ala Ser Ala Asp Val Ala Asn
180 185 190
gtc ggt gga att act ggg atg ttt gcc tca tcc gga gag ggg att caa 624
Val Gly Gly Ile Thr Gly Met Phe Ala Ser Ser Gly Glu Gly Ile Gln
195 200 205
ctc aaa tac ggc aaa cac gcc ggg cgc ctg gtt caa caa ttc ctt ggg 672
Leu Lys Tyr Gly Lys His Ala Gly Arg Leu Val Gln Gln Phe Leu Gly

```

210	215	220	
aaa gtc atc caa tca gac ggt tca aag gtc tcg caa gcc tac agt gtc			720
Lys Val Ile Gln Ser Asp Gly Ser Lys Val Ser Gln Ala Tyr Ser Val			
225	230	235	240
tac agt gac gac ggt ggc gct ata tgg aag atg ggg aaa gtc att ggc			768
Tyr Ser Asp Asp Gly Gly Ala Ile Trp Lys Met Gly Lys Val Ile Gly			
245	250	255	
act ggg atg gat gag aac aaa gtt gtg gag cta tca aac ggc aac ttg			816
Thr Gly Met Asp Glu Asn Lys Val Val Glu Leu Ser Asn Gly Asn Leu			
260	265	270	
atg ctt aac tca cgc ccg agc gat ggt agc gga tat cga aag gtg gca			864
Met Leu Asn Ser Arg Pro Ser Asp Gly Ser Gly Tyr Arg Lys Val Ala			
275	280	285	
acc tca acc gat ggt ggt gaa act tgg tca aca cca gca agc gaa acc			912
Thr Ser Thr Asp Gly Gly Glu Thr Trp Ser Thr Pro Ala Ser Glu Thr			
290	295	300	
caa ctc cct gac cca gga aat aac gga gca att acc agg atg tat cct			960
Gln Leu Pro Asp Pro Gly Asn Asn Gly Ala Ile Thr Arg Met Tyr Pro			
305	310	315	320
gat gcg gca cat ggt tcg gcc aat gcc aag atc ctc ctg ttt acc aat			1008
Asp Ala Ala His Gly Ser Ala Asn Ala Lys Ile Leu Leu Phe Thr Asn			
325	330	335	
gca aac agt aaa aca agc cga agc aat ggt aca atc cgc tat tcc tgt			1056
Ala Asn Ser Lys Thr Ser Arg Ser Asn Gly Thr Ile Arg Tyr Ser Cys			
340	345	350	
gac gac gga aag acc tgg tct tct ggc gca gtg ttc cag tct ggc tcg			1104
Asp Asp Gly Lys Thr Trp Ser Ser Gly Ala Val Phe Gln Ser Gly Ser			
355	360	365	
atg tcc tat tcc act gtc acc gca ctc ggc gat gac agg ttc gga ata			1152
Met Ser Tyr Ser Thr Val Thr Ala Leu Gly Asp Arg Phe Gly Ile			
370	375	380	
ttt tac gag ggg gat agc aac gac ctc gtc tac att gaa gtt tcc aag			1200
Phe Tyr Glu Gly Asp Ser Asn Asp Leu Val Tyr Ile Glu Val Ser Lys			
385	390	395	400
gat ttt att ggg gtt tcc tgc tga			1224
Asp Phe Ile Gly Val Ser Cys			
405			

&lt;210&gt; 3

&lt;211&gt; 407

&lt;212&gt; PRT

&lt;213&gt; Penicillium chrysogenum

&lt;400&gt; 3

Met Leu Ser Ser Leu Met Tyr Leu Ala Arg Glu Cys Ser Ile Leu Arg	
1 5 10 15	
Ala Ile Ser Leu Cys Ala Ile Leu Ala Val Ala Thr Pro Ala Ala Ser	
20 25 30	
Ala Ser Val Thr Ala Lys His Thr Leu Ala Thr Asn Gly Lys Gly Leu	
35 40 45	
Phe Pro Gln Tyr Arg Ile Val Ala Leu Ala Ser Leu Gly Asn Gly Val	
50 55 60	
Leu Leu Ala Ser Tyr Asp Gly Arg Pro Asp Gly Gly Asp Ser Pro Ser	
65 70 75 80	
Pro Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Lys Thr Trp	

				85					90					95					
Gly	Asn	Pro	Thr	Tyr	Ile	Ala	Arg	Gly	Gln	Pro	Ala	Ser	Ser	Thr	Leu				
			100					105					110						
Gln	Gln	Tyr	Gly	Phe	Ser	Asp	Pro	Ser	Tyr	Val	Val	Asp	Ser	Gly	Thr				
		115					120					125							
Gly	Lys	Val	Phe	Asn	Phe	His	Val	Phe	Ser	Lys	Asn	Gln	Gly	Phe	Leu				
	130					135				140									
Asn	Ser	Glu	Ile	Gly	Asn	Asp	Asp	Thr	Asp	Leu	Asn	Ile	Val	Ser	Ala				
145					150					155					160				
Glu	Val	Ser	Val	Ser	Thr	Asp	Gly	Gly	Leu	Ser	Trp	Thr	Thr	Asp	Pro				
				165					170					175					
Asp	His	Glu	Ser	Ser	Leu	Pro	Pro	Val	Ala	Ser	Ala	Asp	Val	Ala	Asn				
			180					185					190						
Val	Gly	Gly	Ile	Thr	Gly	Met	Phe	Ala	Ser	Ser	Gly	Glu	Gly	Ile	Gln				
		195				200						205							
Leu	Lys	Tyr	Gly	Lys	His	Ala	Gly	Arg	Leu	Val	Gln	Gln	Phe	Leu	Gly				
	210					215					220								
Lys	Val	Ile	Gln	Ser	Asp	Gly	Ser	Lys	Val	Ser	Gln	Ala	Tyr	Ser	Val				
225					230					235					240				
Tyr	Ser	Asp	Asp	Gly	Gly	Ala	Ile	Trp	Lys	Met	Gly	Lys	Val	Ile	Gly				
				245					250					255					
Thr	Gly	Met	Asp	Glu	Asn	Lys	Val	Val	Glu	Leu	Ser	Asn	Gly	Asn	Leu				
			260						265				270						
Met	Leu	Asn	Ser	Arg	Pro	Ser	Asp	Gly	Ser	Gly	Tyr	Arg	Lys	Val	Ala				
		275					280					285							
Thr	Ser	Thr	Asp	Gly	Gly	Glu	Thr	Trp	Ser	Thr	Pro	Ala	Ser	Glu	Thr				
	290					295					300								
Gln	Leu	Pro	Asp	Pro	Gly	Asn	Asn	Gly	Ala	Ile	Thr	Arg	Met	Tyr	Pro				
305					310					315					320				
Asp	Ala	Ala	His	Gly	Ser	Ala	Asn	Ala	Lys	Ile	Leu	Leu	Phe	Thr	Asn				
			325						330					335					
Ala	Asn	Ser	Lys	Thr	Ser	Arg	Ser	Asn	Gly	Thr	Ile	Arg	Tyr	Ser	Cys				
			340					345					350						
Asp	Asp	Gly	Lys	Thr	Trp	Ser	Ser	Gly	Ala	Val	Phe	Gln	Ser	Gly	Ser				
		355					360					365							
Met	Ser	Tyr	Ser	Thr	Val	Thr	Ala	Leu	Gly	Asp	Asp	Arg	Phe	Gly	Ile				
	370					375					380								
Phe	Tyr	Glu	Gly	Asp	Ser	Asn	Asp	Leu	Val	Tyr	Ile	Glu	Val	Ser	Lys				
385					390					395					400				
Asp	Phe	Ile	Gly	Val	Ser	Cys													
				405															

&lt;210&gt; 4

&lt;211&gt; 46

&lt;212&gt; DNA

&lt;213&gt; artificial

&lt;220&gt;

<223> 23 nucleotides ZJW coding sequence starting at the ATG start codon, preceeded by a 23 nucleotides sequence including a PacI restriction site

&lt;400&gt; 4

cccttaatta actcataggc atcatgctat cttcattgat gtattt

<210> 5  
<211> 34  
<212> DNA  
<213> Artificial

<220>  
<223> nucleotides complementary to the reverse strand of the region  
downstream of the ZJW coding sequence preceded by an AscI  
restriction site

<400> 5  
ttaggcgcgc cgtacataca tgtacacata gacc