



DNASIS

Maximum Matching [J1(UN8) VS J3(UN8)]

File1: J1(UN8)  
 Mode: Normal 1 - 235  
 File2: J3(UN8)  
 Mode: Normal 3 - 240

Matching Percentage (Total Window: 89%, Alignment Window: 90%)

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          ↓↓   ↓↓
1  TGCACCACCTGTCACCCTGTCCCCCGAAGGGGGAACGCCCAATCTCTTG      50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  ..CACCACCTGTCACCCTGTCCCCCGAAGGGGGAACGCCCTGTCTCCAG      50

51 GGTGTGTCAGGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAA    100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 GGTGTGTCAGGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAA    100

101 TTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAG     150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 TTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAG     150

151 TTTCAGCCTTGCGGCCGTA T CCCCAGGCGGAGTGCTTA T CCGCGTTAGCT  200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 TTTCAGCCTTGCGGCCGTA T CCCCAGGCGGAGTGCTTAACGCGTTAGCT  200

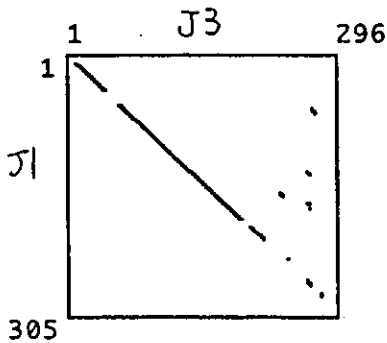
201 ACAGCACTAAAGGG----T---GT-GACCCCTCTAACACTTAG.....      250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 ACAGCACTAAAGGGAAAANCCNTTNANNC-T-TNACNCTTA.....      250
    
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DNASIS

Homology Plot [J1(UN8) VS J3(UN8)]

File: J1(UN8) 1 - 534 5' -> 3'  
 Mode: Normal  
 File: J3(UN8) 1 - 528 5' -> 3'  
 Mode: Normal

Plotting Mode: Left Up Check Size: 10 Matching Size: 10



B.midousuji SH2A株,変異株のデータベース

HA1001	SH2A	COLUMBIA FROZEN	7/95	ATCC	
HA1002	SH2A	JAPAN FROZEN	9/95	J1	pSA101
HA1003	NONE				
HA1004	HA1001	SH4	LARGE		
HA1005	HA1001	SH5	LARGE		
HA1006	HA1001	SH6	LARGE		
HA1007	HA1001	L1	LARGE		
HA1008	HA1001	L2	LARGE		
HA1009	HA1001	L3	LARGE		
HA1010	HA1001	S1	SMALL		
HA1011	HA1001	S2	SMALL		pSA201
HA1012	HA1001	S3	SMALL		

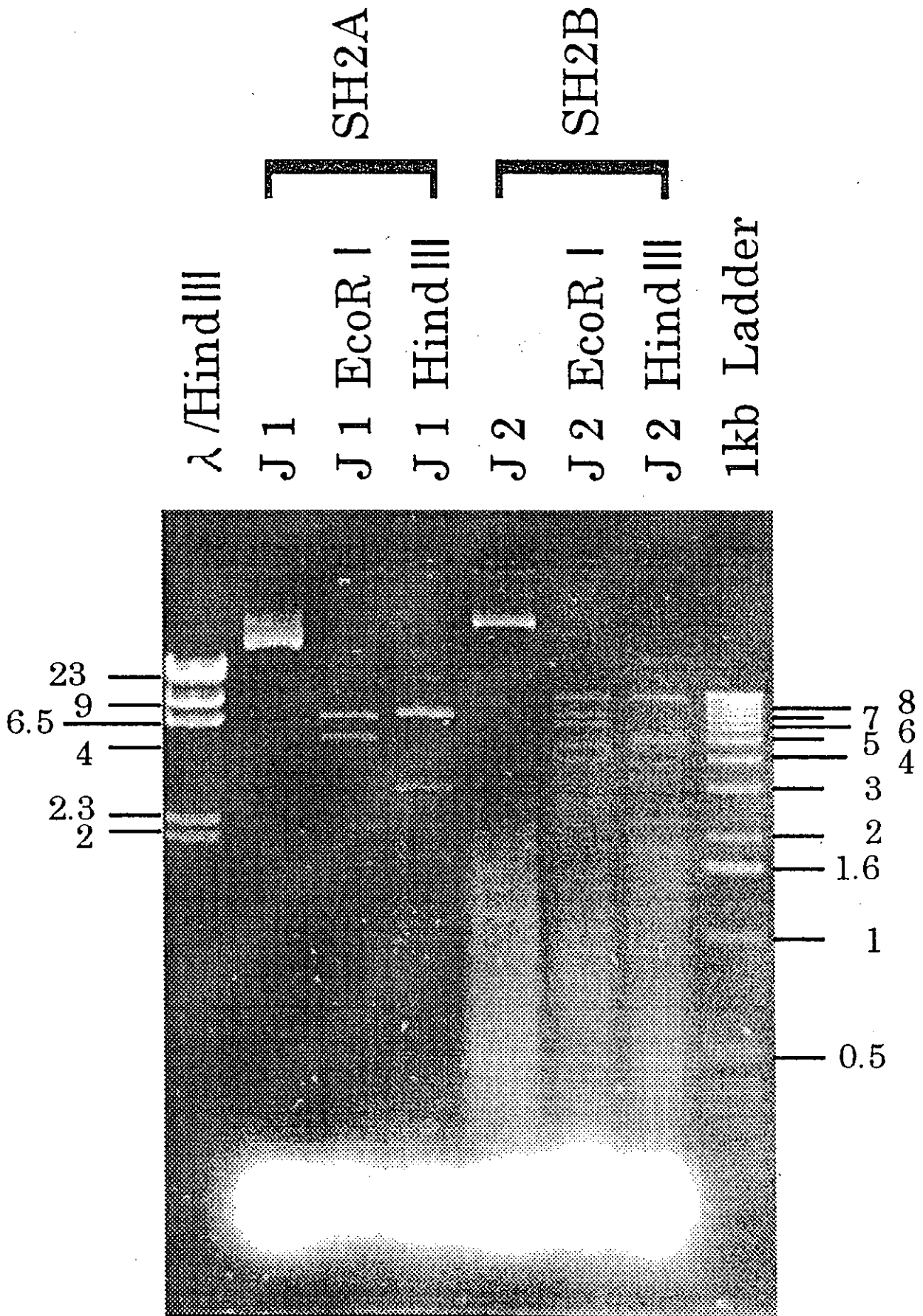
B. midousuji SH2A株, 変異株の履歴

SH2A									
COMPOST									
PLATE			IS VIABLE						
COLUMBIA FROZEN 7/95			ATCC 7/10/97		HA1001				
PLATE									
JAPAN FROZEN 9/14/95			10/96						
HA1002			SH4=AL		HA1004				
STREAK			SH5=AL		HA1005				
CONTINUOUSLY			SH6=AL		HA1006				
12/98									
L1					HA1007				
L2					HA1008				
L3					HA1009				
S1					HA1010				
S2					HA1011				pSA201
S3					HA1012				

*B. midausuji* SH2B株;変異株のデータベース

HB1001	SH2B	COLUMBIA FROZEN 7/95				STICKY	KM	
HB1002	SH2B	JAPAN FROZEN 9/95	pSB201			STICKY	KM1.5	-
HB1003	HB1001	SH3 VERY FAST GROW	COLFRN 96			STICKY	KM<12.5	-
HB1004	HB1002	NON-KM PLATE, KMS-MRINAL'97						
HB1030	HB1001	J3	PASSAGED 5/28			SMOOTH	KM3.125	
HB1033	HB1001	J33		pSB331		SMOOTH	KM<12.5	-
HB1034	HB1001	J34		pSB341		SMOOTH	KM<12.5	LYSIS PROD
HB1040	HB1001	J4	PASSAGED 12/98			SMOOTH		
HB1042	HB1040	J4, B21		pSB421		SMOOTH	KM3.125	LYSIS PROD
HB1045	HB1040	JA, B5		pSB405		SMOOTH	KM3.125	LYSIS PROD
HB1005	HB1002	SH2B10m				SMOOTH	KM<12.5	-
HB1006	HB1002	SH2B20m				SMOOTH	KM100	-
HB1007	HB1002	SH2B21m				SMOOTH	KM100	-
HB1008	HB1001	10/96	COLUMBIA FROZEN			SMOOTH	KM<12.5	-





BLASTN 2.0.8 [Jan-05-1999]

Reference:

Altschul et.al.(1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= (750 letters)

Searching.....done

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Distribution of 511 Blast Hits on the Query Sequence

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Sequences producing significant alignments:	Score (bits)	E Value
emb Z21626 BSGLGBEA B.stearothermophilus glgB gene encoding 1,4...	264	2e-68
gb M63891 PTITETLMOB Plasmid pTB19 (from Bacillus stearothermop...	105	1e-20

emb|Z21626|BSGLGBEA B.stearothermophilus glgB gene encoding 1,4-alpha-glucan branching enzyme Length = 3327

Score = 264 bits (133), Expect = 2e-68  
 Identities = 133/133 (100%)  
 Strand = Plus / Minus

Query: 192 cgatccaagaaaactatattataactatattcatgcctacgccagcgcggtcttgatgga 251  
 |||  
 Sbjct: 336 cgatccaagaaaactatattataactatattcatgcctacgccagcgcggtcttgatgga 277

Query: 252 ctggagatgaaatactcacctggcgccccacgtcgattgaccctgagcaggaagag 311  
 |||  
 Sbjct: 276 ctggagatgaaatactcacctggcgccccacgtcgattgaccctgagcaggaagag 217

Query: 312 ctggctttgatca 324  
 |||  
 Sbjct: 216 ctggctttgatca 204



gbIM63891IPTITETLMOB Plasmid pTB19 (from Bacillus stearothermophilus)  
replication protein

(rep), tetracycline-resistance protein (tetL), mobilizable  
proteins (mob), and bleomycin-resistance (ble0) genes,  
complete cds.

Length = 11887

Score = 105 bits (53); Expect = 1e-20

Identities = 83/93 (89%)

Strand = Plus / Plus

Query: 35 gatcgtctcggtttttcatcggccgcttaattccgtcccttggtgctgtaccacattctaaa 94  
||||| ||||| ||| ||||| ||||| ||||| |||||

Sbjct: 11714 gatcgtctcattttcattggctcgtaattccgtctcttggtgctataccacattctaaa 11773

Query: 95 atcccgttctggaactcttcaaagaactccat 127  
||||| ||||| ||||| |||||

Sbjct: 11774 ttcccgttctggaactcctaaaagaactccat 11806

Title: Bacterium Capable of Biodegradation of toxic and Non-toxic Wastes

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Description: Isolation of novel strains of *Bacillus Midousuji*, a species of thermophilic bacteria which degrades various toxic and non-toxic waste materials including industrial wastes. These particular wastes present various problems under current disposal methods. This thermophilic microorganism has optimal growth at 62 degrees Celcius or higher (up to the boiling point of water) enabling a novel accelerated method for degrading waste in contrast to any other microorganism process in current use. This microorganism degrades fish waste into protein and DHA (a food supplement), plastic into CO<sub>2</sub> and water and hazardous compounds into inert byproducts. Several of the compounds that this microorganism safely degrades now present a difficult and hazardous degradation problem in many superfund and contaminated sights around the world.

Commercial Information:

Applications: This bacterium allows a novel method for the biodegradation of waste material, including fish wastes, plastics and other confidential hazardous compounds. The degraded products could then be more safely stored, more easily be used for agricultural purposes, and provide sources of specific chemicals that would be useful for commercial, industrial, or therapeutic purposes.

Advantages: Since this species is thermophilic, the biodegradation can be accelerated by increasing the temperature. These bacteria have a higher growth rate than previously used species. They are also unique in that they will degrade materials previously resistant to rapid degradation including hazardous wastes.

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Lead Inventors: Drs. I. Bernard Weinstein and Sadayori Hoshina

Patent Status: Patent Application filed.

Licensing Contact: Laura Amos, Associate Director  
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E-mail: amoslau@cuadmin.cis.columbia.edu

Licensing Status: Available for Research Sponsorship and/or Licensing.

Columbia Innovation Enterprise Reference: CIE-657

Related Publications:.

Further Information: May be obtained upon completion of a Confidential Disclosure Agreement.

## Jamaica Bay Biodiversity Abstract

Human Health, Biodiversity and Industrial Pollution in Jamaica Bay, NY

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Anthropogenic pollution of the marine environment has significant adverse effects on endangered species, and on suitability for human recreational use. Pollution is also very likely to impact adversely on human health as regards environmental exposures to teratogens and carcinogens, as well as exposures to toxic algal blooms and human infectious agents. The restoration of the Jamaica Bay National Seashore presents itself as a possible paradigm for highly-urbanized salt marsh ecosystems throughout the industrialized world. Since this ecosystem has been, and continues to be, heavily impacted by exogenous contaminants it provides an excellent opportunity to study the nature of the relationship between biodiversity and pollution.

One aspect of the proposed study would require assessment of biodiversity of macrofauna and macroflora, and its often inverse correlation with increasing levels of pollution. This study would require extensive sampling of soil and water, and testing for industrial contaminants including metals, solvents, polychlorinated biphenyls (PCB), dioxin, polyaromatic hydrocarbons (PAH), and other xenobiotics. Localized and limited sampling of macroflora and macrofauna would permit assessment of

bioaccumulation of specific target chemicals, including mercury, lead, dioxin, PCB and PAH. These studies would require significant expenditures for mass spectrometric analyses of soils, water, and biological samples.

In this way connections could possibly be made linking specific areas of pollution, including their geophysical characters, and oceanographic properties to bioaccumulation in certain elements of the food chain. Only by understanding these relationships could specific steps could be proposed to address problematic components of the ecosystem.

From the anthropocentric perspective, the obvious area of investigation would be determination of the impacts of sewage seepage, storm runoff, and sludge disposal on levels of pathogenic microflora (e.g. coliform bacteria and hepatitis viruses). Traditional bacteriological laboratory methods, and also molecular biology techniques such as the polymerase chain reaction (PCR), would be required for this aspect of the study. In addition, the various sources of pollution may impact on nutrient loading, decline in predators, loss of natural filters, and introduced species, to contribute to red tides and other kinds of harmful algal blooms. Thus, in addition to concerns about infectious agents and unanswered questions of long-term toxicities due to increased cancer and birth defects in local communities, there is a very real concern for acute toxicity in humans including gastrointestinal and neurological symptoms.

A quantitative assessment of these complex biophysical processes on human health would require mathematical modeling including the potential impacts of chaos theory, and application of traditional risk assessment methods.

Finally, an area that is perhaps least well understood is the ability of marine ecosystems, and in particular salt marshes to naturally buffer exogenous impacts. Our specific interest centers on microfauna including species of *Bacillus* to mediate biodegradation of environmental contaminants. Our recent studies indicate that thermophilic bacteria isolated from compost are capable of digesting organic (fish carcasses) and as well as inorganic (plastics) pollutants. Specific plasmid-encoded genes were found to be responsible for these various bio degradative properties, and these were linked to antibiotic resistance genes. Our studies also suggest that bacteriological toxicity toward algae could potentially be a natural method for buffering against anaerobic conditions. The possibility exists that similar bacteriological systems may

exist in industrially impacted salt march ecosystems. Studies of bacterial evolution indicate that under certain environmental conditions processes in addition to random mutation may drive genotypic and phenotypic changes. Taken together these findings suggest the need for investigation of the biodiversity of microflora at various sites within the marshlands with various human impacts. This study would also require bacteriological and molecular biological techniques such as PCR.

厚生科学研究費補助金生活安全総合研究事業  
「ダイオキシン微生物処理技術の研究」プロジェクトメンバー

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