

添付資料3—3

HA1001 のプラスミド pSA101 の DNA の部分塩基配列決定

好熱菌 *Bacillus stearothermophilus* の耐熱性プラスミド pTB19 と 80% の相同性を見出している。また *B. stearothermophilus* に存在する 1,4-alpha-glucan branching enzyme をコードする遺伝子 DNA と 100% 相同性が見られた。

1,4-alpha-glucan branching enzyme は細胞壁合成酵素の一つで、*B. midousuji* の必須遺伝子と考えられることから推察すると、このような重要な遺伝子がプラスミド上に存在することはプラスミドに染色体遺伝子と同等の遺伝情報が搭載されていることが考えられる。またプラスミドと染色体の区別が付けにくい形態である可能性も考えられる。

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

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

emb|Z21626|BSGLGBEA B.stearotherophilus 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 cgatccaagaaaactatattataactatattcatgcctacgcccagcgcggtcttgatgga 251
 |||
 Sbjct: 336 cgatccaagaaaactatattataactatattcatgcctacgcccagcgcggtcttgatgga 277

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

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

添付資料3—4

BphC(dioxygenase の extradiol meta-cleavage 反応)の遺伝子検索

BphC のアミノ酸保存領域、210番目、260番目前後を遺伝子増幅反応のプライマーに相当するところとして選び出した。

BphC のアミノ酸保存領域に相当する部分の塩基配列。5', 3' 側から保存領域の配列に変換した。610番目、775番目前後になった。

抽出した塩基配列のホモロジー検索を *Sphingomonas paucimobilis* SYK-6 の *LigZ*, 遺伝子 *Agrobacterium tumefaciens*、*Rhodococcus erythropolis*、*Rhodococcus globerulus*、*Pseudomonas putida* の *BphC* 遺伝子の保存領域と行い、良好な成績が得られた。

得られた塩基配列をDNA合成し、PCR 遺伝子増幅反応のプライマーとした。アニーリング温度を55°C、1.5mMの塩化マグネシウム濃度で行った。Stringencyは高めに設定したが、写真には明確なバンドが見られ、*B. midousuji* HB1030 に *BphC* 遺伝子の存在が推測された。

		10	20	30	40	50	
bphc(d32142)	1	MS--VORLGY	MGFEVADVPA	---WRAFM	EKLG---AME	ASSSENSARF	50
bphc(aac4474)	1	MSK-VKELAY	VGYEVSDLAA	---WTFHGV	DLLG---MQE	GEKTTSGFTL	50
bphc(x97984)	1	MS--TERLGY	LGFVAVKDVPA	---WDYELT	QNVG---LMA	AGAAGDAALY	50
edo2(RW1)aa	1	MPSPIVALGY	LGFYAQDLAA	---WEWAT	QIEGFVKVRA	PEGISSDHLV	50
ligz -aa	1	VAETV--LGM	WTSHGPTLST	TPEQWTLRVS	ADLKRKHPFR	GVEYSFEELV	50
		60	70	80	90	100	
bphc(d32142)	51	-RVDSRSWRL	MVEKGPSDDI	SLSGYEVDSA	DSLALATKKRL	EANGTEVTITE	100
bphc(aac4474)	51	-RITDHKAHRW	VVEAAGAADDI	VVSGYEVASE	PELDAIVQGL	GSAGFEVTEG	100
bphc(x97984)	51	-RADQRAWRI	AVDPGELDDL	AVAGLEVDDA	AALEERMADKI	ROAGVAFITRG	100
edo2(RW1)aa	51	LRTDERQWR	AVEPGTEGRV	AFIGWLAADA	NALEEVRRL	TAQGTIVVRF	100
ligz -aa	51	SCAAARSWRR	PVP-----	---FPSASD	ARPGAKVPSP	TWPTFAAAKI	100
		110	120	130	140	150	
bphc(d32142)	101	SGELAADRGM	LGLISCTDIA	NTRVEIYYGA	T--ELFEKPF	ISPTGVSGFIT	150
bphc(aac4474)	101	DAALAADRKV	DRIFVTIDPM	GNRVELVSGF	A--DA-ETPF	ESTKLLGSFV	150
bphc(x97984)	101	DEALMQQRKV	MGLLCLQDPF	GLPLEIYYGP	A--ETFDQPF	LPSAPVSGFV	150
edo2(RW1)aa	101	DAELARKRCV	QDLIRCEDPD	GFRLEFFHGH	L---VSREPF	VSPRGI-GFV	150
ligz -aa	101	DVAIVMGNDQ	RELF--LEDV	TPAIVMYLGE	TIWDQPATPE	QAARMPPGTH	150
		160	170	180	190	200	
bphc(d32142)	151	TGDOGFGHYV	L-AVPDIDAA	--LDFYVKGL	GHLSDIIDW	KLNYELITVKL	200
bphc(aac4474)	151	TGDGGAGHOV	L-LTGDVSRE	EYLAFYVDL	GLKTSIDIIE	EVAPGIVADL	200
bphc(x97984)	151	TGDOGIGHFV	R-CVPDITAKA	--MAFYTEVL	GFMVSDIIDI	OMGPEMSVPA	200
edo2(RW1)aa	151	TGDMGLGHIL	I-IVSDIEKS	K--AFYLDL	GFRMSDYIVF	GGN-----KV	200
ligz -aa	151	EAEWGIARPS	AGIIPASPSS	ACM--CAKRW	CRRLRS----	-GGLQDITARA	200
		210	220	230	240	250	
bphc(d32142)	201	HFLHCNRRHH	TLALA-GLPG	A-KKTHHFML	EIKHMDDVGL	AYDK--FDAD	250
bphc(aac4474)	201	HFLHCNRRHH	TVAFG-KLPE	P-KVTHHFML	EVSDTRDVGL	AYDRI-CLDAR	250
bphc(x97984)	201	HFLHCNRRHH	TLALA-AFPT	P-KRTHHFML	QANTLDDVGY	AFDR--LDAA	250
edo2(RW1)aa	201	HFTHTNPRHH	SLAFV-QTSD	RIARLGHFV	EADDVDVGF	ALDR-LYAST	250
ligz -aa	201	RRPLVERRAH	SLGHIYRQII	RDQVVPNLPI	IINIFPPNQ	PTARRCFELG	250
		260	270	280	290	300	
bphc(d32142)	251	GIVMNTLGRH	TNDHMLSFYG	ATPSG-FAVE	YGWGARQVEP	--GWSVVRY-	300
bphc(aac4474)	251	QPFEMTLGMH	TNDRMFSFYV	RTPSG-ENVE	YGWGALLIDD	-ETWEVKTL-	300
bphc(x97984)	251	GRITSLTGRH	TNDHTISFYA	DTPSGPMIEVE	FGWGPRITVDS	--SWTVVRH-	300
edo2(RW1)aa	251	WOLKETLGRH	TNDRMLSFYC	ENPSGS-QTE	FGWGGRKIAH	-PGWLVEITY-	300
ligz -aa	251	RAVYGAIRSW	KEDLPVAVFG	SGGMSHEVID	EDFDRMFEEA	LRNRDAETLC	300
		310	320	330	340	350	
bphc(d32142)	301	-----	-DKISINWGHK	FVAERDRQVS	SNAIE-DELI	DIDATLSAPA	350
bphc(aac4474)	301	-----	-DRRHITWGRH	-----P	QVILA-EOLA	HT----ATDE	350
bphc(x97984)	301	-----	-NRTAMWGHK	-----	-----	-----SVRG	350
edo2(RW1)aa	301	-----	-DAIAFWGHK	VPGTEYSDRG	PQ-----	-----SPRE	350
ligz -aa	301	AIEDKHLQSG	TSELKTIATA	AGALFDITLK	GDDVVGYPECY	RSEAGTGITAN	350
		360	370	380	390	400	
bphc(d32142)	351	Q----A....	400
bphc(aac4474)	351	V----H....	400
bphc(x97984)	351	Q----R....	400
edo2(RW1)aa	351	G----I....	400
ligz -aa	351	GFVAWQ....	400

		10	20	30	40	50	
bphc(D32142)	1	ATG--AGCGT TCAGAGAC--	--TCGGTTAC	ATGGGCTTCG	AGGTTGCGGA		50
bphc(X97984)	1	ATG--AGCAT CGAACGTT--	--TGGGTTAC	CTGGGCTTCG	CCGTCAGGA		50
EDO 2(RW1)	1	ATGCCGTGCG CGATTCGTGCG	CCTGGGCTAT	CTGGGTTTCT	ATGGGCAAGGA		50
ligZ -1	1	ATG----GC CGAA-ATCGT	GCTGGG-TAT	GTGGAGGTC-	--GCACGGGC		50

		60	70	80	90	100	
bphc(D32142)	51	TGTGCCCGCG TGGCGCGCCT	TCATGACGGA	AAAAC TGGGG	GCCATGGAGG		100
bphc(X97984)	51	CGTACCCGCG TGGGACTACT	TTTTGACGCA	AAACG TGGGT	TTGATGGCGG		100
EDO 2(RW1)	51	TCTCGCCGCG TGGGAGGAAT	GGGCGACCA	GATTTTCGGG	TTGCCAAGG		100
ligZ -1	51	CGACCCGTC CACCACGCG	GAGCAATGGA	CGCTCCGGT	ITC-CGCGA		100

		110	120	130	140	150	
bphc(D32142)	101	--CCTCGAGC AGCGAGAATT	--CGGCG--	--CGGTTC-	--GGTTGAC		150
bphc(X97984)	101	--CGGGTTCG TCCGGCGGACG	--CTGCG--	--CTGTACC-	--GTGCCGAT		150
EDO 2(RW1)	101	TTCCGCGCC GGAAGGCAAT	TCCAGCGATC	ATCTCTACT	GCGGATCGAC		150
ligZ -1	101	ITTG-AAGCG GAAGCAKCC	ITCCGTGGC	AGGAATACAG	CTTCGAGGA		150

		160	170	180	190	200	
bphc(D32142)	151	TCCCGCAGTT GGCGCTGAT	GGTCGAAAAG	G-GCCCGTCG	GATGACATCT		200
bphc(X97984)	151	CAGCGTGCTT GGCGCATCGC	CGTGCAGCCG	G-GCGAAKTC	GACGACCTAG		200
EDO 2(RW1)	151	GAGCGCAAT GGCGCTTCGC	GGTCGAGCC	G-GTACGGAA	GGCCGCGTCG		200
ligZ -1	151	CTG-TCTTC TCGCAGCGG	CGAGAGCTG	GCGGAGGCT	GTCCCTTCC		200

		210	220	230	240	250	
bphc(D32142)	201	CGCTCTCGGG CTACGAGGTC	GATAGCGCGG	ACTTCGCT--	ACT--CGCGA		250
bphc(X97984)	201	CCTACGCAAG CTITGGAAGTG	GATGACGCCG	CTGCGCTCGA	GCG--CATGG		250
EDO 2(RW1)	201	CTTTCATCGG CTGGGAGGCC	GCCGACGCCA	ACGCGTTGGA	G----GAGG		250
ligZ -1	201	CGAGCGCGAG CGACCGCGG	CCGGTGCCA	AAATGCCATC	GCCGACATGG		250

		260	270	280	290	300	
bphc(D32142)	251	TCAAGGAGCG TCTCGAAGCG	CATGGCATC	GAGGTGCAA	CAGAGAGCGG		300
bphc(X97984)	251	CCGACAAGCT GCGCCAGGCA	GG--GGTAGC	CTT-CACCCG	CGGTGA-CGA		300
EDO 2(RW1)	251	TCCATCGCG GCTCAACGCC	CAG-GGGATC	GAGGT--CGT	CAGGGA-TGC		300
ligZ -1	251	CCGACTTTCG CGGCCCGAA	GATCGAGGTC	GCGGTCAITCA	TGGCAATGA		300

		310	320	330	340	350	
bphc(D32142)	301	CGAGTTGGCG GCCGATTCGC	GGTGTCTCTG	GACTGATTT	CGTGCACGGA		350
bphc(X97984)	301	AGCGCTCATG CAGCAGCGC	GC AAAGTCATGG	GCCTGTTGTG	CCTGCA-AGA		350
EDO 2(RW1)	301	CGAACTGGCG CGAAAGCGC	GC TGGGTGAGG	ACCTGATCCG	CTTGCAGGAI		350
ligZ -1	301	CGAGCGGAG CTCTTCTTG	AGGATGTCAC	GCCGCGGATC	ACTGTCTATC		350

		360	370	380	390	400	
bphc(D32142)	351	CACGGCAAA CACCCGGGTCG	AGATCTACTA	TGGCGCGACG	GAGCTGTTCG		400
bphc(X97984)	351	CCCCTTCGG CTCCGCTTCG	AGATTTACTA	CGGCCCGCA	GAAACCTTCG		400
EDO 2(RW1)	351	TCCCGACCGG TCCCGGCTGG	AGTTCTTCCA	CGGCATCT	CG--TTTCCC		400
ligZ -1	351	TCCGCGAGAC GATCTGGGAC	CAGCCGGCCA	CG-CCCCGAC	AGGCCGCGG		400

		410	420	430	440	450	
bphc(D32142)	401	AGAAGCCGTT CATCTGCGCG	ACCGGGGTCT	CGGGCTTCA	A-ACC--GGC		450
bphc(X97984)	401	ACCAGCCCTT CTTGCCAGC	GCTCCCGTGT	CGGGCTTCGT	C-ACA--GGC		450
EDO 2(RW1)	401	GCGAGCCGTT CGTCTTCCG	--CGCGGCAT	CGGCTTCGT	C-ACC--GGC		450
ligZ -1	401	G-ATGCCACC CCGCATTCAC	GAGGCGGAAT	GGGGCATAGC	CCGCCCGAGC		450

		460	470	480	490	500	
bphc(D32142)	451	GACCAGG-G GTTCGGCCAC	TACGTGCTGG	CTGTGCCGGA	TATAGATGCT		500
bphc(X97984)	451	GACCAGG-G TATCGGGCAT	ITTCGTGGCG	GCGTCCCCGA	CACCGCCAG		500
EDO 2(RW1)	451	GACATGG-G GCTCGGCCAC	ATCTCTCATCA	CGGTGAGCGA	CATCGAAAAAG		500
ligZ -1	451	GCCGGGACTA TCCCTGCCAG	CCCGAGCTCG	GCAITGCATG-	TGTGCAAAAAC		500

		510	520	530	540	550	
bphc(D32142)	501	GCCCTGGAT TCTATGTCAA	GGGCTGGGC	TTCCAT--	C TGTCCGACAT		550
bphc(X97984)	501	GCGATGGCG TCTACACCGA	AGTGCTGGGC	TTTGTG--	C TGTCCGACAT		550
EDO 2(RW1)	501	TGGAAGGCC TCTACCTGGA	CTTGTCTGGC	TTCAAG--	A TTAGCGAATTA		550
ligZ -1	501	GCTGGTGGCG CAGGCTTCGA	TCTGGCGGTC	TCCAAGACAC	TGCCCGAGCC		550

		560	570	580	590	600	
bphc(D32142)	551	CATCGACTGG	AAGCTCAACT	ATGAACTGAC	GGTCAAACCTC	CACCTTCCTGC	600
bphc(X97984)	551	CATCGACATC	CAGATGGGGC	CGGAAATGAG	CGTGCCCGCG	CACCTTCCTGC	600
EDO 2(RW1)	551	CATCGTCT--	----TCGGC-	-GGGAACAAG	G-----TG	CAATTCACCC	600
ligZ -1	551	CGCCGGCCAC	TGCTCGAGC-	-GGCGGCC	CAATTCCTCG	-GCTTCATCT	600
		610	620	630	640	650	
bphc(D32142)	601	ACTGCAACGG	TCGACACCAC	ACCCTGGCGC	TCG-CCGGTC	TCCCGGGAGC	650
bphc(X97984)	601	ACTGCAATGG	GCGCCACCAC	ACGATCGCC	TGG-CTGGCT	TCCCAATCC	650
EDO 2(RW1)	601	ACATCAACCC	GCGTCACCAC	AGCCTGGCCT	TCGTCCAGAC	CAGCGATCGC	650
ligZ -1	601	ACCGCCAGAT	CATCCGTGAT	CAGGTGGTGC	CAAACCTGCC	GATCATCATC	650
		660	670	680	690	700	
bphc(D32142)	651	AAAGAAGACT	-CA--CCACT	TCATGCTCGA	GACCAAGCAT	ATGGATGACG	700
bphc(X97984)	651	CAAGCGCATC	-CA--CCAT	TCATGCTCGA	AGCCAACACC	ATAAGACGAGC	700
EDO 2(RW1)	651	ATCGCGCGG	-TGGGCCACT	TCATGTTGGA	GGCCGACGAT	GTCGACGCG	700
ligZ -1	651	AACACCTTCT	TCCCGCCGAA	CAAGCCGACC	GCCCGCCGCT	GCTT-CGAGC	700
		710	720	730	740	750	
bphc(D32142)	701	TGGGCCTTGC	CTACGACA-A	GTTCGATGGG	GACG---GGA	CAGTG-----	750
bphc(X97984)	701	TGGGCTATGC	CTTCGATC-G	GCTGGACGGG	GCCG---GGC	GCATC-----	750
EDO 2(RW1)	701	TGGGCTTCGC	GCTCGACC-G	TCTTTATGGC	AGCACHGGC	AGCTG-----	750
ligZ -1	701	TGGGCGCGCC	GGTCGCAAG	GCATCCGCA	GCTGGAAGA	GGACCTGCCC	750
		760	770	780	790	800	
bphc(D32142)	751	GTTCATGACGC	TTCGGC---G	CCACACCAAT	GACCACATGC	TCTCAATCTA	800
bphc(X97984)	751	ACTTCCCTGC	TCGGGC---G	CCACACCAAC	GACCAATCGA	TCTCCTTCTA	800
EDO 2(RW1)	751	AAGGAGACCC	TCGGGC---G	CCACACCAAT	GATTCGATGC	TCTCCTTCTA	800
ligZ -1	751	GTGGCGGTGT	TCGGCTCGGG	CGGATGACG	CACITCGTCA	TCGACGAGGA	800
		810	820	830	840	850	
bphc(D32142)	801	---CGGCGG	ACCCCTCCG	GATTT---TG	CGTCCG	AATACGGCTGGGG	850
bphc(X97984)	801	TGCCGACAG	CGTCCGCCA	TGAT---CG	AAGTCG	AGTTCGGCTGGGG	850
EDO 2(RW1)	801	CTGCGAAA	--ATCCTTCG	GGGT---CG	CAGACGGAGT	TCGGTTGGGG	850
ligZ -1	801	TTTCGACCGC	ATGTTCTTCG	AGGCGCTCGC	CAATCGGGAC	GCGGAGACGC	850
		860	870	880	890	900	
bphc(D32142)	851	CGCTCGCCAG	-GTCCG---AA	CCAGGCTGGT	CCGTCTGGCG	CTACGACAAG	900
bphc(X97984)	851	ACCGCGCAAG	-GTGG---AT	TCTCTCTGGA	CGTGGTGGCG	CCACAAACCGC	900
EDO 2(RW1)	851	CGGCGCAAG	-ATCGCCAC	CCCGCTGGC	TGGTGGAAAC	CTATGATGCG	900
ligZ -1	851	TGTGCGCCAT	CGAGGACAAG	CATCTCCAGT	CCGGCACCTC	CGAGCTCAAG	900
		910	920	930	940	950	
bphc(D32142)	901	ATC-AGCATC	TGG-GGTCA-	CAAAATCGTT	GCC--GAGCG	CGACAGGCAA	950
bphc(X97984)	901	ACC-GCCATG	TGG-GGTCA-	CAAGTCGGT-	-----	-----	950
EDO 2(RW1)	901	ACC-GCATTC	TGG-GGACA-	CAAG--GTT	-CC--GGGCA	C-----CGA	950
ligZ -1	901	ACCTGGATTG	CGGCGGCCGG	CGCGCTGTTC	GACA CGGACC	TGAA GGGCGA	950
		960	970	980	990	1000	
bphc(D32142)	951	-GTGAGCAAG	AACGCAATCG	AGGAT-CAAT	TCA--TTGAC	ATCGATGCCA	1000
bphc(X97984)	951	-----	-ACGCGGCC	-----	-----	-----	1000
EDO 2(RW1)	951	-AT-----	-ATTCGGACA	GGGGT-----C	C-----TCAGT	CTC-----CA	1000
ligZ -1	951	CGTGGTGGG	TATGAGCCCT	GCTACCGCTC	CGAAGCCGGG	ACCGGCAACG	1000
		1010	1020	1030	1040	1050	
bphc(D32142)	1001	CGCTGAGCGC	CCCGCGCAA	GCGTAA.....	1050
bphc(X97984)	1001	---AGCGC	-----	---TGA.....	1050
EDO 2(RW1)	1001	CGCGAAG---	---GA	ATTTGA.....	1050
ligZ -1	1001	CAACGGCTT	CGTCGCCTGG	CAATAA.....	1050

```

      9           18
5' TGC AAY GRH SGM CAC CAC AC 3'
-----
   C  N  X  X  H  H
  
```

Simple Homology Region [bphC 5']

No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
2	ED0 2(RW1)	N	1	562	20	13	65.00%

```

      1           10           20
5' TGCAAYGRHSGMCACCCACAC 3'
   **** ** *****
5' ATCAACCCGCGTCACCCACAG 3'
   562       571       581
  
```

Simple Homology Region [bphC 5']

No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
1	bphc(D32142)	N	1	568	20	20	100.00%

```

      1           10           20
5' TGCAAYGRHSGMCACCCACAC 3'
   *****
5' TGCAACGGTCGACACCCACAC 3'
   568       577       587
  
```

Simple Homology Region [bphC 5']

No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
2	bphc(X97984)	N	1	568	20	19	95.00%

```

      1           10           20
5' TGCAAYGRHSGMCACCCACAC 3'
   *****
5' TGCAATGGGCGCCACCCACAC 3'
   568       577       587
  
```

Simple Homology Region [bphC 5']

No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
3	U57649 n	N	1	574	20	17	85.00%

```

      1           10           20
5' TGCAAYGRHSGMCACCCACAC 3'
   *****
5' TGCAACCCGCGCCACCCACAC 3'
   574       583       593
  
```

Simple Homology Region [bphC 5']

No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
9	ligZ -1	N	1	574	20	13	65.00%

```

      1           10           20
5' TGCAAYGRHSGMCACCCACAC 3'
   * * * * *
5' TTCATCTACCGCCAGATCAT 3'
   574       583       593
  
```

File Name : bphC 3'
 Range : 1 - 21 Mode : Complementary
 Codon Table : Universal

添付資料 3-4-5

5' CGC CAC ACC AAT GAC CAC ATG 3'

 R H T N D H M

Simple Homology Region [bphC 3']

No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
2	EDO 2(RW1)	C	1	718	21	19	90.47%

1 10 20
 5' CGCCACACCAATGACCACATG 3'
 ***** * *****
 5' CGCCACACCAATGATCGCATG 3'
 718 727 737

Simple Homology Region [bphC 3']

No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
1	bphc(D32142)	C	1	718	21	21	100.00%

1 10 20
 5' CGCCACACCAATGACCACATG 3'

 5' CGCCACACCAATGACCACATG 3'
 718 727 737

Simple Homology Region [bphC 3']

No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
1	bphc(X97984)	C	1	718	21	18	85.71%

1 10 20
 5' CGCCACACCAATGACCACATG 3'
 ***** * *
 5' CGCCACACCAACGACCATACG 3'
 718 727 737

Simple Homology Region [bphC 3']

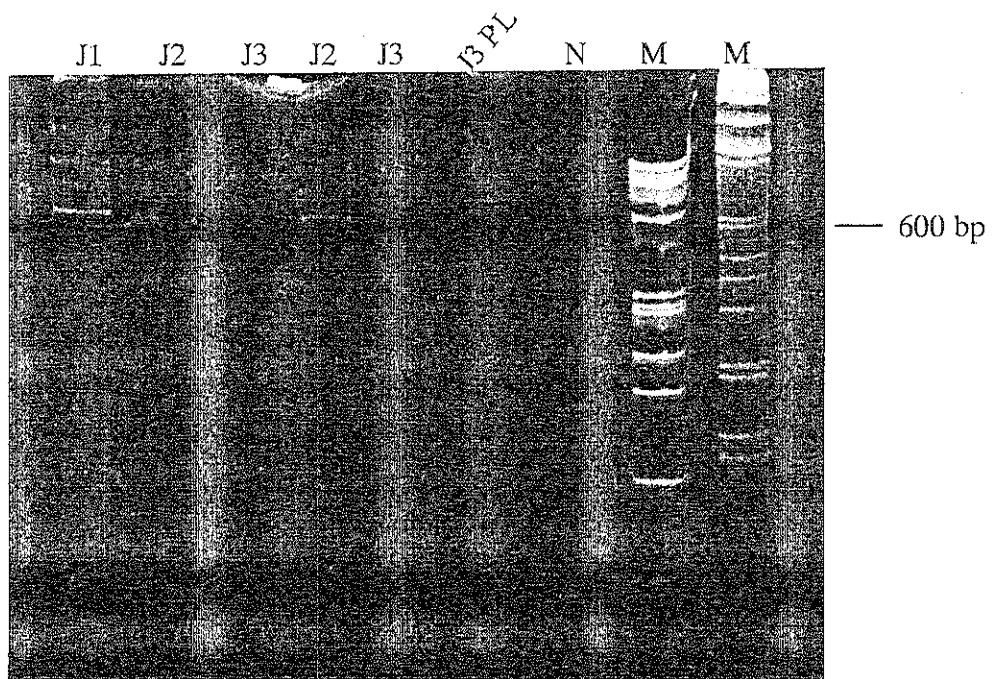
No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
40	U57649 n	C	1	696	21	9	42.85%

1 10 20
 5' CGCCACACCAATGACCACATG 3'
 ***** * *
 5' CGCCAGACAGCCGTTTCGAGAT 3'
 696 705 715

Simple Homology Region [bphC 3']

No.	Target File	Mode	Key	Target	Overlap	Match	Percentage
6	ligZ -1	C	1	706	21	12	57.14%

1 10 20
 5' CGCCACACCAATGACCACATG 3'
 *** * ** * * * *
 5' CGCAGCTGGAAAGAGGACCTG 3'
 706 715 725



添付資料3-5

Bacillus midousuji 16S リボソーム RNA 全塩基配列決定と相同性検索

図は PCR プライマー: U1= Universal primer for PCR amplification 5' cag cag ccg cgg taa tac 3'
U8= Universal Primer for PCR amplification 5' acg aca cga gct gac gac 3' とその他、図に示すと
おり12組の PCR 増幅を行って、DNA 全配列を増幅した(表の数字は *E. coli* の 16S ribosomal
RNA 塩基位置を示す)。

PCR 増幅は AmpliTaq DNA Polymerase, LD (Perkin-Elmer)を用い、その方法に準拠した。

塩基配列決定は PCR 産物を直接片側プライマーを用いて dideoxy termination 法で行った(ABI
PRISM)。

相同性検索はデータ通信により Blast(Basic Local Arignment Search Tool)を用いて行った。

写真は *B. midousuji* HB1001(J1), HB1002(J2), HB1030(J3) の 16S ribosomal DNA 全塩基配列を
遺伝子増幅したもののバンドをしめしている。約 1500 塩基の長さがみられる。

塩基配列のホモロジー検索の結果 *B. midousuji* HB1001(J1)と HB1002(J2)は同一であった。

HB1030(J3)は *B. midousuji* HB1001(J1), HB1002(J2)とは多少塩基配列が異なった。

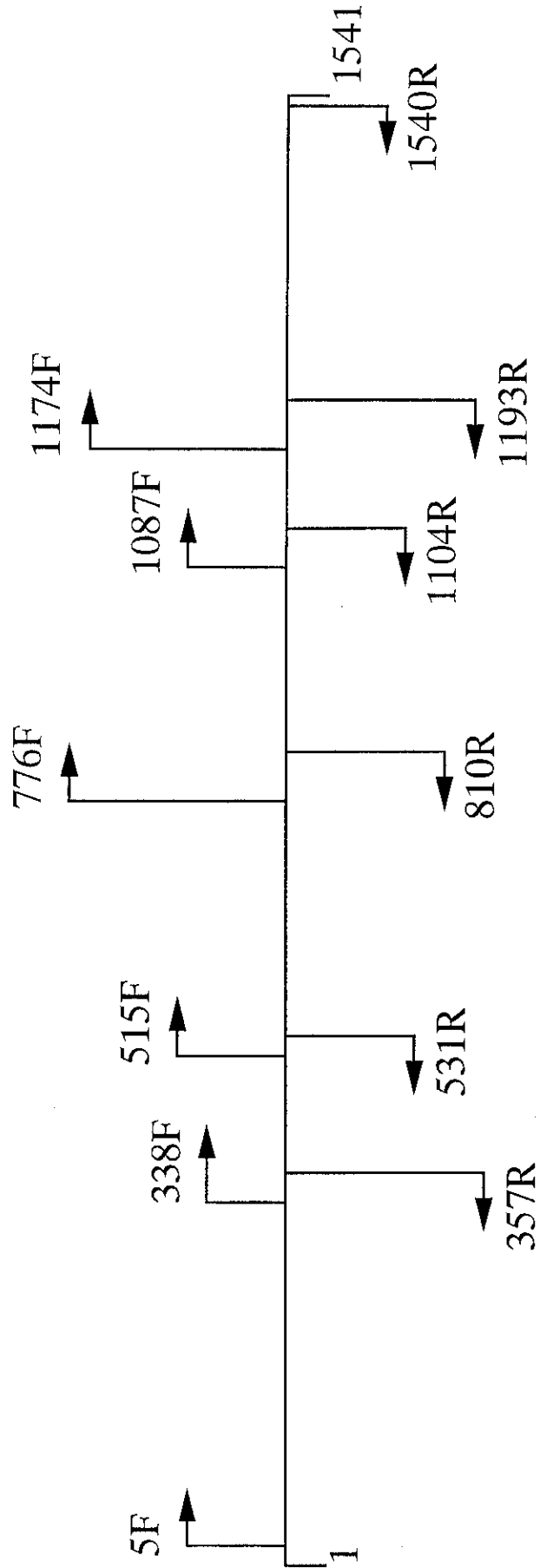
B. midousuji HB1001(J1)と HB1002(J2)の他菌種とのホモロジー検索では *B. thermo-denitrificans*,
B. denitrificans とほぼ同一の 16S ribosomal DNA 全塩基配列を示した。

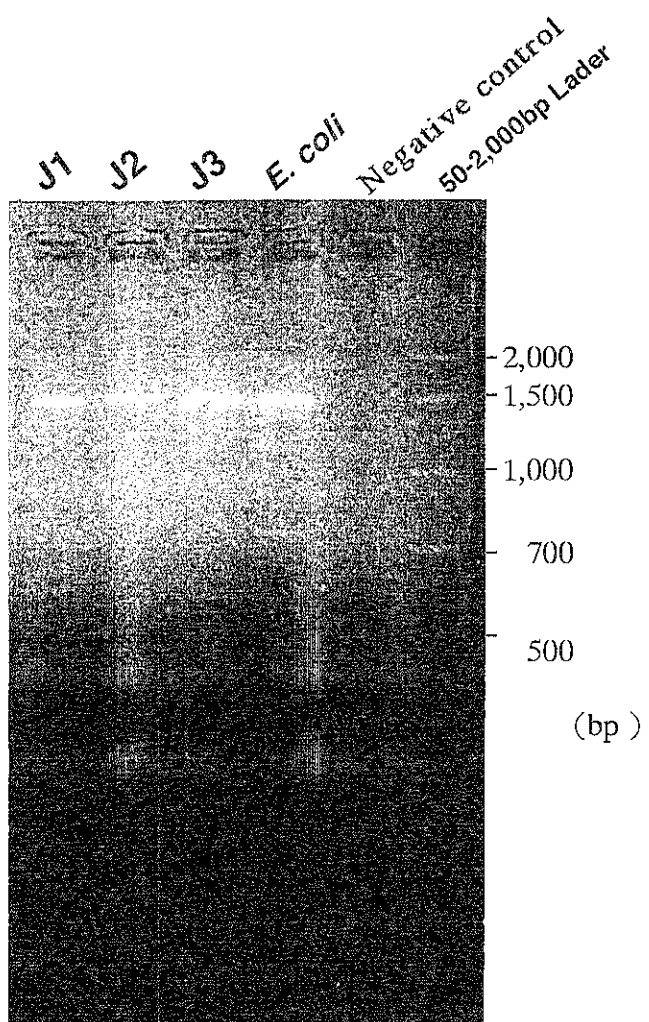
図の「2-J2 contig」は *B. midousuji* HB1001(J1)と HB1002(J2)を示し、「AB0282~1.」は *B. thermo
denitrificans*, 「Z26927~1.」は *B. denitrificans* を示す。

Bacillus midousuji (HB1030) は他菌種とのホモロジー検索で同一、類似の菌種が認められなかつ
た。

次図の Connection は *Bacillus midousuji* (HB1030) を示す。BAC1RR~1., BSU596~1.,
AB0211~1. はそれぞれ *Bacillus* sp., *Bacillus* ICPS6, *B. thermoglucosidasius* の 16S ribosomal
DNA 全塩基配列を示しているが、*Bacillus midousuji* (HB1030)とホモロジーが低いことがわかる。

MicroSeq Full Gene 16S rDNA Kit Sequencing Primer Map





		10	20	30	40	50	
2-J2contig.s	J2	1	10	20	30	40	50
AB0282~1.TXT	B. thr	1	-----	-----	-----	-----	50
Z26927~1.TXT	B. thr	1	-----	-----	-----	-----	50
Connection (J3	1	-----	-----	-----	-----	50
			60	70	80	90	100
2-J2contig.s		51	60	70	80	90	100
AB0282~1.TXT		51	ATGCAAGTCG	AGCGGACCGA	ACGAGAGCTT	GCTCTTGTTT	GGTCAGCGGC
Z26927~1.TXT		51	ATGCAAGTCG	AGCGGACCGA	ACGAGAGCTT	GCTCTTGTTT	GGTCAGCGGC
Connection (51	ATGCAAGTCG	AGCGGACCGA	ACGAGAGCTT	GCTCTTGTTT	GGTCAGCGGC
			110	120	130	140	150
2-J2contig.s		101	110	120	130	140	150
AB0282~1.TXT		101	GGACGGGTGA	GTAACACGTG	GGCAACCTGC	CCGCAAGACC	GGGATAACTC
Z26927~1.TXT		101	GGACGGGTGA	GTAACACGTG	GGCAACCTGC	CCGCAAGACC	GGGATAACTC
Connection (101	GGACGGGTGA	GTAACACGTG	GGCAACCTGC	CCGCAAGACC	GGGATAACTC
			160	170	180	190	200
2-J2contig.s		151	160	170	180	190	200
AB0282~1.TXT		151	CGGGAAACCG	GAGCTAATAC	CGGATAACAC	CAAAGACCCG	ATGGTCTTTG
Z26927~1.TXT		151	CGGGAAACCG	GAGCTAATAC	CGGATAACAC	CAAAGACCCG	ATGGTCTTTG
Connection (151	CGGGAAACCG	GAGCTAATAC	CGGATAACAC	CAAAGACCCG	ATGGTCTTTG
			210	220	230	240	250
2-J2contig.s		201	210	220	230	240	250
AB0282~1.TXT		201	GTTGAAAGGC	GGCITTCGGC	TGTCACCTTG	GGATGGGCC	GCGGCGCATT
Z26927~1.TXT		201	GTTGAAAGGC	GGCITTCGGC	TGTCACCTTG	GGATGGGCC	GCGGCGCATT
Connection (201	GTTGAAAGGC	GGCITTCGGC	TGTCACCTTG	GGATGGGCC	GCGGCGCATT
			260	270	280	290	300
2-J2contig.s		251	260	270	280	290	300
AB0282~1.TXT		251	AGCTAGTTGG	TGAGGTAACG	GCTCACCAAG	GCGACGATGC	GTAGCCGGCC
Z26927~1.TXT		251	AGCTAGTTGG	TGAGGTAACG	GCTCACCAAG	GCGACGATGC	GTAGCCGGCC
Connection (251	AGCTAGTTGG	TGAGGTAACG	GCTCACCAAG	GCGACGATGC	GTAGCCGGCC
			310	320	330	340	350
2-J2contig.s		301	310	320	330	340	350
AB0282~1.TXT		301	TGAGAGGGTG	ACCGGCCACA	CTGGGACTGA	GACACGGCCC	AGACTCCTAC
Z26927~1.TXT		301	TGAGAGGGTG	ACCGGCCACA	CTGGGACTGA	GACACGGCCC	AGACTCCTAC
Connection (301	TGAGAGGGTG	ACCGGCCACA	CTGGGACTGA	GACACGGCCC	AGACTCCTAC
			360	370	380	390	400
2-J2contig.s		351	360	370	380	390	400
AB0282~1.TXT		351	GGGAGGCAGC	AGTAGGGAAT	CTTCCGCAAT	GGACGAAAGT	CTGACGGAGC
Z26927~1.TXT		351	GGGAGGCAGC	AGTAGGGAAT	CTTCCGCAAT	GGACGAAAGT	CTGACGGAGC
Connection (351	GGGAGGCAGC	AGTAGGGAAT	CTTCCGCAAT	GGACGAAAGT	CTGACGGAGC
			410	420	430	440	450
2-J2contig.s		401	410	420	430	440	450
AB0282~1.TXT		401	GACGCCGCGT	GAGCGAAGAA	GGCCTTCGGG	TCGTAAAGCT	CTGTTGTGAG
Z26927~1.TXT		401	GACGCCGCGT	GAGCGAAGAA	GGCCTTCGGG	TCGTAAAGCT	CTGTTGTGAG
Connection (401	GACGCCGCGT	GAGCGAAGAA	GGCCTTCGGG	TCGTAAAGCT	CTGTTGTGAG
			460	470	480	490	500
2-J2contig.s		451	460	470	480	490	500
AB0282~1.TXT		451	GGACGAAGGA	GCGCCGTTTG	AATAAGGCGG	CGCGGTGACG	GTACCTCACG
Z26927~1.TXT		451	GGACGAAGGA	GCGCCGTTTG	AATAAGGCGG	CGCGGTGACG	GTACCTCACG
Connection (451	GGACGAAGGA	GCGCCGTTTG	AATAAGGCGG	CGCGGTGACG	GTACCTCACG
			510	520	530	540	550
2-J2contig.s		501	510	520	530	540	550
AB0282~1.TXT		501	AGAAAGCCCC	GGCTAACTAC	GTGCCAGCAG	CCGCGGTAAT	ACGTAGGGGG
Z26927~1.TXT		501	AGAAAGCCCC	GGCTAACTAC	GTGCCAGCAG	CCGCGGTAAT	ACGTAGGGGG
Connection (501	AGAAAGCCCC	GGCTAACTAC	GTGCCAGCAG	CCGCGGTAAT	ACGTAGGGGG

		560	570	580	590	600	
2-J2contig.s	551	CGAGCGTTGT	CCGGAATTAT	TGGGCGTAAA	GCGCGCGCAG	GCGGTCCTTT	600
AB0282~1.TXT	551	CGAGCGTTGT	CCGGAATTAT	TGGGCGTAAA	GCGCGCGCAG	GCGGTCCTTT	600
Z26927~1.TXT	551	CGAGCGTTGT	CCGGAATTAT	TGGGCGTAAA	GCGCGCGCAG	GCGGTCCTTT	600
Connection (551	CGAGCGTTGT	CCGGAATTAT	TGGGCGTAAA	GCGCGCGCAG	GCGGTCCTTT	600
		610	620	630	640	650	
2-J2contig.s	601	AAGTCTGATG	TGAAAGCCCA	CGGCTCAACC	GTGGAGGGTC	ATTGGAAACT	650
AB0282~1.TXT	601	AAGTCTGATG	TGAAAGCCCA	CGGCTCAACC	GTGGAGGGTC	ATTGGAAACT	650
Z26927~1.TXT	601	AAGTCTGATG	TGAAAGCCCA	CGGCTCAACC	GTGGAGGGTC	ATTGGAAACT	650
Connection (601	AAGTCTGATG	TGAAAGCCCA	CGGCTCAACC	GTGGAGGGTC	ATTGGAAACT	650
		660	670	680	690	700	
2-J2contig.s	651	GGGGGACTTG	AGTGCAGGAG	AGGAGAGCGG	AATTCCACGT	GTAGCGGTGA	700
AB0282~1.TXT	651	GGGGGACTTG	AGTGCAGGAG	AGGAGAGCGG	AATTCCACGT	GTAGCGGTGA	700
Z26927~1.TXT	651	GGGGGACTTG	AGTGCAGGAG	AGGAGAGCGG	AATTCCACGT	GTAGCGGTGA	700
Connection (651	GGGGGACTTG	AGTGCAGGAG	AGGAGAGCGG	AATTCCACGT	GTAGCGGTGA	700
		710	720	730	740	750	
2-J2contig.s	701	AATGCGTAGA	GATGTGGAGG	AACACCAGTG	GCGAAGGCCG	CTCTCTGGCC	750
AB0282~1.TXT	701	AATGCGTAGA	GATGTGGAGG	AACACCAGTG	GCGAAGGCCG	CTCTCTGGCC	750
Z26927~1.TXT	701	AATGCGTAGA	GATGTGGAGG	AACACCAGTG	GCGAAGGCCG	CTCTCTGGCC	750
Connection (701	AATGCGTAGA	GATGTGGAGG	AACACCAGTG	GCGAAGGCCG	CTCTCTGGCC	750
		760	770	780	790	800	
2-J2contig.s	751	TGTAACCTGAC	GCTGAGGCCG	GAAAGCGTGG	GGAGCAAACA	GGATTAGATA	800
AB0282~1.TXT	751	TGTAACCTGAC	GCTGAGGCCG	GAAAGCGTGG	GGAGCAAACA	GGATTAGATA	800
Z26927~1.TXT	751	TGTAACCTGAC	GCTGAGGCCG	GAAAGCGTGG	GGAGCAAACA	GGATTAGATA	800
Connection (751	TGTAACCTGAC	GCTGAGGCCG	GAAAGCGTGG	GGAGCAAACA	GGATTAGATA	800
		810	820	830	840	850	
2-J2contig.s	801	CCCTGGTAGT	CCACGCCGTA	AACGATGAGT	GCTAAGTGTT	AGAGGGGTCA	850
AB0282~1.TXT	801	CCCTGGTAGT	CCACGCCGTA	AACGATGAGT	GCTAAGTGTT	AGAGGGGTCA	850
Z26927~1.TXT	801	CCCTGGTAGT	CCACGCCGTA	AACGATGAGT	GCTAAGTGTT	AGAGGGGTCA	850
Connection (801	CCCTGGTAGT	CCACGCCGTA	AACGATGAGT	GCTAAGTGTT	AGAGGGGTCA	850
		860	870	880	890	900	
2-J2contig.s	851	CACCCTTTAG	TGCTGTAGCT	AACGCGATAA	GCACTCCGCC	TGGGGAGTAC	900
AB0282~1.TXT	851	CACCCTTTAG	TGCTGTAGCT	AACGCGATAA	GCACTCCGCC	TGGGGAGTAC	900
Z26927~1.TXT	851	CACCCTTTAG	TGCTGTAGCT	AACGCGATAA	GCACTCCGCC	TGGGGAGTAC	900
Connection (851	CACCCTTTAG	TGCTGTAGCT	AACGCGATAA	GCACTCCGCC	TGGGGAGTAC	900
		910	920	930	940	950	
2-J2contig.s	901	GGCCGCAAGG	CTGAAACTCA	AAGGAATTGA	CGGGGGCCCC	CACAAGCGG	950
AB0282~1.TXT	901	GGCCGCAAGG	CTGAAACTCA	AAGGAATTGA	CGGGGGCCCC	CACAAGCGG	950
Z26927~1.TXT	901	GGCCGCAAGG	CTGAAACTCA	AAGGAATTGA	CGGGGGCCCC	CACAAGCGG	950
Connection (901	GGCCGCAAGG	CTGAAACTCA	AAGGAATTGA	CGGGGGCCCC	CACAAGCGG	950
		960	970	980	990	1000	
2-J2contig.s	951	TGGAGCATGT	GGTTTAATTC	GAAGCAACGC	GAAGAACCTT	ACCAAGGCTC	1000
AB0282~1.TXT	951	TGGAGCATGT	GGTTTAATTC	GAAGCAACGC	GAAGAACCTT	ACCAAGGCTC	1000
Z26927~1.TXT	951	TGGAGCATGT	GGTTTAATTC	GAAGCAACGC	GAAGAACCTT	ACCAAGGCTC	1000
Connection (951	TGGAGCATGT	GGTTTAATTC	GAAGCAACGC	GAAGAACCTT	ACCAAGGCTC	1000
		1010	1020	1030	1040	1050	
2-J2contig.s	1001	TGACATCCCC	TGACAACCCA	AGAGATTGGG	CGTTCCCCCT	TCGGGGGGAC	1050
AB0282~1.TXT	1001	TGACATCCCC	TGACAACCCA	AGAGATTGGG	CGTTCCCCCT	TCGGGGGGAC	1050
Z26927~1.TXT	1001	TGACATCCCC	TGACAACCCA	AGAGATTGGG	CGTTCCCCCT	TCGGGGGGAC	1050
Connection (1001	TGACATCCCC	TGACAACCCA	AGAGATTGGG	CGTTCCCCCT	TCGGGGGGAC	1050
		1060	1070	1080	1090	1100	
2-J2contig.s	1051	AGGGTGACAG	GTGGTGCATG	GTTGTCGTCA	GCTCGTGTCT	TGAGATGTTG	1100
AB0282~1.TXT	1051	AGGGTGACAG	GTGGTGCATG	GTTGTCGTCA	GCTCGTGTCT	TGAGATGTTG	1100
Z26927~1.TXT	1051	AGGGTGACAG	GTGGTGCATG	GTTGTCGTCA	GCTCGTGTCT	TGAGATGTTG	1100
Connection (1051	AGGGTGACAG	GTGGTGCATG	GTTGTCGTCA	GCTCGTGTCT	TGAGATGTTG	1100

	1110	1120	1130	1140	1150			
2-J2contig.s	1101	GGTTAAGTCC	CGCAACGAGC	GCAACCCTTG	CCTCTAGTTG	CCAGCATTCA	1150	
AB0282~1.TXT	1101	GGTTAAGTCC	CGCAACGAGC	GCAACCCTTG	CCTCTAGTTG	CCAGCATTCA	1150	
Z26927~1.TXT	1101	GGTTAAGTCC	CGCAACGAGC	GCAACCCTTG	CCTCTAGTTG	CCAGCATTCA	1150	
Connection (1101	GGTTAAGTCC	CGCAACGAGC	GCAACCCTTG	CCTCTAGTTG	CCAGCATTCA	1150	
		1160	1170	1180	1190	1200		
2-J2contig.s	1151	GTTGGGCACT	CTAGAGGGA	CTGCCGGCTA	AAAGTCGGAG	GAAGGTGGGG	1200	
AB0282~1.TXT	1151	GTTGGGCACT	CTAGAGGGA	CTGCCGGCTA	AAAGTCGGAG	GAAGGTGGGG	1200	
Z26927~1.TXT	1151	GTTGGGCACT	CTAGAGGGA	CTGCCGGCTA	AAAGTCGGAG	GAAGGTGGGG	1200	
Connection (1151	GTTGGGCACT	CTAGAGGGA	CTGCCGGCTA	AAAGTCGGAG	GAAGGTGGGG	1200	
		1210	1220	1230	1240	1250		
2-J2contig.s	1201	ATGACGTCAA	ATCATCATGC	CCCTTATGAC	CTGGGCTACA	CACGTGCTAC	1250	
AB0282~1.TXT	1201	ATGACGTCAA	ATCATCATGC	CCCTTATGAC	CTGGGCTACA	CACGTGCTAC	1250	
Z26927~1.TXT	1201	ATGACGTCAA	ATCATCATGC	CCCTTATGAC	CTGGGCTACA	CACGTGCTAC	1250	
Connection (1201	ATGACGTCAA	ATCATCATGC	CCCTTATGAC	CTGGGCTACA	CACGTGCTAC	1250	
		1260	1270	1280	1290	1300		
2-J2contig.s	1251	AATGGGCGG	TACAAAGGGC	TGCGAACCCG	CGAGGGGGAG	CGAATCCCAA	1300	
AB0282~1.TXT	1251	AATGGGCGG	TACAAAGGGC	TGCGAACCCG	CGAGGGGGAG	CGAATCCCAA	1300	
Z26927~1.TXT	1251	AATGGGCGG	TACAAAGGGC	TGCGAACCCG	CGAGGGGGAG	CGAATCCCAA	1300	
Connection (1251	AATGGGCGG	TACAAAGGGC	TGCGAACCCG	CGAGGGGGAG	CGAATCCCAA	1300	
		1310	1320	1330	1340	1350		
2-J2contig.s	1301	AAAGCCGCTC	TCAGTT	CGG	ATTGCAGGCT	GCAACTCGCC	TGCATGAAGC	1350
AB0282~1.TXT	1301	AAAGCCGCTC	TCAGTT	CGG	ATTGCAGGCT	GCAACTCGCC	TGCATGAAGC	1350
Z26927~1.TXT	1301	AAAGCCGCTC	TCAGTT	CGG	ATTGCAGGCT	GCAACTCGCC	TGCATGAAGC	1350
Connection (1301	AAAGCCGCTC	TCAGTT	CGG	ATTGCAGGCT	GCAACTCGCC	TGCATGAAGC	1350
		1360	1370	1380	1390	1400		
2-J2contig.s	1351	CGGAATCGCT	AGTAATCGCG	GATCAGCATG	CCGCGGTGAA	TACGTTCCCG	1400	
AB0282~1.TXT	1351	CGGAATCGCT	AGTAATCGCG	GATCAGCATG	CCGCGGTGAA	TACGTTCCCG	1400	
Z26927~1.TXT	1351	CGGAATCGCT	AGTAATCGCG	GATCAGCATG	CCGCGGTGAA	TACGTTCCCG	1400	
Connection (1351	CGGAATCGCT	AGTAATCGCG	GATCAGCATG	CCGCGGTGAA	TACGTTCCCG	1400	
		1410	1420	1430	1440	1450		
2-J2contig.s	1401	GGCCTTGTAC	ACACCGCCCG	TCACACCACG	AGAGCTTGCA	ACACCCGAAG	1450	
AB0282~1.TXT	1401	GGCCTTGTAC	ACACCGCCCG	TCACACCACG	AGAGCTTGCA	ACACCCGAAG	1450	
Z26927~1.TXT	1401	GGCCTTGTAC	ACACCGCCCG	TCACACCACG	AGAGCTTGCA	ACACCCGAAG	1450	
Connection (1401	GGCCTTGTAC	ACACCGCCCG	TCACACCACG	AGAGCTTGCA	ACACCCGAAG	1450	
		1460	1470	1480	1490	1500		
2-J2contig.s	1451	TCGGTGAGGT	AACCCTTACG	GGAGCCAGCC	GCCGAAGGTG	GGGCAAGTGA	1500	
AB0282~1.TXT	1451	TCGGTGAGGT	AACCCTTACG	GGAGCCAGCC	GCCGAAGGTG	GGGCAAGTGA	1500	
Z26927~1.TXT	1451	TCGGTGAGGT	AACCCTTACG	GGAGCCAGCC	GCCGAAGGTG	GGGCAAGTGA	1500	
Connection (1451	TCGGTGAGGT	AACCCTTACG	GGAGCCAGCC	GCCGAAGGTG	GGGCAAGTGA	1500	
		1510	1520	1530	1540	1550		
2-J2contig.s	1501	TTGGGGTGAA	GTCGTAACAA	GGTAGCCGTA	CCGGAAGGTG	CGGCTGGATC	1550	
AB0282~1.TXT	1501	TTGGGGTGAA	GTCGTAACAA	GGTAGCCGTA	CCGGAAGGTG	CGGCTGGATC	1550	
Z26927~1.TXT	1501	TTGGGGTGAA	GTCGTAACAA	GGTAGCCGTA	CCGGAAGGTG	CGGCTGGATC	1550	
Connection (1501	TTGGGGTGAA	GTCGTAACAA	GGTAGCCGTA	CCGGAAGGTG	CGGCTGGATC	1550	
		1560	1570	1580	1590	1600		
2-J2contig.s	1551	ACCTCCTTA	1600	
AB0282~1.TXT	1551	ACCTCCTTA	1600	
Z26927~1.TXT	1551	ACCTCCTTA	1600	
Connection (1551	ACCTCCTTA	1600	

Query=J1 & J2
(1553 letters)

		Score	E
		(bits)	Value
emb Z26927.1 BD16SRRNB	B.denitrificans gene for 16S riboso...	2954	0.0
dbj AB028234.1 AB028234	Bacillus thermodenitrificans gene f...	2944	0.0
emb Z26928.1 BT16SRRNH	B.thermodenitrificans gene for 16S ...	2898	0.0
gb AF114426.1 AF114426	Bacillus thermodenitrificans T4 16S ...	2884	0.0
emb Z26922.1 BC16SRRNB	B.caldotenax gene for 16S ribosomal...	2793	0.0
gb AF114424.1 AF114424	Bacillus thermodenitrificans NS 16S ...	2787	0.0
emb Z26923.1 BT16SRRNF	B.thermoleovorans gene for 16S ribo...	2787	0.0
emb Z26926.1 BT16SRRNG	B.thermocatenulatus gene for 16S ri...	2785	0.0
dbj AB021196.1 AB021196	Bacillus stearothermophilus gene fo...	2777	0.0
dbj AB034836.1 AB034836	Bacillus thermoleovorans gene for 1...	2775	0.0
emb Z26924.1 BC16SRRNC	B.caldolyticus gene for 16S ribosom...	2757	0.0
gb AF114425.1 AF114425	Bacillus thermodenitrificans S 16S r...	2750	0.0
emb AJ005760.1 BSA005760	Bacillus stearothermophilus K1041 ...	2744	0.0
emb Z26925.1 BC16SRRND	B.caldovelox gene for 16S ribosomal...	2742	0.0
emb X57309.1 BS16SRNA	B.stearothermophilus 16S rRNA	2726	0.0
dbj AB021197.1 AB021197	Bacillus thermoglucosidasius gene f...	2631	0.0
gb AF067651.1 AF067651	Bacillus caldolyticus 16S riboso...	2611	0.0
gb U59630.1 BSU59630	Bacillus ICPS6 16S ribosomal RNA gene,...	2607	0.0
dbj AB002647.1 AB002647	Unidentified low G+C gram-positive ...	2585	0.0
gb L29507.1 BAC1RRAAA	Bacillus sp. 16S ribosomal RNA (16S rR...	2567	0.0
emb X60618.1 BKAU16S	B.kaustophilus 16S ribosomal RNA	2553	0.0
gb M77484.1 BACRRSSA	Bacillus caldolyticus (DSM 405) riboso...	2543	0.0
gb M77485.1 BACRRSSB	Bacillus caldovelox (DSM 411) ribosoma...	2529	0.0
gb M77488.1 BACRRSSE	Bacillus thermoleovorans (ATCC 43513) ...	2500	0.0
dbj AB002646.1 AB002646	Unidentified low G+C gram-positive ...	2484	0.0
dbj AB034902.1 AB034902	Bacillus thermoleovorans gene for 1...	2456	0.0
emb X70430.1 ST16SRR	S.thermophilus gene for 16S ribosomal RNA	2446	0.0
gb L09227.1 SAHRDGX	Saccharococcus thermophilus 16S ribosom...	2446	0.0

		10	20	30	40	50	
Connection (1	GAGAGTTTGA	TCCTGGCTCA	GGACGAACGC	TGGCGGCGTG	CCTAATACAT	50
BAC1RR~1.TXT	1	GAG--TTTGA	TCATGGCTCA	GGACGAACGC	TGGCGGCGTG	CCTAATACAT	50
BSU596~1.TXT	1	-AG--TTTGA	TCCTGGCTCA	GGACGAACGC	TGGCGGCGTG	CCTAATACAT	50
AB0211~1.TXT	1	-----	-----	-ACGAACGC	TGGCGGCGTG	CCTAATACAT	50
		60	70	80	90	100	
Connection (51	GCAAGTCGAG	CGGACCGAAC	GGAAGCTTGC	TTCTTGTTCGG	TTAGCGGCGG	100
BAC1RR~1.TXT	51	GCAAGTCGAG	CGGACCGGGC	GGAAGCTTGC	TTCCGCTTGG	TTAGCGGCGG	100
BSU596~1.TXT	51	GCAAGTCGAG	CGGACCGGGC	GGGAGCTTGC	TTCCGCTTGG	TTAGCGGCGG	100
AB0211~1.TXT	51	GCAAGTCGAG	CGGACCGGGC	GGGAGCTTGC	TTCCGCTTGG	TTAGCGGCGG	100
		110	120	130	140	150	
Connection (101	ACGGGTGAGT	AACACGTGGG	TAACCTGCCC	GTAAGACCGG	GATAACTCCG	150
BAC1RR~1.TXT	101	ACGGGTGAGT	AACACGTGGG	TAACCTGCCC	GTAAGACCGG	GATAACTCCG	150
BSU596~1.TXT	101	ACGGGTGAGT	AACACGTGGG	TAACCTGCCC	GTAAGACCGG	GATAACTCCG	150
AB0211~1.TXT	101	ACGGGTGAGT	AACACGTGGG	TAACCTGCCC	GTAAGACCGG	GATAACTCCG	150
		160	170	180	190	200	
Connection (151	GGAAACCGGG	GCTAATACCG	GATAACACCG	AAGACCGCAT	GGTCTTTCGGT	200
BAC1RR~1.TXT	151	GGAAACCGGA	GCTAATACCG	GATAACACCG	AAGACCGCAT	GGTCTTTCGGT	200
BSU596~1.TXT	151	GGAAACCGGG	GCTAATACCG	GATAACACCG	AAGACCGCAT	GGTCTTTCGGT	200
AB0211~1.TXT	151	GGAAACCGGG	GCTAATACCG	GATAACACCG	AAGACCGCAT	GGTCTTTCGGT	200
		210	220	230	240	250	
Connection (201	TGAAAGGTTGG	CTTTTGCTAC	CACTTACGGA	TGGGCCCGCG	GCGCATTAGC	250
BAC1RR~1.TXT	201	TGAAAGGCGG	CTTCGGCTGC	CACTTTCGGA	TGGGCCCGCG	GCGCATTAGC	250
BSU596~1.TXT	201	TGAAAGGCGG	CTTCGGCTGC	CACTTACGGA	TGGGCCCGCG	GCGCATTAGC	250
AB0211~1.TXT	201	TGAAAGGCGG	CTTCGGCTGC	CACTTACGGA	TGGGCCCGCG	GCGCATTAGC	250
		260	270	280	290	300	
Connection (251	TAGTTGGTGA	GGTAACGGCT	CACCAAGGCG	ACGATGCGTA	GCCGGCCTGA	300
BAC1RR~1.TXT	251	TAGTTGGTGA	GGTAACGGCT	CACCAAGGCG	ACGATGCGTA	GCCGGCCTGA	300
BSU596~1.TXT	251	TAGTTGGTGA	GGTAACGGCT	CACCAAGGCG	ACGATGCGTA	GCCGGCCTGA	300
AB0211~1.TXT	251	TAGTTGGTGA	GGTAACGGCT	CACCAAGGCG	ACGATGCGTA	GCCGGCCTGA	300
		310	320	330	340	350	
Connection (301	GAGGGTGACC	GGCCACACTG	GGACTGAGAC	ACGGCCCAGA	CTCCTACGGG	350
BAC1RR~1.TXT	301	GAGGGTGACC	GGCCACACTG	GGACTGAGAC	ACGGCCCAGA	CTCCTACGGG	350
BSU596~1.TXT	301	GAGGGTGACC	GGCCACACTG	GGACTGAGAC	ACGGCCCAGA	CTCCTACGGG	350
AB0211~1.TXT	301	GAGGGTGACC	GGCCACACTG	GGACTGAGAC	ACGGCCCAGA	CTCCTACGGG	350
		360	370	380	390	400	
Connection (351	AGGCAGCAGT	AGGGAATCTT	CCGCAATGGA	CGAAAGTCTG	ACGGAGCGAC	400
BAC1RR~1.TXT	351	AGGCAGCAGT	AGGGAATCTT	CCGCAATGGA	CGAAAGTCTG	ACGGAGCGAC	400
BSU596~1.TXT	351	AGGCAGCAGT	AGGGAATCTT	CCGCAATGGA	CGAAAGTCTG	ACGGAGCGAC	400
AB0211~1.TXT	351	AGGCAGCAGT	AGGGAATCTT	CCGCAATGGA	CGAAAGTCTG	ACGGAGCGAC	400
		410	420	430	440	450	
Connection (401	GCCGCGTGAG	CGAAGAAGGT	CTTCGGATCG	TAAAGCTCTG	TTGTTAGGGG	450
BAC1RR~1.TXT	401	GCCGCGTGAG	CGAAGAAGGT	CTTCGGATCG	TAAAGCTCTG	TTGTTAGGGG	450
BSU596~1.TXT	401	GCCGCGTGAG	CGAAGAAGGT	CTTCGGATCG	TAAAGCTCTG	TTGTTAGGGG	450
AB0211~1.TXT	401	GCCGCGTGAG	CGAAGAAGGT	CTTCGGATCG	TAAAGCTCTG	TTGTTAGGGG	450
		460	470	480	490	500	
Connection (451	AGAAGAAGTA	CCGTTTCGAAT	AGGGCGGTTAC	GGTGACGGTA	CCTAACGAGA	500
BAC1RR~1.TXT	451	AGAAGAAGTG	CCGTTTCGAAC	AGGGCGGCAC	GGTGACGGTA	CCTAACGAGA	500
BSU596~1.TXT	451	AGAAGAAGTG	CCGTTTCGAAC	AGGGCGGCAC	GGTGACGGTA	CCTAACGAGA	500
AB0211~1.TXT	451	AGAAGAAGTG	CCGTTTCGAAC	AGGGCGGCAC	GGTGACGGTA	CCTAACGAGA	500
		510	520	530	540	550	
Connection (501	AAGCCCCGGC	TAACCTACGTG	CCAGCAGCCG	CGGTAATACG	TAGGGGGCGA	550
BAC1RR~1.TXT	501	AAGCCCCGGC	TAACCTACGTG	CCAGCAGCCG	CGGTAATACG	TAGGGGGCGA	550
BSU596~1.TXT	501	AAGCCCCGGC	TAACCTACGTG	CCAGCAGCCG	CGGTAATACG	TAGGGGGCGA	550
AB0211~1.TXT	501	AAGCCCCGGC	TAACCTACGTG	CCAGCAGCCG	CGGTAATACG	TAGGGGGCGA	550

		560	570	580	590	600	
Connection (551	GCGTTGTCCG	GAATTATTGG	GCGTAAAGCG	CGCGCAGGCG	GTCCCTTAAG	600
BAC1RR~1.TXT	551	GCGTTGTCCG	GAATTATTGG	GCGTAAAGCG	CGCGCAGGCG	GTCCCTTAAG	600
BSU596~1.TXT	551	GCGTTGTCCG	GAATTATTGG	GCGTAAAGCG	CGCGCAGGCG	GTCCCTTAAG	600
AB0211~1.TXT	551	GCGTTGTCCG	GAATTATTGG	GCGTAAAGCG	CGCGCAGGCG	GTCCCTTAAG	600
		610	620	630	640	650	
Connection (601	TCTGATGTGA	AAGCCCACGG	CTTAACCGTG	GAGGGTCATT	GGAAACTGGG	650
BAC1RR~1.TXT	601	TCTGATGTGA	AAGCCCACGG	CTTAACCGTG	GAGGGTCATT	GGAAACTGGG	650
BSU596~1.TXT	601	TCTGATGTGA	AAGCCCACGG	CTTAACCGTG	GAGGGTCATT	GGAAACTGGG	650
AB0211~1.TXT	601	TCTGATGTGA	AAGCCCACGG	CTTAACCGTG	GAGGGTCATT	GGAAACTGGG	650
		660	670	680	690	700	
Connection (651	GGACTTGAGT	GCAGAAGAGG	AGAGCGGAAT	TCCACGTGTA	GCGGTGAAAT	700
BAC1RR~1.TXT	651	GGACTTGAGT	GCAGAAGAGG	AGAGCGGAAT	TCCACGTGTA	GCGGTGAAAT	700
BSU596~1.TXT	651	GGACTTGAGT	GCAGAAGAGG	AGAGCGGAAT	TCCACGTGTA	GCGGTGAAAT	700
AB0211~1.TXT	651	GGACTTGAGT	GCAGAAGAGG	AGAGCGGAAT	TCCACGTGTA	GCGGTGAAAT	700
		710	720	730	740	750	
Connection (701	GCGTAGAGAT	GTGGAGGAAC	ACCAGTGGCG	AAGGCGGCTC	TCTGGTCTGT	750
BAC1RR~1.TXT	701	GCGTAGAGAT	GTGGAGGAAC	ACCAGTGGCG	AAGGCGGCTC	TCTGGTCTGT	750
BSU596~1.TXT	701	GCGTAGAGAT	GTGGAGGAAC	ACCAGTGGCG	AAGGCGGCTC	TCTGGTCTGT	750
AB0211~1.TXT	701	GCGTAGAGAT	GTGGAGGAAC	ACCAGTGGCG	AAGGCGGCTC	TCTGGTCTGT	750
		760	770	780	790	800	
Connection (751	AACTGACGCT	GAGGCGCGAA	AGCGTGGGGA	GCAAACAGGA	TTAGATACCC	800
BAC1RR~1.TXT	751	AACTGACGCT	GAGGCGCGAA	AGCGTGGGGA	GCAAACAGGA	TTAGATACCC	800
BSU596~1.TXT	751	AACTGACGCT	GAGGCGCGAA	AGCGTGGGGA	GCAAACAGGA	TTAGATACCC	800
AB0211~1.TXT	751	AACTGACGCT	GAGGCGCGAA	AGCGTGGGGA	GCAAACAGGA	TTAGATACCC	800
		810	820	830	840	850	
Connection (801	TGGTAGTCCA	CGCCGTA AAC	GATGAGTGCT	AAGTGTTAGA	GGGGTTATTC	850
BAC1RR~1.TXT	801	TGGTAGTCCA	CGCCGTA AAC	GATGAGTGCT	AAGTGTTAGA	GGGGTTATTC	850
BSU596~1.TXT	801	TGGTAGTCCA	CGCCGTA AAC	GATGAGTGCT	AAGTGTTAGA	GGGGTTATTC	850
AB0211~1.TXT	801	TGGTAGTCCA	CGCCGTA AAC	GATGAGTGCT	AAGTGTTAGA	GGGGTTATTC	850
		860	870	880	890	900	
Connection (851	CCTTTAGTGC	TGTAGCTAAC	GCGTTAAGCA	CTCCGCCTGG	GGAGTACGGC	900
BAC1RR~1.TXT	851	CCTTTAGTGC	TGTAGCTAAC	GCGTTAAGCA	CTCCGCCTGG	GGAGTACGGC	900
BSU596~1.TXT	851	CCTTTAGTGC	TGTAGCTAAC	GCGTTAAGCA	CTCCGCCTGG	GGAGTACGGC	900
AB0211~1.TXT	851	CCTTTAGTGC	TGTAGCTAAC	GCGTTAAGCA	CTCCGCCTGG	GGAGTACGGC	900
		910	920	930	940	950	
Connection (901	CGCAAGGCTG	AAACTCAAAG	GAATTGACGG	GGGCCCGCAC	AAGCGGTGG	950
BAC1RR~1.TXT	901	CGCAAGGCTG	AAACTCAAAG	GAATTGACGG	GGGCCCGCAC	AAGCGGTGG	950
BSU596~1.TXT	901	CGCAAGGCTG	AAACTCAAAG	GAATTGACGG	GGGCCCGCAC	AAGCGGTGG	950
AB0211~1.TXT	901	CGCAAGGCTG	AAACTCAAAG	GAATTGACGG	GGGCCCGCAC	AAGCGGTGG	950
		960	970	980	990	1000	
Connection (951	AGCATGTGGT	TTAATTCGAA	GCAACGCGAA	GAACCTTACC	AGGTCTTGA	1000
BAC1RR~1.TXT	951	AGCATGTGGT	TTAATTCGAA	GCAACGCGAA	GAACCTTACC	AGGTCTTGA	1000
BSU596~1.TXT	951	AGCATGTGGT	TTAATTCGAA	GCAACGCGAA	GAACCTTACC	AGGTCTTGA	1000
AB0211~1.TXT	951	AGCATGTGGT	TTAATTCGAA	GCAACGCGAA	GAACCTTACC	AGGTCTTGA	1000
		1010	1020	1030	1040	1050	
Connection (1001	CATCCCCTGA	CAACCCTGGA	GACAGGGCGT	TCCTCCCTTG	CGGGAGGACA	1050
BAC1RR~1.TXT	1001	CATCCCCTGA	CAACCCTGGA	GACAGGGCGT	TCCTCCCTTG	CGGGAGGACA	1050
BSU596~1.TXT	1001	CATCCCCTGA	CAACCCTGGA	GACAGGGCGT	TCCTCCCTTG	CGGGAGGACA	1050
AB0211~1.TXT	1001	CATCCCCTGA	CAACCCTGGA	GACAGGGCGT	TCCTCCCTTG	CGGGAGGACA	1050
		1060	1070	1080	1090	1100	
Connection (1051	GGGTGACAGG	TGGTGACATGG	TTGTCGTCAG	CTCGTGTCGT	GAGATGTTGG	1100
BAC1RR~1.TXT	1051	GGGTGACAGG	TGGTGACATGG	TTGTCGTCAG	CTCGTGTCGT	GAGATGTTGG	1100
BSU596~1.TXT	1051	GGGTGACAGG	TGGTGACATGG	TTGTCGTCAG	CTCGTGTCGT	GAGATGTTGG	1100
AB0211~1.TXT	1051	GGGTGACAGG	TGGTGACATGG	TTGTCGTCAG	CTCGTGTCGT	GAGATGTTGG	1100

		1110	1120	1130	1140	1150		
Connection (1101	GTTAAGTCCC	GCAACGAGCG	CAACCCTCGC	CCCTAGTTGC	CAGCATTAG	1150	
BAC1RR~1.TXT	1101	GTTAAGTCCC	GCAACGAGCG	CAACCCTCGC	CCCTAGTTGC	CAGCATTAG	1150	
BSU596~1.TXT	1101	GTTAAGTCCC	GCAACGAGCG	CAACCCTCGC	CCCTAGTTGC	CAGCATTAG	1150	
AB0211~1.TXT	1101	GTTAAGTCCC	GCAACGAGCG	CAACCCTCGC	CCCTAGTTGC	CAGCATTAG	1150	
		1160	1170	1180	1190	1200		
Connection (1151	TTGGGCACTC	TAGGGGGAAC	TGCCGATAAA	AATCCGGGGG	AAGGTGGGGA	1200	
BAC1RR~1.TXT	1151	TTGGGCACTC	TAGGGGGAAC	TGCCGGTGAC	AAACCGGAGG	AAGGTGGGGA	1200	
BSU596~1.TXT	1151	TTGGGCACTC	TAGGGGGAAC	TGCCGGCTAA	AAGTCGGAGG	AAGGTGGGGA	1200	
AB0211~1.TXT	1151	TTGGGCACTC	TAGGGGGAAC	TGCCGGCTAA	AAGTCGGAGG	AAGGTGGGGA	1200	
		1210	1220	1230	1240	1250		
Connection (1201	ATACCTTAA	TCATCATGCC	CCTTATGACC	TGGGCTACAC	ACGTGCTACA	1250	
BAC1RR~1.TXT	1201	TGACGTCAAA	TCATCATGCC	CCTTATGACC	TGGGCTACAC	ACGTGCTACA	1250	
BSU596~1.TXT	1201	TGACGTCAAA	TCATCATGCC	CCTTATGACC	TGGGCTACAC	ACGTGCTACA	1250	
AB0211~1.TXT	1201	TGACGTCAAA	TCATCATGCC	CCTTATGACC	TGGGCTACAC	ACGTGCTACA	1250	
		1260	1270	1280	1290	1300		
Connection (1251	ATGGGCGGT	ACAAAGGGCT	GCGAACCCGC	GAGGGGGAGC	GAATCCCAAA	1300	
BAC1RR~1.TXT	1251	ATGGGCGGT	ACAAAGGGCT	GCGAACCCGC	GAGGGGGAGC	GAATCCCAAA	1300	
BSU596~1.TXT	1251	ATGGGCGGT	ACAAAGGGCT	GCGAACCCGC	GAGGGGGAGC	GAATCCCAAA	1300	
AB0211~1.TXT	1251	ATGGGCGGT	ACAAAGGGCT	GCGAACCCGC	GAGGGGGAGC	GAATCCCAAA	1300	
		1310	1320	1330	1340	1350		
Connection (1301	AAGCCGCTCT	CAGTT	CGGA	TTGCAGGCTG	CAACTCGCCT	GCATGAAGCC	1350
BAC1RR~1.TXT	1301	AAGCCGCTCT	CAGTT	CGGA	TTGCAGGCTG	CAACTCGCCT	GCATGAAGCC	1350
BSU596~1.TXT	1301	AAGCCGCTCT	CAGTT	CGGA	TTGCAGGCTG	CAACTCGCCT	GCATGAAGCC	1350
AB0211~1.TXT	1301	AAGCCGCTCT	CAGTT	CGGA	TTGCAGGCTG	CAACTCGCCT	GCATGAAGCC	1350
		1360	1370	1380	1390	1400		
Connection (1351	-----	-----	-----	-----	-----	1400	
BAC1RR~1.TXT	1351	GGAATCGCTA	GTAATCGCGG	ATCAGCATGC	CGCGGTGAAT	ACGTTCCCGG	1400	
BSU596~1.TXT	1351	GGAATCGCTA	GTAATCGCGG	ATCAGCATGC	CGCGGTGAAT	ACGTTCCCGG	1400	
AB0211~1.TXT	1351	GGAATCGCTA	GTAATCGCGG	ATCAGCATGC	CGCGGTGAAT	ACGTTCCCGG	1400	
		1410	1420	1430	1440	1450		
Connection (1401	-----	-----	-----	-----	-----	1450	
BAC1RR~1.TXT	1401	GCCTTGTA	CACCGCCGT	CACACCACGA	GAGCTTGCAA	CACCCGAAGT	1450	
BSU596~1.TXT	1401	GCCTTGTA	CACCGCCGT	CACACCACGA	GAGCTTGCAA	CACCCGAAGT	1450	
AB0211~1.TXT	1401	GCCTTGTA	CACCGCCGT	CACACCACGA	GAGCTTGCAA	CACCCGAAGT	1450	
		1460	1470	1480	1490	1500		
Connection (1451	-----	-----	-----	-----	-----	1500	
BAC1RR~1.TXT	1451	CGGTGAGGTA	ACCCGCAAGG	GAGCCAGCCG	CCGAAGGTGG	GGCAAGTGAT	1500	
BSU596~1.TXT	1451	CGGTGAGGTA	ACCCGCAAGG	GAGCCAGCCG	CCGAAGGTGG	GGCAAGTGAT	1500	
AB0211~1.TXT	1451	CGGTGAGGTA	ACCCGCAAGG	GAGCCAGCCG	CCGAAGGTGG	GGCAAGTGAT	1500	
		1510	1520	1530	1540	1550		
Connection (1501	-----	-----	-----	-----	-----	1550	
BAC1RR~1.TXT	1501	TGGGGTGAAG	TCGTAACAA	-----	-----	-----	1550	
BSU596~1.TXT	1501	TGGGGTGAAG	TCGTAACAA	-----	-----	-----	1550	
AB0211~1.TXT	1501	TGGGGTGAAG	TCGTAACAA	GTAGCCGTAC	CCGAAGGTGC	GGCTGGATCA	1550	
		1560	1570	1580	1590	1600		
Connection (1551	-----	-----	-----	-----	-----	1600	
BAC1RR~1.TXT	1551	-----	-----	-----	-----	-----	1600	
BSU596~1.TXT	1551	-----	-----	-----	-----	-----	1600	
AB0211~1.TXT	1551	-----	-----	-----	-----	-----	1600	

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Query=

(1482 letters)

	Score	E
Sequences producing significant alignments:	(bits)	Value
gb L29507.1 BAC1RRAAA Bacillus sp. 16S ribosomal RNA (16S rR...	2097	0.0
gb U59630.1 BSU59630 Bacillus ICPS6 16S ribosomal RNA gene,...	2074	0.0
gb AF067651.1 AF067651 Bacillus caldoolyolyticus 16S riboso...	2070	0.0
dbj AB021197.1 AB021197 Bacillus thermoglucosidasius gene f...	2054	0.0
emb AJ005759.1 BSA005759 Bacillus stearothermophilus NUB362...	1877	0.0
dbj AB028234.1 AB028234 Bacillus thermodenitrificans gene f...	1877	0.0
gb AF114426.1 AF114426 Bacillus thermodenitrificans T4 16S ...	1873	0.0
emb X70430.1 ST16SRR S.thermophilus gene for 16S ribosomal RNA	1859	0.0
gb L09227.1 SAHRDGX Saccharococcus thermophilus 16S ribosom...	1859	0.0
emb Z26927.1 BD16SRRNB B.denitrificans gene for 16S riboso...	1848	0.0
emb Z26926.1 BT16SRRNG B.thermocatenulatus gene for 16S ri...	1842	0.0
emb AJ005760.1 BSA005760 Bacillus stearothermophilus K1041 ...	1828	0.0
emb Z26928.1 BT16SRRNH B.thermodenitrificans gene for 16S ...	1820	0.0
emb Z26922.1 BC16SRRNB B.caldotenax gene for 16S ribosomal...	1820	0.0
gb AF114424.1 AF114424 Bacillus thermodenitrificans NS 16S ...	1808	0.0
emb Z26923.1 BT16SRRNF B.thermoleovorans gene for 16S ribo...	1798	0.0
dbj AB021196.1 AB021196 Bacillus stearothermophilus gene fo...	1786	0.0
emb Z26925.1 BC16SRRND B.caldovelox gene for 16S ribosomal...	1784	0.0
emb Z26924.1 BC16SRRNC B.caldolyticus gene for 16S ribosom...	1784	0.0
emb X60618.1 BKAU16S B.kaustophilus 16S ribosomal RNA	1750	0.0
gb M77484.1 BACRRSSA Bacillus caldolyticus (DSM 405) riboso...	1746	0.0
gb M77485.1 BACRRSSB Bacillus caldovelox (DSM 411) ribosoma...	1733	0.0
gb M77488.1 BACRRSSE Bacillus thermoleovorans (ATCC 43513) ...	1729	0.0
emb X60641.1 BTHER16SR Bacillus thermoglucosidasius 16S rib...	1663	0.0
dbj AB002646.1 AB002646 Unidentified low G+C gram-positive ...	1608	0.0
gb M77487.1 BACRRSSD Bacillus thermodenitrificans (NCIMB 11...	1509	0.0
emb X64465.1 BM16SRRN B.methanolicus 16S ribosomal RNA	1495	0.0