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Lampiran 1



**KEMENTERIAN RISET, TEKNOLOGI DAN PENDIDIKAN TINGGI
UNIVERSITAS HASANUDDIN
FAKULTAS KEDOKTERAN
RSPTN UNIVERSITAS HASANUDDIN
RSUP Dr. WAHIDIN SUDIROHUSODO MAKASSAR
KOMITE ETIK PENELITIAN KESEHATAN**



Sekretariat : Lantai 3 Gedung Laboratorium Terpadu
JL.PERINTIS KEMERDEKAAN KAMPUS TAMALANREA KM.10 MAKASSAR 90245.
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REKOMENDASI PERSETUJUAN ETIK

Nomor : 673 / H4.8.4.5.31 / PP36-KOMETIK / 2018

Tanggal: 20 September 2018

Dengan ini Menyatakan bahwa Protokol dan Dokumen yang Berhubungan Dengan Protokol berikut ini telah mendapatkan Persetujuan Etik :

No Protokol	UH18090561		No Sponsor Protokol	
Peneliti Utama	dr. Dewi Kartika Tungadi		Sponsor	Pribadi
Judul Peneliti	Deteksi Gen VEB, OXA-2 PER Pada Pseudomonas aeruginosa Yang Memproduksi Extended Spectrum Beta-Lactamase (ESBL) Di RSUP Dr Wahidin Sudirohusodo Makassar			
No Versi Protokol	1		Tanggal Versi	18 September 2018
No Versi PSP			Tanggal Versi	
Tempat Penelitian	RSUP dr. Wahidin Sudirohusodo dan Laboratorium Mikrobiologi RSUH Makassar			
Jenis Review	<input checked="" type="checkbox"/> Exempted <input type="checkbox"/> Expedited <input type="checkbox"/> Fullboard Tanggal		Masa Berlaku 20 September 2018 sampai 20 September 2019	Frekuensi review lanjutan
Ketua Komisi Etik Penelitian	Nama Prof.Dr.dr. Suryani As'ad, M.Sc.,Sp.GK(K)		Tanda tangan	
Sekretaris Komisi Etik Penelitian	Nama dr. Agussalim Bukhari, M.Med.,Ph.D.,Sp.GK(K)		Tanda tangan	

Kewajiban Peneliti Utama:

- Menyerahkan Amandemen Protokol untuk persetujuan sebelum di implementasikan
- Menyerahkan Laporan SAE ke Komisi Etik dalam 24 Jam dan dilengkapi dalam 7 hari dan Laporan SUSAR dalam 72 Jam setelah Peneliti Utama menerima laporan
- Menyerahkan Laporan Kemajuan (progress report) setiap 6 bulan untuk penelitian resiko tinggi dan setiap setahun untuk penelitian resiko rendah
- Menyerahkan laporan akhir setelah Penelitian berakhir
- Melaporkan penyimpangan dari protokol yang disetujui (protocol deviation / violation)
- Mematuhi semua peraturan yang ditentukan



Lampiran 2

HALAMAN PENGESAHAN
SEMINAR HASIL PROPOSAL PENELITIAN

Program Pendidikan Dokter Spesialis Terpadu
Fakultas Kedokteran Universitas Hasanuddin

**DETEKSI GEN VEB, OXA-2, PER PADA PSEUDOMONAS AERUGINOSA YANG
MEMPRODUKSI *EXTENDED SPECTRUM BETA-LACTAMASE* (ESBL) DI RSUP DR
WAHIDIN SUDIROHUSODO MAKASSAR**


Disetujui untuk diseminarkan :

Nama Mahasiswa	: dr. Dewi Kartika Tungadi
Nomor Pokok	: C108214102
Program Pendidikan	: Dokter Spesialis Terpadu FK.UNHAS
Program Studi	: Patologi Klinik
Tahun Masuk	: Juli 2014
Hari / Tanggal	: Kamis, 31 Januari 2019
Tempat	: Ruang Pertemuan Departemen Ilmu Patologi Klinik Lantai 4 Gedung A RS. UNHAS

Komisi Penasihat :

Ketua

dr. Benny Rusli, SpPK(K)

Sekretaris

Dr. dr. Tenri Esa, M.Si, Sp.PK

Mengetahui,
Manajer PPDS
Fakultas Kedokteran Unhas



Dr. Uleng Bahrun, Sp.PK(K), PhD
NIP. 19680518 199802 2 001



Lampiran 3

Data Primer Hasil Penelitian

No.	RM	No.Lab	Test ID	Jenis Kelamin	Umur (tahun)	Ruangan	Lama Perawatan (hari)	Sampel	Diagnosa	Kedadaan Keluar	Ceftazidime	Gen VEB	Gen OXA-2	Gen PER
1	406454	611/07	DK-1	L	69	Poli Bedah Uro	16	Urine 10 ⁶	Stroke +ISK	Membaik	Resisten	Negatif	Negatif	Negatif
2	846185	676/07	DK-2	L	68	ICU	98	Sputum	Trauma kepala + pneumonia	Membaik	Resisten	Negatif	Negatif	Negatif
3	800664	587/07	DK-3	L	2	PICU	180	Cairan Otak	Hidrocefalus + sepsis + meningitis TB + Marasmus	Membaik	Resisten	Negatif	Negatif	Negatif
4	801653	614/07	DK-4	L	2	PICU	30	ETT	Hidrocefalus + pneumonia	Membaik	Resisten	Negatif	Negatif	Negatif
5	849128	77/08	DK-5	L	56	L1AB	21	Darah	Sirosis hepatis + sepsis	Membaik	Resisten	Negatif	Negatif	Negatif
6	750887	762/07	DK-6	L	58	HCU	184	Sputum	Meningioma + efusi pleura sinistra	Membaik	Resisten	Negatif	Negatif	Negatif
		275/08	DK-7	L	43	L1BB	32	Pus	Ulkus kaki diabetik	Membaik	Resisten	Negatif	Negatif	Negatif
		180/08	DK-8	L	48	ICU	28	ETT	TBI GCS 8	Membaik	Resisten	Negatif	Negatif	Negatif



9	859089	294/11	DK-9	L	55	P.THT	1	Pus	OMSK	Membaik	Resisten	Negatif	Negatif	Negatif
10	843568	206/08	DK-10	P	5	L2	35	Pus	Abses hepar	Membaik	Resisten	Negatif	Negatif	Negatif
11	296222	391A/11	DK-11	L	77	B.Saraf (HCU)	33	Sputum ETT	Hidrosefalus + bronkopneumonia	Membaik	Resisten	Negatif	Negatif	Negatif
12	862412	330/11	DK-12	L	23	IC	13	Pus	HIV + infeksi multipel	Membaik	Resisten	Negatif	Negatif	Negatif
13	851734	140/09	DK-13	P	63	Palem Bawah	49	Darah	Adenokarsinoma rekti	Membaik	Resisten	Negatif	Negatif	Negatif
14	853636	177/09	DK-14	P	51	L2Ortho	14	Pus	Trauma kapitis	Meninggal	Resisten	Negatif	Negatif	Negatif
15	848690	878/08	DK-15	L	47	Poli Bedah Plastik	44	Pus	Luka bakar derajat 3 + sepsis	Membaik	Resisten	Negatif	Negatif	Negatif
16	853321	20/09	DK-16	L	47	L1BD	11	Darah	ISK komplikata	Meninggal	Resisten	Negatif	Negatif	Negatif
17	853608	49/09	DK-17	P	44	L3AB	13	Pus	Ulkus diabetik regio gastroknemius	Membaik	Resisten	Negatif	Negatif	Negatif
18	862396	437/11	DK-18	P	49	L2Ortho	11	Jaringan	Ulkus kaki diabetik	Membaik	Resisten	Negatif	Negatif	Negatif
		380/11	DK-19	L	48	Palem Atas	32	Sputum	Infected bronkiektasis	Membaik	Resisten	Negatif	Negatif	Negatif
		505A/10	DK-20	L	24	L2Ortho	6	Pus	Osteomielitis kronik	Membaik	Resisten	Negatif	Negatif	Negatif



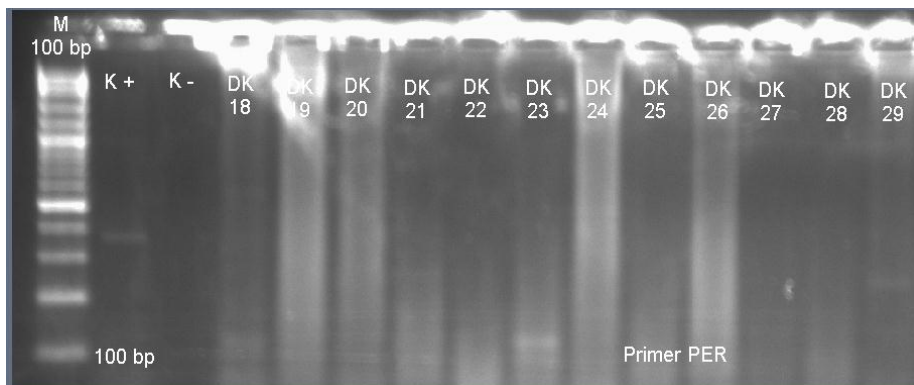
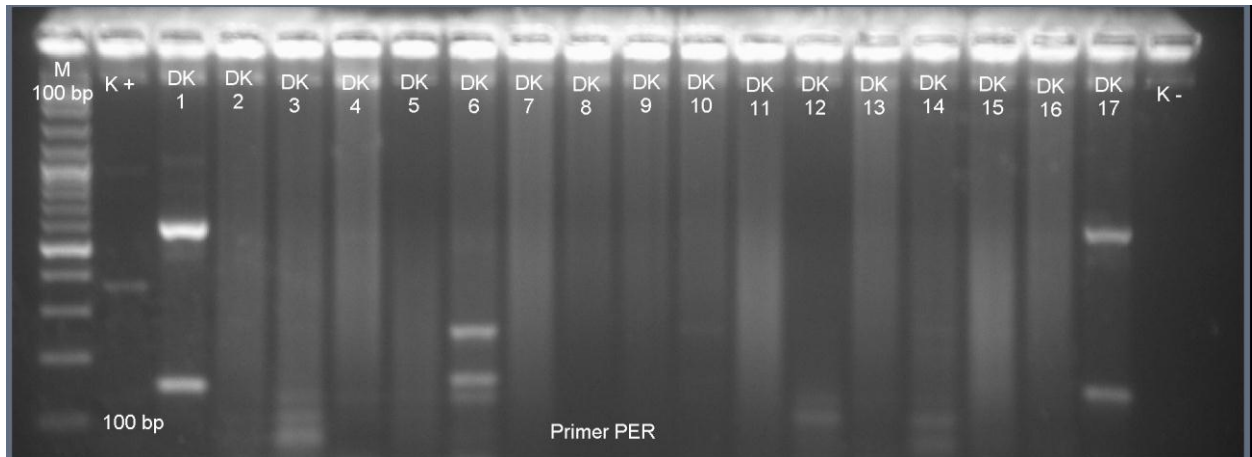
21	596845	465/10	DK-21	P	59	L1BB	28	Pus	Ulkus kaki diabetik	Membaik	Resisten	Negatif	Negatif	Negatif
22	858269	716/10	DK-22	P	10	PJT	35	Pus	Fraktur terbuka tibia dan fibula	Membaik	Resisten	Negatif	Negatif	Negatif
23	855948	39A/11	DK-23	L	20	L2Ortho	56	Pus	Fraktur pubis	Membaik	Resisten	Negatif	Negatif	Negatif
24	861757	150/11	DK-24	L	39	B.Saraf (HCU)	41	Pus	Luka bakar	Membaik	Resisten	Negatif	Negatif	Negatif
25	861559	136/11	DK-25	P	13	L2Ortho	2	Pus	Osteomielitis	Membaik	Resisten	Negatif	Negatif	Negatif
26	857741	658/11	DK-26	L	17	L2Ortho	18	Pus	Disrupsi luka operasi + infeksi	Membaik	Resisten	Negatif	Negatif	Negatif
27	855549	571/10	DK-27	L	44	Luka Bakar (IRNA)	72	Pus	Luka bakar 30-39%	Membaik	Resisten	Negatif	Negatif	Negatif
28	861017	34/11	DK-28	P	36	Palem Bawah	6	Urine 10 ⁶	Infeksi traktus urinarius	Membaik	Resisten	Negatif	Negatif	Negatif
29	849077	21/11	DK-29	P	36	Poli Paru	19	Sputum	GERD with esofagitis + kolelithiasis akut	Membaik	Resisten	Negatif	Negatif	Negatif



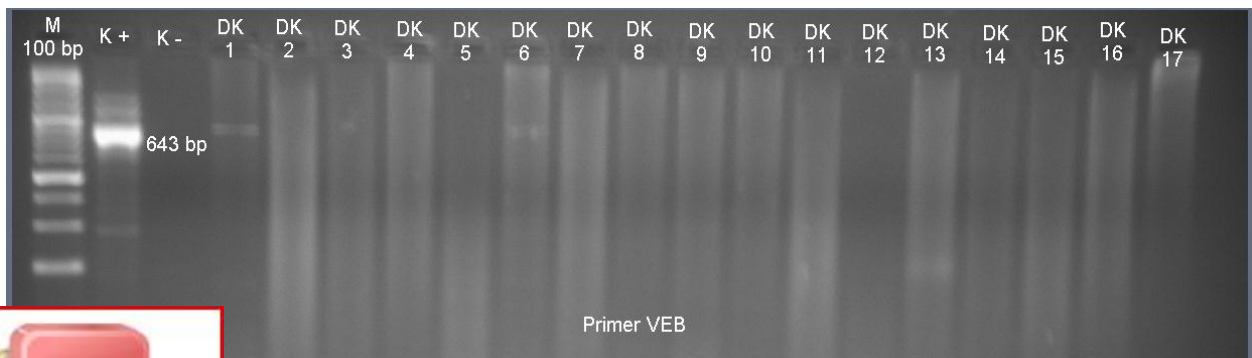
Lampiran 4

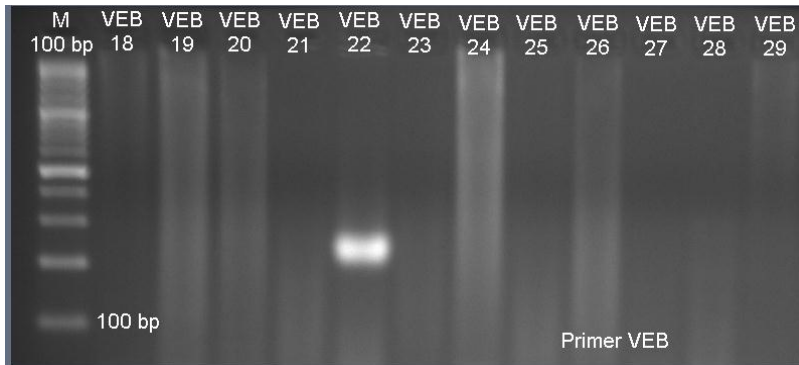
Hasil PCR

Primer PER 340 bp

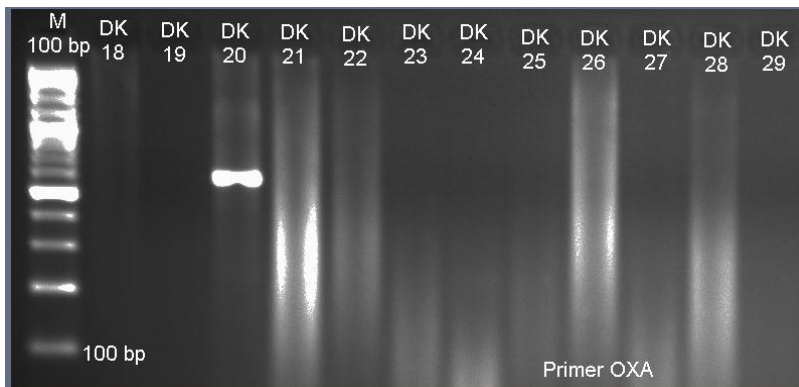
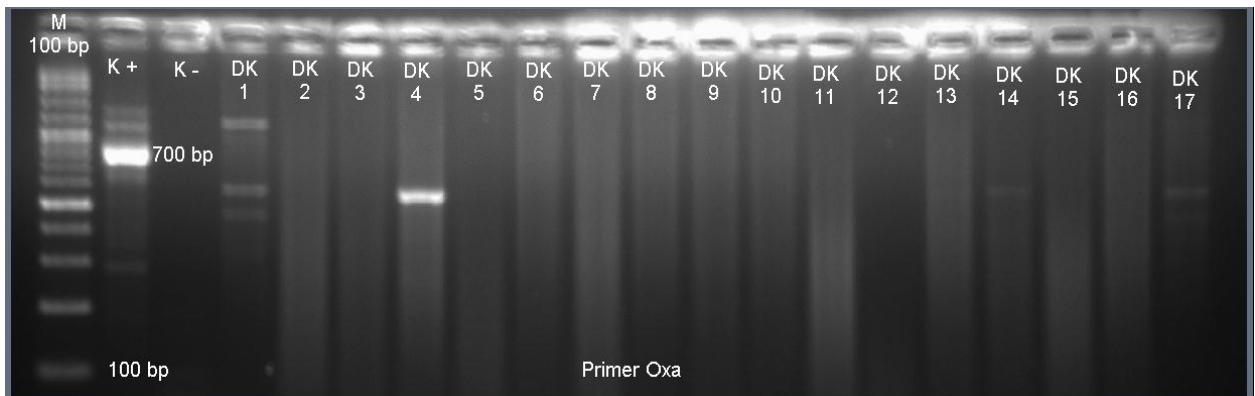


Primer VEB 643 bp





Primer Oxa-2 700 bp



Lampiran 5

LAMPIRAN BLAST PRIMER

PER F : GCAACTGCTGCAATACTCGG

- Your search parameters were adjusted to search for a short input sequence.

Your search is limited to records that include: Pseudomonas aeruginosa (taxid:287) [Full Entrez Query](#)

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#) [How to read this page](#) [Blast report description](#) [Questions/comments](#)

Job title: Nucleotide Sequence (20 letters)

RID

[11G2P30D014](#) (Expires on 12-13 15:01 pm)

BLASTN 2.8.1+ [Citation](#)

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Sequences producing significant alignments:

Select for downloading or viewing reports	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Select seq NG_049960.1	Pseudomonas aeruginosa RNL-1 blaPER gene for class A extended-spectrum beta-lactamase PER-1, complete CDS	40.1	40.1	100%	0.004	100%	NG_049960.1
<input type="checkbox"/> Select seq KU133340.1	Pseudomonas aeruginosa strain RJ248 class 1 integron ISCR1 PER-1, partial sequence	40.1	40.1	100%	0.004	100%	KU133340.1
<input type="checkbox"/> Select seq KU133339.1	Pseudomonas aeruginosa strain RJ246 class 1 integron ISCR1 PER-1, partial sequence	40.1	40.1	100%	0.004	100%	KU133339.1
<input type="checkbox"/> Select seq KU133338.1	Pseudomonas aeruginosa strain RJ242 class 1 integron ISCR1 PER-4, partial sequence	40.1	40.1	100%	0.004	100%	KU133338.1



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PER R : ATGTGCGACCACAGTACCAG

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Job title: Nucleotide Sequence (20 letters)

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Distribution of the top 259 Blast Hits on 100 subject sequences

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Descriptions



Showing significant alignments:

Selected:0

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Sequences producing significant alignments:

Select for downloading or viewing reports	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Select seq MG188750.1	Pseudomonas aeruginosa extended spectrum beta-lactamase PER (blaPER) gene, partial cds	40.1	40.1	100%	0.004	100%	MG188750.1
<input type="checkbox"/> Select seq MF344570.1	Pseudomonas aeruginosa plasmid pA681-IMP, complete sequence	40.1	40.1	100%	0.004	100%	MF344570.1
<input type="checkbox"/> Select seq MF344569.1	Pseudomonas aeruginosa plasmid p12939-OXA, complete sequence	40.1	40.1	100%	0.004	100%	MF344569.1
<input type="checkbox"/> Select seq NG_049960.1	Pseudomonas aeruginosa RNL-1 blaPER gene for class A extended-spectrum beta-lactamase PER-1, complete CDS	40.1	40.1	100%	0.004	100%	NG_049960.1
<input type="checkbox"/> Select seq KU133340.1	Pseudomonas aeruginosa strain RJ248 class 1 integron ISCR1 PER-1, partial sequence	40.1	40.1	100%	0.004	100%	KU133340.1



g 340 bp region from base 6960 to 7299.

Pseudomonas aeruginosa strain RJ248 class 1 integron ISCR1 PER-1, partial sequence

GenBank: KU133340.1

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LOCUS KU133340 340 bp DNA linear BCT 28-MAR-2016
 DEFINITION Pseudomonas aeruginosa strain RJ248 class 1 integron ISCR1 PER-1, partial sequence.
 ACCESSION [KU133340](#) REGION: 6960..7299
 VERSION KU133340.1
 KEYWORDS .
 SOURCE Pseudomonas aeruginosa
 ORGANISM [Pseudomonas aeruginosa](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 340)
 AUTHORS Xie,L., Wu,J., Zhang,F., Han,L., Guo,X., Ni,Y. and Sun,J.
 TITLE Molecular Epidemiology and Genetic Characteristics of Various blaPER Genes in Shanghai, China
 JOURNAL Antimicrob. Agents Chemother. 60 (6), 3849-3853 (2016)
 PUBMED [27067315](#)
 REMARK Publication Status: Online-Only
 2 (bases 1 to 340)
 Xie,L. and Sun,J.
 Direct Submission
 Submitted (10-NOV-2015) Department of Clinical Microbiology, Ruijin Hospital, Shanghai Jiaotong University School of Medicine, 197



Optimization Software:
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```

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              ##Assembly-Data-START##
              Sequencing Technology :: Sanger dideoxy sequencing
              ##Assembly-Data-END##

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                  PER-1"
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                  VLQNTWAPIMKAYQGDEFVSPVQQLLQYSVSHSDNVACDLLFELVGGPAALHDYIQSM
                  GIKETAVVANEAQMHADDQVQYNWTSMKGAEEILKKFEQKTQLSETSQALLWKWME
                  TTTGPERLKGLLPAGTVVAHKTGTSGIKAGKTAATNDLGIILLPDGRPLLVAVFVKDS
                  AESSRTNEAIIAQVAQTAYQFELKKLSALSPN"

ORIGIN

```

PER F: gcaactgctg caatactcgg



```

aactgctg caatactcgg tctcgcacag cgataacgtg gcctgtgatt tgttatttga
tggttggt ggaccagctg ctttgcata ctatatccag tctatgggta taaaggagac
ctgtggtc gcaaatgaag cgcagatgca cgccgatgat caggtgcagt atcaaaactg
cctogatg aaaggtgctg cagagatcct gaaaaagttt gagcaaaaaa cacagctgtc
aaacctcg caggctttgt tatggaagtg gatgggtcgaa accaccacag gaccagagcg

```

```

PER R : atgtgcgacc acagtaccag
        Tacacgctgg tgtcatggtc
        Ctggctactgt ggtcgcacat
301 gttaaaaggt ttgttaccag ctggctactgt ggtcgcacat

```

//

VEBF:cgacttccatttcccgatgc

- Your search parameters were adjusted to search for a short input sequence.

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Job title: Nucleotide Sequence (20 letters)

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alignment scores

Descriptions

Sequences producing significant alignments:

Select:[AllNone](#) Selected:0

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Sequences producing significant alignments:

Select for downloading or viewing reports	Description	<u>Max</u> <u>score</u>	<u>Total</u> <u>score</u>	<u>Query</u> <u>cover</u>	<u>E</u> <u>value</u>	<u>Ident</u>	Accession
<input type="checkbox"/> Select seq CP033439.1	Pseudomonas aeruginosa strain SP4528 chromosome, complete genome	40.1	139	100%	0.004	100%	CP033439.1
<input type="checkbox"/> Select seq CP033432.1	Pseudomonas aeruginosa strain BA15561 chromosome, complete genome	40.1	139	100%	0.004	100%	CP033432.1
<input type="checkbox"/> Select seq MG717453.1	Pseudomonas aeruginosa strain 163869 class A extended-spectrum beta-lactamase VEB-20 (blaVEB) gene, blaVEB-20 allele, complete cds	40.1	40.1	100%	0.004	100%	MG717453.1
	Pseudomonas aeruginosa strain AR_0443 chromosome	40.1	139	100%	0.004	100%	CP029147.1



VEB R: ggactctgcaacaaatcgc

- Your search parameters were adjusted to search for a short input sequence.

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Job title: Nucleotide Sequence (20 letters)

Description

Nucleotide collection (nt)

Program

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Sequences producing significant alignments:

Select for downloading
or viewing reports

Select seq
CP033439.1

Description

Max Total Query E
score score cover value Ident Accession

Pseudomonas aeruginosa strain SP4528 chromosome, complete genome	40.1	114	100%	0.004	100%	CP033439.1
Pseudomonas aeruginosa strain BA15561 chromosome, complete genome	40.1	114	100%	0.004	100%	CP033432.1
Pseudomonas aeruginosa strain 163869 class A extended-spectrum beta-lactamase VEB-20 (blaVEB) gene, blaVEB-20 allele, complete	40.1	40.1	100%	0.004	100%	MG717453.1



Sequences producing significant alignments:

Select for downloading or viewing reports	Description	Max score	Total score	Query cover	E value	Ident	Accession
MG717453.1	cds						
<input type="checkbox"/> Select seq CP029147.1	Pseudomonas aeruginosa strain AR_0443 chromosome	40.1	114	100%	0.004	100%	CP029147.1

- Showing 643 bp region from base 180 to 822.

Pseudomonas aeruginosa strain 163869 class A extended-spectrum beta-lactamase VEB-20 (blaVEB) gene, blaVEB-20 allele, complete cds

GenBank: MG717453.1

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MG717453 643 bp DNA linear BCT 05-AUG-2018
Pseudomonas aeruginosa strain 163869 class A extended-spectrum
beta-lactamase VEB-20 (blaVEB) gene, blaVEB-20 allele, complete
cds.
[MG717453](#) REGION: 180..822

VERSION MG717453.1
 KEYWORDS .
 SOURCE Pseudomonas aeruginosa
 ORGANISM [Pseudomonas aeruginosa](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 643)
 AUTHORS Bour,M. and Plesiat,P.
 TITLE Novel class A extended-spectrum beta-lactamase
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 643)
 AUTHORS Bour,M. and Plesiat,P.
 TITLE Direct Submission
 JOURNAL Submitted (20-DEC-2017) French National Reference Center for
 Antibiotic Resistance, University Hospital of Besancon, 3 boulevard
 Alexandre Fleming, Besancon 25000, France
 COMMENT ##Assembly-Data-START##
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ISIKANEEQMHKDWNTQYQNWATPTAMNKLLIDTYNNKNQLLSKKSDFIWKIMRETT
TGSNRLKGQLPKNTIVAHRGTSGINNGIAAATNDVGVITLPNGQLIFISVFVAESKE
TSEINEKIISDIAKITWNYLKNK"

```

ORIGIN

```

VEB F : cgacttccat ttcccgatgc
1 cgacttccat ttcccgatgc aaagcgttat gaaatttccg attgctttag ccgttttgct
61 tgagatagat aaaggggaatc tttcttttga acaaaaaata gagattacc ccaagacct
121 tttgcctaaa acgtggagtc cgattaaaga ggaattccct aatggaacaa ctttgacgat
181 tgaacaaata ctaaattata cagtatcaga gagcgacaat attgggttg atattttgct
241 aaaattaatc ggaggaactg attctgttca aaaattcttg aatgctaata atttcactga
301 ttttcaatc aaagcaaacg aagaacaaat gcacaaggat tggaaatacc aatatcaaaa
361 ttgggcaacc ccaacagcga tgaacaaact gttaatagat acttataata ataagaacca
421 attactttct aaaaaagtt atgattttat ttggaaaatt atgagagaaa caacaacagg
481 aagtaaccga ttaaaaggac aattacaaa gaatacaatt gttgctcata gaacagggac
541 ttccggaata aataatggaa ttgcagcagc cactaatgat gttggggtaa ttactttacc

```

```

VEB R : ggactct gcaacaaata cgc
Cctgaga cgttgttat gcg
Gcgtatt tgttcagag tcc
atggacaa ttaattttta taagcgtatt tgttcagag tcc

```



OXA 2 F : gccaaaggcacgatagttgt

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Job title: Nucleotide Sequence (20 letters)

Description

Nucleotide collection (nt)

Program

BLASTN 2.8.1+ [Citation](#)

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Alignment scores

Descriptions

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Sequences producing significant alignments:

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Select seq NG_062301.1	Pseudomonas aeruginosa PA145 blaOXA gene for OXA-2 family class D beta-lactamase OXA-681, complete CDS	40.1	40.1	100%	0.004	100%	NG_062301.1
<input type="checkbox"/> Select seq NG_062269.1	Pseudomonas aeruginosa 153304 blaOXA gene for OXA-2 family class D beta-lactamase OXA-737, complete CDS	40.1	40.1	100%	0.004	100%	NG_062269.1
<input type="checkbox"/> Select seq MH986647.1	Pseudomonas aeruginosa strain PA145 OXA-2 family class D beta-lactamase OXA-681 (blaOXA) gene, blaOXA-681 allele, complete cds	40.1	40.1	100%	0.004	100%	MH986647.1
	Pseudomonas aeruginosa strain 24Pae112 chromosome, complete genome	40.1	112	100%	0.004	100%	CP029605.1



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Sequences producing significant alignments:

Select for downloading or viewing reports	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Select seq MH780095.1	Pseudomonas aeruginosa strain 153304 OXA-2 family class D beta-lactamase OXA-737 (blaOXA) gene, blaOXA-737 allele, complete cds	40.1	40.1	100%	0.004	100%	MH780095.1
<input type="checkbox"/> Select seq NG_061615.1	Pseudomonas aeruginosa Pa314 blaOXA gene for class D beta-lactamase OXA-732, complete CDS	40.1	40.1	100%	0.004	100%	NG_061615.1
<input type="checkbox"/> Select seq MH704577.1	Pseudomonas aeruginosa strain 164130 class D beta-lactamase OXA-669 (blaOXA) gene, blaOXA-669 allele, complete cds	40.1	40.1	100%	0.004	100%	MH704577.1
<input type="checkbox"/> Select seq CP027172.1	Pseudomonas aeruginosa strain AR_0353 chromosome, complete genome	40.1	112	100%	0.004	100%	CP027172.1
<input type="checkbox"/> Select seq KY646160.1	Pseudomonas aeruginosa strain PE52 In1215 class 1 integron, partial sequence	40.1	40.1	100%	0.004	100%	KY646160.1

gagttgactgccgg

Search parameters were adjusted to search for a short input sequence.



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Job title: Nucleotide Sequence (20 letters)

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Descriptions

Sequences producing significant alignments:

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Sequences producing significant alignments:

Select for downloading or reports	Description	<u>Max score</u>	<u>Total score</u>	<u>Query cover</u>	<u>E value</u>	<u>Ident</u>	Accession
 Optimization Software: www.balesio.com	Pseudomonas aeruginosa strain FDAARGOS_571 chromosome, complete genome	40.1	139	100%	0.004	100%	CP033833.1

Sequences producing significant alignments:

Select for downloading or
viewing reports

	Description	<u>Max</u> <u>score</u>	<u>Total</u> <u>score</u>	<u>Query</u> <u>cover</u>	<u>E</u> <u>value</u>	<u>Ident</u> <u>value</u>	Accession
CP033833.1							
<input type="checkbox"/> Select seq CP021775.1	Pseudomonas aeruginosa strain Pa58, complete genome	40.1	155	100%	0.004	100%	CP021775.1
<input type="checkbox"/> Select seq CP020603.1	Pseudomonas aeruginosa strain E6130952, complete genome	40.1	139	100%	0.004	100%	CP020603.1
<input type="checkbox"/> Select seq NG_062301.1	Pseudomonas aeruginosa PA145 blaOXA gene for OXA-2 family class D beta-lactamase OXA-681, complete CDS	40.1	40.1	100%	0.004	100%	NG_062301.1
<input type="checkbox"/> Select seq NG_062269.1	Pseudomonas aeruginosa 153304 blaOXA gene for OXA-2 family class D beta-lactamase OXA-737, complete CDS	40.1	40.1	100%	0.004	100%	NG_062269.1
<input type="checkbox"/> Select seq MH986647.1	Pseudomonas aeruginosa strain PA145 OXA-2 family class D beta-lactamase OXA-681 (blaOXA) gene, blaOXA-681 allele, complete cds	40.1	40.1	100%	0.004	100%	MH986647.1
	Pseudomonas aeruginosa strain 24Pae112 chromosome, complete genome	40.1	165	100%	0.004	100%	CP029605.1



- Showing 698 bp region from base 118 to 815.

Pseudomonas aeruginosa strain PA145 OXA-2 family class D beta-lactamase OXA-681 (blaOXA) gene, blaOXA-681 allele, complete cds

GenBank: MH986647.1

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LOCUS MH986647 698 bp DNA linear BCT 10-OCT-2018
DEFINITION Pseudomonas aeruginosa strain PA145 OXA-2 family class D
beta-lactamase OXA-681 (blaOXA) gene, blaOXA-681 allele, complete
cds.
ACCESSION [MH986647](#) REGION: 118..815
VERSION MH986647.1
KEYWORDS .
SOURCE Pseudomonas aeruginosa
ORGANISM [Pseudomonas aeruginosa](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 698)
Arca-Suarez, J., Fraile-Ribot, P.A., Rodriguez-Iglesias, M., Oliver, A.
and Galan-Sanchez, F.
Direct Submission
Submitted (25-SEP-2018) Clinical Microbiology Department, Hospital
Universitario Puerta del Mar, Avenida Ana de Viya 21, Cadiz, Cadiz



Optimization Software:
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11009, Spain
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GSLAISAEQIAFLRKLRYRNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGW
WVGWVEWPTGSVFFALNIDTPNRMDDLKREAIVRILRSIEALPPNPAVNSDAAR"

```

ORIGIN

OXA 2 F : gccaaaggca cgatagttgt

```

1 gccaaaggca cgatagttgt ggcagacgaa cgccaagcgg atcgtgccat gttggttttt
tctctgtgc gatcgaagaa acgctactcg cctgcatcga cattcaagat acctcataca
ttttgcac ttgatgcagg cgctgttcgt gatgagttcc agatTTTTcg atgggacggc
taacaggg gctttgcagg ccacaatcaa gaccaagatt tgcgatcagc aatgcggaat
tactgttt ggggtgatga gctatttgca aaggaaattg gtgatgaaa agctcggcgc
tttgaaga aaatcgacta tggcaacgcc gatccttcga caagtaatgg cgattactgg

```



```

361 aaaggcagcc ttgcaatctc ggcgcaggag caaattgcat ttctcaggaa gctctatcgt
421 aacgagctgc ctttcgggt agaacatcag cgcttggta aggatctcat gattgtggaa
481 gccggtcgca actggatact gcgtgcaaag acgggctggg aaggccgtat gggttgggtg
541 gtaggatggg ttgagtggcc gactggctcc gtattcttcg cactgaatat tgatacgcca
601 aacagaatgg atgatctttt caagaggag gcaatcgtgc gggcaatcct tcgctctatt

```

OXA 2 R : gc gtcgagttg actgcgg

Cg caggctcaac tgacggcc

Cc ggcagtcaac tcggacgc

```

661 gaagcgttac cgccaacc ggcagtcaac tcggacgc

```

//



Lampiran 6

RIWAYAT HIDUP PENULIS

I. Data Pribadi

- | | |
|-----------------------------|--|
| 1. Nama | : dr. Dewi Kartika Tungadi |
| 2. Tempat dan tanggal lahir | : Ujung Pandang, 15 Mei 1987 |
| 3. Alamat | : Jl. Pandang Raya Kompleks Bukit
Villa Mas Blok D/1, Panakukkang Mas |
| 4. Agama | : Katolik |
| 5. Status | : Kawin |
| 6. Nomor Telepon | : 081242782953 |
| 7. Alamat email | : dewitungadi@gmail.com |

II. Riwayat Pendidikan

1. SD YPPK Gembala Baik, Abepura Tahun 1998.
2. SLTP YPPK Santo Paulus, Abepura Tahun 2001.
3. SMU Katolik Rajawali, Makassar Tahun 2004.
4. Fakultas Kedokteran Universitas Hasanuddin, Makassar Tahun 2011.
5. Program Pendidikan Dokter Spesialis Program Studi Patologi Klinik
Fakultas Kedokteran Universitas Hasanuddin Makassar (Mulai Juli 2014).

III. Riwayat Pekerjaan

1. Dokter Internsip: Puskesmas Bantimurung dan RSUD Maros, Makassar,
tahun 2011 – 2012.
2. Dokter Umum : RS Bhayangkara, Makassar, tahun 2012 – 2014.

