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LAMPIRAN

Lampiran 1. Cara menentukan hewan sehat atau sakit secara umum

No.		Hewan sehat:	Hewan sakit:
1	Penglihatan	Tajam	Tidak tajam
2	Makan	Mengunyah	Tidak mengunyah
3	Mata	Mata cerah dan selaput mata merah muda	Mata kusam
4	Urin	Urin normal	Urin berubah warna
5	Feses	Feses normal	Feses abnormal
6	Suhu	Temperatur normal	Temperatur tinggi
7	Cara berjalan	Tidak pincang	Pincang
8	Pernapasan	Respirasi normal	Sesak nafas/batuk
9	Kelompok	Tetap dalam kawanannya	Memisahkan diri dari kawanannya
10	Kebiasaan makan	Makan dan minum seperti biasa	Kehilangan selera makan
11	Nadi	Denyut nadi normal	Denyut nadi tidak normal

Lampiran 2. Hasil Blast sampel *Plasmodium falciparum* dari Desa Gaura

Job Title Nucleotide Sequence

RID [GHJGCAFR01R](#) Search expires on 08-04 12:46 pm [Download All](#) ▾

Program BLASTN [Citation](#) ▾

Database nt [See details](#) ▾

Query ID Icl|Query_376201

Description None

Molecule type dna

Query Length 179

Other reports [Distance tree of results](#) [MSA viewer](#) [?](#)

Filter Results

Organism only top 20 will appear exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity to **E value** to **Query Coverage** to

[Filter](#) [Reset](#)

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments Download ▾ New Select columns ▾ Show 100 ▾ [?](#)

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Lampiran 3: Hasil blast urutan DNA hasil sequencing; *Plasmodium vivax*.

Job Title Nucleotide Sequence

RID [AWGKZ74Z013](#) Search expires on 05-27 20:43 pm [Download All](#) ▾

Program BLASTN [Citation](#) ▾

Database nt [See details](#) ▾

Query ID Icl|Query_20255

Description None

Molecule type dna

Query Length 101

Other reports [Distance tree of results](#) [MSA viewer](#) [?](#)

Filter Results

Organism only top 20 will appear exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity to **E value** to **Query Coverage** to

[Filter](#) [Reset](#)

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments Download ▾ New Select columns ▾ Show 100 ▾ [?](#)

select all 100 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#) New [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Plasmodium vivax isolate YV35 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	126	KT991325.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate YV1 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	126	KT991314.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate W23 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	127	KT991312.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate W15 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	123	KT991309.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate PVX39 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	183	KT991294.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate PVX29 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	128	KT991292.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate PVX14 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	124	KT991282.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate PVX12 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	128	KT991281.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate PVL22 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	132	KT991270.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate PVL17 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	127	KT991266.1
<input checked="" type="checkbox"/>	Plasmodium vivax isolate PVL8 18S ribosomal RNA gene, partial sequence	Plasmodium vivax	145	145	80%	6e-31	98.77%	122	KT991261.1

Lampiran 4: Hasil BLAST sampel filaria dengan primer FI1 dan FI2

Job Title **Nucleotide Sequence**

RID [AWH6EZ5F01R](#) Search expires on 05-27 20:53 pm [Download All](#) ▼

Program **BLASTN** [Citation](#) ▼

Database **nt** [See details](#) ▼

Query ID **lcl|Query_174789**

Description **None**

Molecule type **dna**

Query Length **664**

Other reports [Distance tree of results](#) [MSA viewer](#) ?

Filter Results

Organism *only top 20 will appear* exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity to E value to Query Coverage to

[Filter](#) [Reset](#)

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download ▼ [New](#) Select columns ▼ Show 100 ▼ ?

select all 100 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#) [New](#) [MSA Viewer](#)

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Amoebophrya sp. ex Akashiwo sanguineaum clone KJ47-0-2-13 18S ribosomal RNA gene, partial sequence; inter...	<i>Amoebophrya sp.</i>	73.1	73.1	5%	3e-08	100.00%	1472	KT389975.1
<input checked="" type="checkbox"/> uncultured soil eukaryote genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rR...	uncultured soil e...	73.1	73.1	8%	3e-08	89.47%	1260	HG996134.1
<input checked="" type="checkbox"/> uncultured soil eukaryote clone NS25T_66 18S ribosomal RNA gene, partial sequence; internal transcribed spacer.1...	uncultured eukar...	71.3	71.3	6%	1e-07	97.62%	638	KJ182180.1
<input checked="" type="checkbox"/> uncultured fungus genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gen...	uncultured fungus...	71.3	71.3	9%	1e-07	87.30%	1308	LR993810.1
<input checked="" type="checkbox"/> uncultured fungus genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gen...	uncultured fungus...	71.3	71.3	7%	1e-07	93.62%	1278	LR993738.1
<input checked="" type="checkbox"/> uncultured soil eukaryote genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rR...	uncultured soil e...	71.3	71.3	7%	1e-07	93.62%	1276	HG996207.1
<input checked="" type="checkbox"/> uncultured soil eukaryote genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rR...	uncultured soil e...	71.3	71.3	7%	1e-07	93.62%	786	HG996106.1
<input checked="" type="checkbox"/> uncultured soil eukaryote genomic DNA sequence contains 5.8S rRNA gene, ITS2, 28S rRNA gene, clone 59919ecb	uncultured soil e...	71.3	71.3	7%	1e-07	93.62%	692	HG995772.1
<input checked="" type="checkbox"/> uncultured soil eukaryote genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rR...	uncultured soil e...	71.3	71.3	7%	1e-07	92.00%	1276	HG995671.1
<input checked="" type="checkbox"/> Uncultured eukaryote clone N424T_66 18S ribosomal RNA gene, partial sequence; internal transcribed spacer.1...	uncultured eukar...	71.3	71.3	6%	1e-07	97.62%	655	GU942164.1
<input checked="" type="checkbox"/> uncultured fungus genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gen...	uncultured fungus...	69.4	69.4	8%	4e-07	89.29%	1301	LR993336.1

Lampiran 5: Hasil BLAST sampel filaria dengan primer Hhal

Job Title **Nucleotide Sequence**

RID [AWHD352C01R](#) Search expires on 05-27 20:57 pm [Download All](#) ▼

Program **BLASTN** [Citation](#) ▼

Database **nt** [See details](#) ▼

Query ID **lcl|Query_202095**

Description **None**

Molecule type **dna**

Query Length **560**

Other reports [Distance tree of results](#) [MSA viewer](#) ?

Filter Results

Organism *only top 20 will appear* exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity to E value to Query Coverage to

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Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download ▼ [New](#) Select columns ▼ Show 100 ▼ ?

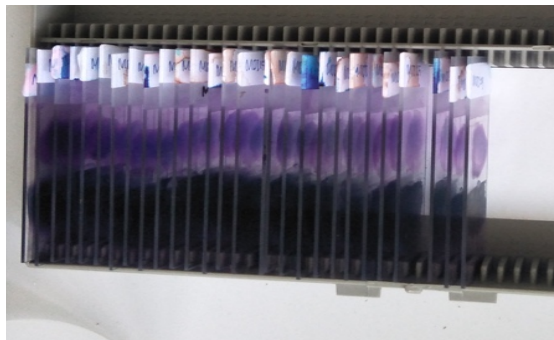
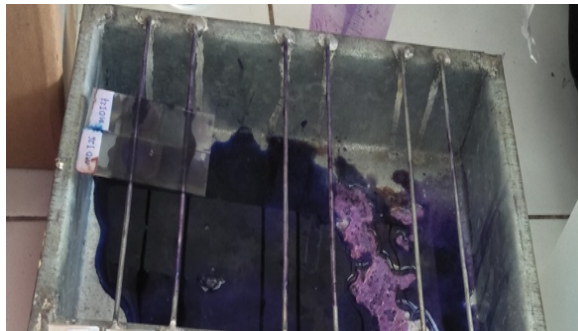
select all 100 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#) [New](#) [MSA Viewer](#)

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Bos taurus Y Chr BAC CH240-462K8 (Children's Hospital Oakland Research Institute Bovine BAC Library (ma...	<i>Bos taurus</i>	220	428	30%	8e-53	90.12%	174759	AC226428.3
<input checked="" type="checkbox"/> Bos taurus Y Chr BAC CH240-297N16 (Children's Hospital Oakland Research Institute Bovine BAC Library (m...	<i>Bos taurus</i>	220	434	30%	8e-53	90.12%	154026	AC225910.2
<input checked="" type="checkbox"/> Bos taurus Y Chr BAC CH240-360L6 (Children's Hospital Oakland Research Institute Bovine BAC Library (mal...	<i>Bos taurus</i>	220	428	30%	8e-53	90.12%	151575	AC225788.2
<input checked="" type="checkbox"/> Bos taurus Y Chr BAC CH240-1113 (Children's Hospital Oakland Research Institute Bovine BAC Library (male)...	<i>Bos taurus</i>	220	428	30%	8e-53	90.12%	181768	AC213444.4
<input checked="" type="checkbox"/> Babesia ovata Retrovirus-related Pol poly LINE-1, putative (BOVATA_050210), partial mRNA	<i>Babesia ovata</i>	219	219	30%	3e-52	89.66%	3366	XM_029013938.1
<input checked="" type="checkbox"/> Bos mutus isolate yakQH1 chromosome 29	<i>Bos mutus</i>	219	7377	30%	3e-52	89.66%	49314950	CP027097.1
<input checked="" type="checkbox"/> Bos mutus isolate yakQH1 chromosome 28	<i>Bos mutus</i>	219	6617	31%	3e-52	89.66%	41841768	CP027096.1
<input checked="" type="checkbox"/> Bos mutus isolate yakQH1 chromosome 27	<i>Bos mutus</i>	219	4553	30%	3e-52	89.66%	43292763	CP027095.1
<input checked="" type="checkbox"/> Bos mutus isolate yakQH1 chromosome 26	<i>Bos mutus</i>	219	3315	30%	3e-52	89.66%	16099052	CP027094.1
<input checked="" type="checkbox"/> Bos mutus isolate yakQH1 chromosome 25	<i>Bos mutus</i>	219	2216	30%	3e-52	89.66%	42522029	CP027093.1
<input checked="" type="checkbox"/> Bos mutus isolate yakQH1 chromosome 24	<i>Bos mutus</i>	219	8045	30%	3e-52	89.66%	61837517	CP027092.1

Lampiran 6: Foto pengambilan sampel darah hewan



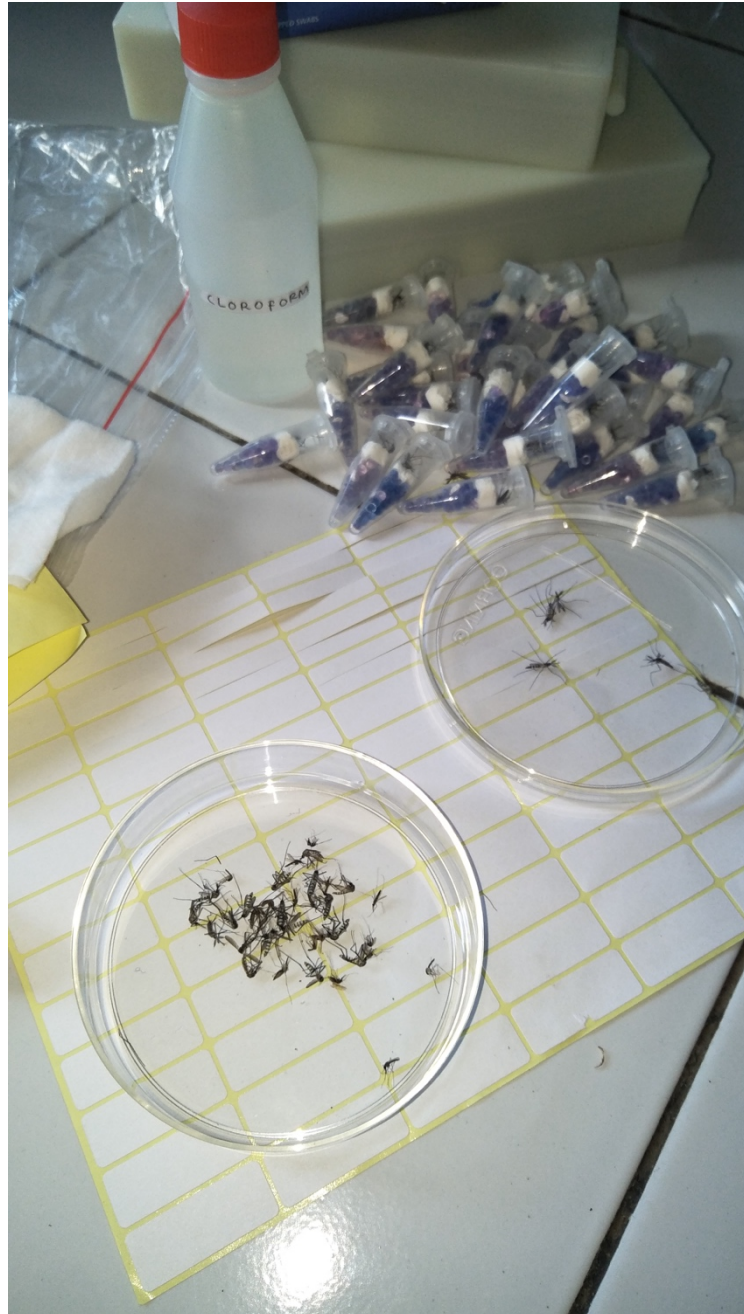
Lampiran 7: Foto pewarnaan giemsa slide darah hewan.



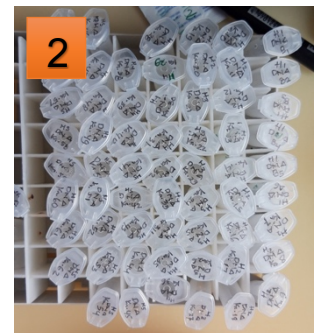
Lampiran 8: Pemeriksaan mikroskopis



Lampiran 9: Penyimpanan nyamuk pada tube yang berisi silica gel



Lampiran 10: Pemeriksaan molekuler



Catatan: 1) Proses Ekstraksi, 2) DNA hasil ekstraksi, 3) Proses Mix PCR, 4) Running PCR, 5) Proses elektroforesis.

Lampiran 11: Hasil PCR primer rPF1, rPF2 (918 bp) dan primer rPV1, rPV2 (714 bp).

