DAFTAR PUSTAKA

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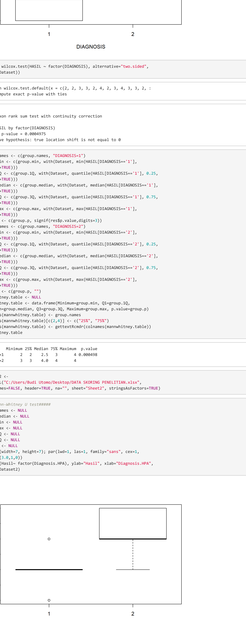
Replace with Main Title

Your Name

2019-11-29 10:31:56

```
> Dataset <-
>   readxl("C:/Users/Rudi Ishmo/Desktop/DATA SCRIPTING PENELITIAN.xlsx",
>   range=cellranger::cell_limits(c(1,1),c(NA,NA)), sheet="Sheet1", stringsAsFactors=TRUE)
```

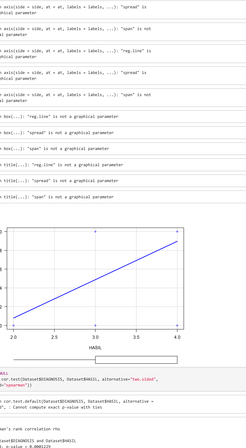
```
> ##########Non-Whitney U test##########
> group.names <- NULL
> group.median <- NULL
> group.min <- NULL
> group.max <- NULL
> group.Q1 <- NULL
> group.Q3 <- NULL
> group.p <- NULL
> window(width=7, height=7); par(lwd=2, las=1, family="sans", cex=1,
>   mgp=c(3.0,1,0))
> boxplot(HA011~ factor(DIAGNOSIS2), ylab="HA011", xlab="DIAGNOSIS",
>   data=Dataset)
```




```
> (res <- wilcox.test(HA011 ~ factor(DIAGNOSIS2), alternative="two.sided",
>   data=Dataset))

Warning in wilcox.test.default(x = c(2, 2, 3, 3, 2, 4, 2, 3, 4, 3, 3, 2, :
cannot compute exact p-value with ties

	Wilcoxon rank sum test with continuity correction

data:  HA011 by factor(DIAGNOSIS2)
W = 63.5, p-value = 0.0004075
alternative hypothesis: true location shift is not equal to 0

> group.names <- c(group.names, "DIAGNOSIS2=1")
> group.median <- c(group.median, with(Dataset, median(HA011[DIAGNOSIS2==1],
>   na.rm=TRUE)))
> group.Q1 <- c(group.Q1, with(Dataset, quantile(HA011[DIAGNOSIS2==1], 0.25,
>   na.rm=TRUE)))
> group.median <- c(group.median, with(Dataset, median(HA011[DIAGNOSIS2==1],
>   na.rm=TRUE)))
> group.Q3 <- c(group.Q3, with(Dataset, quantile(HA011[DIAGNOSIS2==1], 0.75,
>   na.rm=TRUE)))
> group.min <- c(group.min, with(Dataset, min(HA011[DIAGNOSIS2==1],
>   na.rm=TRUE)))
> group.p <- c(group.p, signif(res$p.value,digits=3))
> group.names <- c(group.names, "DIAGNOSIS2=2")
> group.min <- c(group.min, with(Dataset, min(HA011[DIAGNOSIS2==2],
>   na.rm=TRUE)))
> group.Q1 <- c(group.Q1, with(Dataset, quantile(HA011[DIAGNOSIS2==2], 0.25,
>   na.rm=TRUE)))
> group.median <- c(group.median, with(Dataset, median(HA011[DIAGNOSIS2==2],
>   na.rm=TRUE)))
> group.Q3 <- c(group.Q3, with(Dataset, quantile(HA011[DIAGNOSIS2==2], 0.75,
>   na.rm=TRUE)))
> group.max <- c(group.max, with(Dataset, max(HA011[DIAGNOSIS2==2],
>   na.rm=TRUE)))
> group.p <- c(group.p, "")
> manwhitney.table <- NULL
> manwhitney.table <- data.frame(Minimum=group.min, Q1=group.Q1,
>   Median=group.median, Q3=group.Q3, Maximum=group.max, p.value=group.p)
> rownames(manwhitney.table)[1] <- group.names
> colnames(manwhitney.table)[c(1,4)] <- c("25%", "75%")
> colnames(manwhitney.table) <- gettextf(Encoding(colnames(manwhitney.table)))
> manwhitney.table

                Minimum 25% Median 75% Maximum p.value
DIAGNOSIS2=1        2   2    2.5   3       4 0.00408
DIAGNOSIS2=2        1   3    4.0   4       4
```

```
> Dataset2 <-
>   readxl("C:/Users/Rudi Ishmo/Desktop/DATA SCRIPTING PENELITIAN.xlsx",
>   range=cellranger::cell_limits(c(1,1),c(NA,NA)), sheet="Sheet2", stringsAsFactors=TRUE)
```

```
> ##########Non-Whitney U test##########
> group.names <- NULL
> group.median <- NULL
> group.min <- NULL
> group.max <- NULL
> group.Q1 <- NULL
> group.Q3 <- NULL
> group.p <- NULL
> window(width=7, height=7); par(lwd=2, las=1, family="sans", cex=1,
>   mgp=c(3.0,1,0))
> boxplot(Hasil~ Factor(Diagnosis.HPA), ylab="Hasil", xlab="Diagnosis.HPA",
>   data=Dataset2)
```




```
> (res <- wilcox.test(Hasil ~ factor(Diagnosis.HPA), alternative="two.sided",
>   data=Dataset2))

Warning in wilcox.test.default(x = c(3, 3, 3, 3, 3, 3, 3, 2, 3, 2, 2, 2, 2, :
cannot compute exact p-value with ties

	Wilcoxon rank sum test with continuity correction

data:  Hasil by factor(Diagnosis.HPA)
W = 30.5, p-value = 0.00516
alternative hypothesis: true location shift is not equal to 0

> group.names <- c(group.names, "Diagnosis.HPA=1")
> group.min <- c(group.min, with(Dataset2, min(Hasil[Diagnosis.HPA==1],
>   na.rm=TRUE)))
> group.Q1 <- c(group.Q1, with(Dataset2, quantile(Hasil[Diagnosis.HPA==1],
>   0.25, na.rm=TRUE)))
> group.median <- c(group.median, with(Dataset2,
>   median(Hasil[Diagnosis.HPA==1], na.rm=TRUE)))
> group.Q3 <- c(group.Q3, with(Dataset2, quantile(Hasil[Diagnosis.HPA==1],
>   0.75, na.rm=TRUE)))
> group.max <- c(group.max, with(Dataset2, max(Hasil[Diagnosis.HPA==1],
>   na.rm=TRUE)))
> group.p <- c(group.p, signif(res$p.value,digits=3))
> group.names <- c(group.names, "Diagnosis.HPA=2")
> group.min <- c(group.min, with(Dataset2, min(Hasil[Diagnosis.HPA==2],
>   na.rm=TRUE)))
> group.Q1 <- c(group.Q1, with(Dataset2, quantile(Hasil[Diagnosis.HPA==2],
>   0.25, na.rm=TRUE)))
> group.median <- c(group.median, with(Dataset2,
>   median(Hasil[Diagnosis.HPA==2], na.rm=TRUE)))
> group.Q3 <- c(group.Q3, with(Dataset2, quantile(Hasil[Diagnosis.HPA==2],
>   0.75, na.rm=TRUE)))
> group.max <- c(group.max, with(Dataset2, max(Hasil[Diagnosis.HPA==2],
>   na.rm=TRUE)))
> group.p <- c(group.p, "")
> manwhitney.table <- NULL
> manwhitney.table <- data.frame(Minimum=group.min, Q1=group.Q1,
>   Median=group.median, Q3=group.Q3, Maximum=group.max, p.value=group.p)
> rownames(manwhitney.table)[1] <- group.names
> colnames(manwhitney.table)[c(1,4)] <- c("25%", "75%")
> colnames(manwhitney.table) <- gettextf(Encoding(colnames(manwhitney.table)))
> manwhitney.table

                Minimum 25% Median 75% Maximum p.value
Diagnosis.HPA=1       1   2    2   2       3 0.00516
Diagnosis.HPA=2       2   3    3   4       4
```

```
> ##########Spearman's rank correlation test##########
> window(width=7, height=7); par(lwd=2, las=1, family="sans", cex=1,
>   mgp=c(3.0,1,0))
> scatterplot(DIAGNOSIS~HA011, reg.line=lm, smooth=FALSE, spread=FALSE,
>   boxplots='xy', span=0.5, data=Dataset)
```

```
Warning in plot.window(...): "reg.line" is not a graphical parameter

Warning in plot.window(...): "spread" is not a graphical parameter

Warning in plot.window(...): "span" is not a graphical parameter

Warning in plot.xy(xy, type, ...): "reg.line" is not a graphical parameter

Warning in plot.xy(xy, type, ...): "spread" is not a graphical parameter

Warning in plot.xy(xy, type, ...): "span" is not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "reg.line" is
not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "spread" is
not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "span" is not
a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "reg.line" is
not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "spread" is
not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "span" is not
a graphical parameter

Warning in box(...): "reg.line" is not a graphical parameter

Warning in box(...): "spread" is not a graphical parameter

Warning in box(...): "span" is not a graphical parameter

Warning in title(...): "reg.line" is not a graphical parameter

Warning in title(...): "spread" is not a graphical parameter

Warning in title(...): "span" is not a graphical parameter
```

```
> res <- NULL
> (res <- cor.test(Dataset$DIAGNOSIS, Dataset$HA011, alternative="two.sided",
>   method="spearman"))

Warning in cor.test.default(Dataset$DIAGNOSIS, Dataset$HA011, alternative =
"two.sided", : Cannot compute exact p-value with ties

	Spearman's rank correlation rho

data:  Dataset$DIAGNOSIS and Dataset$HA011
S = 2279.9, p-value = 0.00011192
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.519077

> cat(gettextf(round("Spearman's rank correlation coefficient",
>   signif(res$estimate, digits=2), gettextf(round("p.value",), " =",
>   signif(res$p.value, digits=3),
> "\"))

Spearman's rank correlation coefficient 0.519 p.value = 0.00011

> ##########Spearman's rank correlation test##########
> window(width=7, height=7); par(lwd=2, las=1, family="sans", cex=1,
>   mgp=c(3.0,1,0))
> scatterplot(Diagnosis.HPA~Hasil, reg.line=lm, smooth=FALSE, spread=FALSE,
>   boxplots='xy', span=0.5, data=Dataset2)
```

```
Warning in plot.window(...): "reg.line" is not a graphical parameter

Warning in plot.window(...): "spread" is not a graphical parameter

Warning in plot.window(...): "span" is not a graphical parameter

Warning in plot.xy(xy, type, ...): "reg.line" is not a graphical parameter

Warning in plot.xy(xy, type, ...): "spread" is not a graphical parameter

Warning in plot.xy(xy, type, ...): "span" is not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "reg.line" is
not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "spread" is
not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "span" is not
a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "reg.line" is
not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "spread" is
not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "span" is not
a graphical parameter

Warning in box(...): "reg.line" is not a graphical parameter

Warning in box(...): "spread" is not a graphical parameter

Warning in box(...): "span" is not a graphical parameter

Warning in title(...): "reg.line" is not a graphical parameter

Warning in title(...): "spread" is not a graphical parameter

Warning in title(...): "span" is not a graphical parameter
```

```
> res <- NULL
> (res <- cor.test(Dataset2$Diagnosis.HPA, Dataset2$Hasil,
>   alternative="two.sided", method="spearman"))

Warning in cor.test.default(Dataset2$Diagnosis.HPA, Dataset2$Hasil,
alternative = "two.sided", : Cannot compute exact p-value with ties

	Spearman's rank correlation rho

data:  Dataset2$Diagnosis.HPA and Dataset2$Hasil
S = 1912.6, p-value = 0.00000137
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.687254

> cat(gettextf(round("Spearman's rank correlation coefficient",
>   signif(res$estimate, digits=2), gettextf(round("p.value",), " =",
>   signif(res$p.value, digits=3),
> "\"))

Spearman's rank correlation coefficient 0.689 p.value = 0.00000137
```

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thermofisher.com/contactus

Performance guaranteed

CD133 Monoclonal Antibody (5E3)

Catalog Number **MA5-18323**

Product data sheet

Details

Size	100 µl
Host/Isotope	Mouse / IgG2a
Class	Monoclonal
Type	Antibody
Clone	5E3
Immunogen	Recombinant full length human CD133
Conjugate	Unconjugated
Form	Liquid
Purification	Antigen affinity chromatography
Storage buffer	0.1M tris glycine, pH 7.4, with 0.15M NaCl, 50% glycerol
Contains	0.2% sodium azide
Storage Conditions	Store at 4°C short term. For long term storage, store at -20°C, avoiding freeze/thaw cycles.

Species Reactivity

Species reactivity	Human
Published species	Mouse

Tested Applications	Dilution *
Western Blot (WB)	1:500-1:1000

Published Applications

Immunohistochemistry (Paraffin) (IHC (P))	See 1 publications below

* Suggested working dilutions are given as a guide only. It is recommended that the user titrate the product for use in their own experiment using appropriate negative and positive controls.

Product specific information

This antibody detects endogenous protein at a molecular weight of 133 kDa and does not cross-react with related proteins. Purity is >95% by SDS-PAGE.

Background/Target Information

This gene encodes a pentaspan transmembrane glycoprotein.The protein localizes to membrane protrusions and is often expressed on adult stem cells, where it is thought to function in maintaining stem cell properties by suppressing differentiation.Mutations in this gene have been shown to result in retinitis pigmentosa and Stargardt disease.Expression of this gene is also associated with several types of cancer.This gene is expressed from at least five alternative promoters that are expressed in a tissue-dependent manner.Multiple transcript variants encoding different isoforms have been found for this gene.

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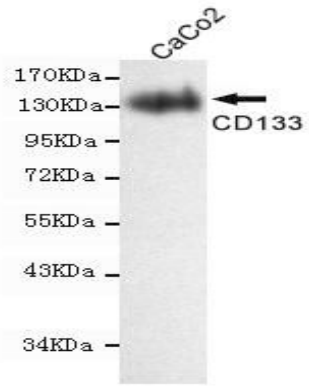

CD133 Antibody (MA5-18323) in WB

Western blot analysis of CD133 in CaCo2 cell lysate using CD133 monoclonal antibody (Product # MA5-18323) at a dilution of 1:1000.

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KARYA AKHIR HUBUNGAN EKSPRESI CD133..... AGUNG DWI S.

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PubMed References For CD133 Monoclonal Antibody (5F3)

1 Immunohistochemistry (Paraffin) References

Species / Dilution	Summary
	MA5-18323 was used in immunohistochemistry - paraffin section to assess the effect of therapy with bone marrow-derived cells an atherosclerotic mouse model.
Mouse / 1:100	Biochemistry and cell biology = Biochimie et biologie cellulaire (2015; 93: 367) **"Structural and ultrastructural evaluation of the aortic wall after transplantation of bone marrow-derived cells (BMCs) in a model for atherosclerosis."** Author(s):Felix AS,Monteiro N,Rocha VN,Oliveira G,Nascimento AL,de Carvalho L,Thole A,Carvalho J PubMed Article URL:http://dx.doi.org/10.1139/bcb-2015-0006

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KARYA AKHIR HUBUNGAN EKSPRESI CD133..... AGUNG DWI S.

Diagnostic BioSystems

IHC Made Affordable

Epidermal Growth Factor Receptor (EGFR) - 111.6

Mouse Monoclonal Antibody

Mob267

Mob267-05

PDM132

Document#: DS-0199-A
Effective Date: 12/01/2014

Immunogen	Clone	Species	Isotype	Primary Antibody Diluent
BALB/C mice were injected with extracellular domain of human recombinant EGFR protein.	111.6	Mouse	IgG1	K004

Lot specific Ig concentration available upon request.

Catalog #	Description
Mob267	1mLconcentrated antibody for use with Diagnostic BioSystems PolyVue™ Plus - Two Step Detection System
Mob267-05	0.5mLconcentrated antibody for use with Diagnostic BioSystems PolyVue™ Plus - Two Step Detection System
PDM132	6mLready to use antibody for use with Diagnostic BioSystems PolyVue™ Plus - Two Step Detection System

Intended Use

For In Vitro Diagnostic Use.**(For Outside U.S Market)**

This product is intended for qualitative immunohistochemistry with normal and neoplastic formalin-fixed, paraffin-embedded tissue sections, to be viewed by light microscopy. Clinical interpretation of staining results should be accompanied by histological studies with proper controls. Patients' clinical histories and other relevant diagnostic tests should be utilized by a qualified person(s) when evaluating and interpreting results.

Summary and Explanation

This antibody is specific to a 170 kDa protein. EGF-Receptor is a member of the type I family of growth factor receptors. The antibody recognizes an epitope mapping in the extracellular domain of EGFR. Overexpression of EGFR has been reported in tumors of breast, brain, bladder, lung, stomach, head and neck, esophagus, cervix, vulva, ovary and endometrium. EGFR is over expressed in squamous cell carcinoma.

Format

This product is supplied as a purified immunoglobulin and contains sodium azide as a preservative.

Principles of the Procedures

Antigen detection by immunohistochemistry (IHC) is a two-step process involving first, the binding of a primary antibody to the antigen of interest, and second, the detection of bound antibody by a chromogen. The primary antibody may be used in IHC using manual techniques or using Diagnostic BioSystems Automated Montage 360™ Staining System.

Dilution of Primary Antibody

Diagnostic BioSystems ready to useantibodies have been optimized for use with the recommended Diagnostic BioSystems Detection System and do not require further dilution. Further dilution may result in loss of sensitivity. The user must validate any such change.

Diagnostic BioSystems concentrated antibodies must be diluted in accordance with the staining procedure when used with the recommended Diagnostic BioSystems detection system. Use of any detection methods other than the recommended systems and protocols require validation by the user. Antibody dilutions should be appropriately adjusted and verified according to the detection system used.

Materials Required But Not Provided

Some of thereagents and materials required for IHC are not provided. Pretreatment reagents, detection systems, control reagents and other ancillary reagents are available from Diagnostic BioSystems. Please refer to the Diagnostic BioSystems website atwww.dbiosys.com

Storage and Handling

Store at 2-8°C. This antibody is suitable for use until the expirationdate when stored at 2-8°C. Do not use product after the expiration date printed on vial. If reagents are stored under conditionsother than those specified here, they must be verified by the user. Diluted reagents should be used promptly. Unused portions of antibody preparation should be discarded after one day.

The presence of precipitate or an unusual odor indicates that the antibody is deteriorating and should not be used.

Positive and negative controls should be run simultaneously with all patient specimens. If unexpected staining is observed which cannot be explained by variations in laboratory procedures and a problem with the antibody is suspected, contact Diagnostic BioSystems Technical Support at (925) 484-3350, extension 2 or techsupport@dbiosys.com.

Specimen Collection and Preparation

Tissues fixed in 10% formalin are suitable for use prior to paraffin embedding. Consult references (Kiernan, 1981: Sheehan &Hrapchak, 1980) for further details on specimen preparation.

The user is advised to validate the use of the products with their tissue specimens prepared and handled in accordance with their laboratory practices.

Precautions

This antibody contains less than 0.1% sodium azide. Concentrations less than 0.1% are not reportable hazardous materials according to U.S. 29 CFR 1910.1200, OSHA Hazard Communication and EC Directive 91/155/EC. Sodium azide (NaN3) used as a preservative is toxic if ingested. Sodium azide may react with lead and copper plumbing to form highly explosive metal azides. Upon disposal, flush with large volumes of water to prevent azide build-up in plumbing. (Center for Disease Control, 1976, National Institute of Occupational Safety and Health,1976). Specimens, before and after fixation and all materials exposed to them, should be handled as if capable of transmitting infection and disposed of with proper precautions. Never pipette reagents by mouth and avoid contacting the skin and mucous membranes with reagents and specimens. If reagents or specimens come in contact with sensitive areas, wash with copious amounts of water.

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Microbial contamination of reagents may result in an increase in nonspecific staining. Incubation times or temperatures other than those specified may give erroneous results. The user must validate any such change. The MSDS is available upon request.

Treatment of Tissues Prior to Staining

Place the slides in the recommended antigen retrieval solution using Diagnostic BioSystems Montage Opus™ Antigen Retrieval System. Allow slides to cool down for 20 minutes prior to staining.

Staining Procedure

Refer to the following table for conditions specifically recommended for this antibody. Refer to the Diagnostic BioSystems PolyVue™ Plus—Two Step Detection System or Montage PolyVue Plus™ Auto Detection Systemfor guidance on specific staining protocols or other requirements.

Parameter	Diagnostic BioSystems Recommendations
Positive Control	Placenta
Concentrated Dilution	1:25-1:50
Pretreatment	HistoZyme
Incubation Time & Temperature	30 min @ RT
Detection System	PolyVue™ Plus - Two Step Detection System or Montage PolyVue Plus™ Auto Detection System for Montage 360 System
Tissue Type	FFPE

Quality Control

Refer to CLSI Quality Standards for Design and Implementation of Immuno-histochemistry Assays; Approved Guideline-Second edition (I/LA28-A2) CLSI Wayne, PA USA (www.clsi.org). 2011.

Troubleshooting

Contact Diagnostic BioSystems Technical Support at (925) 484-3350, extension 2, techsupport@dbiosys.com or your local distributor to report unusual staining.

Cellular Localization

Cell membrane

Limitations of the Procedure

Immunohistochemistry is a complex technique involving both histological and immunological detection methods. Tissue processing and handling prior to immunostaining can also cause inconsistent results. Variations in fixation and embedding or the inherent nature of the tissue may cause variations in results (Nadji and Morales, 1983). Endogenous peroxidase activity or pseudoperoxidase activity in erythrocytesand endogenous biotin may cause non-specific staining depending on detection system used. Tissues containing Hepatitis B surface Antigen (HBsAg) may give a falsepositive with horseradish peroxidase systems (Omata et al, 1980). Improper counterstaining and mounting may compromise the interpretation of results.

Performance Characteristics

The optimum antibody dilution and protocols for a specific application can vary. These include, but are not limited to: fixation, heat-retrieval method, incubation times, and tissue section thickness and detection kit used. Due to the superior sensitivity of these unique reagents, the recommended incubation times and titers listed are not applicable to other detection systems, as results may vary. The data sheet recommendations and protocols are based on exclusive use of Diagnostic BioSystems products. Ultimately, it is the responsibility of the investigator to determine optimal conditions. These products are tools that can be used for interpretation of morphological findings in conjunction with other diagnostic tests and pertinent clinical data by a qualified pathologist.

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KOMITE ETIK PENELITIAN KESEHATAN
RSUD Dr. SOETOMO SURABAYA

KETERANGAN KELAIKAN ETIK
(" ETHICAL CLEARANCE ")

1477/KEPK/Ix/2019

KOMITE ETIK RSUD Dr. SOETOMO SURABAYA TELAH MEMPELAJARI SECARA SEKSAMA RANCANGAN PENELITIAN YANG DIUSULKAN, MAKA DENGAN INI MENYATAKAN BAHWA PENELITIAN DENGAN JUDUL :

" Hubungan Ekspresi CD133 dan EGFR terhadap Derajat Keganasan pada Karsinoma Ovarium "

PENELITI UTAMA : Dyah Fauziah, dr., Sp.PA (K)
PENELITI LAIN : 1. Dr. Gondo Mastutik, drh., M.Kes
2. Agung Dwi Suprayitno, dr
UNIT / LEMBAGA / TEMPAT PENELITIAN : RSUD Dr. Soetomo

DINYATAKAN LAIK ETIK

Berlaku dari : 04/09/2019 s.d 04/09/2020
Surabaya, 4 September 2019
KETUA

(Dr. Eldeus Hanfindito, dr., Sp.An, KIC,KAP)
NIP. 19511007 197903 1 002

) Sertifikat ini dinyatakan sah apabila telah mendapatkan stempel asli dari Komite Etik Penelitian Kesehatan