DAFTAR PUSTAKA

Adán, A., Casaroli-Marano, R., Gris, O. et al. (2008) “Pathological findings in the lens capsules and intraocular lens in chronic pseudophakic endophthalmitis: an electron microscopy study”. Eye 22, hal. 113–119, doi.org/10.1038/sj.eye.6702615.

Agustin FS, Sofia O, Metita M. (2020) “Aspek Klinis Pasien Endoftalmitis Akut Post Operatif Katarak di RSUD Dr. Saiful Anwar Malang.” Ophthalmol Ina;46(2): hal. 124-130.

Au, Cheryl PY; White, Andrew JR; Healey, Paul R (2016) “Efficacy and cost-effectiveness of intrakameral vancomycin in reducing postoperative endophthalmitis incidence in Australia. Clinical & Experimental Ophthalmology,” –. doi:10.1111/ceo.12789.

Barry P, Cordovés L, Gardner S. (2013) “ESCRS guidelines for prevention and treatment of endophthalmitis following cataract surgery: data, dilemmas and conclusions,” www.escrs.org.

Bowen RC, Zhou AX, Bondalapati S, et al. (2018) “Comparative analysis of the safety and efficacy of intrakameral cefuroxime, moxifloxacin and vancomycin at the end of cataract surgery: a meta-analysis.” Br J Ophthalmol; 102, hal. 1268–76.

Braimah IM, Essuman VA, Fordjuor G. Post cataract surgery endophthalmitis in a

Cantor B Louis, Rapuano Canstopher, et al. (2016-2017) “Post operative surgical course and complications Lens and Cataract. BSCS American Academy of Ophtalmology. New York. (11), hal. 209-211.

Carcher C, Bennenim E, Manet A S. (2016) “Incidence of acute pasca operative endophthalmitis after cataract surgery; A nationwide study in France from 2005-2014.” Ophthalmol. 123.1414-20

Chang DF, Rhee DJ. (2021) “Antibiotic prophylaxis of postoperative endophthalmitis following cataract surgery: results of the 2021 ASCRS member survey”. J Cataract Refract Surg.

Chen K-J, Lai C-C, Chen H-C, et al. (2021) Enterococcus faecalis Endophthalmitis: Clinical Settings, Antibiotic Susceptibility, and Management Outcomes. Microorganisms; 9:918.

Chiquet C, Cornut PL, Benito Y, et al. (2008) “Eubacterial PCR for bacterial detection and identification in 100 acute postcataract surgery endophthalmitis.” Invest Ophthalmol Vis Sci. 49(5), hal. 1971–8.

Combey de Lambert A, Campolmi N, Cornut PL, Aptel F, Creuzot-Garcher C, Chiquet C et al. (2013) “Baseline factors predictive of visual prognosis in acute postoperative bacterial endophthalmitis in patients undergoing cataract surgery.” JAMA Ophthalmol 131(9): hal. 1159–1166.

Das T, Padhi TR, Sharma S. (2010) “Endophthalmitis management in India: a decade and half after the Endophthalmitis Vitrectomy Study.” EJ Ophthalmol. www.ejournalofophthalmology.com.

Durand ML. (2017) “Bacterial and fungal endophthalmitis. Clin Microbiol Rev.” 30(3): hal. 597–613.

Friling E, Montan P. (2019) “Bacteriology and cefuroxime resistance in endophthalmitis following cataract surgery before and after the introduction of prophylactic intrakameral cefuroxime: a retrospective single-centre study.” J Hosp Infect 101: hal. 88–92.

Garg P, Roy A, Sharma S. (2017) “Endophthalmitis after cataract surgery: epidemiology, risk factors, and evidence on protection.” Curr Opin Ophthalmol. 2017 Jan;28(1): hal. 67-72. doi: 10.1097/ICU.0000000000000326. PMID: 27661662.

Global eye target. (2023) Available at : https://www.who.int/news/item/27-05-2021-global-eye-care-targets-endorsed-by-member-states-at-the-74th-world-health-assembly . Accessed 1st April , 2023.

Gower EW, Keay LJ, Stare DE, Arora P et al. (2015) “Characteristics of Endophthalmitis after Cataract Surgery in the United States Medicare Population .” AAO Journal. http://dx.doi.org/10.1016/j.ophtha.2015.04.036

Grzybowski A, Turczynowska M, Kuhn F. (2018) "The treatment of postoperative endophthalmitis: should we still follow the endophthalmitis vitrectomy study more than two decades after its publication? Acta Ophthalmol. " ;96:e651-4.

Han DP, Wisniewski SR, Wilson LA, et al. (1996) "Spectrum and susceptibilities of microbiologic isolates in the Endophthalmitis Vitrectomy Study." Am J Ophthalmol. 122:1Y17.

Haripriya A, Chang DF, Ravindran RD. (2019) "Endophthalmitis reduction with intrakameral moxifloxacin in eyes with and without surgical complications: Results from 2 million consecutive cataract surgeries." J Cataract Refract Surg. 45(9): hal. 1226-1233. doi: 10.1016/j.jcrs.2019.04.018. Epub 2019 Jul 29. PMID: 31371152.

Haripriya A, Ravindran RD, Robin AL, Shukla AG, Chang DF. (2023) "Changing operating room practices: the effect on postoperative endophthalmitis rates following cataract surgery." Br J Ophthalmol. 107(6): hal. 780-785. doi: 10.1136/bjophthalmol-2021-320506. Epub 2022 Jan 11. PMID: 35017161.

Hujanen P, Vaajanen A, Felin T, et al *(2022) "Immediate sequential bilateral cataract surgery: a 13-year real-life report of 56 700 cataract operations."* British Journal of Ophthalmology *Published Online First: 13 October 2022. doi: 10.1136/bjo-2021-320588*

Jabbarvand M, Hashemian H, Khodaparast M, Jouhari M, Tabatabaei A, Rezaei S. (2016) "Endophthalmitis Occurring after Cataract Surgery: Outcomes of More Than 480 000 Cataract Surgeries, Epidemiologic Features, and Risk Factors." Ophthalmology. 123(2): hal. 295-301. doi: 10.1016/j.ophtha.2015.08.023. Epub 2015 Dec 15. Retraction in: Ophthalmology. 2020 Apr;127(4):557. PMID: 26704882.

Jeong JH, Cho HJ, Kim HS, Han JI, Lee DW, Kim CG et al. (2017) "Acute endophthalmitis after cataract surgery: 164 consecutive cases treated at a referral center in South Korea." Macmillan Publishers Limited, part of Springer Nature . 2017. 31, 1456–1462

Kementerian Kesehatan RI. (2018). Peta Jalan Penanggulangan gangguan penglihatan di Indonesia Tahun 2017-2030. Jakarta: Direktorat Jenderal Pencegahan dan Pengendalian Penyakit.

Keputusan menteri kesehatan republik indonesia nomor hk.01.07/menkes/557/2018 tentang pedoman nasional pelayanan kedokteran tata laksana katarak pada dewasa.

Kim J, Kim HS, Yoo SJ, Choi MJ et al. (2022) Immediate Vitrectomy for Acute Endophthalmitis in Patients with a Visual Acuity of Hand Motion or Better. Korean J Ophthalmol 36(5), hal. 390-397.

Kim SH, Yu MH, Lee JH, et al. (2019) "Seasonal variation in acute post-cataract surgery endophthalmitis incidences in South Korea." J Cataract Refract Surg. 45(12), hal. 1711–1716.

Kim SH, Yu MH, Lee JH, Kim SW, Rah SH. (2019) Endophthalmitis after Cataract Surgery in Korea: A Nationwide Study Evaluating Incidence and Risk Factors in a Korean Population. Yonsei Med J. 60(5) hal. 467-473.

Kosacki J, Boisset S, Maurin M, et al. (2020) "Specific PCR and quantitative real-time PCR in ocular samples from acute and delayed-onset postoperative endophthalmitis." Am J Ophthalmol. 212(4), hal. 34–42.

Kuhn F, Gini G. (2010) "Complete and Early Vitrectomy for Endophthalmitis (CEVE) as Today's Alternative to the Endophthalmitis Vitrectomy Study. In: Kirchhof," B., Wong, D. (eds) Vitreo-retinal Surgery. *Essentials in Ophthalmology. Springer, Berlin, Heidelberg. https://doi.org/10.1007/978-3-540-33670-9_5*

Kumar A, Pandey RK, Miller LJ, Singh PK, Kanwar M. (2013) "Muller glia in retinal innate immunity: a perspective on their roles in endophthalmitis. Critical Reviews in Immunology." 33(2), hal. 119-135. DOI: 10.1615/critrevimmunol.2013006618. PMID: 23582059; PMCID: PMC3697845.

Kuo G, Lu YA, Sun WC, Chen CY, Kao HK, Lin Y, Lee CH, Hung CC, Tian YC, Hsu HH. (2017) "Epidemiology and outcomes of endophthalmitis in chronic dialysis patients: a 13-year experience in a tertiary referral center in Taiwan". BMC Nephrol 18(1), hal. 270.

Lundstrom M, Wejde G, Stenevi U, et al. (2007) "Endophthalmitis after cataract surgery: a nationwide prospective study evaluating incidence in relation to incision type and location." Ophthalmology. 114 (5), hal. 866–870.

Lutfah Rif'Ati, Aldiana Halim, Yeni Dwi Lestari, Nila F Moeloek & Hans Limburg (2020): Blindness and Visual Impairment Situation in Indonesia Based on Rapid Assessment of Avoidable Blindness Surveys in

15 Provinces, Ophthalmic Epidemiology, DOI: 10.1080/09286586.2020.1853178

Melo GB, Bispo PJ, Yu MC, et al. (2011) "Microbial profile and antibiotic susceptibility of culture-positive bacterial endophthalmitis." Eye (Lond). 25(3), hal. 382–387 quiz 8.

Mishra D, Satpathy G, Chawla R, et al. (2019) "Utility of broad-range 16S rRNA PCR assay versus conventional methods for laboratory diagnosis of bacterial endophthalmitis in a tertiary care hospital." Br J Ophthalmol. 103(1), hal. 152–156.

Nowak MC, Grzybowski A, Michalska-Małecka K, Szaflik JP, Kozioł M, Niemczyk W et al. (2019) "Incidence and Characteristics of Endophthalmitis after Cataract Surgery in Poland, during 2010–2015." MDPI Journal. 16, 2188

Oviano M, Bou G. (2019) "Matrix-assisted laser desorption ionization-time of flight mass spectrometry for the rapid detection of antimicrobial resistance mechanisms and beyond." Clin Microbiol Rev. 32(1)

Pathengay A, Khera M, Das T, Sharma S,Miller D, Flynn HW. (2012) "Acute Postoperative Endophthalmitis Following Cataract Surgery: A Review. Asia Pacific Academy of Ophthalmology."

Peng, K. L., Kung, Y. H., Tsai, H. S., & Wu, T. T. (2021). Treatment outcomes of acute poptoperative infectious endophthalmitis. *BMC ophthalmology*, *21*, 1-9.

Perez da Silva Pereira P, Carvalho Sabini AA, Ferreira de Almeida RM, et al. (2023) "Major outbreak of endophthalmitis after cataract surgery: a retrospective cohort in northern Brazil." medRxiv; DOI: 10.1101/2023.02.08.23285557.

Pusdatin Kemkes RI. (2018). Situasi Gangguan Penglihatan. Jakarta: Kementerian Kesehatan RI.

Syawal ,R. (2007) "The outbreak of acute postoperative cataract endophthalmitis at Dr. Wahidin Sudirohusodo General Hospital Makassar." Journal oftalmologi Indonesia,5, hal. 137-140

Segretín Gutiérrez EFE, García MM, Bursztyn M, Benavente Defferrari MM, Ortiz-Basso T. (2022) Incidence of endophthalmitis post cataract surgery in a Tertiary Hospital of Buenos Aires. Medicina (B Aires). 82(6), hal. 851-855. English. PMID: 36571523.

Shimada H, Arai S, Nakashizuka H, et al. (2011) "Reduction of anterior chamber contamination rate after cataract surgery by intraoperative surface irrigation with 0.25% povidone-iodine." Am J Ophthalmol. 151:11Y17.

Stout JT, Rapuano Canstopher, McCanel CA, et al. (2016-2017) "Vitrectomy for Posterior Segment Complication of Anterior Segment Surgery. BSCS American Academy of Ophtalmology." New York. 12, hal. 388-390.

Sugita S, Ogawa M, Shimizu N, et al. (2013) "Use of a comprehensive polymerase chain reaction system for diagnosis of ocular infectious diseases." Ophthalmology. 120(9), hal. 1761–1768.

Sun J et al (2008-2009) "Surgery: acute infectious endophtalmitis after cataract surgery: Epidemiological Characteristics, Risk Factors and Incidence Trends,"

Sun J, Guo Z, Li H, Yang B, Wu X. (2021) "Acute Infectious Endophthalmitis After Cataract , Surgery: Epidemiological Characteristics, Risk Factors and Incidence Trends, 2008–2019." Dove Press journal. 14, hal. 1231–1238.

Taban M et al (2005) "Acute Endophthalmitis Following Cataract Surgery: A Systematic Review of the Literature." Archives of Ophthalmology; 123; 5/05; p613

Thariya P, Yospaiboon Y, Sinawat S, et al. (2016) "Blood culture bottles are superior to conventional media for vitreous culture." Clin Exp Ophthalmol. 44(6), hal. 488–491.

Wadbudhe AM, Tidke SC, Tidake PK. (2022) "Endophthalmitis After Cataract Surgery: A Postoperative Complication." Cureus Journal. Cureus 14(10): e30110

Wai YZ, Fiona LM, Mohamad AS, Ang CL, Chong YY, Tassha HA et al. (2018) "The Malaysian cataract surgery registry: incidence and risk factors of postoperative infectious endophthalmitis over a 7-year period." Int J Ophthalmol . hal. 10-11.

Wen Q, Xuan R, Ong K (2021) "Incidence of post-cataract surgery endophthalmitis: a chronological review and intercontinental comparison." Asian Journal of Ophthalmology . 19, hal. 19-39.

Yannuzzi NA, Si N, Relhan N, Kuriyan AE, Albini TA, Berrocal AM, Davis JL, Smiddy WE, Townsend J, Miller D, Flynn Jr. HW, (2016) "Endophthalmitis After Clear Corneal Cataract Surgery: Outcomes Over Two Decades, American Journal of Ophthalmology," doi: 10.1016/ j.ajo.2016.11.006.

Zhu Y, Chen X, Chen P, Wu J, Hua H, et al. (2017) "The occurrence rate of acute-onset postoperative endophthalmitis after cataract surgery in Chinese small- and medium-scale departments of ophthalmology." Scientific RepoRts. 7:40776 DOI: 10.1038/srep40776

LAMPIRAN 1

REKOMENDASI PERSETUJUAN ETIK

KEMENTERIAN PENDIDIKAN, KEBUDAYAAN, RISET DAN TEKNOLOGI
UNIVERSITAS HASANUDDIN FAKULTAS KEDOKTERAN
KOMITE ETIK PENELITIAN UNIVERSITAS HASANUDDIN
RSPTN UNIVERSITAS HASANUDDIN
RSUP Dr. WAHIDIN SUDIROHUSODO MAKASSAR
Sekretariat : Lantai 2 Gedung Laboratorium Terpadu
JL.PERINTIS KEMERDEKAAN KAMPUS TAMALANREA KM.10 MAKASSAR 90245.
Contact Person: dr. Agussalim Bukhari.,MMed,PhD, SpGK TELP. 081241850858, 0411 5780103, Fax : 0411-581431

REKOMENDASI PERSETUJUAN ETIK

Nomor : 169/UN4.6.4.5.31/ PP36/ 2024

Tanggal: 15 Maret 2024

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

No Protokol	UH24020069	No Sponsor	
Peneliti Utama	**dr. Dian Puteri Pratami**	Sponsor	
Judul Peneliti	PEMETAAN INSIDENSI, ASPEK KLINIS DAN DETEKSI MOLEKULER PASIEN ENDOFTALMITIS AKUT PASKA OPERASI KATARAK DI RUMAH SAKIT RUJUKAN KOTA MAKASSAR		
No Versi Protokol	2	Tanggal Versi	**13 Maret 2024**
No Versi PSP	2	Tanggal Versi	**13 Maret 2024**
Tempat Penelitian	RS Universitas Hasanuddin, RSUD Tadjuddin Chalid dan Klinik JEC @Orbita Makassar		
Jenis Review	☐ Exempted ☒ Expedited ☐ Fullboard Tanggal	Masa Berlaku **15 Maret 2024** sampai **15 Maret 2025**	Frekuensi review lanjutan
Ketua KEP Universitas Hasanuddin	**Prof. dr. Muh Nasrum Massi,PhD,SpMK, Subsp. Bakt(K)**	Tanda tangan	
Sekretaris KEP Universitas Hasanuddin	**dr. Firdaus Hamid, PhD, SpMK(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 Lapor 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 prokol yang disetujui (protocol deviation / violation)
- Mematuhi semua peraturan yang ditentukan

LAMPIRAN 2
FORMULIR PERSETUJUAN SAMPEL

FORMULIR PERSETUJUAN SETELAH PENJELASAN

Saya yang bertanda tangan di bawah ini :
Nama : ....
Umur : ....tahun
Alamat : ....
Telepon/HP :...
Menyatakan bersedia untuk berpartisipasi pada penelitian ini yang berjudul :

"PEMETAAN INSIDENSI, ASPEK KLINIS DAN DETEKSI MOLEKULER PASIEN ENDOFTALMITIS AKUT PASCA OPERASI KATARAK DI RUMAH SAKIT RUJUKAN KOTA MAKASSAR"

Setelah mendengar/membaca dan mengerti penjelasan yang diberikan mengenai tujuan dan manfaat yang akan didapatkan pada penelitian ini, khususnya bagi kemajuan ilmu kedokteran.

Makassar, ...

Responden/Wali

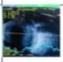
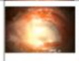
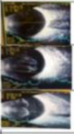
(................................)

Penanggung jawab penelitian :
Nama : dr. Dian Puteri Pratami
Alamat : BTP Blok M1 no. 2
Telp. : 082191109513

Penanggung jawab medik :
Nama : Prof. Dr. dr. Habibah S. Muhiddin, Sp.M(K)
Alamat : Kompleks Dosen UNHAS Tamalanrea GB/66
Telp. : 0811449366

LAMPIRAN 3

DATA INDUK

KODE SAMPLE	USIA	status lensa	jahitan kornea	komplikasi	FUNDUSKOPI INDIREK	USG	DM	TGL OP KATARAK	TGL PERTAMA KELUHAN/ ONSET	TGL MRS/ RUJUKAN	VISUS DATANG	VISUS POST OP VPP	KETERANGAN	KLINIS FOTO	USG FOTO	AB IC	RS PERUJUK	PCR 16sRNA	PCR SEKUENSING	%	PCR 18sRNA	PCR SEKUENSING	%
END 1	69	pseudofakia (IOL +)	none	none	TIDAK TEMBUS , KORNEA EDEMA	CAVUM VITREUS HIPERECHOIC DEBRIS		16/03/24	25/03/2024 POH+9	27/03/2024 POST ONSET+2	VOS LP	VOS LP POH+20	VISUS TETAP			LFX	RS HAPSAH	(+)	Pseudomonas aeruginosa strain SAM10	98%	(-)	Not Identified	NI
END 2	70	pseudofakia (IOL +)	none	suspek panoftalmitis (USG T-Sign , Pachychoroid)	TIDAK TEMBUS, FIBRIN TEBAL DEPAN IOL	"CAVUM VITREUS HIPERECHOIC DEBRIS + T-SIGN	YA	16/03/24	23/03/2024 POH+7	28/03/2024 POST ONSET+5	VOD LP	VOD LP POH+14	VISUS TETAP			LFX	RS HAPSAH	(+)	Pseudomonas aeruginosa strain PSH42	97%	(+)	1. Microsporum canis, 2.Arthroderma multifidum	88%, 86%
END 3	56	pseudofakia (IOL +)	none	none	VITREUS HAZY GRADE 2	TIDAK DILAKUKAN		07/03/24	09/03/2024 POH+2	09/03/2024 POST ONSET+ 0	VOD 1/2 / 60 COUNTING FINGER	VOD 20/70 POH+14	VISUS MAJU ke 2 terbaik	TIDAK TERSEDIA FO	TIDAK TERSEDIA FOTO	LFX	JEC @ORBITA	(+)	Pseudomonas aeruginosa strain Y12	98%	(+)	1. Arthroderma multifidum 90% 2.Trichophyton tonsurans 3. Nannizzia gypsea	90%, 88%, 88%
END 4	74	pseudofakia (IOL +)	none	none	TIDAK TEMBUS , KORNEA EDEMA	MEMBRAN LIKE LESSION		16/03/24	18/03/2024 POH+2	23/03/2024 POST ONSET +5	VOD LP	VOD 1/300 POH+14	VISUS MAJU			LFX	RS HAPSAH	(+)	Zavarzinia sp . strain K1W42B-24	84%	(-)	Not Identified	NI
END 5	58	pseudofakia (IOL +)	none	none	TIDAK TEMBUS , KORNEA EDEMA	MEMBRAN LIKE LESSION		27/03/24	28/03/2024 POH+1	28/03/2024 POST ONSET + 0	VOS 1/300	VOS 20/200 POH+20	VISUS MAJU			LFX	RS MITRA HUSADA	(+)	Zavarzinia sp. strain K1W22B-18	85%	(-)	Not Identified	NI
END 6	79	pseudofakia (IOL +)	1 Jahitan	none	TIDAK TEMBUS , KORNEA EDEMA	MEMBRAN LIKE LESSION		30/03/24	01/04/2024 POH+2	13/04/2024 POST ONSET +12	VOD NLP	VOD 1/300 POH+14	VISUS MAJU			LFX	RS DATU PANCATENA	(+)	Pseudomonas aeruginosa	99%	(+)	1. Microsporum canis 2.Trichophyton interdigitale	90%
END 7	70	afakia	1 jahitan	suspek panoftalmitis (USG T-Sign , Pachychoroid)	TIDAK TEMBUS , KORNEA EDEMA, FIBRIN TEBAL DEPAN IOL	CAVUM VITREUS HIPERECHOIC DEBRIS + T-SIGN	YA	30/03/24	01/04/2024 POH+2	13/04/2024 POST ONSET +12	VOS LP	VOS NLP POH+20	VISUS TURUN			LFX	RS DATU PANCATENA	(+)	Pseudomonas aeruginosa strain XB3	98%	(+)	1. Trichophyton rubrum	90%
END 8	55	pseudofakia (IOL +)	none	none	TIDAK TEMBUS , FIBRIN TEBAL DEPAN IOL	CAVUM VITREUS HIPERECHOIC DEBRIS	YA	26/03/24	12/04/2024 POH+17	26/04/2024 POST ONSET +14	VOS 1/300	VOS 1/300 POH+20	VISUS TETAP			LFX	RS BANTAENG PROF. A.MAKKATUTU	(+)	Zavarzinia sp. strain K1W22B-18	80%	(-)	Not Identified	NI
END 9	81	afakia	3 jahitan	retinal detachment	TIDAK TEMBUS , KORNEA EDEMA	V SHAPE , AFTER MOVEMENT (-)		06/04/24	11/04/2024 POH+5	16/04/2024 POST ONSET +5	VOD LP	VOD LP POH+14	VISUS TETAP			LFX	RS DATU PANCATENA	(+)	Pseudomonas aeruginosa strain PSH7	94%	(+)	1. Trichophyton tonsurans	86%
END 10	58	pseudofakia (IOL +)	none	none	TIDAK TEMBUS , FIBRIN TEBAL DEPAN IOL	MEMBRAN LIKE LESSION		16/04/24	18/04/2024 POH+2	08/05/2024 POST ONSET + 20	VOD 1/2 / 60 COUNTING FINGER	VOD 20/80 POH+14	VISUS MAJU ke 3 terbaik			LFX	KLINIK NURUL BULUKUMBA	(+)	Zavarzinia sp. strain K1W22B-18	83%	(-)	Not Identified	NI
END 11	48	pseudofakia (IOL +)	3 jahitan	none	VITREUS HAZY GRADE 3	MEMBRAN LIKE LESSION	YA	18/04/24	06/05/2024 POH+17	13/05/2024 POST ONSET +7	VOS 1/300	VOS 1/60 POH+20	VISUS MAJU			LFX	HAPSAH	(+)	Bacillus sp. NFN149	80%		Not Identified	NI
END 12	69	pseudofakia (IOL +)	none	none	VITREUS HAZY GRADE 1	POINT LIKE LESSION		07/05/24	09/05/2024 POH+2	**10/05/2024 POST ONSET + 1**	VOS 1/300	VOS 20/60 PH 20/40 P	VISUS MAJU (terbaik)			LFX	RSP UNHAS	(+)	Novosphingobium sp. Y3-5	86%		Not Identified	NI
END 13	68	pseudofakia (IOL +)	none	none	VITREUS HAZY GRADE 3	MEMBRAN LIKE LESSION		26/04/24	29/04/24 POH+3	13/05/2024 POST ONSET +14	VOD 1/60	VOD 2/60 PH 20/100 P	VISUS MAJU			LFX	RSUD I Lagaligo	(+)	Brevundimonas vesicularis strain TK026	98%	(+)	Nannizzia gypsea	**98%**
END 14	48	pseudofakia (IOL +)	1 Jahitan	none	VITREUS HAZY GRADE 3	MEMBRAN LIKE LESSION		12/05/24	10/06/24 POH+29	13/06/2024 POST ONSET + 3	VOS 1/300	VOS 20/160 POH+14	VISUS MAJU			LFX	RS HAPSAH	(+)	UNIDENTIFIED	UNIDEN TIFIED	UNIDENTI	UNIDENTIFIED	NI
END 15	46	pseudofakia (IOL +)	none	none	TIDAK TEMBUS , KORNEA EDEMA	MEMBRAN LIKE LESSION		13/03/24	23/03/24 POH+10	25/03/2024 POST ONSET + 2	VOD 1/300	VOD 20/160 POH+14	VISUS MAJU	TIDAK TERSEDIA FO	TIDAK TERSEDIA FOTO	LFX	RS IBNU SINA	(+)	Bacillus subtilis strain 2014-3557	88%		UNIDENTIFIED	NI
END 16	53	pseudofakia (IOL +)	none	none	TIDAK TEMBUS , KORNEA EDEMA	TIDAK DILAKUKAN	YA	30/04/24	2/05/24 POH+2	10/05/2024 POST ONSET +8	VOS 1/300	VOS 1/300 POH+14	VISUS TETAP		TIDAK TERSEDIA FOTO	LFX	RS DATU PANCATENA	(+)	Pseudomonas aeruginosa strain E11	98%	(+)	Trichophyton rubrum	90%

LAMPIRAN 4

STATISTIK

OUTPUT DATA SPSS

Descriptives

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Usia	16	38.00	81.00	62.0000	12.33423
Onset	16	1.00	31.00	13.8750	9.17878
Valid N (listwise)	16				

Frequency Table

Jenis kelamin

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Laki-laki	8	50.0	50.0	50.0
	Perempuan	8	50.0	50.0	100.0
	Total	16	100.0	100.0	

Usia

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	<45 tahun	1	6.3	6.3	6.3
	45-54 Tahun	3	18.8	18.8	25.0
	55-64 Tahun	4	25.0	25.0	50.0
	65-74 Tahun	6	37.5	37.5	87.5
	75-85 Tahun	2	12.5	12.5	100.0
	Total	16	100.0	100.0	

Onset

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	1-3 hari	3	18.8	18.8	18.8
	4-7 hari	1	6.3	6.3	25.0

	8-14 hari	7	43.8	43.8	68.8
	15-28 hari	3	18.8	18.8	87.5
	29-42 hari	2	12.5	12.5	100.0
	Total	16	100.0	100.0	

Kontrol Sp.M

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Tidak	1	6.3	6.3	6.3
	Ya	15	93.8	93.8	100.0
	Total	16	100.0	100.0	

Diabetes Mellitus

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Tidak	11	68.8	68.8	68.8
	Ya	5	31.3	31.3	100.0
	Total	16	100.0	100.0	

Injeksi

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Tidak	3	18.8	18.8	18.8
	Konjungtiva	3	18.8	18.8	37.5
	Siliar	1	6.3	6.3	43.8
	Mixed	9	56.3	56.3	100.0
	Total	16	100.0	100.0	

Kemosis konjungtiva

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Tidak	10	62.5	62.5	62.5
	Ya	6	37.5	37.5	100.0

	Total	16	100.0	100.0	

Edema kornea

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Tidak	6	37.5	37.5	37.5
	Ya	10	62.5	62.5	100.0
	Total	16	100.0	100.0	

Funduskopi

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Vitreus hazy grade 1	1	6.3	6.3	6.3
	Vitreus hazy grade 2	1	6.3	6.3	12.5
	Vitreus hazy grade 3	3	18.8	18.8	31.3
	Vitreus hazy grade 4	11	68.8	68.8	100.0
	Total	16	100.0	100.0	

USG

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	tidak dilakukan	2	12.5	12.5	12.5
	Point like lesion	1	6.3	6.3	18.8
	Membran like lesion	8	50.0	50.0	68.8
	hiperechoic debris cavum vitreus	2	12.5	12.5	81.3
	T -Sign , pachychoroid	2	12.5	12.5	93.8
	V-shape , after movement (-)	1	6.3	6.3	100.0
	Total	16	100.0	100.0	

Komplikasi

		Frequency	Percent	Valid Percent	Cumulative Percent

Valid	tidak ada	13	81.3	81.3	81.3
	Panoftalmitis	2	12.5	12.5	93.8
	Retinal detachment	1	6.3	6.3	100.0
	Total	16	100.0	100.0	

Status lensa

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Afakia	2	12.5	12.5	12.5
	Pseudofakia	14	87.5	87.5	100.0
	Total	16	100.0	100.0	

Terapi

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	VPP + Vitreous tap + wash out BMD + injeksi AB Intravitreal	14	87.5	87.5	87.5
	VPP + Vitreous tap + injeksi AB Intravitreal	1	6.3	6.3	93.8
	VPP + Sinekiolisis + Vitreous tap + wash out BMD + injeksi AB Intravitreal	1	6.3	6.3	100.0
	Total	16	100.0	100.0	

Visus Masuk

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	1/2 /60 counting finger	2	12.5	12.5	12.5
	1/300 hand wave	8	50.0	50.0	62.5
	Light perception	5	31.3	31.3	93.8
	No light perception	1	6.3	6.3	100.0
	Total	16	100.0	100.0	

Visus Keluar

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	>20/160 snellen chart	4	25.0	25.0	25.0
	20/160 snellen chart	2	12.5	12.5	37.5
	20/200 snellen chart	1	6.3	6.3	43.8
	1/60 sampai 6/60 counting finger	1	6.3	6.3	50.0
	1/300 hand wave	4	25.0	25.0	75.0
	Light perception	4	25.0	25.0	100.0
	Total	16	100.0	100.0	

Status refraksi

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Tetap	6	37.5	37.5	37.5
	Membaik	10	62.5	62.5	100.0
	Total	16	100.0	100.0	

PCR bakteri

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Unidentified	1	6.3	6.3	6.3
	Psudomonas auruginosa	7	43.8	43.8	50.0
	Zavarzinia sp	4	25.0	25.0	75.0
	Brevundimonas vesicularis	1	6.3	6.3	81.3
	Bacillus subtilis	2	12.5	12.5	93.8
	Novosphingobium sp	1	6.3	6.3	100.0
	Total	16	100.0	100.0	

Gram bakteri

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Tidak teridentifikasi	1	6.3	6.3	6.3

	Negatif	13	81.3	81.3	87.5
	Positif	2	12.5	12.5	100.0
	Total	16	100.0	100.0	

Crosstabs

Visus Masuk * Onset

Crosstab

			Onset					
			1-3 hari	4-7 hari	8-14 hari	15-28 hari	29-42 hari	Total
Visus Masuk	1/2 /60 counting finger	Count	1	0	0	1	0	2
		% within Visus Masuk	50.0%	0.0%	0.0%	50.0%	0.0%	100.0 %
	1/300 hand wave	Count	2	0	2	2	2	8
		% within Visus Masuk	25.0%	0.0%	25.0%	25.0%	25.0%	100.0 %
	Light perception	Count	0	1	4	0	0	5
		% within Visus Masuk	0.0%	20.0%	80.0%	0.0%	0.0%	100.0 %
	No light perception	Count	0	0	1	0	0	1
		% within Visus Masuk	0.0%	0.0%	100.0 %	0.0%	0.0%	100.0 %
Total		Count	3	1	7	3	2	16
		% within Visus Masuk	18.8%	6.3%	43.8%	18.8%	12.5%	100.0 %

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	12.610[a]	12	.398
Likelihood Ratio	15.567	12	.212
Linear-by-Linear Association	.000	1	1.000

N of Valid Cases	16		

a. 20 cells (100.0%) have expected count less than 5. The minimum expected count is .06.

Visus Keluar * Onset

Crosstab

			Onset					
			1-3 hari	4-7 hari	8-14 hari	15-28 hari	29-42 hari	Total
Visus Keluar	>20/160 snellen chart	Count	2	0	0	2	0	4
		% within Visus Keluar	50.0%	0.0%	0.0%	50.0%	0.0%	100.0%
	20/160 snellen chart	Count	0	0	1	0	1	2
		% within Visus Keluar	0.0%	0.0%	50.0%	0.0%	50.0%	100.0%
	20/200 snellen chart	Count	1	0	0	0	0	1
		% within Visus Keluar	100.0%	0.0%	0.0%	0.0%	0.0%	100.0%
	1/60 sampai 6/60 counting finger	Count	0	0	0	1	0	1
		% within Visus Keluar	0.0%	0.0%	0.0%	100.0%	0.0%	100.0%
	1/300 hand wave	Count	0	1	2	0	1	4
		% within Visus Keluar	0.0%	25.0%	50.0%	0.0%	25.0%	100.0%
	Light perception	Count	0	0	4	0	0	4
		% within Visus Keluar	0.0%	0.0%	100.0%	0.0%	0.0%	100.0%
Total		Count	3	1	7	3	2	16
		% within Visus Keluar	18.8%	6.3%	43.8%	18.8%	12.5%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	27.905[a]	20	.112
Likelihood Ratio	28.889	20	.090

Linear-by-Linear Association	.233	1	.629
N of Valid Cases	16		

a. 30 cells (100.0%) have expected count less than 5. The minimum expected count is .06.

Status refraksi * Onset

Crosstab

			Onset					
			1-3 hari	4-7 hari	8-14 hari	15-28 hari	29-42 hari	Total
Status refraksi	Tetap	Count	0	0	5	0	1	6
		% within Status refraksi	0.0%	0.0%	83.3%	0.0%	16.7%	100.0%
	Membaik	Count	3	1	2	3	1	10
		% within Status refraksi	30.0%	10.0%	20.0%	30.0%	10.0%	100.0%
Total		Count	3	1	7	3	2	16
		% within Status refraksi	18.8%	6.3%	43.8%	18.8%	12.5%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	7.771[a]	4	.100
Likelihood Ratio	10.022	4	.040
Linear-by-Linear Association	.667	1	.414
N of Valid Cases	16		

a. 10 cells (100.0%) have expected count less than 5. The minimum expected count is .38.

Asal * PCR bakteri Crosstabulation

			PCR bakteri						
			Unidentified	Psudomonas auruginosa	Zavarzinia sp	Brevundimonas vesicularis	Bacillus subtilis	Novosphingobium sp	Total
Asal	Makassar	Count	0	1	1	0	1	1	4
		% within Asal	0.0%	25.0%	25.0%	0.0%	25.0%	25.0%	100.0%
	Bone	Count	1	6	1	0	1	0	9
		% within Asal	11.1%	66.7%	11.1%	0.0%	11.1%	0.0%	100.0%
	Bantaeng	Count	0	0	1	0	0	0	1
		% within Asal	0.0%	0.0%	100.0%	0.0%	0.0%	0.0%	100.0%
	Bulukumba	Count	0	0	1	0	0	0	1
		% within Asal	0.0%	0.0%	100.0%	0.0%	0.0%	0.0%	100.0%
	Luwu Timur	Count	0	0	0	1	0	0	1
		% within Asal	0.0%	0.0%	0.0%	100.0%	0.0%	0.0%	100.0%
Total		Count	1	7	4	1	2	1	16
		% within Asal	6.3%	43.8%	25.0%	6.3%	12.5%	6.3%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	27.825[a]	20	.114
Likelihood Ratio	18.478	20	.556
Linear-by-Linear Association	.022	1	.881
N of Valid Cases	16		

a. 30 cells (100.0%) have expected count less than 5. The minimum expected count is .06.

Crosstabs

Asal * Gram bakteri

Crosstab

			Gram bakteri			Total
			Tidak teridentifikasi	Negatif	Positif	
Asal	Makassar	Count	0	3	1	4
		% within Asal	0.0%	75.0%	25.0%	100.0%
	Bone	Count	1	7	1	9
		% within Asal	11.1%	77.8%	11.1%	100.0%
	Bantaeng	Count	0	1	0	1
		% within Asal	0.0%	100.0%	0.0%	100.0%
	Bulukumba	Count	0	1	0	1
		% within Asal	0.0%	100.0%	0.0%	100.0%
	Luwu Timur	Count	0	1	0	1
		% within Asal	0.0%	100.0%	0.0%	100.0%
Total		Count	1	13	2	16
		% within Asal	6.3%	81.3%	12.5%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	1.829[a]	8	.986
Likelihood Ratio	2.456	8	.964
Linear-by-Linear Association	.364	1	.546
N of Valid Cases	16		

a. 14 cells (93.3%) have expected count less than 5. The minimum expected count is .06.

Asal * Pseudomonas

Crosstab

	Pseudomonas	Total

			Tidak	Ya	
Asal	Makassar	Count	3	1	4
		% within Asal	75.0%	25.0%	100.0%
	Bone	Count	3	6	9
		% within Asal	33.3%	66.7%	100.0%
	Bantaeng	Count	1	0	1
		% within Asal	100.0%	0.0%	100.0%
	Bulukumba	Count	1	0	1
		% within Asal	100.0%	0.0%	100.0%
	Luwu Timur	Count	1	0	1
		% within Asal	100.0%	0.0%	100.0%
Total		Count	9	7	16
		% within Asal	56.3%	43.8%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	4.825[a]	4	.306
Likelihood Ratio	5.974	4	.201
Linear-by-Linear Association	.755	1	.385
N of Valid Cases	16		

a. 9 cells (90.0%) have expected count less than 5. The minimum expected count is .44.

Crosstabs

Visus Masuk * PCR bakteri

Crosstab

	PCR bakteri	Total

			Unidentified	Psudomonas auruginosa	Zavarzinia sp	Brevundimonas vesicularis	Bacillus subtilis	Novosphingobium sp	
Visus Masuk	1/2 /60 counting finger	Count	0	1	1	0	0	0	2
		% within Visus Masuk	0.0%	50.0%	50.0%	0.0%	0.0%	0.0%	100.0%
	1/300 hand wave	Count	1	1	2	1	2	1	8
		% within Visus Masuk	12.5%	12.5%	25.0%	12.5%	25.0%	12.5%	100.0%
	Light perception	Count	0	4	1	0	0	0	5
		% within Visus Masuk	0.0%	80.0%	20.0%	0.0%	0.0%	0.0%	100.0%
	No light perception	Count	0	1	0	0	0	0	1
		% within Visus Masuk	0.0%	100.0%	0.0%	0.0%	0.0%	0.0%	100.0%
Total		Count	1	7	4	1	2	1	16
		% within Visus Masuk	6.3%	43.8%	25.0%	6.3%	12.5%	6.3%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	9.829[a]	15	.830
Likelihood Ratio	12.115	15	.670
Linear-by-Linear Association	1.207	1	.272
N of Valid Cases	16		

a. 24 cells (100.0%) have expected count less than 5. The minimum expected count is .06.

Visus Masuk * Gram bakteri

Crosstab

	Gram bakteri	Total

			Tidak teridentifikasi	Negatif	Positif	
Visus Masuk	1/2 /60 counting finger	Count	0	2	0	2
		% within Visus Masuk	0.0%	100.0%	0.0%	100.0%
	1/300 hand wave	Count	1	5	2	8
		% within Visus Masuk	12.5%	62.5%	25.0%	100.0%
	Light perception	Count	0	5	0	5
		% within Visus Masuk	0.0%	100.0%	0.0%	100.0%
	No light perception	Count	0	1	0	1
		% within Visus Masuk	0.0%	100.0%	0.0%	100.0%
Total		Count	1	13	2	16
		% within Visus Masuk	6.3%	81.3%	12.5%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	3.692[a]	6	.718
Likelihood Ratio	4.857	6	.562
Linear-by-Linear Association	.053	1	.818
N of Valid Cases	16		

a. 11 cells (91.7%) have expected count less than 5. The minimum expected count is .06.

Visus Masuk * Pseudomonas

			Pseudomonas		Total
			Tidak	Ya	
Visus Masuk	1/2 /60 counting finger	Count	1	1	2
		% within Visus Masuk	50.0%	50.0%	100.0%
	1/300 hand wave	Count	7	1	8

		% within Visus Masuk	87.5%	12.5%	100.0%
	Light perception	Count	1	4	5
		% within Visus Masuk	20.0%	80.0%	100.0%
	No light perception	Count	0	1	1
		% within Visus Masuk	0.0%	100.0%	100.0%
Total		Count	9	7	16
		% within Visus Masuk	56.3%	43.8%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	7.162[a]	3	.067
Likelihood Ratio	8.125	3	.043
Linear-by-Linear Association	3.193	1	.074
N of Valid Cases	16		

a. 8 cells (100.0%) have expected count less than 5. The minimum expected count is .44.

Status refraksi * PCR bakteri

			PCR bakteri						
			Unidentified	Psudomonas auruginosa	Zavarzinia sp	Brevundimonas vesicularis	Bacillus subtilis	Novosphingobium sp	Total
Status refraksi	Tetap	Count	0	5	1	0	0	0	6
		% within Status refraksi	0.0%	83.3%	16.7%	0.0%	0.0%	0.0%	100.0%
	Membaik	Count	1	2	3	1	2	1	10
		% within Status refraksi	10.0%	20.0%	30.0%	10.0%	20.0%	10.0%	100.0%
Total		Count	1	7	4	1	2	1	16
		% within Status refraksi	6.3%	43.8%	25.0%	6.3%	12.5%	6.3%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	6.705[a]	5	.244
Likelihood Ratio	8.296	5	.141
Linear-by-Linear Association	2.957	1	.086
N of Valid Cases	16		

a. 12 cells (100.0%) have expected count less than 5. The minimum expected count is .38.

Status refraksi * Gram bakteri

			Gram bakteri			
			Tidak teridentifikasi	Negatif	Positif	Total
Status refraksi	Tetap	Count	0	6	0	6
		% within Status refraksi	0.0%	100.0%	0.0%	100.0%
	Membaik	Count	1	7	2	10
		% within Status refraksi	10.0%	70.0%	20.0%	100.0%
Total		Count	1	13	2	16
		% within Status refraksi	6.3%	81.3%	12.5%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	2.215[a]	2	.330
Likelihood Ratio	3.225	2	.199
Linear-by-Linear Association	.191	1	.662
N of Valid Cases	16		

a. 5 cells (83.3%) have expected count less than 5. The minimum expected count is .38.

Infeksi jamur * Status refraksi

Crosstab

			Status refraksi		
			Tetap	Membaik	Total
Infeksi jamur	Tidak	Count	3	5	8
		% within Infeksi jamur	37.5%	62.5%	100.0%
	Ya	Count	3	5	8
		% within Infeksi jamur	37.5%	62.5%	100.0%
Total		Count	6	10	16
		% within Infeksi jamur	37.5%	62.5%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.000[a]	1	1.000		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.000	1	1.000		
Fisher's Exact Test				1.000	.696
Linear-by-Linear Association	.000	1	1.000		
N of Valid Cases	16				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.00.

b. Computed only for a 2x2 table

Lesi * Pseudomona

Crosstab

			Pseudomonas		
			Tidak	Ya	Total
Lesi	tidak dilakukan	Count	0	2	2
		% within Lesi	0.0%	100.0%	100.0%

	Point like lesion	Count	1	0	1
		% within Lesi	100.0%	0.0%	100.0%
	Membran like lesion	Count	7	1	8
		% within Lesi	87.5%	12.5%	100.0%
	hiperechoic debris cavum vitreus	Count	1	1	2
		% within Lesi	50.0%	50.0%	100.0%
	T -Sign , pachychoroid	Count	0	2	2
		% within Lesi	0.0%	100.0%	100.0%
	V-shape , after movement (-)	Count	0	1	1
		% within Lesi	0.0%	100.0%	100.0%
Total		Count	9	7	16
		% within Lesi	56.3%	43.8%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	10.413[a]	5	.064
Likelihood Ratio	13.129	5	.022
Linear-by-Linear Association	.714	1	.398
N of Valid Cases	16		

a. 12 cells (100.0%) have expected count less than 5. The minimum expected count is .44.

Onset * PCR bakter

Crosstab

		PCR bakteri						
		Unidentified	Psudomonas aurugino sa	Zavarzinia sp	Brevundimonas vesicularis	Bacillus subtilis	Novosphingobium sp	Total
	Count	0	1	1	0	0	1	3

Onset	1-3 hari	% within Onset	0.0%	33.3%	33.3%	0.0%	0.0%	33.3%	100.0%
	4-7 hari	Count	0	0	1	0	0	0	1
		% within Onset	0.0%	0.0%	100.0%	0.0%	0.0%	0.0%	100.0%
	8-14 hari	Count	0	6	0	0	1	0	7
		% within Onset	0.0%	85.7%	0.0%	0.0%	14.3%	0.0%	100.0%
	15-28 hari	Count	0	0	1	1	1	0	3
		% within Onset	0.0%	0.0%	33.3%	33.3%	33.3%	0.0%	100.0%
	29-42 hari	Count	1	0	1	0	0	0	2
		% within Onset	50.0%	0.0%	50.0%	0.0%	0.0%	0.0%	100.0%
Total		Count	1	7	4	1	2	1	16
		% within Onset	6.3%	43.8%	25.0%	6.3%	12.5%	6.3%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	27.660[a]	20	.118
Likelihood Ratio	25.920	20	.168
Linear-by-Linear Association	.540	1	.462
N of Valid Cases	16		

a. 30 cells (100.0%) have expected count less than 5. The minimum expected count is .06.

Onset * Gram bakteri

Crosstab

			Gram bakteri			Total
			Tidak teridentifikasi	Negatif	Positif	

Onset	1-3 hari	Count	0	3	0	3
		% within Onset	0.0%	100.0%	0.0%	100.0%
	4-7 hari	Count	0	1	0	1
		% within Onset	0.0%	100.0%	0.0%	100.0%
	8-14 hari	Count	0	6	1	7
		% within Onset	0.0%	85.7%	14.3%	100.0%
	15-28 hari	Count	0	2	1	3
		% within Onset	0.0%	66.7%	33.3%	100.0%
	29-42 hari	Count	1	1	0	2
		% within Onset	50.0%	50.0%	0.0%	100.0%
Total		Count	1	13	2	16
		% within Onset	6.3%	81.3%	12.5%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	9.319[a]	8	.316
Likelihood Ratio	6.928	8	.544
Linear-by-Linear Association	.213	1	.645
N of Valid Cases	16		

a. 14 cells (93.3%) have expected count less than 5. The minimum expected count is .06.

crosstab

			Pseudomonas		
			Tidak	Ya	Total
Onset	1-3 hari	Count	2	1	3
		% within Onset	66.7%	33.3%	100.0%
	4-7 hari	Count	1	0	1
		% within Onset	100.0%	0.0%	100.0%
	8-14 hari	Count	1	6	7
		% within Onset	14.3%	85.7%	100.0%

	15-28 hari	Count	3	0	3
		% within Onset	100.0%	0.0%	100.0%
	29-42 hari	Count	2	0	2
		% within Onset	100.0%	0.0%	100.0%
Total		Count	9	7	16
		% within Onset	56.3%	43.8%	100.0%

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	9.808[a]	4	.044
Likelihood Ratio	12.369	4	.015
Linear-by-Linear Association	.635	1	.426
N of Valid Cases	16		

a. 10 cells (100.0%) have expected count less than 5. The minimum expected count is .44.

			Lesi						
			tidak dilakukan	Point like lesion	Membran like lesion	hiperechoic debris cavum vitreus	T -Sign , pachychoroid	V-shape , after movement (-)	Total
Infeksi jamur	Tidak	Count	1	0	5	2	0	0	8
		% within Infeksi jamur	12.5%	0.0%	62.5%	25.0%	0.0%	0.0%	100.0%
	Ya	Count	1	1	3	0	2	1	8
		% within Infeksi jamur	12.5%	12.5%	37.5%	0.0%	25.0%	12.5%	100.0%
Total		Count	2	1	8	2	2	1	16
		% within Infeksi jamur	12.5%	6.3%	50.0%	12.5%	12.5%	6.3%	100.0%

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	6.500[a]	5	.261

Likelihood Ratio	8.823	5	.116
Linear-by-Linear Association	.556	1	.456
N of Valid Cases	16		

a. 12 cells (100.0%) have expected count less than 5. The minimum expected count is .50.

IDENTIFIKASI BAKTERI 16sRNA

1. SAMPEL NO. 1

Pseudomonas aeruginosa strain SAM10 16S ribosomal RNA gene, partial sequence
Sequence ID: ON563466.1Length: 1478Number of Matches: 1
Range 1: 46 to 1281GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
2178 bits(1179)	0.0	1217/1236(98%)	5/1236(0%)	Plus/Plus

```
Query  10    GCNTGCT-
CTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTG  68
             || |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  46
GCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTG  105

Query  69
GGGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGG  128
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  106
GGGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGG  165

Query  129
ATCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAA  188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166   ATCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAA
225

Sbjct  1126
TGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCT  1185

Query  1147  ACCACGTGCTACATGGTCGGTACAAA-
GGTTGCCAACCGCCAGGTGGAACTAATCCCNTA  1205
             |||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||  |
Sbjct  1186
ACCACGTGCTACATGGTCGGTACAAAGGGTTGCCAACCGCGAGGTGGAACTAATCCCTAA  1245

Query  1206  AACCCATCTTATTCGGATCC-ATCTGCACTCCACTG  1240
             |||| ||| | | ||||||| ||||||| |||||||
Sbjct  1246  AACCGATCGTGTCCGGATCCAATCTGCAATCCACTG  1281
```

2. SAMPEL NO. 2

Pseudomonas aeruginosa strain PSH42 16S ribosomal RNA gene, partial sequence
Sequence ID: ON563234.1Length: 1396Number of Matches: 1
Range 1: 48 to 1340GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
2187 bits(1184)	0.0	1260/1294(97%)	17/1294(1%)	Plus/Plus

```
Query  12    CTTGCT-
CTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGG  70
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  48
CTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGG  107

Query  71
GGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGGA  130
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  108
GGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGGA  167

Query  131
TCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAAG  190
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  168   TCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAAG
227

Query  191
GCCTACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGA  250
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  228
GCCTACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGA  287

Query  251
GACACGGTCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGC  310
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  288
GACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGC  347

Query  311
CTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTG  370
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  348   CTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTG
407
```

3. SAMPEL NO.3

Pseudomonas aeruginosa strain Y12 16S ribosomal RNA gene, partial sequence
Sequence ID: MH997635.1Length: 1470Number of Matches: 1
Range 1: 37 to 1276GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
2163 bits(1171)	0.0	1218/1240(98%)	10/1240(0%)	Plus/Plus

```
Query  8
AAGGGNACTNGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTG  67
         |||||  || ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  37
AAGGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTG  96

Query  68
GTAGTGGGGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAG  127
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  97
GTAGTGGGGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAG  156

Query  128
TGGGGGATCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGG  187
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  157
TGGGGGATCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGG  216

Query  668
CTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCT  727
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  697
CTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCT  756

Query  728
GGTAGTCCACGCCGTAAACGATGTCGACTAGCCGTTGGGATCCTTGAGATCTTAGTGGCG  787
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  757
GGTAGTCCACGCCGTAAACGATGTCGACTAGCCGTTGGGATCCTTGAGATCTTAGTGGCG  816

Query  788
CAGCTAACGCGATAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGA  847
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  817
CAGCTAACGCGATAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGA  876

Query  848
ATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAA  907
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  877
ATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAA  936

Query  908
CCTTACCTGGCCTTGACATGCTGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACT  967
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

4. SAMPEL NO 4

Zavarzinia sp. strain K1W42B-24 16S ribosomal RNA gene, partial sequence
Sequence ID: MK592783.1Length: 1359Number of Matches: 1
Range 1: 21 to 760GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
686 bits(371)	0.0	624/747(84%)	14/747(1%)	Plus/Plus

```
Query  5    TTCGG--AGG-GTGGCGGACGGGTGAGTAACACGTGGGATTCTGCCCTTAGGTGCGGGAT
61
        |||||  ||| ||||||||||||||||||||||||||||  ||||||  |||| ||||||
Sbjct  21
TTCGGACAGGCGTGGCGGACGGGTGAGTAACACGTGGGAACCTGCCCCGAGGTACGGGAT  80

Query  62   AACCCGGGGAAACTTGGGATAATACCGCATG-ATCTCTGAAGATCAAAGATTGATCCCCT
120
        ||||| ||||||||||||| ||||||| |||   | |||| | | ||||||| ||| |||
Sbjct  81   AACCCAGGGAAACTTGGGACAATACCGTATGTGAC-CTGAGGGTGAAAGATTCATCGCCT
139

Sbjct  380
CCAAAGAAGAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAG  439

Query  421  CTCTGTTCGGAATGACTGGGCGTAAAGGGCG-GTGCGGCGGTTGATCAAATTTACTCTGA
479
        |  |||||||||||||||||||||||||||| ||  ||||||||||||| ||     |||
Sbjct  440  CGTTGTTCGGAATGACTGGGCGTAAAGGGCGCGT-
AGGCGGTTGATCAAGTTGGGGGTGA  498

Query  480
AAGCCCGGGGCTTAACCTCGGAATTGCCTTCGATACTGGTCCCCTTGGCTGTGGAAGAGG  539
        ||||||||||||||||||||||||||||||| | |||||||  ||||  |||||||||||
Sbjct  499
AAGCCCGGGGCTTAACCTCGGAATTGCCTTCAAGACTGGTCAGCTTGAGTGTGGAAGAGG  558

Query  540  ACTGTGGAATTCCCAGTGTAAAGGTAAAATTCTAAAATATTGCGAAAAACACCATGTGCC
599
           ||||||||||||||||| |||| ||||||  | |||||| ||| ||||||| ||| |
Sbjct  559  GTCGTGGAATTCCCAGTGTAGAGGTGAAATTCGTAGATATTGGGAAGAACACCA-GTGGC
617

Query  600  -AATGCGACGACCTGATATCATTACTGAACCTCAATGCGCGAAAGCGTGCGGGACCAGAC
658
         || ||||||||||| |  ||||||||  || |  |||||| |||||| |||| || ||
Sbjct  618  GAAGGCGACGACCTGGTC-CATTACTGACGCTGAG-GCGCGACAGCGTG-GGGAGCAAAC
674

Query  659  TGGATTAAATACCCTGGTAGTCCACGCCGGAAACGAAGAAGACTAGATATTCGGCGGTTT
718
         |||||| ||||||||||||||||||||| |||||| ||   || ||| || |||||||
Sbjct  675  AGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTGGATGTTGGGCGGTTG
734

Query  719  TCCGCT-GTTGTCGATGATAACTCGAT  744
         |||||   |||||| | |||| ||||
Sbjct  735  -CCGCTCAGTGTCGAAGTTAACGCGAT  760
```

5. SAMPEL NO. 5

Zavarzinia sp. strain K1W22B-18 16S ribosomal RNA gene, partial sequence
Sequence ID: MK592784.1Length: 1361Number of Matches: 1
Range 1: 34 to 722GenBankGraphicsNext MatchPrevious Match
Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
712 bits(385)	0.0	591/692(85%)	7/692(1%)	Plus/Plus

```
Query  20   GGCGG-
CGGGTGAGTAACACGTGGGATCCTGCCCTTAGGTGCGGGATAACCCGGGGAAAC  78
            ||||| |||||||||||||||||||| |||||||  |||| ||||||||||| |||||||
Sbjct  34
GGCGGACGGGTGAGTAACACGTGGGAACCTGCCCCGAGGTACGGGATAACCCAGGGAAAC  93

Query  79   TTGGGATAATACCGCATG-ATCTCTTAAGATCAAAGATTCATCCCCTTTGGATGGGCCCG
137
            |||||| ||||||| |||   | || | | | ||||||||||| |||| |||||||||||
Sbjct  94   TTGGGACAATACCGTATGTGAC-CTGAGGGTGAAAGATTCATCGCCTTGGGATGGGCCCG
152

Query  138
CTTCGGAATACGTACTTGGGGAGGTATTGGCTCACCGGTCCTACGATCCCTAGGTGGTCT  197
            | ||||| || ||| ||||   ||||  |||  |||   |||||||||| ||| ||||||
Sbjct  153  CGTCGGATTAGGTAGTTGGTAGGGTAAAGGCCTACCAAGCCTACGATCCGTAGCTGGTCT
212

Query  198
GAGAGGATTATCATCCACACTGGGACTGACACACCGCCCATACTCCTACGGGAGGCCTCA  257
            |||||||| |||| ||||||||||||||| |||| ||||| |||||||||||||||  ||
Sbjct  213
GAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA  272
```

6. SAMPEL NO. 6

Pseudomonas aeruginosa strain Huaian_204_1 16S ribosomal RNA gene, partial sequence
Sequence ID: MN314687.1Length: 995Number of Matches: 1
Range 1: 23 to 223GenBankGraphicsNext MatchPrevious Match
Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
355 bits(192)	3e-93	199/202(99%)	1/202(0%)	Plus/Plus

```
Query  9
GCTTGGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGT  68
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23   GCTT-GCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGT
81

Query  69
GGGGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGG  128
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  82
GGGGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGG  141

Query  129
GATCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAC  188
```

```
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  142  GATCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA
201

Query  189  CGGCCTACCAAGGCGACCATCC  210
           ||||||||||||||||| ||||
Sbjct  202  CGGCCTACCAAGGCGACGATCC  223
```

7. SAMPEL NO. 7

Pseudomonas aeruginosa strain XB3 16S ribosomal RNA gene, partial sequence

Sequence ID: ON795990.1Length: 1268Number of Matches: 1

Range 1: 1 to 1261GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
2200 bits(1191)	0.0	1245/1270(98%)	14/1270(1%)	Plus/Pl

```
Query  23
GATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGATAACGT  82
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGATAACGT
60

Query  83
CCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGGATCTTCGGACC  142
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61
CCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGGATCTTCGGACC  120

Query  143
TCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAG  202
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

8. SAMPEL NO. 8

Zavarzinia sp. strain K1W22B-18 16S ribosomal RNA gene, partial sequence

Sequence ID: MK592784.1Length: 1361Number of Matches: 1

Range 1: 32 to 711GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
490 bits(265)	5e-133	552/694(80%)	19/694(2%)	Plus/Plus

```
Query  14
GTGGCGGACGGGTGAGTAATAACGTGTGAATTCCTGCCCTTAGGTNNGGGATAACCCGGG  73
           |||||||||||||||||||  ||||| |||  |||||||  ||||  |||||||||| ||
Sbjct  32   GTGGCGGACGGGTGAGTAA-CACGTGGGAA--CCTGCCCCGAGGTACGGGATAACCCAGG
88

Query  74   GAAACTTCGGGCTAATACCGCATGATCTCTTGA-GATCAAAGATTGATCCCCCTTGGATG
132
           ||||||| || | ||||||| ||| |  | ||| | | ||||||| ||| || | |||||
Sbjct  89   GAAACTTGGGAC-AATACCGTATG-TGACCTGAGGGTGAAAGATTCATCGCCTTGGGATG
146
```

```
Query  133  GGCCCGCTTCGGATTACCTATTTGGGGTTGTNNTGG-CTCTCAGGTCCTACCATCCCTAG
191
            ||||||| ||||||||  || ||||    ||   || ||  || | ||||| |||| |||
Sbjct  147  GGCCCGCGTCGGATTAGGTAGTTGGTAGGGTAAAGGCCTACCAAG-CCTACGATCCGTAG
205

Query  192
GTGGTCTGACAGGATTATCCTCCNNANTGGGACTGACACACCGCCCATACTCCTACGGGA  251
             |||||||| ||||| |||  ||  | ||||||||| |||| ||||| ||||||||||||
Sbjct  206
CTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGA  265

Query  252
GGCCTCCTTGGGGAATATTGGACGATGGGCATAAGCCTGATCCCGCAATGCCGCGTGAGT  311
            |||  |  ||||||||||||||| ||||||  ||||||||||| ||||||||||||||||
Sbjct  266
GGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCAATGCCGCGTGAGT  325

Query  312  GATGAAGGCCTT-GTGAT-TAAAGACCTCTTTCTGCGGGGAACATTATGACGGTACCaaa
369
            |||||||||||| | | | ||||| | ||||||   |||||  || ||||||||||| ||
Sbjct  326  GATGAAGGCCTTAGGGTTGTAAAG-C-TCTTTCGTTGGGGACGATGATGACGGTACCCAA
383

Query  370  aaaaTATGCCCCGGATAACTTCGTGCCACCGTCCGCGCTAATACAAAGGGGGCTAGCTCT
429
            | || | ||||||| ||||||||||||| |  ||||| |||||| ||||||||||||  |
Sbjct  384
AGAAGAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCGTT  443

Query  430  GTTCGGAATGACTGGGCATAAAGGACGCGTAGGCGGTTTATCAAATTTACTGGTGAATGC
489
            ||||||||||||||||| |||||| ||||||||||||| ||||| ||    |||||| ||
Sbjct  444  GTTCGGAATGACTGGGCGTAAAGGGCGCGTAGGCGGTTGATCAAGTTGGG-
GGTGAAAGC  502

Query  490  ACCGGGGCTCAACTGCGGAATTGCCTTTGATACTGGATCC-
CTTGACTGTGGAAGAGGGC  548
             |||||||| |||  ||||||||||||  | |||||  ||  ||||| ||||||||||||
Sbjct  503  -CCGGGGCTTAACCTCGGAATTGCCTTCAAGACTGG-TCAGCTTGAGTGTGGAAGAGGGT
560
```

9. SAMPEL NO. 9

Pseudomonas aeruginosa strain PSH7 16S ribosomal RNA gene, partial sequence
Sequence ID: ON563192.1Length: 1422Number of Matches: 1
Range 1: 50 to 1367GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
2006 bits(1086)	0.0	1243/1322(94%)	12/1322(0%)	Plus/Plus

```
Query  8    CTTGCT-CTGGATTC-GCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGG
65
            |||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct  50
CTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGG  109

Query  66
GGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGGA  125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110
GGGATAACGTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGGA  169

Query  126
TCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAAG  185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170   TCTTCGGACCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAAG
229

Query  186
GCCTACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGA  245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  230
GCCTACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGA  289

            |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||
Sbjct  530
GGGCGTAAAGCGCGCGTAGGTGGTTCAGCAAGTTGGATGTGAAATCCCCGGGCTCAACCT  589

Query  546
GGGAACTGCATCCAAAACTACTGAGCTAGAGTACGGAAAACGGTGGTGGAATTTCCTGTG  605
            |||||||||||||||||||||||||||||||||||| | | |||||||||||||||||||
Sbjct  590
GGGAACTGCATCCAAAACTACTGAGCTAGAGTACGGTAGAGGGTGGTGGAATTTCCTGTG  649

Query  606
TACCGGTGAAATGCTTACATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACT  665
            || ||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Sbjct  650
TAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACT  709

Query  666
GATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTATATACCCTGGTAGTC  725
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  710
GATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTC  769
```

10. SAMPEL NO. 10

Zavarzinia sp. strain K1W22B-18 16S ribosomal RNA gene, partial sequence
Sequence ID: MK592784.1Length: 1361Number of Matches: 1
Range 1: 35 to 702GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
586 bits(317)	3e-162	554/670(83%)	10/670(1%)	Plus/Plus

```
Query  17   GCGGAC-GGTGAGT-ACACGT-GGATTCTGCCCTTAGGTGCGGGATAACCCGGGGAAACT
73
            |||||| ||||||| |||||| |||  ||||||  |||| ||||||||||| ||||||||
Sbjct  35
GCGGACGGGTGAGTAACACGTGGGAACCTGCCCCGAGGTACGGGATAACCCAGGGAAACT  94

Query  74   TGGGATAATACCGTATGAGCTCTGGGGATGAAAGATTCATCCCCCTTGGATGGGCCCGCT
133
            ||||| ||||||||||| |  ||| || ||||||||||||| || | ||||||||||||
Sbjct  95   TGGGACAATACCGTATGTGACCTGAGGGTGAAAGATTCATCGCCTTGGGATGGGCCCGCG
154

Query  134
TCGGAATACCTACTTGGGGAGGTATTGGCTCACCGGTCCTGCGATCCCTAGGTGGTCTGA  193
            ||||| ||  || ||||   ||||  |||  |||   ||| |||||| ||| ||||||||
Sbjct  155  TCGGATTAGGTAGTTGGTAGGGTAAAGGCCTACCAAGCCTACGATCCGTAGCTGGTCTGA
214

Query  194
GAGGATTATCCTCCACGCTGGGACTGACACACCGCCCATACTCCTACGGGAGGACTCCTT  253
            |||||| |||  |||| |||||||||| |||| ||||| ||||||||||||||   |  |
```

11. SAMPEL NO. 11

Bacillus sp. NFN149 partial 16S rRNA gene, strain NFN149
Sequence ID: LK936596.1Length: 626Number of Matches: 1
Range 1: 446 to 622GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
128 bits(69)	4e-24	141/177(80%)	0/177(0%)	Plus/Plus

```
Query  416  ACCTTGCCAAAAAACCGGGGCTAACTACCGGCCAGCACCCTCGGTAATACTTATGTGGCA
475
            ||||  ||| ||| ||  ||||||||||  |||| || || ||||||||| || ||||||
Sbjct  446  ACCTAACCAGAAAGCCACGGCTAACTACGTGCCACCAGCCGCGGTAATACGTAGGTGGCA
505

Query  476  ACCGTTTGCCCGAATTATTGGGTGTATTGGACTCTCAAGCGCTTTCTTAAATCTGAGGTG
535
            | ||||  || ||||||||||| |||  |  | | |||||| |||||||| ||||| |||
Sbjct  506  AGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAAGCGGTTTCTTAAGTCTGATGTG
565

Query  536  AGCGCCCCCTGCTCTGTCGCGGAAGTTCATTGGAAACTGGGGAACTTCAGTGCGGAA
592
            |  |||||| ||||   || ||| | |||||||||||||||||||||||||||||||
Sbjct  566  AAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGGAACTTCAGTGCGGAA
622
```

12. SAMPEL NO. 12

Novosphingobium sp. Y3-5 16S ribosomal RNA gene, partial sequence
Sequence ID: KT452772.1Length: 1349Number of Matches: 1
Range 1: 19 to 739GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
771 bits(417)	0.0	630/733(86%)	13/733(1%)	Plus/Plus

```
Query  1    GGG-CTAGTGGCGGCACGGGTGAGTAACACGTGGGAATTCTGCCCTTATGTACGGGATAA
59
            ||| |||||||| ||||||||| ||||| |||||||| |||||||||  || ||| ||||
Sbjct  19   GGGTCTAGTGGC-GCACGGGTGCGTAACGCGTGGGAA-TCTGCCCTTGGGTTCGGAATAA
76

Query  60   CCCGGGAGAAACTTCGGGGCTAATACCGCATGATCTCTTCAGATCAAAGATTTAGCCCCC
119
            |  | |||||| || |  |||||||||| ||||| ||||| || |||||||||| | |||
Sbjct  77   C-AGTGAGAAA-TT-GCTGCTAATACCGGATGATGTCTTCGGACCAAAGATTTATCGCCC  133

Query  120  TTGGATGAGCCCGCTTCGGATTACCTATTTGGTGGGGTATTGGCTTACCAGTGCTACGAT
179
            |||||||||||| | |||||| ||| ||||||||||| |||| |||||  || |||||
Sbjct  134  AGGGATGAGCCCGCGTAGGATTAGCTAGTTGGTGGGGTAATGGCCTACCAAGGCGACGAT
193

Query  180
CCTTAGCTGGTCTGAGAGGATGATCCTCCACGCTGGGACTGACACACGGCCCATACTCCT  239
            |||||||||||||||||||||||||  |||| |||||||||| |||||||||| ||||||
```

13. SAMPEL NO. 13

Brevundimonas vesicularis strain TK026 16S ribosomal RNA gene, partial sequence
Sequence ID: MK045801.1Length: 1323Number of Matches: 1
Range 1: 21 to 1248GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
2117 bits(1146)	0.0	1203/1228(98%)	15/1228(1%)	Plus/Plus

```
Query  11
AGTGGCGGACGGGTGAGTAACACGTGGGAACGTGCCTTTAGGTTCGGAATAACTCAGGGA  70
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21
AGTGGCGGACGGGTGAGTAACACGTGGGAACGTGCCTTTAGGTTCGGAATAACTCAGGGA  80

Query  71   AACTTGAGCTAATACCGGATGTGCCCTTCGGGGGAAAGATTTATCGCCTTTAGAGCGGCC
130
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81   AACTTGAGCTAATACCGGATGTGCCCTTCGGGGGAAAGATTTATCGCCTTTAGAGCGGCC
140

Query  131
CGCGTCTGATTAGCTAGTTGGTGAGGTAAAGGCTCACCAAGGCGACGATCAGTAGCTGGT  190
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141
CGCGTCTGATTAGCTAGTTGGTGAGGTAAAGGCTCACCAAGGCGACGATCAGTAGCTGGT  200

Query  191
CTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAG  250
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

14. SAMPEL NO. 15

Bacillus subtilis strain 2014-3557 plasmid pGMrib, complete sequence
Sequence ID: CP045673.1Length: 38647Number of Matches: 1
Range 1: 31941 to 32406GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
551 bits(298)	9e-153	411/466(88%)	5/466(1%)	Plus/Plus

```
Query  133    GTGTGAAATTGTTATCCGCTCACAATTCCTCACAGCATTC-ATCCGGAAGCATAAATTGT
191
              ||||||||||||||||||||||||||||| |||| ||| | | ||||||||||||| |||
Sbjct  31941
GTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGT  32000

Query  192
AAAGCCTGGGGTGCCTAATGAGTGAGGTACGTCACATTAATTGCTTTGCTCTCACAGGCC  251
              |||||||||||||||||||||||||| ||  ||||||||||||| |||| ||||| | ||
Sbjct  32001
AAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCC  32060

Query  252    GCTTTCC-GTCGGGAAACCTGTCggggggggTGGATTAATGAATCGGCCAATTGGCTGGT
310
              ||||||| |||||||||||||||| |   | || |||||||||||||||||   || ||
Sbjct  32061
GCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGG  32120

Query  311    ATATGCGGTTTGCGTGTTGGGTGCTCTTCCGGTTCCTC-
CTCACTTACTCGCTGCGCTCG  369
              | | ||||||||||| ||||| ||||||||| |||||| |||||| ||||||||||||||
```

15. SAMPEL NO. 16

Pseudomonas aeruginosa strain E11 16S ribosomal RNA gene, partial sequence
Sequence ID: MN733280.1Length: 1379Number of Matches: 1
Range 1: 16 to 1298GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
2226 bits(1205)	0.0	1259/1284(98%)	16/1284(1%)	Plus/Plus

```
Query  13    CTTGCT-
CTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGG  71
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16
CTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGG  75

             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  196
GCCTACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGA  255

Query  252
GACACGGTCCAGACTCCTACGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGC  311
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  256
GACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGC  315

Query  312
CTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTG  371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  316   CTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTG
375
```

IDENTIFIKASI GEN (JAMUR)

1. SAMPEL NO. 1

Not Identified

2. SAMPEL NO. 2

Microsporum canis strain No NCCPF 200011 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: KY801942.1Length: 705Number of Matches: 1

Range 1: 5 to 53GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
62.6 bits(68)	8e-09	43/49(88%)	0/49(0%)	Plus/Minus

```
Query  622  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACACTTTTTACTT  670
            ||||||  |||||||||| |||||||  |||||||||| ||||||||||
Sbjct  53   TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGCTTTTTACTT  5
```

Arthroderma multifidum genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2 and 28S rRNA, partial and complete sequence, isolate: 206MOK589NPORAM

Sequence ID: AB861853.1Length: 629Number of Matches: 1

Range 1: 3 to 51GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
58.1 bits(63)	4e-07	42/49(86%)	0/49(0%)	Plus/Minus

```
Query  622  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACACTTTTTACTT  670
            ||||||  |||||||||| |||||||  ||||||||||  |||||||||
Sbjct  51   TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGATTTTTACTT  3
```

3. SAMPEL NO.3

Arthroderma multifidum genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2 and 28S rRNA, partial and complete sequence, isolate: 117MOK395SPKJAM

Sequence ID: AB861765.1Length: 629Number of Matches: 1

Range 1: 4 to 51GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	**Expect**	**Identities**	**Gaps**	**Strand**

65.3 bits(71)	**3e-09**	**43/48(90%)**	**0/48(0%)**	**Plus/Minus**

```
Query  673  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACAACTTTTACT  720
            ||||||  |||||||||| |||||||  ||||||||||||||||||||
Sbjct  51   TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACAACTTTTACT  4
```

Trichophyton tonsurans isolate 1645 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MN295945.1Length: 1461Number of Matches: 1

Range 1: 162 to 209GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
62.6 bits(68)	9e-09	42/48(88%)	0/48(0%)	Plus/Minus

```
Query  673  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACAACTTTTACT  720
            ||||||  |||||||||| |||||||  |||||||||| |||||||||
Sbjct  209  TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACRACTTTTACT  162
```

Nannizzia gypsea isolate J2402 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: PP980712.1Length: 691Number of Matches: 1

Range 1: 5 to 52GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
60.8 bits(66)	3e-08	42/48(88%)	0/48(0%)	Plus/Minus

```
Query  673  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACAACTTTTACT  720
            ||||||  |||||||||| |||||||  |||||||||| |||||||||
Sbjct  52   TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTACT  5
```

4. SAMPEL NO 4

Not identified

5. SAMPEL NO. 6

Microsporum canis strain No NCCPF 200012 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: KY801943.1Length: 705Number of Matches: 1

Range 1: 2 to 52GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	**Expect**	**Identities**	**Gaps**	**Strand**
70.7 bits(77)	**6e-11**	**46/51(90%)**	**0/51(0%)**	**Plus/Minus**

```
Query  679  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACGACTTTTTACTTA  729
            ||||||  |||||||||| |||||||  |||||||||||||||||||||||
Sbjct  52   TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTTACTTA  2
```

Trichophyton interdigitale isolate NCCPF:800055 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MH517558.1Length: 709Number of Matches: 1

Range 1: 4 to 53GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
68.9 bits(75)	2e-10	45/50(90%)	0/50(0%)	Plus/Minus

```
Query  679  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACGACTTTTTACTT  728
            |||||| |||||||||| ||||||| ||||||||||||||||||||||
Sbjct  53   TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTTACTT  4
```

6. SAMPEL NO. 7

Trichophyton rubrum genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene

Sequence ID: OW988659.1Length: 717Number of Matches: 1

Range 1: 3 to 52GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
68.9 bits(75)	2e-10	45/50(90%)	0/50(0%)	Plus/Minus

```
Query  678  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACGACTTTTACTTA  727
            |||||| |||||||||| ||||||| ||||||||||||||||||||||
Sbjct  52   TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTACTTA  3
```

7. SAMPEL NO. 8

Not identified

8. SAMPEL NO. 9

Trichophyton tonsurans strain CEMM-01-3-090 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: MN704386.1Length: 670Number of Matches: 1

Range 1: 4 to 54GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
61.7 bits(67)	3e-08	44/51(86%)	0/51(0%)	Plus/Minus

```
Query  677  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACGAACTTTTTACTT  727
            |||||| |||||||||| ||||||| |||||||||||| |||||||||
Sbjct  54   TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTTTACTT  4
```

9. SAMPEL NO. 10

Not identified

10. SAMPEL NO. 14

Not Identified

11. SAMPEL NO. 11 NOT IDENTIFIED

12. SAMPEL NO. 12 NOT IDENTIIFE

13. SAMPEL NO. 13 NOT IDENTIFIED

14. SAMPEL NOT IDENTIFIED

15. NO. 15 NOT IDENTIFIED

16. SAMPEL NO. 16

Trichophyton rubrum genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene

Sequence ID: OW988659.1Length: 717Number of Matches: 1

Range 1: 3 to 52GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
68.9 bits(75)	2e-10	45/50(90%)	0/50(0%)	Plus/Minus

```
Query  676  TGATCCAGCCGCAGGTTCCCCTACGGCTACCTTGTTACGACTTTTACTTA  725
            ||||||  |||||||||| |||||||  ||||||||||||||||||||||
Sbjct  52   TGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTACTTA  3
```