

# MGIEasy Microbiome DNA Extraction Kit /Nucleic Acid Extraction Kit(MD01T-96)

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MGIEasy Microbiome DNA Extraction Kit/Nucleic Acid Extraction Kit(MD01T-96) could efficiently purify the microbial DNA from various samples such as serum, plasma, CSF (cerebrospinal fluid), BALF (alveolar lavage fluid), sputum, bacterial culture fluid, etc. This kit is suitable for the extraction of DNA from gram-negative bacteria, gram-positive bacteria, fungus, DNA viruses, etc.



## High extraction efficiency from various sample types

Extract high quality microbial DNA from various sample types, such as serum, plasma, CFS, BALF, sputum and bacterial culture fluid.



## Low background bacterial pollution for ultraclean production process

Under ultraclean production process, the kit provides high purified DNA for downstream application, especially for pathogen sequencing.



## Automation friendly

Compatible with the high-throughput automated sample preparation system MGISP-960.



## Product Parameter

Name	MGIEasy Microbiome DNA Extraction Kit/Nucleic Acid Extraction Kit(MD01T-96)
Cat.No.	1000027955/ 940-000639-00
Specification	96 preps
Storage Temperature	Proteinase K and Magnetic Beads H are recommended to be stored at 2-8 °C. The other components are stored at room temperature (15~25°C)
Period of Validity	12 months
Compatible Samples	Swab, serum, plasma, CSF (cerebrospinal fluid), BALF (alveolar lavage fluid), sputum, bacterial culture fluid
Compatible Species	bacteria, fungus, viruses
Application	PCR, RT-qPCR, Microarray and sequencing
Compatible Automatic Platform	MGISP-960, 1.5h; Manual, 45min

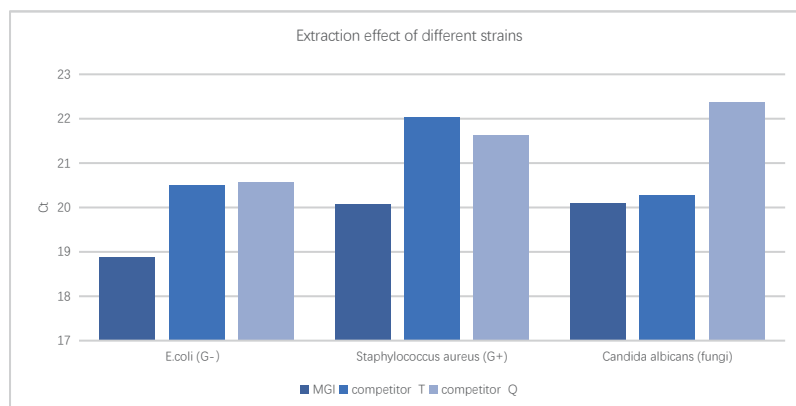


## Order Information

Name	Cat.No.	Model	Specification	Unit	Note
MGIEasy Microbiome DNA Extraction Kit	1000027955	MD01T-96	96 preps	Kit	RUO
Nucleic Acid Extraction Kit	940-000639-00	MD01T-96	96 preps	Kit	CEDoc

## ● High extraction efficiency

Comparing with competitor T and competitor Q, the results showed that MGIEasy microbial DNA extraction kit could efficiently extract microbial DNA from pathogenic bacteria such as E.coli (G-), Staphylococcus aureus (G+), and Candida albicans (fungi). And the extraction effect was better than the competitor.



## ● 2.Suitable for pathogen sequencing

The samples with know microorganism information and the simulated samples with 1% microbial community Meta DNA standard are used as samples. DNA is extracted from MGIEasy Microbiome DNA Extraction Kit, prepared libraries and sequenced on DNBSEQ-G50RS SE50, then analyzed by PFI software. All know microbials including bacteria and fungi are detected. 10 microbials (8 bacteria and 2 fungi) in the standard sample were ranked in top 10 during this identification, which shows the reliability of identification results.

Sample code	Sample type	Sample original pathogen information	Metagenome SE50 Sequencing	
			Detected Reads	Relative abundance
C2	Alveolar lavage fluid	<i>Legionella pneumophila</i>	485	8.930
		<i>Acinetobacter baumannii</i>	18	0.331
		<i>Prevotella melaninogenica</i>	6	0.110
C3	Alveolar lavage fluid	<i>Stenotrophomonas maltophilia</i>	9953	66.531
		<i>Klebsiella pneumoniae</i>	459	3.068
		<i>Klebsiella variicola</i>	401	2.747
		<i>Pseudomonas aeruginosa</i>	411	2.680
		<i>Haemophilus parainfluenzae</i>	62	0.414
		<i>Acinetobacter baumannii</i>	9	0.060
		<i>Human betaherpesvirus 5</i>	50	0.334
C15	sputum	<i>Streptococcus pneumoniae</i>	381	9.568
SH	Meta standard product + human tissue	<i>Lactobacillus fermentum</i>	35977	11.986
		<i>Bacillus subtilis</i>	24372	8.240
		<i>Salmonella enterica</i>	26543	8.813
		<i>Listeria monocytogenes</i>	25890	8.625
		<i>Enterococcus faecalis</i>	29122	9.702
		<i>Staphylococcus aureus</i>	22729	7.572
		<i>Escherichia coli</i>	3114	1.037
		<i>Pseudomonas aeruginosa</i>	3273	1.090
		<i>Cryptococcus neoformans</i>	6936	2.311
		<i>Saccharomyces cerevisiae</i>	4224	1.407

