



Reference list:

NucleoMag® NGS Clean-Up and Size Selection – Efficient Clean-up of PCR products, NGS library preparation reactions, and RNA.

The magnetic bead-based NucleoMag® NGS Clean-Up and Size Select kit is designed for rapid manual and automated clean up and size selection of DNA fragments from a variety of reaction mixtures that are used in the library construction process for next generation sequencing, such as fragmentation, end-repair, A-tailing, Adapter ligation, and PCR amplification mixtures. The following reference list shows latest publications on NucleoMag® NGS Clean-Up and Size Select kit listed by title and publication year of the study, journal, and impact factor.

Please contact us for further information: support@mn-net.com

Title	Year	Journal	Impact Factor	DOI
Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments.	2021	Nature Microbiology	30,964	10.1038/s41564-021-00917-9
The RNA-binding protein RBP33 dampens non-productive transcription in trypanosomes.	2022	Nucleic Acids Research	19,16	10.1093/nar/gkac1123
A novel SHAPE reagent enables the analysis of RNA structure in living cells with unprecedented accuracy.	2021	Nucleic Acids Research	19,16	10.1093/nar/gkaa1255
Genome-wide mapping of SARS-CoV-2 RNA structures identifies therapeutically-relevant elements.	2020	Nucleic Acids Research	19,16	10.1093/nar/gkaa1053
Diurnal oscillations in gut bacterial load and composition eclipse seasonal and lifetime dynamics in wild meerkats.	2021	Nature Communications	17,69	10.1038/s41467-021-26298-5
Histone variant H2A.Z regulates zygotic genome activation.	2021	Nature Communications	17,69	10.1038/s41467-021-27125-7
Unique properties of a subset of human pluripotent stem cells with high capacity for self-renewal.	2020	Nature Communications	17,69	10.1038/s41467-020-16214-8
Wild bees and their nests host Paenibacillus bacteria with functional potential of avail.	2018	Microbiome	14,35	10.1186/s40168-018-0614-1
Geological processes mediate a microbial dispersal loop in the deep biosphere.	2022	Science Advances	14,136	10.1126/sciadv.abn3485
ADAR1 interaction with Z-RNA promotes editing of endogenous double-stranded RNA and prevents MDA5-dependent immune activation.	2021	Cell Reports	9,995	10.1016/j.celrep.2021.109500
Epigenetic priming of immune/inflammatory pathways activation and abnormal activity of	2022	Cell Death & Disease	8,469	10.1038/s41419-022-05483-4



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cell cycle pathway in a perinatal model of white matter injury.				
Identification of a transient state during the acquisition of temozolomide resistance in glioblastoma.	2020	Cell Death & Disease	8,469	10.1038/s41419-019-2200-2
Looks can be deceiving: the deceptive milkcaps (<i>Lactifluus</i> , <i>Russulaceae</i>) exhibit low morphological variance but harbour high genetic diversity.	2019	Ima Fungus	8,044	10.1186/s43008-019-0017-3
A Faithful Gut: Core Features of Gastrointestinal Microbiota of Long-Distance Migratory Bats Remain Stable despite Dietary Shifts Driving Differences in Specific Bacterial Taxa.	2021	Microbiology Spectrum	7,698	10.1128/Spectrum.01525-21
Past climate changes, population dynamics and the origin of Bison in Europe.	2016	Bmc Biology	7,431	10.1186/s12915-016-0317-7
An evolutionary functional genomics approach identifies novel candidate regions involved in isoniazid resistance in <i>Mycobacterium tuberculosis</i> .	2021	Communications Biology	6,548	10.1038/s42003-021-02846-z
Low-Dose Pesticide Mixture Induces Accelerated Mesenchymal Stem Cell Aging In Vitro.	2019	Stem Cells (Dayton, Ohio)	6,277	10.1002/stem.3014
Epigenetic modifier SMCHD1 maintains a normal pool of long-term hematopoietic stem cells.	2022	IScience	6,107	10.1016/j.isci.2022.104684
Halophytophthora fluviatilis Pathogenicity and Distribution along a Mediterranean-Subalpine Gradient.	2021	Journal of Fungi (Basel, Switzerland)	5,724	10.3390/jof7020112
Space and Vine Cultivar Interact to Determine the Arbuscular Mycorrhizal Fungal Community Composition.	2020	Journal of Fungi (Basel, Switzerland)	5,724	10.3390/jof6040317
Zinc Supplementation with or without Additional Micronutrients Does Not Affect Peripheral Blood Gene Expression or Serum Cytokine Level in Bangladeshi Children.	2021	Nutrients	5,719	10.3390/nu13103516
Metabolic responses of thermophilic endospores to sudden heat-induced perturbation in marine sediment samples.	2022	Frontiers in Microbiology	5,59	10.3389/fmicb.2022.958417
Choosing the Right Life Partner: Ecological Drivers of Lichen Symbiosis.	2021	Frontiers in Microbiology	5,59	10.3389/fmicb.2021.769304
Microbial Communities Under Distinct Thermal and Geochemical Regimes in Axial and Off-Axis Sediments of Guaymas Basin.	2021	Frontiers in Microbiology	5,59	10.3389/fmicb.2021.633649
Novel <i>Erwinia persicina</i> Infecting Phage Midgardsormr38 Within the Context of Temperate <i>Erwinia</i> Phages.	2020	Frontiers in Microbiology	5,59	10.3389/fmicb.2020.01245
Unaltered Fungal Burden and Lethality in Human CEACAM1-Transgenic Mice During <i>Candida albicans</i> Dissemination and Systemic Infection.	2019	Frontiers in Microbiology	5,59	10.3389/fmicb.2019.02703
Blue Light Sensing in <i>Listeria monocytogenes</i> Is Temperature-Dependent and the Transcriptional Response to It Is Predominantly SigB-Dependent.	2019	Frontiers in Microbiology	5,59	10.3389/fmicb.2019.02497
Plant Identity Shaped Rhizospheric Microbial Communities More Strongly Than Bacterial Bioaugmentation in Petroleum Hydrocarbon-Polluted Sediments.	2019	Frontiers in Microbiology	5,59	10.3389/fmicb.2019.02144
Bleaching-Associated Changes in the Microbiome of Large Benthic Foraminifera of the Great Barrier Reef, Australia.	2018	Frontiers in Microbiology	5,59	10.3389/fmicb.2018.02404

Title	Year	Journal	Impact Factor	DOI
The Biogeographical Distribution of Benthic Roseobacter Group Members along a Pacific Transect Is Structured by Nutrient Availability within the Sediments and Primary Production in Different Oceanic Provinces.	2017	Frontiers in Microbiology	5,59	10.3389/fmicb.2017.02550
Fast and Simple Analysis of MiSeq Amplicon Sequencing Data with MetaAmp.	2017	Frontiers in Microbiology	5,59	10.3389/fmicb.2017.01461
Determination of Technological Parameters and Characterization of Microbiota of the Spontaneous Sourdough Fermentation of Hull-Less Barley.	2021	Foods (Basel, Switzerland)	5,561	10.3390/foods10102253
Grapevine wood microbiome analysis identifies key fungal pathogens and potential interactions with the bacterial community implicated in grapevine trunk disease appearance.	2021	Environmental Microbiome	5,19	10.1186/s40793-021-00390-1
Spermatic Microbiome Characteristics in Infertile Patients: Impact on Sperm Count, Mobility, and Morphology.	2022	Journal of Clinical Medicine	4,964	10.3390/jcm11061505
Impact of Skin Disinfection on Cutaneous Microbiota, before and after Peripheral Venous Catheter Insertion.	2022	Antibiotics (Basel, Switzerland)	4,94	10.3390/antibiotics11091209
Applications of Blocker Nucleic Acids and Non-Metazoan PCR Improves the Discovery of the Eukaryotic Microbiome in Ticks.	2021	Microorganisms	4,926	10.3390/microorganisms9051051
Systematic Affiliation and Genome Analysis of <i>Subtercola vilae</i> DB165T with Particular Emphasis on Cold Adaptation of an Isolate from a High-Altitude Cold Volcano Lake.	2019	Microorganisms	4,926	10.3390/microorganisms7040107
Whole Genome Sequencing of A(H3N2) Influenza Viruses Reveals Variants Associated with Severity during the 2016-2017 Season.	2019	Viruses	4,911	10.3390/v11020108
Phytomanagement of a Lead-Polluted Shooting Range Using an Aromatic Plant Species and Its Effects on the Rhizosphere Bacterial Diversity and Essential Oil Production.	2022	Plants (Basel, Switzerland)	4,658	10.3390/plants11223024
Mitochondrial genome sequencing, mapping, and assembly benchmarking for Culicoides species (Diptera: Ceratopogonidae).	2022	Bmc Genomics	4,56	10.1186/s12864-022-08743-x
Exploring microbiome engineering as a strategy for improved thermal tolerance in <i>Exiaptasia diaphana</i> .	2022	Journal of Applied Microbiology	4,545	10.1111/jam.15465
Selective enrichment of heterotrophic nitrifiers Alcaligenaceae and <i>Alcanivorax</i> spp. from industrial wastewaters.	2020	Aims Microbiology	4,44	10.3934/microbiol.2020002
Optimisation of sample storage and DNA extraction for human gut microbiota studies.	2021	Bmc Microbiology	4,2	10.1186/s12866-021-02233-y
The Roles of TP53 and FGFR2 in Progress Made Treating Endometrial Cancer.	2022	Diagnostics (Basel, Switzerland)	3,992	10.3390/diagnostics12071737
The Postmedieval Latvian Oral Microbiome in the Context of Modern Dental Calculus and Modern Dental Plaque Microbial Profiles.	2021	Genes	3,96	10.3390/genes12020309
Next-Generation Sequencing and Bioinformatics-Based Protocol for the Full-Length CYP2E1 Gene Polymorphism Analysis.	2022	Pharmacogenomics and Personalized Medicine	3,877	10.2147/PGPM.S371709
Transcriptomic Response of Breast Cancer Cells MDA-MB-231 to Docosahexaenoic Acid: Downregulation of Lipid and Cholesterol Metabolism Genes and Upregulation of Genes of the Pro-Apoptotic ER-Stress Pathway.	2020	International Journal of Environmental Research and Public Health	3,39	10.3390/ijerph17103746

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OverFlap PCR: A reliable approach for generating plasmid DNA libraries containing random sequences without a template bias.	2022	PLoS One	3,24	10.1371/journal.pone.0262968
Jumping the green wall: The use of PNA-DNA clamps to enhance microbiome sampling depth in wildlife microbiome research.	2020	Ecology and Evolution	3,17	10.1002/ece3.6814
Dominance of Fructose-Associated Fructobacillus in the Gut Microbiome of Bumblebees (<i>Bombus terrestris</i>) Inhabiting Natural Forest Meadows.	2022	Insects	2,662	10.3390/insects13010098
Primary Production in the Water Column as Major Structuring Element of the Biogeographical Distribution and Function of Archaea in Deep-Sea Sediments of the Central Pacific Ocean.	2019	Archaea (Vancouver, B.C.)	2,61	10.1155/2019/3717239
RIPiT-Seq: A tandem immunoprecipitation approach to reveal global binding landscape of multisubunit ribonucleoproteins.	2021	Methods in Enzymology	1,682	10.1016/bs.mie.2021.03.019
Draft genome of the <i>Arabidopsis thaliana</i> phyllosphere bacterium, <i>Williamsia</i> sp. ARP1.	2016	Standards in Genomic Sciences	1,339	10.1186/s40793-015-0122-x