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NucleoBond® Xtra / NucleoBond® PC Technology

	NucleoBond® Xtra	NucleoBond® PC
Technology / Separation principle	Anion-exchange chromatography / Solid phase extraction	
Material / Backbone	Modified, macroporous silica gel Very high charge density Very high resolving power Very high binding capacity	Modified, macroporous silica gel High charge density High resolving power High binding capacity
Anion-exchanger group	MAE (methylaminoethanol)	
Format	Gravity-flow columns Midi, Maxi	Gravity-flow columns Mini, Midi, Maxi, Mega, Giga, preparative scale
Lysate clarification	NucleoBond® Xtra Column Filters	NucleoBond® Folded Filters
Procedure	<p>Principle: binding (low-pH) – washing – elution (high-pH) – alcohol precipitation</p> <ul style="list-style-type: none"> • Binding at low pH (interaction between negatively charged DNA backbone and positively charged anion-exchanger material) • Elution at high pH • Alcohol precipitation of eluted plasmid DNA, DNA collection by centrifugation or use of NucleoBond® Finalizer / Finalizer Large 	
Features / Result	Ultra-pure, transfection-grade plasmid DNA The new generation of anion exchangers Xtra fast, Xtra high yields, Xtra convenient	Ultra-pure, transfection-grade plasmid DNA*

*NucleoBond® technology is also available for isolation of genomic DNA and/or total RNA

NucleoBond® principle



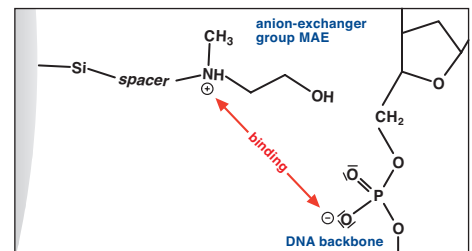
DNA
contaminants

DNA is bound to the anion-exchanger matrix under low-pH conditions
Interaction between positively charged anion-exchanger group and negatively charged DNA backbone

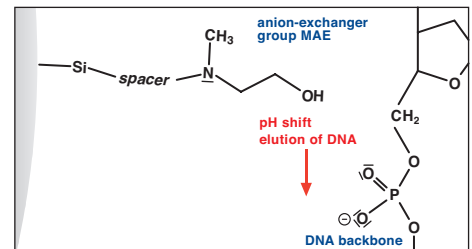
Stringent washing with increasing salt concentration to remove contaminants

DNA is eluted with high-pH buffer

Desalting / Concentration:
Alcohol precipitation of eluted DNA
DNA is collected by centrifugation or use of NucleoBond® Finalizer



Principle of binding



Principle of elution

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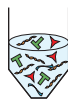
DNA and RNA purification

protein purification

NucleoSpin® Technology

Technology / Separation principle	Silica-membrane technology / Chaotropic salt binding
Material	Silica membrane
Format	Spin columns Low-throughput systems, from extra small to extra large scale
	8-well strips Medium-throughput systems, for vacuum manifolds, centrifuges, and robotic systems
	96-well plates High-throughput systems, for vacuum manifolds, centrifuges, and robotic systems
Procedure	<p>Principle: binding (high-salt) – washing – elution (low-salt)</p> <ul style="list-style-type: none"> • Adsorption of DNA/ RNA in the presence of chaotropic salts (hydrate shell of DNA/ RNA is reversibly removed) • High-salt / ethanolic washing steps to remove contaminants • Low-salt or water elution (hydrate shell is recovered, DNA/ RNA is released from the membrane)
Features / Result	<p>Ready-to-use, sequencing and PCR-grade DNA/ RNA From extra small to extra large scale, from low to high throughput No alcohol precipitation necessary Fast and easy procedure</p>

NucleoSpin® principle

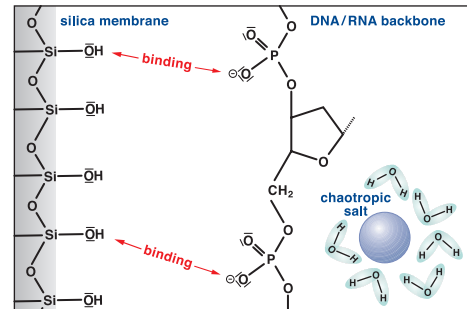


DNA/ RNA
 contaminants

Sample lysis, release of DNA/ RNA from cells, tissue, etc. in the presence of chaotropic salts



DNA/ RNA is bound to the silica membrane under high-salt conditions
Interaction between DNA/ RNA (hydrate shell is reversibly removed by chaotropic salt) and silica membrane



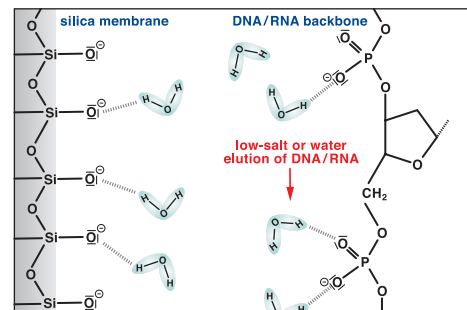
Principle of binding



Contaminants are washed away under high-salt and/or ethanolic conditions to keep the DNA/ RNA bound to the membrane



DNA/ RNA is eluted in low-salt buffer or water, DNA/ RNA is ready to use for downstream applications



Principle of elution

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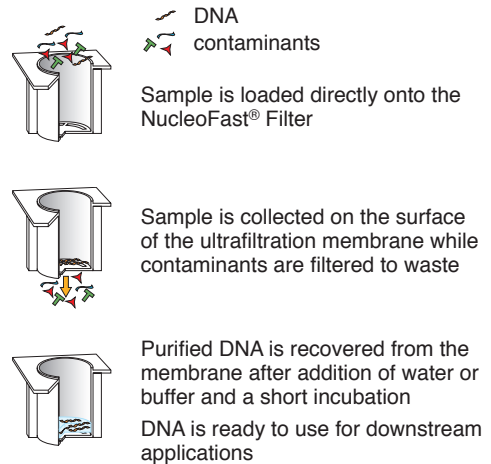
NucleoTrap® Technology

	NucleoTrap®	NucleoTrap® mRNA
Technology / Separation principle	Silica-matrix technology / Chaotropic salt binding	Affinity chromatography
Material	Spherical silica beads	Oligo(dT) latex beads
Format	Silica bead suspension	Latex bead suspension – NucleoTrap® Microfilters for bead separation
Procedure	<p>Principle: binding (high-salt) – washing – elution (low-salt)</p> <ul style="list-style-type: none"> • Adsorption of DNA/RNA in the presence of chaotropic salts (hydrate shell DNA/RNA is reversibly removed) • High-salt / ethanolic washing steps to remove contaminants • Low-salt or water elution (hydrate shell is recovered, DNA/RNA is released from the matrix) 	<p>Principle: binding (high-salt) – washing – elution (low-salt)</p> <ul style="list-style-type: none"> • Adsorption of poly(A) mRNA on oligo(dT) latex beads under high-salt conditions • High-salt washing steps to remove contaminants • Elution of poly(A) mRNA with RNase-free water at elevated temperature
Features / Result	Ready-to-use, sequencing and PCR-grade DNA Scalability Cost efficient	Ready-to-use poly(A) mRNA

NucleoFast® Technology

Technology / Separation principle	Ultrafiltration technology / Filtration
Material	Ultrafiltration membrane
Format	96-well plates High-throughput systems For vacuum manifolds, centrifuges, and robotic systems
Procedure	<p>Principle: filtration</p> <ul style="list-style-type: none"> • Retention of DNA fragments > 150 bp by filtration • Contaminants are filtered to waste • Optional washing step with water • Recovery of DNA from the membrane
Features / Result	Ready-to-use DNA Cost efficient

NucleoFast® principle



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NucleoMag® Technology

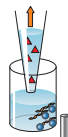
Technology / Separation principle	Magnetic-bead technology / Chaotropic salt binding
Material	Superparamagnetic beads (non-silica)
Format	Flexible
Procedure	<p>Principle: binding (high-salt) – washing – elution (low-salt)</p> <ul style="list-style-type: none"> • Adsorption of DNA / RNA in the presence of chaotropic salts (hydrate shell of DNA / RNA is reversibly removed) • High-salt / ethanolic washing steps to remove contaminants • Low-salt or water elution (hydrate shell is recovered, DNA / RNA is released from the beads)
Features / Result	Highly-pure ready-to-use PCR products, genomic DNA / RNA Easily adapted to automated use, e.g., on KingFisher®, KingFisher® mL, KingFisher® 96, and KingFisher® Flex

NucleoMag® principle



- DNA / RNA
- ▲ contaminants
- NucleoMag® Beads

NucleoMag® Beads are added to the sample, e.g., lysed blood cells, PCR reactions



DNA / RNA is bound to the NucleoMag® Beads

Beads are held in the well by the magnet while contaminants are washed away



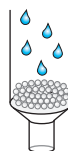
DNA / RNA is eluted from the beads and recovered, while beads are held in the well by the magnet

DNA / RNA is ready to use in downstream applications

NucleoSEQ® Technology

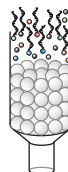
Technology / Separation principle	Gel-filtration / Size exclusion
Material	Size exclusion matrix
Format	Spin columns filled with dry matrix
Procedure	<p>Principle: size exclusion</p> <ul style="list-style-type: none"> • Retention of nucleotides and fluorescence labeled ddNTPs • Direct recovery of the purified sequencing sample by only one centrifugation step
Features / Result	Efficient removal of sequencing dye terminators No alcohol precipitation

NucleoSEQ® principle

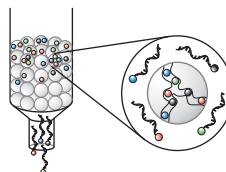


- unincorporated dye-terminators
- labeled DNA fragments

Gel resin is hydrated by addition of water



Sample is loaded onto the column



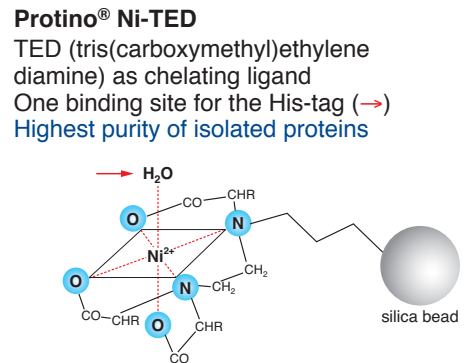
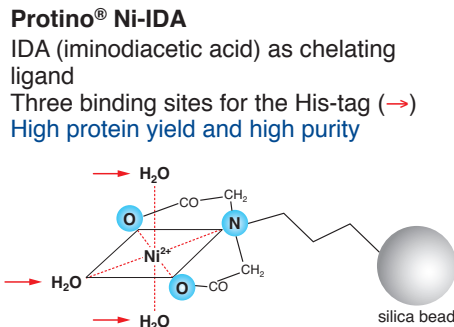
Purified sample is recovered by centrifugation

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Protino® Technology

	Protino® Ni-IDA Purification of polyhistidine (His)-tagged proteins	Protino® Ni-TED Purification of polyhistidine (His)-tagged proteins
Technology	Affinity chromatography (IMAC, immobilized metal ion affinity chromatography)	
Material / Backbone	Macroporous silica with immobilized Ni ²⁺	
Bead size	–	–
Format	Dry material	Dry material
	Dry bulk resin, for gravity-flow chromatography, batch binding, MPLC (e.g., FPLC™)	Dry bulk resin, for gravity-flow chromatography, batch binding, MPLC (e.g., FPLC™)
	Gravity-flow columns filled with dry Ni-IDA	Gravity-flow columns filled with dry Ni-TED
	96-well plates filled with dry Ni-IDA	–
Procedure	Principle: interaction between the His-tag of the recombinant protein and immobilized Ni²⁺ ions <ul style="list-style-type: none"> • Elution with imidazole (structure analogon of histidine, replacement reaction) 	
Features	Dry material, fast and easy handling, storage at room temperature	

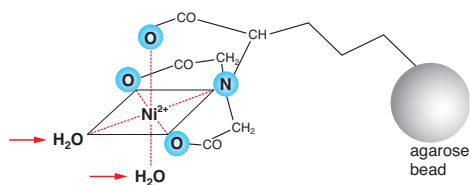


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Protino® Ni-NTA	Protino® Glutathione Agarose 4B
Purification of polyhistidine (His)-tagged proteins	Purification of Glutathione-S-transferase (GST)-tagged proteins
Affinity chromatography (IMAC)	Affinity chromatography
6% beaded agarose (cross-linked), precharged with Ni ²⁺	4% beaded agarose with immobilized glutathione
45 – 165 μm	90 μm
50% aqueous suspension containing 30% ethanol	75% aqueous suspension containing 20% ethanol
Bulk resin, for gravity-flow chromatography, batch binding, MPLC (e.g., FPLC™)	Bulk resin, for gravity-flow chromatography, batch binding, MPLC (e.g., FPLC™)
FPLC™ columns filled with Ni-NTA agarose	FPLC™ columns filled with Glutathione Agarose 4B
–	–
Principle: interaction between the His-tag of the recombinant protein and immobilized Ni²⁺ ions	Principle: interaction between the GST-tag of the recombinant protein and immobilized glutathione
<ul style="list-style-type: none"> Elution with imidazole (structure analogon of histidine, replacement reaction) 	<ul style="list-style-type: none"> Elution with free glutathione (substrate of Glutathione-S-transferase)
High binding affinity and high capacity Ready-to-use and cost-saving	Highest performance and cost-saving, equivalent to Glutathione Sepharose™ 4B Suitable for small proteins, large protein complexes, proteins with low expression rates

Protino® Ni-NTA
 NTA (nitrilotriacetic acid) as chelating ligand
 Two binding sites for the His-tag (→)
 Highest protein yield and high purity



Protino® Glutathione Agarose 4B

