OLIGO

Oligo Service Handbook

www.genscript.com

[2022 Edition]

Make People and Nature Healthier Through Biotechnology

About Us

GenScript Biotech Corporation (stock code: HK.1548) is a leading global provider of life science research, development and manufacturing services. Rooted in solid gene synthesis technology, GenScript has established four major platforms: life science service and product platform, biomedical contract development manufacture organization (CDMO) platform, cell therapy platform and industrial synthetic biological products platform.

Founded in 2002, GenScript established its R&D and manufacturing headquarters in Nanjing, China in 2004. In 2015, GenScript was listed on the Main Board of the Stock Exchange of

Hong Kong, with legal entities in the United States, China, Hong Kong, Japan, Singapore, the Netherlands and Ireland. It operated business in over 100 countries and regions worldwide, providing quality, convenient and reliable services and products for more than 100,000 customers.

As of December 31, 2021, GenScript owned more than 5,200 employees worldwide, with over 40% of them holding a Ph.D. or master's degree. GenScript has a number of intellectual property rights, including more than 180 granted patents and more than 670 patent applications, as well as a high dense technical secrets.

With its mission of "making people and nature healthier with biotechnology", GenScript is committed to be one of the most trusted biotechnology companies in the world. As of

History and Milestones

2002

- GenScript established in New Jersey, USA

2004

- Introduced custom **protein and antibody services**
- Established research and production facilities in **Nanjing, China**

2009

- Received investment from **KPCB China/The Balloch Group**

2011

- Established a new R&D and production base in **Nanjing**
- Participated in the **synthetic yeast genome Sc2.0 project** as the commercial entity selected
- Established **Japanese** subsidiary
- Number of employees reached **1,000**

2013

- **Established Bestzyme** (Industrial Synthetic Bioproducts Division)

2014

- **Established Legend Biotech** (Cell Therapy Division)
- **Awarded the Commissioned Research Institute** Leadership Award

2015

- **Listed on the Hong Kong Stock Exchange** (Stock code: HK.1548)

2017

- Legend Biotech and Janssen Biotech entered into a global strategic partnership for **BCMA products**
- **CFDA** accepted Legend Biotech's IND application
- Acquisition of CustomArray to **acquire gene synthesis technology on a chip**

2018

- **BCMA Product** received **IND approval** in China and U.S.
- **BCMA program** progressed well in China and U.S.
- **Biologics CDMO** business unit officially established

2019

- **New GMP Biologics CDMO R&D Center** was in operation
- LCAR-B38M/JNJ-4528 was granted **Orphan Drug status** by FDA and **Priority Drug status** by EMA
- **LCAR-B38M/JNJ-4528 achieved 100% ORR and 69% CR in US Phase 1b/2 clinical data**

2020

- The Company jointly developed the world's **first neutralization antibody detection kit** with Singapore to combat the epidemic of COVID-19
- **Legend Biotech** goes public on NASDAQ

2021

- **GenScript Flourishing Bio (Biopharmaceutical CDMO)** raised its Series A financing to become the leading gene therapy cell therapy CDMO in China
- Legend Biotech **Cilta-cel** cell therapy product submitted Biologics License Application (BLA) to the U.S. FDA and expected to be approved by the end of February 2022
- With more than **5,200 employees**, the Group serves global markets with life sciences capacity in **Singapore and the US** and cell therapy capacity in **Belgium**

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GenScript Oligo Synthesis

Technology Platform

Based on 20 years of molecular biology platform, GenScript provides DNA Oligo, RNA Oligo, high-throughput oligo pool, large-scale oligo, siRNA, and Trimer oligo synthesis services with superior quality and excellent service, as well as TaqMan probes and NGS adapters, hybridization captured probes, and multiplex PCR Oligo to support molecular diagnostic applications.

In 2022, GenScript's oligo production department moved to a new, self-contained facility, where environmental cleanliness and contamination monitoring are strictly enforced to control exogenous contaminants and other interfering factors to ensure smooth downstream experiments.

Conventional/ modified DNA Oligo synthesis

Conventional/modified RNA Oligo synthesis

High throughput oligo pool synthesis

Large-scale oligo synthesis

Applications

Based on different downstream applications, GenScript has developed targeted process and quality control standards to provide DNA Oligo/RNA Oligo raw materials for basic molecular biology research, molecular diagnostics (qPCR, NGS, etc.), nucleic acid drugs, etc., covering R&D to production stages.

Basic research in molecular biology

Molecular diagnostic
(qPCR, NGS)

Nucleic acid drug
(siRNA, ASO, etc.)

Production Capacity

With our advanced intruments, matured SOP processes and experienced technicians, GenScript is able to guarantee high quality and good homogeneity of DNA and RNA oligo quality.

- Implement SOPs for the entire process from raw materials, production to shipment
- Regular monitoring of quality indicators during the production process
- Optimized independent purification process (HPLC+/PAGE+)
- Strict quality control release criteria

Synthesis Equipment

768-lane oligo synthesizer

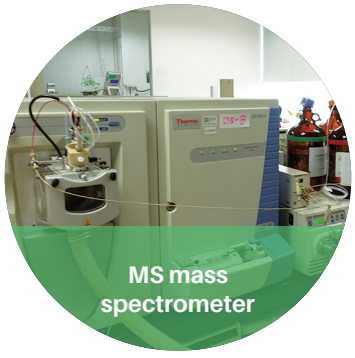
CustomArray chip oligo synthesizer

Purification Equipment

AKTApilot purifier

SCG purifier

QC Equipment



MS mass spectrometer

HPLC high performance liquid chromatograph

Service Advantages

Professional qualification certified

Clean laboratory, ISO 9001, ISO 13485

Meet IVD product registration requirements

Strict quality control standards

Control key points for downstream applications

Improve application success rate and stability

Powerful synthesis capability

Two platforms for single and oligo pool synthesis

Up to 200 nt of DNA and up to 160 nt of RNA synthesis capability

20 years

Rich experience in oligo synthesis

30,000+ lines/day

Stable production throughput

20,000+ customers

Customers' trusted choice

Fast and easy online ordering

Clear price and lead time at a glance

Please visit: www.genscript.com

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Oligo Synthesis Service

DNA Oligo Synthesis Services

The world's preeminent GenScript gene synthesis platform uses GenScript Oligo. GenScript provides desalt, ePAGE, PAGE and HPLC purified oligo and various modified oligo with DNA synthesis lengths up to 200 nt to support PCR amplification, targeted mutation, molecular diagnostics and other molecular biology research with professional quality and superior service.

Service Advantages

Easy and fast online ordering

High purity and low base error rate

Stable quality and fine reproducibility

Service Details

GenScript is ISO 9001 certified, with standardized control of raw materials, production and quality control, ensuring the quality and batch-to-batch stability of DNA Oligo, thus guaranteeing the success rate and consistency of your experiments.

Type	Purification methods	Length (nt)*	Lead time (Calendar days)#	Applications
DNA	Desalt	3-150	1-2	PCR amplification, whole gene synthesis, and DNA sequencing
	ePAGE	15-59	1	Multiplex PCR, site-specific mutation, RNA interference (gene construction) and cloning
	PAGE	10-110	2-3	Molecular diagnostics, mutation libraries, protein binding gel migration electrophoresis analysis, and commercial diagnostic oligo (non-fluorescent modified)
		111-200	4-9	
	HPLC	2-89	3-4	Oligo with hydrophobic group modifications, commercial diagnostic probes and oligo
		90-150	6-8	
	PAGE+	10-150	2-6	Commercialized diagnostic oligo such as NGS adapter (non-fluorescent modified)
	HPLC+	6-89	3-8	Diagnostic nucleic acid raw materials such as TaqMan probes for commercial applications (purity up to 95%, different purity available)

*For information on other DNA Oligo lengths, please contact us for details: email us to oligo@genscript.com.

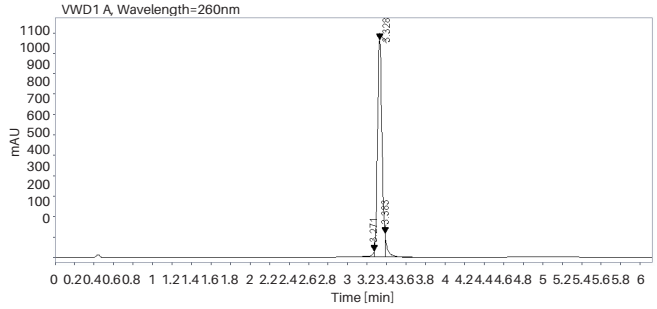
#Delivery lead time will vary according to length and delivery volume, please log on GenScript's website for oligo online ordering system to place your order.

Purification Methods

Type	Purification methods	Principles	Advantages	Applications			
				<10 nt	10-39 nt	40-59 nt	60-120 nt
Research level	Desalt	Purification with reverse silica gel column; it can effectively remove salts; the purity of the purified oligo can meet the needs of most molecular biology experiments.	Fast and short lead time; high throughput and favorable price	Suitable	**Recommended**	Suitable	Suitable
	PAGE Purification	The separation and recovery of oligo chains and impurities of different lengths,such as by denaturing polyacrylamide gel electrophoresis, is more advantageous for the separation of long oligo chains. This purification method can also be applied to the purification of more than 30 types of modified oligo such as phosphate and biotin.	Purity can be > 90% and is particularly effective for purification of long-stranded oligo (> 50 nt), which are strongly recommended for PAGE purification.	Not suitable	Suitable	Suitable	**Recommended**
	HPLC	The purification of oligo with high performance liquid chromatography can achieve high purity and is mainly used for the purification of short chain (< 40 nt) and modified oligo. With higher cost, it is less efficient for batch production.	Purity can > 90% after reversed-phase HPLC purification, which can effectively remove the N-1 short fragment. Modified oligo with hydrophobic groups can currently only be purified by HPLC.	Suitable	**Recommended**	Suitable	Suitable
Molecular diagnostic level	PAGE+	Done in a clean laboratory, the target sequences are separated by denaturing polyacrylamide gel electrophoresis, and each oligo is purified with an independent purification system and disposable consumables to avoid the possibility of mixing with other oligo to the greatest extent. This can also be applied to the purification of more than 30 types of modified oligo such as phosphate and biotin.	It effectively controls the cross-contamination rate to a level as low as 0.01%, **which is especially suitable for the application of NGS adapter purification**.	Not suitable	Suitable	Suitable	**Recommended**
	HPLC+	Done in a clean laboratory; before purification of each oligo, the column is thoroughly cleared of residues by multiple special rinsing procedures, and the different oligo are kept reasonably spaced apart and purified separately to avoid exogenous contamination to the greatest extent.	Exogenous contamination is strictly controlled, and NTC did not peak within 40 cycles; **it is especially suitable for purification of TaqMan probes**.	Suitable	**Recommended**	Suitable	Suitable

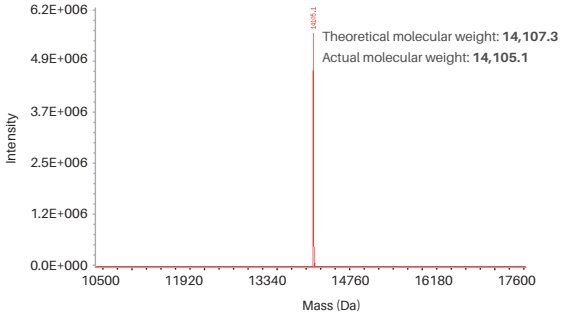
Case Studies

Purity by HPLC



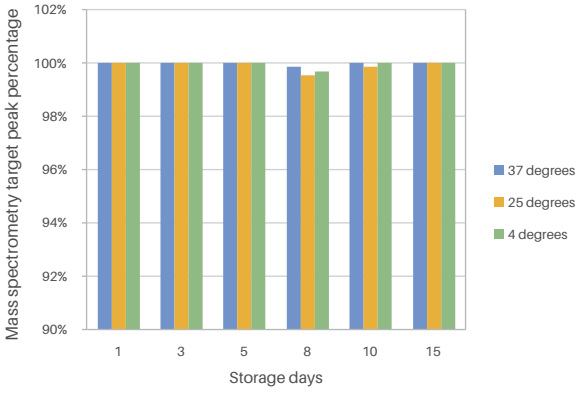
High purity, to avoid interfering factors

Mass spectrometry (MS) detection spectrum

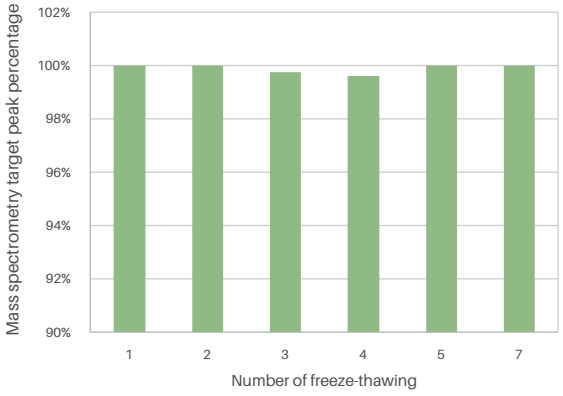


Molecular weight deviation ≤ 0.05% to guarantee experimental success rate

Stability data for phosphate-modified oligo



Freeze-thaw stability data for phosphate-modified oligo



Stable modification, minimum effect of temperature, freeze-thaw and storage time

Learn to order DNA Oligo / RNA Oligo online in 1 minute

Easy to use, clear quotation and delivery details at a glance

RNA Oligo Synthesis Services

Chemically synthesized RNA is an important research tool widely used in gene function analysis, development of novel nucleic acid therapeutic strategies and other research applications.

GenScript offers fast delivery, high quality, and more cost-effective RNA Oligo synthesis services for custom sequences, including common RNA synthesis, RNA Oligo modifications and labeling, chimeric DNA (a hybrid structure of DNA and RNA), 2'-OMe-RNA, and other antisense RNAs. We can test molecular weight by ESI mass spectrometry, purity by HPLC, and strictly enforce QC testing standards. Variety of synthesis specifications, modification types, and customized QC options are available to support the different needs of research or application needs.

Service Advantages

Powerful RNA synthesis capability

Synthesis lengths up to 160 nt with gram-level delivery Available in large scale.

Excellent product quality

Low molecular weight deviation (≥0.05%), high purity, and ISO 9001 certified

20+ years experience in synthesis

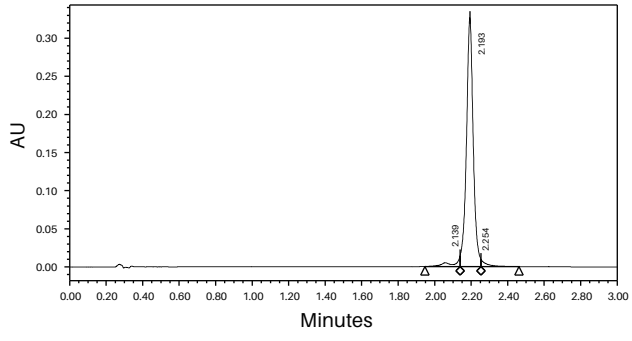
Stable process, good batch-to-batch consistency

Service Details

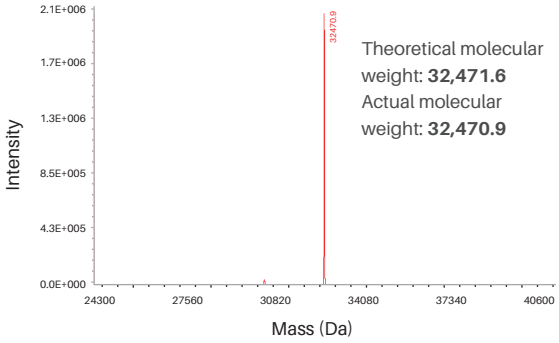
Type	Purification methods	Length (nt)	Lead time (Calendar days)*	Deliverables
RNA	RNase free HPLC PAGE/RPC	6-110	11-15	Lyophilized powder, COA and MS report

*For information on other RNA lengths, please contact us for details: email us to oligo@genscript.com.
#Delivery lead time will vary according to length and delivery volume; please visit GenScript's website for oligo online ordering inquiry and order.

Case Studies



HPLC data shows high purity of RNA



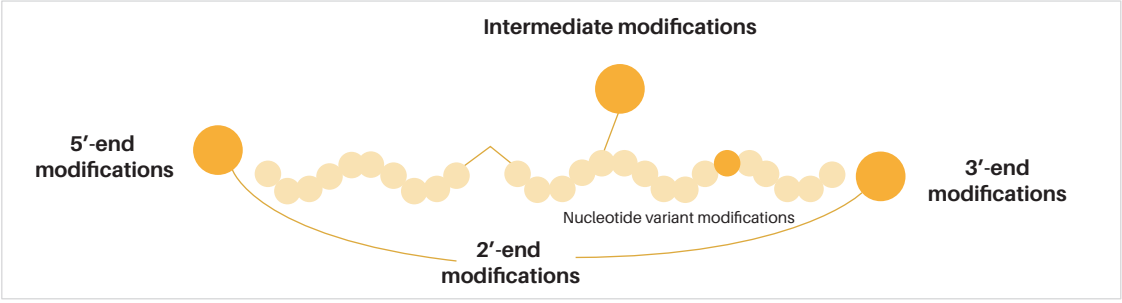
MS report shows RNA molecular weight deviation <0.05%

DNA/RNA Oligo Modifications

Modification Groups Position

The addition of modification groups with various functions during oligo synthesis can support molecular biology studies for a variety of different purposes, e.g:

- Addition of modifications such as Inverted dT to the 3' end of oligos can act as a blocking agent and prevent PCR extension;
- Addition of a fluorescent group at the 3' end and a quenched groups at the 5' end of the oligo allows the preparation of TaqMan probes to test target sequences;
- Addition of modifications such as thio in the middle of the oligo can serve to avoid degradation by exogenous nucleases;
- Addition of modifications such as dI in the middle of the oligo can mimic the bases present in nature.



DNA Modification Group Information

Here is a list of DNA modifications and modification positions that GenScript can provide.
Other modifications can be evaluated based on the availability of raw materials.

★ Linker Modifications

Modification category	Modification name	Modification position
Biotin modifications	Biotin	5'-end / 3'-end
	Biotin dT	5'-end / 3'-end / intermediate modifications
	Biotin-TEG	5'-end / 3'-end / intermediate modifications
	Dual Biotin	5'-end
	Desthiobiotin-TEG	5'-end / 3'-end / intermediate modifications
	PC Biotin	5'-end
Amino modifications	Amino Modifier C3	5'-end
	Amino Modifier C6	5'-end / intermediate modifications

Modification category	Modification name	Modification position
Amino modifications	Amino Modifier C6 dT	5'-end / 3'-end / intermediate modifications
	Amino Modifier C7	3'-end
	Amino Modifier C12	5'-end
	5'-Amino-dT-CE Phosphoramidite	5'-end / 3'-end / intermediate modifications
	iUniAmM	5'-end / 3'-end / intermediate modifications
	AOP-iUniAmM	5'-end / 3'-end / intermediate modifications
Mercaptan modifications	Thiol Modifier C3 S-S	3'-end

Modification category	Modification name	Modification position
Mercaptan modifications	Thiol Modifier C6 S-S	5'-end / 3'-end / intermediate modifications
	Thiol Modifier C6 S-S dT	5'-end / 3'-end / intermediate modifications
	Dithiol Serinol	5'-end / 3'-end / intermediate modifications
Digoxin	Digoxigenin	5'-end / 3'-end
Cholesterol	Cholesteryl	3'-end
	Cholesteryl-TEG	5'-end / 3'-end
Methacrylate	Acrydite	5'-end
Click reaction related modifications	Hexynyl	5'-end
Diphenylcy-clooctyne	DBCO	5'-end

Interarm Modifications

Modification category	Modification name	Modification position
Interarm modifications	Spacer 18	5'-end / 3'-end / intermediate modifications
	Spacer 9	5'-end / 3'-end / intermediate modifications
	Spacer C6	5'-end / 3'-end / intermediate modifications
	Spacer C3	5'-end / 3'-end / intermediate modifications
	dSpacer	5'-end / 3'-end / intermediate modifications
	PC Spacer9	5'-end / intermediate modifications

Quenching Group

Modification category	Modification name	Modification position
Quenching group	BHQ-1	5'-end / 3'-end
	BHQ1-dT	5'-end / 3'-end / intermediate modifications
	BHQ2	3'-end
	BHQ2-dT	5'-end / 3'-end / intermediate modifications
	BHQ3	3'-end
	BlackBerry Quencher 650	5'-end / 3'-end
	BlackBerry Quencher 650 dT	5'-end / 3'-end / intermediate modifications
	Dabcyl	3'-end
	Dabcyl-dT	5'-end / 3'-end / intermediate modifications
	MGB	3'-end

Fluorophore

Modification category	Modification name	Modification position
Fluorophore	6-FAM	5'-end / 3'-end
	6-FAM dT	5'-end / 3'-end / intermediate modifications
	6-TET	5'-end
	6-JOE	5'-end
	6-VIC	5'-end
	6-HEX	5'-end
	6-HEX dT	5'-end / 3'-end / intermediate modifications
	Quasar 570	5'-end / 3'-end
	Quasar 670	5'-end / 3'-end
	CY3	5'-end / 3'-end
	CY5	5'-end / 3'-end
	CY5.5	5'-end / 3'-end
	CY7	5'-end / 3'-end / intermediate modifications
	CY3 dT	Intermediate modifications
	CY5 dT	Intermediate modifications
	NED	5'-end
	6-TAMRA	5'-end / 3'-end
	6-ROX	5'-end / 3'-end
	Texas Red-X	5'-end / 3'-end / intermediate modifications
	Methylene Blue	5'-end
	CAL FLOUR RED 610	5'-end

Stable Modifications

Modification category	Modification name	Modification position
Thiosubstitution	Phosphorothioate	Intermediate modifications
Pentasaccharide 2 and 4 positions	Locked Nucleic Acid	5'-end / 3'-end / intermediate modifications
	5-methyl dC	5'-end / 3'-end / intermediate modifications

Blocking Class Modifications

Modification category	Modification name	Modification position
Nucleotide inversion	inverted dT	5'-end / 3'-end / intermediate modifications
	Inverted abasic	5'-end / 3'-end / intermediate modifications
Pentasaccharide 2 and 3 positions	Dideoxy-bases	3'-end
Phosphorylation modifications	Phosphorylation	5'-end / 3'-end
	Adenylation	5'-end

Other Modification Groups

Modification category	Modification name	Modification position
/	Peptide-oligo conjugates	5'-end / 3'-end
	Aminobutylethyl isoluminol	5'-end
	Thymidine Glycol	5'-end / 3'-end / intermediate modifications
	Palmitate acid	5'-end / 3'-end
	puromycin	3'-end
	Symmetric Doubler	5'-end / 3'-end
	DMT ON	5'-end
	TCO	5'-end / 3'-end / intermediate modifications
	Nitroindole	5'-end / intermediate modifications

Special Bases

Modification category	Modification name	Modification position
Base modifications	Ferrocene dT	5'-end / 3'-end / intermediate modifications
	Ferrocene dI	5'-end / intermediate modifications
	2-Aminopurine	5'-end / 3'-end / intermediate modifications
	5-Fluoro dU	5'-end / 3'-end / intermediate modifications
	U	5'-end / 3'-end / intermediate modifications
	I	5'-end / 3'-end / intermediate modifications
	2'-O-Methyl-5-Methyl C	5'-end / 3'-end / intermediate modifications
	5'Hydroxymethyl dC	5'-end / 3'-end / intermediate modifications
	5-Carboxy dC	5'-end / 3'-end / intermediate modifications
	5-Formyl dC	5'-end / 3'-end / intermediate modifications
	5-Iodo dC	5'-end / 3'-end / intermediate modifications
	Bromodomain	5'-end / 3'-end / intermediate modifications
	iso deoxy bases	5'-end / 3'-end / intermediate modifications
	5-methyl isodeoxycyto sine	5'-end / 3'-end / intermediate modifications
	7-deaza-2'-dG	5'-end / 3'-end / intermediate modifications
	N6-Methyl dA	5'-end / 3'-end / intermediate modifications
	N1-Methyl-dC	5'-end / 3'-end / intermediate modifications
	N3-Methyl-dC	5'-end / 3'-end / intermediate modifications
	O4 Triazolyl dU	5'-end / 3'-end / intermediate modifications
	8-oxo-dG	5'-end / 3'-end / intermediate modifications

RNA Oligo Modifications Group Information

Please check the types of RNA modifications and modification positions that GenScript can provide. Here is the list of RNA modifications and modifcation positions that GenScript can provide. Other modifications can be evaluated based on the availability of raw materials.

Linker Modifications

Modification category	Modification name	Modification position
Biotin modifications	Biotin	5'-end / 3'-end
	Biotin-TEG	5'-end / 3'-end
	Biotin dT	5'-end / 3'-end / intermediate modifications

Modification category	Modification name	Modification position
Biotin modifications	Dual Biotin	5'-end
	Desthiobiotin-TEG	3'-end
	PC Biotin	5'-end

Modification category	Modification name	Modification position
Amino modifications	Amino Modifier C3	5'-end
	Amino Modifier C6	5'-end
	Amino Modifier C6 dT	5'-end / 3'-end / intermediate modifications
	Amino Modifier C6 rU	5'-end / 3'-end / intermediate modifications
	Amino Modifier C7	3'-end
	Amino Modifier C12	5'-end
	iUniAmM	Intermediate modifications
	5-Amino dT	5'-end
Digoxin	Digoxigenin	5'-end / 3'-end
Cholesterol	Cholesteryl	3'-end
	Cholesteryl-TEG	5'-end / 3'-end

Interarm Modifications

Modification category	Modification name	Modification position
Interarm modificati ons	Spacer 18	5'-end / 3'-end / intermediate modifications
	Spacer 9	5'-end / 3'-end / intermediate modifications
	Spacer C6	5'-end / 3'-end / intermediate modifications
	Spacer C3	5'-end / 3'-end / intermediate modifications
	dSpacer	5'-end / 3'-end / intermediate modifications

Quenching Group

Modification category	Modification name	Modification position
Quenching group	BHQ-1	3'-end
	BHQ1-dT	5'-end / 3'-end / intermediate modifications
	BHQ2	3'-end
	BHQ2-dT	5'-end / 3'-end / intermediate modifications
	BHQ3	3'-end
	BlackBerry Quencher 650	5'-end / 3'-end
	BlackBerry Quencher 650 dT	5'-end / 3'-end / intermediate modifications
	Dabcyl	3'-end
	Dabcyl-dT	5'-end / 3'-end / intermediate modifications
	MGB	3'-end

Fluorophore

Modification category	Modification name	Modification position
Fluorophore	6-FAM	5'-end / 3'-end
	6-FAM dT	5'-end / 3'-end / intermediate modifications
	CY3	5'-end / 3'-end / intermediate modifications
	CY5	5'-end / 3'-end
	CY5.5	5'-end / 3'-end
	CY7	5'-end / 3'-end / intermediate modifications
	Quasar 570	5'-end / 3'-end
	Quasar 670	5'-end / 3'-end
	6-TAMRA	5'-end / 3'-end
	6-ROX	5'-end / 3'-end
	6-VIC	5'-end
	Texas Red-X	5'-end / 3'-end / intermediate modifications
	Methylene Blue	5'-end

Stable Modifications

Modification category	Modification name	Modification position
Phosphorothio-ate bond modifications	Phosphorothioate	Intermediate modifications
Pentasaccharide 2 position	2'-O methyl A	5'-end / 3'-end / intermediate modifications
	2'-O methyl G	5'-end / 3'-end / intermediate modifications
	2'-O methyl C	5'-end / 3'-end / intermediate modifications
	2'-O methyl U	5'-end / 3'-end / intermediate modifications
	2'-MethoxyEthoxy A	5'-end / 3'-end / intermediate modifications
	2'-MethoxyEthoxy G	5'-end / 3'-end / intermediate modifications
	2'-MethoxyEthoxy MeC	5'-end / 3'-end / intermediate modifications
	2'-MethoxyEthoxy T	5'-end / 3'-end / intermediate modifications
	2'-Fluoro C	5'-end / 3'-end / intermediate modifications
	2'-Fluoro U	5'-end / 3'-end / intermediate modifications
	2'-Fluoro A	5'-end / 3'-end / intermediate modifications
	2'-Fluoro G	5'-end / 3'-end / intermediate modifications
	2′-Fluoro-Arabinonucleic Acid	5'-end / 3'-end / intermediate modifications

Modification category	Modification name	Modification position
Pentasaccharide 2 and 4 positions	Locked Nucleic Acid	5'-end / 3'-end / intermediate modifications
	5-Methyl dC	5'-end / 3'-end / intermediate modifications
	5-Methyl rC	5'-end / 3'-end / intermediate modifications

Blocking Class Modifications

Modification category	Modification name	Modification position
Nucleotide inversion	inverted dT	5'-end / 3'-end / intermediate modifications
	Inverted abasic	5'-end / 3'-end / intermediate modifications
Pentasaccharide 2 and 3 positions	Dideoxy bases	3'-end
Phosphorylation Modifications	Phosphorylation	5'-end / 3'-end
	Adenylation	5'-end

Other Modification Groups

Modification category	Modification name	Modification position
/	TCO	5'-end / 3'-end
	puromycin	3'-end
	Thymidine Glycol	Intermediate modifications
	Symmetric Doubler	5'-end / 3'-end / intermediate modifications

Special Bases

Modification category	Modification name	Modification position
/	2-Aminopurine	5'-end / 3'-end / intermediate modifications
	5-Fluoro dU	5'-end / 3'-end / intermediate modifications
	2-Fluoro I	Intermediate modifications
	2-methyl I	Intermediate modifications
	Chimeric DNA base	5'-end / 3'-end / intermediate modifications
	rI	5'-end / 3'-end / intermediate modifications
	2'-O-Methyl MeC	5'-end / 3'-end / intermediate modifications
	5-Carboxy dC	5'-end / 3'-end / intermediate modifications
	5-Formyl dC	5'-end / 3'-end / intermediate modifications
	Bromodomain	5'-end / 3'-end / intermediate modifications
	N6-Methyl dA	5'-end / 3'-end / intermediate modifications
	N6-Methyl rA	5'-end / 3'-end / intermediate modifications
	1-Methyl-PseudoUridine	5'-end / 3'-end / intermediate modifications

High-Throughput siRNA Synthesis Service

Small interfering RNA (siRNA) is a double-stranded RNA 20 to 25 nucleotides long that is involved in the RNA interference (RNAi) phenomenon. According to the central law, DNA is transcribed to produce mRNA, which is translated to produce protein. siRNA can bind to mRNA complementary to its sequence and degrade that mRNA, thus interfering with the expression of the corresponding protein of a specific gene. siRNA can be applied to gene function, target validation, and small nucleic acid drug research. siRNA-based drugs can inhibit disease gene expression at the miRNA level and have the advantages of high efficiency, low toxicity, and good specificity, and they have great potential in the fields of drug development such as antiviral, antitumor, and treatment of hyperlipidemia.

Based on the strong oligo synthesis platform, GenScript can provide customers with conventional siRNA, various types of modified and labeled siRNA synthesis services. GenScript strictly implements ISO 9001:2015 quality control standards and ensures delivery of high quality siRNA products to customers through ESI mass spectrometry, HPLC purity testing and other quality control methods.

Service Advantages

High purity, correct sequence

- Purity detected by HPLC, up to 90% purity for full-length double strands
- MS testing of molecular weight with less than 0.05% deviation

Economical price and fast delivery

- Cost-effective to match different research stages
- Ready to use, just dissolve and use directly in experiments

Complete range of chemical modifications

- 2'-Hydroxymethylation, fluorosubstitution, phosphate, thiosubstitution and other modifications
- Stable modification and support downstream application

Powerful synthesis capability

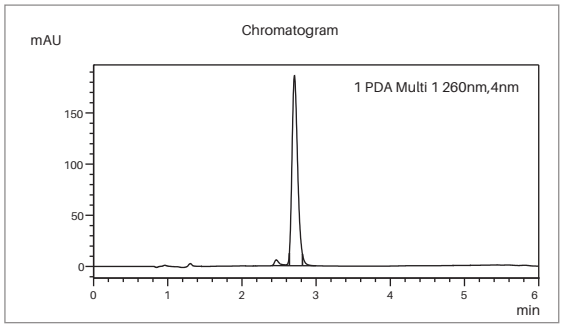
- 20+ years oligo synthesis experience, high throughput
- Strict endotoxin control, support customized QC requirements

Service Details

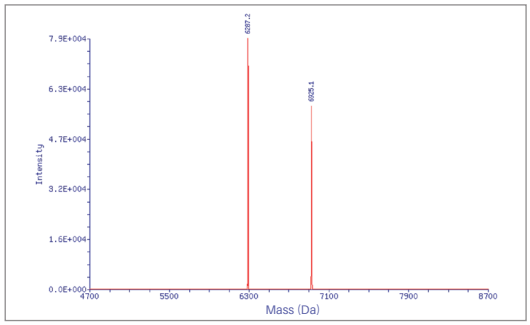
Type*	Full-length double-stranded purity	Scale	QA	Deliverables	Lead time/Price
Research-grade siRNA	>80%	<20 nmol	MS HPLC	Single tube or 96-well plate Dry powder or solution COA files/QA reports	For details, please consult us
Custom-grade siRNA	>90%	≥20 nmol			

*Please refer to the RNA modification group information on page 11 for information on the modification groups that siRNA can undertake

Case Studies



Double-stranded siRNA HPLC profile: high purity



Double-stranded siRNA MS profile: correct molecular weight

Large-Scale Oligo Synthesis Services

GenScript's large-scale oligo synthesis platform is equipped with advanced equipment and technology to enable the synthesis of DNA Oligo and RNA Oligo from milligram to gram level. The platform provides not only standard, unmodified oligos, but also complex oligos requiring multiple modifications, precisely matched for nucleic acid drug development (siRNA, ASO, etc.), molecular diagnostics, and other nucleic acid research areas.

Service Advantages

More synthesis scale

- Synthesis volume from 25 mg to gram level to meet the needs of customers at different stages
- Both DNA and RNA can be

High purity quality

- HPLC purity up to 90% or more
- Optimized purification process, low salt content and reduced cytotoxicity

Full range of modifications

- Multiple chemical modifications (e.g. LNA lock, thio, methylation, 2-OMe, etc.) and fluorescent labels
- Excellent synthesis capabilities to meet customization needs

More customized services

- Customized purity and QC testing
- Senior R&D technical support team to provide you with smooth and professional technical services

Applications

Nucleic acid drug development

siRNA, ASO, miRNA

Molecular Diagnostic Oligo

Genetic diagnosis, concomitant diagnosis, pathogenic microbial detection, early tumor screening, etc.

Nucleic acid structure study

Biophysical studies such as X-ray crystallography and NMR studies

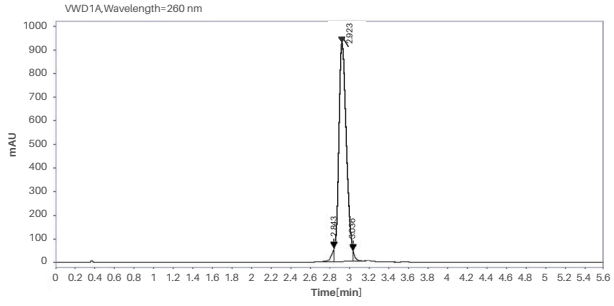
Service Details

Type	Length*	Deliveries to customers*	Delivery form	Lead time	QC
DNA	≤60 nt	25 mg-100 g	Lyophilized powder	≤1g: 10-24 days >1g: Please ask for details	Mass spectrometry testing: molecular weight deviation ≤ 0.05% HPLC testing: purity ≥ 90%*
	61-100 nt	25 mg-10 g			
RNA	≤60 nt	25 mg-100 g			

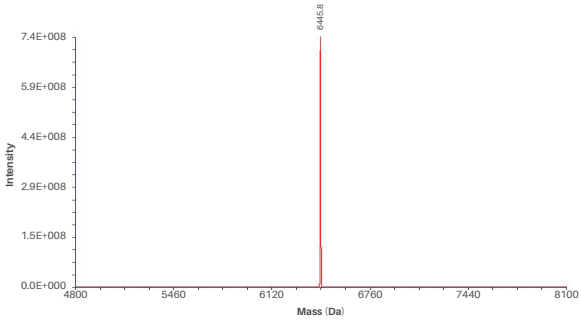
* Information on other lengths, deliverables, and purity are available upon request for customization. Email us at oligo@genscript.com.cn or call us at 400-025-8686 ext. 5812 or 5815 for professional technical support.

Case Studies

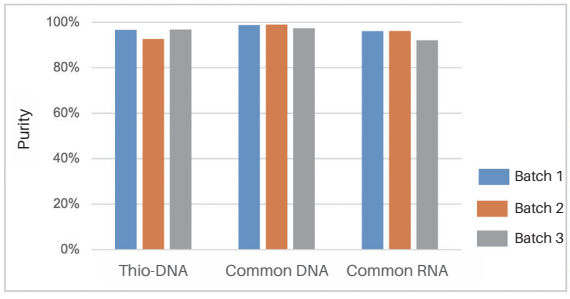
GenScript has ISO 9001 quality management certification, which ensures the quality and batch-to-batch stability of synthetic DNA/RNA by strictly standardizing the process from raw materials, production, quality control and shipping, providing a solid and powerful guarantee for customers' R&D and commercial applications.



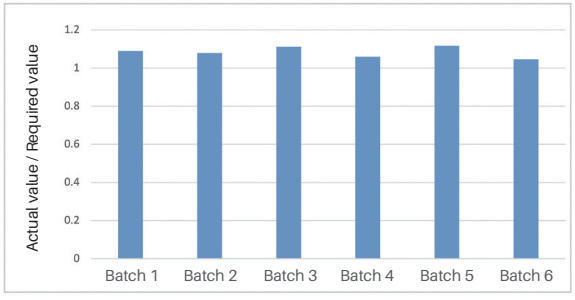
HPLC: purity ≥ 90%



MS: molecular weight deviation ≤ 0.05%



Batch-to-batch stability of oligo purity



Quantitative batch-to-batch stability

Trimer Oligo Synthesis Service

Trimer oligo are triplet nucleosides formed by joining 3 nucleosides in a predetermined species and order. These different triplet nucleosides correspond to different amino acids respectively, and a variety of Trimer oligo are synthesized to predetermined positions in the sequence as a whole synthetic raw material to obtain a oligo library that matches the predetermined sequence.

GenScript provides oligo synthesis services using Trimer oligo raw materials, which can be used for downstream library construction applications and support subsequent research in protein directed evolution, antibody screening, drug target screening and drug discovery, enzyme optimization, etc.

Service Advantages

Precise and customized synthesis

Avoid unintended mutations and stop codons

Support multi-locus and amino acid custom scaling mutations

High coverage and homogeneity

Ensure library diversity and homogeneity

Avoid missing target sequences in library construction/screening

More economical and fast delivery

More cost effective for high diversity libraries

Ensure rapid downstream application

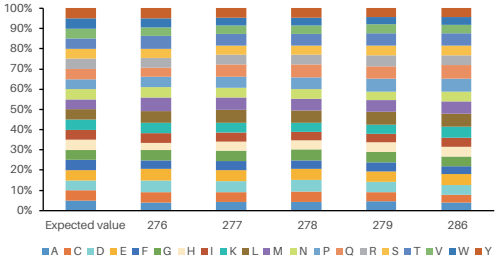
Service Details

By applying Trimer oligo raw materials, GenScript can provide synthesis services for oligo of the following specifications for subsequent library construction, supporting E. coli and Saccharomyces cerevisiae expression systems*. Meanwhile, GenScript can also provide subsequent construction of Trimer combinatorial mytation libraries, including PCR products, plasmids, and glycerol bacteria.

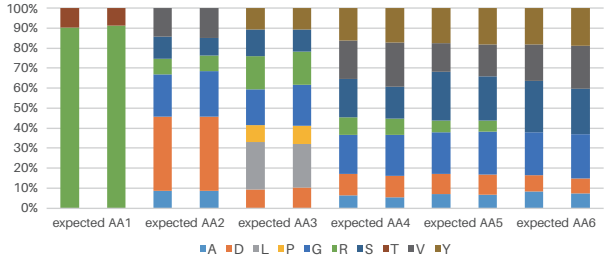
Oligo length*	Number of amino acid sites*	Deliveries to customers*	Lead time	Deliverables	QC
≤100 nt	≤12	Approx. 2 nmol#	10 calendar days	Lyophilized powder (mixed oligo)	Mass spectrum NGS sequencing (customization)

*Welcome for enquiry about other expression systems, oligo lengths, codon numbers, and deliveries, and we will provide customization service. Email us at oligo@genscript.com.cn or call us at 400-025-8686 ext. 5812 or 5815 for professional technical support.
#Deliveries varies according to oligo length.

Case Studies



The sequence coverage is 100%, and the proportional distribution of 20 amino acids at 5 saturation mutation sites is **highly uniform**



Support non-equal proportional custom mutation, and various amino acid proportional distributions highly match with design proportion

High-Throughput Oligo Pool Synthesis Service

GenScript's electrochemical semiconductor chip technology can synthesize up to 90,000 nucleotide sequences on 1 chip, providing you with a faster and more economical library construction solution to support subsequent high-throughput screening.

Service Advantages

Flexibility for Your Application

Two chip sizes allows for construction of any size pool

No sequence restrictions or minimum order required

High Screening Efficiency

Top-notch sequence accuracy ensures target specificity

>99% coverage rate ensures maximum targeting

Low Batch Variations

High consistency between oligo pools

More confidence in your results when using multiple oligo pool batches

Service Details

GenScript oligo pools use electrochemical semiconductor chips to precisely control the accuracy of each oligo sequence. It is synthesized in a closed structure instrument, and the reaction efficiency is not affected by external moisture and air.

Chip specifications	Length (nt)	Synthetic oligo number/chips	Lead time (weeks)
12 K	10-170 nt	12,472	1-2
92 K		91,766	3

QC Standards:

Delivery testing: Nano Drop quantification

Effective sequence length detection: Standard QC sequence amplification monitoring*

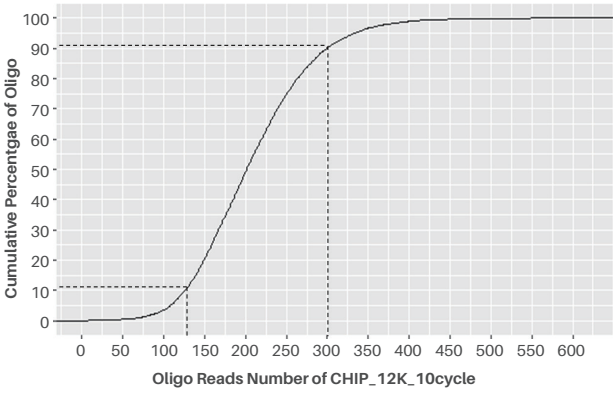
Sequence homogeneity testing: NGS testing*

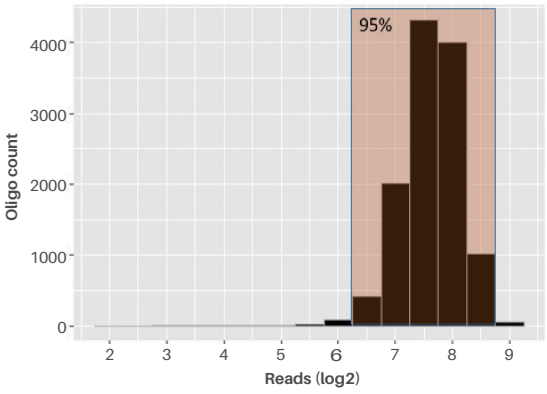
Case Study

Customer orders: Oligo pool of 12,000 nucleotide sequences, 125 mer in length

GenScript Solution: 12 K-chip, synthesized by semiconductor technology, delivered within one week, synthesized and amplified in small quantities

QC testing results: Sequencing with NGS





Testing results:

- ✓ 12,000 custom Oligos evenly distributed
- ✓ 99.74% coverage
- ✓ Homogeneous degree: 90%/10% < 2.5

Oligo Pool Applications and Advantages

1 CRISPR sgRNA Libraries Construction

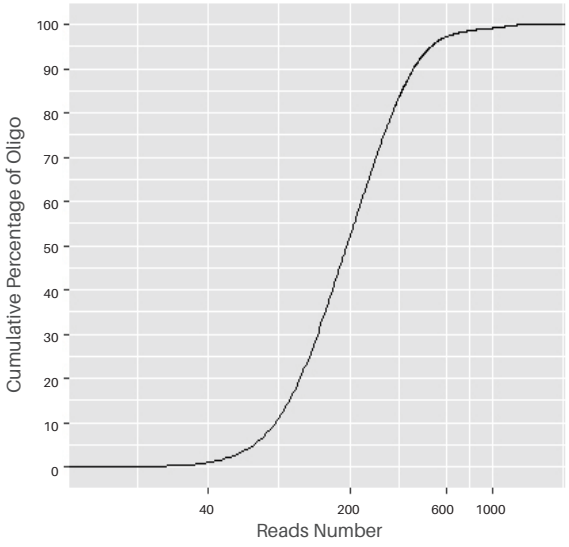
In gene editing experiments, sgRNA libraries can be built by oligo pool, which can be used to screen sgRNA sequences with high editing efficiency for target genes, or to screen target genes that meet research requirements.

sgRNA library, a GenScript oligo pool application that prepared by amplification and cloning, has the superior performance of high diversity and homogeneity, i.e., it can cover all designed sequences and the synthesis amount of each sequence is basically the same, ensuring efficient and parallel subsequent high-throughput

Process of using oligo pool for CRISPR sgRNA library construction

Case Sharing

Experiment: A sgRNA library containing 62,804 sequences was synthesized using a oligo pool, and the coverage and homogeneity of the sgRNA library was tested by NGS.



Number of sequencing	62804
Sequencing data volume (GB)	0.67
Reads number (million)	14.90
Q30	85.30%
Coverage (sequencing depth ≥ 1×)	100%
Reads number of 10% sequence*	88
Reads number of 90%sequence*	412
90%/10%* (after cloning)	4.68

Full coverage: GenScript synthesizes a oligo pool in which all design sequences are sequenced at least once, characterizing the synthetic sequences delivered to cover all the design sequences required by the customer.

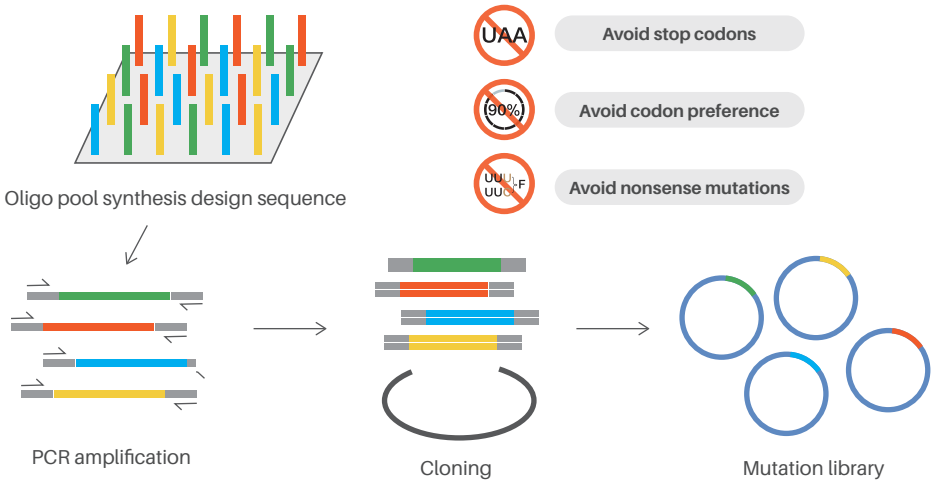
High homogeneity: The 90%/10% value characterizes the homogeneity of different sequences synthesized in the library, with lower values representing better homogeneity. sgRNA librarry construcyed on GenScript oligo pools have 90%/10% values as low as 4.68, avoiding the loss of sequences with lower abundance during amplification.

2 Mutation Library Construction

When studying the regulation and association between molecular sequences and protein functions, mutation libraries are constructed using oligo pooling technology to synthesize a large number of regulatory regions or mutation sequences of DNA to find sequences that match the study target.

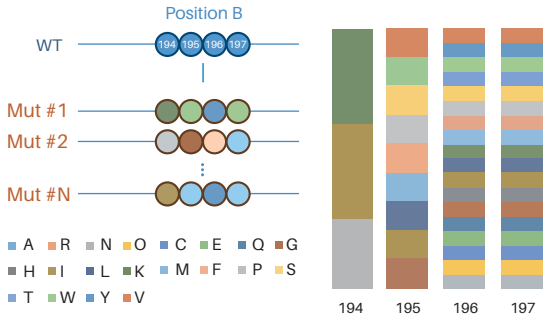
GenScript oligo pools are amplified and cloned to obtain mutation libraries with better sequence diversity than traditional library building schemes, high coverage and homogeneity, i.e., they can cover all designed sequences with little difference in the amount of each sequence synthesized. Meanwhile, the library construction cost based on oligo pool synthesis technology will be much lower than the traditional gene synthesis followed by targeted mutation scheme.

Process of Oligo Pool for Mutation Library Construction



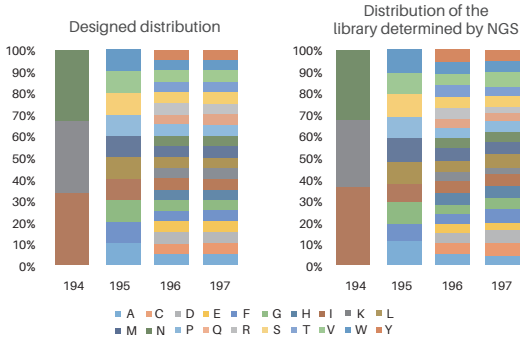
Case Sharing

Experiment: For a wild-type protein, amino acids at positions 194-197 were mutated, of which amino acids at positions 196 and 197 were required to be saturated (i.e., the specified amino acids were replaced by all 19 amino acids), while position 194 was required to be mutated to the specified 3 amino acids and position 195 was required to be mutated to the specified 10 amino acids, with equal probability of mutation into each amino acid, as shown in the figure on the right. Meanwhile, the library quality was verified by NGS sequencing results.



High coverage: NGS sequencing results show that the mutant library sequences, when translated into amino acid sequences (right panel below), are consistent with the designed amino acid sequences (left panel below) and cover the designed amino acid mutation species at all loci, as expected from the experimental design.

High homogeneity: After translation of mutant library sequences into amino acid sequences (right panel below), the percentage of each amino acid mutation is very homogeneous, avoiding concentration differences to interfere with downstream experiments and ensuring parallel and reliable downstream experiments.

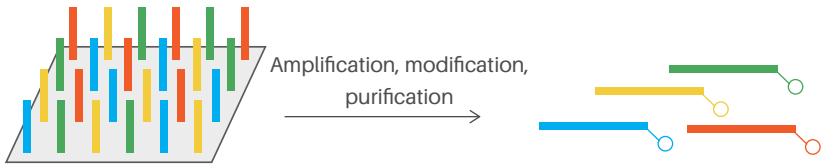


3 NGS Hybridization Capture Probe Libraries Construction

NGS constructs hybridization capture probe libraries by oligo pool synthesis, which can be used for both target gene capture and testing, as well as specific probe sequences for target sequence screening.

The hybridization capture libraries prepared by amplification, modification and purification based on GenScript's oligo pool demonstrates high coverage, high capture efficiency and reproducibility with similar capture effect at a much lower price than the finished hybridization capture library (single oligo synthesis and mixing), which is more economical.

Process of Oligo Pools for Hybridization Capture Probe Library Construction



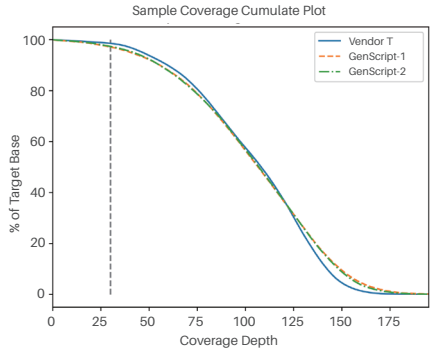
Oligo pool synthesis design sequence

Hybridization capture probe libraries

*NGS hybrid capture probe libraries: only modified and purified libraries are available for direct use in downstream experiments

Case Sharing

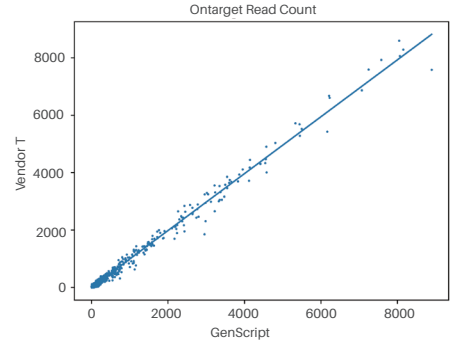
Experiment: Fragments of 127 gene sequences from 12 tumor tissues on an 800 kb human genome were captured, and the capture coverage, capture efficiency, and reproducibility between parallel experiments of hybridization capture probe libraries (microarray synthesis technology) constructed using GenScript oligo pools versus finished hybridization capture probe libraries (Supplier T, single-strip synthesis technology) were compared.



Capturing base sequence coverage of target fragments

High fragment coverage: When the sequencing depth is ≥ 30×, the base sequence coverage of the target fragment captured by the capture probe library is as high as 97.15%, which is consistent with the base sequence coverage of the finished capture probe library, and the base sequence coverage of the two is similar at different sequencing depths, which can satisfy the capture and subsequent detection of the target gene, indicating that the microarray technology can be used for hybridization capture probe library construction at a lower price instead of single synthesis technology.

High reproducibility: The batch-to-batch consistency of the microarray in 2 parallel experiments based on oligo pool synthesis strongly ensures the reproducibility of the experiments.



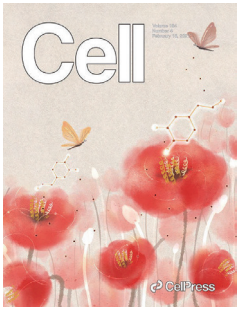
Comparison of reads number captured for the target fragment

High capture efficiency: Under the same experimental conditions, the reads number of target fragments captured by the capture probe library construction based on GenScript oligo pools is similar to that of the finished capture probe library, which can successfully capture a sufficient proportion of target fragments for subsequent amplification and up-sequencing.

GenScript Oligo Pool - The Trusted Choice of Library Construction

GenScript and its acquired CustomArray have been focusing on oligo pool synthesis technology for more than 10 years, gaining the trust and favor of more and more molecular biology scientists and library construction experts with high quality and stable delivery, helping more and more high impact factor papers to shine in the international academic arena.

Selective papers published with CustomArray (GenScript) oligo pool synthesis:



Reference 1. Massively parallel assessment of human variants with base editor screens

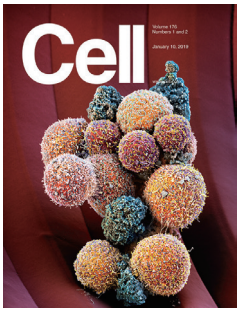
CRISPR/Cas9 cytosine base editor gene pool screening method is used for massively parallel assessment of human single nucleotide variants, where sgRNA libraries based on oligo pool synthesis are used to accelerate research.

Cell. 2021. **IF 38.637**

Reference 2. Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells.

The CRISPR-Cas9 GeCKO libraries constructed based on the sequences synthesized by CustomArray oligo pools has successfully edited 18,080 genes using 64,751 specific guide sequences for subsequent positive and negative screening on human-derived cell models.

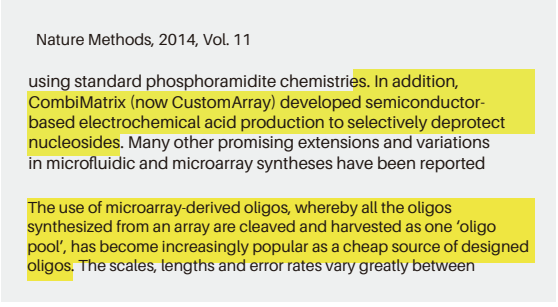
Science, 2014. **IF 41.058**



Reference 3. A Genome-wide Framework for Mapping Gene Regulation via Cellular Genetic Screens

The sgRNA libraries constructed using sequences synthesized from CustomArray oligo pools allow stable gene editing to find and study enhancer sequences by randomly combining the products of CRISPR/Cas9 editing and subsequently performing RNA sequencing of single cells.

Cell, 2019. **IF 31.398**



Nature Methods, 2014, Vol. 11

using standard phosphoramidite chemistries. In addition, CombiMatrix (now CustomArray) developed semiconductor-based electrochemical acid production to selectively deprotect nucleosides. Many other promising extensions and variations in microfluidic and microarray syntheses have been reported

The use of microarray-derived oligos, whereby all the oligos synthesized from an array are cleaved and harvested as one 'oligo pool', has become increasingly popular as a cheap source of designed oligos. The scales, lengths and error rates vary greatly between

Reference 4. Large-scale *de novo* DNA synthesis: technologies and applications.

The oligo pool synthesis technologies, represented by CustomArray semiconductor technology, can be applied to functional research and editing of regulatory elements, protein editing, gene regulatory networks and metabolic pathway research at a more economical price.

Nature Methods, 2014. **IF 26.919**

03

Molecular Diagnostic Oligo

qPCR Probes and Oligo Synthesis Services

The consistent quality of GenScript's qPCR probes and oligo comes from superior R&D, standardized manufacturing processes and stringent quality control standards, as well as in-depth analysis by biological application scientists of influencing factors that may interfere with qPCR diagnostic applications, and strict control of these factors during the manufacturing process, which is a solid foundation for the accuracy and consistency of your testing.

In 2022, GenScript's oligo production department moved to a new, self-contained facility, where environmental cleanliness and contamination monitoring are strictly enforced to control exogenous contaminants and other interfering factors to ensure smooth downstream experiments.

Service Advantages

ISO 9001 clean laboratory

provides ISO 13485 certified manufacturing conditions

Very low exogenous contamination rate, eliminating NTC interference peaks

Environmental monitoring to control exogenous contamination

Stable fluorescent dyes to ensure high positive amplification signal

Low impact of storage time and conditions

Applications

Pathogen testing

Tumor screening

Personalized drug administration

Service Details

Type	Purification Methods*	Length (nt)	Deliverables	Lead Time and Price
qPCR probes	HPLC+	15-30	• Single tube or 96-well plate • Dry powder or solution • COA file	Please inquire
qPCR oligo	HPLC+	15-59		

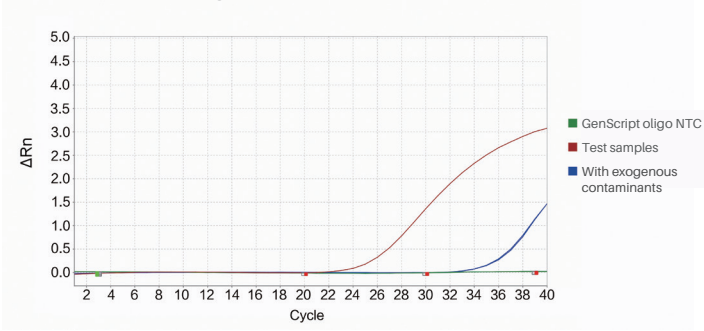
* HPLC + purification: The purification process developed and optimized for molecular diagnostics is completed in a clean laboratory. Before purification of each oligo, the column is thoroughly cleared of residues by multiple special rinsing procedures, and the different oligo are kept reasonably spaced apart and purified separately to avoid exogenous contamination to the greatest extent, with no peaks at NTC within 40 cycles. For more information on other purification methods, please ask for details.

GenScript provides ISO 13485 certified qPCR probes and oligo for customers who need clinical declaration of kits.

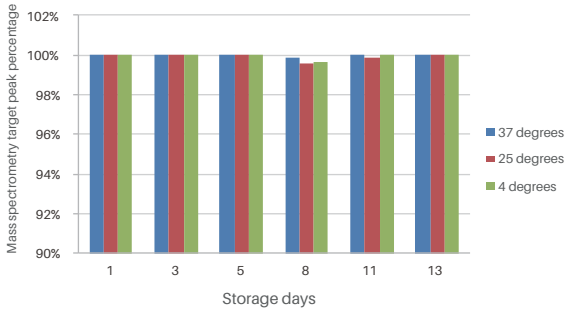
Welcome to inquire qPCR probes and oligo synthesis service: email to **oligo@genscript.com** get professional technical support.

Case Studies

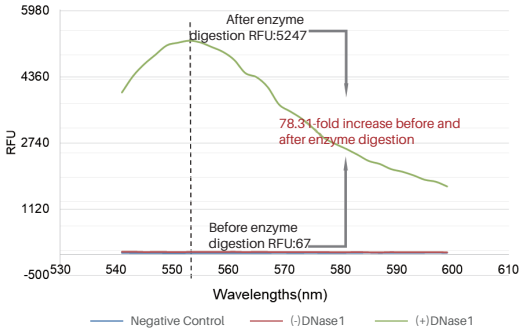
Low exogenous contamination rate, eliminating NTC interference peaks



Stable fluorescent labeling to ensure positive amplification signal



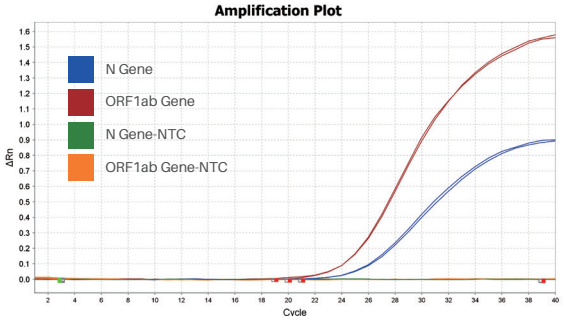
Significant fluorescence value enzymatic cut increment



After DNase I hydrolysis of TaqMan probes (i.e. after separation of fluorescence from quenched groups), the fluorescence increment is 78-fold and the probe can be used for target sequence testing.

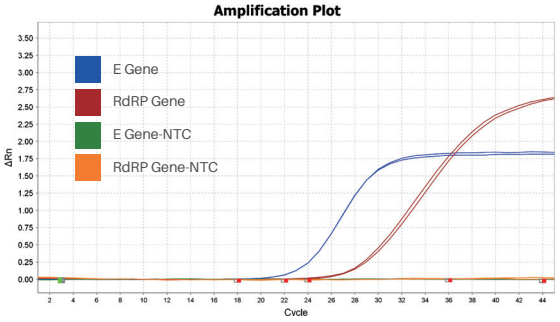
Multiplex PCR testing: successful testing of positive control and without peaks at NTC

N+O combination **FAM & NED**



Samples	Ct value
ORF1ab Positive Plasmid Control	24
N Positive Plasmid Control	25
NTC	ND

R+E combination **FAM & VIC**



Samples	Ct value
RdRP Positive Plasmid Control	27
E Positive Plasmid Control	23
NTC	ND

Analysis of Key Factors for qPCR Probe Application

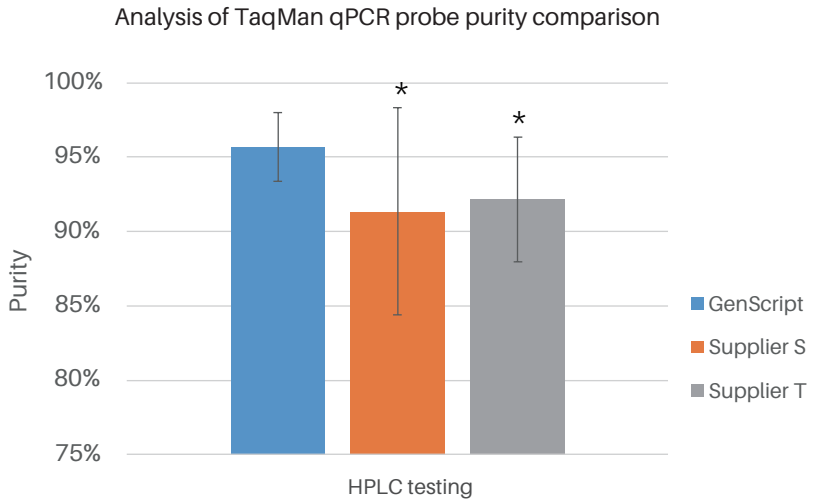
GenScript understands that the standard of conventional oligo is not enough to meet the strict requirements of qPCR probe quality for qPCR diagnostic applications. Which quality control standards are the key to the success or failure of qPCR experiments? GenScript's R&D team of professional chemical synthesis and biological application scientists will explain each of them to you.

1 Purity

The purity of qPCR probes is the percentage of full-length probes to all probes. A lower purity means that there are more probes with missing sequences (i.e., a higher percentage of N-X), which may lead to a decrease in amplification efficiency during the experiment, resulting in a large Ct value and affecting the testing results.

Experimental comparison methods:

The purity of the qPCR probes from GenScript, Supplier S and Supplier T were compared by HPLC for purity and by mass spectrometry for molecular weight, and the mean and standard deviation of more than 10 sets of probe samples were tested and counted respectively.



*$p < 0.05$, there are significant differences between Supplier S & Supplier T and GenScript

Experimental results show that:

The purity of GenScript's qPCR probes was significantly higher than that of Supplier S and Supplier T. The difference in purity between multiple groups of probes was small, indicating good batch-to-batch consistency. The Error Bar of the purity of multiple sets of qPCR probes from Supplier S and Supplier T was large, indicating a greater difference in purity between oligo batches and poorer batch-to-batch consistency.

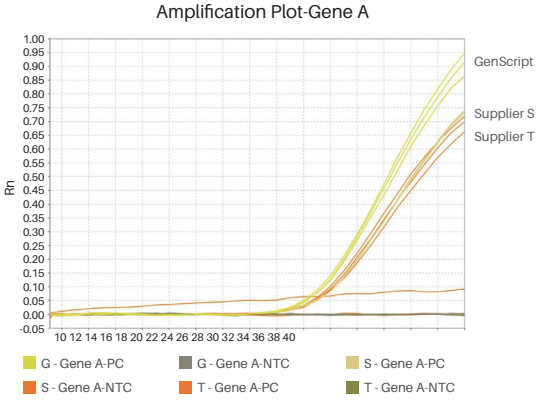
2 Fluorescence Intensity and CT Value

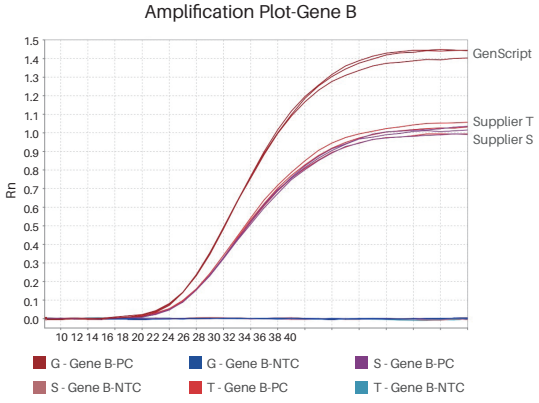
The Ct value is an important parameter for the qPCR probe testing and can be characterized based on whether the Ct value of the sample to be tested matches that of the positive control. The range of Ct value is 15-35, and under conditions of similar specificity, the probe with small Ct value, i.e. high amplification efficiency, should be preferably selected for the experiment.

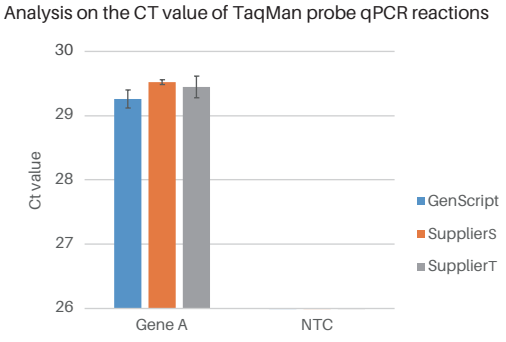
The qPCR experiment detects the target sequence by testing the fluorescence signal, so in general, the fluorescence signal intensity is also one of the important experimental parameters.

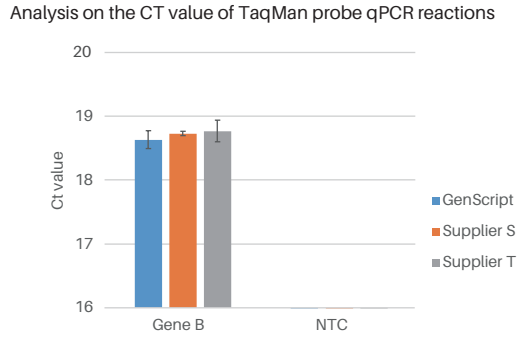
Experimental comparison methods:

For Gene A and Gene B, the fluorescence intensity and Ct values of GenScript, Supplier S and Supplier T qPCR probes were compared by qPCR amplification curve under the same experimental conditions.









Experimental results show that:

The fluorescence intensity of GenScript's qPCR probes was significantly higher than that of Supplier S and Supplier T.

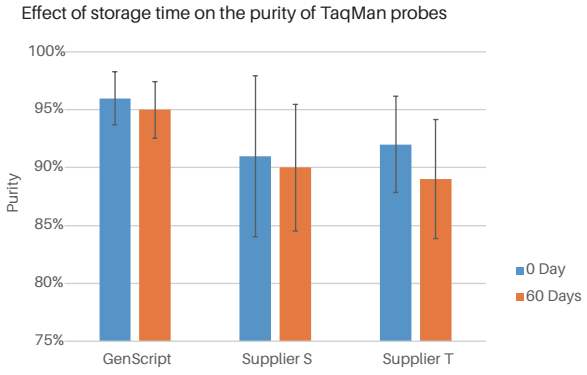
The Ct value of GenScript's qPCR probes was within the normal range and the Ct value is smaller than those of Supplier S and Supplier T, indicating that the amplification efficiency was higher than that of Supplier S and Supplier T.

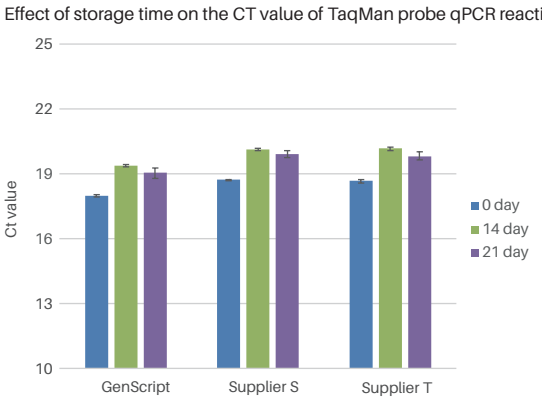
3 Stability

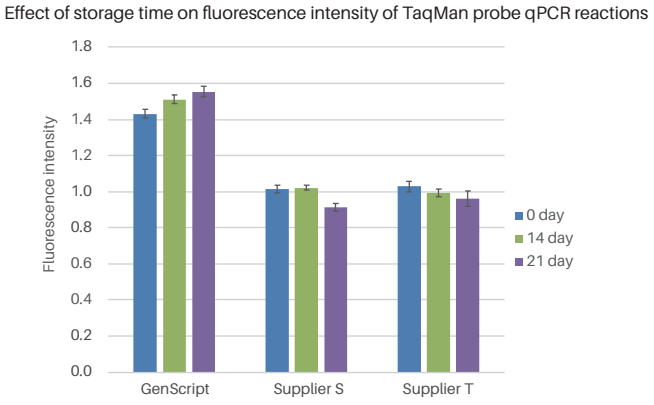
The stability of the qPCR probe determines the stability of the experiment, especially for products for molecular diagnostic applications. The stability of the probe, which is the core raw material, directly determines the stability of the molecular diagnostic kit.

Experimental comparison methods:

Under the same storage Buffer and storage concentration conditions, the qPCR probes from GenScript, Supplier S and Supplier T were tested for purity of the qPCR probes using HPLC after being placed at 4°C for 2 months, and both fluorescence intensity and Ct values were measured.







Experimental results show that:

After 2 months of storage at 4°C, GenScript's qPCR probes showed little change in purity, while the purity of Supplier S and Supplier T decreased, with large differences between sample groups.

The Ct values obtained by applying GenScript's qPCR probes were smaller and the fluorescence intensity was higher than that of Supplier S and Supplier T. Moreover, the Ct values and fluorescence intensity changed less with storage time, ensuring consistency between experiments.

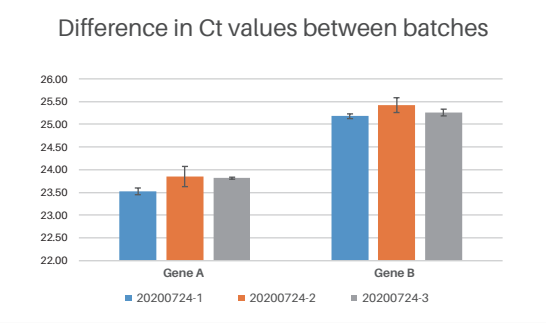
In summary, GenScript's qPCR probes are less affected by storage time and more stable, making them a high-quality choice for qPCR experiments and molecular diagnostic kit materials.

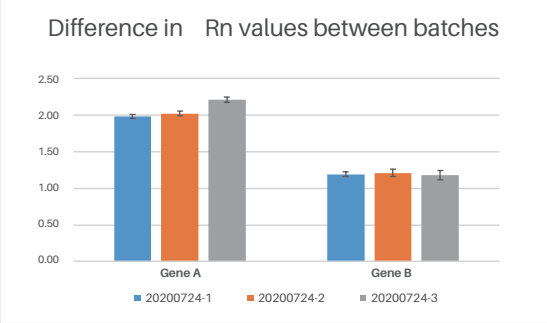
4 Batch-to-batch Consistency

GenScript implements strict SOPs to ensure good batch-to-batch QC consistency of qPCR probes, which in turn ensures better reproducibility between experiments.

Experimental comparison methods:

The Ct values and fluorescence intensities of qPCR probes from different batches produced at different times were measured for different Gene A and Gene B to compare the differences in the results of the probes between batches.





Experimental results show that:

The Ct values and fluorescence intensities obtained by using GenScript's qPCR probes for Gene A and Gene B from 3 batches are not significantly different, which can ensure the reproducibility of subsequent experiments and the stability of the diagnostic kit's test results.

Summary of the Advantages of GenScript qPCR Probes

Safeguards	qPCR Probe Advantages	Downstream Application Advantages
Clean laboratory Optimized purification process Strict quality control standards	**Very low exogenous contamination rate**	Eliminate NTC interference peaks Avoid non-sample factors interfering with experimental results
High quality fluorescent dyes Optimized fluorescence modification scheme	**Stable modifications and fluorescence signals**	Ensure that the positive signal of sample detection is stable
Precise quantification ISO 9001 and ISO 13485 Quality management certification Full SOP operation and monitoring	**Excellent batch-to-batch quality consistency**	Stable experimental data Fine experimental reproducibility

NGS Oligo Synthesis Services

For NGS library construction and target region enrichment applications, GenScript provides library construction adapter, Hybridization capture probes, and multiplex PCR Oligo, each with professional quality control and strict standards to match its application, providing high quality raw materials for NGS technology in molecular biology research and molecular diagnosis applications.

Service Advantages

Multiple library construction adapters

Low cross-contamination rate

Avoid misassignment of indexes and samples

Hybridization capture probes

Stable modifications and low base error rate

Eliminate probe off-target problems

Multiplex amplification oligo

Precise and uniform quantification

Improve target fragment amplification efficiency

Service Details

Type	Purification Methods	Length (nt)	Deliverables	Lead Time and Price
Library construction adapters	PAGE +/HPLC +/Desalting (RPC)	15 - 80	• Single tube or 96-well plate • Dry powder or solution • COA file	Please inquire
Hybridization capture probes (single synthesis/chip synthesis)		50 - 150		
Multiplex PCR Oligo		15 - 110		

***Purification process developed and optimized for molecular diagnostics:**

HPLC + purification: done in a clean lab, before purification of each oligo, the column is thoroughly cleared of residues by multiple special rinsing procedures, and the different oligo are kept reasonably spaced apart and purified separately to avoid exogenous contamination to the greatest extent, with no peaks at NTC within 40 cycles.

PAGE + purification: done in a clean laboratory; the target sequences are separated by denaturing polyacrylamide gel electrophoresis, and each oligo is purified with an independent purification system and disposable consumables to avoid the possibility of mixing with other oligo to the greatest extent. It effectively controls the cross-contamination rate to a level as low as 0.01%, which is especially suitable for the application of NGS adapter purification.

GenScript provides ISO 13485 certified NGS oligo for customers who have a need for clinical declaration of kits.

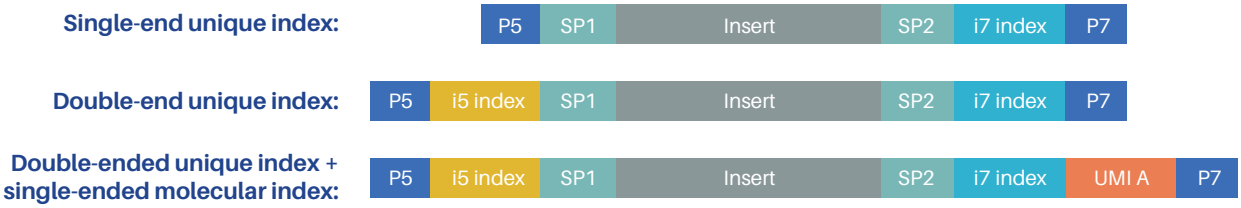
Welcome to inquire NGS Oligo synthesis service: email to **oligo@genscript.com** get professional technical support.

Adapter Oligo Synthesis Service

For NGS library construction, whether the sample is directly fragmented or the target region is obtained by hybridization capture, multiplex PCR amplification, etc., it is necessary to add adapter to each sample fragment by Enzyme-linked method (TA cloning adapter) or transposase method.

Sample indexes are included in the adapter sequence. After each sample is fragmented, all the fragments are connected to the same index, and the data of different samples can be categorized and processed by the different indexes.

Types of GenScript Adapters



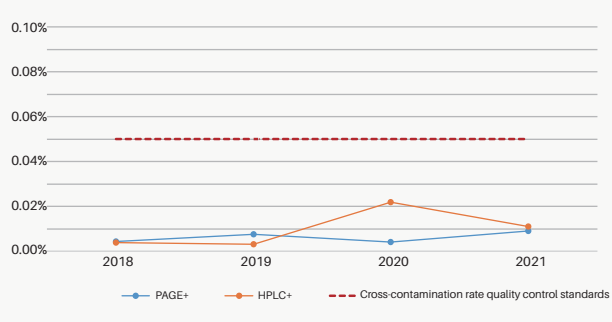
Single-end unique index: Only i7 Index is needed, and is suitable for sequencing of genotyping tests that are not sensitive to sample crosstalk, such as mutations at the somatic cellular level in genetic diseases.

Double-end unique index: Both i7 Index and i5 Index are needed, is suitable for high sensitivity tests, which effectively reduce Index misassignment by double-sided testing and eliminate sample cross-contamination of interfering data.

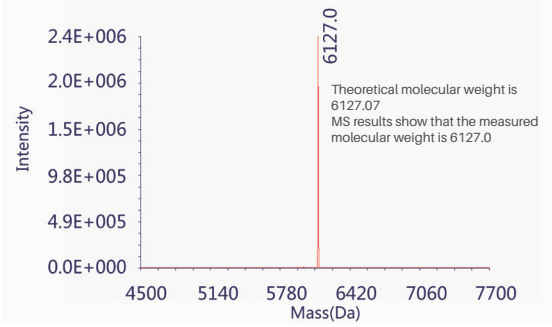
Double-ended unique index + single-ended molecular index: i7 Index and i5 Index are needed to effectively reduce misassignment and false sequence interference at all stages of NGS, it distinguishes low-frequency mutations using UMI, and excludes errors generated in amplification, and can be used to detect low-frequency mutations, such as liquid biopsies.

Advantages of GenScript

Low cross-contamination rate:
Avoid adapter-sample misassignment



Low base error rate: Ensure correct sample index sequence and accurate subsequent sequencing data



Hybrid Capture Probe Synthesis Services

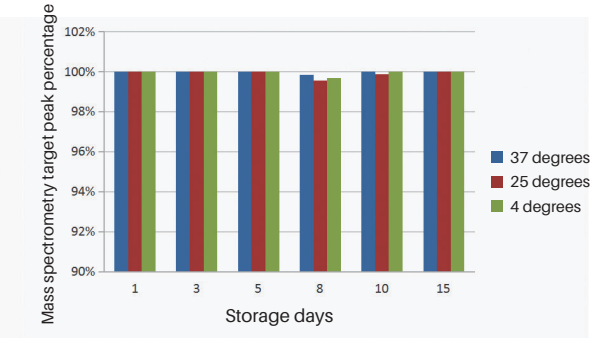
High sensitivity of target capture sequencing detection can reduce the workload of subsequent sequencing and data analysis, and is suitable for whole exon sequencing and target region sequencing. Hybrid capture technology isolates target region sequences by designing and synthesizing probes that bind specifically to the target region, and is one of the mainstream techniques for obtaining target fragments.

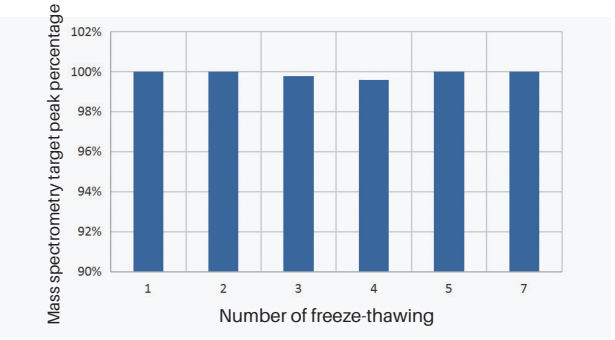
As a supplier with both single oligo synthesis and microarray synthesis platforms, GenScript can provide both high coverage and homogeneous microarray probe libraries for R&D stage and single synthetic probes for production stage with single quality control at a super high cost, which can provide cost-effective solutions for various target region capture, covering the whole process from R&D to production.

GenScript's single synthetic hybrid capture probes, with precise quantification, full automated dispensing, and optional deep desalination process, ensure good homogeneity of hybrid capture probe libraries, correct oligo profiles per strip, and throughputs up to 10,000+ probes/day. The high quality and high throughput production line provides stable support for NGS hybrid capture probe library needs.

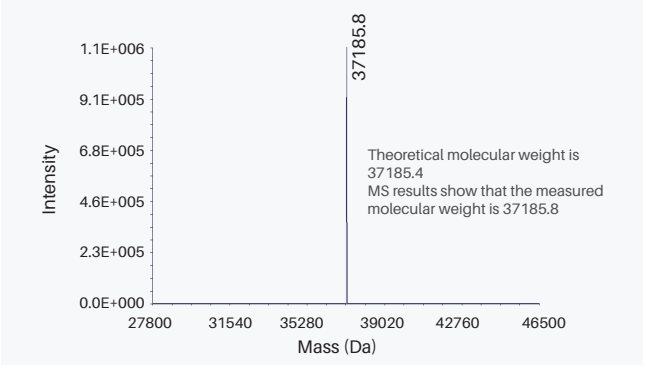
Advantages of GenScript

Stable modification: Storage time, temperature and number of freeze-thawing have very little effect on oligo modification stability and are more stable





Low base error: Ensure specific binding of probes to target fragments



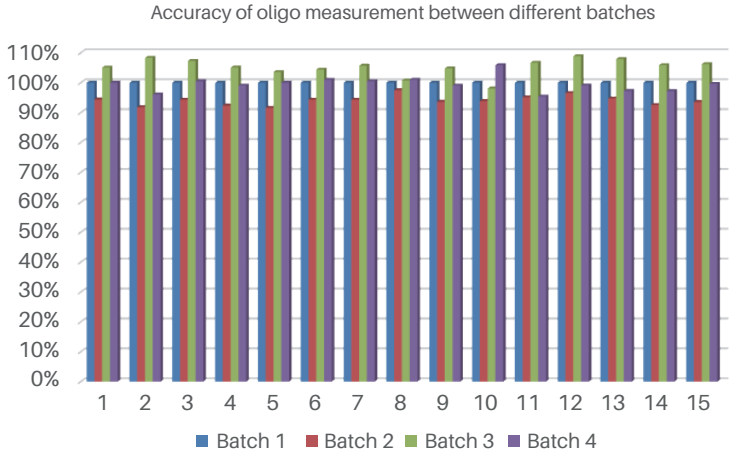
Multiplex PCR Oligo Synthesis Service

Multiplex PCR is one of the techniques used in targeted sequencing to obtain target regions. Using a sample as a template, multiple pairs of forward and antisense oligo are designed to amplify multiple target sequences, thereby obtaining multiple target fragments at once. It is difficult to design multiplex PCR Oligo because of the need to add as many as thousands of oligo pairs simultaneously in the reaction system and the need to avoid mutual interference and poor homogeneity of amplification efficiency.

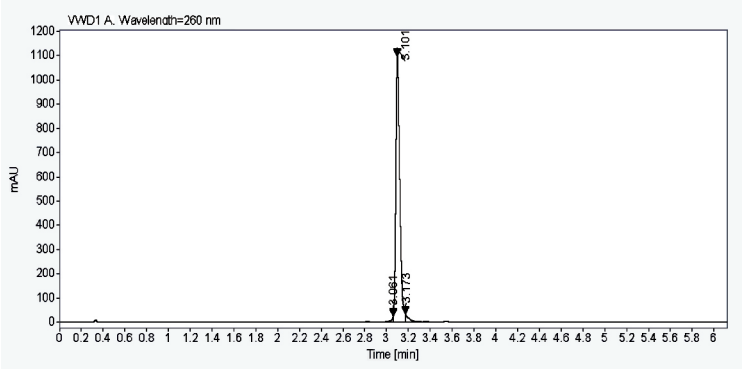
Meanwhile, it is necessary to accurately quantify the oligo to ensure that the concentration of each oligo pair in the multiplex amplification system is consistent or in accordance with the theoretical concentration ratio, so as to avoid the decrease of amplification efficiency caused by too high oligo concentration or the low amplification product of the target fragment caused by too low oligo concentration.

Advantages of GenScript

Precise quantification: Low batch-to-batch difference, fine homogeneity of multiple target fragments obtained



Purity assurance: Low proportion of N-X fragments for higher amplification efficiency



Analysis of Key Factors for NGS Applications

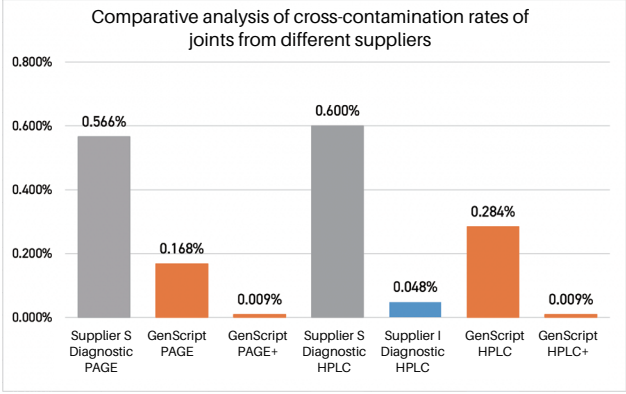
Are your NGS experiments always failing to get the desired data? Perhaps you have neglected the fact that the quality standards required for NGS Oligo materials are much higher than those for conventional oligo. GenScript senior scientists will explain which oligo quality standards are critical to NGS results.

1 Cross-contamination Rate

The cross-contamination rate characterizes the rate of mixing other oligo in the adapter oligo. The adapter must strictly control the cross-contamination rate to ensure that each sample fragment is attached to an exclusive index, so that cross-contamination will not cause mismatch of samples and adapter, which will lead to wrong results when multiple samples are mixed for sequencing. GenScript NGS Oligo are purified by optimized PAGE+ and HPLC+, and the cross-contamination rate can be as low as 0.01% with strict control.

Experimental comparison methods:

NGS was performed using Illumina TruSeq library construction kits and MiSeq instruments to detect the cross-contamination rate of adapter oligo from different domestic and international suppliers.



Experimental results show that:

The cross-contamination rate of GenScript conventional PAGE and HPLC Oligo is significantly lower than that of Supplier S.

GenScript's PAGE+ and HPLC+ Oligo optimized for molecular diagnostic oligo have significantly lower cross-contamination rates than conventional PAGE and HPLC, and far lower than Supplier S's diagnostic-grade PAGE and HPLC.

Cross-contamination rates of GenScript's HPLC+ Oligo are also significantly lower than those of Supplier's diagnostic-grade HPLC.

2 Oligo Purity

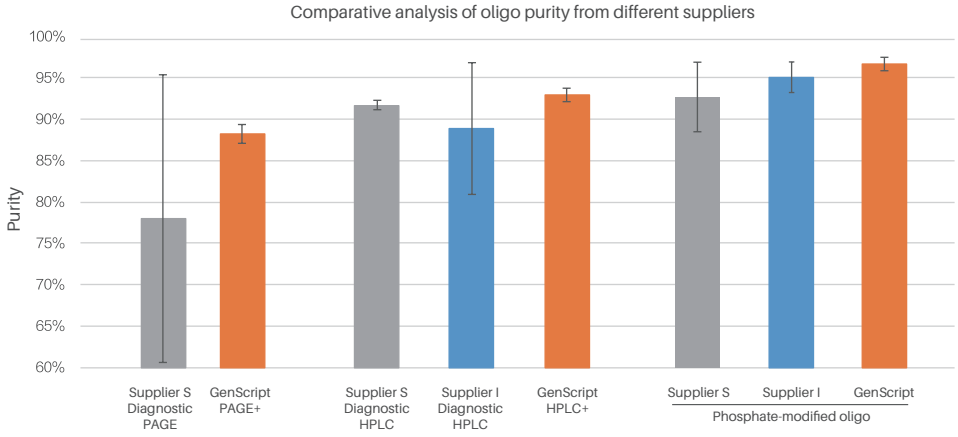
Oligo purity is a measure of the proportion of intact oligo sequences, with higher oligo purity indicating a lower proportion of N-X by-products in the oligo.

- For adapters, higher purity allows a higher proportion of intact sequence adapters to bind to sample fragments or Flow Cells.
- For hybrid capture probes, higher purity allows a higher proportion of intact probes to bind to the target fragment, ensuring capture efficiency.
- For multiplex PCR Oligo, high purity helps to ensure a higher proportion of intact sequence oligo can bind to the template to ensure the efficiency of subsequent amplification.

Meanwhile, the stability of parameters such as purity between different oligo samples and between batches is an important factor to ensure consistency between experiments.

Experimental Comparison Methods:

The purity of oligo and phosphorylated oligo from different domestic and foreign suppliers was tested by HPLC.



Experimental Results Show That:

The purity of GenScript PAGE+ oligo, HPLC+ oligo and phosphate-modified oligo were higher than that of Supplier S and Supplier I.

The difference in purity between samples of GenScript oligo was significantly lower than that of Supplier S and Supplier I, suggesting a small batch-to-batch difference, which was conducive to experimental reproducibility and batch-to-batch consistency of molecular diagnostic products.

GenScript NGS Oligo Advantages Summary

Safeguards	Advantages of GenScript	Downstream Application Advantages
Optimized independent purification process Strict quality control standards	Adapter oligo **Low cross-contamination rate**	Avoid sample fragment and adapter mismatches
Optimized modification scheme 19-year synthesis technology and experience	Hybrid capture probes (single synthesis) **Stable modifications** **Low base error rate**	Improve capture efficiency
More precise control of semiconductor chips Low interference in closed synthesis system	Hybrid capture probes (microarray synthesis) **Fine homogeneity**	High throughput and cost-effective choice
Precise quantification technology Full SOP operation and monitoring ISO 9001 and ISO 13485 quality management certified	Multiple PCR oligo **Small batch-to-batch difference**	Avoid high quantification affecting amplification efficiency or low quantification causing low target fragments

04

Oligo Resource Center

FAQ

Conventional Oligo Chapter

Q: What are the basic principles of oligo design?

A: The following principles of oligo design are for your reference:

1) oligo should preferably be designed within the conserved region of the template cDNA.
2) Oligo length is generally between 15-30 bases.
3) The GC content of the oligo should be between 40%-60%, and the temperature should preferably be close to 72°C.
4) The 3′ end of the oligo should avoid the 3rd position of the codon.
5) The 3' end of the oligo cannot be A, but preferably T.
6) The bases should be randomly distributed.
7) There should be no complementary sequence within the oligo or between different oligo.
8) The oligo should have relatively high ΔG values at the 5′ end and middle ΔG values, and low ΔG values at the 3′ end.
9) The 5′ end of oligo can be modified, but the 3′ end cannot be modified.
10) The single strand of the amplification product should not form a secondary structure.
11) The oligo should be specific.

Oligo 6 and Oligo Premier 5.0 are the most commonly used software. You are welcome to use our oligo design tools in the "Oligo Resource Center" on GenScript website.

Q: How to store the oligo?

A: After the oligo are synthesized, they undergo a series of processing and purification steps, and are spin-dried to form a flake. The undissolved oligo are very stable and can be stored at -20°C for 2-3 years orlonger. The dissolved oligo can be stored for at least half a year at -20°C avoiding repeated freeze-thawing.
If the requirement of repeatability for the experiment is high, the OD value of the synthesis is large or the synthesis amount of a single oligo is large, it is recommended to dilute the dissolved oligo into a 100 M storage solution beforehand and store it in several portions at -20°C in the refrigerator. Before use, dilute the concentrated solution into working solution (10-20 M) and then perform the experiment.
The fluorescent modified oligo need to be stored away from light.

Q: Will the oligo degrade if they are transported at room temperature?

A: No, the lyophilized oligo can be stored stably at room temperature for at least 2 weeks. The normal transport time is usually 1-3 days, so the oligo you receive will not degrade.

Q: How to dissolve the oligo?

A: The oligo are very loose after drying, therefore, it is best to centrifuge the oligo at 3,000-4,000 rpm for 1 minute or tap the tube vertically upwards on the table several times before opening the cap to collect the oligo powder at the bottom of the tube and prevent the oligo from scattering when opening the cap.
Add calculated volume of deionized sterile water or 10 mM Tris pH 7.5 buffer, leave at room temperature for a few minutes, mix and shake up and down, and centrifuge to collect the solution to the bottom of the tube. Generally, do not use distilled water to dissolve oligo because some distilled water has a relatively low pH (pH 4-5) and oligo are not stable under such conditions.
Our synthesis report sheet shows the amount of water to be added for each tube of oligo diluted to 100 M (i.e. 100 pmol/ l), but
you can add the appropriate amount of nuclease-free double distilled water (pH > 6.0) or TE buffer (pH 7.5-8.0) depending on your experimental needs.

Q: Why does a dissolved oligo work fine at first, but not well after a period of time?

A: If the pH of the water you dissolved the oligo is too low or contaminated with bacteria or nucleases, it will degrade the oligo. Insufficient thawing or mixing when using the oligo may also result in inaccurate oligo addition. It is recommended to split the oligo, avoid repeated freeze-thawing, and use 10 mM Tris pH7.5 buffer to dissolve the oligo. Another possibility is that there is no problem with the oligo, but that the quality of the materials used for PCR, especially the template, is not exactly the same as previously used.

qPCR Oligo Chapter

Q: What are the basic principles of TaqMan probe design?

A: The following principles are for your reference:

1) TaqMan probes should be positioned as close as possible to the amplification oligo (50-150 bp of amplification product), but not overlapping with the oligo.
2) The length is usually 18-40 mer.
3) The G-C content should be controlled to around 40-80%.
4) Avoid the appearance of consecutive identical bases, especially to avoid the appearance of GGGG or more G.
5) Avoid using G at the 5' end of the oligo.
6) Choose more bases C.
7) The annealing temperature should be controlled to around 68-70°C.

Design tools of our company: https://www.genscript.com/tools/real-time-pcr-taqman-oligo-design-tool

Q: What are the selections of common fluorescence spectra and quenching groups?

A: Choose according to the qPCR instrument model, and the recommended fluorescence groups will be available in the qPCR instrument description. At the probe level, ensure that the quenching groups can efficiently absorb the emission wavelength of the reporter groups, and that the excitation and emission wavelengths of each dye can be distinguished when multiplexed tests are performed to avoid cross-talk. Common fluorescence spectra and quenching groups are shown in the following figure for reference:

Fluorophore	Excitation Max [nm]	Emission Max [nm]	Quenching group	Quenching range
6-FAM	494	518	BHQ-1 / TAMRA	BHQ-1 480-580 nm TAMRA 520-600 nm
6-JOE	520	548	BHQ-1 / TAMRA	
6-TET	521	542	BHQ-1 / TAMRA	
6-HEX	533	559	BHQ-1 / TAMRA	
6-VIC	538	554	BHQ-1	
NED	546	575	BHQ-2	BHQ-2 559-670 nm
Quasar 570	548	567	BHQ-2	
CY3	555	570	BHQ-2	
6-TAMRA	559	583	BHQ-2	
6-ROX	588	608	BHQ-2	
Texas red-X	598	617	BHQ-2	
CY5	646	662	BHQ-2	
Quasar 670	647	666	BHQ-2	
CY5.5	684	710	BHQ-3	BHQ-3 620-730 nm

Q: What is the difference in the use of double-labeled fluorescent probes with quenching groups as TAMRA, Eclipse or BHQ series dyes?

A: Double-labeled fluorescent probes consisting of quenching groups as TAMRA, Eclipse or BHQ series dyes are often used as Hydrolysis Probes, or TaqMan probes, for real-time fluorescent qPCR experiments.

1) TAMRA is a fluorescent dye that emits fluorescence at a higher wavelength while quenching the reporter group. The Eclipse and BHQ series are non-fluorescent dyes that do not emit fluorescence themselves while quenching the reporter group. The fluorescence background of the probe is lower than that of TAMRA and the detection sensitivity is higher.

2) TAMRA has a narrow absorption spectrum and can be matched with fewer reporter groups, while Eclipse has a wider absorption range (390 nm-625 nm) and can be quenched with many reporter groups, such as FAM, HEX, TAMRA, ROX, etc.; the absorption spectrum of the BHQ series dyes used in combination covers a wider range, from 430 nm to near infrared, and can be quenched by a wider variety of reporter groups, including Cy3, Cy5, etc. Therefore, a set of double-labeled fluorescent probes can be composed of Eclipse or BHQ series dyes for multiplex PCR.

Q: Taqman method of qPCR system and program reference settings

A:

Taqman method qPCR system

Component	Volume (μL)
Master Mix	10
Nuclease-free water	8
Template sample (1 pg/μL)	1
Forward/reverse oligo (10 μM)	0.4
Probe (10 μM)	0.2
Total volume of each reaction	20

Taqman method qPCR procedure

Temperature	Time	Cycle number
37	2 min	/
95	5 min	/
95	15 s	45X
60	30 s	

Q: How should synthetic fluorescent labeled probes be preserved?

A: Fluorescent probes should be stored as follows:

1) Fluorescent probes must be stored away from light.

2) Dry products can be stored at -80°C for more than one year. If there is no such storage condition, please store at -20°C.

3) It is highly recommended to dissolve the probes in RNase-free TE (pH8.0) buffer, as this will result in a more stable probe solution and longer storage time. Usually, the probe is prepared as a 100 M stock solution, divided into several portions (each portion is repeatedly freeze-thawed up to 5 times), and stored at -20°C. Before use, the prepared stock solution is diluted into a working solution (10 M or 20 M) and store the remaining portion at -20°C.

NGS Oligo Chapter

Q: How do I standardize NGS sample handling?

A: The quality control of sample preparation should not be neglected because the standardized sample handling directly affects the results of NGS assay. The recommendations of Technical Guideline for Individualized Tumor Therapy Testing (Trial) are as follows.

1) **Surgical and biopsy tissues:** Samples are fixed with 10% neutral formalin and taken according to the pathology operation specification; biopsy specimens are fixed for 24 hours, and the fixation time of puncture samples controlled in 6-24 hours is preferable; some DNA will be fragmented after samples are immersed for a long time for more than 1 week, and mutations cannot be detected, which will affect the diagnostic results.

2) **Tissue sectioning:** It is recommended to cut 5 consecutive sections, one of which is stained with HE to confirm the content of tumor cells. Too low tumor tissue content will directly affect tumor gene mutation abundance and cause false negatives, therefore, the tumor tissue content of each section should be at least 70%.

3) **Puncture paraffin specimens:** 1-2 paraffin sections (2 ng DNA) can meet the sequencing needs. The starting amount of DNA samples varies among different assays, and currently, with the continuous optimization of library construction products, the requirement of sample input quantity for library construction is also decreasing.

4) **For plasma samples:** Peripheral blood is collected to extract circulating DNA (cfDNA) for testing. Samples are collected using a disposable closed EDTA anticoagulated vacuum blood collection tube; 6-10 mL of whole blood is collected, transported under refrigeration; plasma is separated within 6 hours; free DNA is extracted, and stored in a -80°C refrigerator and repeated freeze-thawing should be avoided. If peripheral blood needs to be transported for a long time, it is recommended to use commercial free DNA sample preservation tubes. cfDNA can be stably preserved in whole blood for 7 days under room temperature conditions.

5) **For sample quality control:**

Percentage of tumor cell: Routine pathological examination and diagnosis (H&E staining) is required to determine the percentage of tumor cells prior to testing, and if necessary, a tumor cell enrichment method, such as manual scraping or microdissection, should be used. Tissues with predominantly tumor cells without significant necrotic, mucinous and inflammatory changes are selected for testing to avoid false negative results. Ideally, the proportion of tumor cells should be not less than 50% in paraffin samples and not less than 25% in fresh samples. For more sensitive methods such as ARMS, the content and proportion of tumor cells can be lower, depending on the DNA extraction method used and the sensitivity of the mutation detection method, etc.

Nucleic acid purity: It can be determined by the extract OD260/OD280 ratio, which is 1.8 for DNA and 2.0 for RNA. If the DNA ratio is higher than 1.8, it means that the RNA has not been removed from the preparation. The presence of phenols and proteins in the RNA and DNA solutions will result in a lower ratio.

Q: How do I choose the library construction solution?

A: 1. **Enzyme-linked library construction mode:** It covers 3 steps: end repair after ultrasound fragmentation, flat end with A-tail, splice and amplification, which requires low DNA quality and high genome coverage, and is suitable for general gene pooling.

Advantages: Cost-effective, low sequence preference and wide application.

Limitations: Fragment damage; it requires more operation steps and takes about 2.5h.

2. Transposase library construction mode: It covers 2 steps: transposase fragment interruption and PCR with splice and amplification; it is easy to operate, suitable for processing a large number of samples; with low starting amount of library construction and low fragment damage, it is suitable for sample construction with limited sample volume.

Advantages: It requires less operation steps and takes about 1.5h.

Limitations: There is a sequence preference for transposase interruption.

Q: How do I choose the target region enrichment solution?

A: 1. **Hybridization capture technique:** According to the principle of DNA base complementary pairing, the target fragment is captured by probes designed to be specific and complementary to the target region, and enriched by amplification; the remaining fragments are removed by elution and NGS can be performed directly afterwards. The hybrid capture technology can capture a large target region at one time, from Mb size to exome, and can detect SNV, InDel, CNV, SV, gene fusion and other variants.

Advantages: The capture region is large and homogeneous. In tumor tissues, the structural variation is very large, and hybrid capture can detect unknown mutation sites of known genes and larger regions of insertion/deletion and gene fusion phenomena.

Limitations: Poor specificity - as the sample is randomly interrupted, the fragments captured by hybridization may be partly in the target region and partly in the non-target region, which cannot achieve 100% on-target rate. For special regions, such as high GC, tandem repeat regions, etc., the probe specificity are difficult to optimize and the hybridization time is long.

2. **Multiplex PCR amplification:** Design multiple pairs of upstream and downstream oligo to amplify multiple target fragments from sample templates at one time, and then perform library construction and NGS. It is more suitable for small target regions and point mutations, detecting tens to thousands of loci, or regions below 500 Kb, with less influence from the background genome. The specific amplification ability of ultra-multiplex PCR for trace DNA signals has higher sensitivity in areas such as cfDNA detection and identification of MRD.

Advantages: Low template starting volume, low oligo raw material cost, simple operation and short time.

Limitations: Oligo design is difficult; you need to ensure the specificity of amplification, and avoid oligo dimer, etc. There are some limitations for the detection of some unknown structures, and the oligo region will be lost if SNP occurs in the amplicon, etc. The number of amplified regions is limited.

Q: How to improve hybridization capture efficiency?

A: 1. **Apply closed non-specific sequences:** The Cot-1 sequence needs to be used to close the naturally occurring repetitive sequences (Homologous Recombination Deficiency, HRD) of varying degrees in genomic DNA, and the blocking oligo is used to close the adapter sequence of the sample fragment to avoid non-specific capture caused by hybridization between the capture probe and the sequence of these two regions, improving capture efficiency and subsequent sequencing data quality.

2. **Calibrate experimental instruments for temperature:** Even a slight change in temperature, e.g. ±2°C, during NGS hybridization elution operation may have an impact on the on-target rate of the Flanking region as well as GC bias. Slightly higher elution temperatures will result in a loss of capture of the AT region; slightly lower elution temperatures will result in increased non-specific capture and a decrease in the on-target rate.

3. **Avoid over-amplification:** For post-capture amplification, it is recommended to select the corresponding number of amplification cycles based on hybridization time and number of hybrids to avoid over-amplification. The lower the number of PCR cycles used, the less non-specific amplification and the higher the library construction efficiency when obtaining a yield library that meets the requirements of the machine.

Literature Published by Customers

In terms of services and products, GenScript have been cited by more than 1,300 international famous academic journals such as Cell, Science and PNAS. GenScript's oligo synthesis services and products have been used by a number of world-renowned institutions to publish their scientific achievements, demonstrating once again GenScript's ability to help scientists “Make Research Easy” in the industry.

The following are some scientific articles selected

Title: N6-methyladenine in DNA antagonizes SATB1 in early development

Journal: *Nature* IF 43.07

Doi: 10.1038/s41586-020-2500-9

Title: MAFG-driven astrocytes promote CNS inflammation

Journal: *Nature* IF 43.07

Doi: 10.1038/s41586-020-1999-0

Title: Genetic interaction mapping and exon-resolution functional genomics with a hybrid Cas9-Cas12a

Journal: *Nat Biotechnol* IF 41.667

Doi: 10.1038/s41587-020-0437-z

Title: Mammalian ALKBH1 serves as an N6-mA demethylase of unpairing DNA

Journal: *Cell Res* IF 17.848

Doi: 10.1038/s41422-019-0237-5

Title: Dysbiosis-Induced Secondary Bile Acid Deficiency Promotes Intestinal Inflammation

Journal: *Cell Host Microbe* IF 14.946

Doi: 10.1016/j.chom.2020.01.021

Title: Myelin-specific CD8+ T cells exacerbate brain inflammation in CNS autoimmunity

Journal: *J Clin Invest* IF 12.784

Doi: 10.1172/JCI132531

Title: Engineering and functionalization of large circular tandem repeat protein nanoparticles

Journal: *Nat Struct Mol Biol* IF 12.595

Doi: 10.1038/s41594-020-0397-5

Title: Utilization of Lanthipeptide Synthetases is a General Strategy for the Biosynthesis of 2-Aminovinyl-Cysteine Motifs in Thioamitides

Journal: *Angew Chem Int Ed Engl* IF 12.257

Doi: 10.1002/ange.202012871

Title: Quantitative assessment of the determinant structural differences between redox-active and inactive glutaredoxins

Journal: *Nat Commun* IF 12.124

Doi: 10.1038/s41594-020-0397-5

Title: Timing of exposure to environmental adjuvants is critical to mitigate peanut allergy

Journal: *J Allergy Clin Immunol* IF 12.047

Doi: 10.1016/j.jaci.2020.09.011

Title: Large-Scale, Quantitative Protein Assays on a High-Throughput DNA Sequencing Chip

Journal: *Mol Cell* IF 14.714

Doi: 10.1016/j.molcel.2019.02.019

Title: CRISPR screen identifies genes that sensitize AML cells to double-negative T-cell therapy

Journal: *Blood* IF 13.164

Doi: 10.1182/blood.2019004108

Title: Phospho-ERK is a biomarker of response to a synthetic lethal drug combination of sorafenib and MEK inhibition in liver cancer

Journal: *J Hepatol* IF 12.486

Doi: 10.1016/j.jhep.2018.07.004

Title: High-resolution characterization of gene function using single-cell CRISPR tiling screen

Journal: *Nat Commun* IF 12.124

Doi: 10.1038/s41467-021-24324-0

Title: Programmable human histone phosphorylation and gene activation using a CRISPR/Cas9-based chromatin kinase

Journal: *Nat Commun* IF 12.124

Doi: 10.1038/s41467-021-21188-2

Title: Low cost DNA data storage using photolithographic synthesis and advanced information reconstruction and error correction

Journal: *Nat Commun* IF 12.124

Doi: 10.1038/s41467-020-19148-3

05

Ordering Guide and Contact Information

Order Method

GenScript provides a simple and fast online ordering system for you to quickly submit your oligo synthesis orders anytime, anywhere, supporting different delivery forms, purification methods, modification types and other parameters to provide you with clear quotation/lead time information, which not only helps you complete your orders in time and carry out experiments on time, but also allows you to understand all the information of your orders at a glance.

Advantages of Online Ordering

Simple Operation

Excel mode, only 3 steps, as fast as 30 seconds

Complete Functions

Dry powder/liquid, single tube/96-well plate options

Clear Quotation

Quote one by one; quotation for synthesis/purification/modification

Email US: You can send your demand information to protein@genscript.com

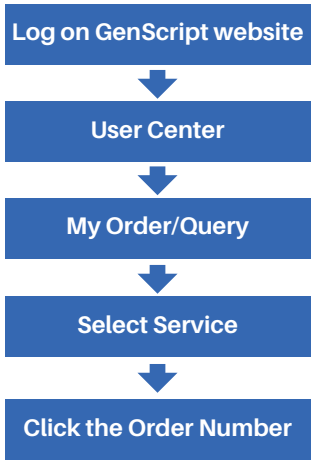
Call US: USA: +1-732-885-9188
Netherlands: +31 (0) 71 569 0120
United Kingdom: +44 (1865) 679988
Singapore: +65 3159 1898
Japan: +81-3-6811-6572
Korea: +82-10-9311-9208

Order Query

How to Query?

1. Log in to your GenScript account
2. Click Account Name - User Center
3. Click "My Order/Query" in the taskbar on the left of the page
4. Select "Oligo Synthesis" service for the order type
5. Click the order number to enter the "Order Details" page to view the order progress.

For delayed and difficult orders, please feel free to send us an email for consultation and confirmation and we will reply and follow up as soon as possible.



How do I Download the Report?

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- Electronic reports can be downloaded from the list of "**User Center - My Order/Query**" on the official website by clicking "↓" in the column of "**Invoices & Documents**".

GenScript has always been committed to meeting the needs of its customers and to bringing advanced technology to millions of labs.

More events

please visit **"GenScript Oligo Synthesis Service"**