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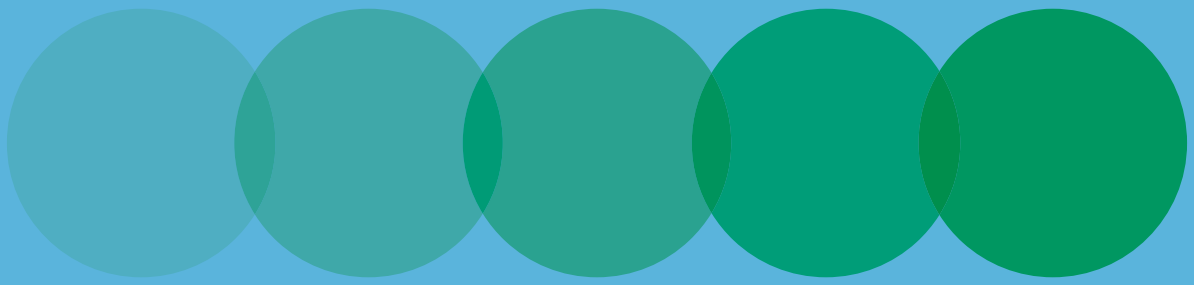
OLIGO SYNTHESIS



Humanizing Genomics
macrogen

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OLIGO SYNTHESIS SERVICE

Custom DNA Oligos

INTRODUCTIONS

Macrogen has prepared a total automation system for the synthesis process as supplemented with very recent synthesis equipment.

Oligonucleotides are synthesized as making the reaction on the column after binding 3'end of nucleosides to the support (controlled pore glass, CPG) for fixing. In this process, one of the important factors influencing the oligonucleotide's quality is the CPG size. Macrogen use 1000Å CPG and provide high quality of products.

- Synthesis scales from 0.025 ~1umole
- Free MOPC purification(cartridge method)
- Sequence length from 3~130bases
- Free shipping: ≥ 300bases of primers
- Liquid Handing System (normalization)

PURIFICATION

- Salt free(Desalt)
  - For only 25nmole unmodified(standard) DNA oligos
  - Length from 3~35bases
- MOPC™ Purification(Cartridge purfication)
  - Available for all unmodified and most modified oligos
  - Guaranteed purity of >85%
  - Suitable for PCR ,sequencing, SNP analysis, mutation studies, cloning, expression, and siRNA expression
  - Free of charge
- HPLC purification
  - Available for all unmodified and modified oligos
  - Recommend less than 50base of oligos
  - Guaranteed purity of >90%
- PAGE purification
  - Available for all unmodified and modified oligos
  - Recommend less than 50base of oligos
  - Guaranteed purity of >=95%

Guaranteed yields:

PURIFICATION	Synthesis Scale			
	0.025	0.05	0.2	1
DESALT	3			
MOPC		6	8	20
PAGE		2	4	8
HPLC		2	4	8

The minimum yield guarantees are valid for unmodified oligos ≥25bases

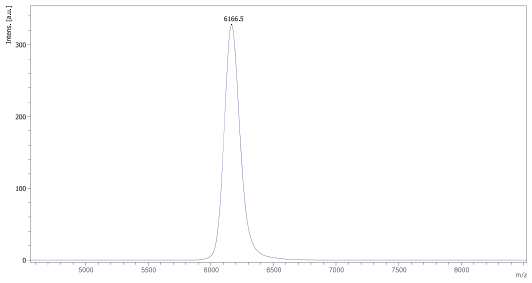
100% QC FOR ALL OLIGOS

All oligonucleotides are taken for MALDI-TOF analysis for the purpose of quality control before delivered to customers. If the error range between the calculated molecular weight and measured molecular weight exceeds 0.2%, an acceptable range, the product is automatically failed for shipping process.

Poor oligonucleotide which might be made during the synthesis process is completely selected out via this process.

Oligo synthesis report including MALDI-TOF result(QC report) is providing with oligos.

Result of MALDI-TOF Analysis



MODIFICATION TYPE

Fluorescent dyes	- FAM, HEX, TET, JOE, TAMRA, CY3, CY5, CY3.5, CY5.5 - CAL Fluor560 - ATTO565 NHS-ester, ROX NHS-ester, TexasRed NHS-ester
Non Fluorescent Modifications	- Phosphorylatioin, Biotin, NH2C6, NH2C12, C3 Spacer, dSpacer - Thiol C6 S-S
Dark Quenchers	- Black Hole Quencher (BHQ1, BHQ2, BHQ3) - Blackberry Quencher (BBQ650) - Dabcyl and Eclipes quencher
Internal Modification	- Deoxylnosine (dI)

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DUAL-LABELED DNA PROBES

5' Fluorophore	3' Quencher
FAM	TAMRA, BHQ1, Dabcyl
HEX	TAMRA, BHQ1, BHQ2, Dabcyl
TET	TAMRA, BHQ1, BHQ2, Dabcyl
JOE	TAMRA, BHQ1, BHQ2, Dabcyl
CY3	BHQ1, BHQ2, BHQ3
CY3.5	BHQ2
CY5	BHQ2, BHQ3
CY5.5	BHQ2, BHQ3, BBQ650
TAMRA	BHQ1, BHQ2, Dabcyl
CAL Fluor560	BHQ1
ATTO565 NHS-ester	BHQ1, BHQ2, BBQ650
ROX NHS-ester	TAMRA, BHQ2, BBQ650
TexasRed NHS-ester	BHQ1, BHQ2, BBQ650

DUPLEX OLIGOS (DOUBLE-STRANDED OLIGOS)

- Annealed oligos are supplied dry in tubes
- Synthesis scales from 0.05 ~1umole
- Liquid Handing System (normalization)
- Modified oligos are also available.

PREMADE OLIGOS

- 5nmol (20ug) of ≥ 95% pure primer in tubes (PAGE purification)
- Checking the purity through the HPLC
- Random primer, Sequencing primer, 16s/18s rRNA PCR & Sequencing primer

SEQUENCING PRIMERS

Primer Name	Sequence	Base
a-Factor	TACTATTGCCAGCATTGCTGC	21
AD Reverse	AGATGGTGCACGATGCACAG	20
AOX1 Forward	GACTGGTTCCAATTGACAAGC	21
AOX1 Reverse	GCAAATGGCATTCTGACATCC	21
BGH-R	TAGAAGGCACAGTCGAGG	18
Bluescript SK	CGCTCTAGAACTAGTGGATC	20
Bluescript KS	TCGAGGTCGACGGTATC	17
CMV-F	CGCAAATGGGCGGTAGGCGTG	21
CYC1 Reverse	GCGTGAATGTAAGCGTGAC	19
DsRed1-C	AGCTGGACATCACCTCCCACAACG	24
DsRed1-N	GTACTGGAACTGGGGGGACAG	21
EBV-RP	GTGGTTTGTCCAAACTCATC	20
EGFP-N	CGTCGCCGTCCAGCTCGACCAG	22
EGFP-C	CATGGTCCTGCTGGAGTTCGTG	22
EGFP-CF	AGCACCCAGTCCGCCCTGAGC	21
EGFP-CR	CGTCCATGCCGAGAGTG	17
EGFP-NR	CGTCGCCGTCCAGCTC	16
GAL1 Forward	AATATACCTCTATACTTTAACGTC	24
Gal4AD	TACCACTACAATGGATG	17
GLprimer1	TGTATCTTATGGTACTGTAACTG	23
GLprimer2	CTTTATGTTTTTGGCGTCTTCCA	23
LCO1490	GGTCAACAAATCATAAAGATATTGG	25
HCO2198	TAAACTTCAGGGTGACCAAAAAATCA	26
KAN2-FP	ACCTACAACAAAGCTCTCATCAACC	25
KAN2-RP	GCAATGTAACATCAGAGATTTTGAG	25
M13R-pUC(-40)	CAGGAAACAGCTATGAC	17
M13F	GTAAAACGACGGCCAGT	17
M13R	GCGGATAACAATTTCACACAGG	22
M13-FP	TGTAAAACGACGGCCAGT	18
MT Forward	CATCTCAGTGCAACTAAA	18
pGEX5	GGCAAGCCACGTTTGGTG	18
pGEX3	GGAGCTGCATGTGTCAGAGG	20
pMalE	TCAGACTGTCGATGAAGC	18
pQE-F	CCCGAAAAGTGCCACCTG	18
pQE-R	GTTCTGAGGTCATTACTGG	19
pBAD-F	ATGCCATAGCATTTTTATCCA	21

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SEQUENCING PRIMERS

Primer Name	Sequence	Base
pBAD-FP	ATGCCATAGCATTTTTATCC	20
pBAD-R	GATTTAATCTGTATCAGG	18
pTrcHis Forward	GAGGTATATATTAATGTATCG	21
pJET1.2F	CGACTCACTATAGGGAGAGCGGC	23
pJET1.2R	AAGAACATCGATTTTCCATGGCAG	24
pEGFP_N	CCGTCCAGCTCGACCAG	17
pEGFP-FP	TTTAGTGAACCGTCAGATC	19
pEGFP-RP	AACAGCTCCTCGCCCTTG	18
pBacPAC-RP	GTCTGTAAATCAACAACGC	19
pDONOR-FP	TAACGCTAGCATGGATCTC	19
pESP-RP	TCCAAAAGAAGTCGAGTGG	19
pET-24a	GGGTTATGCTAGTTATTGCTCAG	23
pET-RP	CTAGTTATTGCTCAGCGG	18
pREP-fwd	GCTCGATACAATAAACGCC	19
pRH Forward	CTGTCTCTATACTCCCCTATAG	22
pRH Reverse	CAAAATTCAATAGTTACTATCGC	23
RVprimer3	CTAGCAAAATAGGCTGTCCC	20
RVprimer4	GACGATAGTCATGCCCCGCG	20
SP6	ATTTAGGTGACACTATAG	18
SV40-pArev	CCTCTACAAATGTGGTATGG	20
SV40-Promoter	GCCCCTAACTCCGCCCATCC	20
STag 18mer Primer	GAACGCCAGCACATGGAC	18
QE Promoter	CCGAAAAGTGCCACCTG	17
T3	ATTAACCCTCACTAAAG	17
T7terminator	GCTAGTTATTGCTCAGCGG	19
T7promoter	TAATACGACTCACTATAGGG	20
T7 EEV	ATGTCGTAATAACCCCGCCCCG	22
T7	AATACGACTCACTATAG	17
U-19mer Primer	GTTTTCCCAGTCACGACGT	19
35S-A	AAGGGTCTTGCGAAGGATAG	20
35S-B	AGTGGAAAAGGAAGGTGGCT	20

PRIMER FOR MICROBE IDENTIFICATION

Primer Name	Sequence	Base
27F	AGAGTTTGATCMTGGCTCAG	20
337F	GACTCCTACGGGAGGCWGCAG	21
518F	CCAGCAGCCGCGGTAATACG	20
785F	GGATTAGATACCCTGGTA	18
800R	TACCAGGGTATCTAATCC	18
907R	CCGTCAATTCMTTTRAGTTT	20
1100R	GGGTTGCGCTCGTTG	15
1492R	TACGGYTACCTTGTTACGACTT	22
NS1	GTAGTCATATGCTTGTCTC	19
NS8	TCCGCAGGTTCACCTACGGA	20
LR0R	ACCCGCTGAACTTAAGC	17
LR7	TACTACCACCAAGATCT	17
ITS1	TCCGTAGGTGAACCTGCGG	19
ITS2	GCTGCGTTCTTCATCGATGC	20
ITS3	GCATCGATGAAGAACGCAGC	20
ITS4	TCCTCCGCTTATTGATATGC	20
ITS5	GGAAGTAAAAGTCGTAACAAGG	22

RANDOM PRIMER

Primer Name	Sequence	Base
Oligo dT(15)	TTTTTTTTTTTTTTT	15
Oligo dT(18)	TTTTTTTTTTTTTTTTTT	18
Oligo dT(20)	TTTTTTTTTTTTTTTTTTTT	20
Random Hexamer	NNNNNN	6
Random Nonamer	NNNNNNNNN	9

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