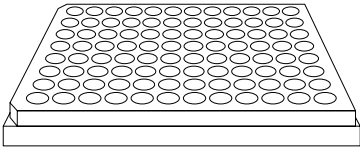
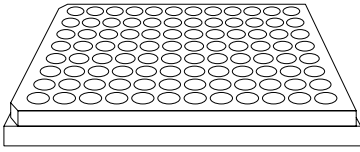
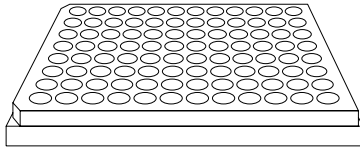


Order instructions 96-well sequencing

OPTION A: 96-WELL SEQUENCING

1. SAMPLES

PURIFIED DNA	RAW PCR PRODUCT	BACTERIA IN 96-WELL PLATE
Minimal volume 15 µl/well	Minimal volume 15 µl/well	Glycerol stocks on dry ice or as cultures in LB medium
		
Plasmid DNA 50 - 200 ng/µl	or	PRC product 5 ng/µl

Notes

- Samples should be normalised over the plate.
- DNA preferably column purified dissolved in water or 10mM Tris pH8.0.
- DNA samples should be free of EDTA and ethanol since trace amounts of these compounds will inhibit the sequence reaction.
- 2 µl of the PCR product on agarose gel should give a single clear and sharp band.

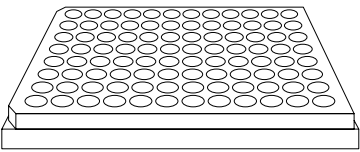
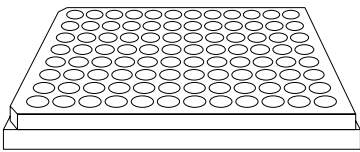
2. PRIMERS

Maximum of one primer per half plate which will be added by BaseClear.

If you want to use multiple primers per plate, you can submit a 'mirror-plate' with the corresponding primers.

- For a full 96-well plate please send in 200 µl primer with a concentration of 10 pmol/µl.
- For a half 96-well plate please send in 100 µl primer with a concentration of 10 pmol/µl.
- For a mirror-plate please add 20 µl primer with a concentration of 10 pmol/µl per well in a 96-well plate.

OPTION B: 96-WELL PREMIX SEQUENCING

PURIFIED PLASMID DNA	PURIFIED PCR PRODUCT
0,75 µg DNA 25 pmol primer	15 ng DNA/100 bp 25 pmol primer
	
Make up to a final volume of 20 µl with ultra pure water or 10 mM Tris (pH 8.0)	Make up to a final volume of 20 µl with ultra pure water or 10 mM Tris (pH 8.0)

CREATE ONLINE ORDER

Create your order using our convenient online portal <https://orders.baseclear.com>. Print the generated order form to send with your samples

WE PERFORM

- Optional plasmid isolation or PCR product purification
- Sequencing run on ABI 3730(XL) DNA Analyzer
- Data analysis by KB caller, for superior base calling and sequence data interpretation

YOU RECEIVE

- Data within 1-2 working days
- Results provided via secure online portal
- E-mail notification when results are ready to download
- Full report, including sequence data in FASTA, SCF and ABI format.
- Sequence length of up to 1100 bp (long run) or 550 bp (short run)

STANDARD PRIMER LIST

NAME	PRIMER SEQUENCE
3-AOX1	GCAAATGGCATTCTGACATCC
5-AOX1	GACTGGTTCCAATTGACAAGC
AmpL1	ACAGTCCAGTTACGCTGGAGTC
AmpR1	CTTTCTGCTATGGAGGTCAGGTATG
attL1-Fw	ACTTAAGCTCGGGCCCCAAA
attL2-Rv	TGTAACATCAGAGATTTTGAGACA
BGH2	GAAGTAGAAGGCACAGTCGAGG
CMV-fw2	CGTGTACGGTGGGAGGTCT
MF	TTTCCCAGTCACGACGTTG
MF (-47)	CGCCAGGGTTTTCCCAGTCACGAC
MF-20i	GTA AACGACGGCCAG
MR	GGATAACAATTCACACAGG
MR-invitrogen	CAGGAAACAGCTATGACC

NAME	PRIMER SEQUENCE
pBAD Forward	ATGCCATAGCATTTTTATCC
pBAD Reverse	GATTTAATCTGTATCAGG
pDonR F1T	CGCGTTAACGCTAGCATGGATCTC
pDonR R1	GTAACATCAGAGATTTTGAGACAC
pECFP-C1-FW	CAAAGACCCCAACGAGAAGC
pECFP-C1-RV	CATTCATTTTATGTTTCAGGTTCA
pGEX forward	ATAGCATGGCCTTTGACAGG
pGEX reverse	GAGTGCATGTGTCAGAGG
poly-A	TTTTTTTTTTTTTTTTTTTTT
pQE60-FW	CCC AAAAGTGCCACCTG
pQE60-Rv	GTTCTGAGGTCATTACTGG
pRSforward	CCCTGAACCTCCTCGTTTCGACC
pRSReverse	GAGACGTGCTACTTCCATTGTC

NAME	PRIMER SEQUENCE
pRSseq	GCTGACGTCATCAACCCGCT
pTrcHis Forw.	GAGGTATATATTAATGTATCG
pTrcHis Rev.	GATTTAATCTGTATCAGGCTG
SL1C	AGTCCAGTTACGCTGGAGTC
Sp6i	GATTTAGGTGACACTATAG
SR2	GGTCAGGTATGATTTAAATGGTCAGT
T3ext.	AATTAACCTCACTAAAGGG
T3i	AATTAACCTCACTAAAG
T7	TAATACGACTCACTATAGGG
T7-R	GCTAGTTATTGCTCAGCGG
Tk PolyA Rev	CTTCCGTGTTTCAGTTAGC