



Roche use only:

Internal Reference No.: _____

Key Account Manager Email: _____

Design Specification Form

SeqCap EZ Enrichment System

Complete this form in its entirety to ensure accurate processing of your order by Roche Sequencing Solutions (Roche). Note that a NimbleDesign account is now required before completing this form (see sequencing.roche.com/products/software/nimbledesign-software.html). If you are ordering multiple designs, complete one form for each design. If you have questions, contact Customer Service (refer to page 6 for contact details).

BACKGROUND INFORMATION

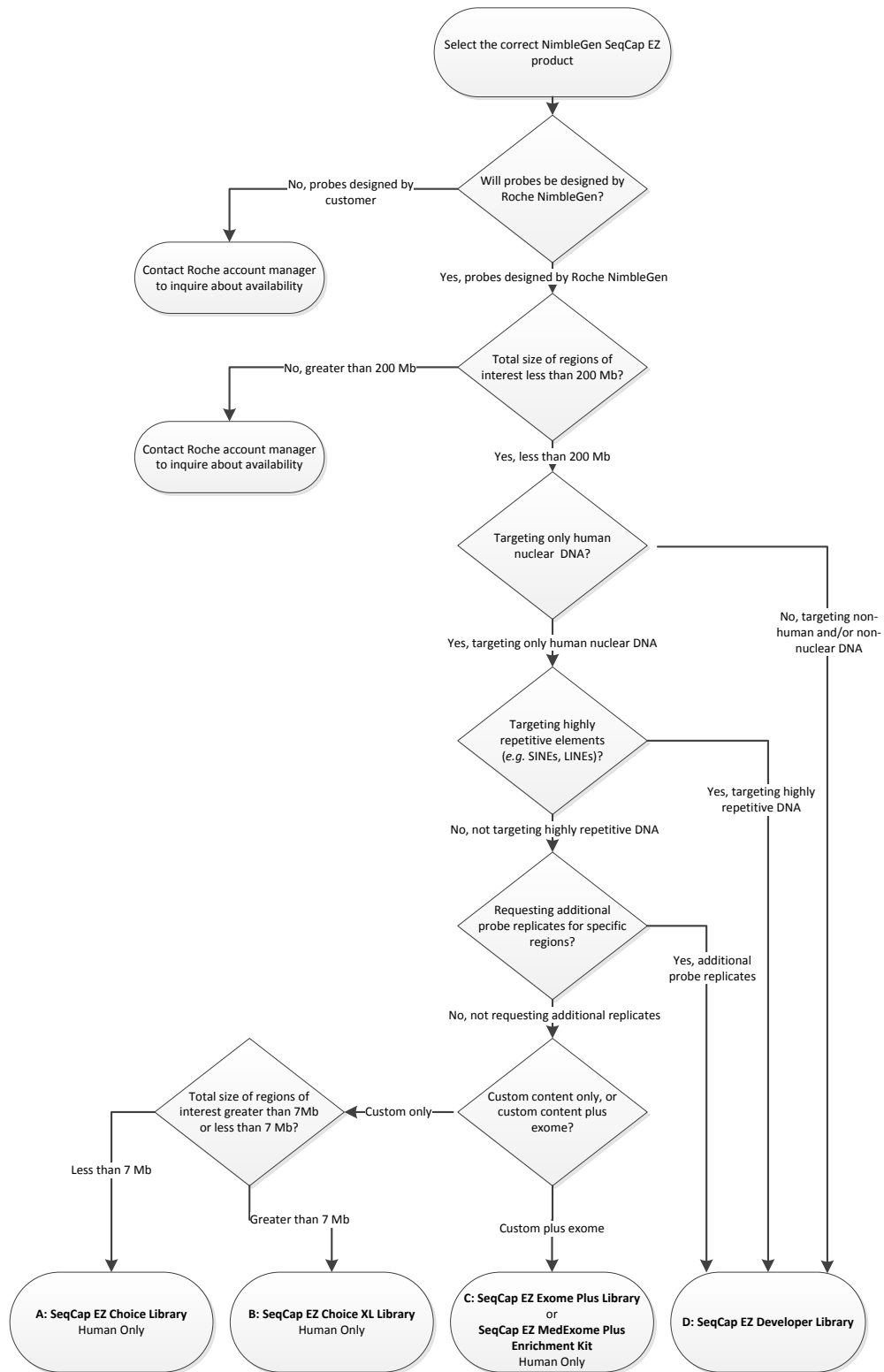
The SeqCap EZ enrichment system provides a convenient method to enrich for targeted regions in the human or any other sequenced genome. The selected region(s) of interest can be contiguous (*e.g.* disease associated regions) or noncontiguous (*e.g.* exons of a candidate gene panel, or single nucleotide polymorphisms). Based on regions selected by the researcher, Roche will design capture probes using proprietary algorithms and send the design proposal to the researcher for approval. After the design has been approved, Roche will produce the capture probes and ship the probes to the address on the Purchase Order.

The performance of targeted enrichment methods may be unpredictable due to variability among genomes and other properties intrinsic to the targeted region(s). Examples of such factors include: target sequence complexity (*e.g.* G/C content), repetitive element distribution (*e.g.* Alu, LINE, LTR), evolutionary history of the targeted region (*e.g.* conserved pseudogenes and gene family relationships), and population variation from the reference genome (*e.g.* CNV and hypervariable regions). When using a previously untested capture design, it is recommended to perform a small-scale experiment to determine the capture characteristics of a specific target before beginning a larger study.

SELECT ENRICHMENT PRODUCT(S)

Four SeqCap EZ enrichment system products are available, which differ in target genome, the size of the custom regions, and/or the nature of the regions of interest. Please use the flowchart on the next page to select the appropriate product(s) for your experiment.

Enrichment Product Selection Flowchart



ENRICHMENT KIT INFORMATION

Specify the kit quantity.

You may combine two or more configurations if the number of reactions needed is not listed below. For example, you can order two 96-reaction kits and two 12-reaction kits to get a total of 216 reactions for your design.

- A.** If ordering SeqCap EZ Choice kits, please enter the quantity needed in the table below.

Enrichment Kit Name	Cat. No.	Quantity
SeqCap EZ Choice Library, 4 Reactions	06740251001	
SeqCap EZ Choice Library, 12 Reactions	06266282001	
SeqCap EZ Choice Library, 24 Reactions	06266304001	
SeqCap EZ Choice Library, 48 Reactions	06266312001	
SeqCap EZ Choice Library, 96 Reactions	06266339001	
SeqCap EZ Choice Library, 384 Reactions	06266347001	
SeqCap EZ Choice Library, 960 Reactions	06266355001	

- B.** If ordering SeqCap EZ Choice XL kits, please enter the quantity needed in the table below.

Enrichment Kit Name	Cat. No.	Quantity
SeqCap EZ Choice XL Library, 4 Reactions	06740260001	
SeqCap EZ Choice XL Library, 12 Reactions	06266363001	
SeqCap EZ Choice XL Library, 24 Reactions	06266371001	
SeqCap EZ Choice XL Library, 48 Reactions	06266380001	
SeqCap EZ Choice XL Library, 96 Reactions	06266398001	
SeqCap EZ Choice XL Library, 384 Reactions	06266401001	
SeqCap EZ Choice XL Library, 960 Reactions	06266517001	

- C.** If ordering SeqCap EZ Exome Plus or SeqCap EZ MedExome Plus kits, please enter the quantity needed in the table below. To add custom content to SeqCap EZ Exome v3, select one of the SeqCap EZ Exome Plus options. Select SeqCap EZ MedExome Plus Enrichment Kit to add content to SeqCap EZ MedExome.

Enrichment Kit Name	Cat. No.	Quantity
SeqCap EZ Exome Plus Library, 12 Reactions	06740189001	
SeqCap EZ Exome Plus Library, 48 Reactions	06740235001	
SeqCap EZ Exome Plus Library, 96 Reactions	06740243001	
SeqCap EZ MedExome Plus Enrichment Kit, 48 Reactions	07681364001	

- D.** If ordering SeqCap EZ Developer kits, please enter the quantity needed in the table below.

Enrichment Kit Name	Cat. No.	Quantity
SeqCap EZ Developer Library, 4 Reactions	06740278001	
SeqCap EZ Developer Library, 12 Reactions	06471684001	
SeqCap EZ Developer Library, 24 Reactions	06471706001	
SeqCap EZ Developer Library, 48 Reactions	06471714001	
SeqCap EZ Developer Library, 96 Reactions	06471722001	
SeqCap EZ Developer Library, 384 Reactions	06471749001	
SeqCap EZ Developer Library, 960 Reactions	06471757001	

DESIGN INFORMATION

1. **Please specify the taxonomic name, genomic build, and source for your design.** Many genome builds can be found in the UCSC Genome database (genome.ucsc.edu) or ENSEMBL (www.ensembl.org). If the genome build is not available in either of these databases, provide a link to a publicly available source for the build. If your reference sequence is not publicly available, please provide a FASTA-formatted genome sequence when possible. This reference sequence will be used to screen out probes targeting repetitive elements of the genome in order to enhance capture efficiency.

Homo sapiens (HG19/GRCh37)

Homo sapiens (HG38/GRCh38)

Other: _____

Example: *Mus musculus* (mm10) from UCSC.

2. **Provide a brief description of the design:**

Description: _____

Example: design targeting transcripts from a cancer gene panel, version 3.

3. **Provide a design identifier (optional).** Roche can include a design identifier of up to 10 characters in the final design name. The provided design identifier will go after the build in the final design name.

Design Identifier: _____

Example: CancerV3 (final design name will be 130130_HG19_CancerV3_EZ_HX1).

4. **Submit (attach) the regions of interest in one of the following formats:**

Coordinates for the regions of interest. Coordinates must be supplied in tab-delimited BED format; (genome.ucsc.edu/FAQ/FAQformat.html#format1). Exact coordinates of each region are required.

Coordinates for regions to receive additional probe copies. Add a 4th column to the BED file with the relative number of probe copies for each region; *e.g.*, if the region should have 5x probe replicates relative to other regions, the fourth column value should be 5.

List of gene/transcript identifiers. Please provide the identifier list source (database or URL) and database version.

Source: _____ Version: _____

Examples: Ensembl Gene IDs, Ensembl Transcript IDs, Ensembl Exon IDs, HGNC Gene Symbols, RefSeq ncRNA IDs, RefSeq mRNA IDs, or CCDS IDs.

FASTA formatted target sequences (if coordinates or identifiers cannot be obtained).



For small target regions of <100 bp in size, Roche extends the regions to 100 bp to increase capture efficiency.

5. **Specify the total size of your regions of interest using the information contained in the BED file and/or FASTA files created in step 4:**

Total size of regions of interest: _____

6. **Email the BED file and/or FASTA files and this form to Customer Service.**

(madison.customerservice@roche.com).

7. **Review and approve the design.** Roche will email probe coverage summaries for each design. Instructions for viewing and approving the design are provided along with these files. Approval of the design is required before processing of your order can continue. By approving the design, you represent to Roche that you have the right to submit the data to Roche for purposes of manufacture, and confirm that the design is according to your specifications.

CUSTOMER SERVICE

If you have questions about completing this form, contact Customer Service:

Email madison.customerservice@roche.com

TECHNICAL SUPPORT

If you have technical questions, contact your local Roche Technical Support. Go to sequencing.roche.com/support.html for contact information.

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