**Request Pricing Estimate**

**Step 1:** Please refer to the services section that you require estimates for and complete.

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| --- | --- |
| **Study Contact** | |
| Responsible Investigator | First and last name |
| Funding agency or potential funding agency |  |

**Step 2:** Once the services responses are completed, please email request to:

[**IBX-NJ-NIMH-ServiceInquiries@infinity-biologix.com**](mailto:IBX-NJ-NIMH-ServiceInquiries@infinity-biologix.com)

**Services Requested**

**Kitting and Fulfillment**

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| --- | --- |
| **Kit Specification Questions** | |
| How many subjects are expected in this study? |  |
| What samples/ processing/ analysis will you need kits for?  And what tubes will be needed for each sample? *Please list out any timepoints for PK kits if necessary.* |  |
| Will you need venipuncture supplies for each kit? |  |
| Will the kits require aliquots?  How many? What volume? |  |
| How will the samples be shipped back to the lab? Frozen, refrigerated, or ambient? |  |

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| **Logistics Specification Questions** | |
| Frequency of shipment of samples to IBX? |  |
| Frequency of shipment of samples from IBX to testing lab? |  |

**Bioprocessing**

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| --- | --- |
| **Sample Prep Service Questions** | |
| Source material  Is this request going to use NRGR requested samples?  If Yes, will it be material from your studies or material from someone else’s study? |  |
| Total number of tubes  Is this for serum isolation, plasma isolation or PBMC? |  |
| Is pooling required prior to fractionation? |  |
| How many aliquots per tube do you require? |  |

**Nucleic Acid Extraction**

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| --- | --- |
| **Nucleic Acid Extraction Questions** | |
| Source material   * Whole blood * Saliva * Tissue * Other |  |
| Nucleic Acid Extraction   * DNA * RNA |  |
| How many aliquots per tube do you require? |  |

**Cell Services**

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| --- | --- |
| **Cell Services Questions** | |
| Total number of Samples to be processed |  |
| What is the outcome material?   * Cryopreserved Lymphocytes * Lymphoblastoid Cell Lines * Fibroblast Cell Lines * Induced Pluripotent Cell Lines |  |
| If iPSC, how many clones per subject? |  |
| If iPSC, how many vials per subject?   * Standard: 6-8 vials * Large scale: 40-60 vials |  |
| What are the QC level requirements?   * Standard QC is inclusive of sterility, identity, FACS for Tra-1-60 and Oct-4, and viability and expression of Alkaline phosphatase   Optional:   * Karyotyping (G-banding) * Expression Array (Illumina HT12) analysis * Includes RNA extraction, QC, and cDNA synthesis * Immunocytochemistry |  |

**Analytical Services**

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| --- | --- |
| **Genetic and Genomic Analysis Questions** | |
| How many samples will be processed? |  |
| Source material   * DNA * RNA * Other |  |
| What are the target and reference genes/ SNPs of interest (include rs # if available) |  |
| Are you targeting any special chemistry/ platform that may have been used for prior samples?   * Low, Medium or High Throughput Genotyping |  |
| Do you require raw data only in FastQ files or will they require bioinformatics analysis? |  |

|  |  |
| --- | --- |
| **Sequencing Questions** | |
| How many total samples will be processed and per batch? |  |
| What type of sequencing service are you interested in?   * i.e.: mRNASeq, Total RNASeq, WGS, Whole Exome Seq, Sequencing from already prepared libraries or Targeted Sequencing |  |
| Coverage and depth of sequencing?  Are you looking at expression per gene, or including detection of splice variants and non-coding RNA? |  |
| What read lengths are you interested in? Single-end or base paired-end?  How many million reads per sample are you interested in? (forward and reverse) |  |
| What are the data delivery requirements? Fastq data, VCF, BAM files |  |

**Sample Storage**

|  |  |
| --- | --- |
| **Sample Storage Questionnaire** | |
| Sample Quantity |  |
| Sample Size |  |
| Sample Type |  |
| Sample Temperature |  |
| Storage Duration |  |
| Inbound/Outbound Transportation needed. If yes, shipment origin and destination required. |  |