|  |
| --- |
| **DFCI - DS In-house Centralized Data Access Request Form** |
| Please complete and email (also copy your PI/Supervisor) this form to **Selvi Guharaj at** [**selvi@ds.dfci.harvard.edu**](mailto:selvi@ds.dfci.harvard.edu)if you need access to the centralized datasets (open-/controlled-access) resident on our DFCI - DS UNIX servers and the kraken cluster. Please submit a separate request for each individual dataset. Please refer to the **centralized\_dataset\_list\_DFCI-DS** google sheet [https://docs.google.com/spreadsheets/d/16\_iT4zMc3Akk4LWBwMvN7fsOC\_CDvmi6NC07iqyOg6M/edit?usp=sharing] for the current list of centralized datasets.  Any questions regarding your request will be sent to the email address you provide below.  **NOTE:** By completing this form, the data access requester agrees **NOT** to distribute controlled-access datasets and data derivatives of controlled-access datasets to any entity or individual. |
| **Date (YYYY/MM/DD):** |
| **Requester/Submitter Name:** |
| **Requester/Submitter DFCI - DS Email:** |
| **Requester/Submitter Position Title:** |
| **Requester/Submitter eRA Commons - NIH ID:** |
| **Principal Investigator/Supervisor Name:** |
| **Dataset Access Type (open, controlled):** |
| **If Dataset Access Type is controlled-access,**   * Have you submitted all annual renewal/closeout reports for previously requested controlled-access datasets by the deadline to Selvi Guharaj **(Yes/No)**? If “No”, this request will not be processed and will be rejected. * Will you submit annual renewal/closeout reports for this dataset by the deadline to Selvi Guharaj **(Yes/No)**? Failure to do so will result in suspension of access to the requested controlled-access dataset(s) and rejection of future data download and access requests. |
| **Dataset Name** (TCGA, GTEx, TARGET, CPTAC, RefSeq, Genome Assembly)**:** |
| **Dataset Category** (Sequencing Reads, Simple Nucleotide Variation, Copy Number Variation, Transcriptome Profiling, Biospecimen, Clinical, DNA Methylation): |
| **Dataset Type** (Raw Reads, Aligned Reads, Expression Quantification, Mutation, Copy Number Segment, Copy Number Scores, Biospecimen Supplement, Clinical Supplement): |
| **Experimental Protocol** (RNA-Seq, miRNA-Seq, ATAC-Seq, WXS, WGS, Genotyping Array, Methylation Array): |
| **Dataset Format** (FASTQ, BAM, CRAM, TXT, TSV, VCF, MAF, SVS, XML): |
| **Other:** |
| **Comments:** |