1. All VCFs go to ./raw
2. 0\_gather.py
   1. All\_VCF.vcf
   2. forVEP.vcf
3. VEP forVEP.vcf
4. Get VCF file (allVCF) and VEP file (allVEP)
5. 2\_fromVEP.py
6. 3\_consolidate.py
7. common.txt -> Excel
8. Clinical significance:
   1. Clinvar ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/vcf\_GRCh38/
   2. OncoKB https://oncokb.org/dataAccess
   3. CGI https://www.cancergenomeinterpreter.org/mutations
   4. DoCM http://www.docm.info/
   5. ICGC https://dcc.icgc.org/api/v1/mutations/pql?query=select(\*)%2Cin(mutation.clinvarClinicalSignificance%2C%27Uncertain%20significance%27%2C%27Likely%20pathogenic%27%2C%27Pathogenic%27%2C%27not%20provided%27%2C%27Benign%27%2C%27Pathogenic%2FLikely%20pathogenic%27%2C%27Likely%20benign%27%2C%27other%27%2C%27Conflicting%20interpretations%20of%20pathogenicity%27%2C%27association%27%2C%27drug%20response%27%2C%27Benign%2FLikely%20benign%27%2C%27no%20interpretation%20for%20the%20single%20variant%27%2C%27risk%20factor%27%2C%27Pathogenic%2FLikely%20pathogenic%2C%20drug%20response%27%2C%27Pathogenic%2FLikely%20pathogenic%2C%20other%27%2C%27Likely%20pathogenic%2C%20other%27%2C%27Likely%20pathogenic%2C%20risk%20factor%27%2C%27Benign%2C%20other%27%2C%27Conflicting%20interpretations%20of%20pathogenicity%2C%20other%27%2C%27Likely%20pathogenic%2C%20drug%20response%27%2C%27Pathogenic%2FLikely%20pathogenic%2C%20risk%20factor%27%2C%27association%20not%20found%27)%2Climit(3145)
   6. http://p53.iarc.fr/ ???