| Code | title | correspond |
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| 10003414 | A pilot study on the assessment of the effectiveness of whole genome sequencing (WGS) technique in determining and estimating the frequency of genotypes of human leukocyte antigen (HLA) alleles in 20 Iranian individuals | Dr.Hossein Najmabadi |
| 10003536 | Pharmacogenetic analysis of whole genome sequencing data in 20 Iranian individuals | Dr. Hossein Najmabadi |
| 10003538 | Whole Genome Sequencing (WGS) data analysis for 20 families with intellectual disabilities | Dr. Hossein Najmabadi |
| 10003541 | Investigating monogenic causes of premature familial coronary artery disease in 20 families, using the whole exome sequencing (WES) technique. | Dr. Kimia Kahrizi |
| 1128 | Investigating the functional significance of the BCL11A SNPs rs142407 and rs4761393 by using the CRISPR-Cas9 system in K562 cells | Dr. Mehdi Banan |
| 1190 | Identification of known and novel varients of non syndromic Retinitis Pigmentosa among 25 affected families refered from Province of Yazd, using Whole Exome Sequencing | Dr. Hamid Reza Khorram Khorshid |
| 1337 | Functional study of CAPN10 gene involved in autosomal recessive intelectual disability | Dr. Kimia Kahrizi |
| 1340 | Genetic investigation of Iranian old age people by Whole Genome Sequencing (WGS) | Dr. Hossein Najmabadi |
| 1411 | Idnetifying Candidate Variants responsible for transfusion dependent anemia of unknown genomic origin in Five Iranian Families using Whole Exome Sequencing | Dr. Maryam Neishabury |
| 1437 | Mutation analysis of tRNA metyltransferase (TRMT1) on its enzymatic activity and function in parents with intellectual disability | Dr. Hossein Najmabadi |
| 1439 | The identification of different genetic variants of seven Iranian ethnic groups and residents of Persian Gulf’s islands | Dr. Hossein Najmabadi |

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| 1502 | Investigation of 100 intellectual disabled families with consanguineous marriage in Ghazvin province using Whole Exome Sequencing. | Dr. Hossein Najmabadi |
| 1518 | The Functional Effect of Retinitis Pigmentosa Variant on related Protein-Protein Interactions; Using Yeast Two Hybrid System | Dr. Hamid Reza Khorram Khorshid |
| 1616 | aEvaluation of trisomy 21 mosaicism and chromosomal fragility in 20 individuals with early Alzheimer's disease and comparison with 20 normal individuals using cytogenetic techniques and fluorescent in situ hybridization (FISH). | Dr. Farkhondeh Behjati |
| 1617 | aEvaluation of genomic instability (chromosomal and aniosomal fragility) in 20 patients with early-onset Parkinson's disease and comparison with 20 normal individuals | Dr. Farkhondeh Behjati |
| 1632 | Evaluate the achievement of strategic plan goals Genetic Research Center of the University of Social Welfare and Rehabilitation Sciences and the factors affecting it | Dr. Payam Roshanfekr |
| 1660 | Evaluation of the relationship between chromosome 8 abnormalities and prognosis (some indicators of immunohistochemistry and survival) in 25 women with primary invasive breast cancer using fluorescence incisor hybridization (FISH) | Dr. Farkhondeh Behjati |
| 1674 | Prevalence of autosomal and X-dependent mental retardation in Guilan province | Dr. Hossein Najmabadi |
| 1726 | Comparison of the tendency of RUNX1 transcription factor to bind to two oligonucleotides indicating polymorphism in the central nucleotide of the 5'HS4 palindromic sequence of the beta locus regulatory region | Dr. Maryam Neishabury |

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| 1842 | Evaluation of the relationship between TGFa genetic polymorphism (Taq1) and the occurrence of non-syndromic cleft lip and palate in the Iranian population | Dr. Hamid Reza Khorram Khorshid |
| 1969 | Searching for causative genes in 10 Iranian patients affected to hereditary spastic paraplegia (HSP) using whole exome sequencing | Dr. Afagh Alavi |
| 2129 | Genetic investigation in 20 rare syndromic families using whole exome sequencing | Dr. Kimia Kahrizi |
| 2131 | Investigation into leukocyte telomere length in subjects with high body mass index and completely matched controls | Dr.Farzaneh Larti |
| 2237 | Strengthening the infrastructure of Iranian National Genome Center “Iranome” as the main substruction of gene editing and gene therapy studies | Dr. Hossein Najmabadi |
| 2277 | Exome sequencing in blood transfusion dependent individuals suspected to rare types of anemia, who are faced with challenges in clinical management due to ambiguity in diagnosis | Dr. Maryam Neishabury |
| 2348 | Biobanking and Genetic Investigation of Premature Cardiac Death/Arrest in Iran | Dr. Kimia Kahrizi |
| 2389 | The implementing consequences of NIPT in screening of chromosomal aberrations in the first trimester of gestation based on the contingent protocol, using reflexed-DNA testing in Iranian population during 1398-1399 | Dr. Hamid Reza Khorram Khorshid |
| 2405 | Identification of genetic causes responsible for hearing loss in five Iranian families using Whole Genome Sequencing | Dr.Mojghan babanejad |
| 2418 | Studying the effect of non-deletional HPFH mutations in K562 cells harboring an EGFP to γ-globin knock-in | Dr. Mehdi Banan |

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| 2469 | The diagnostic yield of whole exome sequencing data reanalysis in 50 genetically undiagnosed patients presenting neuromuscular disorders. | Dr.Zohreh Fattahi |
| 2476 | Identification the new corona virus genome (2019-nCov) in 5 patients using NGS | Dr. Hossein Najmabadi |
| 2493 | Genome study of New Corona virus (SARS-Cov2) in 50 Iranian patients using NGS method (pilot study) | Dr. Hossein Najmabadi |
| 2495 | Developing and upgrading of Iranian population database “Iranome” by adding genomic data from 400 Iranian samples subjected to Whole Genome Sequcning (WGS) (1st phase). | Dr. Hossein Najmabadi |
| 2514 | Using a Drosophila Melanogaster model to investigate the function of 3 novel genes causing intellectual disability in a cohort of Iranian families with autosomal recessive intellectual disability in Genetics Research Center of University of Social Welfare and Rehabilitation of Sciences from 2006 to 2017. | Dr. Hossein Najmabadi |
| 2517 | Investigating the unknown genetic causes of hemochromatosis in Iranian population using whole exome sequencing in 10 families with single or multiple affected individuals (phase I) | Dr. Maryam Neishabury |
| 2571 | Monitoring of the SARS-Cov2 genome in Iranian population by combination of NGS and Conventional Sequencing | Dr. Hossein Najmabadi |
| 2592 | Searching for causative genes in 15 Iranian patients affected to hereditary spastic paraplegia (HSP) using whole exome sequencing | Dr. Afagh Alavi |
| 2819 | Genetic Identification of familial premature coronary artery disease in 30 Iranian families using Whole Exome Sequencing | Dr. Kimia Kahrizi |

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| 2821 | Combination of technologies that included Sanger, exome sequencing, and linkage analysis to identify rare mutations and genes related to hereditary hearing loss in five families that had no result in previous studies. | Dr. Marzieh Mohseni |
| 2834 | Exome sequencing in several families of Qazvin province with one or more patients with autosomal recessive GJB2-negative deaf syndrome | Dr. Reza Najafipour |
| 2875 | Identification of genetic causes of autosomal dominant non-syndromic hearing loss in two Iranian affected families without detected mutations in GJB2 gene using Whole Exome Sequencing | Dr. Niloofar Bazazzadegan |
| 2878 | Study of human mitochondrial genome diversity in 100 indivituals with Fars ethnicty | Dr. Hossein Najmabadi |
| 2888 | Searching for causative genes in five Iranian patients affected to idiopathic calcification of basal ganglia (FAHR) using whole exome sequencing | Dr. Afagh Alavi |
| 2913 | The two-year program to enhance the scientific capacity of our country in the region; in terms of advances in medical genetics | Dr. Hossein Najmabadi |
| 2920 | Identification of genetic causes of autoinflammatory diseases in 7 Iranian affected families without common mutations in MEFV gene using Whole Exome sequencing | Dr. Niloofar Bazazzadegan |
| 2936 | Estimating the compatibility of screen positive with clinical positive cases and determining pathologic and borderline cutoffs of metabolites in inborn error of metabolism, in Hope Gene Medical Institute from 1389 to 1400 | Dr.sedigheh madani |
| 3030 | Genetic analysis of the second group of Iranian patients affected to idiopathic calcification of basal ganglia (FAHR) | Dr. Afagh Alavi |

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| 3049 | Decoding the Genetic Complexity of Intellectual Disability and Determining Causative Genetic Factors via Whole Genome Sequencing in Pedigrees that have not been diagnosed with common diagnostic approaches | Dr. Hossein Najmabadi |
| 3068 | Re-analysis of whole-exome sequencing data and family re-examination in 15 individuals with severe transfusion-dependent anemia who have not yet reached a definitive molecular diagnosis. | Dr. Maryam Neishabury |
| 3072 | Re-exploration of the data obtained from the sequencing of 10 Hereditary Hearing loss families in which the cause of HL has not been determined so far, using updated software and databases | Dr. Marzieh Mohseni |
| 3084 | Exploring the genetic factors of intellectual disability through advanced whole-genome sequencing approach in 10 families with at least 3 affected individuals lacking a genetic diagnosis via whole-exome sequencing | Dr. Hossein Najmabadi |
| 3090 | Investigating monogenic causes of premature familial coronary artery disease in 20 families, using whole exome sequencing (WES) technique | Dr. Kimia Kahrizi |
| 3103 | Investigating the methylation status of OAS2, OAS3, IFI44L, FOXP3 and TET2 genes of autoimmune rheumatoid arthritis disease patients | Dr. Hamid Reza Khorram Khorshid |
| 3104 | DNA methylation analysis of OAS2, OAS3, IFI44L, FOXP3 and TET2 genes of 70 patients with systemic lupus erythematosus | Dr. Hamid Reza Khorram Khorshid |
| 3105 | Investigating genetic factors of intellectual disability through advanced whole genome sequencing in 10 families with at least 2 or more affected individuals lacking a genetic diagnosis via whole exome sequencing | Dr. Hossein Najmabadi |

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| 3124 | HbF induction in peripheral blood hematopoietic stem and progenitor cells via CRISPR/Cas9-mediated genome editing | Dr. Mehdi Banan |
| 3141 | Exome sequencing to identify known and new genes and mutations in 25 Iranian families with autosomal recessive hereditary hearing loss that did not show mutations in the GJB2 gene | Dr. Reza Najafipour |
| 3210 | The study of five non-syndromic hearing loss individuals with autosomal recessive inheritance did not reach results by panel-based method with whole exome analysis method | Dr. Niloofar Bazazzadegan |
| 3230 | Genetic studies in 10 families suspected of rare blood diseases that face uncertainty in clinical diagnosis | Dr. Maryam Neishabury |
| 3231 | Evaluating of transcriptome and gene expression alteration in a family with hereditary spastic paraplegia (HSP) using RNA-sequencing method | Dr. Afagh Alavi |
| 3320 | Evaluating the stemness and engraftment of BCL11A-edited human hematopoietic stem and progenitor cells (HSPCs) in immunodeficient mice | Dr. Mehdi Banan |
| 3321 | Investigation of hereditary hearing loss causes in 4 Iranian deaf families that have not reached conclusions in previous studies, using exome sequencing in the second affected individual | Dr. Marzieh Mohseni |
| 3327 | Investigating the detection rate of hereditary eye diseases using targeted sequencing (panel) and comparing it with new generation whole exome sequencing (WES) | Dr. Hamid Reza Khorram Khorshid |
| 3331 | Comprehensive genomic profiling to detect off-target impacts of CRISPR/Cas9 editing in human hematopoietic stem and progenitor cell clones focusing on modifications to the BCL11A gene. | Dr. Mehdi Banan |

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| 3353 | Molecular Epidemiology of the c.716T>A Variant in SLC26A4 Gene: A Population-Based Study in Southeastern Region of Sistan and Baluchestan Province | Dr. Reza Najafipour |
| 3447 | Investigation and reporting of pathogenic variants in carriers and affected individuals referred to the Kariminejad-Najmabadi Pathology and Genetics Laboratory, a 20-year retrospective study | Dr.Hossein Najmabadi |
| 3450 | Identification of genes and variants associated with leukodystrophy in 15 Iranian families affected by this disease using whole exome sequencing technique | Dr. Afagh Alavi |