DrSeq

nucleome
LEARN I SERVE I DISCOVER SCIENCE

Name :
Sex/Age : Unknown/0 Year(s)
Date Received : Apr 03 2025
Indication :

Whole Exome Sequencing on the Illumina Novaseq 6000 NGS Platofrm

Clinical Indication:
A 0.0 Year(s) old baby with gender - (not specified) born to parents with unknown consanguinity was referred for genetic evaluation. No clinical symptoms / phenotypes were mentioned.

*

Variant Interpretation & Clinical correlation:

A Heterozygous variant NM_001009944.3:c.7531G>A, [NP_001009944.3:p.Ala2511Thr] in PKD1[MIM*601313] gene was identified by Whole Exome Proband-Only analysis. The Heterozygous variations in the PKD1 gene are known to cause Autosomal dominant POLYCYSTIC KIDNEY DISEASE 1 WITH OR WITHOUT POLYCYSTIC LIVER DISEASE [MIM#173900]. This variant is not present in publicly available databases like ['1000 Genomes', 'Genome Aggregation Database Exome (gnomAD_exome)', 'Genome Aggregation Database Genome (gnomAD_genome)', 'Inhouse exome database']. This variant is present in [['Exome Variant Server', '0.0']].

DrSeq

nucleome
LEARN I SERVE I DISCOVER SCIENCE

Name :
Sex/Age : Unknown/0 Year(s)
Date Received : Apr 03 2025
Indication :

Variant Evidence	Gene Impact
Chromosome: Position: Genotype: phred quality score:	RefSeq Gnese 110, NCBI

Allele	DP	%
Heterozygous		

Gene: {d.dynamic.variantInfo.data.rowData[0][2]	Transcript:
Effect:	Protein:
Exon:	Coding:

DrSeq

nucleome
LEARN I SERVE I DISCOVER SCIENCE

Name :
Sex/Age : Unknown/0 Year(s)
Date Received : Apr 03 2025
Indication :

Based on the evidence, this variant
is classified as likely to be
variant

OMIM Phenotype

Case Specific Recommendations:

Recommendations
Genetic counselling is advised. For assistance in locating nearby genetic counseling services, please contact the laboratory [Ph.No. -------].,Validation of the variant detected by Sanger sequencing is recommended.,Targeted mutation analysis in the parents is recommended to document possible de novo status of the variant detected in the proband.,Please note that the classification of variants may change over time if additional information becomes available.

Methodology:
To be filled by organization based on the test methodology.

Signature 1 Siganture 2 Signature 3 Nucleome Address

DrSeq

nucleome
LEARN I SERVE I DISCOVER SCIENCE

Name :
Sex/Age : Unknown/0 Year(s)
Date Received : Apr 03 2025
Indication :

Limitations/Disclaimer:
Absence of a plausible explanation for the reported phenotype by exome sequencing does not exclude a genetic basis of the patient's condition. Some types of genetic abnormalities, such as copy number changes, variants in non-coding regions, large insertions or deletions etc. may not be detectable in this exome analysis test. It is possible that the genomic region where a disease causing mutation exists in the proband was not captured in the current test and therefore was not detected. Additionally, it is possible that a particular genetic abnormality may not be recognized as the underlying cause of the genetic disorder due to incomplete scientific knowledge about the function of all genes in the human genome and the impact of variants in those genes. Only variants in genes associated with the medical condition, or thought to be clinically relevant potentially for the probands medical condition, are reported here. Intronic and untranslated region variants are not assessed using this method.,The classification of variants may change over time.,Although all precautions have been taken during the test, the currently available data indicate that the chances of technical error are 2-3%.,For any further questions please contact the laboratory [Ph.No. -------].

Variant Classification as per ACMG guidelines:

Name	Description

References:

McLaren, William, et al. The Ensembl Variant Effect Predictor. Genome Biology, vol. 17, no. 1, 6 June 2016, p. 122, doi:10.1186/s13059-016-0974-4.,1000 Genomes Project Consortium, et al. A Global Reference for Human Genetic Variation. Nature, vol. 526, no. 7571, 2015, pp. 68-74 doi:10.1038/nature15393.,Karczewski, Konrad J., et al. The ExAC Browser: Displaying Reference Data Information from over 60,000 Exomes. Nucleic Acids Research, vol. 45, no. D1, 2017, pp. D840-D845, doi:10.1093/nar/gkw971.,Chen, Shamil, et al. A Genomic Mutational Constraint Map Using Variation in 76,156 Human Genomes. Nature, vol. 625, no. 7993, 4 Jan. 2024, pp. 92-

Signature 1 Siganture 2 Signature 3 Nucleome Address

DrSeq

nucleome
LEARN I SERVE I DISCOVER SCIENCE

Name	:	
Sex/Age	:	Unknown/0 Year(s)
Date Received	:	Apr 03 2025
Indication	:	

100.,Sherry, Stephen T., et al. dbSNP: The NCBI Database of Genetic Variation. Nucleic Acids Research, vol. 29, no. 1, 1 Jan. 2001, pp. 308-11.,Amberger, Joanna S., et al. OMIM.org: Online Mendelian Inheritance in Man (OMIMÂ®), an Online Catalog of Human Genes and Genetic Disorders. Nucleic Acids Research, vol. 43, no. D1, 28 Jan. 2015, pp. D789-98.,Landrum, Melissa J., et al. ClinVar: Public Archive of Interpretations of Clinically Relevant Variants. Nucleic Acids Research, vol. 44, no. D1, 4 Jan. 2016, pp. D862-8.,Ng, Pauline C., and Steven Henikoff. Predicting Deleterious Amino Acid Substitutions. Genome Research, vol. 11, no. 5, 1 May 2001, pp. 863-74.,Kumar, Prateek, Steven Henikoff, and Pauline C. Ng. Predicting the Effects of Coding Non-synonymous Variants on Protein Function Using the SIFT Algorithm. Nature Protocols, vol. 4, no. 7, July 2009, pp. 1073-81.,Adzhubei, Ivan A., et al. A Method and Server for Predicting Damaging Missense Mutations. Nature Methods, vol. 7, no. 4, Apr. 2010, pp. 248-9.,Kircher, Martin, et al. A General Framework for Estimating the Relative Pathogenicity of Human Genetic Variants. Nature Genetics, vol. 46, no. 3, Mar. 2014, pp. 310-5.,Schwarz, Johannes M., et al. MutationTaster2: Mutation Prediction for the Deep-Sequencing Age. Nature Methods, vol. 11, no. 4, Apr. 2014, pp. 361-2.,Quan, Lihua, and Kai Wang. InterVar: Clinical Interpretation of Genetic Variants by ACMG-AMP 2015 Guideline. American Journal of Human Genetics, vol. 100, 2017, pp. 267-80.,Richards, Sue, et al. Standards and Guidelines for the Interpretation of Sequence Variants: A Joint Consensus Recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genetics in Medicine, vol. 17, no. 5, May 2015, pp. 405-23.,Green, Robert C., et al. ACMG Recommendations for Reporting of Incidental Findings in Clinical Exome and Genome Sequencing. Genetics in Medicine, vol. 15, no. 7, July 2013, pp. 565-74.,Rehm, Heidi L., et al. ACMG Clinical Laboratory Standards for Next-Generation Sequencing. Genetics in Medicine, vol. 15, no. 9, Sept. 2013, pp. 733-47.,Kalia, Sarah S., et al. Recommendations for Reporting of Secondary Findings in Clinical Exome and Genome Sequencing, 2016 Update (ACMG SF v2.0): A Policy Statement of the American College of Medical Genetics and Genomics. Genetics in Medicine, vol. 19, no. 2, Feb. 2017, pp. 249-55.,Miller, D. T., et al. Recommendations for Reporting of Secondary Findings in Clinical Exome and Genome Sequencing, 2021 Update: A Policy Statement of the American College of Medical Genetics and Genomics (ACMG). Genetics in Medicine, vol. 23, no. 8, Aug. 2021, pp. 1391-8.,Raney, Brian J., et al. The UCSC Genome Browser Database: 2024 Update. Nucleic Acids Research, vol. 52, no. D1, 2024, pp. D1082â€“D1088, https://doi.org/10.1093/nar/gkad987.,Nassar, Laila R., et al. The UCSC Genome Browser Database: 2023 Update. Nucleic Acids Research, vol. 51, no. D1, 2023, pp. D1188â€“D1195, https://doi.org/10.1093/nar/gkac1072.,ThorvaldsdÃ³ttir, Helga, James T. Robinson, and Jill P. Mesirov. Integrative Genomics Viewer (IGV): High-Performance Genomics Data Visualization and Exploration. Briefings in Bioinformatics, vol. 14, no. 2, Mar. 2013, pp. 178-92, doi:10.1093/bib/bbs017.,Gargano, Maria A., et al. The Human Phenotype Ontology in 2024:

DrSeq

nucleome
LEARN I SERVE I DISCOVER SCIENCE

Name :
Sex/Age : Unknown/0 Year(s)
Date Received : Apr 03 2025
Indication :

Phenotypes around the World. Nucleic Acids Research, vol. 52, no. D1, 5 Jan. 2024, pp. D1333-D1346, doi:10.1093/nar/gkad1005.,Riggs, Elizabeth R., et al. Technical Standards for the Interpretation and Reporting of Constitutional Copy-Number Variants: A Joint Consensus Recommendation of the American College of Medical Genetics and Genomics (ACMG) and the Clinical Genome Resource (ClinGen). Genetics in Medicine, vol. 22, no. 2, 2020, pp. 245â€“257. https://doi.org/10.1038/s41436-019-0686-8.,Geoffroy, Vincent, et al. AnnotSV: An Integrated Tool for Structural Variations Annotation. Bioinformatics, vol. 34, no. 20, 2018, pp. 3572â€“3574. https://doi.org/10.1093/bioinformatics/bty304.,Babadi, Mehrtash, et al. GATK-gCNV Enables the Discovery of Rare Copy Number Variants from Exome Sequencing Data. Nature Genetics, vol. 55, no. 9, 2023, pp. 1589â€“1597.,Gargano, Maria A., et al. The Human Phenotype Ontology in 2024: Phenotypes Around the World. Nucleic Acids Research, vol. 52, no. D1, 2024, pp. D1333-D1346. https://doi.org/10.1093/nar/gkad1005.,Bruford, Elspeth A., et al. Guidelines for Human Gene Nomenclature. Nature Genetics, vol. 52, no. 8, 2020, pp. 754â€“758. https://doi.org/10.1038/s41588-020-0669-3.,Orphanet. https://www.orpha.net/.

Appendix 1: Sample Data and Statistics

Appendix 2: Coverage Summary

Mean Depth	Percentage target base pairs covered

Signature 1 Siganture 2 Signature 3 Nucleome Address

DrSeq

nucleome
LEARN I SERVE I DISCOVER SCIENCE

Name :
Sex/Age : Unknown/0 Year(s)
Date Received : Apr 03 2025
Indication :

Appendix 3: Coverage of Analyzed Genes (Percentage of coding region covered)

Gene	Region Covered	Gene	Region Covered	Gene	Region Covered