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अखिल भारतीय आयुर्विज्ञान संस्थान, नई दिल्ली

All India Institute Of Medical Sciences, New Delhi

t'ittb:

Patient Name :

Invested 18

Age : Lab Name:

Reg Date : Recommended By: Mr KULDEEP VERMA

2Y 8m

Dept of Laboratory Medicine 28-Dec-2023 16:33 PM

Sex :

Sample Received Date :

Department : Lab Sub Centre:

Sample Collection Pate:

Lab Reference No: Sample Type : Serum Make

28-1 kg-2021 20 26 PM

Pardiatries

Smart Lab New OPD Block 28-Dec-2023 (2.5) PM

2311164746

Reference

Sample Details : LC2812231775

Report

BIOCHEMISTRY

Test Name (Methodology)

Dr. Sudip Kumar Datta (Biochemistry & Immunoassay)

Dr. Tushar Schgal (Hematology & Congulation) Dr. Suneeta Meena (Serology)

UOM

Dr. Devendra Kr. Verma (Laboratory Medicine) 29-Dec-2023 11:22

IMMUNOASSAY

Test Name Oteshadaings

1113.00

Result

----End of Report---

UOM

pg/mL

15 - 65

Reference

Intact PTH action

Dr. Sudip Kumar Datta

(Biochemistry & Immunoassay)

Dr. Tushar Schgal (Hematology & Coagulation) Dr. Sunceta Meena (Serology)

Dr. Devendra Kr. Verma Laboratory Medicine) 29-Dec-2023 11:22

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- Flu in OPD for any factor is

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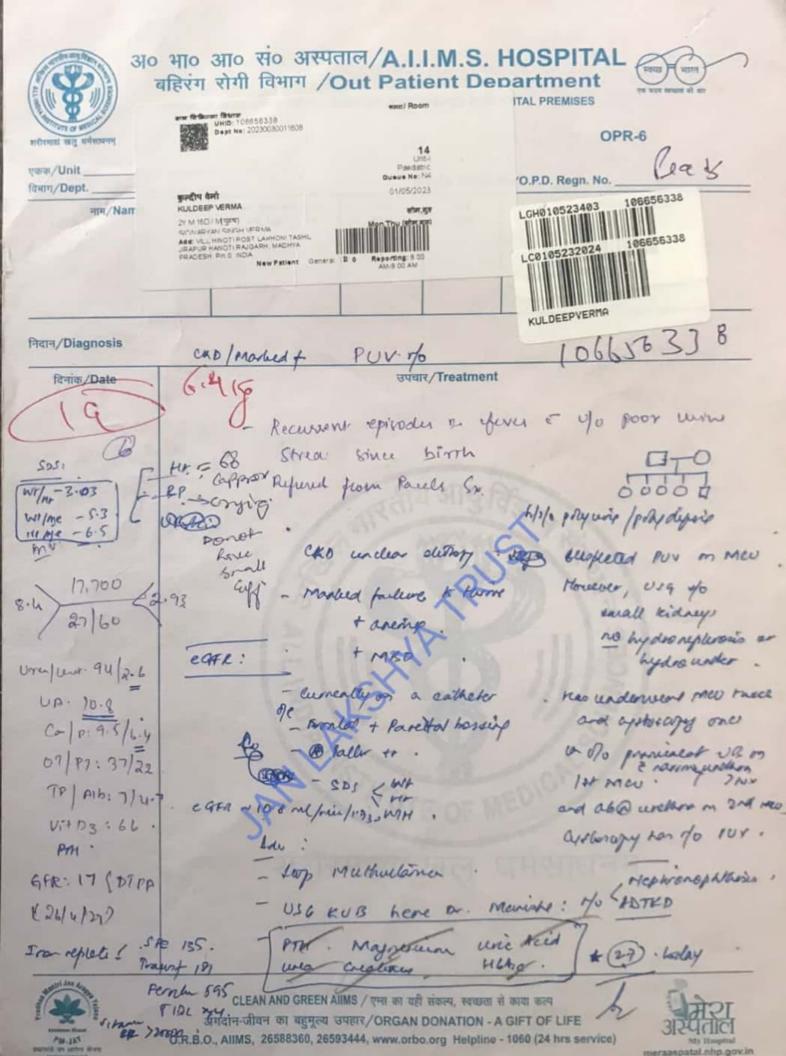
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Adu- I person intake.

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अखिल भारतीय आयुर्विज्ञान संस्थान, नई दिल्ली All India Institute Of Medical Sciences, New Delhi

UHID:

106656338

Male

Patient Name:

Mr KULDEEP VERMA

Sample Received Date: Department :

04-May-2023 18:17 PM

Age: Lab Name:

Paediatrics

Reg Date :

Dept of Laboratory Medicine

Smart Lab New OPD Block

Lab Sub Centre:

04-May-2023 17:16 PM

Sample Collection Date:

04-May-2023 14:55 PM

Recommended By:

Lab Reference No:

2312366420

Sample Details: LC0405231892

Sample Type: Serum

Report

BIOCHEMISTRY			
Test Name (Methodology)	Result	UOM	Reference
Urea (Urana GLDH)	90	mg/dL	17 - 49
Creatinine (Jaffe compensated)	2.3	mg/dL	0.2 - 0.4
Frie Acid (enzymatic colorimetric)	10.5	mg/dL	3.4 - 7.0
Calcium (5-Nitro-5'-methyl-RAPTA)	9.4	mg/dL	8.8 - 10.8
Phosphorus (molybdate U1)	4.8	mg/dL	2.5-4,5
odium (Ion Selective Electrodes)	134	mmol/L	135 - 145
Otassium (Ion Selective Electrodes)	3.5	mmol/L	3.5-5.1
Chloride (Ion Selective Electrodes)	100	mmol/L	98-107
illirubin (T) (Coberimetric diazo)	0.53	mg/dL	0 - 1
ilirublin (D) (Diaza Gen.2 Jendemsik-Graf)	0.52	mg/dL	0 - 0.2
ilirubin (I) (Calculated)	0.01	mg/dL	0 - 0.9
LT (IFCC without pyridoxal phissphate)	262	U/L	0 - 26
ST (IFCC without pyridoxal phosphate)	56	U/L	<=40
LP areco	710	U/L	142 - 335
otal protein (Hisrae)	7.3	g/dL	6.0 - 8.0
Ibumin (mcra)	5.1	g/dL	3.8 - 5.4
lobulin (Catenhatod)	2.3	g/dL	3.0 - 3.7
G ratio (Culculated)	2.2		0.8-2.0
r, Sudip Kumar Datta Dr. Tushar	Schgal De S	unecta Meena	Dr Hemang (Biochemistry &

(Biochemistry & Immunoassay)

(Hematology & Coagulation)

(Serology)

Immunoassay) 04-May-2023 21:22

SEROLOGY

Test Name (Methodology)	Result	UOM	Reference
HIV Combo (HIV 1, 2) (ECLE)	0.24	COI	< 1.0 Non Reactive > 1.0 Reactive
Anti HAV IgM (ECLL)	0.29	COI	< 1.0 Non Reactive ≥ 1.0 Reactive

Attention: Please collect blood samples by puncturing the rubber cap of the vacutainers. Manual opening of caps and filling it must be avoided strictly. Lab reports are subjected to pre-analytical errors due to inappropriate patient preparation, phlebotomy practices, storage and transport. Please inform SMART Lab in case of any discrepancies with the expected results on the same day on Ext.no. 2526

NAME OF THE PATIENT:	Kuldery	>	AGE	/SEX: 20	IM	UHID:	106656336
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			14				
INVESTIGATION			7				
НВ			13				
PLATELATES		- 5	1				
TLC(N/L/E/M/B)				-			
PH		V					
PCO2		2					
P02		V					
HC03)				_ 0	
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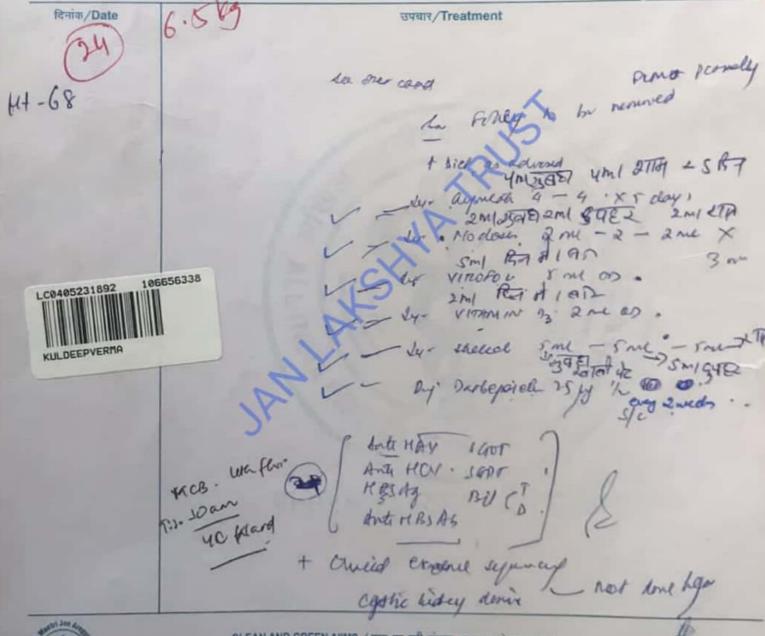
अ० भा० आ० सं० अस्पताल/A.I.I.M.S. HOSPITAL बहिरंग रोगी विभाग /Out Patient Department



अरपताल के अन्दर धूमपान मना है।/SMOKING IS PROHIBITED IN HOSPITAL PREMISES

शरीरवाचं कर्तु वर्गतावनम् एकक्/Unit		THE BOOM BATE 100056338 STATE Dept No. 2023003001908	wwei Room	OPR-6
विभाग/Dept.			14 (m)	Regn. No.
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निवान/Diagnosis





CLEAN AND GREEN AIIMS / एम्स का यही संकल्प, खच्छता में कावा कल्प अंगदान-जीवन का बहुमूल्य उपहार/ORGAN DONATION - A GIFT OF LIFE O.R.B.O., AIIMS, 26588360, 26593444, www.orbo.org Helpline - 1060 (24 hrs service)

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अ० भा० आ० सं० अस्पताल/A.I.I.M.S. HOSPITAL बहिरंग रोगी विभाग /Out Patient Department



अस्पताल के अन्दर धूम्रपान मना है। SMOKING IS PROHIBITED IN HOSPITAL PREMISES



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CLEAN AND GREEN AIIMS / एम्स का यही संकल्प, स्वकाता से कावा कल्प अंगदान-जीवन का बहुमूल्य उपहार /ORGAN DONATION - A GIFT OF LIFE O.R.B.O., AlIMS, 26588360, 26593444, www.orbo.org Helpline - 1060 (24 hrs service)



अo भाo आo संo अस्पताल/A.I.I.M.S. HOSPITAI में नोगी विभाग /Out Patient Department अस्तिका अन्दर धूमपान मना है।/SMOKING IS PROHIBITED IN HOSPITAL PREMISES अपर ाराय शरीरमाध खतु धर्मसायनम् UHID: 106856338 एकक/Unit Dept No: 20230220002007 tegn. No. विभाग/Dept. G-31 पता/Address नाग/Name कुल्दीप वेर्मा KULDEEP VERMA 29/04/2023 2Y M 14D / M(GFW) SIONARYAN SINGH VERMA ASE VILL HINOT: POST LAKHON: TASHI JRAFUR HANOT: RAJOARH, MADHYA Follow Up ... General Fo निदान/Diagnosis उपचार/Treatment दिनांक/Date mcu (9/4/23) Appointment on Depti./GI

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CLEAN AND GREEN AIIMS / एम्स का यही संकल्प, खच्छता से काया कल्प

अंगदान-जीवन का बहुमूल्य उपहार/ORGAN DONATION - A GIFT OF LIFE

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अ० भा० आ० सं० अस्पताल/A.I.I.M.S. HOSPITAL



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UHD: 106856338 Dept No: 202X0330014808	OPR-6
C-212 Und Paedatric Queue Ne: F26	बल्रोविक पंजीकृत संव/O.P.D. Regn. No
要で見せ 後月 KULDEEP VERMA 27 1M 27D / NGPR RRUNG VERMA SIONARYINA SINGH VERMA MAIL JEPP MAIL J	आयु पता/Address Age
निदान/Diagnosis	(CKD)
दिनांक/Date	उपचार/Treatment
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- Vaet	5 pallol, Yartine
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CLEAN AND GREEN AIMS / एम्स का यही संकल्प, स्वध्वना से काया कल्प अंगदान-जीवन का बहुमूल्य उपहार/ORGAN DONATION - A GIFT OF LIFE O.R.B.O., AIIMS, 26588360, 26593444, www.orbo.org Helpline - 1060 (24 hrs service)





Sri Aurobindo Institute of Medical Sciences

Sri Aurobindo Medical College & P.G. Institute
SAIMS HOSPITAL, INDORE (M.P.)

QUANTITATIVE DATA:

Devemotors	Left kidney	Right kidney
Parameters GFR (ml/min)	4.95	2.5
2 min diff. (% of relative function)		77
T _{max} (mins)		
Retention (%)		

CLINICAL IMPRESSION:

1. Almost bilateral non-functioning kidneys.

2. Scan pattern is compatible with chronic parenchymal dysfunction leading to chronic renal failure pattern.

3. Poor visualization of bladder activity.

Thanks for the referral.

Checked By: -- 13742 DR G N MAHAPATRA

Dr. G. N. Mahapatra

Sr. Consultant and Director,
Department of Nuclear Medicine & PET-CT

Note: This report is purely for diagnostic correlation with the other reports and clinical data of the patient by the treating physician. This cannot be used for medico legal purposes. For any clarification, corrections and missed findings the referring Physician may kindly call 9962784274/9820801633 directly to the above signatories. Direct enquiry by patient/relatives will not be entertained.

MedGenome Labs Ltd.

3rd Floor, Narayana Nethralaya Building, Narayana Health City, #258/A, Bommasandra, Hosur Road, Bangalore - 560 099, India. Tel: +91 (0)80 67154989 / 990, Web: www.medgenome.com



Average sequencing	Average on-target	Percentage target base pairs covered		
depth (x)	sequencing depth (x)	Ox	≥5x	≥20x
453	163.30	0.07	99.82	99.50

Total data generated (Gb)	7.45
Total reads aligned (%)	99.99
Reads that passed alignment (%)	92.21
Data ≥Q30 (%)	96.71

The classification of the variants is done based on American College of Medical Genetics as described below [PMID: 25741868].

Variant	A change in a gene. This could be disease causing (pathogenic) or not disease causing (benign).
Pathogenic A disease causing variant in a gene which can explain the patient's symptoms has been detected. This usually meather that a suspected disorder for which testing had been requested has been confirmed.	
Likely Pathogenic	A variant which is very likely to contribute to the development of disease however, the scientific evidence is currently insufficient to prove this conclusively. Additional evidence is expected to confirm this assertion of pathogenicity.
Variant of Uncertain Significance	A variant has been detected, but it is difficult to classify it as either pathogenic (disease causing) or benign (non- disease causing) based on current available scientific evidence. Further testing of the patient or family members as recommended by your clinician may be needed. It is probable that their significance can be assessed only with time, subject to availability of scientific evidence.

*The transcript used for clinical reporting generally represents the canonical transcript (MANE Select), which is usually the longest coding transcript with strong/multiple supporting evidence. However, clinically relevant variants annotated in alternate complete coding transcripts could also be reported:

Variants annotated on incomplete and nonsense mediated decay transcripts will not be reported.

*The in-silico predictions are based on Variant Effect Predictor (v104), [SIFT version - 5.2.2; PolyPhen - 2.2.2; LRT version (November, 2009); CADD (v1.6); Splice Al; deNSFPv4.2] and MutationTaster2 predictions are based on NCBI/Ensembl 66 build (GRCh38 genomic coordinates are converted to hg19 using UCSC LiftOver and mapped to MT2).

Diseases databases used for annotation includes ClinVar (updated on 5082021), OMIM (updated on 5082021), HGMD (v2021.3), LOVD (Nov-18), DECIPHER (population CNV) and SwissVar.

LIMITATIONS

Genetic testing is an important part of the diagnostic process. However, genetic tests may not always give a definitive
answer. In some cases, testing may not identify a genetic variant even though one exists. This may be due to limitations
in current medical knowledge or testing technology. Accurate interpretation of test results may require knowing the true
biological relationships in a family. Failing to accurately state the biological relationships in (my/my child's) family may
result in incorrect interpretation of results, incorrect diagnoses, and/or inconclusive test results.

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The sensitivity of NGS assay to detect copy number variants (CNV) is 70-75%. We recommend discussing alternative
testing methodology options with MedGenome Tech Support (techsupport@medgenome.com) as required. In case
clinician is suspecting CNV as an important genetic etiology, alternate tests like microarray/ MLPA or qPCR may be
considered after discussing with the MedGenome TechSupport team.

Sandly

R. Suliv

Main

Consultant - Clinical Geneticist

Sandhya Nair, Ph.D Sr. Manager -Variant Interpretation

Balaji Rajashekar, Ph.D Director - Clinical Bioinformatics Dr. Vibha Jain, MBBS, DNB (Obs & Gynae), DNB-SS (Medical Genetics); PGDHHM, FICCM

APPENDIX

TEST METHODOLOGY

Targeted gene sequencing: Selective capture and sequencing of the protein coding regions of the genome/genes is performed. Variants identified in the exonic regions are generally actionable compared to variants that occur in non-coding regions. Targeted sequencing represents a cost-effective approach to detect variants present in multiple/large genes in an individual.

DNA extracted from blood was used to perform targeted gene capture using a custom capture kit. The libraries were sequenced to mean depth of >80-100X on Illumina sequencing platform. We follow the GATK best practices framework for identification of germline variants in the sample using Sentieon [Sentieon]. The sequences obtained are aligned to human reference genome (GRCh38) using BWA aligner [Sentieon, PMID:20080505] and analyzed using Sentieon for removing duplicates, recalibration and re-alignment of indels [Sentieon]. Sentieon haplotype caller is then used to identify variants in the sample. The germline variants identified in the sample is deeply annotated using VariMAT pipeline. Gene annotation of the variants is performed using VEP program [PMID: 20562413] against the Ensembl release 99 human gene model [PMID: 29155950]. In addition to SNVs and small Indels, copy number variants (CNVs) are detected from targeted sequence data using the ExomeDepth method PMID: 22942019]. This algorithm detects CNVs based on comparison of the read-depths in the sample of interest with the matched aggregate reference dataset.

Clinically relevant mutations in both coding and non-coding regions are annotated using published variants in literature and a set of diseases databases: ClinVar,OMIM, HGMD, LOVD, DECIPHER (population CNV) and SwissVar [PMID: 26582918, 18842627, 28349240, 21520333, 19344873, 20106818]. Common variants are filtered based on allele frequency in 1000Genome Phase 3, gnomAD (v3.1 & 2.1.1), dbSNP (GCF_000001405.38), 1000 Japanese Genome, TOPMed (Freeze_8), Genome Asia,HmtDB and our internal Indian population database (MedVarDb v2.1) [PMID: 26432245, 32461613, 11125122, 26292667, 33568819, 31802016, 22139932]. Non-synonymous variants effect is calculated using multiple algorithms such as PolyPhen-2, SIFT, MutationTaster2 and LRT. Clinically significant variants are used for interpretation and reporting.

MedGenome Labs Ltd.

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- In a very few cases genetic test may not show the correct results, e.g. because of the quality of the material provided to MedGenome. In case where any test provided by MedGenome fails for unforeseeable or unknown reasons that cannot be influenced by MedGenome in advance, MedGenome shall not be responsible for the incomplete, potentially misleading or even wrong result of any testing if such could not be recognised by MedGenome in advance.
- Variants of uncertain significance (VUS) which are mentioned in the report need to be further correlated with the clinical
 phenotype, reports of other investigations, segregation analysis in the parents or affected/unaffected family members.
 MedGenome shall not be responsible for the inappropriate interpretation/ communication/ clinical actions/ reproductive
 decisions based on the VUS reported. The classification of VUS may change as the clinical phenotype evolves or more
 information is available in the scientific literature/ annotated databases.
- This is a laboratory developed test and the development and the performance characteristics of this test was determined by MedGenome.

END OF REPORT

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