INVOICE



Receipt No. 23 - 24/5145 05/10/2023



Patient Name	Mst. MAYANK MEHTA IRCH-305416	P. ID No.	P10001000	18251
Mobile No	8860001135	Accession No	. 100023010	696
Email ID		Age / Sex	9 Yrs	Male
Refd By	DR SAMEER BAKSHI	Billing Date	05/10/2023	19:30:17

Received with thanks a sum of Rs. 12000 from Mst. MAYANK MEHTA By: Paytm on a/c of:

Sr. No. Investigation Charges (Rs.)

1 AML Prognostication Panel 17999

 Total Amount
 Rs.
 17999

 Discount
 Rs.
 5999

 Net
 Rs.
 12000

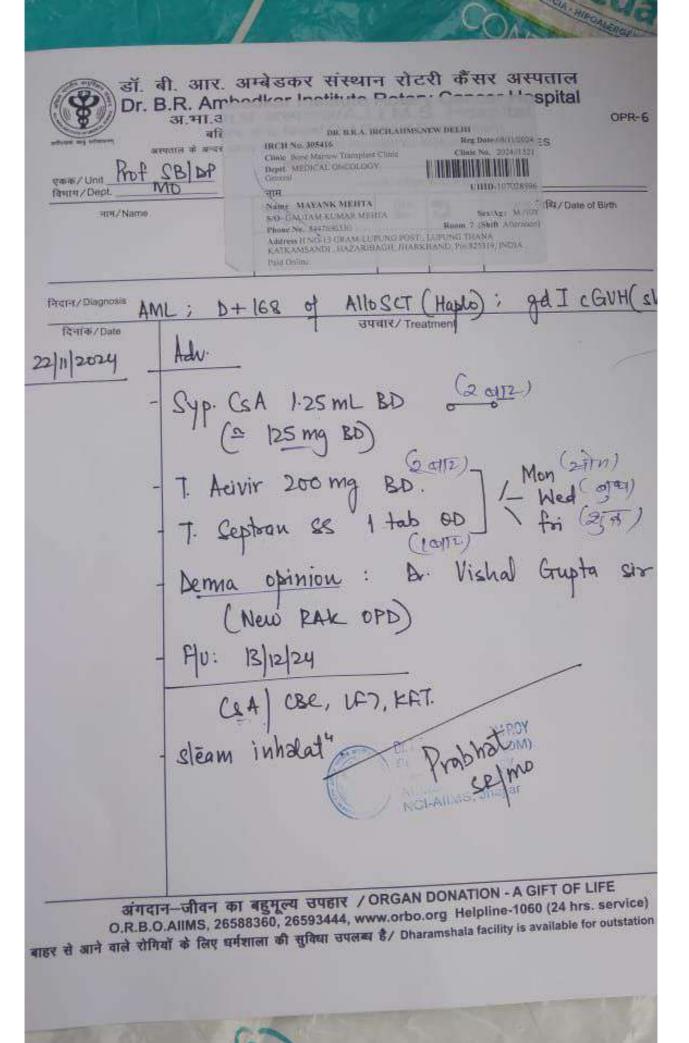
 Received
 Rs.
 12000

 Balance
 Rs.
 0

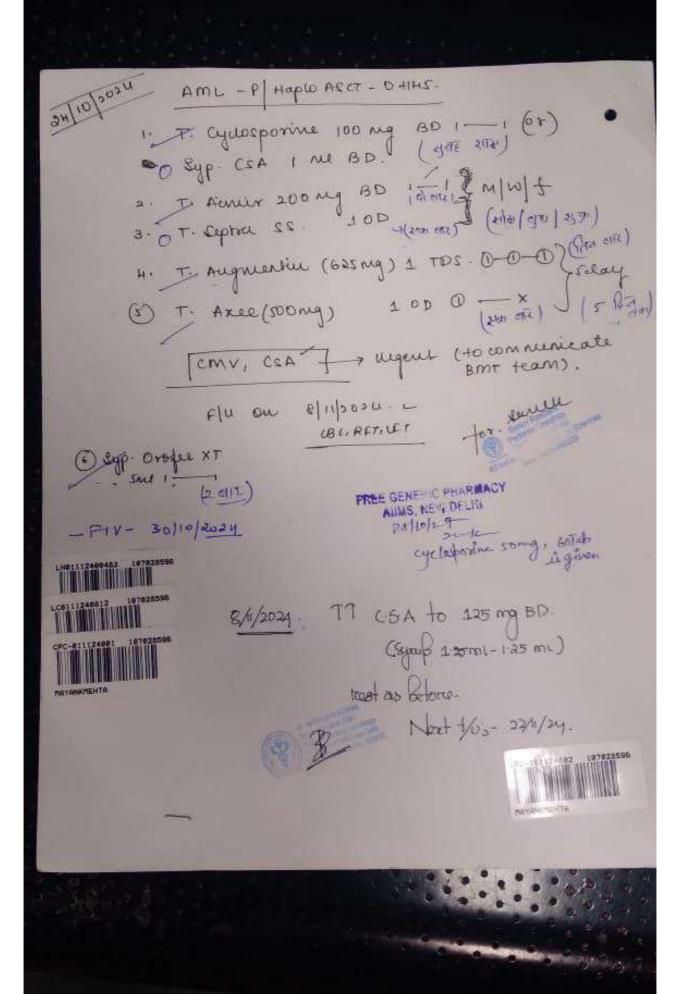
Online ID / Password 100023010696 / 28D72E80 User : Sylvia.P740

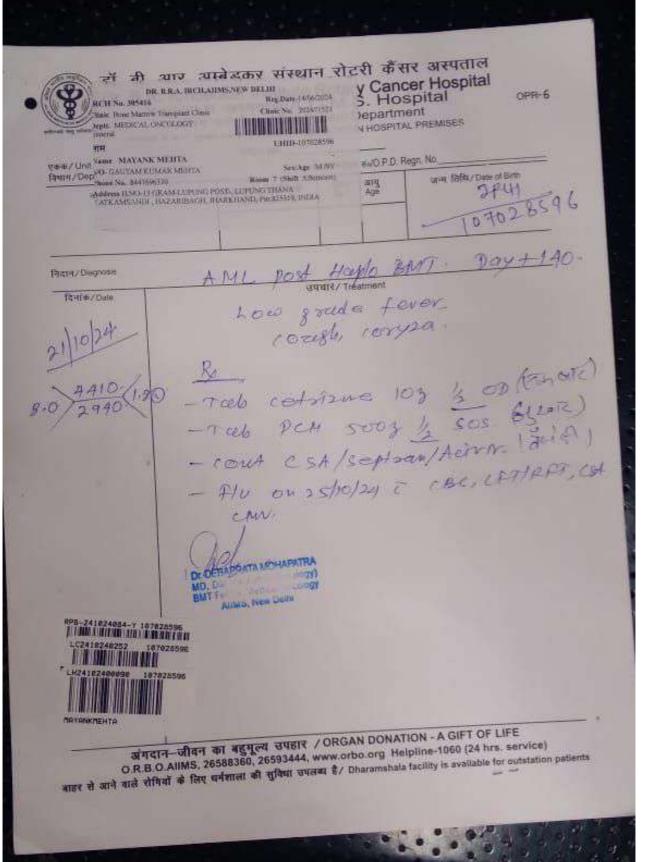
Pathkind Diagnostics Pvt. Ltd. (CIN - U74999DL2016PTC306874)

National Reference Lab: Plot No. 55-56, UdyogViharPh-IV, Gurugram - 122015. Ph No:75000-75111 E-mail: customercare@pathkindlabs.com



Dr. Vishal Gupta Dept of Dematology Allms. Delhi (N. PAR OPD). 22/11/2024. lesp Sir, Hereby referring this case: AML Post HADOA Haplo-identical Allogenic stem cell transplant)
D+ 168. for your epinion. Current issue: ? gd I chronic Slain GUHD kindly opine if regarding the same. Thank you. A. Righhat My SR Med Onco (Faculty: Dr. Deepam Phohpam)











Download Date: 11/12/2020



मयंक मेहता Mayank Mehta जन्म तिथि/DOB: 16/08/2014 gen MALE

Issue Date: 28/11/2020

9989 2057 7665

VID: 9135 7501 1273 9198

मेरा आधार, मेरी पहचान



Gurugram

Age

Sex

Pathkind Diagnostics Pvt. Ltd.

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

: 9 Yrs

: Male

Processed By

Pathkind Diagnostics Pvt. Ltd.

Billing Date

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

05/10/202319:30:17

05/10/2023 11:00:55

05/10/2023 19:36:40

: Mst. MAYANK MEHTA IRCH-305416 Name

Sample Collected on Sample Received on

P. ID No. : P1000100018251 Report Released on 11/10/2023 17:50:29

: 100023010696 Barcode No. 995326626 **Accession No**

Referring Doctor: DR SAMEER BAKSHI

Referred By Ref no.

Report Status - Preliminary Report

Toot Norma	Result	Biological Ref. Interval	Unit	
Test Name	resuit	biological Rel. Iliterval	Unit	

AML Prognostication Panel AML-ETO1 t(8;21) RTPCR Qualitative

Sample: Whole Blood EDTA Method: RTPCR & Electrophoresis

AML1-ETO (RUNX1-RUNX1T1) Qualitative Assay

Specimen type: EDTA P Bld

Methodology: RTPCR & Gel Electrophoresis

Translocation Screened	Effect of Mutation	Molecular Status
AML1-ETO/ t(8;21)(q22;q22.1)	Pathogenic	Not Detected

Result & Interpretation:

The hybrid transcript for AML1-ETO was not detected in the leukocytes of the specimen.

Clinical Information:

AML1-ETO or t(8:21)(q22;q22.1) is a balanced reciprocal translocation between AML1 gene on chromosome 21 and ETO gene on chromosome 8. It is observed in 5-12% cases of AML and most closely associated with AML-M2, though it may rarely be seen in AML-M1 or M4. Immunophenotypically, a close association has been reported between expression of CD19 in AML and occurrence of AML1-ETO translocation. At the genetic level, AML1 breakpoints are located within intron 5 and ETO breakpoint occur upstream of exon 2. Presence of the translocation denotes a good prognosis and patients often achieve CR in 85-90% cases

The result of this test should be interpreted in correlation with the clinical and hematological parameters observed.

Methodology, Test Attributes and Limitations:

Whole Blood RNA was extracted using commercial Kit. This assay is based on the qualitative estimation of presence of AML1-ETO hybrid transcript. The analytical sensitivity of this Test allows detection of 1 leukemic cell carrying the abnormal transcript in 100,000 normal cells. This Test is designed for diagnostic evaluation of the said transcript and should not be used for Monitoring purposes. Samples must be received at the laboratory under appropriate conditions within 48hrs of aspiration to ensure preservation of RNA. PCR is a highly sensitive technique; reasons for apparently contradictory results may be due to improper quality control during sample collection, selection of inappropriate specimen and/or presence of PCR inhibitors.

Note: This Test has been validated and its performance evaluated at Pathkind Diagnostics Pvt Ltd

Inv(16) RTPCR Qualitative





@ Customer Care: 75000-75111

Page No: 1 of 6



Sex

Gurugram

Pathkind Diagnostics Pvt. Ltd.

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

Processed By

Pathkind Diagnostics Pvt. Ltd.

Billing Date

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

05/10/202319:30:17

05/10/2023 11:00:55

05/10/2023 19:36:40

11/10/2023 17:50:29

: Mst. MAYANK MEHTA IRCH-305416 Name Age : 9 Yrs

Sample Collected on : Male Sample Received on P. ID No. : P1000100018251 Report Released on

: 100023010696 Barcode No. 995326626 **Accession No**

Referring Doctor: DR SAMEER BAKSHI

Referred By Ref no.

Report Status - Preliminary Report

Test Name	Result	Biological Ref. Interval	Unit
iest ivallie	Nesuit	Divivgical Net. Hitel Val	Oill

inv16 (CBFB-MYH11) Qualitative Assay

Specimen type: EDTA P Bld

Methodology: RTPCR & Gel Electrophoresis

Translocation Screened	Effect of Mutation	Molecular Status
CBFB-MYH11/ inv16(p13q22)	Pathogenic	Not Detected

Result & Interpretation:

The hybrid transcript for CBFB-MYH11 was not detected; hence the specimen is negative for inv16 mutation .

It may be noted that this RTPCR assay is designed to interrogate the presence of type A, D and E fusion transcripts only. A false negative due to the presence of other rare transcripts cannot be ruled out.

Clinical Information:

Pericentric inversion of chromosome 16, inv (16) (p13q22) is found in 8-9% cases of AML. It is most closely associated with AML-M4Eo. This inversion results in the fusion of CBFB gene to smooth muscle myosin heavy chain gene, MYH11. So far, 10 different CBFB-MYH11 fusion transcripts have been reported. More than 85% cases have the transcript A; type D & E together represent another 10% cases. CBFB-MYH11 or inv (16) positive AMLs are considered to have a good prognosis with more than 50% cases reaching CR. This RTPCR assay is designed to investigate the presence of type A, D and E transcripts only.

The result of this test should be interpreted in correlation with the clinical and hematological parameters observed.

Methodology, Test Attributes and Limitations:

Whole Blood RNA was extracted using commercial Kit. This assay is based on the qualitative estimation of presence of CBFB-MYH11 hybrid transcript. The analytical sensitivity of this Test allows detection of 1 leukemic cell carrying the abnormal transcript in 100,000 normal cells. This Test is designed for diagnostic evaluation of the said transcript and should not be used for Monitoring purposes. Samples must be received at the laboratory under appropriate conditions within 48hrs of aspiration to ensure preservation of RNA. PCR is a highly sensitive technique; reasons for apparently contradictory results may be due to improper quality control during sample collection, selection of inappropriate specimen and/or presence of PCR inhibitors.

Note: This Test has been validated and its performance evaluated at Pathkind Diagnostics Pvt Ltd

PML-RARA t(15:17) RTPCR Qualitative

Sample: Whole Blood EDTA

@ Customer Care: 75000-75111





Page No: 2 of 6



Gurugram

Pathkind Diagnostics Pvt. Ltd.

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

Processed By

Pathkind Diagnostics Pvt. Ltd.

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

: Mst. MAYANK MEHTA IRCH-305416 **Billing Date** 05/10/202319:30:17 Name Sample Collected on 05/10/2023 11:00:55 Age : 9 Yrs Sex : Male Sample Received on 05/10/2023 19:36:40 P. ID No. : P1000100018251 Report Released on 11/10/2023 17:50:29

: 100023010696 Barcode No. 995326626 **Accession No**

Referring Doctor: DR SAMEER BAKSHI

Referred By Ref no.

Report Status - Preliminary Report

Test Name	Result	Biological Ref. Interval	Unit	
iest ivallie	ncouit	Diological Nel. Ilitei vai	Onit	

PML-RARa Qualitative Assay

Specimen type: EDTA P Bld

Methodology: RTPCR & Gel Electrophoresis

Translocation Screened	Effect of Mutation	Molecular Status
PML-RARa/ t(15;17)(q22;q12)	Pathogenic	Not Detected

Result & Interpretation:

The hybrid transcript for PML-RARa was not detected in the leukocytes of the specimen.

Clinical Information:

PML-RARa or t(15;17)(q22;q12) is a balanced reciprocal translocation between PML gene on chromosome 15 & RARa gene on chromosome 17. This translocation is present in all cases of Acute Promyelocytic Leukemia/ AML-M3 & stratifies the patients for treatment with ATRA (all trans retinoic acid). At the genetic level, RARa breakpoints always occur in intron 2. PML breakpoints may occur in intron 6 (bcr1; 55-57%), exon 6 (bcr2; 3-5%) or intron 3 (bcr3; 40%).

This test detects the bcr1, bcr2, and bcr3 forms of the hybrid transcript.

The result of this test should be interpreted in correlation with the clinical and hematological parameters observed.

Methodology, Test Attributes and Limitations:

Whole Blood RNA was extracted using commercial Kit. This assay is based on the qualitative estimation of presence of PML-RARa hybrid transcript. The analytical sensitivity of this Test allows detection of 1 leukemic cell carrying the abnormal transcript in 10,000 normal cells. This Test is designed for diagnostic evaluation of the said transcript and should not be used for Monitoring purposes. Samples must be received at the laboratory under appropriate conditions within 48hrs of aspiration to ensure preservation of RNA. PCR is a highly sensitive technique; reasons for apparently contradictory results may be due to improper quality control during sample collection, selection of inappropriate specimen and/or presence of PCR inhibitors.

Note: This Test has been validated and its performance evaluated at Pathkind Diagnostics Pvt Ltd

NPM1 Mutation Detection

Sample: Whole Blood EDTA

NPM1 Mutation Analysis

@ Customer Care: 75000-75111







Gurugram

Name

Referred By

Pathkind Diagnostics Pvt. Ltd.

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

Processed By

Pathkind Diagnostics Pvt. Ltd.

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

: Mst. MAYANK MEHTA IRCH-305416

Billing Date Sample Collected on

05/10/202319:30:17 05/10/2023 11:00:55

Age : 9 Yrs Sex : Male

Sample Received on

05/10/2023 19:36:40

: P1000100018251 P. ID No.

Report Released on

11/10/2023 17:50:29

: 100023010696 **Accession No**

Barcode No.

995326626

Referring Doctor: DR SAMEER BAKSHI

Ref no.

Report Status - Preliminary Report

Test Name Result Biological Ref. Interval Unit

Specimen: EDTA Whole Blood Methodology: Real Time PCR

Mutations Screened in: Exon 12 of NPM1 gene (RefSeq NM_002520)

Gene/ Exon	Mutation Screened	Effect of Mutation	Molecular Status
NPM1/Exon 12	Mutations A, B & D	Pathogenic	Mutation 'A' Detected

Result & Interpretation:

Mutation 'A' was observed in exon 12 of NPM1 gene.

Clinical Information:

Acute myeloid leukemias (AMLs) are a heterogeneous group of disorders characterized by the clonal expansion of myeloid blasts (eg, undifferentiated myeloid precursors) in the peripheral blood, bone marrow, and/or other tissues, which results in impaired hematopoiesis and bone marrow failure.

While cytogenetic aberrations detected at the time of diagnosis are the most used prognostic feature, approximately 50% of AML cases show a normal karyotype, which is considered an intermediate-risk feature. A comprehensive evaluation of several molecular markers (eg, FLT3, NPM1, CEBPA, KIT, IDH1 and IDH2) is important for risk assessment and prognostication in certain patients with AML and may guide treatment decisions.

- 1. An NPM1 alteration is a common finding in de novo AML (25%-30% of cases) and consists of small insertion (typically 4 base pair) or insertion/deletion events involving exon 12.
- 2. Three variants are highly recurrent, termed types A, B, and D and together account for approximately 90% of NPM1 alterations in de novo AML.
- 3. Thus, in patients with newly diagnosed AML, those with normal karyotype, no FLT3 variant, and a NPM1 alteration are considered to have a better prognosis than patients in the same group with neoplasms lacking a NPM1 alteration.
- 4. Furthermore, the presence of a NPM1 alteration serves as a sensitive marker for evaluating minimal disease and therapeutic response following treatment

Methodology, Test Attributes and Limitations:

Whole Blood DNA was extracted using commercial Kit. The Kit utilizes real-time quantitative PCR (qPCR) double-dye oligonucleotide hydrolysis principle, in which specific primers and an internal double-dye probe with a reporter and a quencher (FAM™-TAMRA™) for the amplification reactions is being used. In addition, a 3'-end modified phosphate oligonucleotide is used that perfectly matches the wildtype NPM1 gene and does not allow polymerization. This test is designed to detect NPM1-mutant transcripts of types A, B, and D only. Samples must be received at the laboratory under appropriate conditions within 72hrs of aspiration to ensure preservation of high molecular weight DNA. PCR is a highly sensitive technique; reasons for apparently contradictory results may be due to improper quality control during sample collection, selection of inappropriate specimen and/or presence of PCR inhibitors.

Results of this test must always be interpreted within the patient's clinical context and in conjunction with other relevant data and should not be used alone for a diagnosis of malignancy.

Note: This Test has been developed and its performance evaluated at Pathkind Diagnostics Pvt. Ltd.



@ Customer Care: 75000-75111





Gurugram

Pathkind Diagnostics Pvt. Ltd.

Processed By

Pathkind Diagnostics Pvt. Ltd.

Billing Date

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

05/10/202319:30:17

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

Name : Mst. MAYANK MEHTA IRCH-305416

Age : 9 Yrs Sample Collected on : 05/10/2023 11:00:55 Sex : Male Sample Received on : 05/10/2023 19:36:40

P. ID No. : P1000100018251 Report Released on : 11/10/2023 17:50:29

Accession No : **100023010696** Barcode No. : 995326626

Referring Doctor: DR SAMEER BAKSHI

Referred By : Ref no. :

Report Status - Preliminary Report

Test Name Result Biological Ref. Interval Unit

FIT3 Mutation Detection

Sample: Whole Blood EDTA

FLT3 (ITD & D835) Mutation Detection Assay (Qualitative)

Specimen: EDTA Whole Blood

Methodology: PCR & Gel Electrophoresis

Mutations Screened in: FLT3 gene (Ref Seg NC 000013.11)

Gene/ Exon	Mutation Screened	Effect of Mutation	Molecular Status
FLT3/ Exon 14	ITD	Pathogenic	Detected
FLT3/ Exon 20	D835	Pathogenic	Not Detected

Result & Interpretation:

ITD Mutation was **DETECTED** in the FLT3 gene of the sample provided.

Clinical Information:

Acute myeloid leukemias (AMLs) are a heterogeneous group of disorders characterized by the clonal expansion of myeloid blasts (eg, undifferentiated myeloid precursors) in the peripheral blood, bone marrow, and/or other tissues, which results in impaired hematopoiesis and bone marrow failure.

Gene alterations, along with translocations and inversions, carry prognostic importance in AML. In addition to large chromosomal rearrangements, molecular changes have also been implicated in the development of AML. In fact, genetic mutations are identified in more than 97% of cases, often in the absence of any large chromosomal abnormality. A comprehensive evaluation of several molecular markers (eg, FLT3, NPM1, CEBPA, KIT, IDH1 and IDH2) is important for risk assessment and prognostication in certain patients with AML and may guide treatment decisions.

- 1. This test is designed to detect FLT3 mutations in acute myeloid leukemia (AML). FLT3 mutation incidence is 20-30 percent in cytogenetically normal AML and represents an important diagnostic and prognostic marker.
- 2. Up to 70 percent of *FLT3*-mutated patients harbor internal tandem duplication (ITD) mutations in exon 14 of the juxtamembrane domain and 30 percent demonstrate tyrosine kinase domain (TKD) D835 mutations in exon 20. Aspartic acid at amino acid 835 most often changes either to Tyrosine (D835Y) or Valine (D835V).
- 3. This test is designed to detect both ITD and D835 mutations. The presence of FLT3 mutations is associated with a poor prognosis, unless it occurs concurrently with an NPM mutation
- 4. FLT3 Positive AMLs are candidates for treatment with Midostaurin in combination with standard cytarabine and daunorubicin induction and cytarabine consolidation

Methodology, Test Attributes and Limitations:

Whole Blood/BM DNA was extracted using commercial Kit. The Mutation analysis was carried out using an LDT. PCR reactions were carried out to amplify the region involved in ITD and D835 point mutations. The amplified product for D835 was digested with EcoRV and resolved on gel electrophoresis.

Samples must be received at the laboratory under appropriate conditions within 72hrs of aspiration to ensure preservation of high molecular weight DNA. PCR is a highly sensitive technique; reasons for apparently contradictory results may be due to improper quality control during sample collection, selection of inappropriate specimen and/or presence of PCR

FLT3 mutations other than ITD and D835 will not be detected with this assay. Results of this tests are be interpreted within the patient's clinical context and in conjunction with other relevant data and should not be used at the patient's remainded by the patient's clinical context and in conjunction with other relevant data and should not be used at the page of the page of

Plot No. 55-56, Udyog Vihar, Phase-4, Gurugram
Referencespathkindlabs.com | @ www.pathkindlabs.com
 Customer Care: 75000-75111

जांच सही तो इलाज सही (





Gurugram

Name

Sex

Pathkind Diagnostics Pvt. Ltd.

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

Processed By

Pathkind Diagnostics Pvt. Ltd.

Billing Date

Sample Collected on

Plot No. 55-56, Udhyog Vihar Ph-IV, Gurugram - 122015

05/10/202319:30:17

05/10/2023 11:00:55

: Mst. MAYANK MEHTA IRCH-305416

: 9 Yrs Age : Male

Sample Received on 05/10/2023 19:36:40 P. ID No. : P1000100018251 Report Released on 11/10/2023 17:50:29

Accession No : 100023010696 Barcode No. 995326626

Referring Doctor: DR SAMEER BAKSHI

Referred By Ref no.

Report Status - Preliminary Report

Test Name	Result	Biological Ref. Interval	Unit	
iest ivallie	nesuit	Diological Rel. Ilitel val	Oiiit	

- 1. M Carmen Chillón, Carina Fernández, Ramón García-Sanz, Ana Balanzategui et al. FLT3-activating mutations are associated with poor prognostic features in AML at diagnosis. Hematol J. 2004; 5(3):239-46.
- 2. Naval Daver, Richard F. Schlenk, Nigel H. Russell & Mark J. Levis. Targeting FLT3 mutations in AML: review of current knowledge and evidence. Leukemia 2019. Vol 33; 299-312
- 3. Alexander J Ambinder, Mark Levis . A. Potential targeting of FLT3 acute myeloid leukemia. Review Haematologica. 2021 Mar 1;106 (3):671-681

Note: This Test has been validated and its performance evaluated at Pathkind Diagnostics Pvt Ltd

** End of Report **

Result Awaited: AML Prognostication(Karyotyping HM Disor, CEPBA Mutation Det.)

Dr. Avijit Guha Scientist (Molecular) PhD (Molecular)





@ Customer Care: 75000-75111