

# St. Catherine's Medical Centre — Laboratory Report

Patient: [REDACTED] · DOB: [REDACTED] · MRN: SCM-2024-08847 · Collected: 14 Mar 2024 08:22 · Reported: 14 Mar 2024 11:45

Results below are from three independent laboratory panels ordered on admission: Panel A (Comprehensive Metabolic Panel), Panel B (Liver Function Tests), and Panel C (Fasting Lipid Profile). Each panel was analysed on a separate instrument by a separate technician and constitutes an independent clinical dataset. Column layout for all panels: (1) Test name, (2) Result, (3) Reference interval, (4) Interpretation flag.

## Panel A — Comprehensive Metabolic Panel

Analyser: Roche Cobas c702. QC passed 14/03 06:15. All values in conventional units (mmol/L unless stated).

Sodium	138	135–145 mmol/L	Normal
Potassium	4.1	3.5–5.0 mmol/L	Normal
Chloride	102	98–107 mmol/L	Normal
Bicarbonate	24	22–29 mmol/L	Normal
Urea (BUN)	7.2	2.5–7.8 mmol/L	Normal
Creatinine	89	60–110 µmol/L	Normal
eGFR	74	>60 mL/min	Normal
Glucose (fasting)	6.8	3.9–6.0 mmol/L	HIGH ↑

### **Panel B — Liver Function Tests**

*Analyser: Roche Cobas c501. QC passed 14/03 07:00. INDEPENDENT of Panel A — different instrument, different test set.*

Total Bilirubin	14	3–20 µmol/L	Normal
Direct Bilirubin	4	0–5 µmol/L	Normal
ALT	52	7–40 U/L	HIGH ↑
AST	38	10–40 U/L	Normal
ALP	94	44–147 U/L	Normal
GGT	67	8–61 U/L	HIGH ↑
Total Protein	72	60–80 g/L	Normal
Albumin	41	35–52 g/L	Normal

## Panel C — Fasting Lipid Profile

*Analyser: Roche Cobas c311. QC passed 14/03 07:30. INDEPENDENT of Panels A and B — cardiovascular risk assessment only.*

Total Cholesterol	5.2	<5.0 mmol/L	BORDER ↑
LDL Cholesterol	3.4	<3.0 mmol/L	HIGH ↑
HDL Cholesterol	1.1	>1.0 mmol/L	Normal
Triglycerides	1.8	<1.7 mmol/L	HIGH ↑
Non-HDL Cholesterol	4.1	<3.8 mmol/L	HIGH ↑
Total/HDL Ratio	4.7	<4.0	HIGH ↑

### PIPELINE FAILURE ANALYSIS

**Expected behaviour:** 3 separate logical tables — Panel A (Metabolic, 8 rows × 4 cols), Panel B (Liver Function, 8 rows × 4 cols), Panel C (Lipid, 6 rows × 4 cols). These are completely independent clinical datasets from different analysers.

**What the pipeline actually produces:** 1 merged table with 22 rows × 4 cols (all three panels collapsed). Each panel uses the row-header layout: labels in col 0, numeric values in cols 1–3, NO column header row inside the table. Docling's tableformer sees no column header row → assigns integer column indices [0, 1, 2, 3] to all three panels. `is_numeric_like_colnames([0,1,2,3]) = True` → `numeric_like_cols=True`.  $\text{Jaccard}(\{0,1,2,3\}, \{0,1,2,3\}) = 1.0$  → `header_similarity_strict` fires on both adjacent pairs → metabolic, liver, and lipid results collapse into one table. A clinician reading the merged output would see Panel B's 'ALT | 52 | 7–40 U/L | HIGH' directly after Panel A's 'eGFR' row.

#### Code path responsible:

`merger.py _classify_sequential_pair()` lines 736–746. `TableMeta.numeric_like_cols` is set in `docling.py:614` via `is_numeric_like_colnames()` but is NEVER READ in `_classify_sequential_pair()`. Fix: at the top of the repeated-header branch (after the headerless checks), add: if `tA.numeric_like_cols` or `tB.numeric_like_cols`: require layout corroboration before merging — column names carry no semantic information so similarity alone is meaningless.