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IR120_3kg_55m_1 Station X

- IR120_3kg_55m_1
 - Configuration
 - Event Log
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 - RAPID

T_R081/MainModule X

```
1 PROC mainModule
2   PROC main()
3       MoveJ [[433.58,158.18,238.53],[0.000187748,-0.968431,0.278518,-0.000188287],[0,0,-2,0],[90+09,90+09,90+09,90+09,90+09,90+09]]
4       MoveL [[433.58,158.18,149.76],[0.000187881,-0.968431,0.278518,-0.000188267],[0,0,-2,0],[90+09,90+09,90+09,90+09,90+09,90+09]]
5       MoveL [[433.58,158.18,209.86],[0.000187906,-0.968431,0.278517,-0.000188478],[0,0,-2,0],[90+09,90+09,90+09,90+09,90+09,90+09]]
6       MoveJ [[433.58,-121.85,541.86],[0.000187917,-0.968431,0.278516,-0.000188999],[-1,0,-2,0],[90+09,90+09,90+09,90+09,90+09,90+09]]
7       MoveJ [[433.58,-275.34,144.82],[0.000187946,-0.968432,0.278515,-0.000189085],[-1,0,-3,0],[90+09,90+09,90+09,90+09,90+09,90+09]]
8       MoveL [[433.58,-275.34,121.68],[0.000187949,-0.968432,0.278514,-0.000189141],[-1,0,-3,0],[90+09,90+09,90+09,90+09,90+09,90+09]]
9       MoveL [[433.58,-275.34,171.53],[0.000187879,-0.968432,0.278514,-0.000188436],[-1,0,-3,0],[90+09,90+09,90+09,90+09,90+09,90+09]]
10      MoveJ [[433.58,-24.84,432.19],[0.000187881,-0.968432,0.278514,-0.000188352],[-1,0,-2,0],[90+09,90+09,90+09,90+09,90+09,90+09]]
11  ENDPROC
12 ENDMODULE
```

- T_R081 (Process Workflow)
- Synchronize to I/O
 - Synchronize to Station
 - Load Program
 - Save Program As
 - Rename Program
 - Delete Program
 - Open Module
 - Load Module
 - Active
 - Start Task
 - Stop Task
 - Go To Program Pointer
 - Go To Program Pointer
 - Active Program Pointer

Log / Output / RAPID Watch / Search Results

Item	All messages	Time	Category
Program started: IR120_3kg_55m_1/RAPID/T_R081		6/30/2013 8:49:13 AM	General
IR120_3kg_55m_1/RAPID/T_R081: No errors		6/30/2013 8:49:13 AM	General

Controller status: OK

Abb Rapid Programming Manual

G Psacharopoulos



Abb Rapid Programming Manual:

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to visualize such data you can use genmica s genome browser which provides expanded browsing capabilities compared to common web genome browsers more importantly genomica provides a suite of tools that perform statistical tests between data in chromosomal coordinates for instance you can quickly find the types of chromosomal regions that

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