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Contextual information

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The Cronshaw Archive of Early Technology

About this document

Contextual information provided by Andrew Cronshaw

Protein Instrumental Analysis
The Cronshaw Archive of Early Technology c.1960s to 2017
 - compiled by Dr Andy Cronshaw

Introduction

There were a series of major changes in the analysis of proteins that occurred between the 1960s and 2017. Analyses in the 1960s relied on fairly basic, now perhaps considered primitive techniques. These were principally, paper chromatography, thin layer chromatography (TLC) and automated amino acid analysis (AAA). In the early 1980s most researchers worked in laboratories without very high cost instrumental analysers. Separate distinct processes were linked but often the different stages were carried out manually.

The advent of computing and later, the sequencing of the DNA from the human and multi-species genomes enabled rapid technological advances. In the mid-1980s HPLC with Edman sequencing was the dominant process of protein identification but the by 1990s mass spectrometry emerged as the replacement and remains the dominant technique today.

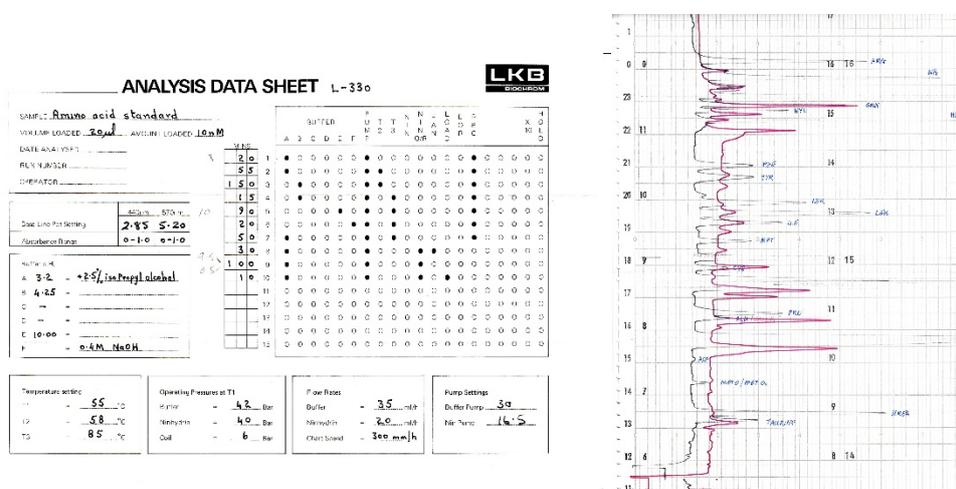


Fig.1 Control sheet and output from LKB4400 AAA c.1984.

Contents and Provenance

These items were rescued from several clear outs and laboratory moves, were curated and deemed important for future generations. I believe, having worked with each of Prof Michael Gardner, Prof Richard Ambler, Prof Alastair Aitken and others at the University of Edinburgh over a 36+-year period, there would have been approval for archiving this material in the University Archive.

1. Instrumental promotion documents 1960s - 2017 (several)
2. Textbook (1), instrument booklets (several)
3. Outdated correspondence and documents relating to difficulties in obtaining funding for the Edman protein sequencer in the 1980s – Prof Richard Ambler’s ambition.
4. Instrument data outputs, representative standard and sample runs 1980s – 2017 (several)

List of Protein Analyser instruments used at the University of Edinburgh

1. Model 120c (likely model) Amino acid analyser (Beckman Instruments) 1960s - 1980 Darwin Building, Kings Buildings (KB)
 Features: manual control, pen chart recorder and manual dot counting analysis.
2. An early spinning cup sequencer – was talked about believed to have existed at prior to 1987 at KB?
3. LKB4400 amino acid analyser (AAA) c.1984 – 87 – Hugh Robson Building
 Features: diode pin programmer, pen chart recorder and early integrator with heat sensitive paper.
4. High Pressure Liquid Chromatography (HPLC) various manufacturers c.1980 to 2017 +
 universally used. The early instruments were modular with manual syringe injection, separate pumps,

UV detectors and pen recorders. Fractions were collected manually. The technology was later adapted to interface with mass spectrometers.

5. Fast Protein Liquid Chromatography (FPLC) instruments (Pharmacia) c.1985 to 2002 universally used. Later replaced by Akta series of instruments.

Features: self-automated, heat sensitive integrator, pen chart recorder, fraction collector. Later addition: Early autosampler and motor valves.

6. 477A Edman protein sequencer (Applied Biosystems Inc) 1987 - 2000

Features: early touchscreen with diode grid, 5.25-inch floppy discs + 120A HPLC (ABI).

Features: self-automated, pen chart recorder

Later updated to the Procise Edman Sequencer (AB) c.2000-5

7. 130A HPLC (ABI) 1987 - 2004

Features: self-automated, pen chart recorder

8. 420A Amino acid analyser (ABI)1987 - 1999

Features: early touchscreen with diode grid, 5.25-inch floppy discs, pen chart recorder

9. BioIon Plasma Desorption Mass spectrometer c.1991 – 3 months collaborative access with Odense University, Denmark

10. Lasermat Matrix-Assisted Laser Desorption Mass Spectrometer with Time-of-flight detector (FinniganMAT) 1992-1993

11. Voyager DE-STR Matrix-Assisted Laser Desorption Mass Spectrometer with Time-of-flight detector (MALDI-TOF MS, ABI) 2001 – 2016.

Hands on instrument used by many students after careful training

Features: early CRT computer, laser printer

12. Procise Protein Sequencer (AB) 2000 - c.2008 – became outdated with rapid advances in mass spec.

13. 173 Microblotter Capillary HPLC System (AB) – 2001 - 4

14. LCQ mass spectrometry (FinniganMAT) 1997-1999

Features: manual injection, CRT computer, Xcalibur/Chromelion software, laser printer

15. LC + LCQ deca (ThermoFinnigan) – upgrade from LCQ instrument c.1999-2010

Features: early autosampler, early CRT computer, Xcalibur/Chromelion software, laser printer

16. LTQ Orbitrap series of instruments (ThermoScientific) c.2010

Features: advanced pc computer with flat screen, Xcalibur/Chromelion software

17. QExactive (ThermoScientific) c.2014

18. OrbitrapFusion (ThermoScientific) 2016

The high cost of dedicated instruments and the specialist nature of the analyses led to the establishment of central core facilities at UK universities. Open access was provided to scientists and advice and help was freely provided. Today, scientific advances allowed small amounts of precious complex samples to be analysed very quickly generating very large data files. Sample preparation is a highly skilled process which must allow for statistical analysis of data. Processing data involves an ever-improving range of software packages. The complexity of instruments brought a new language of scientific acronyms. It is frequently impossible for a non-scientist to understand a technical scientific email relating to the modern mass spectrometer. Older scientists and non-specialists have to work extra hard to keep up-to-date with changing technology and software. The cost of analytical instruments and maintenance increases almost exponentially with time. As a consequence, modern instruments are run 24/7. Today state-of-the-art instrument would cost in excess of £0.5 million and they are very costly to maintain and new improved models are launched annually.

15/11/18