

Chris Anthony

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Click Ctl plus +
Normal text click Ctl plus 0

Methylotroph stories; dedicated to research students everywhere (May 2024)

This is a power point presentation of a lecture I gave on
20th May to the Microbiology group in Biological Sciences,
University of Southampton

The lecture summarised my 40 years of work on methylotroph metabolism in 40 minutes.

I have added a few extra slides to make the stories complete.

VIDEOS can be speeded up by
downloading an [accelerator](#)

HOME



Methylo troph stories

Dedicated to research students everywhere

My CV

Born Watford in 1939, son of a brewery labourer.

1950 – 1957 Watford Grammar School

1957 – 1960 Reading University BSc Microbiology

1960 – 1963 Reading University PhD Thesis: The microbial metabolism of one-carbon compounds

1963 – 1966 Reading University Post Doc: A novel methanol dehydrogenase

1966 - 1967 Sheffield University Post Doc: glutamate fermentation in Clostridia

1967 – 2004 Southampton University: Lecturer etc

2005 – present time: Southampton University: Emeritus Professor

Thank you to my research students (1969 – 2008)

Methanol dehydrogenase	Cytochromes and electron transport	Metabolic pathways	3D structures
Steven Ford	Jim Elliott	Pat Dunstan	Peter James
Dudley Page	Steven Froud	Iain Taylor	Paul Williams
Darren Day	David O'Keefe	John Bolbot	Gyles Cozier
Jonathan Cox	Andrew Cross		Simon Dales
Ian Richardson	Mathew		[John Read]
Alain Avezoux	Beardmore-Gray		[Chenyi]
Karen Amaratunga	Anthony Long		[Leigh Felton]
Tosin Majekodunmi	Claude Chan		
Paul Afolabi	Helen Ashworth		
	Also Bill Keevil (Post-doc); Paul Skipp (Technician)		
Amino acid transport	Electron transport and nitrogen fixation	Neomycin biosynthesis	Electron transport in methylamine metabolism
Jeff Robinson	Andrew Smith	Cedric Pearce	Ashley Lawton
Bob Cook	Nick Juty		Kevin Auton

Methylotroph stories

Methylotrophs are bacteria that grow with compounds with a single carbon atom as their sole source of carbon and energy. 'Ordinary bacteria' never grow methylotrophically.

1. The rise of the methylotrophs. Only 2 species in 1960. Many hundreds now – with enormous genetic and metabolic diversity.
2. Methanol dehydrogenase (**MDH**); the first Quinoprotein.
3. A special electron transport chain for methanol oxidation.
4. A remarkable resurgence of interest in MDH.

My PhD project (1960 – 1963): Isolate a bacterium able to grow on methanol and therefore able to oxidise it. Then find the enzyme responsible.

1. The rise of the methylotrophs.

Always specialised genera; never the usual types of bacteria
Many grow well on 'ordinary' substrates – succinate, lactate etc

Only 2 species in 1960. Only 4 papers in my PhD introduction

Many hundreds of species now – with enormous genetic diversity

A wealth of novel metabolic pathways for conversion of formaldehyde to cell material

Unusual energy transduction

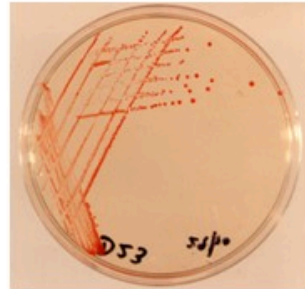
Regular international symposia (from 1970 to present day)

Industrial exploitation. This is because of their metabolic diversity and because their growth substrate, methanol, is inexpensive

The main 'workhorses' in the study of methylotrophs

- *Pseudomonas* AM1 (Peel & Quayle, 1961)
- *Pseudomonas* sp. M27 (Anthony & Zatman, 1964)

***Methylobacterium extorquens*.** A pink facultative methylotroph



Me in 1963



J Rod Quayle



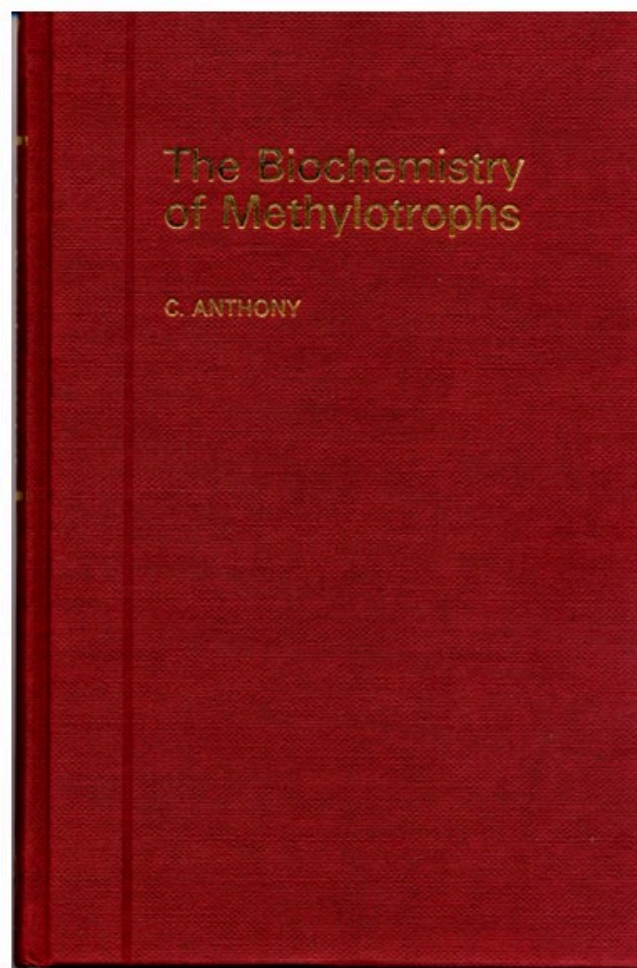
My PhD supervisor and my first research student (Len Zatman and Pat Dunstan, now Goodwin)



Young Howard & Rod Quayle

Howard Dalton, Rod and me

The Biochemistry of Methylootrophs 1982



The Biochemistry of Methylootrophs

C. ANTHONY

*Department of Biochemistry
University of Southampton
England*

Chapters 12

Text pages 350

Index 48 pages

Tables 60

Figures 57

References 1300

1982



ACADEMIC PRESS

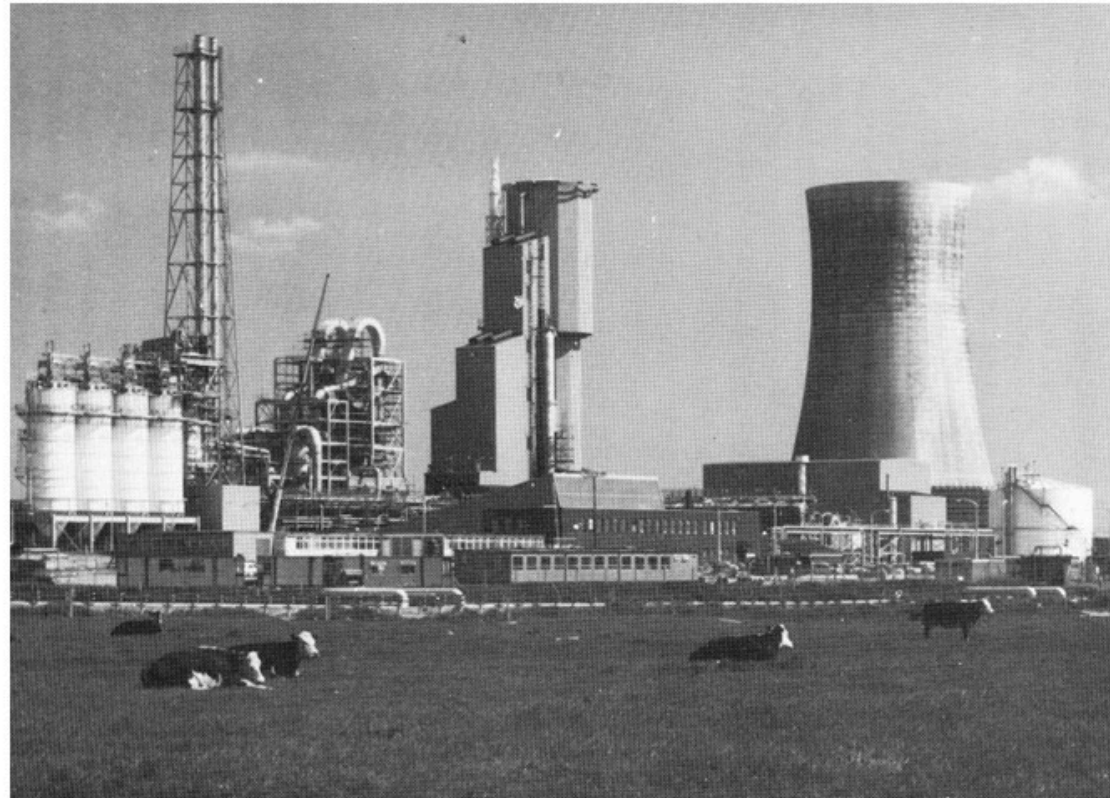
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São Paulo · Sydney · Tokyo · Toronto

Methylootrophic bacteria
Ribulose biphosphate path
Ribulose monophosphate cy
The Serine pathway
The TCA cycle and growth
on multicarbon compound
Oxidation of methane, metha
formaldehyde and format
Oxidation of methylated ami
Electron transport and
energy transduction
Growth yields and bioenerge
Methylootrophic yeasts
Methanogens and
methanogenesis
Commercial exploitation

A CD version is available and the complete b
is on my website: chris-anthony.co.uk

The ICI 'Pruteen' plant at Billingham, UK 1980 For production of protein supplement for cattle feed



The centre tower is the 1.5 million litre fermenter

It contains about 100,000,000,000,000,000,000 methylotrophs
10% of their soluble protein is Methanol dehydrogenase

2nd Story: Methanol dehydrogenase

*An enzyme with a remarkable structure and novel type of prosthetic group - **PQQ** (the first Quinoprotein). The false claim that PQQ is a new vitamin*

Oxidising enzymes.

Most common: alcohol + NAD⁺ → aldehyde + NAD + H⁺

Alternative oxidising enzymes are membrane bound and have FAD or FMN as a bound prosthetic group: succinate + Enz-FAD → fumarate + Enz-FADH₂

Most living things have an NAD-linked alcohol dehydrogenase
BUT none oxidises methanol so my supervisor, Len Zatman, thought there might be an interesting dehydrogenase in bacteria able to oxidise methanol to formaldehyde.

My project: Isolate a bacterium able to grow on methanol and therefore able to oxidise it. Then find the enzyme responsible.

I thought this was a trivial problem but it was not.

My first paper was on a novel methanol dehydrogenase (1964)

My last paper was on the very high (atomic) resolution of this enzyme (2004)

We published 2 papers together. The first described our new methylotroph and the next slide is the second.

Methanol dehydrogenase

Responsible for all bacterial methanol oxidation

The Microbial Oxidation of Methanol

2. THE METHANOL-OXIDIZING ENZYME OF *PSEUDOMONAS* SP. M 27

BY C. ANTHONY AND L. J. ZATMAN
Department of Microbiology, University of Reading

(Received 21 November 1963)

A soluble enzyme – now known to be in the periplasm

Dye-linked assay (PMS/PIP); pH optimum 9.2; pI 8.2

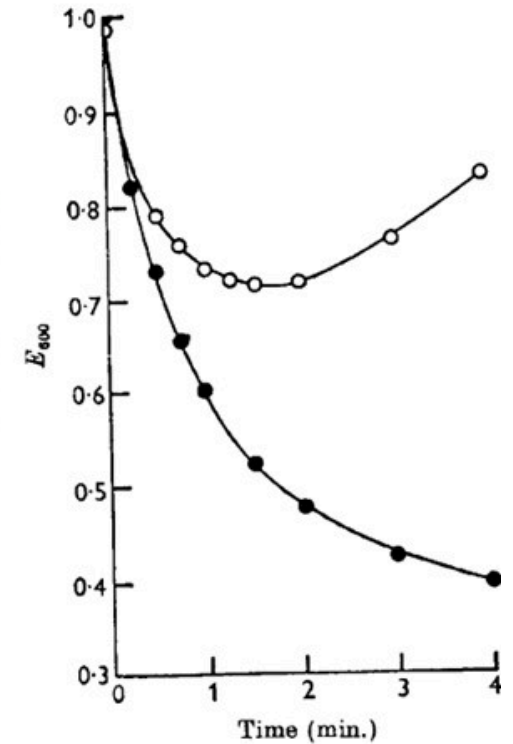
Methanol + PMS $\rightarrow$ Formaldehyde + PMSH₂
PMSH₂ is oxidised by blue PIP which loses its colour

Activator is ammonia (not NH₄⁺ ion) (this is unique)

Wide substrate specificity

Unusual absorption spectrum – not FAD or FMN **so novel prosthetic group??**

High proportion of tryptophans



MDH assay
with PMS/indophenol

Isolation of the prosthetic group

The prosthetic group is the part of the enzyme that is not the amino acid chain.

It is FAD or FMN in flavoproteins, or haem in cytochromes

Grow huge amounts of bacteria on methanol. Harvest and break (ultrasound)
Purify the enzyme from the soluble fraction (Ion exchange, Sephadex etc)

Precipitate the protein and release the fluorescent prosthetic group by acid treatment

Purify the prosthetic group (ion exchange etc). After 3 months I had a few red grains.

Characterised by its excitation and emission fluorescence. A beautiful green colour.

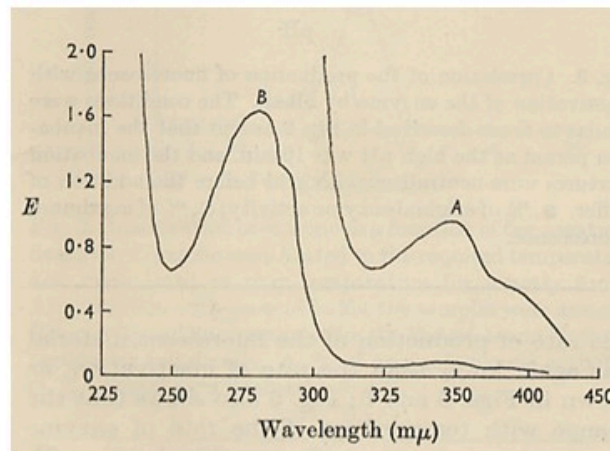
The only known compound with a maximum excitation at 360nm with this maximum occurring at low pH. It is tightly bound to the enzyme.

SO a completely new compound. Thirteen years later its structure was determined by X-ray crystallography at Cambridge; then confirmed by us a further 15 years later with the X-ray structure of the whole enzyme.

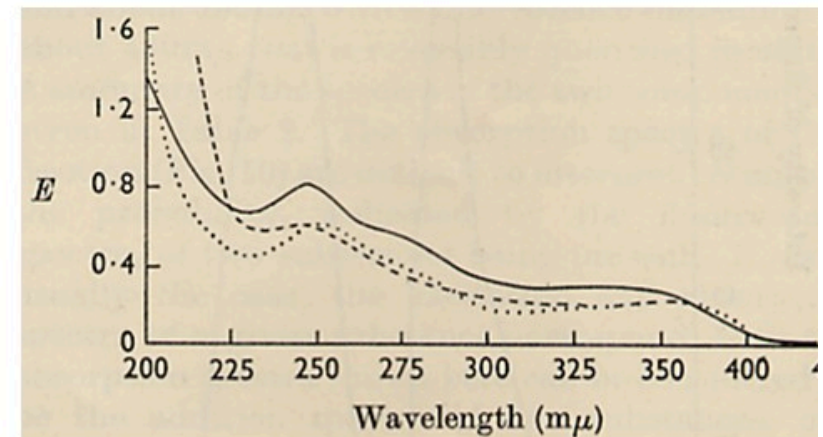
A new type of enzyme prosthetic group

Note: all other dehydrogenases use NAD(P) as hydrogen acceptor or they are membrane flavoproteins that use FMN or FAD as prosthetic group

The Microbial Oxidation of Methanol
 THE PROSTHETIC GROUP OF THE ALCOHOL DEHYDROGENASE OF
PSEUDOMONAS SP. M27:
 A NEW OXIDOREDUCTASE PROSTHETIC GROUP
 BY C. ANTHONY* AND L. J. ZATMAN
Department of Microbiology, University of Reading
 (Received 30 December 1966)



Spectrum of MDH



Spectrum of prosthetic group

PQQ and other quinoproteins The novel prosthetic group of MDH was later in other dehydrogenases and Hans Duine and Hans Frank called these Quinoproteins. These include the alcohol dehydrogenase of acetic acid bacteria and the typical glucose dehydrogenase in *Pseudomonas*, *E. coli*.



Hauge described GDH and PQQ very early on



Friends from Yamaguchi, Japan:
Matsushita, Urugami (?), Ameyama, Adachi.
Found many new quinoproteins especially in
Acetic acid bacteria

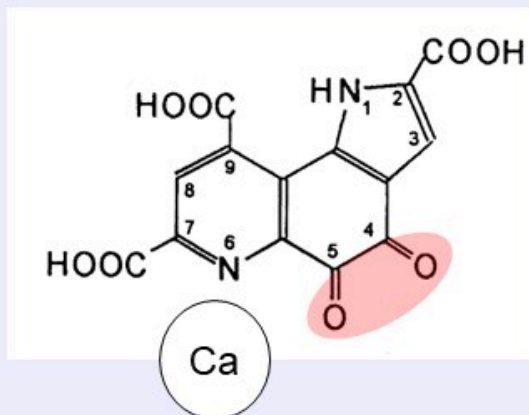


Hans Duine and Hans Frank
'invented' quinoproteins

Note: No PQQ-containing quinoproteins have been described in anything other than bacteria

PQQ and Quinoproteins

Pyrroloquinoline Quinone PQQ)



First isolated and purified
by Anthony & Zatman
in 1967 from bacterial
methanol dehydrogenase

Structure determined by
Kennard's group in 1979

Remains tightly bound
throughout reaction cycle

PQQ-containing Quinoproteins

All bacterial dehydrogenases

Usually responsible for 1st step in
the oxidation of growth substrate

Mainly alcohols and aldoses

eg ethanol oxidation to acetic acid
in acetic acid bacteria

Reaction occurs in the periplasm

Electron acceptors are
cytochromes, blue copper proteins
or ubiquinone

May be soluble or membrane-bound

May also contain haem

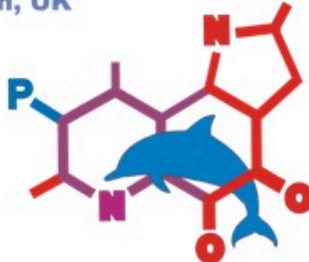
**None has been described in
eukaryotic organisms**

From 1988 onwards there have been International Symposia on PQQ and Quinoproteins The 5th was in Southampton in 2002



3rd International Symposium on Vitamin B₆, PQQ, Carbonyl Catalysis and Quinoproteins

 **University of Southampton, UK**
April 14th-19th 2002



Comprising the
 11th International Symposium on Vitamin B₆ and Carbonyl Catalysis
 and the 5th International Symposium on PQQ and Quinoproteins



Boldrewood conference Centre

Programme book and Abstracts

The following slide was included to show what was lost when Boldrewood was demolished. This was my room, complete with coffee machine and comfort. Murali with back showing was a 4th year medical student solving a problem with his project and the other is a research student friend Leigh Felton. Staff rooms were always available for students to see members of staff.



My office with Murali and Leigh

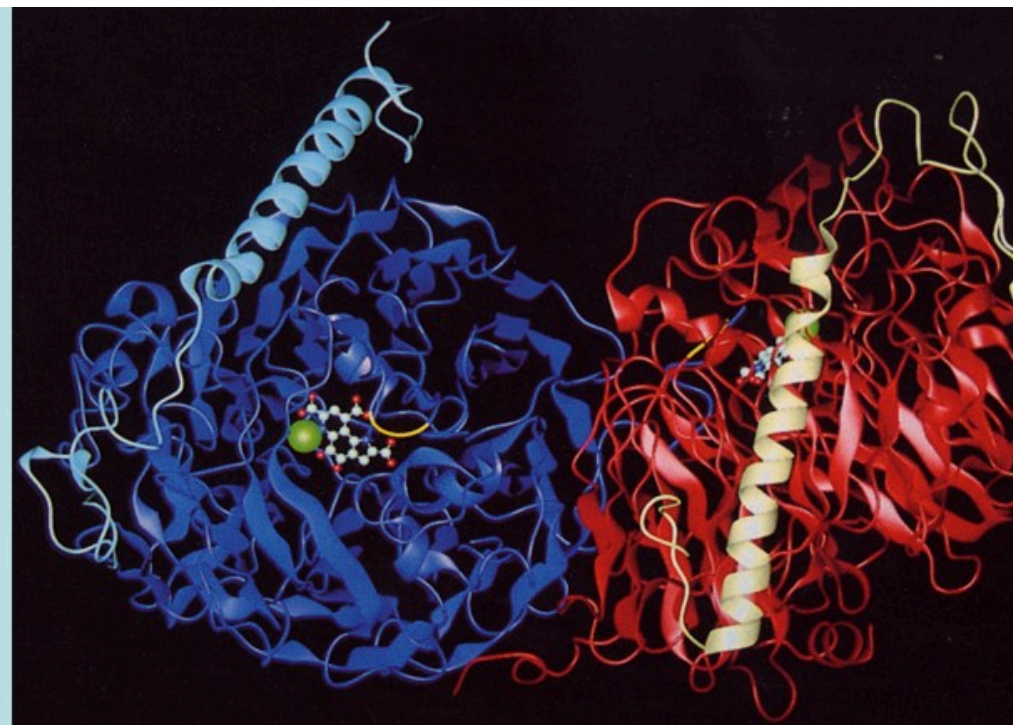
The following section describes our work with MDH which was done some years later in collaboration with Meenakshi Ghosh who came to Oxford from Calcutta to learn how to do X-ray crystallography of proteins. She had previously had experience only with inorganic crystals. She needed a project so I provided it.

The X-ray structure of MDH 1992-2004

Southampton:
Chris Anthony
Alain Avezoux

Oxford:
Meenakshi Ghosh,
Colin Blake

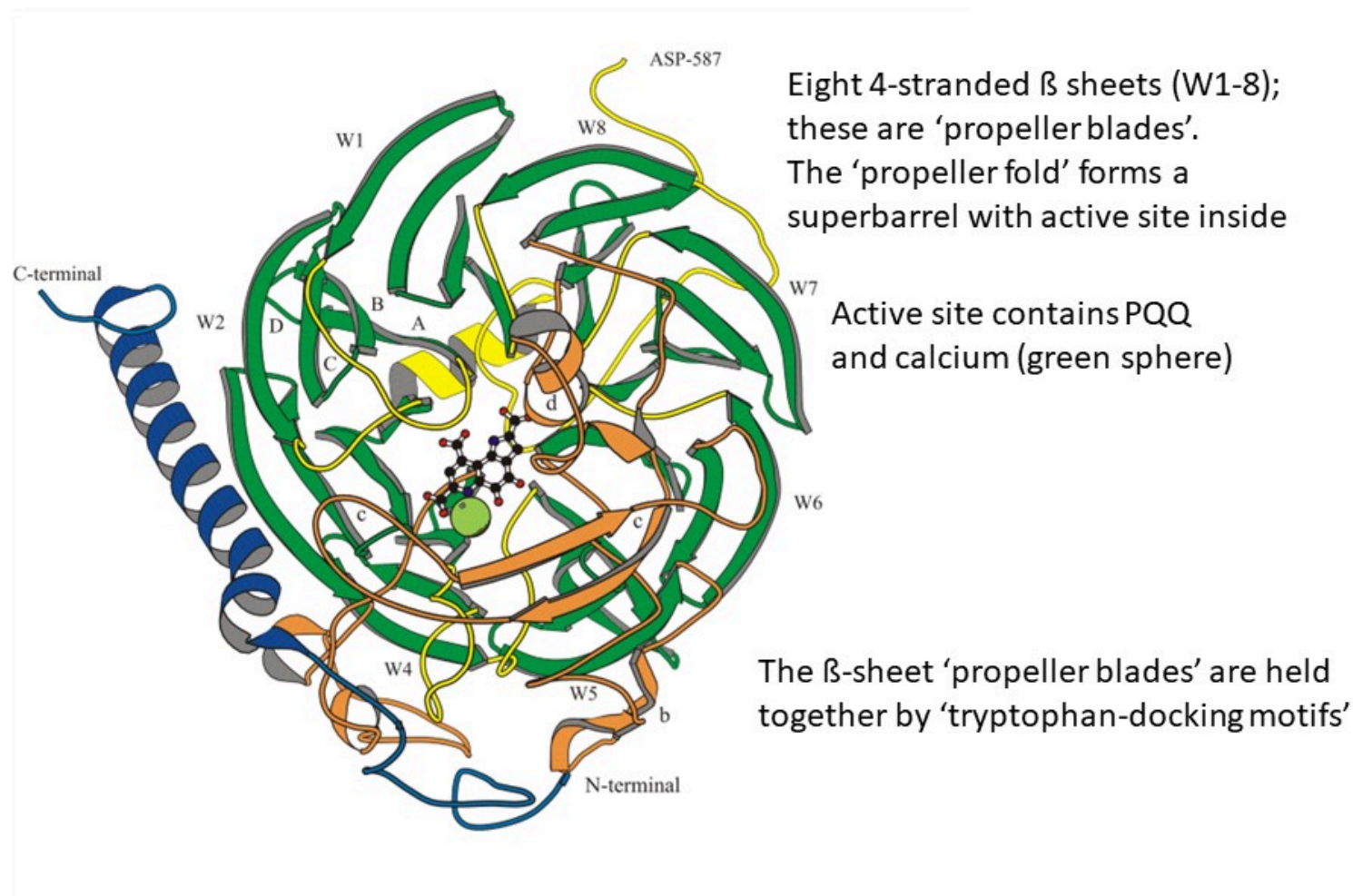
MDH is a dimer
Large subunit is 60k
Small subunit is 9k



Meenakshi
Ghosh

A wonderful collaboration; Meenakshi knew no biochemistry and i knew no crystallography and its interpretation

The β -propeller structure of MDH



We made the mistake of relying on an 'expert' to assay our enzyme for metal ion content and he found none. After our Japanese friends showed that their Ethanol dehydrogenase contained calcium we found it in MDH. Our work with a mutant lacking calcium enabled us to reconstitute it with strontium or barium.

The calcium ion in MDH

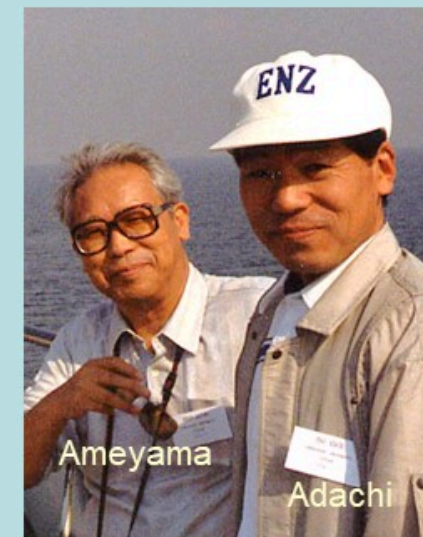
1965-1989 'MDH contains no metal ion' [Anthony & Zatman]

1986 MDH from mutants (*mxmA*, *K* & *L*) was inactive and had unusual spectrum [Nunn & Lidstrom]

1990 MDH contains Calcium (or strontium) [Adachi et al.]

1992 Other MDHs contain calcium.
MDH from *mxmA*, *K* & *L* lacked Calcium;
incubation with Ca produced active enzyme
& normal spectrum [Ian Richardson]

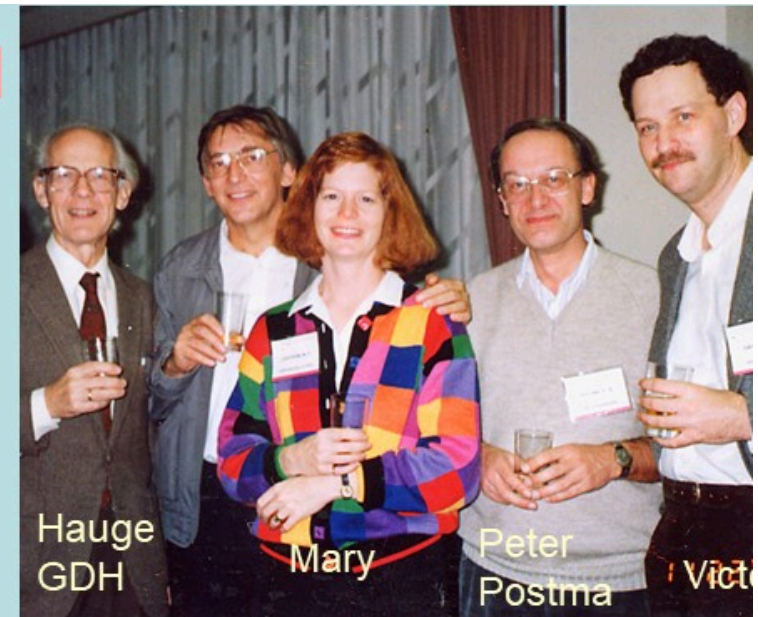
1992 MDH isolated from marine *Methylophaga Marina* is red and inactive;
incubation with Ca produced
normal green active enzyme [Claude Chan]

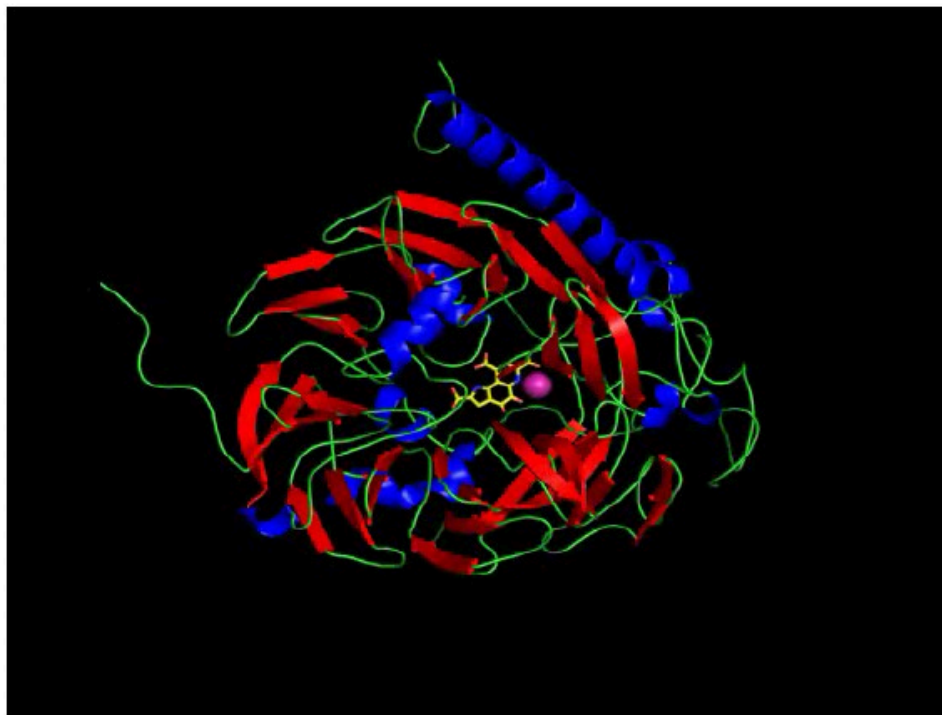


The calcium ion in MDH

1994 Kinetics of MDH containing strontium *[Harris & Victor Davidson]*

1996 Incubation with Barium produced MDH which was more active than wild-type MDH [Matt Goodwin, Alain Avezoux & Simon Dales]

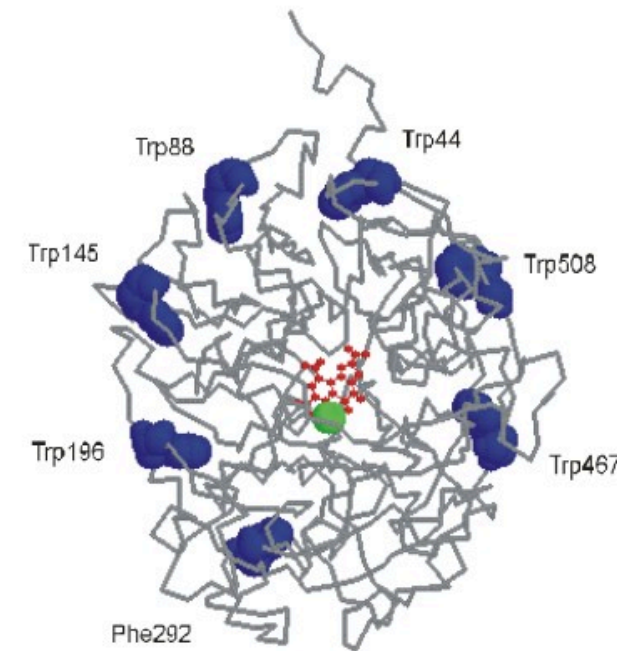
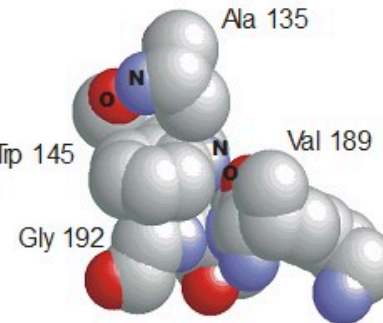
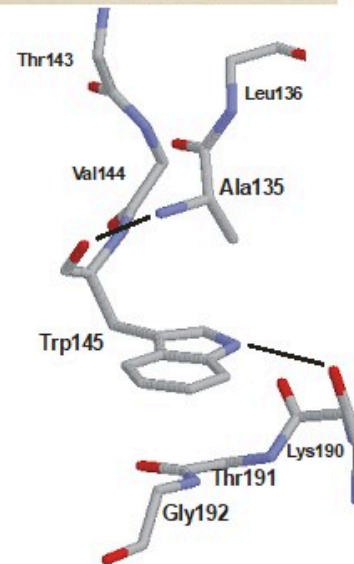
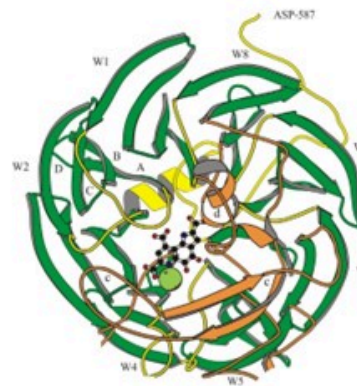
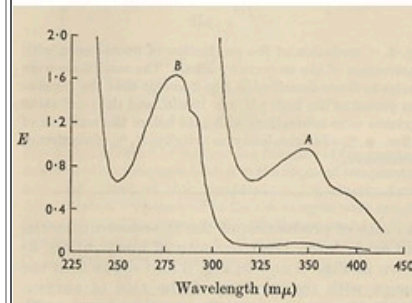




Tryptophan docking system

High proportion of tryptophans;
19 per α subunit

The β -sheet 'propeller blades' are held together by 'tryptophan-docking motifs'



The following slide shows the consensus sequence involved in the docking motifs which demonstrated to Kashahara and Kato that they had a propeller structure which they wrongly interpreted as evidence for a quinop

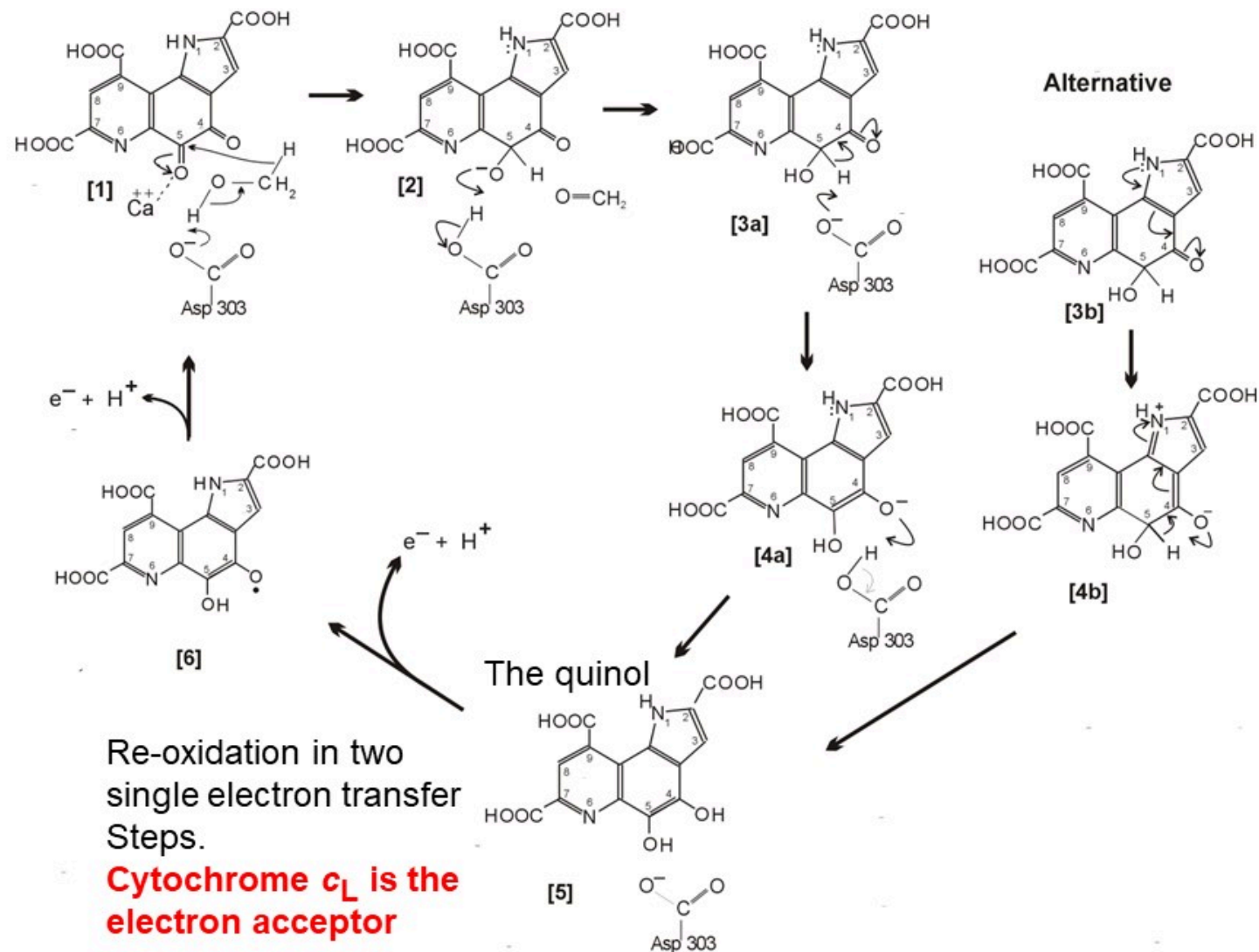
The consensus sequence in the tryptophan-docking motifs

Propeller blades W1-W8

Position	1	2	3	4	5	-	6	7	8	9	10	11
Motif	C	C	C				D	D	D	D	D	D
W1	Ala 77	Leu	Gly	Leu	Asp	Asp	Pro	Gly	Thr	Ile	Leu	Trp 88
W2	Ala135	Leu	Asn	Ala	Glu	-	Thr	Gly	Glu	Thr	Val	Trp145
W3	Ala 186	Tyr	Asp	Val	Lys	-	Thr191-Gly192		Glu	Gln	Val	Trp 196
W4	Gly 282	Arg	Asp	Ala	Asp	-	Thr	Gly	Glu	Ala	Lys	Phe 292
W5	Thr 337	Leu	Asp	Arg	Thr	-	Asp	Gly	Ala	Glu	Val	Ser 347
W6	Ala 457	Tyr	Asn	Ala	Ile	-	Thr	Gly	Asp	Tyr	Lys	Trp 467
W7	Ala 489	Arg	Asp	Ser	Asp	-	Thr	Gly	Asp	Leu	Leu	Trp 508
W8	Val 577	Phe	Ser	Leu	Asp 581	-	Gln 39	Leu	Arg	Pro	Ala	Trp 44
MDH Consensus	Ala	X	Asp/ Asn	X	X	-	Thr	Gly	Asp/ Glu	X	X	Trp
GDH/ADH Consensus	Ala	X	Asp/ Asn	X	X	-	Thr	Gly	Lys	X	X	Trp

For example: **Trp145** of strand D in W2 is stacked between **Ala135** in strand C in W2 and **Thr-Gly** at position **6-7** in W3

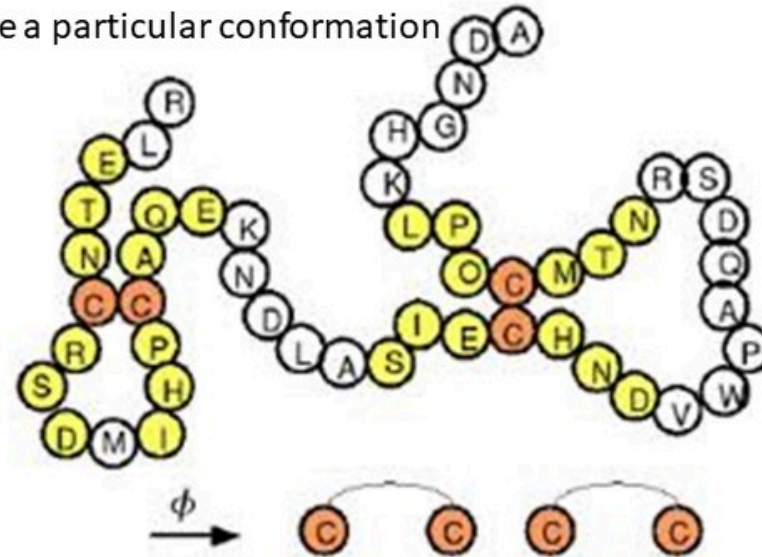
The Direct hydride transfer mechanism Anthony et al (1993--)



The mechanism involves an initial proton abstraction (by Asp 303) and a hydride transfer from the methyl group of methanol. The quinol then passes its electrons one at a time to the specific cytochrome electron acceptor. After a single electron has been transferred the free radical PQQH is stable, and MDH is usually isolated with PQQ in this form (Shown by Frank and Duine)

The unique disulphide ring structure in the MDH active site

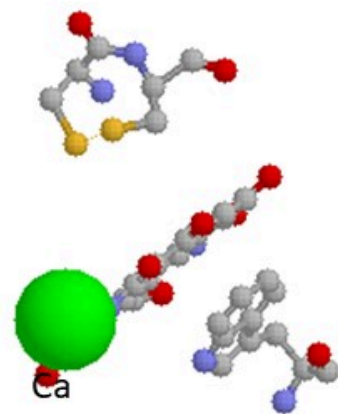
Two distant Cysteine residues in proteins can be oxidised to form a disulphide bridge that is used to stabilise a particular conformation



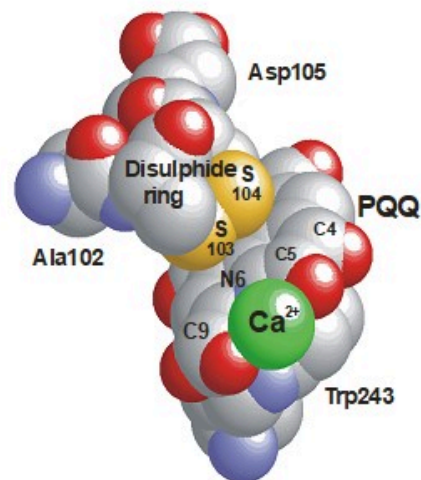
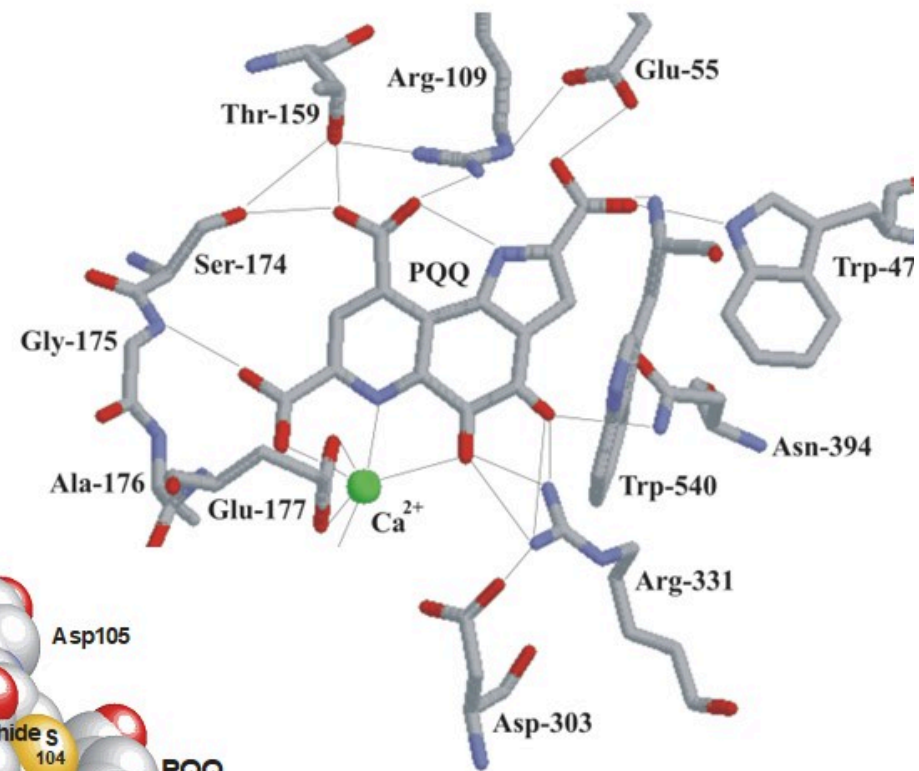
Ramachandran stated that 2 adjacent cysteines would never form a bridge. BUT if they did then they would form an 8-membered ring structure with a 'strained' peptide bond.

**None has ever been seen except in the active site of MDH.
It is very easily reduced, so breaking the bond and inactivating the enzyme.**

The active site of MDH



Novel disulphide ring structure
from adjacent cysteines



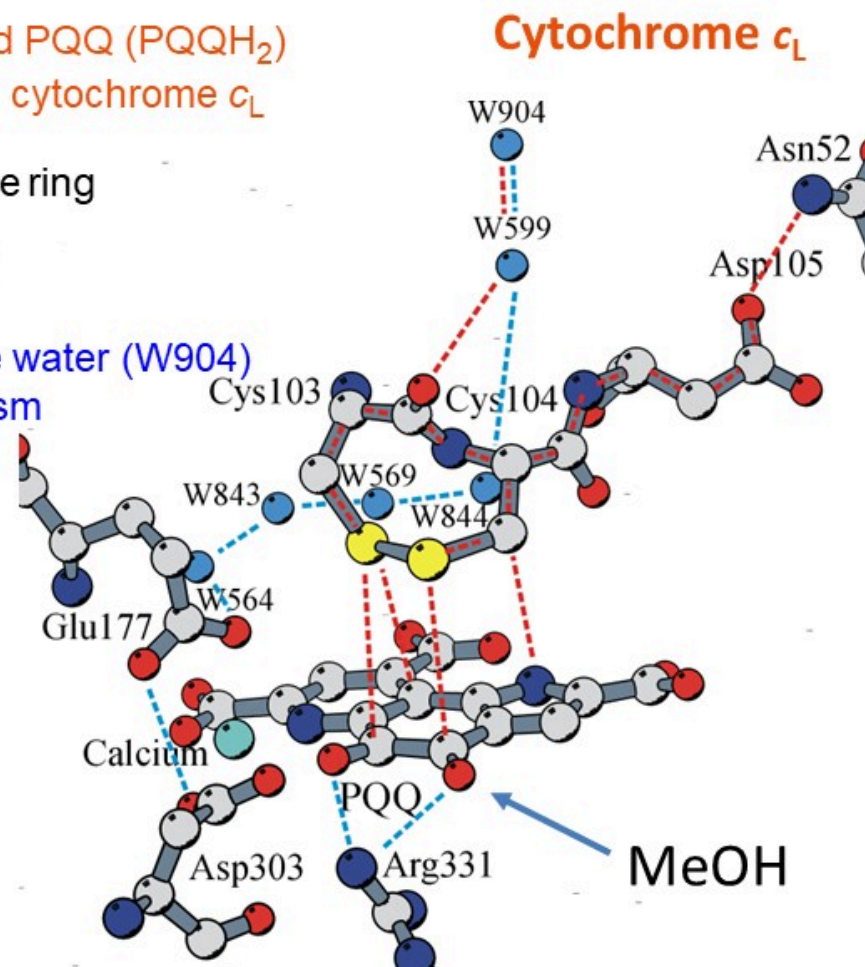
The path of electrons and protons during the oxidative part of the reaction mechanism of MDH

Electrons must pass from reduced PQQ (PQQH₂) to a unique type of cytochrome - cytochrome c_L

Note involvement of the disulphide ring

Protons must pass from PQQH₂ by way of its hydroxyls, and the hydrogen-bonding network, to the water (W904) which is accessible to the periplasm

The pathways are based on those proposed for the quinohaemoprotein alcohol dehydrogenase by Oubrie, Dijkstra *et al*, and Chen, Matsushita, Toyama, Scott Mathews *et al*.



False claim that PQQ is vitamin

Most enzyme cofactors cannot be made in humans so have to be provided as their precursors – vitamins. Eg: NAD (Niacin), FAD (riboflavin)

If mammals do have quinoprotein enzymes then PQQ is almost certainly a vitamin.

In 2003 Kashara and Kato published a paper in Nature claiming to have found a gene coding for a quinoprotein and announcing that this meant that PQQ is “The first new vitamin for 55 years”.

This was welcomed with a great fanfare

Their argument was so obviously false so I ignored it.

BUT two years later Mitsubishi announced that they were investing 4 million dollars in producing this new vitamin. So I contacted them and published a paper in Nature explaining why it is not. But Mitsubishi went ahead and now it is on the market as a growth nutrient!

Premature announcement that PQQ is a vitamin for mammals

brief communications

Nutritional biochemistry

A new redox-cofactor vitamin for mammals

Takaoki Kasahara, Tadafumi Kato
Laboratory for Molecular Dynamics of Mental Disorders, Brain Science Institute, RIKEN, Japan



NATURE | VOL 422 | 24 APRIL 2003 | www.nature.com/nature

Scientists Add New Member to Vitamin B Family

---Sarah Graham, Scientific American, April 24, 2003.

A new page may need to be added to the vitamin B family album.

According to a report published today in the journal Nature, researchers have determined that the compound known as pyrroloquinoline quinone (PQQ) should be classified as a vitamin in the same class as vitamins E and B3. Scientists first isolated PQQ from bacteria in 1979.



MITSUBISHI GAS CHEMICAL COMPANY, INC.

Biological Products

September 24, 2003

Mitsubishi Gas Chemical Company Inc. speeds the development of application of coenzyme PQQ-vitamin.

IN THE NEWS

Japanese Discover First New Vitamin in 55 Years

April 24, 2003
 By REUTERS

Mind your PQQ - properties of pyrroloquinoline quinine, nutrient - vitamins and supplements in a bodybuilder's diet

The argument by Kasahara and Kato

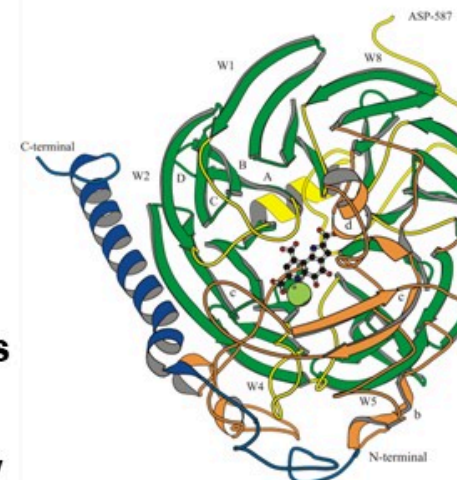
Search engines 'identified' PQQ-binding sites in a protein in mice [predicted from a gene sequence]

Our argument against

We cannot identify PQQ-binding sites in a database

In fact, the search engine found 7 'propeller blades' that typically occur in PQQ-containing quinoproteins

The 'propeller blades' – wrongly identified by the search engine as 'PQQ-binding sites' are not directly involved in binding PQQ; they are purely structural



All trees are green

All PQQ enzymes have propeller structure

My coat is green

My protein has a propeller structure

SO: My coat is a tree

SO: My protein is a PQQ enzyme

Therefore PQQ is a vitamin

brief communications

Nutritional biochemistry

A new redox-cofactor vitamin for mammals

Premature announcement that PQQ is a vitamin for mammals

Leigh M. Felton and Chris Anthony:
Nature; Communication Arising

The only evidence that the proposed dehydrogenase is PQQ-dependent is that the Smart and Pfam databases 'identified' '7 PQQ-binding sites' in the C-terminal region.

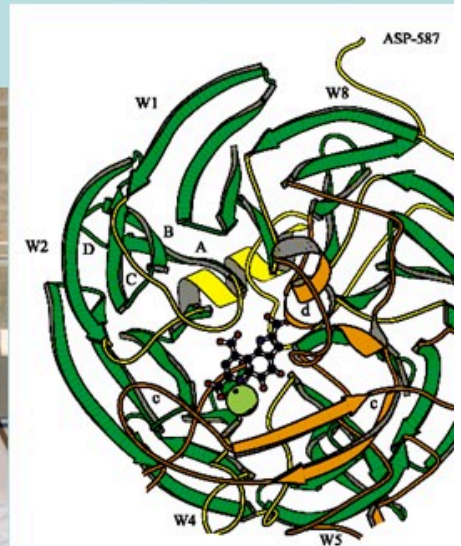
In fact, the 'sites' are sequences predicted to form a series of β -sheet 'blades' in a 'propeller fold' as seen in PQQ-dependent dehydrogenases.

This fold has nothing to do with PQQ binding and is found in many other proteins.

The proposed enzyme has no sequence similarity to any PQQ-dependent dehydrogenase.

There is still no evidence that PQQ
Is a cofactor for a eukaryotic enzyme
Or that it is a vitamin

Thank you,
Goodbye and Good luck





REGARDED AS A SUPERCHARGED COQ10, PQQ IS AN ALL NATURAL NUTRIENT THAT PLAYS AN IMPORTANT ROLE IN ENERGY PRODUCTION

Nutritional information

Serving Size: 1 capsule
Servings Per Container: 60

Ingredient	Amount Per serving	%DV*
pyrroloquinoline quinone (as PQQ disodium salt)	30 mg	**

*Percent Daily Values (DV) are based on a  **No DV established.

INGREDIENTS:
Pyrroloquinoline quinone (fruiting agent), vegetable magnesium stearate (for vegetable binding), hydroxypropyl methylcellulose (capsule shell).

DIRECTIONS FOR USE:
Take one capsule daily, preferably with a meal. Do not exceed stated dose.

Best before date: 05/2022
Lot: PQQ097
510603819533400

Triple Strength PQQ (Pyrroloquinoline Quinone) 30 x 60 Veggie Capsules

★★★★★ 11 reviews ⌚ Delivery in 1-2 days 🚚 Free Delivery

Get a daily dose of this all new super potent anti-oxidant, regarded by many as Supercharged CoQ10. Our super strength PQQ has a potent 30mg of the finest-quality Pyrroloquinoline Quinone, triple the strength of most PQQ supplements.



Available options (please select one)

1 Bottle - £27.99 Per Bottle	2 Bottles £22.39 Per Bottle
4 Bottles £20.99 Per Bottle	6 Bottles £18.19 Per Bottle

1 £27.99

3rd Story. Before we knew the structure of MDH we started working on how this enzyme with a novel prosthetic group interacts with an electron transport chain so that the oxidation of methanol will be coupled to ATP production.

3rd Story: A special electron transport chain for methanol oxidation involves a novel type of cytochrome c

Methylobacterium has a 'normal' system for NADH and succinate oxidation

Inhibitors of NADH and succinate oxidation **did not** inhibit methanol oxidation

Inhibitors of the cytochrome oxidase **did** inhibit methanol oxidation

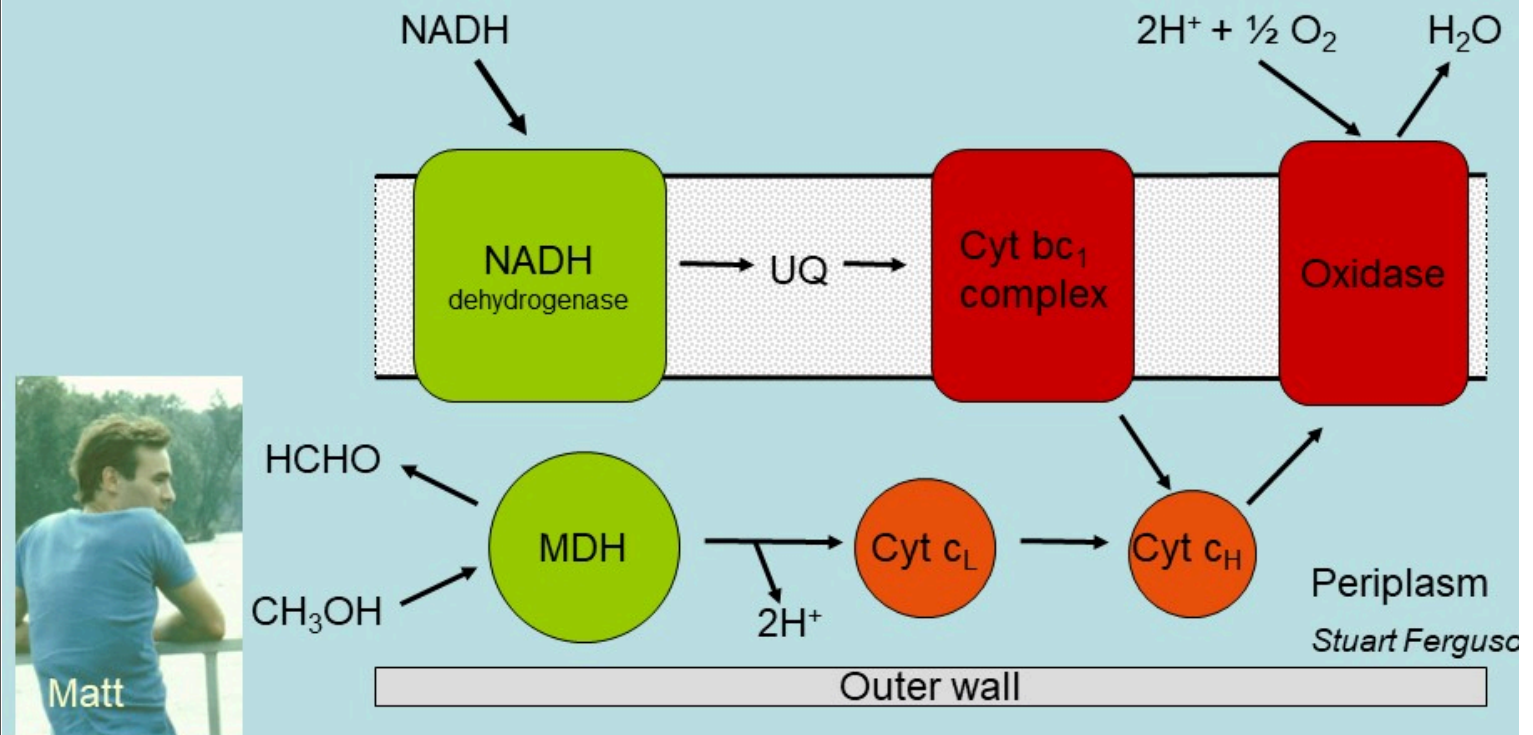
Addition of lactate (giving NADH) or succinate reduced cytochromes b, c and oxidase

BUT: Addition of methanol only reduced cytochromes c and oxidase

Methylobacterium and all methylotrophs have an extra cytochrome c called cytochrome c_L . This is the specific electron acceptor for MDH. They react in the periplasm.

A student David O'Keefe boldly went against my advice, staying up most of the night and found it after months of my failure.

Electron transport during methanol oxidation



During oxidation of MeOH 2 protons are released into the periplasm and consumed inside, setting up a protonmotive force supporting production of about 0.6 ATP/MeC

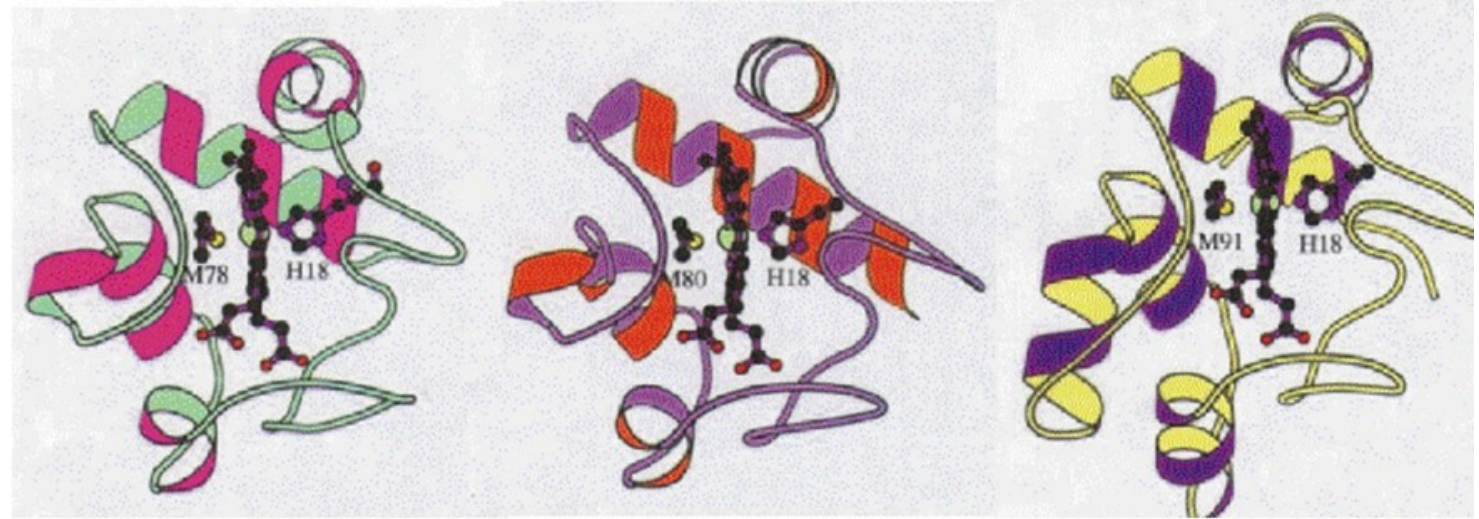
1975 - 1985 David O'Keefe; Sandy Cross; Mathew Beardmore-Gray; Claude Chan;
Jon Cox; Darren Day; Steve Froud; Andy Elliott; Bill Keevil; Sasha Netrusov; Pat Goodwin

NOTE: The ATP yield from methanol is very low but this does not matter because almost every atom of carbon in these bacteria comes by way of this oxidation process so there is ATP to spare. Cell yields are not limited (as in other bacteria) by ATP but by availability of NADH. Matt Beardmore-Gray calculated that the large amount of cytochrome and MDH in these bacteria is sufficient to cover the surface in a mono-molecular layer.

The solution of the unusual MDH structure helped us get an X-ray crystallography unit set up in the Department,

with the appointment of John Cooper and Steve Wood, and they helped solve the structure of the two methylotroph cytochromes.

Structure of cytochrome c_H



M. extorquens
cytochrome c_H

Mammalian
cytochrome c

Bacterial
cytochrome c_2

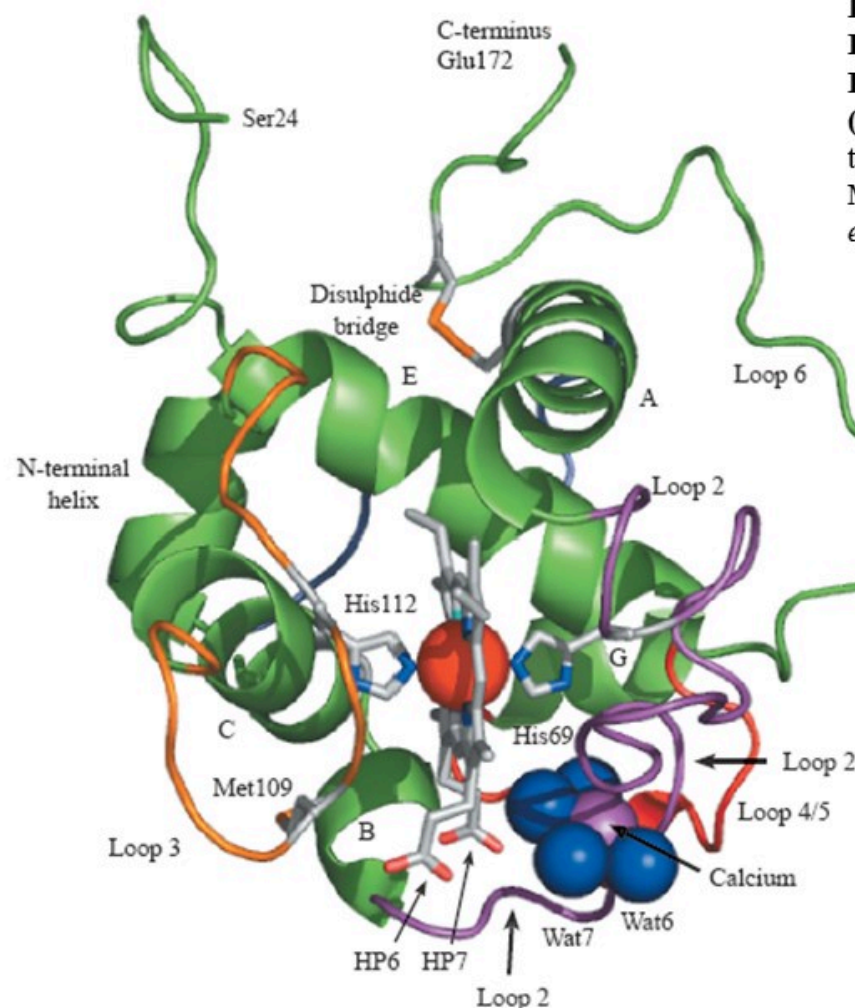
Remarkably, cytochrome c_H is unique for a bacterial cytochrome in being similar in structure to mammalian cytochrome c

Its internal structure 'disproves' a key proposal for cytochrome function: All other cytochromes c have a tyrosine bonded to water in the haem cleft: Cytochrome c_H has tryptophan and no water. So the water has no function.

The X-ray structure of cytochrome c_L , the electron acceptor from methanol dehydrogenase

Paul Williams and Southampton X-ray structure group

Paul Williams, Leighton Coates, Fiyaz Mohamm Raj Gill Peter Erskine, Dominique Bourgeois, St P. Wood, Chris Anthony and Jonathan B. Coope (2006). The 1.6 Å X-ray Structure of the Unusual c type Cytochrome, Cytochrome c_L , from the Methylophilic Bacterium *Methylobacterium extorquens*. *J. Mol. Biol.* 357, 151–162



The amino acid sequence is unique for cytochromes

The core structure is exactly as seen in other cytochromes c

Two cytochromes c have evolved in the same organism, functioning in the same electron transport chain, having similar core structure but no sequence identity

NOTE: the unique calcium ion and the exposed haem propionates

4. A resurgence of interest in MDH

In 1986 Mary Lidstrom and David Nunn published the methanol operon.

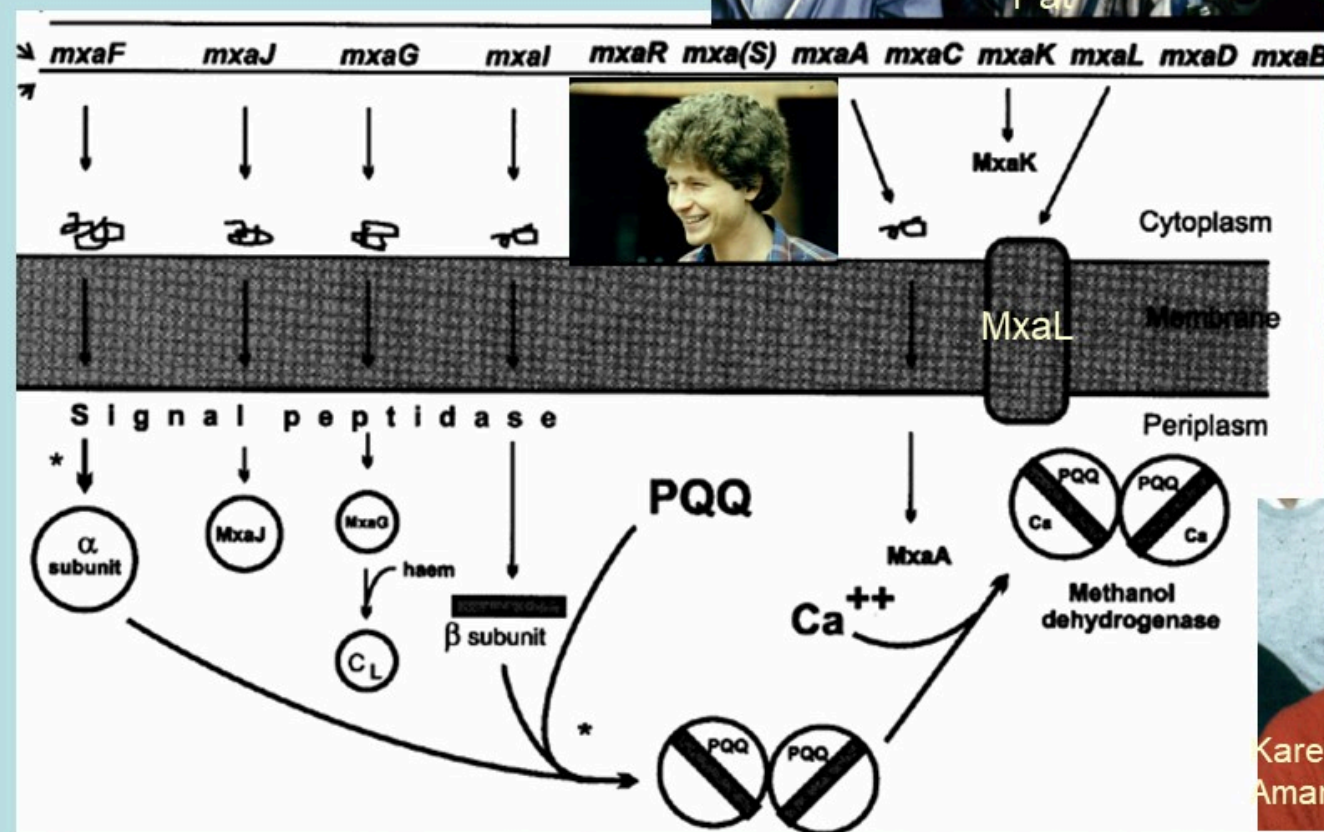
David came to work in my lab and he sequenced the genes for MDH and cytochrome c_L

A very remarkable observation

Mary Lidstrom showed that all methylotrophs have two methanol oxidation operons.

The 2nd (Mox2) is never expressed. Mutations in Mox2 do not affect growth on methanol.

Expression of the mxa operon



The genes: Nunn, Lidstrom, Amaratunga, Anderson, Anthony, Goodwin, Morris, O'Connor

NOTE: the immense amount of difficult work on the genetics of our *Methylobacterium* by Karen Amaratunga and Simon Dales led them to provide important evidence for all our ideas about structure, mechanism and electron transport by a programme of site-directed mutagenesis.

A novel methanotroph (Methanotrophs grow on methane which is oxidised to methanol which is then oxidised by MDH)

In 2017 a novel methanotroph (*Methylacidiphilum fumariolicu*) was isolated from acidic volcanic mud. It grows at high temperature and low pH.

It requires a rare earth element for growth (eg Lanthanum, Cerium, Neodymium).

It only uses the 2nd methanol oxidation operon to produce MDH which uses one of the lanthanides instead of calcium at the active site. As a result during the last few years I have weekly reports on ResearchGate of my 1964 paper being cited!

A final strange thing

In 2018 Colin Murrell's group at UEA described a novel methylotroph isolated from seawater using a methanol medium containing lanthanum salts.

"We propose the name *Marinibacterium anthonyii* (in honour of the British microbiologist Professor Christopher Anthony)". Note: I was Colin Murrell's tutor here and he played second violin in my string quartet.

Marinibacterium anthonyii is the only methylotroph that does **not have 'my' MDH; it only has the 2nd methanol oxidation operon.**

Our last publication on MDH 40 years after my first

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**P. A. Williams, L. Coates,
 F. Mohammed, R. Gill,
 P. T. Erskine, A. Coker,
 S. P. Wood, C. Anthony and
 J. B. Cooper***

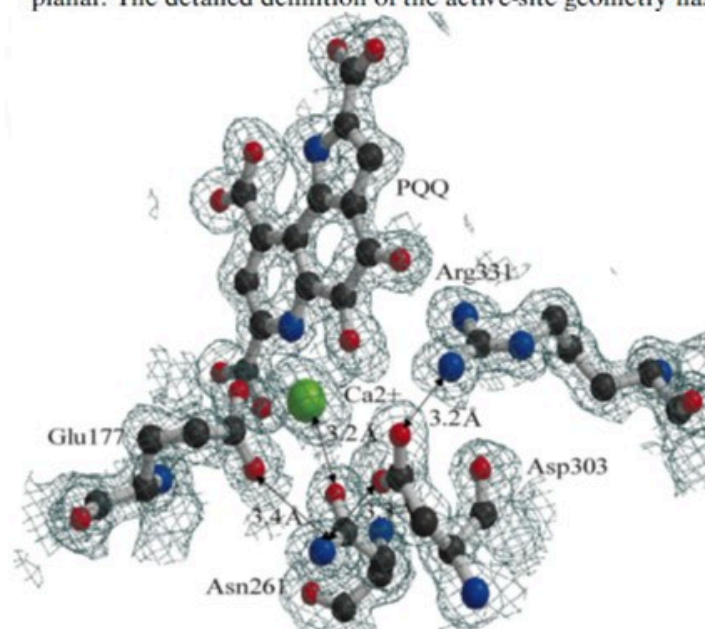
School of Biological Sciences, University of
 Southampton, Bassett Crescent East,
 Southampton SO16 7PX, England

The atomic resolution structure of methanol dehydrogenase from *Methylobacterium extorquens*

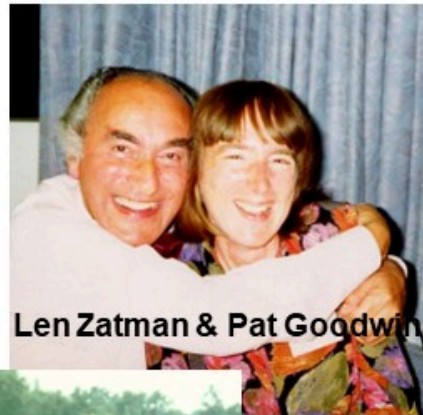
The crystal structure of methanol dehydrogenase (MDH) from *Methylobacterium extorquens* has been refined without stereochemical restraints at a resolution of 1.2 Å. The high-resolution data have defined the conformation of the tricyclic pyrroloquinoline quinone (PQQ) cofactor ring as entirely planar. The detailed definition of the active-site geometry has

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PDB Reference: methanol
 dehydrogenase, 1w6s,
 r1w6ssf.



Acknowledgements



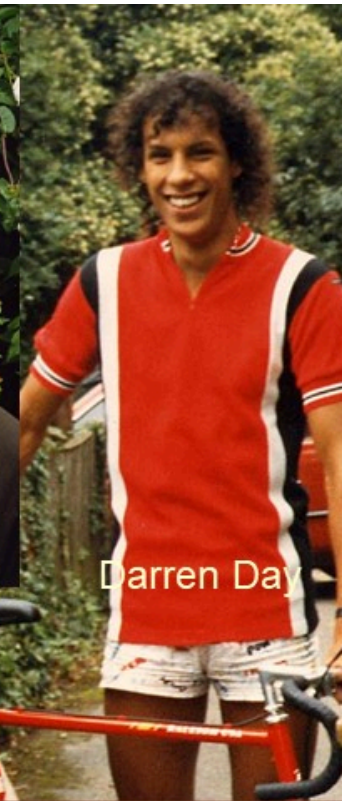
Len Zatman & Pat Goodwin



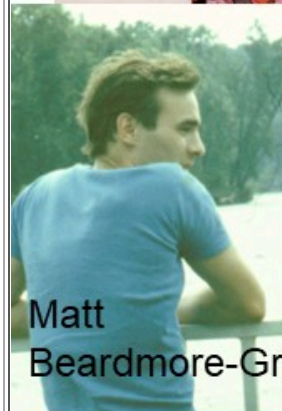
Kevin Auton



Claude Chan



Darren Day



Matt
Beardmore-Gray



H. Dalton



Paul Skipp



Karen
Amaratunga



Wolfgang
Babel

Pat
Sasha
Netrusov

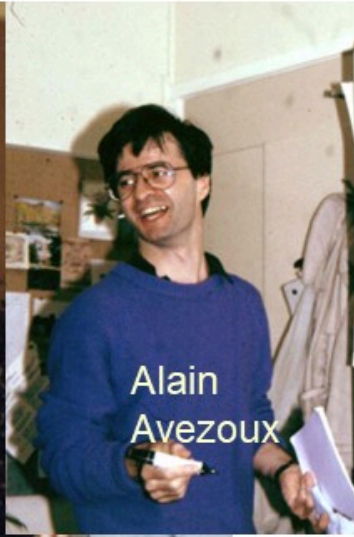
Hiro
Toyama

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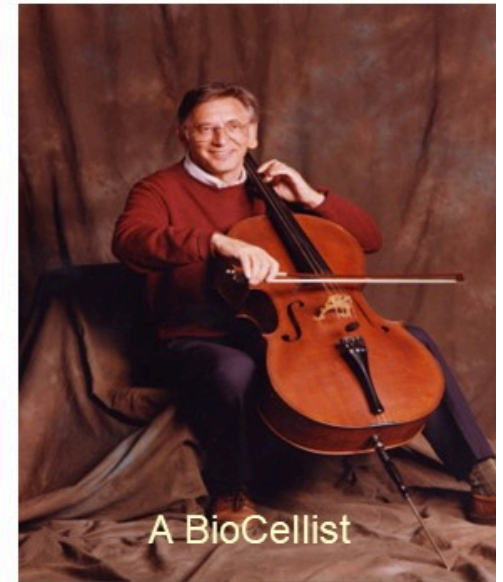


David N.

A few more pictures of methylotroph friends



Chris
1959

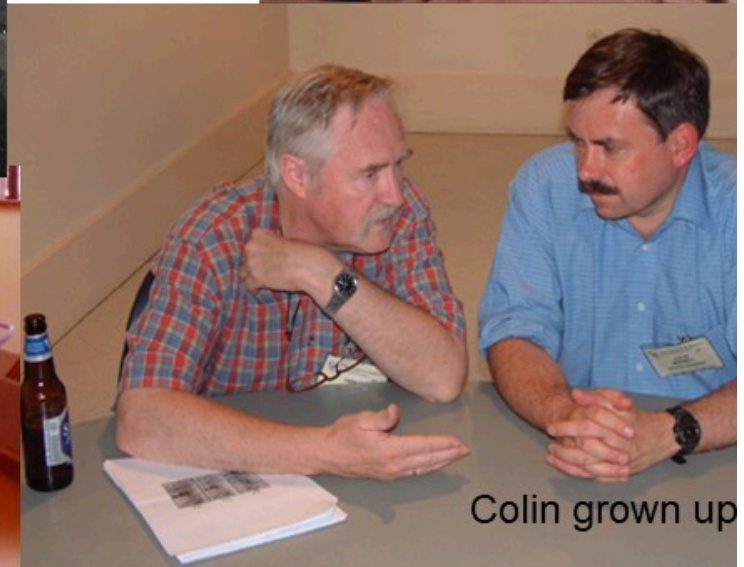


A BioCellist



Colin Murrell
2nd fiddle

1977



Colin grown up

More friends



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