

A geometric pattern that distinguishes the “Iron sulfur” group of Cytochrome p450 enzymes

James A Studier
Urbana Illinois 61801
studier@life.illinois.edu

Abstract:

Given a phylogenetic tree of the P450 enzymes we describe a geometric pattern that distinguishes a major subtree.

If we consider a phylogenetic tree of the cytochrome p450 enzymes there is a large subtree in which most of the enzymes receive electrons from an “iron-sulfur” reductase. We refer to enzymes on the entire subtree as IRSU enzymes.

They are all bacterial or Archaeal except for family 55, which contains lower eukaryotes.

There are some patterns that are present in most of the cytochrome p450 enzymes such as the cysteine containing loop that is right below the the heme iron.

We now describe a geometrical pattern that is conserved in the IRSU but does not occur in the non-IRSU. The pattern occurs at the beginning of the E_helix. The first feature can be seen in a sequence alignment.

The IRSU sequences all have a one residue insert relative to the non IRSU.

The alpha carbon chain has a 4-alpha carbon segment that has a very flat torsion (the 4 consecutive alpha carbons are almost in the same plane). The non IRSU's have a more common helix pattern.

An 8 residue segment was extracted from 21 IRSU alpha carbon chains.

By repeatedly superimposing each segment on the centroid of all of them, a multiple superposition was constructed.

There is close agreement.

The pattern in the non IRSU does not have as much agreement but it is clearly different from the IRSU.

There are 2 residues whose backbone oxygen makes a hydrogen bond with an NH that is 5 residues in the carboxyl direction (in a typical alpha helix the number is 4). There are also hydrogen bonds with the strand at the carboxyl end of the enzyme.

CYP167A1	1Q5D	142	EFDVVRDYAEG	409	LNV
CYP101A1	2CPP	147	QCNFTEDYAEP	402	LPL
CYP105	2Z36	144	PVDLVQALSLP	403	LPV
CYP105P1	3E5J	135	PVDLVKTFANA	395	LPV
CYP165B3	1LFK	136	PADLIAFVADK	394	LMV
CYP165D3	3003	127	PVDFVRHAAWP	380	LPL
CYP121	1M40	130	PADLRNDFADP	392	LPV
CYP107	10XA	137	VVDIVDRFAHP	398	LPV
CYP245A1	2Z3T	145	RPDLVEGFAAP	409	LLL
CYP248A	3BUJ	126	AMDVVDELAYP	389	LPI
CYP119	1F4T	114	EDDIVKKLAVP	360	LVV
CYP119st	3B4X	111	EFDVIESFAIP	360	LVV
CYP109	4RM4	128	EFDLVHDFSYP	392	FRV
CYP231A2	2RFB	100	NKDIISEYAVR	349	LFL
CYP151	3P30	136	DFDFVQHFAHP	399	LPL
CYP153	3RWL	148	EFDWDRVSIE	410	MMV
CYP154A1	10D0	137	PVDLRQELAYP	401	LPV
CYP154C1	1GWI	140	VVDLKAAFAYP	402	LPV
CYP176	1T2B	137	EGDAATWLANE	392	VPI
CYP158A1	2DKK	144	PADLVERVLEP	403	LPC
CYP055	IJFB	137	PVDLVKEFALP	399	LPV

