Information about molecular changes in am mutants

Mutant	Peptide analysis	DNA sequence analysis	Enzyme properties
am1	Ser336 → Phe	TCC → TTC inferred	Enzymically inactive - failure to bind NADPH
am2	His142 → Gln	CAC → GAC inferred	Stabilised in inactive conformation, heat labile
am21	Second-site ?	" + ?	Activated by warming
am3	Glu393 → Gly	GAG → GGG	Stabilised in inactive conformation, reduced negative charge
am3a	Second site ?		Greatly increased Kms for NH4. NAD, glutamate
am3b	Second site ?	GAG → GGG + ?	Needs activation by high α-oxoglutarate + NADPH
am3-18	Second site ?		Needs activation by EDTA
am4	Gly112 → Asp (inferred)	GGC → GAC	Enzymically inactive
am6	Various double f/s sequences	Single bp deletion in Ser1 codon inferred	No enzyme frameshift
am7	Gly372 → Ser	GGT → TGT inferred	Enzymically inactive
am8	-	795-796 TA → GT	No enzyme - intron 2 not spliced or frameshift splice
am9	-	1671-1673 CAT→TA	No enzyme - frameshift
am14	Leu20 → His	CTPy → CAPy inferred	Osmotically reparable - weak 4-ary structure
am14R1	His20 → Tyr	CAPy → TAPy inferred	Both improved stability but further improved by high osmotic pressure
am14R5	Second site ?	?	
am15	Various double f/s sequences	Deletion of C in AAC Asn56 codon	No enzyme - frameshift
am17	Suppressible to Tyr313	Gln313 CAG → TAG (inferred)	No enzyme
am17RN35	Gln313 → Tyr	TAG → TAPy inferred	Both high Km glutamate
am17RU4	Gln313 → Leu	TAG → TTG inferred	