Genotypes of patients with prothrombin deficiency

Mutation (Name)	Location	Domain	Type	Genotype	Origin	Activity U/dL	Antigen U/dL	Studies of dysfunctional protein	Comments	reference
Arg-39Gln	Exon 1	Prepro	Missense	Hom	Italy	10	12			1
Arg-4Qln (Edmonton) Del half of intron 10 and most of exon 11	Exon 2 Intron 10 /Exon 11	Prepro Catalytic	Missense Deletion	Comp het	Caucasian	8				2
Arg-2Trp*	Exon 2	Prepro	Missense	Hom	Iran	8	8			3
Arg-2Trp*	Exon 2	Prepro	Missense	Hom	Iran	9	6			3
Arg-1Gln*	Exon 2	Prepro	Missense	Homo	Iran	9	14			3
Glu7Lys (Nijmegen)	Exon 2	Prepro	Missense	Homo	Netherlands					4
Glu16Gln (Puerto Rico II) Arg457Gln* (Puerto Rico I)	Exon 2 Exon 12	Gla Catalytic	Missense Missense	Comp het	Puerto Rico	9	35			3,5
Glu29Gly (Shanghai)	Exon 2	Gla	Missense	Hom	China	7	32			6
IVS2-25 C>G Trp569stop	Intron 2 Exon 14	- Catalytic	Splicing Nonsense	Comp het	Netherlands	3	2			7
Tyr44Cys*	Exon 3	Kringle 1	Missense	Hom	Netherlands	2	5			8,9
Tyr44Cys* (Carora)	Exon 3	Kringle 1	Missense	Hom	Venezuela	4	<5			10
IVS5+1 G>A Arg457Gln*	Intron 5 Exon 12	- Catalytic	Splicing Missense	Comp het	Puerto Rico	8	18			5
Asp118Tyr Arg220Cys	Exon 6 Exon 7	Kringle 1 Kringle 2	Missense Missense	Comp het	Italy	26	14			3
nt 468 insT Arg418Trp*	Exon 6 Exon 11	Kringle 1 Catalytic	Frameshift Missense	Comp het	Japan	12	42	Purified		11,12

(Tokushima)										
Cys138Tyr Trp357Cys	Exon 6 Exon 10	Kringle 1 Catalytic	Missense Missense	Comp het	Italy	<1	<1		Prophylaxis	13
nt 877 del G Arg340Trp	Exon 8 Exon 10	Kringle 2 Catalytic	Frameshift Missense	Comp het	African American	8	4			14,15
Arg271Cys* (Barcelona)	Exon 8	Activation cleavage site	Missense	Hom		5	100		Based on amino acid sequencing	16,17
Arg271Cys* (Madrid)	Exon 8	Activation cleavage site	Missense	Hom	Spain	3	103	Purified	Based on amino acid sequencing	18,19,20
Arg271Cys* (Obihiro)	Exon 8	Activation cleavage site	Missense	Hom	Japan	18	105			21
Arg271Cys*	Exon 8	Activation cleavage site	Missense	Hom	India	10				22
Arg271His* (Padua)	Exon 8	Activation cleavage site	Missense	Het		52	100	Plasma studied		23,24
Arg271His* (Dhahran)	Exon 8	Activation cleavage site	Missense	Hom	Saudi Arabia	5	95			25
Arg271His* nt 1718 del GT and His562Arg	Exon 8 Exon 14	Activation cleavage site Catalytic	Missense Frameshift	Comp het	Bangladesh	2	26			26
Phe299Val (Suresnes)	Exon 9	Catalytic	Missense	Hom	Algeria	<5	23			27
Glu300Lys Glu309Lys* (Denver)	Exon 9 Exon 9	Catalytic Catalytic	Missense Missense	Comp het		5	21	Plasma studied		28,29
nt 1032 del GAA*	Exon 9	Catalytic	Del Amino acid 302	Hom	Iran	7	15	Expressed		3,30,31
nt 1032 del GAA*	Exon 9	Catalytic	Del Amino acid 302	Hom	Iran	1	10			3
nt 1032 del GAA*	Exon 9	Catalytic	Del Amino acid 302	Hom	India	5				22
Glu309Lys*	Exon 9	Catalytic	Missense	Hom	India	8				22

Gly319Arg (Segovia)	Exon 9	Catalytic	Missense	Hom		7	130	Purified		32,33,34
Arg320His* (San Antonio)	Exon 9	Activation cleavage site	Missense	Het		44	115	Plasma studied		35
Gly330Ser	Exon 9	Catalytic	Missense	Hom	Italy	5	40	Expressed		3,36
Met337Thr (Himi I) Arg388His* (Himi II)	Exon 10 Exon 10	Catalytic Catalytic	Missense Missense	Comp het	Japan	10	Normal	Purified		37,38
Ser354Arg	Exon 10	Catalytic	Missense	Hom		14	14			3
Ala362Thr (Vellore I) Arg-1Gln*	Exon 10 Exon 2	Catalytic Prepro	Missense	Comp het		18				22
Arg382His	Exon 10	Catalytic	Missense	Hom	Iran	1	61	Expressed		3,39
Arg382Cys* (Quick I) Gly558Val (Quick II)	Exon 10 Exon 14	Catalytic Catalytic	Missense Missense	Comp het		<2		Purified	Based on amino acid sequencing	40,41
Arg382Cys* (Corpus Christi) Gln541stop	Exon 10 Exon 14	Catalytic Catalytic	Missense Nonsense	Comp het	Hispanic	2	25	Purified		25
Arg388His*	Exon 10	Catalytic	Missense	Hom	Turkey	12	64			42
Arg418Trp Unknown (Molise)	Exon 11	Catalytic	Missense	Comp het		10	50	Purified		43,44,45
Arg457Gln* nt19771 del 5 bp	Exon 12 Exon 13	Catalytic Catalytic	Missense Frameshift	Comp het	Puerto Rico	6	15			5
Arg457Gln*	Exon 12	Catalytic	Missense	Hom	Puerto Rico	15	28			5,46
Arg457Gln*	Exon 12	Catalytic	Missense	Hom	Puerto Rico	19	40			5
Glu466Ala* (Salakta)	Exon 12	Catalytic	Missense		Tunis	15-18	100	Purified		47,48,49
Glu466Ala* (Frankfurt)	Exon 12	Catalytic	Missense	Hom	Tunis	13,20	91			50
Gln476stop	Exon 12	Catalytic	Nonsense	Comp het		<1	31			51

Ala520Val	Exon 13	Catalytic	Missense							
Arg517Gln (Greenville)	Exon 13	Catalytic	Missense	Het	Caucasian	51	102	Plasma studied		52
Arg538Cys*	Exon 14	Catalytic	Missense	Hom	Italy- Cicely	7	6			3
Arg538Cys*	Exon 14	Catalytic	Missense	Hom	Italy- Cicely	4	4			3
Gly548Ala* (Perija)	Exon 14	Catalytic	Missense	Hom	Yukba Indian- Venezuela	2	70	Plasma studied	High (35%) prothrombin deficiency frequency in the village	53,54,55
Asp552Glu (Saint Denis)	Exon 14	Catalytic	Missense	Hom		<3	60	Partially purified		56
Lys556Thr (Scranton)	Exon 14	Catalytic	Missense	Het	USA	58	110			57

Nucleotide numbers are based on the Genebank file NM_000506 using the A (nucleotide 32) of the ATG initiator methionine as +1.
*A mutation that was identified in more than 1 family

Mutations causing Prothrombin deficiency according to their types

Missense			Nonsense	Splice	Deletion/Insertion
R-39Q	E309K*	R517Q	Q541STOP	IVS5+1 G TO A	nt 468 ins T
R-4Q	G319R	A520V	W569STOP	IVS2-25 C TO G	nt 877 del G
R-2W*	R320H*	R538C*	G476STOP		nt 1032 del GAA*
R-1Q*	G330S	G548A*			nt 1718 del GT
E7K	M337T	D552E			nt 19771 del 5 BP
E16Q	R340W	K556T			Deletion int 10-ex 11
E29G	S354R	G558V			
Y44C*	W357C	H562R			
D118Y	A362T				
C138Y	R382H				
R220C	R382C*				
R271C*	R388H*				
R271H*	R418W*				
F299V	R457Q*				
E300K	E466A*				

* Mutations that were identified in more than one family

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