## Clinical aspects and pathogenesis of congenital dyserythropoietic anemias: from morphology to molecular approach

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Citation: Iolascon A, Esposito MR, and Russo R. Clinical aspects and pathogenesis of congenital dyserythropoietic anemias: from morphology to molecular approach. Haematologica 2012;97(12): 1786-1794. doi:10.3324/haematol.2012.072207

Exon	Nucleotide change°/*	Legacy name <sup>a/b</sup>	Reference
missense			
	c.156 C>G	F52L	(Ref. 2)
			(Ref. 4)
			(Ref. 1)
			(Ref. 1)
14	c.2062 C>T	R688W	(Ref. 2)
14	c.2069 T>C	V690A	(Ref. 5)
14	c.2092 G>A	E698K	(Ref. 1)
14	c.2140 C>T	R714W	(Ref. 1)
14	c.2173 C>T	R725W	(Ref. 4)
		G750C	(Ref. 4)
19	c.2602 T>A	F868I	(Ref. 1)
19	c.2605 G>A	V869M	(Ref. 1)
20	c.2650 A>G	T884A	(Ref. 2)
24	c.3107 C>A	S1036F	(Ref. 1)
24			(Ref. 1)
24			(Ref. 1)
24	c.3194 G>A		(Ref. 4)
26	c.3389 C>T	-	(Ref. 1)
nonsense			
14	c.2044 C>T	R682X	(Ref. 1)
			(Ref. 2)
		R998X	(Ref. 1)
27			(Ref. 4)
splicing		•	
	c.1367+1 G>A		(Ref. 2)
12			(Ref. 2)
			(Ref. 4)
28			(Ref. 4)
	c.3024 insTT	G1008Gfs23X	(Ref. 4)
24			(Ref. 4)
small deletion			
	c.1117_19delGTT	V373del	(Ref. 3)
			(Ref. 4)
missense			
	c.40 C>T	R14W	(Ref. 7)
2	C 401 ( N 1		(Ref ()
	missense   2   6   12   14   14   14   14   14   14   14   14   14   14   14   14   14   14   14   14   14   15   19   20   24   24   24   24   24   24   25   nonsense   14   18   23   27   splicing   8   12   21   28   frameshift   23   24	missense   2 c.156 C>G   6 c.1078 T>C   12 c.1796 A>G   14 c.2015 C>T   14 c.2062 C>T   14 c.2020 G>A   14 c.2020 G>A   14 c.2017 C>T   14 c.2020 G>A   14 c.2173 C>T   15 c.2248 G>T   19 c.2602 T>A   19 c.2605 G>A   20 c.2650 A>G   24 c.3107 C>A   24 c.3124 C>T   24 c.3128 A>T   24 c.3138 A>T   24 c.3139 C>T <i>nonsense</i> 14   14 c.2032 C>T   23 c.2992 C>T   23 c.2392 C>T   24 c.3167+1 G>A   12 c.1360+5 G>A   21 c.2868+2 insCCG   28 c.3358 del -10 to +31 <i>frameshift</i> 23   23 c.3024 insTT   24 c.3145 insT   23 c.3024 insTT	missense   2   c.156 C>G   F52L     6   c.1078 T>C   F360L     12   c.1796 A>G   N599S     14   c.2015 C>T   P672L     14   c.2062 C>T   R688W     14   c.2099 T>C   V690A     14   c.2092 G>A   E698K     14   c.2092 G>A   E698K     14   c.2140 C>T   R714W     14   c.2173 C>T   R725W     15   c.2248 G>T   G750C     19   c.2602 T>A   F8681     19   c.2602 T>A   F8681     19   c.2605 G>A   V869M     20   c.2650 A>G   T884A     24   c.3107 C>A   S1036F     24   c.3124 C>T   R1042W     24   c.3134 A>T   D1043V     24   c.3194 G>A   R1065Q     26   c.3389 C>T   P1130L <i>Inonsense</i> I   Q447X     23   c.2929 C>T   R998X     27

## Online Supplementary Table 1S. Mutational spectrum of CDAN1/CDAN2

continued on the next page

2	c.74 C>A	P25H	(Ref. 13)
2	c.197 G>A	C66Y	(Ref. 8)
4	c.325 G>A	E109K	(Ref. 7)
6	c.640 C>T	Q214X	(Ref. 12)
7	c.716 A>G	D239G	(Ref. 7)
8	c.938 G>A	R313H	(Ref. 7)
8	c.953T>C	I318T	(Ref. 7)
9	c.1043 A>C	D348A	(Ref. 6)
10	c.1157 A>G	Q386R	(Ref. 7)
11	c.1254 T>G	I418M	(Ref. 10)
11	c.1307 C>T	S436L	(Ref. 10)
12	c.1385 A>G	Y462C	(Ref. 7)
13	c.1453 A>G	T485A	(Ref. 12)
13	c.1489 C>T	R497C	(Ref. 7)
13	c.1508 G>A	R503Q	(Ref. 9)
14	c.1571 C>T	A524V	(Ref. 7)
14	c.1588 C>T	R530W	(Ref. 7)
14	c.1589 G>A	R530Q	(Ref. 9)
14	c.1654 C>T	L552F	(Ref. 10)
15	c.1685 A>G	Y562C	(Ref. 9)
15	c.1733 T>C	L578P	(Ref. 10)
15	c.1735 T>A	Y579N	(Ref. 10)
16	c.1808 C>T	S603L	(Ref. 6)
16	c.1832 G>C	R611P	(Ref. 10)
16	c.1858 A>G	M620V	(Ref. 10)
17	c.1910 T>G	V637G	(Ref. 12)
17	c.1968 T>G	F656L	(Ref. 9)
18	c.2101 C>T	R701C	(Ref. 6)
18	c.2129 C>T	T710M	(Ref. 11)
19	c.2166 A>C	K723Q	(Ref. 9)
19	c.2180 C>T	S727F	(Ref. 12)
20	c.2270 A>C	H757P	(Ref. 10)
nonsense			
2	c.71 G>A	W24X	(Ref. 13)
3	c.235 C>T	R79X	(Ref. 7)
5	c.367 C>T	R123X	(Ref. 10)
5	c.568 C>T	R190X	(Ref. 6)
6	c.649 C>T	R217X	(Ref. 7)
7	c.790 C>T	R264X	(Ref. 7)
8	c.970 C>T	R324X	(Ref. 7)
9	c.1015 C>T	R339X	(Ref. 10)
10	c.1201C>T	R401X	(Ref. 7)
14	c.1603 C>T	R535X	(Ref. 10)
14	c.1648 C>T	R550X	(Ref. 9)
14	c.1660 C <t< td=""><td>R554X</td><td>(Ref. 6)</td></t<>	R554X	(Ref. 6)
splicing			
2	c.221+31 A>G		(Ref. 10)
3	c.279+3 A>G		(Ref. 10)
6	c.689+1 G>A		(Ref. 7)
9	c.1109+1 G>A		(Ref. 10)
9	c.1109+5 G>A		(Ref. 10)
19	c.2149-2 A>G		(Ref. 10)
frameshift			
3	c.222-817_366+4242del	Q75EfsX7	(Ref. 7)
0	0.222 011_000 1 12 12001		(Rel. 1)

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5	c.428_428delAinsCG	D143AfsX35	(Ref. 6)	
9	c.1063delG	D355IfsX8	(Ref. 7)	
16	c.1821delT	H608IfsX7	(Ref. 6)	
17	c.1962-64 (delT)	T654TfsX13	(Ref. 9)	
19	c.2150 (delC)	A717VfsX7	(Ref. 10)	
small deletion				
16	c.1857_1859delCAT	I619del	(Ref. 10)	

° CDAN1: the nucelotides are numbered from the A of the ATG initiation codon (ENST00000356231). All mutations have been revised according to the rules of nomenclature of the HGVS database (http://www.hgvs.org/mutnomen/). \* CDAN2: the nucelotides are numbered from the A of the ATG initiation codon (ENST00000377475) "CODANIN-1: Accession number: Q8IWY9 (UniProtKB/Swiss-Prot)." SEC23B: Accession number: Q15437 (UniProtKB/Swiss-Prot).

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