سهامی خاص
شماره ثبت : ۴۱۰۴۵

Hearing Impairment Gene List
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تاریخ : .....
شماره : .....
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ABHD12				
ACTG1	EDNRB	MARVELD2	OTOA	TIMM8A
ALMS1	ESPN	MIR96	OTOF	TJP2
ATP2B2	ESRRB	MIRN96	OTOG	TMC1
BSND	EYA1	MITF	OTOGL	TMIE
CACNA1D	EYA4	MSRB3	PAX2	TMPRSS3
CCDC50	FGF3	MT_CO1	PAX3	TNFRSF11B
CCOL11A1	FGFR1	MT_CO2	PCDH15	TPRN
CDH23	FGFR2	MT_CYB	PDSS1	TRIOBP
CEACAM16	FGFR3	MT_ND1	PDZD7	USH1C
CHD7	FOXI1	MT_ND4	PHEX	USH1G
CIB2	GATA3	MT_ND6	POU3F4	USH2A
CLDN14	GFER	MT_RNR1	POU4F3	WFS1
CLRN1	GIPC3	MT_TC	PRPS1	
COCH	GJA1	MT_TE	PRRX1	
COL11A1	GJB2	MT_TF	PTPRQ	
COL11A2	GJB3	MT_TH	RDX	
COL2A1	GJB6	MT_TK	SEMA3E	
COL4A3	GLI3	MT_TL1	SERAC1	
COL4A4	GPR98	MT_TS1	SERPINB6	
COL4A5	GPSM2	MT_TS2	SIX1	
COL9A1	GRHL2	MT_TV	SIX5	
COL9A2	GRXCR1	MT_TW	SLC17A8	
CRYM	HGF	MTATP8	SLC19A2	
DFNA5	HOXA1	MTCO1	SLC26A4	
DFNB31	HOXA2	MTND1	SLC26A5	
DFNB59	IGF1	MTRNR1	SLC4A11	
DFNB59/PJVK	ILDR1	MYH14	SMAD4	
DIABLO	KCNE1	MYH9	SMPX	
DIAPH1	KCNJ10	MYO15A	SNAI2	
DIAPH3	KCNQ1	MYO1A	SOBP	
DLX5	KCNQ4	MYO3A	SOX10	
DSPP	LHFPL5	MYO6	SOX9	
E160	LOXHD1	MYO7A	STRC	
E160:E161	LRP2	NDP	TCOF1	
E161	LRTOMT	OPA1	TECTA	
EDN3				

نشانی: شیراز، خیابان انقلاب، خیابان شکیبا، روبه روی پارک انقلاب، ساختمان رز، طبقه اول، واحد۲ / کد پستی: ۷۱۶۳۷۶۶۵۱۵
تلفن: ۳۸۲۶۳۰۶۹-۰۷۱ / (۳۲۴۲) ۲۳۰۵۸۸۶-۰۷۱

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Importnat Notes:

1- Only known exons of these genes will be examined

2- Repeat expansion disorders will not be covered

3- Genomic regions beside exons of protein-coding genes, genes that are not listed here in this list, repeat expansions and mutations in the upstream and downstream regulatory regions will not be investigated.

4- Additional Comments:

- **Although next generation sequencing (NGS) is a method of choice for high throughput sequencing purposes, NGS has not been approved for clinical and diagnostic use; therefore, Sanger sequencing must be done to confirm the sequencing data, particularly on identified mutations.**
- **Genetic counseling is recommended to explain risks and potential**

5- pitfalls of the experiment.

- **It is of utmost importance for all clinicians involved in the care of families requesting molecular genetic diagnostic tests and the families themselves to be aware of the risk of errors in DNA analysis. Incorrect analysis may result from 1) incorrect data and clinical diagnosis 2) incomplete family studies and history 3) mix-up of DNA samples and mislabeling 4) rare molecular events5) new or spontaneous mutations 6) paternity problems, adaptation, IVF, egg donor, bone marrow transplantation, recent blood product transfusion 7) maternal DNA contamination of CVS or amniotic fluid samples 8) technical errors. The risk of errors from various reasons mentioned above and several others is about 0.5%, while the chance of technical errors of all types is estimated to be around 0.5%. The risk of errors due to DNA recombination in diagnosis is approximately 0.3%. We take no responsibility about patient identity and possible mis-labeling of the DAN samples. Any feedback from our colleagues in the clinical field would be most welcomed. Comments can be given in writing or by calling my number listed below or by e-mail to: Mohammad.ali.faghihi@gmail.com**

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