

A

Q7RTT9 S29A4_HUMAN	1	MGSVGSQRLEEPSVAGTDPDGVVMSFTFDSHQLEEAEEAAQGGQLRARGVPAFTDITL	59
Q9BZD2 S29A3_HUMAN	1	MAVVSDEDDQHS-----S-----NSTYRITSSSLRAD-QEALLEKLLDR	38
Q7RTT9 S29A4_HUMAN	60	----EVPVDDRYHAIYFAMLLAGVGFLLPYNSFITDVDYLHKKYPGTISI-----	104
Q9BZD2 S29A3_HUMAN	39	PPGLQRPEDRFCGTYIIFSLGIGSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSD	98
Q7RTT9 S29A4_HUMAN	105	VFDMSLTYILV----ALAAVLLNNVVERLTLHTRITAGYLLALGPLLFLIS-----ICD	154
Q9BZD2 S29A3_HUMAN	99	ILNYFESYLAVASTVPSMCLVANFLLVNRVAVHVRVLAISLTVLILAFMVIATLVKVDTS	158
Q7RTT9 S29A4_HUMAN	155	VWLQFSDQAYAINLAAVGTVAFGCTVQSSFFGYTGMPLPKRYTQGVMTGESTAGVMIS	214
Q9BZD2 S29A3_HUMAN	159	SWTRGF-----FAVITVCMVILSGASTVFSSSIYGMTGSFPMRNSQALISGGAMGGTVSA	213
Q7RTT9 S29A4_HUMAN	215	LSRILTKLLLPDERASTLIFFLVSVALELLCFLHLLVRRSRFVLYFTRPRDSDHRGPRG	274
Q9BZD2 S29A3_HUMAN	214	VASLVDLAASSDVRNSALAFFLTATVFLVLCMGLYLLSRLEYARYMRPVLAAHV----	269
Q7RTT9 S29A4_HUMAN	275	LGRGYGYRVHHDVVDVHFEHPAPALAPNESPKDSPAHEVTGSSGAYMRFDVPRPRVQR	334
Q9BZD2 S29A3_HUMAN	270	-----FSGEE-----LFDQSLSAP--SVASRFIDS-----	293
Q7RTT9 S29A4_HUMAN	335	SWPTFRALLLHRYVVARVIWADMLSIATVYFITLCLFPGLESEIRHCIL-----GEW	386
Q9BZD2 S29A3_HUMAN	294	HTPPLRPILKKTAS-----LGFVCTVYVFFITSLIYPAICTNIESLNKGGSSLWTKFF	346
Q7RTT9 S29A4_HUMAN	387	LPFLIMAVFNLSDFVKGKILAAALPVD--WRGTHLLACSCLRVVFIPFLFVLCVYPSGMP---	441
Q9BZD2 S29A3_HUMAN	347	IPLTFLLYNFADLCGRQLTAWIQVPGPNKALPGFVLRTCLIPFLFVLCVYPSGMP---	406
Q7RTT9 S29A4_HUMAN	442	--ALRHPAWPCIFSLLMGINSNGYFGSVPMILAAGKVPSPKQRELAGNMTVSYMSGLTLGSA	500
Q9BZD2 S29A3_HUMAN	407	VVQSDVYFALLSLLGLSNGYSLTALLYGPKIVPRELAEATGVVSYMSGLTLGSA	466
Q7RTT9 S29A4_HUMAN	501	VAYCTYSLTRDAHGSCLHASTANGSILAGL	530
Q9BZD2 S29A3_HUMAN	467	CTLLVHLI-----	475

B

Q99808 S29A1_HUMAN	1	-----MTTS	4
Q7RTT9 S29A4_HUMAN	1	MGSVGSQRLEEPSVAGTDPDGVVMSFTFDSHQLEEAEEAAQGGQLRARGVPAFTDITLDE	60
Q99808 S29A1_HUMAN	5	HQPQDRYKAVWLIFMFLGLTLLPWNFFMTATQYFTNRLDMSQNVSLVTAELSKDAQASA	64
Q7RTT9 S29A4_HUMAN	61	FVPDDRYHAIYFAMLLAGVGFLLPYNSFITDVDYLHKKYPGTISIVFDMSLTY-----	109
Q99808 S29A1_HUMAN	65	APAAPLPERNSLSAIFNNVMTLCAMLPLLFTYLNLSFLHQRIPQSVRILGSL-VAILLVF	123
Q7RTT9 S29A4_HUMAN	110	-----LT-----YILVALAAVLLNNVVERLTLHTRITAGYLLALGPLL	148
Q99808 S29A1_HUMAN	124	LITAILVKVQL-DALFFVITMIKIVLINSFG-AILQGSFLGAGLLPASTAPIMSGGQ	181
Q7RTT9 S29A4_HUMAN	149	FISICDVLQFLSRDQAYAINLAAVGTVAFGCTVQSSFFGYTGMPLPKRYTQGVMTGES	207
Q99808 S29A1_HUMAN	182	LAGEFFASVAMICAIASGSELSAFAFGYFITACAVIILTIICYL--GLPRLEFYRYQQQL	238
Q7RTT9 S29A4_HUMAN	208	TAGVMISLSRILTKLLLPDERASTLIFFLVSVVA--LELLCFLHLLVRRSRFVLYFTR	264
Q99808 S29A1_HUMAN	239	KLEG---PGEQ-----ETKLDLISKGEEPGRAGK---ES-GVSVS	271
Q7RTT9 S29A4_HUMAN	265	PRDSHRGRPGLGRGYRVHHDVVDVHFEHPAPALAPNESPKDSPAHEVTGSSGAYMR	324
Q99808 S29A1_HUMAN	272	NSQPTNE---SHSIKAILKN-----ISVLAFVCFIFTITIGMFAVIVEVKSSIAG	320
Q7RTT9 S29A4_HUMAN	325	FVDRPRVQRSWPTFRALLLHRYVVARVIWADMLSIATVYFITLCLFPGLESEIRHCILG	384
Q99808 S29A1_HUMAN	321	SSTWERYFIPVSCFLTFNFIWDWLRSLTAV-FMWPGKDSRWLPSVLVRLVFLVLLLCN	379
Q7RTT9 S29A4_HUMAN	385	E-----WLPILIMAVFNLSDFVKGKILAAALPVDWRGTH--LLACSCLRVVFIPFLFVLCV	435
Q99808 S29A1_HUMAN	380	IKPRRYLTVVFEHDAWFIFFMAAFSNGYLAFLCFCMFPKPKVPAEAEATAGAIMAFFLFC	439
Q7RTT9 S29A4_HUMAN	436	YPSG--MPALRHPAWPCIFSLLMGINSNGYFGSVPMILAAGKVPSPKQRELAGNMTVSYM	492
Q99808 S29A1_HUMAN	440	LGLALGAVFSFLFRAIV-----	456
Q7RTT9 S29A4_HUMAN	493	SGLTIGSAVAYCTYSLTRDAHGSCLHASTANGSILAGL	530

C

Q14542 S29A2_HUMAN	1	-----MARG	4
Q7RTT9 S29A4_HUMAN	1	MGSVGSQRLEEPSVAGTDPDGVVMSFTFDSHQLEEAEEAAQGGQLRARGVPAFTDITLDE	60
Q14542 S29A2_HUMAN	5	DAPRDSYHLVGSIFFILGLTLLPWNFFITAIPIYFQARLAGAGNSTARILSNHTGPEDA	64
Q7RTT9 S29A4_HUMAN	61	FVPDDRYHAIYFAMLLAGVGFLLPYNSFITDVDYLHKKYPGTISIVFDMSLTY-----	112
Q14542 S29A2_HUMAN	65	FNFNWVTLLSQLPLLFTLLNSFLYQCVPETVRIL-GSLLAILL-LFALTAALVKVDMS	122
Q7RTT9 S29A4_HUMAN	113	-----ILVA----LAAVLLNNVVERLTLHTRITAGYLLALGPLLFLISICDVLQFLS	161
Q14542 S29A2_HUMAN	123	PGPFFSITMASVCFINSFSAVLQGSFLGQGTMPSTYSTILFSGQGLAGIFAALMLLSM	182
Q7RTT9 S29A4_HUMAN	162	RDQAYAINLAAVGTVAFGCTVQSSFFGYTGMPLPKRYTQGVMTGESTAGVMISLSRILTK	221
Q14542 S29A2_HUMAN	183	ASGVDAETSAALGYFITPCVGIILMSIVCYLSLPHL---KFARYLANKSSQAQAQ-EL---	235
Q7RTT9 S29A4_HUMAN	222	LLLPDERASTLIFFLV--SVALELLCFLHLLVRRSRFVLYFTRPRDSDHRGPRGLGRG	278
Q14542 S29A2_HUMAN	236	---ETKAEALLQSDENGIPSSPQKVALTLDLLEKEPESEPEDEP-----QKPF	279
Q7RTT9 S29A4_HUMAN	279	YGYRVHHDVVDVHFEHPAP-----ALAPNESPKDSPAHEVTGSSGAYMRFDVPRPR	331
Q14542 S29A2_HUMAN	280	-----KPSVFTVQKIWLTAALCLVLFVFTVLSVFPATAMVTSSTSPGKWSQFF	328
Q7RTT9 S29A4_HUMAN	332	VQRSWPTFRALLLHRYVVARVIWADMLSIATVYFITLCLFPGLESEIRH-CILGEWL---	387
Q14542 S29A2_HUMAN	329	NPICCFLLFNIMDWLGRSLTSYFLWPEDEDSRLLPLLVCLRFLFVPLFMLCHVQSRSLPI	388
Q7RTT9 S29A4_HUMAN	388	-PILIMAVFNLSDFVKGKILAAALPVD--DWRGTHLLACSCLRVVFIPFLFVLCVYPSGMPA--	442
Q14542 S29A2_HUMAN	389	LFPQDAYFITFMLLFAVSNGLVSLTMCLAPRQVLPHEREVAGALMTFFLALGLSCGASL	448
Q7RTT9 S29A4_HUMAN	443	--LRHPAWPCIFSLLMGINSNGYFGSVPMILAAGKVPSPKQRELAGNMTVSYMSGLTLGSAV	501
Q14542 S29A2_HUMAN	449	SFLFKALL-----	456
Q7RTT9 S29A4_HUMAN	502	AYCTYSLTRDAHGSCLHASTANGSILAGL	530

Fig S1: Sequence comparison of hEN4 with its paralogs hENT1, 2 and 3. A) hENT4 and hENT3 sequence comparison: Identity - 20.175, Similarity - 165. B) hENT1 and hENT4 sequence comparison: Identity - 19.37, Similarity - 148. C) hENT2 and hENT4 sequence comparison: Identity - 20.035, Similarity - 146. The sequences were obtained and aligned using Uniprot server.