1

International Journal of Advanced Research in Biological Sciences ISSN: 2348-8069 www.ijarbs.com

(A Peer Reviewed, Referred, Indexed and Open Access Journal) DOI: 10.22192/ijarbs Coden: IJARQG (USA) Volume 9, Issue 5 -2022

Research Article

Special Issue on Potential Applications of Bioinformatics in Biological Sciences -PABBS 2022

DOI: http://dx.doi.org/10.22192/ijarbs.2022.09.05.01.001

In silico analysis of AMMECR1 protein-protein and its phylogenetic interaction

Jeyabaskar Suganya^{1*}, Nishandhini.M², Mark Antony. J³, Rajesh Kumar.G⁴, Mahendran Radha⁵ ^{1*}Assistant Professor, ²Assistant Professor, ³Student, ⁴Assistant Professor, ⁵Professor.

 ^{1*}Assistant Professor, ²Assistant Professor, ³Student, ⁴Assistant Professor, ⁵Professor.
 ^{1,2,3,5}Department of Bioinformatics, School of Life Sciences, VISTAS, Pallavaram, Chennai-600117, Tamil Nadu, India.
 ⁴Assistant Professor, Department of Pharmacology, Govt. Kilpauk Medical College, Chennai,

Tamil Nadu, India.

Abstract

Protein-protein interactions are particularly essential among these relationships because of their diversity, specificity, and adaptability. Protein-protein interactions (PPIs) are important for understanding protein function, disease occurrence, and therapeutic development. Phylogenetics and Evolutionary Biology is a branch of biology that studies evolutionary relationships between groups of species as well as computational modelling approaches for studying biological, behavioural, and social systems. The AMMECR1 gene was found to be the main cause of Alport syndrome in humans in a recent study, but the actual function of the gene is still anonymous. As a result, determining the function of either genes or proteins was critical, as it would aid in the development of a novel medication for the protein AMMECR1. The protein-protein interaction and phylogenetic analysis of the AMMECR1 protein were used in this study to anticipate the activities of the protein that causes Alport syndrome. The function of the AMMECR1 protein were used in this study to anticipate the activities of the current *in silico* protein analysis, which will be useful for further investigation.

Keywords: AMMECR1 protein, Alport syndrome, Protein-protein Interaction, Phylogenetic analysis.



Introduction

The AMMECR1 gene is found on chromosome Xq22.3 and encodes the AMMECR1 protein [Zhou HM et al., 2015]. In humans, the symptoms of contiguous gene deletion syndrome include A: Alport disorder, M: Mental retardation, M: Midface impairment, and E: Elliptocytosis, as well as generalised hypoplasia and heart issues [Cai C et al., 2019]. The syndrome is caused mainly byanomissionofXq22.3 Chromosome, which encompasses with several genes. For AMMECR1 example: encodes anunknown function for nuclear-localized protein. On analysing the C-terminal domain(residues 122 to 333) of protein AMMECR1 was found to have a extremely conserved region, with homologues in bacteria, archaea, and eukaryotes [Andreoletti Get al., 2017].

The excessive tenacity of the AMMECR1 domain recommends an essential biological function i.e Central dogma of life. The LRGCIG - 6-amino acid motif has been revealed to be functionally significant during the evolutionary analysis in the AMMECR1 domain. The AMMECR1 domain is broken into two smaller subdomains. Five alphahelices and five beta-strands make up the big subdomain, which encompasses both the N- and C-terminal sections. An antiparallel beta-sheet is formed by these five beta-strands [Moyses-Oliveira Met al., 2018].

The small subdomain which also forms an antiparallel sheet is made up of 4 helices and 3 strands. The conserved motif (LRGCIG) is positioned at in N-terminal loop structure and itsside chains pointed towards the crossing point of 2 subdomains. Only 2 loops connected 2 subdomains and found that there is minute interaction between domains. As a result, these subdomains might migrate vigorously when substrate enters the domains or cleft. The cleft's enormous size indicates a large substrate such as a nucleic acid or protein. Negatively charged nucleic acids on the other hand are unable to travel across the gap because the inner side is devoid of positively charged residues [Basel-Vanagaite Let al., 2017].

Interaction evidence from a variety of sources must be considered when building a functional association network for an organism's proteins; the applicability of these sources varies depending on the proteins in question, their biological roles, and the extent to which they have been studied experimentally [Andreoletti G et al., 2017]. Data integration across different evidence sources has been shown to improve overall network quality and it is also thought to be required given the various modalities by which proteins can be connected. There are three types of sources of interaction evidence: I prior information gleaned from curated route databases or scientific papers, (ii) computational interaction predictions gleaned from a range of algorithms, and (iii) direct lab trials gleaned from a variety of assays in both low- and high-throughput [Damian Szklarczyk et al., 20211.

One of several online sites dedicated to organismwide protein association networks is the STRING database [Huang JK et al., 2018]. The HumanBase/GIANT, FunCoupGeneMANIA, IMP, IID, ConsensusPathDB and HumanNetfields are all frequently used as resources in String database [Ogris Cet al., 2018]. These resources differ in the types of interaction evidence they include, the organisms they cover, and the online interface elements [Warde-Farley Det al., 2010]. attempts to prioritise coverage, STRING completeness of evidence sources and usability [Greene CS et al., 2015]. It allows users to log in and save their searches, as well as provide online viewers to aid in the examination of the supporting material for protein-protein interaction [Wong AK et al., 2015].

STRING is a database of protein-protein interactions that is both known and predicted [Kotlyar M *et al.*, 2019]. The interactions arise from computer prediction, knowledge transfer across species, and interactions gathered from other (primary) databases [Kamburov A *et al.*, 2013], and they include both direct (physical) and

Materials and Methods

Method for protein-protein interaction:

The AMMECR1 protein's interactions with other

proteins were identified using the STRING

indirect (functional) correlations [Hwang Set al., 2019]. Currently, the STRING database contains 24'584'628 proteins from 5'090 species [Doncheva NT et al., 2019]. STRING 10 versions now supports5090 species, which is more than double the previous version [Szklarczyk D et al.,2015]. The most significant new feature is the ability to the upload complete datasets of genome as input in the database which the allow users to analyse subclasses as interaction complexes and perform gene-set enhancement investigation across the database [Franceschini A et al., 2013]. STRING also uses the well-known taxonomy systems like GO and KEGG for enrichment analysis, but it also offers innovative classification systems based on high-throughput text mining [Von Mering C et al., 2005].

MEGA (Molecular **Evolutionary** Genetics Analysis) 5.03 software has evolved throughout time to satisfy the growing demand for advanced evolutionary analysis to uncover organismal and genome evolutionary patterns and processes [Koichiro Tamura et al., 2021]. It was first launched in 1993 as an interactive interface for statistical molecular evolution methods on the Microsoft Disk Operating System [Caspermeyer J 2018.]. MEGA's scope and utility have evolved over the years as additional methodologies, tools, and interfaces have been added, resulting in current integrated software for comparative sequence analysis [Claramunt S et al., 2015]. For molecular phylogenetic analysis, MEGA initially included distance-based and maximum parsimony approaches [Hipsley CA et al., 2014].

MEGA's scope was expanded by adding data gathering and integration of major methodologies for aligning sequences [Kumar S *et al.*, 2018].For molecular evolutionary analyses, maximum likelihood (ML) and Bayesian approaches were included later [Stecher G *et al.*, 2020]. MEGA now includes tools for finding the best-fit substitution model(s), calculating evolutionary distances and divergence periods, reconstructing phylogenies, predicting ancestral sequences, detecting selection, and diagnosing disease mutations [Patel R *et al.*, 2018]. database (http://string-db.org/). The AMMECR1 protein of Alport syndromewas employed as a query, and the results were analysed. The STRING database seeks to bring together all known and projected protein interactions, including both physical and functional interactions. STRING accomplishes this by gathering and scoring evidence from a variety of sources, including I automated text mining of scientific literature, (ii) databases of interaction experiments and complexes/pathways, (iii) annotated computational interaction predictions based on co-expression and conserved genomic context, and (iv) systematic transfers of interaction evidence from one organism to another. STRING aspires for broad coverage: the resource's next version 11.5 will include around 14 000 creatures. We also show how to utilise STRING to query genome-wide, experimental data, including how to find enriched functionality and potential biases in the user's query data automatically. STRING is a useful online resource available at https://stringdb.org/.

Method for Phylogenetic Tree Reconstruction:

The amino acid sequences retrived from the string database were aligned and a phylogenetic tree was constructed using MEGA 5.03. We saved and analysed a phylogenetic tree. The Molecular Evolutionary Genetics Analysis (MEGA) software is a desktop tool for comparing homologous gene sequences from various species or multigene families, with a focus on inferring evolutionary relationships and patterns of DNA and protein evolution. This is the most recent stable release with bug fixes. This application methods includes several for measuring evolutionary distances from nucleotide and amino acid sequence data, three phylogenetic inference methods (UPGMA, neighborjoining, and maximum parsimony), and two statistical tests for

topological differences. Biologists can use this integrated workbench to mine data from the web, align sequences, perform phylogenetic analyses, test evolutionary hypotheses, and create publication-quality displays and descriptions.

Results and Discussion

The interaction of AMMECR1 protein with other proteins in *Homasapaiens* was found using STRING database. The AMMECR1 protein sequence of *Homasapaiens* was used as a query. The results showed the protein interaction network with 11 different proteins that includes (Figure 1):

- HR Lysine-specific demethylase hairless with the score of 0.930
- J THOC2 THO complex subunit 2with the score of 0.823

- EMC2 ER membrane protein complex subunit 2 with the score of 0.819
-) TMEM164 Transmembrane protein 164 with the score of 0.755
- RGAG1 Retrotransposon gag domain containing 1 with the score of 0.747
-) NXT2 Nuclear transport factor 2 like export factor 2 with the score of 0.734
-) COL4A5 Collagen alpha-5(IV) chain with the score of 0.733
- ACSL4 Long-chain-fatty-acid--CoA ligase 4 with the score of 0.689
-) KCNE1L Potassium voltage-gated channel isk-related subfamily e member 1-like with the score of 0.671
- J GUCY2F Guanylate Cyclase 2F with the score of 0.644

S.No	Protein Name	Function
1.	AMMECR1	AMME syndrome applicant gene 1 protein; chromosomal region gene 1 for Alport syndrome, mental retardation, midface hypoplasia, and elliptocytosis
2.	HR	Histone demethylase that precisely demethylates both mono- and dimethylated 'Lys-9' of histone H3. Hair biology (through collagen targeting), brain activity, and cell cycle may all be controlled by this transcription regulator.
3.	THOC2	It is required for the efficient export of polyadenylated RNA and spliced mRNA. The THO subcomplex of the TREX complex is thought to link mRNA transcription, processing, and nuclear export by binding with spliced mRNA rather than unspliced pre-mRNA.
4.	EMC2	It contains a tetratricopeptide repeat domain
5	TMEM164	It is a member of the TMEM164 family.
6.	RGAG1	It contains Retrotransposon gag domain containing 1
7.	NXT2	Protein export regulator for NES-containing proteins and it's also involved in mRNA nuclear export.
8.	COL4A5	Type IV collagen is the most important structural component of glomerular basement membranes (GBM), which forms a 'chicken- wire' meshwork with laminins, proteoglycans, and entactin/nidogen.
9.	ACSL4	Long-chain fatty acids are activated for both cellular lipid production and breakdown via beta-oxidation. Arachidonate and eicosapentaenoate are the preferred substrates.

Table 1: Predicted proteins for AMMECR1 along with its functions using String database

Int. J. Adv. Res. Biol. Sci. (2022). 9(5): Special Issue 1: 1-11

10.	KCNE1L	KCNQ1 is a repolarizing cardiac potassium ion channel that
		functions as an inhibitory beta-subunit.
11.	GUCY2F	It's likely that it has a specialised function in photoreceptor rods
		and/or cones. Guanylate cyclase receptors are enzymes involved in
		the resynthesis of cGMP, which is essential for the return of the
		dark state after phototransduction.

Figure 2: Sequences Alignment for 11 protein sequences using MEGA software

<u></u>			MILE /	ugnme	ent Expl	orer (a	alignme	nt exp	lorer.m	as)				- 🗆 ×
Data Edit Search Alignme	nt Web	Sequence	r Di	splay	Help									
	6 1 1		0 3	< 🖪	× 9	+	🔁 🔳	11	🔍 ନ୍ମ	7	P			
Protein Sequences														
Species/Abbry		CITAL IS	1.1	1010101	SI KINI				1.121		SE LONGES FOR	151 1		
1. TMEM164 ENSP00000361143 Homo sapiens	MSRYSY	CELLDY	VLYCA	VDP	SFAC	IC C P	DCAA	FLS	WOOR	LE	VVVLTLA	LEILVA	LRHILR	O T K E D C R C
2. THOC2 ENSI/00000245838 Homo saplens											RUFQQAL			
3. RGAG1 ENSP00000419786 Homo saprens											HSHVUL			
4 NX12 ENSP00000218004 Homo capere											IPIIPF-		AISIDE	K Y V 10 A C
5 KOVE1LENSP0000361173 Homo capieres	MNCSES	GHIRI	SR	I I I F	I H H H	a N A S	G I G A	G P R	- 5 M G I		PIPFVGH			III MIEY
5 US ENSP00000370625 Home septens	MESTES										SI GEPAPE			
7. GUCY2F ENSP00000218006 Home sapiens											SLPQQVW			
EMC2 ENSP00000220800 Homo sapiens COL4A5 ENSP00000301902 Homo sapiens											ICYASKLG IKGEKGE			
10. AMMECR1 ENSP0000262844 Homo sapen														
11. ACSL4 ENSP00000330787 Homo sapiens		VL II.					IPWY				AKRIKAK			
Jocies/Abbiv				11		11	1111						11 11	
IMEM164 ENSP00000361143 Homo saprens	IVVERLC		OALL	ALL	F P V V	N R L	. L 🛛 - E	LEI	YYIC	нум	LYVYPIYL	LWKCCA	YELL	SSFRWALL
THOC2 ENSI 100000245838 Homo sapiens	QFNQKEN	KKKK	L-Y	QQK	- NLLI	LEN	EGYA	K L 1	ALLC	QUL	565 150	ILEN K	SLIGCE	NLDPNRVL
RGAG11 NSP00000419706 Home sagress I NXT2 ENSP00000218004 Home sagress				GN		I A M		C S T	= NN =	V	ISSSIANS IASDOFS	O DWS S G	D G GT I	IS PI MADV
KCNE1L ENSP00000351173 Homo sapiens														
HR ENSP00000370826 Homo sopiens	CPFLLET		APEN	VVPT	CLPP	YLVS	GLPP	EHP	C DWP	LTP	HPWVYSGG	Q P K V P S	AFSLGS	KGFYYKDP
CUCY2F ENSI*00000218006 Homo saprens	DKCIFEV	ACVNY		IK IE	Y II E	5 1 1	1 8 19 1	RVL	V I V M	KYF	U VAHAUVI	SEDEDI	NVHIAN	RVASALRS
EMC2 ENSP00000220853 Homo sapiens COL4A6 ENSP00000021902 Homo sapiens	ELNEYLE	QFVGE	QEAV	HEL	ALLY	INEH	A	AAF	CLEE	LMM	INPANHLY	CUQYAE	VKYICC	GLENLELS
COL4891 INSPOSIOUUUU1902 Fromo sapiens AMMEGE1 ENSP00000362844 Fromo sapiens	YAYAAPE		NEPN	PIF	VTWK	GRD		C C L	GTES	AMA		TITSA	KBBREP	
ACSL4 ENSP00000339757 Homo sapiens	TALGLAP	K TIA	IFC	TRA	EWMIN	AAQT	CEKY	= P	LVTL	YA-	LGKEAVVH	GLNESE	ASYLIT	SVELLESK
ecies/Abby								· · /						
	LLULLRL	PAKK	0			-		-						
	YVHLLPA	DNCIV	DEH	RE	AEAK	VE	KLTV	IV V L	SSEK	NDE	REKEKEKE	EEKVEK	PFDNQK	LGLLEALL
	PTSTQNS			DID							SVEDAGEN			MSPAIMTA
NX12 LNSP00000218004 Homo sapiens														
KCNE1L ENSP00000361173 Homo sapiene														
	GIVHTIC	NVWAC	PGDC	NIC	YOLGI	AT	PRCF	SPF	PPVT	Q R C	COSSYPPT	KCCCLC	PCGKCQ	FGIFGCAS
											AFTEAAAR			
	VEDMLET													
	and the second se	Conception of the set		GKO	GENG		FGLF	GDP	GYPG	EPG	RDGEKGCK	GDTGPP	GFPGLV	IPRPGTGI
AMMECR1 ENSP00000262844 Homo sapien:														
											ELIAEISC		IGYSSP	LILSDCSS
IMEM164 ENSP00000361143 Horod suprens						-								
	G II W Q H A C	N MIC	MPHY	YAA	SHK		I C K I	HI	1 E =	YH	RVGVPRGA	KGSPVN	ALQNKR	APKQAPSH
											VMSAPPVR			
NXT2 ENSP00000218004 Home supiens	100 C									1.1.1	18 State 199			Contraction of the second
KONE11 ENSE00000351173 Harmo supiens		-	1.1	_	-	1	-	-	-			-	1000	
											OPEVEE RP			
	INCINCA	A V N V N	K T K C	OVE	A A S I I		FNM C	F II G	L N O I	MR T	DSNGNG	LAALI U	TVIKLM	FII STYTV
EMC2 ENGP00000220053 Homo sapians COL4A5 ENGP00000331902 Homo sapians			CEK	EPC				-		CPC		PCOKCO		
AMMECR1 ENSPECTION C1902 from aspiens	GEKGNIG		HINK C	A A A	- 12 I I		A1 P 8		AVM		GPPGFPGF	N IS CAN IS II		
	KKGSKGE	CVIK	PTLN	AAV	PEM		KNVN	SKV	C E M N	YID	KTLFKIGY		KKGYD	APLONLI
Species/Abbry														
1. IMEM164 ENSP00000361143 Homo supiens		and the first												The first of the first of the
2 THOC2 ENSP0000245838 Homo sapiens		NMECYI	CPH	SHD	PILE	AKVV	3 IGK	S F M	KFFQ	DO	KOFDKFK	EVII S C	IISITD	QVIIDSIS
3. RGAG1 ENSP00000419705 Homo saplens	LOKTVP	ASGAM	TSL	VTVP	SSSV	NSTE	O M S A	TAS	RVMS	ACL	MAKTOGA	IPTGSM 8	AVAKQY	KRATASER
4. NX12 ENSP00000218004 Homo sapiens												Statistics and		ALC: NO.
5 KONFIL ENSP0000361173 Homo sopiens	La constante													
5. HR ENSP00000370825 Homo sapiens	APKRPP										C P Q D C Q A		CDIPCL	ALPAKLAC
7. GUCY2I_LNSP00000218006 Tomo sapiens	LMLLLR	133 -	III P	GRP	PRAD	AKCM	VI ALG	KIC	1331) - A I	AMMVCLI	LIALL	INGLAY	I I RREINS
8 EMC2 ENSP00000220853 Home sapere				100				_			A CONTRACTOR			
the second s														
9. COL4A5 ENSP00000331992 Homo sapiens 10. AMMECR1 ENSP00000262844 Homo sapien		LPGPP		PHIP	PSDE	CEL	CPPC	P.P.C	SPGD	< C L C	CEQCVKCI	OKODTCF	NCICTC	ISCPPCC

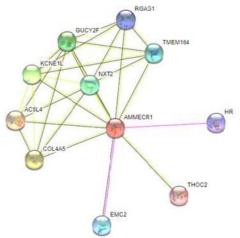
Int. J. Adv. Res. Biol. Sci. (2022). 9(5): Special Issue 1: 1-11

Species/Abbry	- 2 × 2 × 2 × 2 × 2 × 2 × 2 × 2 × 2 × 2
TMEM164 ENSP00000361143 Homo sapiens 2. THOC2 ENSP00000245838 Homo sapiens	MUCNACKSEELWGMFKIFPYGFRYRLYGOWKNEIYNSHPLLVKVKAC IURAKYIMKRL KENVKPSGK
3. RGAC1 ENSP00000419785 Homo sepiens 4. NXT2 ENSP00000218004 Homo capiens	STPLERAPTSCANSTOPY ATASET NSMPOLTYPASCENSMLOWRAFVSEANSMPOMRTMASCLTSAAD
5. KCNL1L LNSF00000361173 Homo sapiens 5. HR ENSF00000370826 Homo sapiens	OSCAQAAGEGGCHACHSCOVERSPLOGELOGEEDTATISSSEECPGSOPDSRISTGLAKHTISG GDRI
7. GUCY2F ENSP00000218006 Homo saprens	UL KSPNR LU LEUVIE NPH FUSKRUSRASVSFUI SEVUSGRSFRLSFSSGSL PA VENSNIATY
EMC2 ENSP00000220353 Homo sepiens	L P G L P G P P G S L G F P G Q K G E K G Q A S A T G F K G L P G I P G A P G A P G A P G S K G E P G D I L T F P G M K G D K G E L G S P
10. AMMLCR1 LNSP000002020041 I cmo sapren 11. ACSI 4 ENSP00000339757 Homo saprens	
1.0000000	+ 1 1 + 1 + 1 + 1 + 1 + 1 + 1 + 1 + 1 +
THEM164 ENER/00000361143 Homo sapiens	GKIGHANPELLEDVILGO OKYDNILTEVYDS KYLTSINYDVLAYCI FALANPEKERMKHDDITI 65
3. RGAC1 ENSP00000419786 Homo sapiens 5. NDT2 ENSP00000218004 Liomo sapiens 5. KCNE1L ENSP00000361173 Homo sapiens	AM SOAKS PLWIAD SUSIS LIMRUIASOVKSCPOMRSLASCALSKPLMIPKASCIME EKMII AS
5 HR ENSP00000370826 Homo supiers	I I REFERAL AWAOREGOGRAVEEDSPOLERCOSRCHHG, FNTHWROPECSHRICVACORVAGTORAEEK
8. EMC2 ENSP00000220853 Homo captons 9. COL4A5 ENSP00000031902 Homo sapiens	DWYWLKKFELGDFGDLKGIKGRASDYFEMMKDLRIEN HPLLGFFYDSGMFAIVTEFCGRGGLEDILTN PGIPGIPGTPGCDGLPGLPGPKGEPGGIETKGERGPPGHPGLPGLPGLPGLASMGPPGFGPKGEKGIG
 AMMECRI ENSI 20000262844 Homo sapien ACSI 4 ENSP00000039787 Homo sapiens 	DRKKDIVKIQAG VVSISKVTAAIKNCELIDNICATAKSDOSYVISTVVPNOKRITIIADOKSVTSTWV
Species/Abbry 1. TML M1641, NSP000000611401, Iomo sapiens	a a a a a a a a a a a a a a a a a a a
2. THOC2 ENSP00000246838 Homo sapiens 3. IROAC1 ENSP00000419785 Homo sapiens	OLS LASECSAVER KYFT DLAGLLOYVANGLKAGKSEDLLILK VOKNAGIEITEENT NEGLEANTGGEG MP INRD VSGATSMPONTU ASCCISASIMED ASCAMSING VIA VSCCMSMPINKAODPCVMPAN
4. NX12 LNSP00000218004 Homo sapiens 5. KCNE11 ENSP00000351173 Homo sapiene	
3. TR LNS-60000370826 fismo sapiens 7. CUCY2E ENSP00000218006 Homo sapiens	A KIDAWA EKE SITI DI KOWKATHHSE EAHOUTKE SWOAAD GEATKAE DAGENDITEN UISEEKEKE Istoryyf FC Laf Vel vycai wrtai Assaytr fra ywnig Amarki Dikallokog yn yr amybe y soger
I. MC21 N3P00000220961 Homo septens OCL4A5 ENSP00000331902 Homo septens	ASNPSCPS PSP X CD P COT I TO PSK PSL PCN PGR DGD VGL PGD PGL PGD PG L PG I PGSK CE PS PG I GL
 AMMECRI ENS/20000262844 Homo sapien ACSL4 ENSP00000039787 Homo sapiens 	CNNPAMEAEILKEIREAANAMKLERIEIRKYRLEPERWTPETGLYTDAFKLKRKELRNIYLKDIERMY
Species/Abbry	
1. TMEM164 ENSP00000361143 Homo sapiens 2. THOC2 ENSP00000245838 Homo sopiens	AF GGY FGO RNTKKS SORTKDALL DHDLAL PLOLIMACORS GV FOR FGG FKHLKLYGKLYDOCHDTLYD
8. RCAC1 ENSP00000419785 Homo sepiens	RAKVSCKMLSQPKSTQDPCCMSKSPKKSKTACCMQKNSPTSDVMSTPTVRAWTSETMSTPLMRTSDPCE
1. NX12 LNSP00000218004 Homo sapiens 5. KCNE11 ENSP00000361173 Homo sapiens	
6. HR ENSP00000370826 Homo sapiens 7. GUCY2F ENSP00000210006 Homo sapiens	TO KIPPITPOPSCHODIHR KS. KEETPOSAETPAEDRAGROPLPOPSLCELLASTAVKLOLOFERIHMA LWTAPELLRAPRGSRLGSFASOVYSTALIMGEVNVRSTPFCKMDLPAGEILNRLKKEPPVYRPVVPPCI
EMC2 ENSP00000220853 Homo supress	
0. COL4A5 ENSP00000331002 Homo sepiens 10. AMMECR1 ENSP00000262044 Homo sepien	PROPECTED IN DEPOTE AN OFFICE CONCEPCENCE AL POPPORE OF FCALOR KOD 30 F
1 ACSI 4 ENSP0000339787 Huma sapens	ĸ
Species/Abbiv 1. TMFM164 ENSP00000361143 Homo capions	
2. THOC2 ENSP00000245838 Homo sapiens	OF LASH LSTEDY IKRVPSIDVLCNEFH PHDAAFFLSRPMYAHHISSKYDELKKSEKOSKQQHKVHKYI
0. RGAG1 ENSP00000119705 Homo sapiens 1. NX12 ENSP00000218004 Homo sapiens	SILTRASSOCINGUP LMRAPAGGE I ATPLISPAYOAMGAPOMTATASGMMGSMPOVKAPI GSAKSMPLT
5 KONE1L ENSP00000361173 Homo appiers 5 HR ENSP00000370826 Homo sapiens	PVTPAUPSDDRITH LDSIIAQVVERKIQEKALOPOLRACPOLRKOLOLPUSPVRPRLPPPCALLWUGE
	PECLELNKOCWAEAAEQRPTFDEI FNGFKTFNKGKKTNI DSMLRMLEQYSSNLEDLIRERTEELEIEK
EMC2 ENSP00000220853 Homo suprens COL4A5 ENSP00000331902 Homo suprens	
0. AMMECR1 ENSP00000262844 Homo sapien	
11. ACSL4 ENGP00000009767 Homo sapiens Species/Abby	
. TMEM164 ENSP00000361143 Iomo sapiens	
	KKKEKERCI ALQOKLLEEEKKOMEHVORVLORLKLEKONWLLAKSIKNEIIIKFLOLCIFPRCIFSAID Steimaasassaschistaottanvsgemskeimaapasgempimsamasgemsmeinetmasgatstio
L NXT2 ENSP00000218004 Homo sapiens	
5. KCNL1L LNSP00000361173 Homo sapiens 5. HR ENSP00000370826 Homo sapiens	PELRPKSDEGSVITTHRATGDEDTSRVENTAASIETPEVCATHCKINTASYTPEGTATREFEPCTWAAY
	D Y Y K Y E T I C D A Y M Y A S C L T K R A C S R H A A E I A M M S L D I L S S Y C T F K M R H M P E Y P Y R I R I C L H S C T Y Y A C Y
EMC2 ENGP00000220053 Homo sapiens COLAAS ENGP0000033 1902 Homo septens	DIG DGGPG PGPTAEKASKAEPGIPGPPGPMDPN IGSKGEKSEPGIPGIPGVSGFKGYDGIPGDPG
0. AMMECR1 ENSP00000262844 Homo sapien	
11. ACSL4 ENSP00000039787 Homo saplens Species/Abby	
1. TMEM164 ENSP00000361143 Homo sepiens 2. THOC2 ENSP00000245838 Homo sepiens	YCARFVELVHOCKTONEST ICYDRVESDIIYTVASCEENFASRYORFICCMIETV RWHRDRATYEKE
IRCAC1 ENSPIREMENT ISOAC1 ENSPIREMENT NSI2 ENSPIREMENT NSI2 ENSPIREMENT	VANSREVSIND TVEVSORMA AP RASANDARS SEMEASVSCRMPMPITRA ANDODOMOMSMPONTA
 KGN: 11-1 NSE0000091171 Thmo sapiens RELNSE0000079820 Tomo sapiens 	S PHRSHLS TKNLSVEVADLVSTLVMADT PLPAMIRAQKDILDGLGLWSPGSQVSTVMHVIRAQAD
7. GUCY2F ENGP00000210006 Homo sepiens 3. EMC2 ENSP00000220853 Homo sepiens	SHIRSHLS KHLCVLYADLYS LYHADIYLYAMIKARKDILGGLGLGLGLGLGLGLAGYGYYHYNNYTKARACA LTMPRYCLFGD YNTAGRMCGTGLPYRIIYSLGTYTILGNLGCGYCYLLRGRTLKGKGTCTFWLYG
0. COL4A5 ENSP00000331902 Homo sapiens 10. AMMECR1 ENSP00000262844 Homo sapien	LSCOPOLICIPOPICACONPOLICIPOLICIPOLICICO COMO FICIPOCICIPOLICO CONCERCIPOLICO CONCERCIPOLICO CONCERCIPOLICO CONC
1 ACSI 4 ENSP0000339787 Homo sapens	
Species/Abbry 1. TMLM101 LNSP00000301143 Homo sapiens	• X X • X
7 THOC2 ENSP00000245838 Home septens 3. RCAC1 ENSP00000419786 Home septens	Y PRET TETRA TOF DOG NKA TOF BY EN - REVY EKWEYKTEKA SVECTETOFY EHRNTT FVT TKTTPWYF Revertekrascectystotafovmstofikatosceastsein tascskotshwtattpetakroo
. NXT2 ENGP00000210004 Homo sapiens	IN NAME OF A DESCRIPTION OF A DESCRIPTIO
KCNL1LLNSP00000611/0 Homo sapiens HD ENSD0000970826 Homo continue	
5 HR ENSP00000370826 Harma capiens 7. CUCY2F ENSP00000218006 Homo sapiens	RELOMVCPARAGALFERAFGARYINAGIRARI REFWGVSCWTILGAPGEAVIVPAGARHGVQGIVSTVS NKELPVERVOKOCQVCHCLQPVELAAFGRRKAERGLVRHKE
0. EMC2 ENGP00000220953 Homo sapiens	
9. COL4A5 ENSP00000331902 Homo sapiens	DPG SS GL FGL FGF FGL FGL FGL FG FFG FFG FFG F
10 AMMECR1 ENSP00000262844 Homo capien	

Int. J. Adv. Res. Biol. Sci. (2022). 9(5): Special Issue 1: 1-11

Species/Abby	A + a + 0 + a + 1 + a + 0 + a + 0 + a + 1 + a + 0 + a + a + a + a + a + a + a + a
1. IMEM164 ENSP00000361143 Homo saprens 2. THOC2 ENGP00000245638 Homo saprens	IN SCALERRVIKICOFFKFKFFFF YALANGYSGOLKGRKSYN PENFFUHKOPPERNAVASVONGPSGGP
3. RCAC1 ENSP00000419785 Homo sapiens 1. NXT2 ENSP00000218004 Homo sapiens	V SFCKI PALCYLLEECEAAROECSVEEEMETDEEKOMKC-LDDSERMA-LVSLFLCAAERW-ILQMEVC
5. KCNE1L ENSPROYOU351173 Homo sapiens 5. IIR ENSPROYOU3526 Homo sapiens	
7. CUCY2F ENSP00000218006 Homo sapiens	
	PRONTOLICE POPVCCCCHPCQPCPPCEKSKPSQDC PCPACQKCETCQTCFCHPCPPCLPCLSCQKCDCC
10. AMMECR1 ENSP00000262844 Homo sapien 11. ACSL4 ENSP00000039787 Homo sapiens	
 A second sec second second sec	
1. TMEM164 ENSP00000361143 Homo sapiens 2. THOC2 ENSP00000245838 Homo sapiens	SSSSIGSASKSDESSIEE DKSRENSOCGVKAVNKASSIIFKGKSSNGNSGSNSNKAVKENDKEKGKEKE
3. RGAG1 ENSP00000419786 Homo sopiens 4. NXT2 ENSP00000218004 Homo sopiens	FPISHENKSFIRRSQGIYDSISFIDIISAVICHPKQGQKSVRQYATOFIIIARH SWSDAIIR RFIFGIS
5. KCNL1L LNSP00000361173 Tomo sapiens 5. HR ENSP00000370826 Homo sapiens	
7. CUCY2F ENSP00000218006 Homo sapiens	-
EMC2 ENGP00000220053 Homo sapiens COL4A5 ENSP0000033 1902 Homo suprens	TPGTPGNPGTPGPKG <mark>P</mark> PGFHGFPGV0GPPGPPGSPGPA
0. AMMECR1 ENSP00000262844 Homo sapien 1. ACSL4 ENSP00000339707 Homo sapiens	
Species/Abby	-
IMEM164 ENSP0000361143 Homo suprens 2. THOC2 ENSP00000245838 Homo suprens	EKKENT PATTPEARVLOKDOKEKPKEERDNKDEKARETKERTPKEDKEKEKEKEKEKAKDEKFKTTVPNAE
). RGAG1 ENGP00000119705 Homo sapiens	AVTTKNGRI FLKVAGGLKELI DRSLYTECOLAEEKDSPGNSSQVLPTACKRNNEEAMGNELSSQQQTEE I
NXT2 ENSP00000218004 Homo supiens KCNE1L ENSP00000351173 Homo sapiens	
6. HR ENSP00000370826 Homo sapiens 1. CUCY2E ENSP00000218006 Homo sapiens	
0. EMC2 ENGP00000220053 Homo sapiens	
9 COL4A5 ENSP00000331902 Homo sequens 10. AMMECR1 ENSP00000262844 Homo sequen	PENGETKEFKSNPSCPSTPSTPSTPSTSSTSSTCGPPSTCGNPGRPGTNGKKEEPSTPSTFPSMKSPSGVPSSA
11. ACSL4 ENGP00000039787 Homo sapiens	
Species/Abbiv 1. TMEM161 ENSP00000361143 Homo sapiens	
2. THOC2 ENSP00000245838 Homo sapiens	ISKSTGEREREKEPSRERDIAKEMKSKENVKCCEK TPYSOSLKSTVPRSDIDEDEREGKRAKIDTHDSPSH
4. NXT2 ENSP00000218004 Homo sapiens	IQH V <mark>SKRCYYLKEHBOPQEGLHDHLGQS GHHQKAHINK</mark>
5 KONE11 ENSP00000361173 Homo separate 5 HR ENSP00000370826 Homo sepiena	
7. CUCY2F ENSP00000218006 Homo sapiens	
	GRECEPOLI CPROPROLPOPSOUS I II KODACPROLPOPCLKC_POPUCPUCLPOPTOPCOPCRUCL
10 AMMECR1 ENSP00000262844 Homo capitan 11. ACSL/ ENSP00000339787 Homo saplens	
Species/Abby	<u></u>
TMEM164 ENSP00000361143 Homo sapiens THOC2 ENSP00000245838 Homo sapiens	S ST VK DNI I FI K FS SAKI YINHI FPPI SK SK FR FKDKKDI DKSRFR SRFR FK KDFKDFKDRK FRKRDHSMM. RF
3. RCAC1 ENSP00000419785 Homo sapiens 4. NX12 ENSP00000218004 Homo sapiens	
5. KCNE1L ENGP00000361173 Homo sapiens	
5. HR ENSP00000370826 Homo sapiens 7. GUCY2F ENSP00000218006 Homo sapiens	
8. EMC2 ENSP0000220853 Homo sapiens 9. COL4A5 ENSP00000331902 Homo soprens	SHDSAGG4KSDPGIPGDPGI4GIDGPPGPDG DGPPGPPGISSVAHGHIITRHSDITDAPQCPQ4 QVYP
10. AMMECR1 ENSP00000262044 Homo sapien 11. ACSL4 ENSP00000339787 Homo sapiens	E Contraction of the second
Species/Abbry	
	। বিশিৎ কৰ্মমান কৰিন কৰিন আৰম্ভ নিৰ্বাহ কৰ্মমান মাৰ কৰ্মক জনবিধ কৰ্মমান প্ৰথম বিশাহ কৰিন কৰিন কৰিন আৰম্ভ নিৰ্বাহ স
2. THOC2 ENSP00000245838 Homo saplens	I I NE ANELNE ALENGT KÖV <mark>SKHKSES</mark> PCESPYRNEKÖK EKNKSKSSCK EKCSDSFKSE KMÖK I SSCOKKESR
IMEM164 ENSP0000361143 Homo septens THOC2 ENSP0000245638 Homo septens RGAG1 ENSP00000119706 Homo septens NXT2 ENSP00000218004 Homo septens	
2. THOC2 ENSP00000245838 Homo septens 3. RGAG1 ENSP00000419705 Homo septens 4. NXT2 ENSP00000218004 Homo septens 5. KCNE1L ENSP00000351173 Homo septens	
2. THOC2 ENSPRING/24538 Homo sepens 3. RGAGI ENSPRING/19706 Homo sepens 4. MRT ENSPRING/241844 Homo septems 5. KONETL ENSPRING/25173 Homo septems 5. HK ENSPRING/2570826 Homo septems 7. CIC/27E ENSPRING/2016/2616 Homo septems	
2. THCC2 ENSP00002445838 Homo sepens 3. RGAG1 ENSP0000197351 Homo sepens 4. M072 FXSP00002197351 Homo sepiens 5. KCNE1L ENSP00000251737 Homo sepiens 5. HCNE1X50000270224 homo sepiens 7. CILCY2F ENSP00002200531 Homo sepiens 5. LCC2 ENSP00002200531 Homo sepiens	V P P D L TKRRKEENGT WOVEKHKSEEPCESPYPHEKDKEKNKEKSECKEKSEDSFKSEKMD K I SEGCKKEER
2. THCC2 ENSP000024838 Homo sepens D. RGAG1 ENSP0000019705 Homo sepens b. MC2 ENSP0000071004 Homo sepens 5. KCNE1L ENSP0000037103 Homo sepens 5. HC HSH00000370826 Homo sepens 0. EMC2 ENSP0000027080 Homo sepens 1. EMC2 ENSP000002003 Homo sepens 1. EMC2 ENSP000002013 Homo sepens 1. EMC2 ENSP000002013 Homo sepens 1. EMC2 ENSP000002013 Homo sepens 1. CMC4 ENSP000002013 Homo sepens 1. CMMECR1 ENSP00002144 Homo sepens	VPPDLEKRRKEENGTVOVEKHKSESPCESPYPNEKDKEKNKEKSSOKEKSSDSFKSEKMD (ISSOCKKESR GFSLIVVOGNKHAHSDDIGTAGSCIRRFSTMF-MFCNINNVCNFASRSDYSYWISTFEPMPMSMDPIKMOS
2. THCC2 ENSP000024838 Homo sepens D. RGAG1 ENSP0000019706 Homo sepens M072 ENSP0000091804 Homo sepens S. KCHC1, ENSP000039103 Homo septens S. KCHC1, ENSP000039103 Homo septens O. CIC/27 ENSP0000021030 Homo septens J. CIC/22 ENSP000002033 Homo septens J. CIC/22 ENSP000002033 Homo septens J. CIC/22 ENSP0000039107 Homo septens	VPPDLTKRRKEENGTWOVEKHKSESPCESPYPHEKDKEKNKSKSSCKEKSSDSFKSEKMD (ISSCOKKESR GFRTYVDGHKRAHBODIGTAGNCIRRFSTMPFMFCNIMVCNFASRNDYSYNISTFEPMPMSMOPIKHOS
2. THCC2 ENSP0000245838 Homo sepens 3. RGACI ENSP000019730 Homo sepens 4. M072 ENSP0000219730 Homo sepiens 5. KCNE1L ENSP0000021973 Homo sepiens 5. KCNE1L ENSP0000218306 Homo sepiens 7. CICY2E ENSP0000220033 Homo sepiens 1. CICX2 ENSP0000220033 Homo sepiens 1. CICX2 ENSP000002844 Homo sepiens 10. AMMECR1 ENSP0000028444 Homo sepiens 11. ACSL4 ENSP00000282644 Homo sepiens SpectradeValue	VPPDL KRRKEENGTVOVEKHKSESPCESPYPNEKDKEKNKEKSSOKEKSSDSFKSEKMD KRKEENGTVOVEKHKSESPCESPYPNEKDKEKSSOKEKSSDSFKSEKMD KRFS KFS
2. THOC2 ENSP0000245838 Homo sepens D. RGAG1 ENSP0000245838 Homo sepens D. RGAG1 ENSP0000278004 Homo sepiens S. KOLETS-ENSP0000270826 Homo sepiens S. KOLETS-ENSP0000270826 Homo sepiens D. CMC2 ENSP0000027081 Homo sepiens D. CMC2 ENSP0000025031 Homo sepiens D. CMC2 ENSP00000233424 Homo sepiens D. CMC2 ENSP00000239767 Homo sepiens Systems/Matw D. THOC2 ENSP00000245838 Homo sepiens	VPPDLTKRRKEENGTWOVEKHKSESPCESPYPHEKDKEKNKSKSSCKEKSSDSFKSEKMD (ISSCOKKESR GFRTYVDGHKRAHBODIGTAGNCIRRFSTMPFMFCNIMVCNFASRNDYSYNISTFEPMPMSMOPIKHOS
2. THOC2 ENSP000024838 Homo sepens 2. RGAG1 ENSP000024838 Homo sepens 3. RGAG1 ENSP000021804 Homo sepens 5. RCHETL ENSP000021804 Homo sepens 5. RCHETL ENSP000021806 Homo sepens 6. RCHETL ENSP000021806 Homo sepens 0. RCHETLENSP000021804 Homo sepens 10. RCHETLENSP0000239707 Homo sepens 5. PROMOCIDENSP0000239707 Homo sepens 5. PROMOCIDENSP0000235707 Homo sepens 1. RGS11 ENSP0000235707 Homo sepens 1. RGS11 ENSP0000235707 Homo sepens 1. RGS11 ENSP0000235707 Homo sepens 1. RGS11 ENSP0000235707 Homo sepens	VPPDL KRRKEENGTVOVEKHKSESPCESPYPNEKDKEKNKEKSSOKEKSSDSFKSEKMD KRKEENGTVOVEKHKSESPCESPYPNEKDKEKSSOKEKSSDSFKSEKMD KRFS KFS
2. THCC2 ENSP0000244838 Homo sepens 3. RGACI ENSP00002419736 Homo sepens 4. M077 ENSP00002419736 Homo sepiens 5. KCNE1L ENSP000025173 Homo sepiens 5. KCNE1L ENSP00002503 Homo sepiens 6. RCA2 ENSP000025030 Homo sepiens 4. XXI Adv ENSP0000251807 Homo sepiens 4. XXI Adv ENSP0000251807 Homo sepiens 1. AMSECT ENSP00002538 Homo sepiens 1. ACSLI ENSP00002351131 Homo sepiens 4. XXI Adv ENSP00002351807 Homo sepiens 5. THCC2 ENSP00002351807 Homo sepiens 4. XXI Adv ENSP0000235181 Homo sepiens 4. XXI Adv ENSP0000235181 Homo sepiens 4. XXI ENSP00002419748 Homo sepiens 4. XXI ENSP00002419748 Homo sepiens 4. XXI ENSP00002419748 Homo sepiens 4. XXI ENSP00002419745 Homo sepiens 5. HCNE1L ENSP00002419745 HOMO Homo sepiens 5. HCNE1L ENSP00002419745 HOMO Homo sepiens 5. HCNE1L ENSP00002419745 HOMO Homo sepiens 5. HCNE1L ENSP0000419745 HOMO Homo sepiens 5. HCNE1L ENSP00004	VPPDL KRRKEENGTVOVEKHKSESPCESPYPNEKDKEKNKEKSSOKEKSSDSFKSEKMD KRKEENGTVOVEKHKSESPCESPYPNEKDKEKSSOKEKSSDSFKSEKMD KRFS KFS
2. THCC2 ENSP0000245838 Homo sepens RGAG1 ENSP0000245838 Homo sepens MT2 FNSP0000218004 Homo sepiens 5. KCNE1L ENSP000021804 Homo sepiens 5. KCNE1L ENSP000021024 homo sepiens 6. KCNE1L ENSP000021030 Homo sepiens 1. CMC2 ENSP0000021030 Homo sepiens 1. CMC4 ENSP0000021044 Homo sepiens 1. CMAN ENSP0000021400 Homo sepiens 5. HC2 ENSP0000021838 Homo sepiens 5. HC2 ENSP0000021838 Homo sepiens 1. MC4 ENSP0000021978 Homo sepiens 1. KC2 ENSP0000021978 Homo sepiens 1. KC2 ENSP0000021978 Homo sepiens 1. KC2 ENSP000021978 Homo sepiens 1. KC2 ENSP000021978 Homo sepiens 5. HC4 ENSP000021978 Homo sepiens 5. HC4 ENSP0000319787 Homo sepiens 5. HC4 ENSP0000319787 Homo sepiens 5. HC4 ENSP0000319787 Homo sepiens 5. HC4 ENSP0000319787 Homo sepiens 5. HC4 ENSP000021978 Homo sepiens 5. HC4 ENSP000022633 Homo sepiens	WPPDL KRRKEENGTWOVEKHKSESPCESPYPNEKDKEKDSGKEKGEDSFKSEKMDKISSEKMDKISSGKEKGEDSFKSEKMDKISSGKEKESR GFB I Y VOGNKHAHBDDIKTAGNCINKFSINF-NFCHINNYCNFANKSDYSYNISIFEYNYKANAMOPIKSGS H KEKIEKRDSSOSKEEKKHHKSSDKHR
2. THOC2 ENSP000024938 Homo sepens 3. RGA01 ENSP000014938 Homo sepens 4. RGA01 ENSP0000218004 Homo sequens 5. RCH2T ENSP0000218004 Homo sequens 6. RCH2T ENSP0000218064 Homo sequens 7. RCH2T ENSP00002033 Homo sequens 10. RMMECR1 ENSP0000262884 Homo sequens 10. AMMECR1 ENSP0000262844 Homo sequens 10. AMMECR1 ENSP00000262844 Homo sequens 10. AMMECR1 ENSP00000262844 Homo sequens 10. AMMECR1 ENSP00000262844 Homo sequens 10. RCH2T ENSP00000262844 Homo sequens 10. RCH2T ENSP00000262844 Homo sequens 10. RCH2T ENSP00000262838 Homo sequens 10. RCH2T ENSP000003611/3 Homo sequens 10. RCH2T ENSP00000218004 Homo sequens 10. RCH2T ENSP00000218004 Homo sequens 10. RCH2T ENSP00000218004 Homo sequens 10. RCH2T ENSP0000021803 Homo sequens 10. RCH2T ENSP00000218004 Homo sequens 10. RCH2T ENSP0000021804 Homo sequents 10. RCH2T ENSP00000001804 Homo sequents 10. RCH2T ENSP0000001804 Homo sequ	VPPDL KRRKEENGT VOVEKHKSESPCESPYPHEKDKEKNKEKSSCKEKSSDSFKSEKMD (15500 KKESR GFS. 1 YVQGHKHAHGDDIG AGN GIRRFSIMF - MFCNINNYCNFASR DYSYWISIF PMPM2MSMOPIKGOS GFS. 1 YVQGHKHAHGDDIG AGN GIRRFSIMF - MFCNINNYCNFASR DYSYWISIF PM2MSMOPIKGOS H X K K K E K R D S C O X E K K H H K S D K H R 1 D P F S R C A Y C A F A Y Y A Y A Y A Y A Y A Y A Y A Y A
2. THOC2 ENSP0000245838 Homo sepens D. RGAG1 ENSP00002419705 Homo sepens MRT ENSP00002718204 Homo sepens 5. KCNE1L ENSP0000035173 Homo sepens 5. KCNE1L ENSP0000025083 Homo sepens 1. CILCYZE ENSP0000025080 Homo sepens 1. CILCYZE ENSP0000025080 Homo sepens 1. CILCYZE ENSP00000250824 Homo sepens 1. CILCYZE ENSP00000251807 Homo sepens 1. CILCYZE ENSP00000251807 Homo sepens 1. CILCYZE ENSP00000251807 Homo sepens 5. HCME1L ENSP00000251807 Homo sepens 5. HCME1L ENSP00000251808 Homo sepens 5. HCME1L ENSP00000251838 Homo sepens 5. HCME1L ENSP00000245838 Homo sepens 4. HCME1L ENSP0000245838 Homo sepens 4. HCME1L ENSP00000245838 Homo sepens 4. HCME1L ENSP00000245838 Homo sepens 4. HCME1L	VPPDL KRRKEENGTWOVEKHKSESPCESPYPNEKDKEKNKEKSSOKEKSEDSFKSEKMD (15500KKESR GFRIIVVWGNKHAHEDDIGTAGNAGNCIRRFSTWH-WFCMINNVCMFASRINUYSYWISTFEYMPMSMOPIKGGS H X K K I K K K K K K SOOK EE K K H H K SOOK H R 1 M P F S K C A V C A R A V V A V R SO 10 1 P H C POGWDSIWISI WIEKT SA A A A F G SGO A A SPECIEFFS A A
2. THCC2 ENSP000024838 Homo sepens D. RGAG1 ENSP0000219706 Homo sepens MR75 ENSP0000271804 Homo sepens 5. KCNETL ENSP0000271826 Homo sepens 5. KCNETL ENSP0000271826 Homo sepens 1. TALC2E ENSP00002033 Homo sepens 1. TALC2E ENSP000020338767 Homo sepens 1. TALC2E ENSP0000239767 Homo sepens 5. KCNETL ENSP000024588 Homo sepens 1. TALC2E INSP000024588 Homo sepens 5. KCNETL ENSP000024588 Homo sepens 5. KCNETL ENSP000024588 Homo sepens 5. KCNETL ENSP000024588 Homo sepens 5. KCNETL ENSP000024598 Homo sepens 5. KCNETL ENSP000024594 Homo sepens 5. KCNETL ENSP000024594 Homo sepens 1. COLV2E ENSP000024594 Homo sepens 1. COLV2E ENSP000024594 Homo sepens 1. COLV2E ENSP000024594 Homo sepens 1. CALA ENSP000024594 Homo sepens 1. CALA ENSP0000239787 Homo sepens 1. CALA ENSP0000339787 Homo sepens 1. CAMELCET. ENSP0000339787 Homo sepens	VPPDL KRRKEENGT VOVEKHKSESPCESPYPHEKDKEKNKEKSSCKEKSSDSFKSEKMD (15500 KKESR GFS. 1 YVQGHKHAHGDDIG AGN GIRRFSIMF - MFCNINNYCNFASR DYSYWISIF PMPM2MSMOPIKGOS GFS. 1 YVQGHKHAHGDDIG AGN GIRRFSIMF - MFCNINNYCNFASR DYSYWISIF PM2MSMOPIKGOS H X K K K E K R D S C O X E K K H H K S D K H R 1 D P F S R C A Y C A F A Y Y A Y A Y A Y A Y A Y A Y A Y A
2. THOC2 ENSP0000248938 Homo segens 3. RGAG1 ENSP000031103 Homo segens 4. M07 ENSP000031103 Homo segens 5. KOR51L ENSP000031103 Homo segens 7. CUCY2F ENSP0000318006 Homo segens 7. CUCY2F ENSP0000218006 Homo segens 7. CUCY2F ENSP0000318006 Homo segens 10. AMMECR1 ENSP000031707 Homo segens 10. AMMECR1 ENSP000031707 Homo segens 5. Procest ENSP0000031101 Homo segens 5. Procest ENSP0000031101 Homo segens 5. KOR51L ENSP0000031707 Homo segens 5. KOR51L ENSP00000318173 Homo segens 5. KOR51L ENSP0000021006 Homo segens 6. KOR51L ENSP000021006 Homo segens 6. KOR51L ENSP0000021006 Homo segens 6. KOR51L ENSP000002106 Homo segens 6. KOR51L ENSP000002106 Homo segens	VPPDL KRRKEENGTWOVEKHKSESPCESPYPNEKDKEKNKEKSSOKEKSEDSFKSEKMD (15500KKESR GFRIIVVWGNKHAHEDDIGTAGNAGNCIRRFSTWH-WFCMINNVCMFASRINUYSYWISTFEYMPMSMOPIKGGS H X K K I K K K K K K SOOK EE K K H H K SOOK H R 1 M P F S K C A V C A R A V V A V R SO 10 1 P H C POGWDSIWISI WIEKT SA A A A F G SGO A A SPECIEFFS A A
2. THCC2 ENSP0000245838 Homo sepens D. RGAG1 ENSP0000245838 Homo sepens MRT2 ENSP00002718204 Homo sepens 5. KCNE1L ENSP00000351173 Homo sepens 5. KCNE1L ENSP0000025083 Homo sepens 1. CILCY2E ENSP0000025080 Homo sepens 1. CILCY2E ENSP00000251807 Homo sepens 1. CILCY2E ENSP00000251807 Homo sepens 1. CILCY2E ENSP00000251807 Homo sepens 1. CILCY2E ENSP0000025484 Homo sepens 1. CILCY2E ENSP0000025488 Homo sepens 5. KCNE1L ENSP0000024588 Homo sepens 5. KCNE1L ENSP00000245838 Homo sepens 5. KCNE1L ENSP0000024598 Homo sepens 5. KCNE1L ENSP0000024598 Homo sepens 5. KCNE1L ENSP00000245976 Homo sepens	VPPDL KRRKEENGTWOVEKHKSESPCESPYPNEKDKEKNKEKSSOKEKSEDSFKSEKMD (15500KKESR GFRIIVVWGNKHAHEDDIGTAGNAGNCIRRFSTWH-WFCMINNVCMFASRINUYSYWISTFEYMPMSMOPIKGGS H X K K I K K K K K K SOOK EE K K H H K SOOK H R 1 M P F S K C A V C A R A V V A V R SO 10 1 P H C POGWDSIWISI WIEKT SA A A A F G SGO A A SPECIEFFS A A
2. THCC2 ENSP000024838 Homo sepens D. RGAG1 ENSP0000219706 Homo sepens MR7 ENSP0000271804 Homo sepens S. KCNETL ENSP0000271826 Homo sepens S. KCNETL ENSP0000271826 Homo sepens D. KCZE ENSP0000270820 Homo sepens 1.001476 ENSP00000239757 Homo sepens D. KCZE ENSP00000245838 Homo sepens S. KCNETL ENSP0000245838 Homo sepens D. KCZE ENSP0000245838 Homo sepens S. KCNETL ENSP0000245837 Homo sepens S. KCNETL ENSP0000245837 Homo sepens D. GUCYZ ENSP0000245838 Homo sepens S. KCNETL ENSP00002393757 Homo sepens S. THE MSC ENSP0000451738 Homo sepens S. THE ENSP00002458173 Homo sepens S. KCNETL ENSP00002458173 Homo sepens S. KCNETL ENSP0000245938 Homo sepens	VPPDL KRRKEENGTWOVEKHKSESPCESPYPNEKDKEKNKEKSSOKEKSEDSFKSEKMD (15500KKESR GFRIIVVWGNKHAHEDDIGTAGNAGNCIRRFSTWH-WFCMINNVCMFASRINUYSYWISTFEYMPMSMOPIKGGS H X K K I K K K K K K SOOK EE K K H H K SOOK H R 1 M P F S K C A V C A R A V V A V R SO 10 1 P H C POGWDSIWISI WIEKT SA A A A F G SGO A A SPECIEFFS A A
2. THCC2 ENSP000024838 Homo sepens 3. RGAG1 ENSP0000219706 Homo sepens 4. MD7 ENSP0000219706 Homo sepens 5. KCNETL ENSP0000251973 Homo sepens 5. KCNETL ENSP0000251973 Homo sepens 5. KCNETL ENSP0000251926 Homo sepens 1. CILC2E ENSP0000252053 Homo sepens 4. COLC2E ENSP0000252053 Homo sepens 5. KCNETL ENSP0000251973 Homo sepens 5. KCNETL ENSP0000254588 Homo sepens 5. KCNETL ENSP0000254588 Homo sepens 5. KCNETL ENSP0000251973 Homo sepens 5. KCNETL ENSP0000251974 Homo sepens	VPPDL KRRKEENGT WOVEKHKSESPCESPYPHEKDKEKNKEKSSCKEKSSDSFKSEKMD (15000 KKESPCKESP 64 + 8 + 1 × VQ600 KHA H H H H H H H H H H H H H H H H H H
2. THCC2 ENSP0000248/88 Homo sepens 3. RGAG1 ENSP0000319804 Homo sepens 4. R017 ENSP000031103 Homo sepens 4. R017 ENSP000031103 Homo sepens 5. RCHC11_ENST0000351173 Homo sepens 5. RCHC11_ENST00000351173 Homo sepens 5. RCHC12_ENSP0000021031 Homo sepens 5. RCHC12_ENSP0000021031 Homo sepens 10.114AP_ENDP0000021031 Homo sepens 10.114AP_ENDP0000021031 Homo sepens 7. RCHC1_ENSP0000021031 Homo sepens 1. RCHC1_ENSP00000245838 Homo sepens 1. RCHC1_ENSP00000245771 Homo sepens 1. RCHC1_ENSP0000025777 Homo sepens	

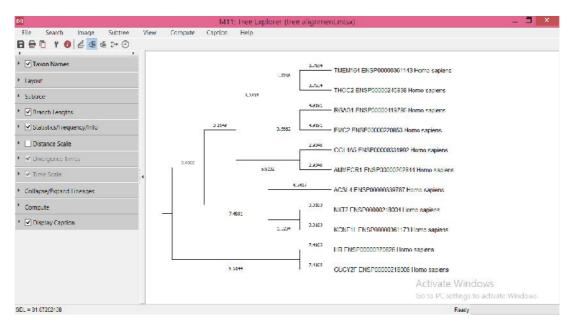
Figure 1: The interactions of AMMECR1 using String database



Your Input:

AMMECR1	MECR1 AMME syndrome candidate gene 1 protein; Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1 (333 aa)					Score
AMME syndrome candidate gene 1 protein; Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1 (333 aa) Predicted Functional Partners:						Score
e ACSL4	Long-chain-fatty-acid–CoA ligase 4; Activation of long-chain fatty acids for both synthesis of cellular lipids, and degradation				٠	0.930
😑 COL4A5	Collagen alpha-5(IV) chain; Type IV collagen is the major structural component of glomerular basement membranes (GBM),				٠	0.823
😁 KCNE1L	Potassium voltage-gated channel isk-related subfamily e member 1-like; Potassium voltage-gated channel subfamily E regul				٠	0.819
GUCY2F	Retinal guary/yl cyclase 2; Probably plays a specific functional role in the rods and/or cones of photoreceptors. It may be th		. 0		٠	0.755
NXT2	Nuclear transport factor 2 like export factor 2; NTF2-related export protein 2; Regulator of protein export for NES-containing				٠	0.747
TMEM164	Transmembrane protein 164; Belongs to the TMEM164 family		. 0			0.734
EMC2	ER membrane protein complex subunit 2; Tetratricopeptide repeat domain containing			٠		0.733
RGAG1	Retrotransposon Gag-like protein 9; Retrotransposon gag domain containing 1		. 0		۰	0.689
😁 HR	Hr, lysine demethylase and nuclear receptor corepressor; Lysine-specific demethylase hairless; Histone demethylase that sp			•		0.671
THOC2	THO complex subunit 2; Required for efficient export of polyadenylated RNA and spliced mRNA. Acts as component of the		. 0		.0	0.644

Figure 3: Phylogenetic treegenetrated by MEGA 5.03



The multiple sequence alignment file was used for the phylogenetic analysis by MEGA 5.03. From the multiple sequence alignment of AMMECR1, it is clear that the sequences analyzed in 11 protein sequences share the strong similarity among themselves. On analysing the phylogenetic tree based upon the protein sequences of Homo sapiens demonstrate the presence of 5 clusters among the 11 different proteins. The phylogenetic analysis was carried out by using distance method and clustering by UPGMA (Unweighted Pair Group Method with Arithmetic Mean). A tree of AMMECR1 drawn by using MEGA 5.03 reveals the formation of an outgroup comprising of HR, THOC2,EMC2,TMEM164, RGAG1, NXT2. COL4A5. ACSL4. KCNE1L.GUCY2F protein sequence. The sequences of AMMECR1 and COL4A5 show the considerable similarity between each other with the distance of 2.9048. The remaining 9 sequences of Homo sapiens from different protein form 4 groups.

- First group comprises of THOC2 and TMEM164 with the distance of 3.70634.
- Second group comprise of RGAG1 and EMC2 with the distance of 4.9191.
-) Third group comprise of ACSL4, NXT2 and KCNE1L with the distance of 4.5417 & 3.0183.
- Fourth group comprise of HR and GUCY2F with the distance of 7.4105

Conclusion

The study showed the protein-protein and evolutionary relationship of AMMECR1of Homo sapiens which plays a role in Alport syndrome. The string database showed that AMMECR1protein interacts with 11 different proteins of Homo sapiens that includes HR, THOC2, EMC2, TMEM164, RGAG1, NXT2. COL4A5, ACSL4, KCNE1L and GUCY2F. The maximum protein protein interaction was observed in COL4A5 protein when compared with other protein. The evolutionary relationship shows that AMMECR1of Homo sapiens is highly conserved across all 11 proteins of Homo sapiens and that the AMMECR1 is closest to COL4A5with good evolutionary distance of 2.9048. From the results of present *in silico* protein analysis predicted that the function of AMMECR1 protein can be more or less same as COL4A5.

Acknowledgments

We acknowledge Vels Institute of Science, Technology and Advanced Studies (VISTAS) for providing us with required infrastructure and support system needed.

Conflict of interest:

The authors declare they have no competing interests.

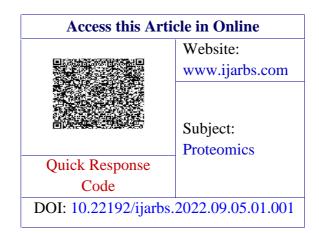
References

- Andreoletti G, Seaby EG, Dewing JM., O Kelly I, Lachlan K, Gilbert RD and Ennis S. 2017. AMMECR1: a single point mutation causes developmental delay, midface hypoplasia and elliptocytosis. Journal of medical genetics. 54(4); 269-277.
- Andreolett G,Seaby EG, Dewing JM, Kelly I, Lachlan K, Gilbert RD. 2017.
 AMMECR1: A Single Point Mutation Causes Developmental Delay, Midface Hypoplasia and Elliptocytosis. J Med Genet. 54: 269-277.
- Basel-Vanagaite, L, Pillar N, Isakov O, Smirin-Yosef, P, Lagovsky, I, Orenstein N, 2017.X-Linked Elliptocytosis with Impaired Growth Is Related to Mutated AMMECR1. Gene, 606:47-52.
- Cai C, Xu M, Su Y and Zhou H. 2019. Phosphorylation of AMMECR1 at Serine16 Is Not Essential for Its Nuclear Localization. Journal of Biosciences and Medicines. 7:146-153.
- Caspermeyer J. 2018. MEGA software celebrates silver anniversary. MolBiolEvol. 35(6): 1558-1560.

- Claramunt S andCracraft J.2015. A new time tree reveals Earth history's imprint on the evolution of modern birds. Sci Adv. 1(11):e1501005.
- Damian Szklarczyk, Annika L Gable, Katerina C Nastou, David Lyon, Rebecca Kirsch, SampoPyysalo, Christian von Mering.2021.The STRING database in 2021: customizable protein–protein networks, and functional characterization of user-uploaded gene/measurement sets. Nucleic Acids Research. 49(D1): D605-D612.
- Doncheva NT, Morris JH, Gorodkin J, Jensen LJ.2019. CytoscapeStringApp: network analysis and visualization of proteomics data. J Proteome Res. 18: 623-632.
- Drysdale R, Cook CE, Petryszak R, Baillie-Gerritsen V, Barlow M.,Gasteiger E, Gruhl F, Haas J, Lanfear J, Lopez R.2020.The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. Bioinformatics. 36: 2636-2642.
- Franceschini A, Szklarczyk D, Frankild S, Kuhn M, Simonovic M, Roth A, Lin J, Minguez P, Bork P, Von Mering C.2013.STRING v9.1: protein-protein interaction networks with increased coverage and integration. Nucleic Acids Res. 41:D808-D815.
- Greene CS, Krishnan A, Wong AK, Ricciotti E, Zelaya RA, Himmelstein DS, Zhang R, Hartmann BM, Zaslavsky E, Sealfon SC.2015. Understanding multicellular function and disease with human tissuespecific networks. Nat. Genet. 47: 569-576.
- Hipsley CA and Muller J. 2014. Beyond fossil calibrations: realities of molecular clock practices in evolutionary biology. Front Genet. 5:138.
- Huang JK, Carlin DE, Yu MK, Zhang W, Kreisberg JF,2018; Tamayo P, Ideker T. Systematic evaluation of molecular networks for discovery of disease genes. Cell Syst. 6: 484-495.

- Hwang S, Kim CY, Yang S, Kim E, Hart T, Marcotte EM, Lee I. 2019.HumanNet v2: human gene networks for disease research. Nucleic Acids Res. 47: D573-D580.
- Kamburov A, Stelzl U, Lehrach H, Herwig R.2013 The ConsensusPathDB interaction database: 2013 update. Nucleic Acids Res. 41: D793-D800.
- Koichiro Tamura, Glen Stecher, Sudhir Kumar, 2021. MEGA11: Molecular Evolutionary Genetics Analysis Version 11. Molecular Biology and Evolution. 38(7):3022-3027.
- Kotlyar M, Pastrello C, Malik Z, Jurisica I. 2019. IID 2018 update: context-specific physical protein-protein interactions in human, model organisms and domesticated species. Nucleic Acids Res. 47:D581-D589.
- Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular Evolutionary Genetics Analysis across computing platforms. MolBiolEvol. 35(6): 1547-1549.
- Moyses-Oliveira M, Giannuzzi G, Fish RJ, Rosenfeld JA, Petit F, Soares MF.2018 Inactivation of AMMECR1 Is Associated with Growth, Bone and Heart Alterations. Hum Mutat. 39. 281-291.
- Ogris C, Guala D, Sonnhammer ELL.2018.FunCoup 4: new species, data and visualization. Nucleic Acids Res. 46: D601-D607.
- Patel R and Kumar S. 2019. On estimating evolutionary probabilities of population variants. BMC Evol Biol. 19(1): 133.
- Stecher G, Tamura K and Kumar S. 2020. Molecular Evolutionary Genetics Analysis (MEGA) for macOS. MolBiolEvol. 37(4): 1237-1239.
- Szklarczyk D, Franceschini A, Wyder S, Forslund K, Heller D, Huerta-Cepas J, Simonovic M, Roth A, Santos A, Tsafou KP.2015.
 STRING v10: Protein-protein interaction networks, integrated over the tree of life. Nucleic Acids Res. 43: D447-D452.

- Von Mering C, Jensen LJ, Snel B, Hooper SD, Krupp M, Foglierini M, Jouffre N, Huynen M.A, Bork P.2005. STRING: known and predicted protein-protein associations integrated and transferred across organisms. Nucleic Acids Res. 33: D433-D437.
- Warde-Farley D, Donaldson SL, Comes O, Zuberi K, Badrawi R, Chao P, Franz M, Grouios C, Kazi F, Lopes CT. 2010. The GeneMANIA prediction server: biological network integration for gene prioritization and predicting gene function. Nucleic Acids Res. 38: W214-W220.
- Wong AK, Krishnan A, Yao V, Tadych A, Troyanskaya OG. 2015. IMP 2.0: A multispecies functional genomics portal for integration, visualization and prediction of protein functions and networks. Nucleic Acids Res. 43: W128-W133.
- Zhou HM, Cai C, Xu M and Li G. 2015. Research advances of AMMECR1. Biophysics. 3:1-6.



How to cite this article:

Jeyabaskar Suganya, Nishandhini.M, Mark Antony. J, Rajesh Kumar.G, Mahendran Radha. (2022). *In silico* analysis of AMMECR1 protein-protein and its phylogenetic interaction. Int. J. Adv. Res. Biol. Sci. 9(5): Special Issue 1: 1-11.

DOI: DOI: http://dx.doi.org/10.22192/ijarbs.2022.09.05.01.001