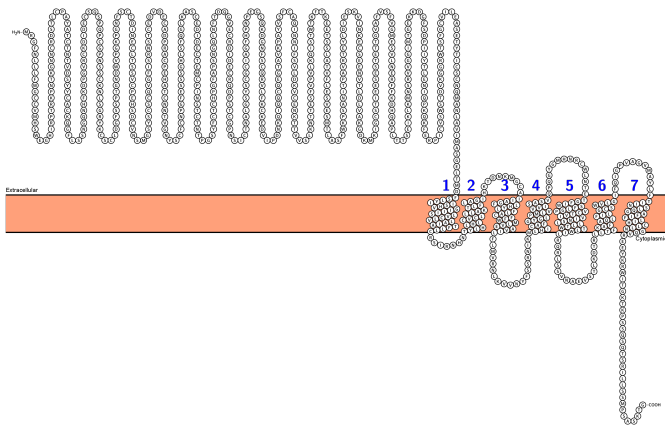


# Adhesion G protein-coupled receptor E1

Organism: Homo sapiens (Human) | Gene names: ADGRE1, EMR1, TM7LN3



Entry: Q14246

Mass: 97.683 Da

Transmembrane: 7

Subcellular location: Cell membrane

{ECO:0000269|PubMed:24530099}, Multi-pass membrane protein {ECO:0000255}.

Cofactor: -

Extinction coefficient: 1.13

Isoelectric Point: 6.42

PubMed ID: 7601460, 14702039, 15057824, 15489334, 17823986, 24530099, 25713288

Family: -

## Function:

Orphan receptor involved in cell adhesion and probably in cell-cell interactions specifically involving cells of the immune system. May play a role in regulatory T-cells (Treg) development. {ECO:0000250|UniProtKB:Q61549}.

## Data from experiment(s): Hek293 membrane pellets

DIBMA 10	No data	DIBMA 12	No data
DIBMA Glycerol	No data	DIBMA Glucosamine	No data
Amphipol 17	No data	Amphipol 18	No data
AASTY 6-45	No data	AASTY 11-45	No data
AASTY 6-50	No data	AASTY 11-50	No data
AASTY 6- 55	No data	AASTY 11- 55	No data
SMALP 502-E	No data	SMALP 140-I	No data
SMALP 300	No data	SMALP 200	No data
SMALP 140	No data	DDM	No data
DM	No data	LMNG	No data
Fos-12	No data	Digitonin-A	No data
RIPA	No data		

Data from experiment(s): Hek293 membrane pellets 1 %

DIBMA 10	No data	DIBMA 12	No data
DIBMA Glycerol	No data	DIBMA Glucosamine	No data
Amphipol 17	No data	Amphipol 18	No data
AASTY 6-45	No data	AASTY 11-45	No data
AASTY 6-50	No data	AASTY 11-50	No data
AASTY 6- 55	No data	AASTY 11- 55	No data
SMALP 502-E	No data	SMALP 140-I	No data
SMALP 300	No data	SMALP 200	No data
SMALP 140	No data	DDM	No data
DM	No data	LMNG	No data
Fos-12	No data	Digitonin-A	No data
RIPA	No data		

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**Involvement in disease:**

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**Binding site:**

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**Tissue specificity:**

Expression is restricted to eosinophils. {ECO:0000269|PubMed:17823986, ECO:0000269|PubMed:24530099}.

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**3D (X-ray crystallography):**

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**Pharmaceutical use:**

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**AS sequence:**

MRGFNLLLFWGCCVMHSEWEGHIRPTRKPNKGNCRDSTLCPAYATCTNTVDSYYCACKQGFLSSNGQNHFKDPGVRCKDID  
ECSQSPQPCGPNSSCKNLSGRYKCSCLDGFSSPTGNDWVPGKPGNFSCDINECLTSSVCPEHSDCVNSMGSYSCSCQVGFISR  
NSTCEDVDECADPRACPEHATCNNTVGNYSFCFNPGFESSGHLFSFQGLKASCEDIDECTEMCPINSTCTNTPGSYFCTCHPGF  
APSNQQLNFTDQGVVECRDIDECRQDPSTCGPNSICTNALGSYSCGCIAGFHPNPEGSQKDGNFSCQRVLFKCKEDVIPDNKQIQQ  
CQEGTAVKPAYVSFCAQINNIFSVLDKVCENKTTVVSLKNTTESFVPLKQISTWTKFTEETSSLATVFLESVESMTLASFWKPS  
ANITPAVRTEYLDIESKVINKECSEENVTLDLVAKGDKMKIGCSTIEESESTETTGVAFVSFVGMESVLNERFFKDHQAPLTTSEIKL  
KMNSRVVGGIMTGEKKDGFSDPIIYTLNIQPKQKFERPICVSWSTDVKGGRWTSFGCVILEASETYTICSCNQMANLAVIMASG  
ELTMDFSLYIISHVGIISLVCLVLAIAATFLLCRSIRNHNTYLHLHLCVCLLAKTLFLAGIHKTDNKMGCIIAGFLHYLFLACFFWML  
VEAVILFLMVRNLKVVNYFSSRNIMLHICAFGYGLPMLVVVISASVQPQGYGMHNRCWLNTETGFIWSFLGPVCTVIVINSLLLT  
WTLWILRQRLSSVNAEVSTLKDTRLLTFKAFAQLFILGCSWVLGIFQIGPVAGVMAYLFTIINSLQGAFILIHCLLNGQVREEYKR  
WITGKTKPSSQSQTSRILLSSMPSASKTG

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**Creditnotes:**

The protein visualizations are generated with the help of Protter:

Omasits, U., Ahrens, C.H., MÃ¼ller, S., Wollscheid, B. "Protter: interactive protein feature visualization and integration with experimental proteomic data". *Bioinformatics*. 2014 Mar 15; **30**(6):884-6. doi: 10.1093/bioinformatics/btt607.

IP and extinction coefficients are gathered from Protparam by ExPASy:

Gasteiger, E., Hoogland, C., Gattiker, A., Duvaud, S., Wilkins, M.R., Appel, R.D., Bairoch, A. "Protein Identification and Analysis Tools on the ExPASy Server". (In) *John M. Walker (ed): The Proteomics Protocols Handbook*, Humana Press (2005). pp. 571-607

The basic knowledge is found on UniProt:

The UniProt Consortium. "UniProt: the universal protein knowledgebase in 2021". *Nucleic Acids Res.* **49**:D1 (2021)

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