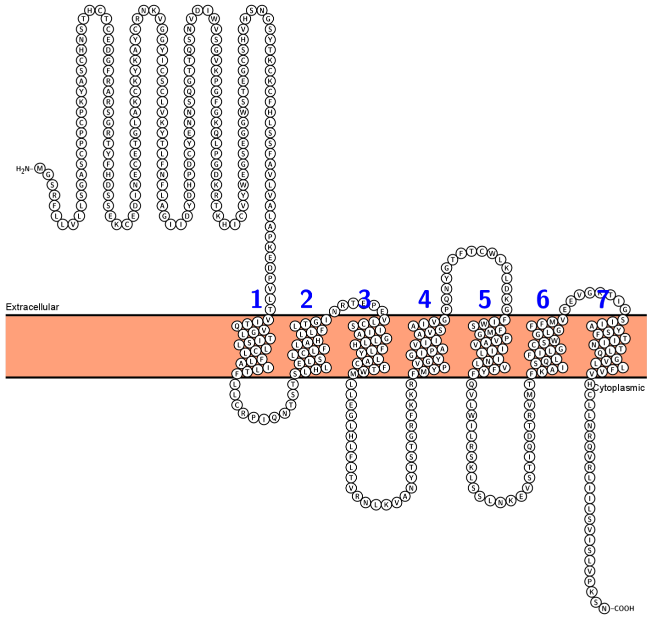
Cube Biotech

Putative adhesion G protein-coupled receptor E4P

Organism: Homo sapiens (Human) | **Gene names:** ADGRE4P, EMR4, EMR4P, GPR127, PGR16



Entry: Q86SQ3

Mass: 50.903 Da

Transmembrane: 7

Subcellular location: [Isoform 1]: Cell membrane {ECO:0000250|UniProtKB:Q91ZE5}, Multi-pass membrane protein {ECO:0000305}., [Isoform 2]: Secreted {ECO:0000305}.

Cofactor: -

Extinction coefficient: 1.391

Isoelectric Point: 8.7

PubMed ID: 12565841, 12731063, 12679517, 16753812, 25713288

Family: -

Function:

May mediate the cellular interaction between myeloid cells and B-cells. {ECO:0000250|UniProtKB:Q91ZE5}.

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		

Involvement in disease:

-

Binding site:

-

Tissue specificity:

-

3D (X-ray crystallography):

-

Pharmaceutical use:

-

AS sequence:

MGSRFLLVLLSGASCPPCPKYASCHNSTHCTCEDGFRARSGRTYFHDSSEKCEDINECETGLAKCKYKAYCRNKVGGYICSCLVK
YTLFNFLAGIIDYDHPDCYENNSQGTTQSNVDIWVSGVKPGFGKQLPGDKRTKHICVYWEGSEGGWSTEGCSHVHSNGSYTKC
KCFHLSSFAVLVALAPKEDPVLTVITQVGLTISLLCLFLAILTFLLCRPIQNTSTSLHLELSLCLFLAHLLFLTGINRTEPEVLCSIIAGLL
HFLYLACFTWMLLEGLHLFLTVRNLKVANYTSTGRFKKRFMYPVGYGIPAVIIAVSAIVGPQNYGTFTCWLKLDKGFIWSFMGPV
AVIILINLVFYFQVLWILRSKLSSLNKEVSTIQDTRVMTFKAISQLFILGCSWGLGFFMVEEVGKTIGSIIAYSFTIINTLQGVLLFVVHC
LLNRQVRLIILSVISLVPKSN

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)