Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

CEACAM family

Carcinoembryonic antigen cell adhesion family, CD66 family, C-CAM family

Members

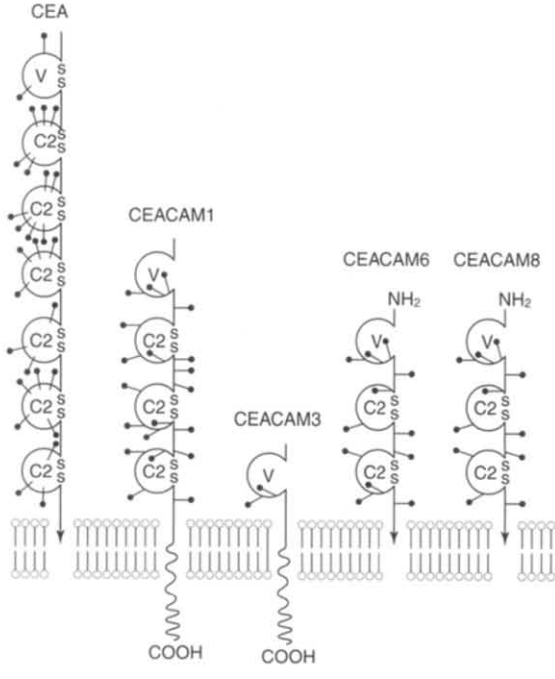
CEA	CEACAM5, CD66e
CEACAM1	CD66a, Cell-CAM 105, BGP, biliary glycoprotein, NCA-160
CEACAM3	CD66d, CGM1
CEACAM4	CGM7
CEACAM6	CD66c, NCA, NCA-90, CGM6
CEACAM7	CGM2
CEACAM8	CD66b, CGM6, CGM8, NCA-95

Note: The carcinoembryonic antigen (CEA) family nomenclature has recently been redefined[1,2].

Family

Immunoglobulin superfamily

Structure



Molecular weights

Amino acids	CEA	702
	CEACAM1	526
	CEACAM3	252
	CEACAM6	344
	CEACAM8	349
Polypeptide	CEA	76 795
	CEACAM1	57 560
	CEACAM3	27 077
	CEACAM6	37 161
	CEACAM8	38 154

SDS-PAGE reduced	CEA	180–200 kDa
	CEACAM1	140–180 kDa
	CEACAM3	35 kDa
	CEACAM6	90–95 kDa
	CEACAM8	95–100 kDa

Carbohydrate

N-linked sites	CEA	28
	CEACAM1	20
	CEACAM3	2
	CEACAM6	12
	CEACAM8	11
O-linked sites		

Gene location 19q13.1–19q13.2

Gene structure The CEA family comprises at least 28 separate genes.

Alternative forms

CEACAM1, CEACAM3 and CEACAM7 are alternatively spliced. The largest isoforms are shown here.

Structure

The human CEA family is part of a cluster of at least 28 genes divided into two functional groups. By genomic mapping, the CEACAM subgroup contains seven members and the PSG (pregnancy-specific glycoprotein) subgroup of secreted molecules contains 11 members. The remaining genes are thought to be pseudogenes[1]. Within the best characterized CEACAM members, CEACAM1 and CEACAM3 encode type 1 transmembrane proteins while CEACAM8, CEACAM6 and CEA are GPI anchored in the membrane. All members possess an N-terminal V-type Ig domain followed by between 0 and 6 C2-type Ig domains. Apart from CEACAM3, the extracellular domains are extensively *N*-glycosylated. CEACAM1 and CEACAM3 have putative tyrosine phosphorylation sites in their cytoplasmic domains, which could bind signalling components such as the tyrosine phosphatases SHP-1 and SHP-2; CEACAM1 can associate with the cytoplasmic tyrosine kinases Src, Lyn and Hck[3,4]. Alternative splicing results in CEACAM1, 3 and 7 isoforms with varying numbers of Ig domains and/or shorter cytoplasmic domains[1]. Further structural and sequence information on other CEACAM family members and members of the PSG family can be found in refs 1 and 2.

Ligands

The CEACAM family can mediate homophilic cell–cell adhesion and in certain combinations, heterophilic interactions with other family members[5]. Binding is via the V-type domain[6,7]. In addition, CEACAM1 and CEACAM6 have been reported to bind E-selectin, CEACAM1 and CEACAM3 can act as a receptors for *Neisseria gonorrhoeae* and *Neisseria meningitidis*[8], murine CEACAM1 and CEACAM2 are receptors for murine coronaviruses[9], and CEACAM6 can bind galectins.

Function

Binding assays indicate a role for CEACAM family members in mediating adhesion between granulocytes and/or between granulocytes and epithelial cells, and as microbial receptors. In addition, signalling via CEACAM1 and CEACAM3 cytoplasmic domains[4] may regulate the adhesive activity of the β_2 integrins[10] and the cytolytic function of intraepithelial lymphocytes[11]. Different splice variants of CEACAM1 and 3 display different bacterial tropism and invasion[4]. Importantly, members of the CEACAM family are strongly down-regulated in malignancies, implicating these receptors as putative tumour suppressors[4]. It should be noted that Cell-CAM 105 originally identified in rats and described as a homophilic adhesion molecule involved in the formation and maintenance of hepatocyte polarization and exhibiting ecto-ATPase activity[12,13], is CEACAM1.

Distribution

CEACAM1 and CEACAM6 are abundant on granulocytes and epithelial cells, CEACAM8 and CEACAM3 are restricted to granulocytes, and CEA is mostly found on epithelial cells.

Disease association

OMIM CEA, 114890; CEACAM1, 109770; CEACAM6, 163980.
CEACAM1 and CEA are strongly down-regulated in colon and other carcinomas. Evidence that CEACAM proteins can act as tumour suppressors comes from studies in which transfection of CEACAM1 in carcinoma cells resulted in an inhibition of tumour development in nude mice and conversely down-regulation in benign cells resulted in increased tumourigenicity[4]. CEA levels in serum are used routinely as clinical markers in the diagnosis and serial monitoring of cancer patients for recurrent disease or response to therapy.

Knockout

MGI:1347245 (CEACAM1)

Amino acid sequence of human CEA

```
  1 MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVHNLPQ
 61 HLFGYSWYKG ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY
121 TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTCEPE TQDATYLWWV
181 NNQSLPVSPR LQLSNGNRTL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP
241 TISPLNTSYR SGENLNLSCH AASNPPAQYS WFVNGTFQQS TQELFIPNIT VNNSGSYTCQ
301 AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWWVNN
361 QSLPVSPRLQ LSNDNRTLTL LSVTRNDVGP YECGIQNELS VDHSDPVILN VLYGPDDPTI
421 SPSYTYYRPG VNLSLSCHAA SNPPAQYSWL IDGNIQQHTQ ELFISNITEK NSGLYTCQAN
481 NSASGHSRTT VKTITVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWWVNGQS
541 LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDTPIISP
601 PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQQHTQVL FIAKITPNNN GTYACFVSNL
661 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI
```

In CEA the C-terminus is proteolytically cleaved and a GPI anchor attached. However, the site of cleavage has not been unambigously determined.

Amino acid sequence of human CEACAM1

```
  1 MGHLSAPLHR VRVPWQGLLL TASLLTFWNP PTTAQLTTES MPFNVAEGKE VLLLVHNLPQ
 61 QLFGYSWYKG ERVDGNRQIV GYAIGTQQAT PGPANSGRET IYPNASLLIQ NVTQNDTGFY
121 TLQVIKSDLV NEEATGQFHV YPELPKPSIS SNNSNPVEDK DAVAFTCEPE TQDTTYLWWI
181 NNQSLPVSPR LQLSNGNRTL TLLSVTRNDT GPYECEIQNP VSANRSDPVT LNVTYGPDTP
241 TISPSDTYYR PGANLSLSCY AASNPPAQYS WLINGTFQQS TQELFIPNIT VNNSGSYTCH
301 ANNSVTGCNR TTVKTIIVTE LSPVVAKPQI KASKTTVTGD KDSVNLTCST NDTGISIRWF
361 FKNQSLPSSE RMKLSQGNTT LSINPVKRED AGTYWCEVFN PISKNQSDPI MLNVNYNALP
421 QENGLSPGAI AGIVIGVVAL VALIAVALAC FLHFGKTGRA SDQRDLTEHK PSVSNHTQDH
481 SNDPPNKMNE VTYSTLNFEA QQPTQPTSAS PSLTATEIIY SEVKKQ
```

Amino acid sequence of human CEACAM3

```
  1 MGPPSASPHR ECIPWQGLLL TASLLNFWNP PTTAKLTIES MPLSVAEGKE VLLLVHNLPQ
 61 HLFGYSWYKG ERVDGNSLIV GYVIGTQQAT PGAAYSGRET IYTNASLLIQ NVTQNDIGFY
121 TLQVIKSDLV NEEATGQFHV YQENAPGLPV GAVAGIVTGV LVGVALVAAL VCFLLLAKTG
181 RTSIQRDLKE QQPQALAPGR GPSHSSAFSM SPLSSAQAPL PNPRTAASIY EELLKHDTNI
241 YCRMDHKAEV AS
```

Amino acid sequence of human CEACAM6

```
  1 MGPPSAPPCR LHVPWKEVLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLAHNLPQ
 61 NRIGYSWYKG ERVDGNSLIV GYVIGTQQAT PGPAYSGRET IYPNASLLIQ NVTQNDTGFY
121 TLQVIKSDLV NEEATGQLHV YPELPKPSIS SNNSNPVEDK DAVAFTCEPE VQNTTYLWWV
181 NGQSLPVSPR LQLSNGNMTL TLLSVKRNDA GSYECEIQNP ASANRSDPVT LNVLYGPDGP
241 TISPSKANYR PGENLNLSCH AASNPPAQYS WFINGTFQQS TQELFIPNIT VNNSGSYMCQ
301 AHNSATGLNR TTVTMITVSG SAPVLSAVAT VGITIGVLAR VALI
```

The sequences sequences underlined and in italics are cleaved off to form mature CEACAM6 and a GPI anchor is added.

Amino acid sequence of human CEACAM8

```
  1 MGPISAPSCR WRIPWQGLLL TASLFTFWNP PTTAQLTIEA VPSNAAEGKE VLLLVHNLPQ
 61 DPRGYNWYKG ETVDANRRII GYVISNQQIT PGPAYSNRET IYPNASLLMR NVTRNDTGSY
121 TLQVIKLNLM SEEVTGQFSV HPETPKPSIS SNNSNPVEDK DAVAFTCEPE TQNTTYLWWV
181 NGQSLPVSPR LQLSNGNRTL TLLSVTRNDV GPYECEIQNP ASANFSDPVT LNVLYGPDAP
241 TISPSDTYYH AGVNLNLSCH AASNPPSQYS WSVNGTFQQY TQKLFIPNIT TKNSGSYACH
301 TTNSATGRNR TTVRMITVSD ALVQGSSPGL SARATVSIMI GVLARVALI
```

The sequences sequences underlined and in italics are cleaved off to form mature CEACAM8 and a GPI anchor is added.

Database accession

	EMBL/GenBank	*SwissProt*
CEA	M17303	P06731
CEACAM1	X16354	P13688
CEACAM3	L00692	P40198
CEACAM6	M29541	P40199
CEACAM8	X52378	P31997

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