Fig. 1 ; SEQ ID No 1

```
GFTPSGTTGT TKLTVTEECQ VRVGDLTVAK TRGQLTDAAP IGPVTVQALG 50
CDARQVALKA DTDNFEQGKF FLISDNKRDK LYVNIRPTDN SAWTTDNGVF 100
YKNDVGSWGG IIGIYVDGQQ TNTPPGNYTL TLTGGYWAK            139
```

CLUSTAL 2.0.8 multiple sequence alignment of in each case one representative of each adhesin group (acc. to Korotkova, 2007)

Fig. 2

```
AfaE-5          AFTGSGSTGTTKLTVTEQCQVLVTGSD--VTKTRGELTDGARVGVLSVTAKGCNT-EHAA 57
DrbE-122        AFTASGNTGTTKLTVTEQCQVMVTGSA--STKTRGELIDGARVGALSLNARGCNT-EHAA 57
DraE            GFTPSGTTGTTKLTVTEECQVRVGDLT--VAKTRGQLTDAAPIGPVTVQALGCDA-RQVA 57
SM254           QFSYSGNTGTVKVTVTEECQIQVGDFS--TTKPRSQLTNGAAIGPINVTARGCDT-RQIA 57
DaaE            TFQASGTTGITTLTVTEECRVQVGNVT--ATLARSKLKDDTAIGVIGVTALGCNG-LQAA 57
AfaE-2          -AVDKHATGTYTLNVTEECAVHLTDNT--ESLRKTDLTEGKLLAGVGLSATGCAN-SKVA 56
AfaE-1          NFTSSGTNGKVDLTITEECRVTVESKS--ESFLRSGLVANRHITNLGIQSTGCGTGQRVA 58
NfaE-111        GIRLGTATASGTITNMESCTVNLTIATPDAKMNRAGMQENREITKFKVASNDCPTDTYAV 60
                      *9   :10 *.* : :          : :    : . : : .*     .

AfaE-5          LRAQPDNYHQGK-IVLIRDDYQARINVRLQAT-----DGRAWNTNGDTVYRADAGNWGGS 111
DrbE-122        LRAQADNYHNGK-IVLLREDQQARINVRLVAS-----DGGQWTNDGATTYRDAAGDWGGS 111
DraE            LKADTDNFEQGK-FFLISDNNRDKLYVNIRPT-----DNSAWTTDNGVFYKNDVGSWGGI 111
SM254           LQAGADNIEGDK-LYMRSDNGGDKLYVVLSAL-----DGSNWTTDNGVFYNTVPGNWGGT 111
DaaE            LQADPDNYDATN-LYMTSRN-HDKLNVKLKAT-----DGSSWTYGNGVFYKTEGGNWGGH 110
AfaE-2          FSADAGNLKGTN-ILLKGADKTSFIPVYWETATAAGDDSHNWTATTEGIHRNSNGPWEGT 115
AfaE-1          LKLGAGSYDDTNGAHMTHENGTDKLLVSMGSA------TGDGTQDGGVYYINRDGNWNGQ 112
NfaE-111        WFKEIDNVANGI--AQGKSEYQTRFYLRMAST-----NGTESQKDISVGNKTGKGLSGKL 113
                     ..           :   : :  .                        *

AfaE-5          LF------VVVDGDNVDKPTGSYTLNLDWGYWVS 139
DrbE-122        LY------VVVDGDNTSNQAGSYTLNMDGGYWAS 139
DraE            IG------IYVDGQQTNTPPGNYTLTLTGGYWAK 139
SM254           IG------VKVQGDQTRTPTGNYTLTLTGGYWAK 139
DaaE            VG------ISVDGNQTDKPTGEYTLNLTGGYWTN 138
AfaE-2          IR------LRVIGDQTSAKAQAYTLVLNGGTWIE 143
AfaE-1          MV------FIVRNDQQHLPTGKYTLNLEGGFWTK 140
NfaE-111        ANGAFEGKITLAQDTTGVPVDVYTYNLMAAVYSQ 147
                       . :  :       **  :  . : .
```

without signal sequence

Fig. 3 , SEQ ID No 2

```
XXXXXXXXXXXXXXXXXEXCXXXXXXXX--XXXXXXXXXXXXXXXXXXXXXXXXCXX-
XXXXXXXXXXXXXXXXX-XXXXXXXXXXXXXXXXXXX-----
XXXXXXXXXXXXXXXXXXGXXXXXXX------XXXXXXXXXXXXXXXYTXXXXXXXXXX
```

CLUSTAL 2.0.8 multiple sequence alignment of adhesins of the DraE group (acc. to Korotkova, 2007)

```
G2152          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
SM297          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
JJB30          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
SM437          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
SM249          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
SM246          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
SM245          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
SM54           GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
G2171          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
G2166          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
G2106          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
G2102          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
G2097          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
G2096          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
DraE           GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
G2099          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
G2100          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCNARQVALKA 60
SM252          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
JJB17          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
SM293          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
G2076          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
SM513          GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKA 60
AfaE-III       GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCNARQVALKA 60
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G2152          TNTPPGNYTLALTGGYWAK 139
SM297          TNTPPGNYTLTLTGGYWAK 139
JJB30          TNTPPGNYTLNLTGGYWAK 139
SM437          TNTPPGNYTLTLTGGYWAK 139
SM249          TNTPPGNYTLTLTGGYWAK 139
SM246          TNTPPGNYTLTLTGGYWAK 139
SM245          TNTPPGNYTLTLTGGYWAK 139
SM54           TNTPPGNYTLTLTGGYWAK 139
G2171          TNTPPGNYTLTLTGGYWAK 139
G2166          TNTPPGNYTLTLTGGYWAK 139
G2106          TNTPPGNYTLTLTGGYWAK 139
G2102          TNTPPGNYTLTLTGGYWAK 139
G2097          TNTPPGNYTLTLTGGYWAK 139
G2096          TNTPPGNYTLTLTGGYWAK 139
DraE           TNTPPGNYTLTLTGGYWAK 139
G2099          TNTPPGNYTLTLTGGYWAK 139
G2100          TNTPPGNYTLTLTGGYWAK 139
SM252          TNTPPGNYTLTLTGGYWAK 139
JJB17          TNTPPGNYTLTLTGGYWAK 139
SM293          TNTPPGNYTLTLTGGYWAK 139
G2076          TNTPPGNYTLTLTGGYWAK 139
SM513          TNTPPGNYTLTLTGGYWAK 139
AfaE-III       TNTPPGNYTLTLTGGYWAK 139
               ********** ********

G2152          DTDNFEQGKFFLISDNNRDKLYVNMRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
SM297          DTDNFEQGKFFLISDNNRDKLYVNMRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
JJB30          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
SM437          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
SM249          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
SM246          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
SM245          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
SM54           DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
G2171          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
G2166          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
G2106          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
G2102          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
G2097          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
G2096          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
DraE           DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
G2099          GTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGTIGIYVDGQQ 120
G2100          GTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
SM252          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSTWTTDNGVFYKNDVGSWGGVIGIYVDGQQ 120
JJB17          DTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGGTIGIYVDGQQ 120
SM293          DTDNFEQGKFFLISDNNRDKLYVNIRPADNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
G2076          DTDNFEQDKFFLISDNNRDKLYVNIRPMDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
SM513          DTDNFEQGKFFLISDNNRDKLYVNIRPMDNSAWTTDNGVFYKNDVGSWGGIIGIYVDGQQ 120
AfaE-III       DTDNFEQGKFFLISDNNRDKLYVNIRPMDNSAWTTDNGVFYKNDVGSWGGTIGIYVDGQQ 120
               .******.*****************:** ***:****************** *********
```

Fig. 4

GFTPSGTTGTTKLTVTEECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCXARQVALKAXT
DNFEQXKFFLISDNKRDKLYVNXRPXDNSXWTTDNGVFYKNDVGSWGGXIGIYVDGQQTNTP
PGNYTLXLTGGYWAK

Fig. 5 , SEQ ID No 3

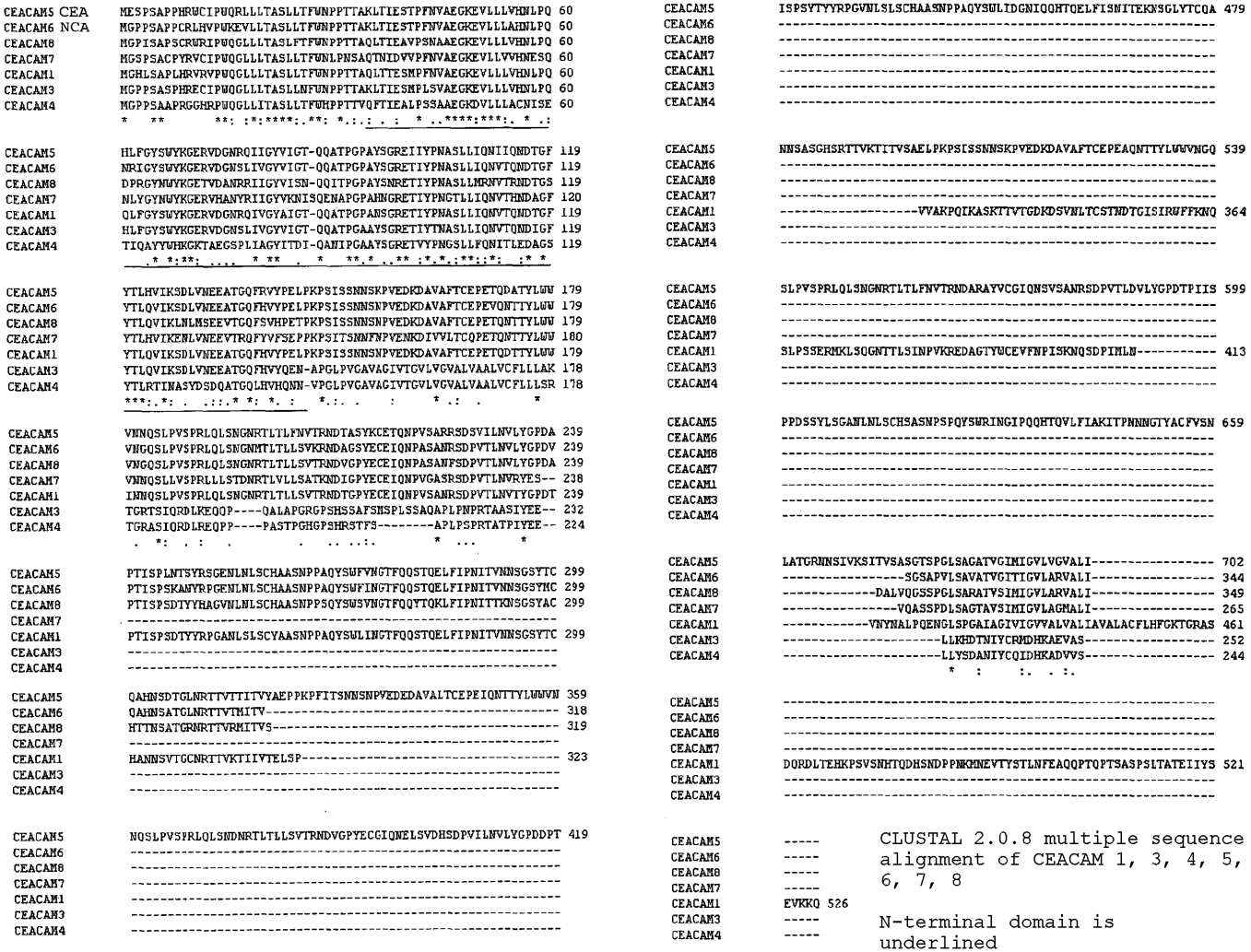
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DNFEQGKFFLISDNNRDKLYVNIRPXDNSAWTTDNGVFYKNDVGSWGGXIGIYVDGQQTNTP
PGNYTLTLTGGYWAK

Fig. 6
SEQ ID No 4

XXXXXXXPXXXAEGKXVLLXXXNXXXXXXXYXWXKGXXXXXXXXIXGYXXXX-
QXXXPGXAXXXREXXYXNXXLLXXNXXXXDXGXYTLXXIXXXXXXXXXTXQXXVXXXXXXPX
XXXXXXXXXXXXXXXVXXXXXXXXXXXXXXLXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXAXXXXXXXXXXXXYXX

Fig. 7
SEQ ID No 5

Fig. 8


CEACAM5 CEA
CEACAM6 NCA
CEACAM8
CEACAM7
CEACAM1
CEACAM3
CEACAM4
CLUSTAL 2.0.8 multiple sequence alignment of CEACAM 1, 3, 4, 5, 6, 7, 8
N-terminal domain is underlined

KLTIESTPFNVAEGKEVLLLXHNLPQXXXGYSWYKGERVDGNXXIXGYVIGTQQATPGPAYS
GREXIYPNASLLIQNXXQNDTGFYTLXVIKSDLVNEEATGQFXVYPELPKPSISSNNSXPVE
DKDAVAFTCEPEXQXXTYLWWVNXQSLPVSPRLQLSNGNXTLTLXXVXRNDXXSYXCEXQNP
XSAXRSDXVXLNVLYGPDXPTISPXXXXYRXGENLNLSCHAASNPPAQYSWFXNGTFQQSTQ
ELFIPNITVNNSGSYXCQAHNSXTGLNRTTVTXITVYAEPPKPFITSNNSNPVEDEDAVALT
CEPEIQNTTYLWWVNNAHNSATGLNRTTVTMITVQSLPVSPRLQLSNDNRTLTLLSVTRNDV
GPYECGIQNELSVDHSDPVILNVLYGPDDPTISPSYTYYRPGVNLSLSCHAASNPPAQYSWL
IDGNIQQHTQELFISNITEKNSGLYTCQANNSASGHSRTTVKTITVSAELPKPSISSNNSKP
VEDKDAVAFTCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQ
NSVSANRSDPVTLDVLYGPDTPIISPPDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQH
TQVLFIAKITPNNNGTYACFVSNLATGRNNSIVKSITVSASGXXPXLSAXATVGIXIGVLXX
VALI

Fig. 9
SEQ ID No 6

KLTIESTPFNVAEGKEVLLLVHNLPQHLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYS
GREIIYPNASLLIQNIIQNDTGFYTLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVE
DKDAVAFTCEPETQDATYLWWVNNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNP
VSARRSDSVILNVLYGPDAPTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQ
ELFIPNITVNNSGSYTCQAHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALT
CEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDP
VILNVLYGPDDPTISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNIT
EKNSGLYTCQANNSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNT
TYLWWVNGQSLPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYG
PDTPIISPPDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYA
CFVSNLATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI

Fig. 10
SEQ ID No 7

KLTIESTPFNVAEGKEVLLLAHNLPQNRIGYSWYKGERVDGNSLIVGYVIGTQQATPGPAYS
GRETIYPNASLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVE
DKDAVAFTCEPEVQNTTYLWWVNGQSLPVSPRLQLSNGNMTLTLLSVKRNDAGSYECEIQNP
ASANRSDPVTLNVLYGPDVPTISPSKANYRPGENLNLSCHAASNPPAQYSWFINGTFQQSTQ
ELFIPNITVNNSGSYMCQAHNSATGLNRTTVTMITVSGSAPVLSAVATVGITIGVLARVALI

Fig. 11
SEQ ID No 8

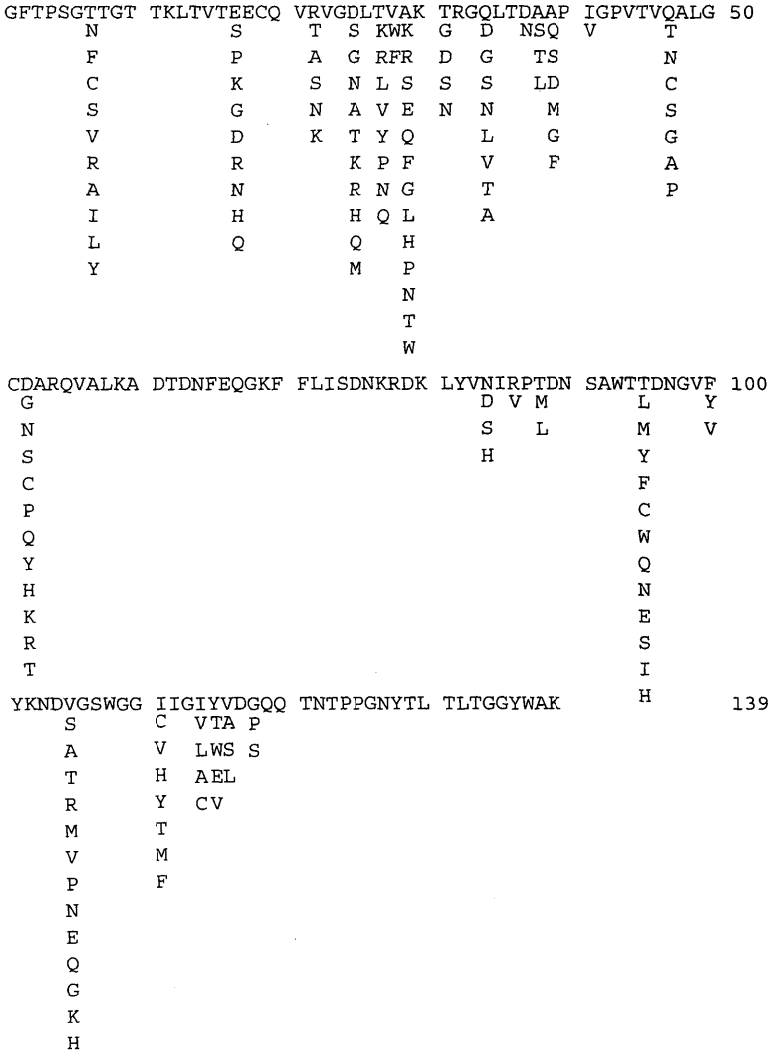

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CDARQVALKA DTDNFEQGKF FLISDNKRDK LYVNIRPTDN SAWTTDNGVF 100
YKNDVGSWGG IIGIYVDGQQ TNTPPGNYTL TLTGGYWAK 139

Fig. 12

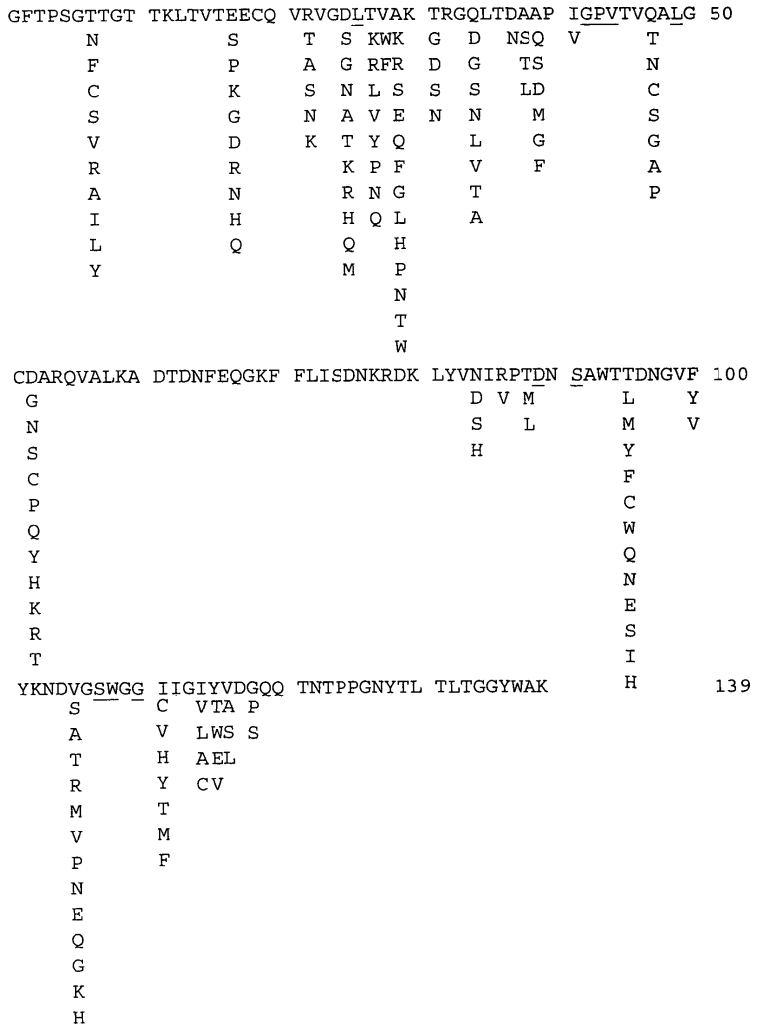

GFTPSGTTGT TKLTVTEECQ VRVGDLTVAK TRGQLTDAAP IGPVTVQALG 50
N S T S KWK G D NSQ V T
F P A G RFR D G TS N
C K S N LS D S S LD C
S G N A V E N N M S
V D K T Y Q L G G
R R K P F V F A
A N R N G T A P
I H H Q L A
L Q Q H
Y M P
N
T
W
CDARQVALKA DTDNFEQGKF FLISDNKRDK LYVNIRPTDN SAWTTDNGVF 100
G D V M L Y
N S L M V
S H Y
C F
P C
Q W
Y Q
H N
K E
R S
T I
YKNDVGSWGG IIGIYVDGQQ TNTPPGNYTL TLTGGYWAK H 139
S C VTA P
A V LWS S
T H AEL
R Y CV
M T
V M
P F
N
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Q
G
K
H

Fig. 13

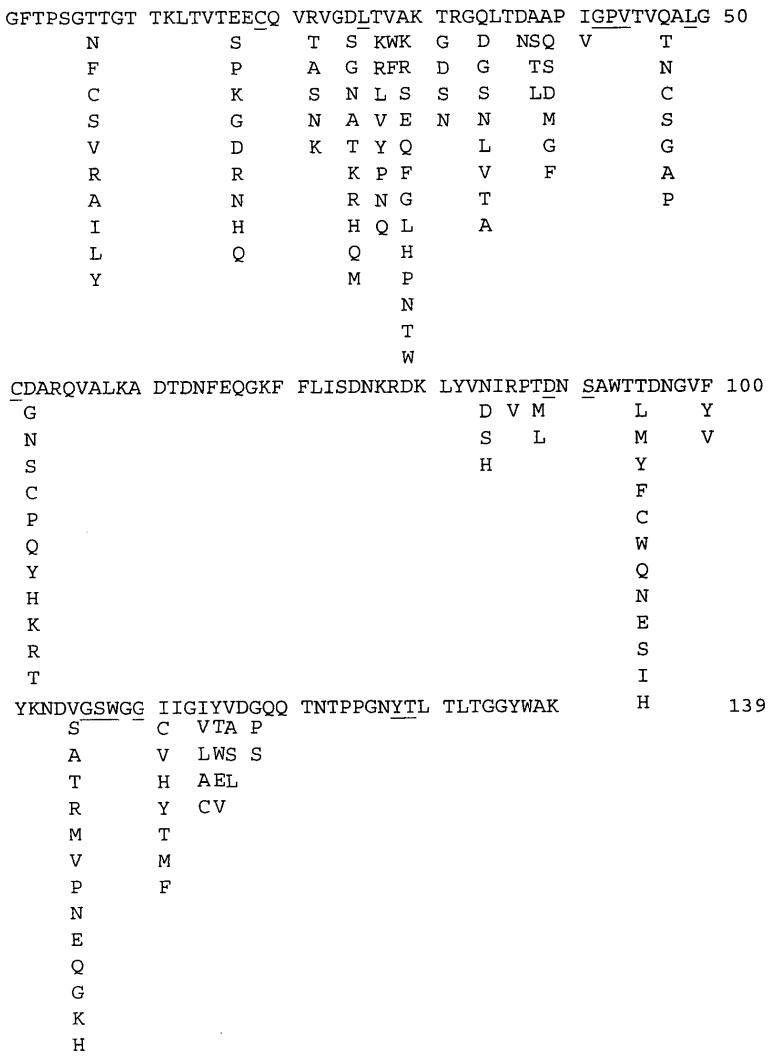

GFTPSGTTGT TKLTVTEECQ VRVGDLTVAK TRGQLTDAAP IGPVTVQALG 50
CDARQVALKA DTDNFEQGKF FLISDNKRDK LYVNIRPTDN SAWTTDNGVF 100
YKNDVGSWGG IIGIYVDGQQ TNTPPGNYTL TLTGGYWAK 139

Fig. 14

EECQVRVGDLTVAKTRGQLTDAAPIGPVTVQALGCDARQVALKADTDNFEQGKFFLISDNKR
DKLYVNIRPMDNSAWTTDNGVFYKNDVGSWGGVIGVYADGQQTNTPPGNYTLTLTGGYWAKD
NKQGFTPSGTTGTTKLTVT

Fig. 15
SEQ ID 12

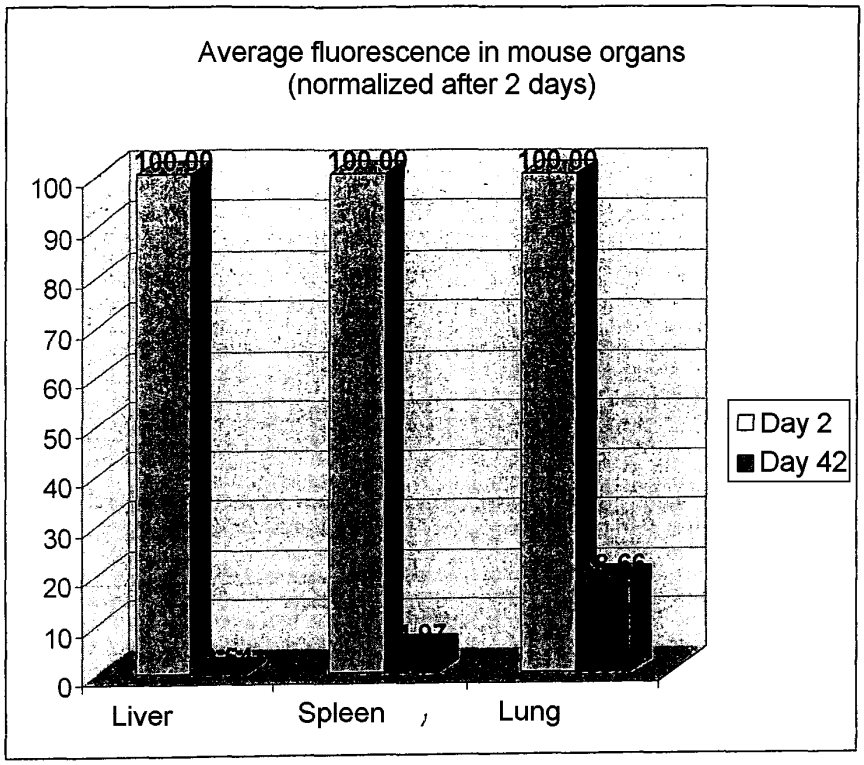

Average fluorescence in mouse organs
(normalized after 2 days)
100
90
80
70
60
50
40
30
20
10
0
Liver
Spleen
Lung
Day 2
Day 42

Fig. 16