

SEQ protocol Nachanmeldung 2013-03-22.txt
SEQUENCE LISTING

<110> Universität Stuttgart

<120> The IgM and IgE heavy chain domain 2 as covalently linked homodimerization modules for the generation of fusion proteins with dual specificity

<160> 36

•<170> BISSAP 1.0

<210> 1

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> SOURCE

<222> 1..111

<223> /mol_type="protein"
/organism="Homo sapiens"

<400> 1

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Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg Asp Gly
1      5      10      15
Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly
20      25      30
Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln
35      40      45
Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu
50      55      60
Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu
65      70      75      80
Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp His Arg
85      90      95
Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro Asp
100      105      110
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<210> 2

<211> 106

<212> PRT

<213> Homo sapiens

<220>

<221> SOURCE

<222> 1..106

<223> /mol_type="protein"
/organism="Homo sapiens"

<400> 2

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Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly
1      5      10      15
Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly
20      25      30
Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val
35      40      45
Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu
50      55      60
Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser
65      70      75      80
Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu
85      90      95
Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn
100      105
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<210> 3

<211> 265

<212> PRT

<213> Homo sapiens

<220>

<221> SOURCE

<222> 1..265

<223> /mol_type="protein"
/organism="Homo sapiens"

<400> 3

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1      5      10      15
Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly
20      25      30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35      40      45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
50      55      60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65      70      75      80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
85      90      95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
100     105     110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
115     120     125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130     135     140
Gly Gly Ser Gly Gly Gly Ser Gly Gly Thr Gly Asp Ile Gln
145     150     155     160
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
165     170     175
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp
180     185     190
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala
195     200     205
Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser
210     215     220
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
225     230     235     240
Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly
245     250     255
Gln Gly Thr Lys Val Glu Ile Lys Arg
260     265

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<210> 4

<211> 264

<212> PRT

<213> Homo sapiens

<220>

<221> SOURCE

<222> 1..264

<223> /mol_type="protein"
/organism="Homo sapiens"

<400> 4

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1      5      10      15
Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly
20      25      30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35      40      45
Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ala Pro Gly
50      55      60
Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp
65      70      75      80
Tyr Asn Thr Pro Phe Thr Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser
85      90      95

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Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110
Ala Val Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe
115 120 125
Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
130 135 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu
145 150 155 160
Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr
165 170 175
Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr
180 185 190
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys Tyr Ala Ser
195 200 205
Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220
Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
225 230 235 240
Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala
245 250 255
Gly Thr Lys Leu Glu Ile Lys Arg
260

<210> 5
<211> 472
<212> PRT
<213> artificial sequences

<220>
<221> SOURCE
<222> 1..472
<223> /mol_type="protein"
/note="sCTNF"
/organism="artificial sequences"

<400> 5
Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn
1 5 10 15
Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala
20 25 30
Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro
35 40 45
Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln
50 55 60
Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile
65 70 75 80
Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser
85 90 95
Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr
100 105 110
Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg
115 120 125
Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser
130 135 140
Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Ser
145 150 155 160
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
165 170 175
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
180 185 190
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Pro Ser
195 200 205
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
210 215 220
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
225 230 235 240
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
245 250 255

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Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 260 265 270
 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 275 280 285
 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 290 295 300
 Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Ser Ser
 305 310 315 320
 Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln
 325 330 335
 Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu
 340 345 350
 Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu
 355 360 365
 Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys
 370 375 380
 Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val
 385 390 395 400
 Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys
 405 410 415
 Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro
 420 425 430
 Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser
 435 440 445
 Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln
 450 455 460
 Val Tyr Phe Gly Ile Ile Ala Leu
 465 470

<210> 6
 <211> 580
 <212> PRT
 <213> artificial sequences

<220>
 <221> SOURCE
 <222> 1..580
 <223> /mol_type="protein"
 /note="SCTRAIL"
 /organism="artificial sequences"

<400> 6
 Thr Arg Gly Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln
 1 5 10 15
 Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala
 20 25 30
 Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
 35 40 45
 Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu
 50 55 60
 Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
 65 70 75 80
 Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln
 85 90 95
 Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
 100 105 110
 Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
 115 120 125
 Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
 130 135 140
 Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
 145 150 155 160
 Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
 165 170 175
 Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly
 180 185 190
 Gly Ser Gly Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln
 195 200 205

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Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
 210 215 220
 Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
 225 230 235 240
 Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
 245 250 255
 Ser Trp Glu Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
 260 265 270
 Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
 275 280 285
 Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
 290 295 300
 Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
 305 310 315 320
 Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
 325 330 335
 Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
 340 345 350
 Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
 355 360 365
 Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
 370 375 380
 Gly Gly Gly Gly Ser Gly Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser
 385 390 395 400
 Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg
 405 410 415
 Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
 420 425 430
 Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg
 435 440 445
 Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
 450 455 460
 Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe
 465 470 475 480
 Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys
 485 490 495
 Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr
 500 505 510
 Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser
 515 520 525
 Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
 530 535 540
 Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr
 545 550 555 560
 Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
 565 570 575
 Phe Leu Val Gly
 580

<210> 7

<211> 410

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..410

<223> /mol_type="protein"

/note="scFvEGFR-MHD2"

/organism="artificial sequences"

<400> 7

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu
 20 25 30
 Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
 35 40 45

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```

Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp
50 55 60
Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
65 70 75 80
Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Phe Thr
85 90 95
Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
100 105 110
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu Thr
115 120 125
Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr
130 135 140
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
145 150 155 160
Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser
165 170 175
Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly
180 185 190
Thr Asn Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
195 200 205
Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe
210 215 220
Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu
225 230 235 240
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp
245 250 255
Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Gly Ser
260 265 270
Leu Gly Gly Ser Gly Gly Ala Glu Leu Pro Pro Lys Val Ser Val Phe
275 280 285
Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu
290 295 300
Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp
305 310 315 320
Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val
325 330 335
Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser
340 345 350
Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr
355 360 365
Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser
370 375 380
Met Cys Val Pro Asp Gly Gly Ser Gly Gly Thr Gly Ser Glu
385 390 395 400
Phe Ala Ala Ala His His His His His
405 410

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<210> 8

<211> 413

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..413

<223> /mol_type="protein"

/note="MHD2-sCFVHER2"

/organism="artificial sequences"

<400> 8

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Ser Ala Gly Ala Gly Ser
20 25 30
Leu Gly Gly Ser Gly Gly Ala Glu Leu Pro Pro Lys Val Ser Val Phe
35 40 45
Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu
50 55 60

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Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp
65      70      75      80
Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val
      85      90      95
Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser
      100      105      110
Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr
      115      120      125
Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser
      130      135      140
Met Cys Val Pro Asp Gly Gly Gly Ser Gly Gly Thr Gly Ser Gly
145      150      155      160
Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
      165      170      175
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp
      180      185      190
Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
      195      200      205
Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser
      210      215      220
Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala
225      230      235      240
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
      245      250      255
Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly
      260      265      270
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
      275      280      285
Gly Gly Ser Gly Gly Gly Thr Gly Asp Ile Gln Met Thr Gln Ser Pro
      290      295      300
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
305      310      315      320
Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
      325      330      335
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser
      340      345      350
Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr
      355      360      365
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
      370      375      380
Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val
385      390      395      400
Glu Ile Lys Arg Ala Ala Ala His His His His His His
      405      410

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<210> 9
 <211> 653
 <212> PRT
 <213> artificial sequences

<220>
 <221> SOURCE
 <222> 1..653
 <223> /mol_type="protein"
 /note="scFVEGFR-MHD2-scFVHER2"
 /organism="artificial sequences"

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<400> 9
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1      5      10      15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu
      20      25      30
Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
      35      40      45
Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp
      50      55      60
Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
65      70      75      80

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```

Ser Gly Gly Asn Thr 85 Asp Tyr Asn Thr 90 Phe Thr Ser Arg Phe Thr 95
Ile Ser Arg Asp Asn Ser Lys Asn Thr 105 Leu Tyr Leu Gln Met Asn Ser 110
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu Thr 125
Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr 140
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly 160
145 Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser 175
Val Gly Asp Arg 180 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly 190
Thr Asn Ile 195 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu 205
Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe 220
Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu 240
225 Gln Pro Glu Asp Phe 245 Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp 255
Pro Thr Thr Phe 260 Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Gly Ser 270
Leu Gly Gly Ser Gly Gly Ala Glu Leu Pro Pro Lys Val Ser Val Phe 285
Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu 300
Ile 305 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp 320
Leu Arg Glu Gly Lys 325 Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val 335
Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser 350
Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr 365
Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser 380
Met 385 Cys Val Pro Asp Gly Gly Ser Gly Gly Gly Thr Gly Ser Gly 400
Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly 415
Gly Ser Leu Arg 420 Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp 430
Thr Tyr Ile 435 His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp 445
Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser 460
Val 465 Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala 480
Tyr Leu Gln Met Asn 485 Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr 495
Cys Ser Arg Trp 500 Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly 510
Gln Gly Thr 515 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly 525
Gly Gly Ser Gly Gly Gly Thr Gly Asp Ile Gln Met Thr Gln Ser Pro 540
Ser 545 Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg 560
Ala Ser Gln Asp Val 565 Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro 575
Gly Lys Ala Pro 580 Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser 590
Gly Val Pro 595 Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr 605
Leu Thr 610 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys 620

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Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val
625 630 635 640
Glu Ile Lys Arg Ala Ala Ala His His His His His His
645 650

<210> 10
<211> 648
<212> PRT
<213> artificial sequences

<220>
<221> SOURCE
<222> 1..648
<223> /mol_type="protein"
/note="MHD2-sCTNF"
/organism="artificial sequences"

<400> 10
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Ser Ala Gly Ala Gly Ser
20 25 30
Leu Gly Gly Ser Gly Gly Ala Glu Leu Pro Pro Lys Val Ser Val Phe
35 40 45
Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu
50 55 60
Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp
65 70 75 80
Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val
85 90 95
Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser
100 105 110
Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr
115 120 125
Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser
130 135 140
Met Cys Val Pro Asp Gly Gly Ser Gly Gly Thr Gly Ser Glu
145 150 155 160
Phe Met Arg Gly Ser His His His His His Gly Ser Ala Ser Ser
165 170 175
Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn
180 185 190
Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala
195 200 205
Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro
210 215 220
Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln
225 230 235 240
Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile
245 250 255
Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser
260 265 270
Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr
275 280 285
Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg
290 295 300
Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser
305 310 315 320
Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Ser
325 330 335
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
340 345 350
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
355 360 365
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
370 375 380
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
385 390 395 400

SEQ protocol Nachanmeldung 2013-03-22.txt

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
405 410 415
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
420 425 430
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
435 440 445
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
450 455 460
Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
465 470 475 480
Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Ser Ser
485 490 495
Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln
500 505 510
Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu
515 520 525
Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu
530 535 540
Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys
545 550 555 560
Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val
565 570 575
Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys
580 585 590
Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro
595 600 605
Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser
610 615 620
Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln
625 630 635 640
Val Tyr Phe Gly Ile Ile Ala Leu
645

<210> 11
<211> 888
<212> PRT
<213> artificial sequences

<220>
<221> SOURCE
<222> 1..888
<223> /mol_type="protein"
/note="SCFVEGFR-MHD2-sCTNF"
/organism="artificial sequences"

<400> 11
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu
20 25 30
Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
35 40 45
Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp
50 55 60
Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
65 70 75 80
Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Phe Thr
85 90 95
Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
100 105 110
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu Thr
115 120 125
Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr
130 135 140
Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
145 150 155 160
Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser
165 170 175

SEQ protocol Nachanmeldung 2013-03-22.txt

Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Gly
			180					185					190		
Thr	Asn	Ile	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu
		195					200					205			
Leu	Ile	Lys	Tyr	Ala	Ser	Glu	Ser	Ile	Ser	Gly	Val	Pro	Ser	Arg	Phe
	210					215					220				
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu
225					230					235					240
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Asn	Asn	Asn	Trp
			245						250					255	
Pro	Thr	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Gly	Ser
			260					265					270		
Leu	Gly	Gly	Ser	Gly	Gly	Ala	Glu	Leu	Pro	Pro	Lys	Val	Ser	Val	Phe
		275					280					285			
Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg	Lys	Ser	Lys	Leu
	290					295					300				
Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln	Ile	Gln	Val	Ser	Trp
305					310					315					320
Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val	Thr	Thr	Asp	Gln	Val
				325					330					335	
Gln	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	Thr	Ser
			340					345					350		
Thr	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Gly	Gln	Ser	Met	Phe	Thr
		355					360					365			
Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln	Gln	Asn	Ala	Ser	Ser
	370					375					380				
Met	Cys	Val	Pro	Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Thr	Gly	Ser	Glu
385					390					395					400
Phe	Met	Arg	Gly	Ser	His	His	His	His	His	Gly	Ser	Ala	Ser	Ser	
				405				410					415		
Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn
			420					425					430		
Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala
		435					440					445			
Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro
	450					455					460				
Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln
465					470					475					480
Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile
				485					490					495	
Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys	Ser
			500					505					510		
Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr
		515					520					525			
Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg
	530					535					540				
Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe	Ala	Glu	Ser
545					550					555					560
Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	Gly	Gly	Gly	Gly	Ser	Ser
				565					570					575	
Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro
			580					585					590		
Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu
		595					600					605			
Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser
	610					615					620				
Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly
625					630					635					640
Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala
				645					650					655	
Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Ser	Ala	Ile	Lys	Ser	Ser	Pro
			660					665					670		
Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr	Glu
		675					680					685			
Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg	Leu
	690					695					700				
Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe	Ala	Glu	Ser	Gly
705					710					715					720

SEQ protocol Nachanmeldung 2013-03-22.txt

Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Ser Ser
725 730 735
Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln
740 745 750
Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu
755 760 765
Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu
770 775 780
Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys
785 790 795 800
Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val
805 810 815
Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys
820 825 830
Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro
835 840 845
Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser
850 855 860
Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln
865 870 875 880
Val Tyr Phe Gly Ile Ile Ala Leu
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<210> 12

<211> 724

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..724

<223> /mol_type="protein"
/note="MHD2-sCTRAIL"
/organism="artificial sequences"

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Ala His Ser Leu Asp Asp Tyr Lys Asp Asp Asp Lys Glu Phe Ala
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Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe
35 40 45
Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe
50 55 60
Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val
65 70 75 80
Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser
85 90 95
Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser
100 105 110
Asp Trp Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly
115 120 125
Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro Asp Glu Phe
130 135 140
Thr Arg Gly Thr Ser Glu Thr Ile Ser Thr Val Gln Glu Lys Gln
145 150 155 160
Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala
165 170 175
Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
180 185 190
Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu
195 200 205
Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
210 215 220
Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Ile Tyr Ser Gln
225 230 235 240
Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
245 250 255

SEQ protocol Nachanmeldung 2013-03-22.txt

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
 260 265 270
 Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
 275 280 285
 Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
 290 295 300
 Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
 305 310 315 320
 Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly
 325 330 335
 Gly Ser Gly Gly Gly Ser Thr Ser Glu Thr Ile Ser Thr Val Gln
 340 345 350
 Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
 355 360 365
 Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
 370 375 380
 Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
 385 390 395 400
 Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
 405 410 415
 Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
 420 425 430
 Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
 435 440 445
 Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
 450 455 460
 Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
 465 470 475 480
 Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
 485 490 495
 Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
 500 505 510
 Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
 515 520 525
 Gly Gly Gly Gly Ser Gly Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser
 530 535 540
 Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg
 545 550 555 560
 Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
 565 570 575
 Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg
 580 585 590
 Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
 595 600 605
 Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe
 610 615 620
 Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys
 625 630 635 640
 Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr
 645 650 655
 Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser
 660 665 670
 Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
 675 680 685
 Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr
 690 695 700
 Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
 705 710 715 720
 Phe Leu Val Gly

<210> 13

<211> 978

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

SEQ protocol Nachanmeldung 2013-03-22.txt

<222> 1..978

<223> /mol_type="protein"
/note="SCFVEGFR-MHD2-SCTRAIL"
/organism="artificial sequences"

<400> 13

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Gly Ser Thr Gly Asp Tyr Lys Asp Asp Asp Lys Gly Gly Gly Gly
20      25      30
Ser Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly
35      40      45
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
50      55      60
Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ala
65      70      75      80
Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn
85      90      95
Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Phe Thr Ile Ser Arg Asp
100     105     110
Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
115     120     125
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr
130     135     140
Glu Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
145     150     155     160
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile
165     170     175
Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg
180     185     190
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His
195     200     205
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Lys Tyr
210     215     220
Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225     230     235     240
Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
245     250     255
Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Trp Pro Thr Thr Phe
260     265     270
Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu
275     280     285
Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly
290     295     300
Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro
305     310     315     320
Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser
325     330     335
Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro
340     345     350
Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp
355     360     365
Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr
370     375     380
Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro Asp Glu Phe Thr Arg
385     390     395     400
Gly Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn
405     410     415
Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His
420     425     430
Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser
435     440     445
Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser
450     455     460
Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu
465     470     475     480
Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr
485     490     495

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SEQ protocol Nachanmeldung 2013-03-22.txt

Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln
 500 505 510
 Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu
 515 520 525
 Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr
 530 535 540
 Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn
 545 550 555 560
 Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp
 565 570 575
 His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Ser
 580 585 590
 Gly Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys
 595 600 605
 Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val
 610 615 620
 Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser
 625 630 635 640
 Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp
 645 650 655
 Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg
 660 665 670
 Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser
 675 680 685
 Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn
 690 695 700
 Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
 705 710 715 720
 Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
 725 730 735
 Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
 740 745 750
 Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile
 755 760 765
 Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly
 770 775 780
 Gly Gly Ser Gly Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val
 785 790 795 800
 Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro
 805 810 815
 Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
 820 825 830
 Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
 835 840 845
 Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
 850 855 860
 His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
 865 870 875 880
 Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
 885 890 895
 Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
 900 905 910
 Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
 915 920 925
 Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
 930 935 940
 Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
 945 950 955 960
 His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
 965 970 975
 val Gly

<210> 14
 <211> 1217
 <212> PRT
 <213> artificial sequences

SEQ protocol Nachanmeldung 2013-03-22.txt

<220>

<221> SOURCE

<222> 1..1217

<223> /mol_type="protein"

/note="sCDbEpCAMxEGFR-MHD2-sCTRAIL"

/organism="artificial sequences"

<400> 14

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Gly Ser Thr Gly Asp Tyr Lys Asp Asp Asp Lys Gly Gly Gly Gly
20      25      30
Ser Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly
35      40      45
Pro Gly Leu Val Gln Pro Gly Gly Ser Val Arg Ile Ser Cys Ala Ala
50      55      60
Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala
65      70      75      80
Pro Gly Lys Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly
85      90      95
Glu Ser Thr Tyr Ala Asp Ser Phe Lys Gly Arg Phe Thr Phe Ser Leu
100     105     110
Asp Thr Ser Ala Ser Ala Ala Tyr Leu Gln Ile Asn Ser Leu Arg Ala
115     120     125
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Phe Ala Ile Lys Gly Asp
130     135     140
Tyr Trp Gly Gln Gly Thr Leu Leu Thr Val Ser Gly Gly Gly Gly
145     150     155     160
Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val
165     170     175
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr
180     185     190
Asn Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
195     200     205
Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser
210     215     220
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
225     230     235     240
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro
245     250     255
Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly
260     265     270
Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Glu Val Gln Leu
275     280     285
Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
290     295     300
Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp
305     310     315     320
Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
325     330     335
Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Phe Thr
340     345     350
Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
355     360     365
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu Thr
370     375     380
Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr
385     390     395     400
Val Ser Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
405     410     415
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
420     425     430
Ser Thr Lys Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp
435     440     445
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gln Met
450     455     460
Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Ser Ser Gly Ser
465     470     475     480

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SEQ protocol Nachanmeldung 2013-03-22.txt

Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe
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Ala	Thr	Tyr	Tyr	Cys	Ala	Gln	Asn	Leu	Glu	Ile	Pro	Arg	Thr	Phe	Gly
			500					505					510		
Gln	Gly	Thr	Lys	Val	Glu	Leu	Lys	Arg	Ala	Ala	Ala	Ala	Glu	Leu	Pro
		515					520					525			
Pro	Lys	Val	Ser	Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn
	530					535					540				
Pro	Arg	Lys	Ser	Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg
545					550					555					560
Gln	Ile	Gln	Val	Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly
				565					570					575	
Val	Thr	Thr	Asp	Gln	Val	Gln	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr
			580					585					590		
Thr	Tyr	Lys	Val	Thr	Ser	Thr	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu
		595					600					605			
Gly	Gln	Ser	Met	Phe	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe
							615				620				
Gln	Gln	Asn	Ala	Ser	Ser	Met	Cys	Val	Pro	Asp	Glu	Phe	Thr	Arg	Gly
625					630					635					640
Thr	Ser	Glu	Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile
				645					650					655	
Ser	Pro	Leu	Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala	His	Ile
			660					665					670		
Thr	Gly	Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys
			675				680					685			
Asn	Glu	Lys	Ala	Leu	Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser	Ser	Arg
	690					695					700				
Ser	Gly	His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu
705					710					715					720
Val	Ile	His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe
				725					730					735	
Arg	Phe	Gln	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	
			740				745						750		
Val	Gln	Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu
		755					760					765			
Met	Lys	Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly
	770					775					780				
Leu	Tyr	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp
785					790					795					800
Arg	Ile	Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His
				805					810					815	
Glu	Ala	Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly	Gly	Gly	Gly	Ser	Gly
			820					825					830		
Gly	Gly	Ser	Thr	Ser	Glu	Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu	Lys	Gln
		835					840					845			
Gln	Asn	Ile	Ser	Pro	Leu	Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala
	850					855					860				
Ala	His	Ile	Thr	Gly	Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro
865					870					875					880
Asn	Ser	Lys	Asn	Glu	Lys	Ala	Leu	Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu
				885					890					895	
Ser	Ser	Arg	Ser	Gly	His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn
			900					905					910		
Gly	Glu	Leu	Val	Ile	His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln
		915					920					925			
Thr	Tyr	Phe	Arg	Phe	Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp
						935					940				
Lys	Gln	Met	Val	Gln	Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro
945					950					955					960
Ile	Leu	Leu	Met	Lys	Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala
				965					970					975	
Glu	Tyr	Gly	Leu	Tyr	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys
			980					985					990		
Glu	Asn	Asp	Arg	Ile	Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp
		995						1000				1005			
Met	Asp	His	Glu	Ala	Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly	Gly	Gly
	1010					1015					1020				

SEQ protocol Nachanmeldung 2013-03-22.txt

Gly Ser Gly Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln
1025 1030 1035 1040
Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
1045 1050 1055
Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1060 1065 1070
Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
1075 1080 1085
Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
1090 1095 1100
Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
1105 1110 1115 1120
Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
1125 1130 1135
Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
1140 1145 1150
Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
1155 1160 1165
Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
1170 1175 1180
Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
1185 1190 1195 1200
Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
1205 1210 1215
Gly

<210> 15
<211> 405
<212> PRT
<213> artificial sequences

<220>
<221> SOURCE
<222> 1..405
<223> /mol_type="protein"
/note="scFvEGFR-EHD2"
/organism="artificial sequences"

<400> 15
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu
20 25 30
Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
35 40 45
Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp
50 55 60
Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
65 70 75 80
Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Phe Thr
85 90 95
Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
100 105 110
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu Thr
115 120 125
Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr
130 135 140
Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
145 150 155 160
Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser
165 170 175
Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly
180 185 190
Thr Asn Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
195 200 205
Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe
210 215 220

SEQ protocol Nachanmeldung 2013-03-22.txt

Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu
 225 230 235 240
 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp
 245 250 255
 Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Gly Ser
 260 265 270
 Leu Gly Gly Ser Gly Gly Asp Phe Thr Pro Pro Thr Val Lys Ile Leu
 275 280 285
 Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu
 290 295 300
 Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp
 305 310 315 320
 Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr
 325 330 335
 Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser
 340 345 350
 Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr
 355 360 365
 Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn
 370 375 380
 Gly Gly Gly Ser Gly Gly Thr Gly Ser Glu Phe Ala Ala Ala His
 385 390 395 400
 His His His His His
 405

<210> 16
 <211> 731
 <212> PRT
 <213> artificial sequences

<220>
 <221> SOURCE
 <222> 1..731
 <223> /mol_type="protein"
 /note="EHD2-sCTRAIL"
 /organism="artificial sequences"

<400> 16
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Tyr Lys Asp Asp Asp Lys Gly Gly Gly Gly
 20 25 30
 Ser Ala Ala Gln Pro Ala Asp Phe Thr Pro Pro Thr Val Lys Ile Leu
 35 40 45
 Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu
 50 55 60
 Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp
 65 70 75 80
 Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr
 85 90 95
 Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser
 100 105 110
 Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr
 115 120 125
 Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn
 130 135 140
 Gly Gly Ser Gly Gly Glu Phe Thr Arg Gly Thr Ser Glu Glu Thr Ile
 145 150 155 160
 Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu
 165 170 175
 Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg
 180 185 190
 Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly
 195 200 205
 Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu
 210 215 220
 Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly
 225 230 235 240

SEQ protocol Nachanmeldung 2013-03-22.txt

Phe Tyr Tyr Ile Tyr 245 Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile 255
 Lys Glu Asn Thr Lys 260 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys 270
 Tyr Thr Ser Tyr 275 Pro Asp Pro Ile Leu Leu Met Lys Ser 285 Ala Arg Asn
 Ser Cys Trp Ser Lys 290 Asp Ala Glu Tyr Gly Leu Tyr 300 Ser Ile Tyr Gln
 Gly Gly Ile Phe 310 Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val 320
 Thr Asn Glu His 325 Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly 335
 Ala Phe Leu Val 340 Gly Gly Gly Gly Ser Gly Gly Gly Ser Thr Ser Glu 350
 Glu Thr Ile Ser 355 Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu 365
 Val Arg Glu Arg Gly 370 Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr 380
 Arg Gly Arg Ser Asn 390 Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys 400
 Ala Leu Gly Arg Lys 405 Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His 415
 Ser Phe Leu Ser 420 Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His 430
 Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln 445
 Glu Glu Ile Lys Glu Asn Thr Lys 450 Asn Asp Lys Gln Met Val Gln Tyr 460
 Ile Tyr Lys Tyr Thr 470 Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser 480
 Ala Arg Asn Ser Cys 485 Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser 495
 Ile Tyr Gln Gly 500 Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe 510
 Val Ser Val Thr 515 Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser 525
 Phe Phe Gly Ala Phe 530 Leu Val Gly Gly Gly Gly Ser Gly Gly Gly Ser 540
 Thr Ser Glu Glu Thr 550 Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile 560
 Ser Pro Leu Val 565 Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile 575
 Thr Gly Thr Arg 580 Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys 590
 Asn Glu Lys Ala 595 Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg 605
 Ser Gly His Ser Phe 610 Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu 620
 Val Ile His Glu Lys 615 Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe 640
 Arg Phe Gln Glu Glu 630 Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met 655
 Val Gln Tyr Ile Tyr 645 Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu 670
 Met Lys Ser Ala 675 Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly 685
 Leu Tyr Ser Ile Tyr 690 Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp 700
 Arg Ile Phe Val Ser 710 Val Thr Asn Glu His Leu Ile Asp Met Asp His 720
 Glu Ala Ser Phe Phe 725 Gly Ala Phe Leu Val Gly 730

<210> 17

<211> 983

<212> PRT

<213> artificial sequences

SEQ protocol Nachanmeldung 2013-03-22.txt

<220>

<221> SOURCE

<222> 1..983

<223> /mol_type="protein"
/note="scFVEGFR-EHD2-scTRAIL"
/organism="artificial sequences"

<400> 17

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1      5      10      15
Gly Ser Thr Gly Asp Tyr Lys Asp Asp Asp Lys Gly Gly Gly Gly
20      25      30
Ser Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly
35      40      45
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
50      55      60
Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ala
65      70      75      80
Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn
85      90      95
Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Phe Thr Ile Ser Arg Asp
100     105     110
Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
115     120     125
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr
130     135     140
Glu Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
145     150     155     160
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
165     170     175
Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg
180     185     190
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His
195     200     205
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys Tyr
210     215     220
Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225     230     235     240
Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
245     250     255
Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe
260     265     270
Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Gly Gly Ser
275     280     285
Gly Gly Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys
290     295     300
Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val
305     310     315     320
Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly
325     330     335
Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly
340     345     350
Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp
355     360     365
Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr
370     375     380
Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn Gly Gly Ser Gly
385     390     395     400
Gly Glu Phe Thr Arg Gly Thr Ser Glu Glu Thr Ile Ser Thr Val Gln
405     410     415
Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
420     425     430
Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
435     440     445
Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
450     455     460
Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
465     470     475     480

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SEQ protocol Nachanmeldung 2013-03-22.txt

Leu Arg Asn Gly Glu 485 Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile 495
 Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr 510
 Lys Asn Asp 515 Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr 525
 Pro Asp 530 Pro Ile Leu Leu Met 535 Lys Ser Ala Arg Asn 540 Ser Cys Trp Ser
 Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe 560
 545 Glu Leu Lys Glu Asn 565 Asp Arg Ile Phe Val Ser Val Thr Asn Glu His 575
 Leu Ile Asp Met 580 Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val 590
 Gly Gly Gly 595 Gly Ser Gly Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser 605
 Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg 620
 Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser 640
 625 Asn Thr Leu Ser Ser 645 Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg 655
 Lys Ile Asn Ser 660 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser 670
 Asn Leu His 675 Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe 685
 Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys 700
 690 Glu Asn Thr Lys Asn Asp 710 Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr 720
 705 Thr Ser Tyr Pro Asp 725 Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser 735
 Cys Trp Ser Lys 740 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly 750
 Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr 765
 Asn Glu His 770 Leu Ile Asp Met 775 Asp His Glu Ala Ser Phe Phe Gly Ala 780
 Phe 785 Leu Val Gly Gly Gly 790 Gly Ser Gly Gly Gly Ser Thr Ser Glu Glu 800
 Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val 815
 Arg Glu Arg Gly 820 Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg 830
 Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala 845
 Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser 860
 Phe 865 Leu Ser Asn Leu His 870 Leu Arg Asn Gly Glu Leu Val Ile His Glu 880
 Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu 895
 885 Glu Ile Lys Glu Asn Thr Lys Asn Asp 905 Lys Gln Met Val Gln Tyr Ile 910
 Tyr Lys Tyr Thr Ser Tyr Pro Asp 920 Pro Ile Leu Leu Met Lys Ser Ala 925
 Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile 940
 930 Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val 960
 945 Ser Val Thr Asn Glu 965 His Leu Ile Asp Met 970 Asp His Glu Ala Ser Phe 975
 Phe Gly Ala Phe 980 Leu Val Gly

<210> 18
 <211> 5
 <212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..5

<223> /mol_type="protein"
/note="peptide linker 1"
/organism="artificial sequences"

<400> 18

Gly Gly Gly Gly Ser
1 5

<210> 19

<211> 10

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..10

<223> /mol_type="protein"
/note="peptide linker 2"
/organism="artificial sequences"

<400> 19

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 20

<211> 15

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..15

<223> /mol_type="protein"
/note="peptide linker 3"
/organism="artificial sequences"

<400> 20

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 21

<211> 8

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..8

<223> /mol_type="protein"
/note="peptide linker 4"
/organism="artificial sequences"

<400> 21

Gly Ser Leu Gly Gly Ser Gly Gly
1 5

<210> 22

<211> 8

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

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<222> 1..8
<223> /mol_type="protein"
      /note="peptide linker 5"
      /organism="artificial sequences"

<400> 22
Gly Gly Gly Ser Gly Gly Gly Thr
1           5

<210> 23
<211> 10
<212> PRT
<213> artificial sequences

<220>
<221> SOURCE
<222> 1..10
<223> /mol_type="protein"
      /note="peptide linker 6"
      /organism="artificial sequences"

<400> 23
Gly Gly Gly Ser Gly Gly Gly Thr Gly Ser
1           5                10

<210> 24
<211> 12
<212> PRT
<213> artificial sequences

<220>
<221> SOURCE
<222> 1..12
<223> /mol_type="protein"
      /note="peptide linker 7"
      /organism="artificial sequences"

<400> 24
Gly Gly Gly Ser Gly Gly Gly Thr Gly Ser Gly Gly
1           5                10

<210> 25
<211> 8
<212> PRT
<213> artificial sequences

<220>
<221> SOURCE
<222> 1..8
<223> /mol_type="protein"
      /note="peptide linker 8"
      /organism="artificial sequences"

<400> 25
Gly Gly Gly Ser Gly Gly Gly Ser
1           5

<210> 26
<211> 5
<212> PRT
<213> artificial sequences

<220>
<221> SOURCE
<222> 1..5
<223> /mol_type="protein"
      /note="peptide linker 9"
      /organism="artificial sequences"

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<400> 26

Glu Phe Thr Arg Gly
1 5

<210> 27

<211> 3

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..3

<223> /mol_type="protein"
/note="peptide linker 10"
/organism="artificial sequences"

<400> 27

Ala Ala Ala
1

<210> 28

<211> 405

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..405

<223> /mol_type="protein"
/note="Anti-CEA scFv-EHD2"
/organism="artificial sequences"

<400> 28

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu
20 25 30
Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Thr Ser Val Lys Leu
35 40 45
Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser Tyr Met His Trp
50 55 60
Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp
65 70 75 80
Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Gln Gly Lys Ala
85 90 95
Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu Ser
100 105 110
Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Asn Glu Gly Thr
115 120 125
Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
130 135 140
Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
145 150 155 160
Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala
165 170 175
Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val
180 185 190
Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu
195 200 205
Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe
210 215 220
Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met
225 230 235 240
Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr
245 250 255
Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Gly Ser
260 265 270

SEQ protocol Nachanmeldung 2013-03-22.txt

Leu Gly Gly Ser Gly Gly Asp Phe Thr Pro Pro Thr Val Lys Ile Leu
 275 280 285
 Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu
 290 295 300
 Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp
 305 310 315 320
 Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr
 325 330 335
 Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser
 340 345 350
 Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr
 355 360 365
 Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn
 370 375 380
 Gly Gly Gly Ser Gly Gly Gly Thr Gly Ser Glu Phe Ala Ala Ala His
 385 390 395 400
 His His His His His
 405

<210> 29
 <211> 391
 <212> PRT
 <213> artificial sequences

<220>
 <221> SOURCE
 <222> 1..391
 <223> /mol_type="protein"
 /note="Anti-HER2 scFv-EHD2"
 /organism="artificial sequences"

<400> 29
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
 20 25 30
 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn
 35 40 45
 Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly
 50 55 60
 Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
 65 70 75 80
 Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
 85 90 95
 Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 100 105 110
 Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp
 115 120 125
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
 130 135 140
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
 145 150 155 160
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 165 170 175
 Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln
 180 185 190
 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe
 195 200 205
 Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr
 210 215 220
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 225 230 235 240
 Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly
 245 250 255
 Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Gly Gly Ser Gly Gly Asp
 260 265 270
 Phe Thr Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly
 275 280 285

SEQ protocol Nachanmeldung 2013-03-22.txt

Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr
 290 295 300
 Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met
 305 310 315 320
 Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala
 325 330 335
 Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp
 340 345 350
 Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp
 355 360 365
 Ser Thr Lys Lys Cys Ala Asp Ser Asn Gly Gly Ser Gly Gly Ala Ser
 370 375 380
 Ser His His His His His His
 385 390

<210> 30
 <211> 393
 <212> PRT
 <213> artificial sequences

<220>
 <221> SOURCE
 <222> 1..393
 <223> /mol_type="protein"
 /note="Anti-HER3 scFv-EHD2"
 /organism="artificial sequences"

<400> 30
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
 20 25 30
 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 35 40 45
 Phe Ser His Tyr Val Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly
 50 55 60
 Leu Glu Trp Val Ser Ser Ile Ser Ser Ser Gly Gly Trp Thr Leu Tyr
 65 70 75 80
 Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 85 90 95
 Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 100 105 110
 Val Tyr Tyr Cys Thr Arg Gly Leu Lys Met Ala Thr Ile Phe Asp Tyr
 115 120 125
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 130 135 140
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln
 145 150 155 160
 Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys
 165 170 175
 Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr Asn Val Val Ser Trp Tyr
 180 185 190
 Gln Gln His Pro Gly Lys Ala Pro Lys Leu Ile Ile Tyr Glu Val Ser
 195 200 205
 Gln Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly
 210 215 220
 Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Thr Glu Asp Glu Ala
 225 230 235 240
 Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Ser Ser Ile Phe Val Ile Phe
 245 250 255
 Gly Gly Gly Thr Lys Val Thr Val Leu Ala Ala Ala Gly Gly Ser Gly
 260 265 270
 Gly Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp
 275 280 285
 Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser
 290 295 300
 Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln
 305 310 315 320

SEQ protocol Nachanmeldung 2013-03-22.txt

Val Met Asp Val Asp 325 Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu 335
 Leu Ala Ser Thr Gln 340 Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu 350
 Ser Asp Arg Thr Tyr Thr Cys 360 Val Thr Tyr Gln Gly His Thr Phe 365
 Glu Asp Ser Thr Lys Lys Cys 375 Ala Asp Ser Asn Gly Gly Ser Gly Gly 380
 Ala Ser Ser His His His His His His
 385 390

<210> 31
 <211> 645
 <212> PRT
 <213> artificial sequences

<220>
 <221> SOURCE
 <222> 1..645
 <223> /mol_type="protein"
 /note="Anti-CEAXCD3 scDb-EHD2"
 /organism="artificial sequences"

<400> 31
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro 15
 1 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu 30
 20 Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Thr Ser Val Lys Leu 45
 35 Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser Tyr Met His Trp 60
 50 Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp 80
 65 70 Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Gln Gly Lys Ala 95
 85 Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu Ser 110
 100 Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Asn Glu Gly Thr 125
 115 Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val 140
 130 Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser 160
 145 150 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys 175
 165 Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys 190
 180 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu Glu 205
 195 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr 220
 210 Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr 240
 225 230 Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys 255
 245 Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly 270
 260 Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val 285
 275 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser 300
 290 Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly 320
 305 310 Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr 335
 325 Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val Asp Lys Ser Lys 350
 340 345

SEQ protocol Nachanmeldung 2013-03-22.txt

Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 355 360 365
 Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr
 370 375 380
 Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
 385 390 395 400
 Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala
 405 410 415
 Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val
 420 425 430
 Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu
 435 440 445
 Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe
 450 455 460
 Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met
 465 470 475 480
 Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr
 485 490 495
 Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Gly Ser
 500 505 510
 Leu Gly Gly Ser Gly Gly Asp Phe Thr Pro Pro Thr Val Lys Ile Leu
 515 520 525
 Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu
 530 535 540
 Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp
 545 550 555 560
 Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr
 565 570 575
 Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser
 580 585 590
 Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr
 595 600 605
 Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn
 610 615 620
 Gly Gly Gly Ser Gly Gly Gly Thr Gly Ser Glu Phe Ala Ala Ala His
 625 630 635 640
 His His His His His
 645

<210> 32
 <211> 394
 <212> PRT
 <213> artificial sequences

<220>
 <221> SOURCE
 <222> 1..394
 <223> /mol_type="protein"
 /note="Anti-EGFR scFv-L3-EHD2"
 /organism="artificial sequences"

<400> 32
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Gln Val Gln Leu Lys Gln Ser Gly Ala Glu Leu Val
 20 25 30
 Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Thr
 35 40 45
 Phe Thr Glu Asn Ile Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly
 50 55 60
 Leu Glu Trp Ile Gly Trp Phe His Pro Gly Ser Gly Ser Ile Lys Tyr
 65 70 75 80
 Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
 85 90 95
 Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala
 100 105 110
 Val Tyr Phe Cys Ala Arg His Gly Gly Thr Gly Arg Gly Ala Met Asp
 115 120 125

SEQ protocol Nachanmeldung 2013-03-22.txt

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Cys Gly
130 135 140
Ser Gly Gly Gly Gly Ser Gly Gly Ser Ala Gln Ile Leu Met Thr Gln
145 150 155 160
Ser Pro Ala Ser Ser Val Val Ser Leu Gly Gln Arg Ala Thr Ile Ser
165 170 175
Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ala Tyr Ser Tyr Met His
180 185 190
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu
195 200 205
Ala Ser Asn Leu Glu Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly
210 215 220
Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp
225 230 235 240
Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Tyr Thr Phe
245 250 255
Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Gly Ser
260 265 270
Gly Gly Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys
275 280 285
Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val
290 295 300
Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly
305 310 315 320
Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly
325 330 335
Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp
340 345 350
Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr
355 360 365
Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn Gly Gly Ser Gly
370 375 380
Gly Ala Ser Ser His His His His His
385 390

<210> 33

<211> 645

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..645

<223> /mol_type="protein"
/note="Anti-EGFR scFv-L3-EHD2-scFv"
/organism="artificial sequences"

<400> 33

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Gln Val Gln Leu Lys Gln Ser Gly Ala Glu Leu Val
20 25 30
Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Thr
35 40 45
Phe Thr Glu Asn Ile Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly
50 55 60
Leu Glu Trp Ile Gly Trp Phe His Pro Gly Ser Gly Ser Ile Lys Tyr
65 70 75 80
Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
85 90 95
Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala
100 105 110
Val Tyr Phe Cys Ala Arg His Gly Gly Thr Gly Arg Gly Ala Met Asp
115 120 125
Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Cys Gly
130 135 140
Ser Gly Gly Gly Gly Ser Gly Gly Ser Ala Gln Ile Leu Met Thr Gln
145 150 155 160

SEQ protocol Nachanmeldung 2013-03-22.txt

Ser	Pro	Ala	Ser	Ser	Val	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser
				165					170					175	
Cys	Arg	Ala	Ser	Lys	Ser	Val	Ser	Thr	Ser	Ala	Tyr	Ser	Tyr	Met	His
			180					185					190		
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Leu
		195				200						205			
Ala	Ser	Asn	Leu	Glu	Ser	Gly	Val	Pro	Pro	Arg	Phe	Ser	Gly	Ser	Gly
	210					215					220				
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Glu	Asp
225					230				235						240
Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Ser	Arg	Glu	Leu	Pro	Tyr	Thr	Phe
				245					250					255	
Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Gly	Gly	Ser
			260					265					270		
Gly	Gly	Asp	Phe	Thr	Pro	Pro	Thr	Val	Lys	Ile	Leu	Gln	Ser	Ser	Cys
		275					280					285			
Asp	Gly	Gly	Gly	His	Phe	Pro	Pro	Thr	Ile	Gln	Leu	Leu	Cys	Leu	Val
290						295					300				
Ser	Gly	Tyr	Thr	Pro	Gly	Thr	Ile	Asn	Ile	Thr	Trp	Leu	Glu	Asp	Gly
305					310					315					320
Gln	Val	Met	Asp	Val	Asp	Leu	Ser	Thr	Ala	Ser	Thr	Thr	Gln	Glu	Gly
				325					330					335	
Glu	Leu	Ala	Ser	Thr	Gln	Ser	Glu	Leu	Thr	Leu	Ser	Gln	Lys	His	Trp
			340					345					350		
Leu	Ser	Asp	Arg	Thr	Tyr	Thr	Cys	Gln	Val	Thr	Tyr	Gln	Gly	His	Thr
		355					360					365			
Phe	Glu	Asp	Ser	Thr	Lys	Lys	Cys	Ala	Asp	Ser	Asn	Gly	Gly	Ser	Gly
	370					375					380				
Gly	Ala	Ser	Ser	Glu	Phe	Gln	Val	Gln	Leu	Lys	Gln	Ser	Gly	Ala	Glu
385					390					395					400
Leu	Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Leu	Ser	Cys	Lys	Thr	Ser	Gly
				405					410					415	
Tyr	Thr	Phe	Thr	Glu	Asn	Ile	Ile	His	Trp	Val	Lys	Gln	Arg	Ser	Gly
			420					425					430		
Gln	Gly	Leu	Glu	Trp	Ile	Gly	Trp	Phe	His	Pro	Gly	Ser	Gly	Ser	Ile
		435					440					445			
Lys	Tyr	Asn	Glu	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys
	450					455					460				
Ser	Ser	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	Arg	Leu	Thr	Ser	Glu	Asp
465					470					475					480
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	His	Gly	Gly	Thr	Gly	Arg	Gly	Ala
				485					490					495	
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Gly	Gly
			500					505					510		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Gln	Ile	Leu	Met
		515					520					525			
Thr	Gln	Ser	Pro	Ala	Ser	Ser	Val	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr
	530					535					540				
Ile	Ser	Cys	Arg	Ala	Ser	Lys	Ser	Val	Ser	Thr	Ser	Ala	Tyr	Ser	Tyr
545					550					555					560
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile
				565					570					575	
Tyr	Leu	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Val	Pro	Pro	Arg	Phe	Ser	Gly
			580					585					590		
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Glu
		595					600					605			
Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Ser	Arg	Glu	Leu	Pro	Tyr
	610					615					620				
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	His
625					630					635					640
His	His	His	His	His											
				645											

<210> 34
 <211> 652
 <212> PRT
 <213> artificial sequences

SEQ protocol Nachanmeldung 2013-03-22.txt

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<220>
<221> SOURCE
<222> 1..652
<223> /mol_type="protein"
      /note="MHD2-sCTNFR2"
      /organism="artificial sequences"

<400> 34
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1      5      10      15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Gly Gly Gly Ala Ala Ala
20      25      30
His His His His His His Gly Gly Thr Gly Gly Gly Gly Ser Gly Gly
35      40      45
Lys Leu Gly Gly Ser Gly Gly Ala Glu Leu Pro Pro Lys Val Ser Val
50      55      60
Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys
65      70      75      80
Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser
85      90      95
Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln
100      105      110
Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr
115      120      125
Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe
130      135      140
Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser
145      150      155      160
Ser Met Cys Val Pro Asp Gly Gly Gly Ser Gly Gly Gly Thr Gly Ser
165      170      175
Glu Phe Leu Ala Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
180      185      190
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
195      200      205
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
210      215      220
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
225      230      235      240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
245      250      255
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
260      265      270
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
275      280      285
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
290      295      300
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asn
305      310      315      320
Phe Arg Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly
325      330      335
Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
340      345      350
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
355      360      365
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
370      375      380
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
385      390      395      400
Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
405      410      415
Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
420      425      430
Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
435      440      445
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
450      455      460
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asn Phe
465      470      475      480

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Arg Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly
485 490 495
Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val
500 505 510
Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala
515 520 525
Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val
530 535 540
Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys
545 550 555 560
Gly Gln Gly Cys Pro Ser Thr His Val Leu Thr His Thr Ile Ser
565 570 575
Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile
580 585 590
Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro
595 600 605
Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly
610 615 620
Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asn Phe Arg
625 630 635 640
Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
645 650

<210> 35
<211> 647
<212> PRT
<213> artificial sequences

<220>
<221> SOURCE
<222> 1..647
<223> /mol_type="protein"
/note="EHD2-sCTNFR2-L16aa"
/organism="artificial sequences"

<400> 35
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Gly Gly Gly Ala Ala Ala
20 25 30
His His His His His His Gly Gly Thr Gly Gly Gly Gly Ser Gly Gly
35 40 45
Lys Leu Gly Gly Ser Gly Gly Asp Phe Thr Pro Pro Thr Val Lys Ile
50 55 60
Leu Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln
65 70 75 80
Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr
85 90 95
Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser
100 105 110
Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu
115 120 125
Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr
130 135 140
Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser
145 150 155 160
Asn Gly Gly Gly Ser Gly Gly Gly Thr Gly Ser Glu Phe Leu Ala Ser
165 170 175
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
180 185 190
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
195 200 205
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
210 215 220
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
225 230 235 240
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
245 250 255

SEQ protocol Nachanmeldung 2013-03-22.txt

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Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
260 265 270
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
275 280 285
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
290 295 300
Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asn Phe Arg Glu Ser Gly
305 310 315 320
Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Ser Ser
325 330 335
Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln
340 345 350
Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu
355 360 365
Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu
370 375 380
Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys
385 390 395 400
Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val
405 410 415
Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys
420 425 430
Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro
435 440 445
Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser
450 455 460
Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asn Phe Arg Glu Ser Gly Gln
465 470 475 480
Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Ser Ser Arg
485 490 495
Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala
500 505 510
Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala
515 520 525
Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly
530 535 540
Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro
545 550 555 560
Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser
565 570 575
Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln
580 585 590
Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile
595 600 605
Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala
610 615 620
Glu Ile Asn Arg Pro Asp Tyr Leu Asn Phe Arg Glu Ser Gly Gln Val
625 630 635 640
Tyr Phe Gly Ile Ile Ala Leu
645

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<210> 36

<211> 660

<212> PRT

<213> artificial sequences

<220>

<221> SOURCE

<222> 1..660

<223> /mol_type="protein"
/note="EHD2-sCTNFR2-L28aa"
/organism="artificial sequences"

<400> 36

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Gly Gly Gly Ala Ala Ala
20 25 30

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SEQ protocol Nachanmeldung 2013-03-22.txt

His	His	His	His	His	His	Gly	Gly	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly
		35				40					45				
Lys	Leu	Gly	Gly	Ser	Gly	Gly	Asp	Phe	Thr	Pro	Pro	Thr	Val	Lys	Ile
	50				55					60					
Leu	Gln	Ser	Ser	Cys	Asp	Gly	Gly	Gly	His	Phe	Pro	Pro	Thr	Ile	Gln
65				70					75						80
Leu	Leu	Cys	Leu	Val	Ser	Gly	Tyr	Thr	Pro	Gly	Thr	Ile	Asn	Ile	Thr
				85					90					95	
Trp	Leu	Glu	Asp	Gly	Gln	Val	Met	Asp	Val	Asp	Leu	Ser	Thr	Ala	Ser
			100					105						110	
Thr	Thr	Gln	Glu	Gly	Glu	Leu	Ala	Ser	Thr	Gln	Ser	Glu	Leu	Thr	Leu
		115					120					125			
Ser	Gln	Lys	His	Trp	Leu	Ser	Asp	Arg	Thr	Tyr	Thr	Cys	Gln	Val	Thr
	130				135						140				
Tyr	Gln	Gly	His	Thr	Phe	Glu	Asp	Ser	Thr	Lys	Lys	Cys	Ala	Asp	Ser
145					150					155					160
Asn	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly
				165					170					175	
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Glu	Phe	Leu	Ala	Ser	Ser	Arg	Thr
			180					185						190	
Pro	Ser	Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro	Gln	Ala	Glu
		195					200					205			
Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn
	210				215						220				
Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser	Glu	Gly	Leu
225				230					235						240
Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser
				245					250					255	
Thr	His	Val	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	
			260				265					270			
Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg
		275					280					285			
Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr
	290				295						300				
Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu
305					310					315					320
Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asn	Phe	Arg	Glu	Ser	Gly	Gln	Val	Tyr
				325					330					335	
Phe	Gly	Ile	Ile	Ala	Leu	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Arg	Thr	Pro
			340					345					350		
Ser	Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly
		355					360					365			
Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly
	370				375						380				
Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr
385				390						395					400
Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr
				405					410					415	
His	Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln
			420					425					430		
Thr	Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu
		435					440					445			
Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu
	450					455					460				
Gly	Gly	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile
465				470					475						480
Asn	Arg	Pro	Asp	Tyr	Leu	Asn	Phe	Arg	Glu	Ser	Gly	Gln	Val	Tyr	Phe
				485					490					495	
Gly	Ile	Ile	Ala	Leu	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Arg	Thr	Pro	Ser
			500					505					510		
Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln
		515					520					525			
Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val
	530					535					540				
Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu
545					550					555					560
Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His
				565					570					575	

SEQ protocol Nachanmeldung 2013-03-22.txt

Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr
			580					585					590		
Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr
		595					600					605			
Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly
	610					615					620				
Gly	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn
625					630					635					640
Arg	Pro	Asp	Tyr	Leu	Asn	Phe	Arg	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly
				645					650					655	
Ile	Ile	Ala	Leu												
			660												