

SEQUENCE LISTING

<110> HANALL BIOPHARMA CO., LTD.

<120> ANTIBODY BINDING TO FCEN FOR TREATING AUTOIMMUNE DISEASES

<130> PF-B1783

<140> PCT/KR2015/004424

<141> 2015-04-30

<150> 61/986,742

<151> 2014-04-30

<160> 44

<170> PATENTIN VERSION 3.2

<210> 1

<211> 363

<212> DNA

<213> ARTIFICIAL

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<223> HV OF HL161A

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120

CCCGGCAAGG GCCTGGAATG GGTGTCCGTG ATCTCCGGCT CCGGCGGCTC CACCTACTAC
180

GCCGACTCTG TGAAGGGCCG GTTCACCATC TCCCGGGACA ACTCCAAGAA CACCCTGTAC
240

CTGCAGATGA ACTCCCTGCG GGCCGAGGAC ACCGCCGTGT ACTACTGCGC CAAGACCCCC
300

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TCC

363

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GLU VAL GLN LEU LEU GLU SER GLY GLY GLY LEU VAL GLN PRO GLY GLY
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SER LEU ARG LEU SER CYS ALA ALA SER GLU PHE THR PHE GLY SER CYS
20 25 30

VAL MET THR TRP VAL ARG GLN ALA PRO GLY LYS GLY LEU GLU TRP VAL
35 40 45

SER VAL ILE SER GLY SER GLY GLY SER THR TYR TYR ALA ASP SER VAL
50 55 60

LYS GLY ARG PHE THR ILE SER ARG ASP ASN SER LYS ASN THR LEU TYR
65 70 75 80

LEU GLN MET ASN SER LEU ARG ALA GLU ASP THR ALA VAL TYR TYR CYS
85 90 95

ALA LYS THR PRO TRP TRP LEU ARG SER PRO PHE PHE ASP TYR TRP GLY
100 105 110

GLN GLY THR LEU VAL THR VAL SER SER
115 120

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120

CAGCCTCCCG GAAAAGGGTT GGAGTGGATT GGCACAATAT ACTACTCCGG CAACACTTAC
180

TATAACCCCA GCCTGAAGAG CAGGCTGACT ATCTCTGTCTG ACACCAGTAA AAATCACTTT
240

TCTCTGAATC TGTCTTCAGT GACCGCAGCC GACACCGCCG TGTATTATTG CGCTCGGCGC
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GCCGGGATTC TGACAGGCTA TCTGGATTCA TGGGGCCAGG GGACATTGGT TACAGTGTCT

360

AGT

363

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GLN LEU LEU LEU GLN GLU SER GLY PRO GLY LEU VAL LYS PRO SER GLU
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THR LEU SER LEU THR CYS THR VAL SER GLY GLY SER LEU SER SER SER
20 25 30

PHE SER TYR TRP VAL TRP ILE ARG GLN PRO PRO GLY LYS GLY LEU GLU
35 40 45

TRP ILE GLY THR ILE TYR TYR SER GLY ASN THR TYR TYR ASN PRO SER
50 55 60

LEU LYS SER ARG LEU THR ILE SER VAL ASP THR SER LYS ASN HIS PHE
65 70 75 80

SER LEU ASN LEU SER SER VAL THR ALA ALA ASP THR ALA VAL TYR TYR
85 90 95

CYS ALA ARG ARG ALA GLY ILE LEU THR GLY TYR LEU ASP SER TRP GLY
100 105 110

GLN GLY THR LEU VAL THR VAL SER SER
115 120

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ACCTGCACCG TGTCCGGCGG CTCCCTGTCC TCCAGCTTCT CCTACTGGGT CTGGATCCGG
120

CAGCCCCCTG GCAAGGGCCT GGAATGGATC GGCACCATCT ACTACTCCGG CAACACCTAC
180

TACAACCCCA GCCTGAAGTC CCGGCTGACC ATCTCCGTGG ACACCTCCAA GAACCACTTC
240

AGCCTGAAGC TGTCTCCGT GACCGCCGCT GACACCGCCG TGTACTACTG TGCCAGAAGG
300

GCCGGCATCC TGACCGGCTA CCTGGACTCT TGGGGCCAGG GCACCCTGGT GACAGTGTCC
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TCC 363

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<400> 6

GLN LEU LEU LEU GLN GLU SER GLY PRO GLY LEU VAL LYS PRO SER GLU
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THR LEU SER LEU THR CYS THR VAL SER GLY GLY SER LEU SER SER SER
20 25 30

PHE SER TYR TRP VAL TRP ILE ARG GLN PRO PRO GLY LYS GLY LEU GLU
35 40 45

TRP ILE GLY THR ILE TYR TYR SER GLY ASN THR TYR TYR ASN PRO SER
50 55 60

LEU LYS SER ARG LEU THR ILE SER VAL ASP THR SER LYS ASN HIS PHE
65 70 75 80

SER LEU LYS LEU SER SER VAL THR ALA ALA ASP THR ALA VAL TYR TYR
85 90 95

CYS ALA ARG ARG ALA GLY ILE LEU THR GLY TYR LEU ASP SER TRP GLY
100 105 110

GLN GLY THR LEU VAL THR VAL SER SER
115 120

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120

CCCGGACAAG GCTTGGAATG GATGGGGCGT ATCAACCCAA ACTCTGGCGG GACTAATTAC
180

GCCCAGAAGT TTCAGGGAAG GGTGACTATG ACAAGGGACA CATCCATATC CACCGCTTAT
240

ATGGACCTGT CTCGACTGCG GTCTGATGAT ACAGCCGTTT ATTACTGCGC CAGAGACTAC
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AGCGGATGGA GCTTCGATTA TTGGGGGCAG GGTACTTTGG TCACAGTTTC AAGT 354

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<220>
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<400> 8

GLN VAL GLN LEU VAL GLN SER GLY ALA GLU VAL LYS LYS PRO GLY ALA
1 5 10 15

SER VAL LYS VAL SER CYS LYS ALA SER GLY TYR THR PHE THR GLY CYS
20 25 30

TYR MET HIS TRP VAL ARG GLN ALA PRO GLY GLN GLY LEU GLU TRP MET
35 40 45

GLY ARG ILE ASN PRO ASN SER GLY GLY THR ASN TYR ALA GLN LYS PHE
50 55 60

THR LEU SER LEU THR CYS THR VAL SER GLY GLY SER ILE SER SER SER
20 25 30

SER TYR TYR TRP GLY TRP ILE ARG GLN PRO PRO GLY LYS GLY LEU GLU
35 40 45

TRP ILE GLY ASN ILE TYR TYR SER GLY SER THR TYR TYR ASN PRO SER
50 55 60

LEU MET SER ARG VAL THR ILE SER VAL ASP THR SER LYS ASN GLN PHE
65 70 75 80

SER LEU LYS LEU SER SER VAL THR ALA ALA ASP THR ALA VAL TYR TYR
85 90 95

CYS ALA ARG GLN LEU SER TYR ASN TRP ASN ASP ARG LEU PHE ASP TYR
100 105 110

TRP GLY GLN GLY THR LEU VAL THR VAL SER SER
115 120

<210> 11
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<212> DNA
<213> ARTIFICIAL

<220>
<223> LV OF HL161A

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ACCTGTGGCG GCAACAACAT CGGCTCCACC TCCGTGCACT GGTATCAGCA GAAGCCCGGC
120

CAGGCCCCCG TGCTGGTGGT GCACGACGAC TCCGACCGGC CTTCTGGCAT CCCTGAGCGG
180

TTCTCCGGCT CCAACTCCGG CAACACCGCC ACCCTGACCA TCTCCAGAGT GGAAGCCGGC
240

GACGAGGCCG ACTACTACTG CCAAGTGCGA GACTCCTCCT CCGACCACGT GATCTTCGGC
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GGAGGCACCA AGCTGACCGT GCTGGGCCAG CCTAAGGCCG CTCCCTCCGT GACCCTG 357

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SER TYR VAL LEU THR GLN PRO PRO SER VAL SER VAL ALA PRO GLY GLN
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THR ALA ARG ILE THR CYS GLY GLY ASN ASN ILE GLY SER THR SER VAL
20 25 30

HIS TRP TYR GLN GLN LYS PRO GLY GLN ALA PRO VAL LEU VAL VAL HIS
35 40 45

ASP ASP SER ASP ARG PRO SER GLY ILE PRO GLU ARG PHE SER GLY SER
50 55 60

ASN SER GLY ASN THR ALA THR LEU THR ILE SER ARG VAL GLU ALA GLY
65 70 75 80

ASP GLU ALA ASP TYR TYR CYS GLN VAL ARG ASP SER SER SER ASP HIS
85 90 95

VAL ILE PHE GLY GLY GLY THR LYS LEU THR VAL LEU GLY GLN PRO LYS
100 105 110

ALA ALA PRO SER VAL THR LEU
115

<210> 13
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<400> 13

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60

ACCTGTGGCG GCAACAACAT CGGCTCCAAG TCCGTGCACT GGTATCAGCA GAAGCCCGGC
120

CAGGCCCCCG TGCTGGTGGT GTACGACGAC TCCGACCGGC CCTCTGGCAT CCCTGAGCGG
180

TTCTCCGCCT CCAACTCCGG CAACACCGCC ACCCTGACCA TCTCCAGAGT GGAAGCCGGC
240

GACGAGGCCG ACTACTACTG CCAAGTGTGG GACTCCTCCT CCGACCACGT GGTGTTCCGGC
300

GGAGGCACCA AGCTGACCGT GCTGGGCCAG CCTAAGGCCG CTCCTCCGT GACCCTG 357

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<400> 14

SER TYR VAL LEU THR GLN SER PRO SER VAL SER VAL ALA PRO GLY GLN
1 5 10 15

THR ALA ARG ILE THR CYS GLY GLY ASN ASN ILE GLY SER LYS SER VAL
20 25 30

HIS TRP TYR GLN GLN LYS PRO GLY GLN ALA PRO VAL LEU VAL VAL TYR
35 40 45

ASP ASP SER ASP ARG PRO SER GLY ILE PRO GLU ARG PHE SER ALA SER
50 55 60

ASN SER GLY ASN THR ALA THR LEU THR ILE SER ARG VAL GLU ALA GLY
65 70 75 80

ASP GLU ALA ASP TYR TYR CYS GLN VAL TRP ASP SER SER SER ASP HIS
85 90 95

VAL VAL PHE GLY GLY GLY THR LYS LEU THR VAL LEU GLY GLN PRO LYS
100 105 110

ALA ALA PRO SER VAL THR LEU
115

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<220>

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ACCTGTGGCG GCAACAACAT CGGCTCCAAG TCCGTGCACT GGTATCAGCA GAAGCCCGGC
120

CAGGCCCCCG TGCTGGTGGT GTACGACGAC TCCGACCGGC CCTCTGGCAT CCCTGAGCGG
180

TTCTCCGCCT CCAACTCCGG CAACACCGCC ACCCTGACCA TCTCCAGAGT GGAAGCCGGC
240

GACGAGGCCG ACTACTACTG CCAAGTGTGG GACTCCTCCT CCGACCACGT GGTGTTCCGGC
300

GGAGGCACCA AGCTGACCGT GCTGGGCCAG CCTAAGGCCG CTCCTCCGT GACCCTG 357

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<212> PRT

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<223> Lv of HL161BK

<400> 16

SER TYR VAL LEU THR GLN SER PRO SER VAL SER VAL ALA PRO GLY GLN
1 5 10 15

THR ALA ARG ILE THR CYS GLY GLY ASN ASN ILE GLY SER LYS SER VAL
20 25 30

HIS TRP TYR GLN GLN LYS PRO GLY GLN ALA PRO VAL LEU VAL VAL TYR
35 40 45

ASP ASP SER ASP ARG PRO SER GLY ILE PRO GLU ARG PHE SER ALA SER
50 55 60

ASN SER GLY ASN THR ALA THR LEU THR ILE SER ARG VAL GLU ALA GLY
65 70 75 80

ASP GLU ALA ASP TYR TYR CYS GLN VAL TRP ASP SER SER SER ASP HIS
85 90 95

VAL VAL PHE GLY GLY GLY THR LYS LEU THR VAL LEU GLY GLN PRO LYS
100 105 110

ALA ALA PRO SER VAL THR LEU
115

<210> 17
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ATCACCTGCA GGGCTTCTCA AGGTATTTC AACTACCTCG CCTGGTTCCA GCAAAGCCA
120

GGTAAAGCCC CAAAGAGCTT GATCTACGCC GCTTCTAGTC TGCAGAGTGG AGTTCCTAGT
180

AAGTTCTCCG GCTCTGGCAG TGGCACAGAT TTTACCTTGA CCATTTCAG CCTGCAGTCT 240

GAGGATTCG CTACCTACTA TTGTCAGCAG TATGACAGCT ATCCCCCAC ATTTGGGGGG
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GGCACTAAGG TGGAGATAAA ACGGACAGTG GCTGCCCTT CTGTCTTTAT T 351

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<400> 18

ASP ILE GLN MET THR GLN SER PRO SER SER LEU SER ALA SER VAL GLY
1 5 10 15

ASP ARG VAL THR ILE THR CYS ARG ALA SER GLN GLY ILE SER ASN TYR
20 25 30

LEU ALA TRP PHE GLN GLN LYS PRO GLY LYS ALA PRO LYS SER LEU ILE
35 40 45

TYR ALA ALA SER SER LEU GLN SER GLY VAL PRO SER LYS PHE SER GLY

50 55 60

SER GLY SER GLY THR ASP PHE THR LEU THR ILE SER SER LEU GLN SER
65 70 75 80

GLU ASP PHE ALA THR TYR TYR CYS GLN GLN TYR ASP SER TYR PRO PRO
85 90 95

THR PHE GLY GLY GLY THR LYS VAL GLU ILE LYS ARG THR VAL ALA ALA
100 105 110

PRO SER VAL PHE ILE
115

<210> 19
<211> 351
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<213> ARTIFICIAL

<220>
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ACCTGTGGCG GCAATAACAT AGGATCCAAA AATGTTCACT GGTATCAGCA AAAACCTGGC
120

CAAGCTCCCG TGCTCGTGAT CTACCGGGAC TCTAACCGAC CCAGTGGAAT CCCCGAACGC
180

TTTAGCGGTT CCAACTCTGG AAATACAGCT ACTCTGACTA TCTCCAGGGC TCAGGCCGGG
240

GATGAGGCCG ATTACTACTG CCAGGTGTGG GACTCAAGCA CAGTGGTCTT CGGCGGAGGT
300

ACCAAGTTGA CTGTTCTTGG GCAGCCAAAG GCCGCACCTT CAGTGACCCT G 351

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<212> PRT
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<400> 20

SER TYR GLU LEU THR GLN PRO LEU SER VAL SER VAL ALA LEU GLY GLN

1 5 10 15

THR ALA ARG ILE THR CYS GLY GLY ASN ASN ILE GLY SER LYS ASN VAL
20 25 30

HIS TRP TYR GLN GLN LYS PRO GLY GLN ALA PRO VAL LEU VAL ILE TYR
35 40 45

ARG ASP SER ASN ARG PRO SER GLY ILE PRO GLU ARG PHE SER GLY SER
50 55 60

ASN SER GLY ASN THR ALA THR LEU THR ILE SER ARG ALA GLN ALA GLY
65 70 75 80

ASP GLU ALA ASP TYR TYR CYS GLN VAL TRP ASP SER SER THR VAL VAL
85 90 95

PHE GLY GLY GLY THR LYS LEU THR VAL LEU GLY GLN PRO LYS ALA ALA
100 105 110

PRO SER VAL THR LEU
115

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<400> 21

SER CYS VAL MET THR
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VAL ILE SER GLY SER GLY GLY SER THR TYR TYR ALA ASP SER VAL LYS
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GLY

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<220>
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THR PRO TRP TRP LEU ARG SER PRO PHE PHE ASP TYR
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<210> 24
<211> 11
<212> PRT
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<400> 24

GLY GLY ASN ASN ILE GLY SER THR SER VAL HIS
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<400> 25

ASP ASP SER ASP ARG PRO SER
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<210> 26
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<400> 26

VAL ARG ASP SER SER SER ASP HIS VAL ILE
1 5 10

<210> 27
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<400> 27

PHE SER TYR TRP VAL
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<210> 28
<211> 16
<212> PRT
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<223> HV CDR2 OF HL161B OR HL161BK

<400> 28

THR ILE TYR TYR SER GLY ASN THR TYR TYR ASN PRO SER LEU LYS SER
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<210> 29
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<212> PRT
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<223> HV CDR3 OF HL161B OR HL161BK

<400> 29

ARG ALA GLY ILE LEU THR GLY TYR LEU ASP SER
1 5 10

<210> 30
<211> 11
<212> PRT
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<220>
<223> LV CDR1 OF HL161B OR HL161BK

<400> 30

GLY GLY ASN ASN ILE GLY SER LYS SER VAL HIS
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<400> 31

ASP ASP SER ASP ARG PRO SER
1 5

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GLN VAL TRP ASP SER SER SER ASP HIS VAL VAL
1 5 10

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GLY CYS TYR MET HIS
1 5

<210> 34
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<400> 34

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1 5 10 15

GLY

<210> 35

<211> 9

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<400> 35

ASP TYR SER GLY TRP SER PHE ASP TYR

1 5

<210> 36

<211> 11

<212> PRT

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<223> LV CDR1 OF HL161C

<400> 36

ARG ALA SER GLN GLY ILE SER ASN TYR LEU ALA

1 5 10

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<211> 7

<212> PRT

<213> ARTIFICIAL

<220>

<223> LV CDR2 OF HL161C

<400> 37

ALA ALA SER SER LEU GLN SER

1 5

<210> 38

<211> 10

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<223> LV CDR3 OF HL161C

<400> 38

GLN GLN TYR ASP SER TYR PRO PRO THR PHE
1 5 10

<210> 39

<211> 5

<212> PRT

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<223> HV CDR1 OF HL161D

<400> 39

SER TYR TYR TRP GLY
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<212> PRT

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<223> HV CDR2 OF HL161D

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ASN ILE TYR TYR SER GLY SER THR TYR TYR ASN PRO SER LEU MET SER
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<210> 41

<211> 13

<212> PRT

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<223> HV CDR3 OF HL161D

<400> 41

GLN LEU SER TYR ASN TRP ASN ASP ARG LEU PHE ASP TYR
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<210> 42

<211> 11

<212> PRT

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<220>

<223> LV CDR1 OF HL161D

<400> 42

GLY GLY ASN ASN ILE GLY SER LYS ASN VAL HIS
1 5 10

<210> 43
<211> 7
<212> PRT
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<220>
<223> LV CDR2 OF HL161D

<400> 43

ARG ASP SER ASN ARG PRO SER
1 5

<210> 44
<211> 9
<212> PRT
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<220>
<223> LV CDR3 OF HL161D

<400> 44

GLN VAL TRP ASP SER SER THR VAL VAL
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