

SEQUENCE LISTING

<110> CENTRE HOSPITALIER RÉGIONAL ET UNIVERSITAIRE DE BREST
ÉTABLISSEMENT FRANÇAIS DU SANG
INSERM (Institut National de la Santé et de la Recherche
Médicale)
UNIVERSITÉ DE BRETAGNE OCCIDENTALE

<120> BLOOD BIOMARKERS OF STROKE

<130> CV - 1192/PCT

<150> EP18305600.1

<151> 2018-05-16

<160> 18

<170> BiSSAP 1.3.6

<210> 1

<211> 604

<212> PRT

<213> Homo sapiens

<220>

<223> PTGS2 - Accession number NP_000954.1

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Phe	Lys	Gly	Phe	Trp	Asn	Val	Val	Asn	Asn	Ile	Pro	Phe	Leu	Arg	Asn
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<212> DNA
<213> Homo sapiens

<220>

<223> PTGS2 - Accession number NM_000963.4

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<211> 288
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 <213> Homo sapiens

<220>

<223> HMOX1 - Accession number NP_002124.1

<400> 3

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35     40     45
Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu
50     55     60
Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro
65     70     75     80
Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp
85     90     95
Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln
100    105    110
Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
115    120    125
Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
130    135    140
Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145    150    155    160
Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
165    170    175
Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
180    185    190
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195    200    205
Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
210    215    220
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<223> HMOX1 - Accession number NM_002133.3

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1554

<210> 5

<211> 860

<212> PRT

<213> Homo sapiens

<220>

<223> LDLR - Accession number NP_000518.1

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<211> 641

<212> PRT

<213> Homo sapiens

<220>

<223> HSPA1B - Accession number NP_005337.2

<400> 7

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Asn	Thr	Val	Phe	Asp	Ala	Lys	Arg	Leu	Ile	Gly	Arg	Lys	Phe	Gly	Asp
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Pro	Val	Val	Gln	Ser	Asp	Met	Lys	His	Trp	Pro	Phe	Gln	Val	Ile	Asn
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Asp	Gly	Asp	Lys	Pro	Lys	Val	Gln	Val	Ser	Tyr	Lys	Gly	Glu	Thr	Lys
						100				105				110	
Ala	Phe	Tyr	Pro	Glu	Glu	Ile	Ser	Ser	Met	Val	Leu	Thr	Lys	Met	Lys
						115				120				125	
Glu	Ile	Ala	Glu	Ala	Tyr	Leu	Gly	Tyr	Pro	Val	Thr	Asn	Ala	Val	Ile
						130				135				140	
Thr	Val	Pro	Ala	Tyr	Phe	Asn	Asp	Ser	Gln	Arg	Gln	Ala	Thr	Lys	Asp
145							150				155				160
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						165				170				175	
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						210				215				220	
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Phe	Val	Glu	Glu	Phe	Lys	Arg	Lys	His	Lys	Lys	Asp	Ile	Ser	Gln	Asn
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Lys	Arg	Ala	Val	Arg	Arg	Leu	Arg	Thr	Ala	Cys	Glu	Arg	Ala	Lys	Arg
						260				265				270	
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Leu	Arg	Asp	Ala	Lys	Leu	Asp	Lys	Ala	Gln	Ile	His	Asp	Leu	Val	Leu
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Lys Ala Asn Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu Ser Lys		495
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Glu Glu Ile Glu Arg Met Val Gln Glu Ala Glu Lys Tyr Lys Ala Glu		510
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Asp Glu Val Gln Arg Glu Arg Val Ser Ala Lys Asn Ala Leu Glu Ser		525
	530	535
Tyr Ala Phe Asn Met Lys Ser Ala Val Glu Asp Glu Gly Leu Lys Gly		540
545	550	555
Lys Ile Ser Glu Ala Asp Lys Lys Lys Val Leu Asp Lys Cys Gln Glu		560
	565	570
Val Ile Ser Trp Leu Asp Ala Asn Thr Leu Ala Glu Lys Asp Glu Phe		575
	580	585
Glu His Lys Arg Lys Glu Leu Glu Gln Val Cys Asn Pro Ile Ile Ser		590
	595	600
Gly Leu Tyr Gln Gly Ala Gly Gly Pro Gly Pro Gly Gly Phe Gly Ala		605
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Gln Gly Pro Lys Gly Gly Ser Gly Ser Gly Pro Thr Ile Glu Glu Val		620
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Asp		640

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 <212> DNA
 <213> Homo sapiens

<220>
 <223> HSPA1B - Accession number NM_005346.5

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<210> 9
 <211> 103
 <212> PRT
 <213> Homo sapiens

<220>
 <223> G0S2 - Accession number NP_056529.1

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35          40          45
Pro Phe Thr Ala Ala Arg Arg Leu Arg Asp Gln Glu Ala Ala Val Ala
50          55          60
Glu Leu Gln Ala Ala Leu Glu Arg Gln Ala Leu Gln Lys Gln Ala Leu
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<210> 10
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 <212> DNA
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 <211> 575
 <212> PRT
 <213> Homo sapiens

<220>
 <223> BAG3 - Accession number NP_004272.2

<400> 11

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Gln	Thr	Gly	Trp	Pro	Phe	Phe	Val	Asp	His	Asn	Ser	Arg	Thr	Thr	Thr
		35					40					45			
Trp	Asn	Asp	Pro	Arg	Val	Pro	Ser	Glu	Gly	Pro	Lys	Glu	Thr	Pro	Ser
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Ser	Ala	Asn	Gly	Pro	Ser	Arg	Glu	Gly	Ser	Arg	Leu	Pro	Pro	Ala	Arg
65					70				75					80	
Glu	Gly	His	Pro	Val	Tyr	Pro	Gln	Leu	Arg	Pro	Gly	Tyr	Ile	Pro	Ile
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Pro	Val	Leu	His	Glu	Gly	Ala	Glu	Asn	Arg	Gln	Val	His	Pro	Phe	His
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Val	Tyr	Pro	Gln	Pro	Gly	Met	Gln	Arg	Phe	Arg	Thr	Glu	Ala	Ala	Ala
	115						120					125			
Ala	Ala	Pro	Gln	Arg	Ser	Gln	Ser	Pro	Leu	Arg	Gly	Met	Pro	Glu	Thr
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Thr	Gln	Pro	Asp	Lys	Gln	Cys	Gly	Gln	Val	Ala	Ala	Ala	Ala	Ala	Ala

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Ser	Asp	Cys	Ser	Ser	Ser	Ser	Ser	Ser	Ala	Ser	Leu	Pro	Ser	Ser
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Arg	Ser	Ser	Leu	Gly	Ser	His	Gln	Leu	Pro	Arg	Gly	Tyr	Ile	Ser
		195					200				205			Ile
Pro	Val	Ile	His	Glu	Gln	Asn	Val	Thr	Arg	Pro	Ala	Ala	Gln	Pro
	210					215					220			Ser
Phe	His	Gln	Ala	Gln	Lys	Thr	His	Tyr	Pro	Ala	Gln	Gln	Gly	Glu
225					230				235					240
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Pro	Arg	Pro	Leu	Arg	Ala	Ala	Ser	Pro	Phe	Arg	Ser	Ser	Val	Gln
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Ser	Pro	Ser	Pro	Ile	Arg	Val	His	Thr	Val	Val	Asp	Arg	Pro	Gln
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Pro	Met	Thr	His	Arg	Glu	Thr	Ala	Pro	Val	Ser	Gln	Pro	Glu	Asn
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Pro	Glu	Ser	Lys	Pro	Gly	Pro	Val	Gly	Pro	Glu	Leu	Pro	Pro	Gly
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Gln	Lys	Pro	Pro	Pro	Pro	Ser	Glu	Lys	Val	Glu	Val	Lys	Val	Pro
	355					360					365			Pro
Ala	Pro	Val	Pro	Cys	Pro	Pro	Pro	Ser	Pro	Gly	Pro	Ser	Ala	Val
	370				375				380					Pro
Ser	Ser	Pro	Lys	Ser	Val	Ala	Thr	Glu	Glu	Arg	Ala	Ala	Pro	Ser
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Gln	Gly	Leu	Glu	Gln	Ala	Val	Asp	Asn	Phe	Glu	Gly	Lys	Lys	Thr
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Lys	Lys	Tyr	Leu	Met	Ile	Glu	Glu	Tyr	Leu	Thr	Lys	Glu	Leu	Leu
	450			455					460					Ala
Leu	Asp	Ser	Val	Asp	Pro	Glu	Gly	Arg	Ala	Asp	Val	Arg	Gln	Ala
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Lys	Ala	Ile	Asp	Val	Pro	Gly	Gln	Val	Gln	Val	Tyr	Glu	Leu	Gln
			500				505					510		Pro
Ser	Asn	Leu	Glu	Ala	Asp	Gln	Pro	Leu	Gln	Ala	Ile	Met	Glu	Met
	515					520					525			Gly
Ala	Val	Ala	Ala	Asp	Lys	Gly	Lys	Lys	Asn	Ala	Gly	Asn	Ala	Glu
	530				535				540					Asp
Pro	His	Thr	Glu	Thr	Gln	Gln	Pro	Glu	Ala	Thr	Ala	Ala	Ala	Thr
545				550					555					560
Asn	Pro	Ser	Ser	Met	Thr	Asp	Thr	Pro	Gly	Asn	Pro	Ala	Ala	Pro
			565					570					575	

<210> 12
<211> 2608
<212> DNA
<213> Homo sapiens

<220>
<223> BAG3 - Accession number NM_004281.3

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atttccagac acttccaccc ctctctggcc acgtcacccc cgcctttaat tcataaaggt 180
gcccggcgcc ggcttcccgg acacgtcggc ggcgagagagg ggcccacggc ggcgggcccg 240
ccagagactc ggcgcccgga gccagcgccc cgcacccgcg ccccagcggg cagaccccaa 300
cccagcatga gcgccgccac ccactcgccc atgatgcagg tggcgtccgg caacggtgac 360
cgcgaccctt tgccccccgg atgggagatc aagatcgacc cgcagaccgg ctggcccttc 420
ttcgtggacc acaacagccg caccactacg tggaacgacc cgcgcgtgcc ctctgagggc 480
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ctccatgaag gcgctgagaa ccggcaggtg caccctttcc atgtctatcc ccagcctggg 660
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caccagctcc cgcgggggta catctccatt ccggtgatac acgagcagaa cgttaccgg 960
ccagcagccc agccctcctt ccaccaagcc cagaagacgc actaccagc gcagcagggg 1020
gagtaccaga cccaccagcc tgtgtaccac aagatccagg gggatgactg ggagccccgg 1080
cccctgcggg cggcatcccc gttcaggtca tctgtccagg gtgcatcgag ccgggagggc 1140
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gtcgacaggc ctgagcagcc catgacccat cgagaaactg cacctgtttc ccagcctgaa 1260
aacaaccag aaagtaagcc aggcccagtt ggaccagaac tccctcctgg acacatccca 1320

attcaagtga tccgcaaaga ggtggattct aaacctgttt cccagaagcc cccacctccc	1380
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gccaggagag acggtgtcag gaaggttcag accatcttgg aaaaacttga acagaaagcc	1800
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gctggaaatg cagaagatcc ccacacagaa acccagcagc cagaagccac agcagcagcg	1980
acttcaaacc ccagcagcat gacagacacc cctggtaacc cagcagcacc gtagcctctg	2040
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ttcagagact ttaagtcagt tggtttttat tagctgcttg gtatgcagta acttgggtgg	2160
aggcaaaaca ctaataaaag ggctaaaaag gaaaatgatg cttttcttct atattcttac	2220
tctgtacaaa taaagaagtt gcttgttgtt tgagaagttt aaccccgttg cttgttgttc	2280
tgcagccctg tctacttggg cacccccacc acctgttagc tgttggttggtg cactgtcttt	2340
tgtagctctg gactggaggg gtagatgggg agtcaattac ccatcacata aatatgaaac	2400
atttatcaga aatgttgcca ttttaatgag atgattttct tcatctcata attaaaatac	2460
ctgactttag agagagtaaa atgtgccagg agccatagga atatctgtat gttggatgac	2520
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<210> 13

<211> 239

<212> PRT

<213> Homo sapiens

<220>

<223> TM4SF1 - Accession number XP_016861874.1

<400> 13

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20     25     30
Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg Phe Val Trp
35     40     45
Phe Phe Ser Gly Ile Val Gly Gly Gly Leu Leu Met Leu Leu Pro Ala
50     55     60
Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly Cys Cys Gly
65     70     75     80
His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser Val Leu Ala
85     90     95
Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile Val Ala Ala
100    105    110
Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu Gly Gln Trp
115    120    125
Asn Tyr Thr Phe Ala Ser Thr Glu Gly Gln Tyr Leu Leu Asp Thr Ser
130    135    140
Thr Trp Ser Glu Cys Thr Glu Pro Lys His Ile Val Glu Trp Asn Val
145    150    155    160
Ser Leu Phe Ser Ile Leu Leu Ala Leu Gly Gly Ile Glu Phe Ile Leu
165    170    175
Cys Leu Ile Gln Val Ile Asn Gly Val Leu Gly Gly Ile Cys Gly Phe
180    185    190
Cys Cys Ser His Gln Gln Val Arg Thr Cys Met Lys Ile Asn Met Thr
195    200    205
Ala Lys Arg Thr Asn Pro Gly Gln Ser His Asn Leu Pro Leu Phe His
210    215    220
Cys Asn Leu Tyr Ile Ser Leu Val Phe Ile Cys Lys Thr Leu Tyr
225    230    235
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<210> 14

<211> 972

<212> DNA

<213> Homo sapiens

<220>

<223> TM4SF1 - Accession number XM_017006385.2

<400> 14

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gaatgggctg agagtgggtgt ttgctttctc caccagaagg gcacactttc atctaatttg      180
gggtatcact gagctgaaga caaagagaag ggggagaaaa cctagcagac caccatgtgc      240
tatgggaagt gtgcacgatg catcggacat tctctggtgg ggctcgcctt cctgtgcatc      300
gcggtctaata ttttgcttta ctttcccaat ggggaaacaa agtatgcctc cgaaaaccac      360
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ctcagccgct tcgtgtgggt cttttctggc atcgtaggag gtggcctgct gatgctcctg      420
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aactgtggca aacgatgtgc gatgctttct tctgtattgg ctgctctcat tgggaattgca      540
ggatctggct actgtgtcat tgtggcagcc cttggcttag cagaaggacc actatgtctt      600
gattccctcg gccagtggaa ctacaccttt gccagcactg agggccagta ctttctggat      660
acctccacat ggtccgagtg cactgaaccc aagcacattg tggaatggaa tgtatctctg      720
ttttctatcc tcttggctct tgggtggaatt gaattcatct tgtgtcttat tcaagtaata      780
aatggagtgc ttggaggcat atgtggcttt tgctgctctc accaacaggt aagaacctgc      840
atgaaaatca atatgactgc taaaagaacc aaccaggac agagccacaa tcttcctcta      900
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<210> 15
 <211> 367
 <212> PRT
 <213> Homo sapiens

<220>
 <223> DUSP1 - Accession number NP_004408.1

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

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

<210> 16
 <211> 2013
 <212> DNA
 <213> Homo sapiens

<220>
 <223> DUSP1 - Accession number NM_004417.4

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tggttcggcg cagagagacc cgggggtcta gcttttcctc gaaaagcgcc gccctgcctt	180
tggccccgag aacagacaaa gagcaccgca gggccgatca cgctgggggc gctgaggccg	240
gccatgggtca tggaagtggg caccctggac gctggaggcc tgcgggcgct gctgggggag	300
cgagcggcgc aatgcctgct gctggactgc cgctccttct tcgctttcaa cgccggccac	360
atcgccggct ctgtcaacgt gcgcttcagc accatcgtgc ggcgccgggc caaggcgcc	420
atgggcctgg agcacatcgt gcccaacgcc gagctccgcg gccgcctgct ggccggcgcc	480
taccacgccg tggtgttgct ggacgagcgc agcgccgcc tggacggcgc caagcgcgac	540

ggcaccctgg ccctggcggc cggcgcgctc tgccgcgagg cgcgcgccgc gcaagtcttc	600
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tcgaccccca tggggctcag ccttcccctg agtactagcg tccctgacag cgcggaatct	720
gggtgcagtt cctgcagtac cccactctac gatcagggtg gcccggtgga aatcctgccc	780
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gccattgact tcatagactc catcaagaat gctggaggaa gggtgtttgt ccactgccag	1020
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gaggctggga gccccgcat ggctgtgctc gaccgaggca cctccaccac caccgtgttc	1260
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accagtgttg ggtttttttt tagttgccaa cagttgtatg tttgctgatt atttatgacc	1920
tgaaataata ttttcttct tctaagaaga cattttgta cataaggatg acttttttat	1980
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<210> 17

<211> 185

<212> PRT

<213> Homo sapiens

<220>

<223> ADM - Accession number NP_001115.1

<400> 17

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Leu Gly Ala Asp Thr Ala Arg Leu Asp Val Ala Ser Glu Phe Arg Lys
20     25     30
Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met
35     40     45
Ser Ser Ser Tyr Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala
50     55     60
Gln Thr Leu Ile Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro
65     70     75     80
Glu Asp Ser Ser Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg
85     90     95
Gln Ser Met Asn Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe
100    105    110
Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr
115    120    125
Asp Lys Asp Lys Asp Asn Val Ala Pro Arg Ser Lys Ile Ser Pro Gln
130    135    140
Gly Tyr Gly Arg Arg Arg Arg Arg Ser Leu Pro Glu Ala Gly Pro Gly
145    150    155    160
Arg Thr Leu Val Ser Ser Lys Pro Gln Ala His Gly Ala Pro Ala Pro
165    170    175
Pro Ser Gly Ser Ala Pro His Phe Leu
180    185
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<210> 18

<211> 1492

<212> DNA

<213> Homo sapiens

<220>

<223> ADM - Accession number NM_001124.3

<400> 18

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tctccttcaa gtacttggca gatcactctc ttagcagggt ctgcgcttcg cagccgggat      180
gaagctgggt tccgtcgccc tgatgtacct gggttcgctc gccttcctag gcgctgacac      240
cgctcggttg gatgtcgcgt cggagtttcg aaagaagtgg aataagtggg ctctgagtcg      300
tgggaagagg gaactgcgga tgtccagcag ctaccccacc gggctcgctg acgtgaaggc      360
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cgggcctgcc cagaccctta ttcggcccca ggacatgaag ggtgcctctc gaagccccga	420
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cttccagggc ctccggagct ttggctgccg cttcgggacg tgcacgggtgc agaagctggc	540
acaccagatc taccagttca cagataagga caaggacaac gtcgccccca ggagcaagat	600
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tgctgtcaag attttttttg taacttcaaa tatagagata tttttgtacg ttatatattg	1260
tattaagggc attttaaaag caattatatt gtcctcccct attttaagac gtgaatgtct	1320
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cataaaatgg gtgatatgcg aacagcaaac caataaactg tctcaatgct ga	1492