NM_153730.2 Rattus norvegicus kelch-like family member 12 (Klhl12), mRNA			CDS: 81714														
[siDirect v.2.0 2020-06-11 04:47:13]																	
blue=coding																	
yellow=noncoding																	
bolded are the ones we ordered.																	
1		DNA disa side		C and and a DNA and and						- (4/.)	2/.)	24.1	0()	4/)	2/ \	2/ \	
target position 13-35	target sequence CGGCATTATGGCCCCTAAAGACA	RNA oligo, guide UCUUUAGGGGCCAUAAUGCCG	passenger GCAUUAUGGCCCCUAAAGACA	URA	on seed-duplex stapasseng		min. number of mismatches against off-targets	t passenger	number of	0 1(+)	2(+)	3(+)	0(-)	1(-)	2(-)	3(-)	target posit
23-45	GCCCCTAAAGACATAATGACAAA	UGUCAUUAUGUCUUUAGGGGC	CCCUAAAGACAUAAUGACAAA	UA	15.8 16.1	5.6 15.8	3		3 2	1	0	0	2	0	0	0	12
24-46	CCCCTAAAGACATAATGACAAA	UUGUCAUUAUGUCUUUAGGGG	CCUAAAGACAUAAUGACAAAU	UA	20.5	11.7	3		ე ე	1	0	0	6	n	0	2	10
25-47	CCCTAAAGACATAATGACAAAT	UUUGUCAUUAUGUCUUUAGGG	CUAAAGACAUAAUGACAAAUA	URA	20.5	14.6	3		2	1	0	0	6	0	0	3	16
27-49	CTAAAGACATAATGACAAATACT	UAUUUGUCAUUAUGUCUUUAG	AAAGACAUAAUGACAAAUACU	R	14.8	19.2	3		2	1	0	0	14	0	0	1	13
218-240	AAGCCATATGTTGACATTCAAGG	UUGAAUGUCAACAUAUGGCUU	GCCAUAUGUUGACAUUCAAGG	URA	20.5	18.8	3		3	1	0	0	8	0	0	0	6
225-247	ATGTTGACATTCAAGGTTTAACT	UUAAACCUUGAAUGUCAACAU	GUUGACAUUCAAGGUUUAACU	UA	18.6	20.5			2	1	0	1	9	0	0	1	7
236-258	CAAGGTTTAACTGCTTCTACAAT	UGUAGAAGCAGUUAAACCUUG	AGGUUUAACUGCUUCUACAAU	R	18.9	14	2		2	1	0	0	6	0	0	1	12
237-259	AAGGTTTAACTGCTTCTACAAT	UUGUAGAAGCAGUUAAACCUU	GGUUUAACUGCUUCUACAAUG	URA	20.3	8.2	3		2	1	0	n ·	1/1	n	0	1	1/1
238-260	AGGTTTAACTGCTTCTACAATG	AUUGUAGAAGCAGUUAAACCU	GUUUAACUGCUUCUACAAUGG	UA	20.3	4.9	2		2	1	0	1	2	n	0	2	16
275-297	TTCGTGTATACAGAAACAGTACA	UACUGUUUCUGUAUACACGAA	CGUGUAUACAGAAACAGUACA	UA	17.8	15.8	2	•	3	1	0	0	2	0	0	0	6
347-369	CAGTTGAAAGGTGTAAAACAAGC	UUGUUUACACCUUUCAACUG	GUUGAAAGGUGUAAAACAAGC	URA	7.2	12.2	3		2	1	0	0	15	0	0	1	11
421-443	CAGGGATTTTGCTGAAACTCACA	UGAGUUUCAGCAAAAUCCCUG	GGGAUUUUGCUGAAACUCACA	UA	21.5	14.2	3		3	1	0	0	5	0	0	0	8
430-452	TGCTGAAACTCACAATTGCGTTG	ACGCAAUUGUGAGUUUCAGCA	CUGAAACUCACAAUUGCGUUG	UA	20.6	19.2	3		3	1	0	0	5	0	0	0	3
565-587	TGAGATTCAGGTGGATTCTGAAG	UCAGAAUCCACCUGAAUCUCA	AGAUUCAGGUGGAUUCUGAAG	R	20.4	20.4	2		2	1	0	1	16	0	0	2	4
695-717	AGGTACATTACAGATGTGATTGA	AAUCACAUCUGUAAUGUACCU	GUACAUUACAGAUGUGAUUGA	UA	20.5	8.5	3		3	1	0	0	6	0	0	0	8
697-719	GTACATTACAGATGTGATTGATG	UCAAUCACAUCUGUAAUGUAC	ACAUUACAGAUGUGAUGAUG	R	20.5	13.5	3		2	1	0	0 :	11	0	0	2	13
724-746	GCCTTTTATCCGCTGTAGTTTAC	AAACUACAGCGGAUAAAAGGC	CUUUUAUCCGCUGUAGUUUAC	UA	19	2.1	3		3	1	0	0	12	0	0	0	4
933-955	GGAGCTTTTTGCCAAGTATCACT	UGAUACUUGGCAAAAAGCUCC	AGCUUUUUGCCAAGUAUCACU	R	14.5	12.3	2		3	1	0	2	10	0	0	0	5
1137-1159	TGGGAGATATGATTTACGTTTCT	AAACGUAAAUCAUAUCUCCCA	GGAGAUAUGAUUUACGUUUCU	UA	15	15.9	3		3	1	0	0	6	0	0	0	1
1138-1160	GGGAGATATGATTTACGTTTCTG	GAAACGUAAAUCAUAUCUCCC	GAGAUAUGAUUUACGUUUCUG	Α	15	13.3	3		3	1	0	0	10	0	0	0	2
1302-1324	GAGGATATGATGGCTTGAATATA	UAUUCAAGCCAUCAUAUCCUC	GGAUAUGAUGGCUUGAAUAUA	URA	12	17.4	3		3	1	0	0	10	0	0	0	7
1303-1325	AGGATATGATGGCTTGAATATAT	AUAUUCAAGCCAUCAUAUCCU	GAUAUGAUGGCUUGAAUAUAU	UA	8.9	8.5	3		2	1	0	0	1	0	0	1	7
1304-1326	GGATATGATGGCTTGAATATATT	UAUAUUCAAGCCAUCAUAUCC	AUAUGAUGGCUUGAAUAUAUU	R	8.7	14.9	2		3	1	0	1	3	0	0	0	11
1312-1334	TGGCTTGAATATATTAAATTCAG	GAAUUUAAUAUUUCAAGCCA	GCUUGAAUAUUAAAUUCAG	A	-9.7	12	3		3	1	0	0	5	0	0	0	8
1313-1335	GGCTTGAATATATTAAATTCAGT	UGAAUUUAAUAUUUCAAGCC	CUUGAAUAUUAAAUUCAGU	UA	2.1	8.9	2		3	1	0	1	6	0	0	0	11
1413-1435	CCCTACTGAATGACCATATTTAT	AAAUAUGGUCAUUCAGUAGGG	CUACUGAAUGACCAUAUUUAU	URA	12.6	20.3	3	3	3	1	0	0	4	0	0	0	7
1414-1436	CCTACTGAATGACCATATTTATG	UAAAUAUGGUCAUUCAGUAGG	UACUGAAUGACCAUAUUUAUG	R	-1.8	19.2	3		3	1	0	0	5	0	0	0	9
1415-1437	CTACTGAATGACCATATTTATGT	AUAAAUAUGGUCAUUCAGUAG	ACUGAAUGACCAUAUUUAUGU	A	-8	18.1	3		3	1	0	0	2	0	0	0	9
1468-1490	TTCTTCTGTTGAAGCTTATAACA	UUAUAAGCUUCAACAGAAGAA	CUUCUGUUGAAGCUUAUAACA	URA	14.9	19.2	2		3	1	0	1	10	0	0	0	3
1471-1493	TTCTGTTGAAGCTTATAACATTC	AUGUUAUAAGCUUCAACAGAA	CUGUUGAAGCUUAUAACAUUC	UA	8.5	20.5	2		2	1	0	1	15	0	0	2	7
1619-1641	GAGTGTTATGACCCTATCATCGA	GAUGAUAGGGUCAUAACACUC	GUGUUAUGACCCUAUCAUCGA	A	13.3	13.5	3		4	1	0	0	6	0	0	0	0
1700-1722	CTCCGAGAAAAGTAACTGTTATT	UAACAGUUACUUUUCUCGGAG	CCGAGAAAAGUAACUGUUAUU	URA	17.8	21	3		3	1	0	0	13	0	0	0	6
1701-1723	TCCGAGAAAAGTAACTGTTATTT	AUAACAGUUACUUUUCUCGGA	CGAGAAAAGUAACUGUUAUUU	URA	19	14.8	3		3	1	0	0	8	0	0	0	16
1702-1724	CCGAGAAAAGTAACTGTTATTTG	AAUAACAGUUACUUUUCUCGG	GAGAAAAGUAACUGUUAUUUG	UA	11.6	10.3	3		3	1	0	0	5	0	0	0	26
1703-1725	CGAGAAAAGTAACTGTTATTTGG	AAAUAACAGUUACUUUUCUCG	AGAAAAGUAACUGUUAUUUGG	A	6.9	13.3	2		2	1	0	1	20	0	0	2	12
1737-1759	GAACAGTTTGTGGGAGAATGAAG	UCAUUCUCCCACAAACUGUUC	ACAGUUUGUGGGAGAAUGAAG	R	20.4	16.7	3		2	1	0	0	19	0	0	1	14
1738-1760	AACAGTTTGTGGGAGAATGAAGG	UUCAUUCUCCCACAAACUGUU	CAGUUUGUGGGAGAAUGAAGG	UA	20.4	17.8	3		2	1	0	0	9	0	0	1	27