Supplementary Data

Figure S1: Effects of ethanol on rat brain slices viability

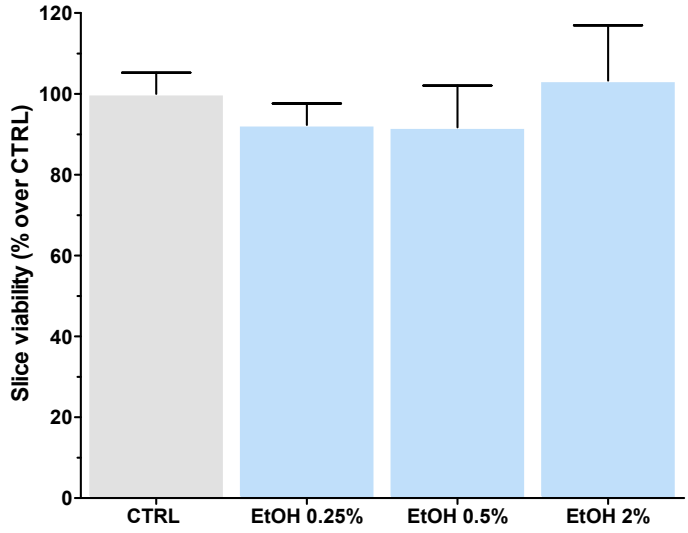

Figure S1: Effect of ethanol (0.25%-2% v/v) on the viability of rat brain slices after 2 hours of treatment. Data are shown as mean ± SEM (n=3-4); controls (CTRL) represent slices treated with ACSF.

Figure S2: Effects of MOE on prolonged oxidative stress

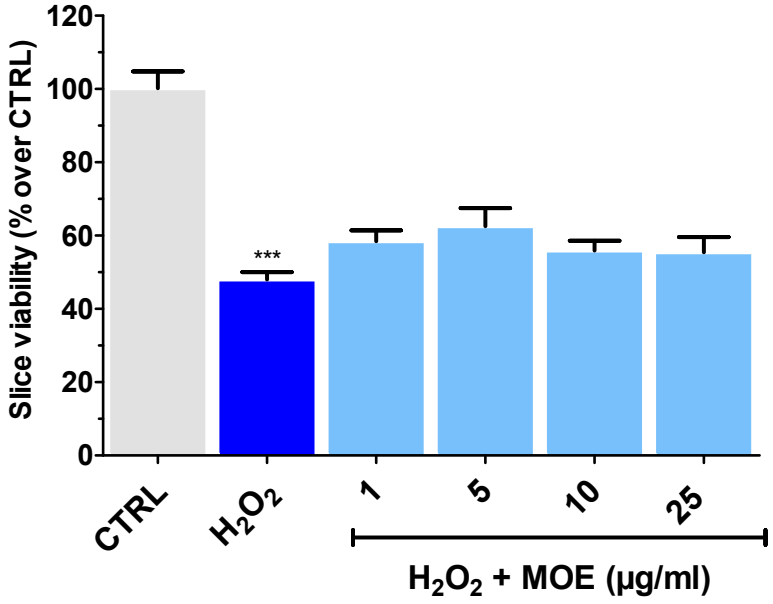

Figure S2: Effect of MOE (1-25 µg/ml) on prolonged oxidative stress- (H_2O_2 20 mM for 2h) induced injury, in rat brain slices. Data were reported as mean ± SEM (n=3-4). Statistical analysis was performed by ANOVA followed by Bonferroni post-hoc test. ***P<0.001 vs CTRL.

Figure S3: Antioxidant activity of MOE

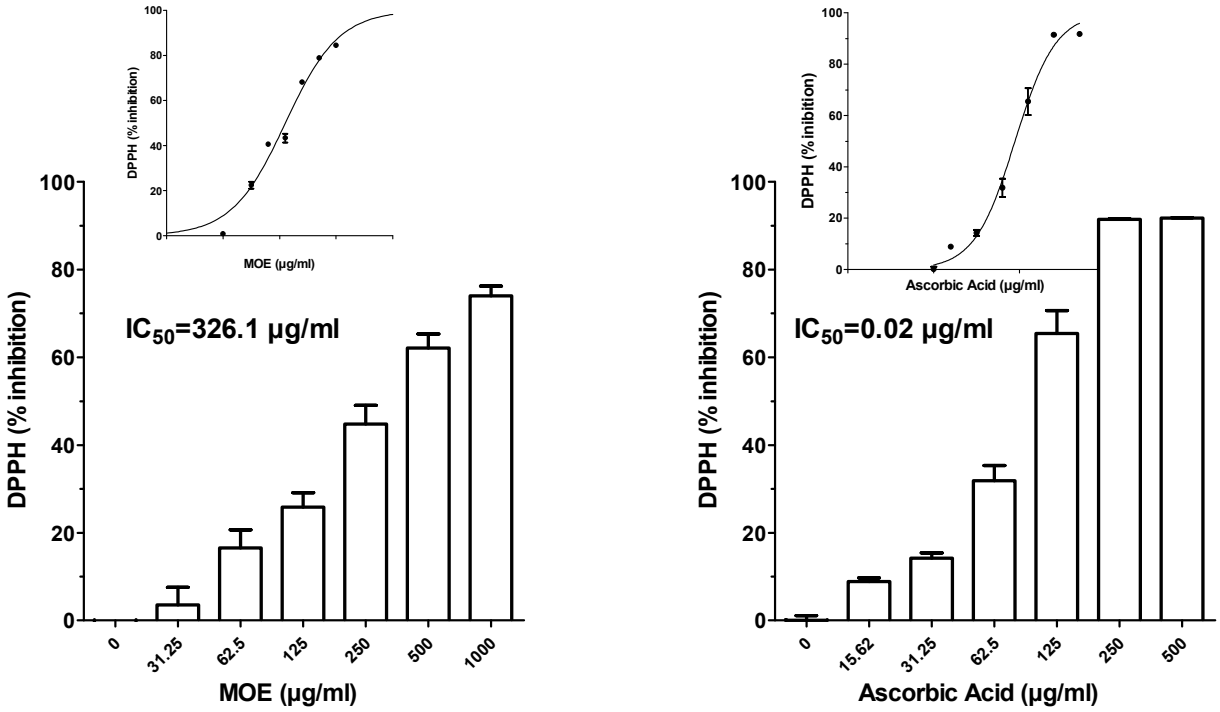

Figure S3: MOE (left) and Ascorbic acid (right) antioxidant activity as measured by DPPH assay. Absorbance was measured at 517 nm after 30 min of incubation with DPPH 100 µM. DPPH scavenged (%) is represented in Y-axis. Data are reported as mean ±SEM (n=4). IC_{50} values were calculated by fitting the data according to a sigmoidal curve (log inhibitor vs normalized response, see insert).

Figure S4: Stability of MOE solution

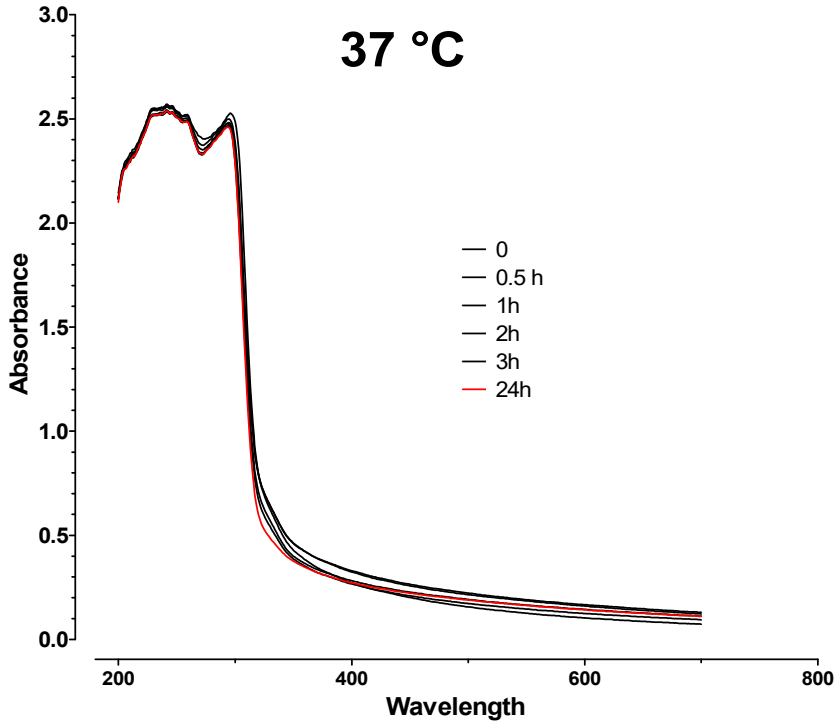

Figure S4: UV-visible spectra of MOE solutions (0.3 mg/ml) incubate at 37°C for different times. The stability of MOE solutions kept at different temperatures and times were checked by recording UV-Vis spectra in the wavelength range of 200-600 nm in quartz cuvette with 1 cm optical path length. No significant changes were detected in the spectra of solutions up to 24h.

Table S1. List of identified proteins in the proteomics experiment

See file excel

Table S2

Sequences of gene promoters retrieved by using EPD and control random sequences. When the gene may have more than one promoter all the promoters were considered (they can be distinguished by _1 and _2 in the Gene Name column). Uppercase is used to distinguish 100 bp downstream the TSS.

Gene Name	Ensembl	Promoter Sequence
Vcp	ENSRNOG00000034242	>FP004192 Vcp_1 :+U EU:NC; range -900 to 100. ctggcttcaaactgtcaatctcctgcctttagcctctggagtactgagatctagggtgtacaccaccatacccacttg tttttgcttgttttaaaatttttatttacttagttttgagtatcatttggctggctggaactctttttttataggccaggctga cttaaaactcacagagagccgcctgcctccgaagtgctgacattaaatgcatgtactaccacactgcttttaaaatt tattgagatactgtttgagactagaattatagctatgtgccattacgccgacatggttttgttttttcagaaaaggtctt gtatcctgggttgatctccatctaatagtcctcctgcctcagcttcccaattgctaaaaatacagacctagcccatcc accacgcccttcgttggagccagtgttttaaaggagcacgaaggattttagtatggtggagtaagaggatccctag gattggcgagaaatgaactatgtggattattattacaactcagctaaactaataagggttcaagcctttgtgcgag gttctcccagctgcttataaactaaggagccaatcaattggagccaagtagaggaaacctccttcggagggataa agactctccttttaccagaggatctggcctattgcttttgtcgattggtcaagactccctatgcgtcgaggaagcgta gtgctacggccaattgacgtggcgttactaggcgtgttgcagccttgaggcggggctaggccacaaacgaattttc tgattggttatcgtctgtgggttgctggggagaggcacggagaggcgggcacgagtcctaaggcagtcgctgattg gttgaggttagagcagctttccttccgatgattcggcttttctcggttcAGTCTCCGTGAAGCGTTTGCAGC CGTCGTTTGATTAGTCGCCTCTCGCGGATTAGGAGCTAGCGTCTCCCGCCCGCCTGCCG CCCCGGTGCCGCTGGGAGG
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Skp1	ENSRNOG00000005828	>FP007693 Skp1_1 :+U EU:NC; range -900 to 100. taaaggttaagattatccaacaaggtggtgcctgcctcccagcgctgagctattggaaacacagatctgaatttaa agccagcctggtctaaatagcgagttccaaacctggtttatctagtaagaccctgtttcaaaacaaaacaaaacaa aacaaaaagagtataaggcgagtatatgtggtgaaaaaaaaaagccggtaatctcacgagttttagaccaacct ggtctacgcaatgaatttgcagtcactctgtgccaaacgagaccccgtcttaaaatgcaaagaaaataaaaacta agcaggtgcaccaagtcaggagtatttagagacaccttgactcaacatccgtaatttttaaagctcagttatcagt ggagtaaggttcaagtccttaattccaggtcggaaaaaaaaaaaaaaaaccaaacaaaccaaaaaccctttattt ccttgggttattaggagagtaacagtggtcaggctgaggtgactcctttaaagcacacccacccacaaccggtttt gcggtttgttctttccaggcttttcaggactggggtctttcaagcagtttaagacagcctctgcctgaaagacccttc gggtcgcgatggttccccagccggtgccggcgtccgcacggaaggagagcacggcgttgttcaggacggcggag taaagtggaagtccccctcctgctcagccacccttccacccatcgccgctcagcacctctccaggagacctctgcgg cgcccagaacctgccacccgccttccgcatgccgtcaggcactctcaacggccagcccggccggctgtgtgacgtc acgaactcggggtcctcggtgccctcttcccgctcctataaaagctgacgccgcgcggcgctgctgtAGTGGCC TTGTTCTCGAGACTTCTATTCGGTTGTGAACTCTGTTCGGCAGCCTCAGGCCTGCGGTC TTGAGACCGAGCACGGTGAGTAGCAGCCCGCGAGC
Psma6_1	ENSRNOG00000007114	>FP005130 Psma6_1 :+U EU:NC; range -900 to 100. gaagaaaaattaactcgagaaattaaaactttcttatgaagaatctcttcaaatgttttgctttaaaataagtgcttt tagagagaataccacagatctgagtatttcagtattaaatcagtaaattgttacaaatattggtgtgaacgaaactt tttttatctaggggaaaattatgcctcaacttttagattcaccaaataggagttgtgtcctggtgtgcactatgtgtag aattttagagtttgaaaaaccagttttccaggagctatttcaccgacttggaattactctccagtattcagccagcac agcaacacaggaaccgcaagttcccattacttgtatctcaacttcaacttcacttttaaggcaaaaaaacaaacca aaccaaaacaacatcaacgaaaaaccctgggccgctgtccaaagaaaagtcttgccagactagaagaaaactat tgttatttccagtggcttcttccattagccctctttcagggcttacatttaagggtggctgctgctcccccaaaacgta ggaagagaagtggcaagtgaaatgaagttaggaagaacaaagccagaactccagtaagacaagatagcaagt acaggcgccaaaactgactatcatactgtctcctgaagtcacaagtaggcaaatcacaactgcgaacttcctctttt ggacaatatgttctccagaatgcactaacggccgcgacccaaatccaccacccaaaagcacacccgaccacaga atgagctcggggccccgcccacttagaggcggtgctttggaactcctccactggaacccacccccgccagtacctt accagagcggaagcagctaggccggtgctccggaagcagtagccataacttccgggagggGCTTGTGTGCC TGGTGTGTGTGTGTGTGTGTGCGCTACGGGGTGTAGACTGTGTCTGAAATAGCGGGA ACGCCATGTCCCGTGGTTCCAGCGCCGGTTTTG
Psma6_2	ENSRNOG00000007114	>FP005129 Psma6_2 :+U EU:NC; range -900 to 100. gggtttaggtattattgttagtgacggtggtgtttttatgcttgctggtgaggatatcaaagtgtctagaaatgcata cctgtctggtcaggaacctgcagcccttcacttgcctgaactcccaagtgctaggttgtaggcatgagctgccaagc ccacttagattgaattattaaaatcacgtgaaagggctggggagatggctcagttggcagtgtttgttccccaagg acctgaggacctgaatttgaccccagtgctcacatgcagaggctgagcataggggcatatgcttaaaaagaagca ctaagggagtgaagacaggctcactggtcaccttgcctatcaggtgacctttacgacacagaacaagcctgtcgc

		aaagttcaaggtggcttctgaggaacaatgatggaggttgccctctagcctattcatgtacatgcacgcccacatg aacacggaatagatagctggaagttattatcatcagtagttaacagctgaaagatttttggtaactctggcaaaaa aaaaatattttcaactaagctaaaattaatgcaccagtctttttttttttttttttttttttttttggtgctacttaaaaa aaaatctactccaagaagcaaatgcctgcgaagtcactggtagcaacttaatcgctaatatgttagcgaaataaat tcaagatgtcaggtcaggcaacctcatccctctcaactgagcagaacatgattagagatcaagttcggctgccatc taaatatttaaagtccattactaaaggtatctcagactgtctatgattacataagaatagaatgtctgtgtccactag gttccagtggaattccggacagttctatccgtttggcgtttctggggcagggttGAGTCCTAGGCTGAGGG GTTGGGACAAAGCATCCACCTCCACGGAACAGCTACTTTTAGGTGGATAATGGCCAAT CTCCGAAAAAGTAAGTGCCTAATTGT

Table S3

Random DNA sequences used as background for promoter analyses.

Sequence Name	Sequence
Random 1	>random sequence 1 consisting of 1000 bases. gaagcctgtcactcagattgatgttacaactcagacaggctagggacttgcggtgaagaatagtctacgaacgtcga aagacgttacaagaggcttgatggtttacggccacgctggacttctgttggggtgagaaacgaaggtcagccgccgt ctaaagggcccgattccacctaggagcgcgatgtgataaccccgactcagcccagcggtgattgatcctacccacag acaagtatctttacagtgaggaagtccacgcctggtcctacgcgcacatagttggtctatgtcacttcagtaccccgat acgcacaatgcgtgacactggaggtcccaaatactcgcgacttataaaggactcgtccgtcggctaaccgcatggtt atacgtgttgcggttgggccggtatcgcccgatagtgactatcggcgattcgatagaagaggagatttaccgcttgcc ccggcaagcggtggcgttgcgtgttcggagcgctattaactgaaccggggacgccgggttatacacccggggtgtac tatattgtgcgcgctacgtttctcacacgcgtcacaccgcttagaagcgtctactagttatcgcatgcgcccaatgatgt attgcatcgagacttctcccatagcgtcctgaaggggctcgacttcgcgcatcgtttctggagggatagctgggactag taccgtatcctaaggtgacctaccattggctgtcatttttaagcgctaatccctttcaggccttgtgtctcatcagactg cggacccgcctaaactgatgtaggagctggccataacacccataatatagggcggccgtttcagcaaatttagaacg aacaatatgctggcagtcttgtctaccggggtgtccaacataatcgaccatcatcccctgccggaattccggtggttgc tgtggggttgtgttgagttttgtatgataaatatctagaatcaaagaaacaactaacccaga
Random 2	>random sequence 2 consisting of 1000 bases. gtataaccgtctttagagccgggctacaccgttcgccgatatatcttttgcgggtaagaggccacaatgttaccggac gcgtgtgcaggcgagctcaagcgcggcgggaagctcaaacgttacctaaagcactcaatgagttcttggttctatca acgcgtccacctggccctactattgtggatagcaagcatgtcacttcggtcgtcgggtgcgtgatggtctagcaaaag acacgatcgagggacgccgtgtccttctgccgcgaacgctgtcggcgagggtcctatcaagcaggccggtcgccagg tgaggaatgacggtacgcggtaccagacgagaaaaaaacttatggctgaatcctctgtgatactagccatatagagt ctacctcccggttcgctgtagatctacaagactggcggcaaactttgggatagcattaacaattatttgccatatgtatt cttggcggcgctgactggctgtctttggaaagcacatgattgatgaaataatggagatcaaccagtgaactgtaaggt tctcctcaatccaacaactccccggggtaggctatcaacgtccaggcctgaatatagcttcatcgtagaggatgtagt accgaaggttaggcactttccggtctcagcgaacctcagagatgtcgttgaacattgtgcgcatcactaggcgcggca cggcaatatcccgctagtgacttaatcagtaaatggaaattgggaatgcgactaatagactaagctaagcagaccca gcgaccatagtttcttgcggagactgtatacgagtgcagtcagaccgtcgtacgcttagtttacacacgaccgatcca ctgatgtccaggtagatgaaatggcttgctgtcactccgcccgtaattcgtagttctgcagatccacgttcccctgaatg cagttcagtgcatgatcagattttagtcagcataatctatcataaacctcccaaagtggccggc
Random 3	>random sequence 3 consisting of 1000 bases. acagcccaatttgtgtctacattttgtcacacatctgcgtgacgcccacttcctcgcgcatcagaccggaatcgggcgc ggagaggttcattggctgcaatggtatcacatgcgtctcactggtgggtagacttctgatgctttgtagctaactctgac cttcgctaaaaagtgccagggcacgactaccccatgtgtcgtcgaatagacatgcctacctcaacgtttccatcacta caaagcattgcagcatggtaccactcagctcccgtatggatgcttcaacgagtacgtaaatgcgcgtcctttataaaa cgtacatttgaacccaatatccaacgcctcgatcggacaagcgccatgcgtgtgagacataatcatttccggacgggc gcataagcaaagtgagggtccagcggtagtccatgtggccggacgccggcacgcgtgcttaatcgcgaattgctgaa aacggctacacctcacagaaagattgttgcacattggtccgctcgttctgagtttggtttcttattaatatcgaacggca tgtctgtgactgttaaagttcggcaaagtcttatagaaaggattcaggtagggcgcttgcgagacttgttgagcaaga gattagggatttgagaattggccattcgtcctcacggggcctgtattcactgcgtgcacgtacagtgttgcgcgctggg cgatttgtgacttcggtctgtgcaattttagctggatggttaggggcggatgtgcaggtaaactaatcacagtgagtgc acatggcaagcgcatatctagcagaggcccaggaaacaccgggccatgtatagaaagaatcccgggctggtttttac gtccatggttgtataatgcccgtacttgcacggtgaaactcactgttctgggggcgcaacgcgggatatccaccagag tttgagtgctacagattcgtcggtggcagtcgataggcggtattgaccatctgcgttcc

Random 4	>random sequence 4 consisting of 1000 bases. tctccaacgaaaggacttcggcccccaatgcttgacacatggctatgattgaggtgctgttccgctttctcccgccgct aatctcgtaagtagacttgatcgacgcacgtgaatccttgctccctcagctcgcaggcactccctggcggcccggggt agaattcaccgcacggggcgcctcgtgctgggggcctctgaaggagccgccacgatcaagcatcgctttggtctacct tccttaatggacgaacaaggagtcgcccattattccgactggtgaaaagaggtgctactgatacaggcgacattgcc atacgcgtgcactggccaacaataaagccttgcgtcctgatcaatgtgaggcgcaagaggcaaccgcttattacggt gtcttccgataaagatggcgtctacttgatcccatcgcattagcgggagctataaggcagtgggctgaggagccattc gcagcccactgaatccgaccttagatatgtgtcccgtcgtcgggcaggcccatggcttttcagaattataagtcataag gaacgttttggcactcgaacgggataaagatacatgtacagtaacttacttaattcagagtccagccccagaccgca gagagctaagaatcccctacgcgccctgataatatcttttgcgtgtggtgacggtgcatagaccgtgactagacgttta tccgtatctggcaggcaacctcagagcatctgccgaatgcccaaacgccccgctggtaacctttttagaccttccgggg agacctgggatgggtttcgtgccgcctaccaatgatgctgaaatacgacggatacgcgacctcaaggtgagatctag gacacaaacccttctactgttcttagagtagcaatccctccttagctactgtacgctgcactcccttacaaagcaccat gtgcgtaggtgttagactgtttgctcctgagaatggtactaacggctacctcgagtaaaacaac
Random 5	>random sequence 5 consisting of 1000 bases. tttaggctttagacgtcctccctagttgccgagcgttgcccctcgcgagctggggtagctcatttagcctcaacatagg ggagtctttacactgcgacccggcgggcattccttcataacccaaacctggacggcgcaagggacccgatccgcgag gagactgttgtgtctcagacgtcgagtctgttggaatcgggatcgacctcagtatcagtgatagccggtggagctggg gacccccggtgctagagatcgacgaagcagaataattgccccccagagagctgtaaggtcagaagcggacgccctg ggcccggatcgttggcatgatggtctgagtaggggcctctctcgtccgatcatttagagtactctcagtaccttgctata atagtttcggatcatgccgaacctaggtcggatgatcgacacgggatttggttagggcaaggcgaggaaacctgaga aaaactgagggattcatggattttctgttcggggatgagttcttggtttgagctggtgatccatattaagcaactgtccc cacactgtatgcggactacctcatgttctcaaatttcataccacgcattaagcactggctgactgaagataagaagac cacaagctcttcccccgcccgctactaacgttataaagggaaacctaaagaacctacttaggtcgctgaggcatttttc tatgctatatgttgctgggatccttaaaaccaagattctggagtatacgcatggtcatacctctccgagtaggttacag gctaatcccggcgttgtcacaggctacaccccggccagctaaggtgaagcgcacagctgagtcgtaaatgcagtctt cctcaagttccggcatcaagcatagtgttacttgacgccacgaatataccgacgcccgctttcccattgccgtcctgtc agagtaaggccctaggacttgttccagctcacatccacgttaatacgattaacgtctggca
Random 6	>random sequence 6 consisting of 1000 bases. gttaaacttgttagatggcctgaactccgtacgtagagtgggatgcggaacgggtttttttctcatttcatcatcgccgcc aacgaagtctcggtattacctgtgacgtgttcgataggacatactcgccaccaccaggtccttctatccccctctgacc ttgtccacgaggaacactatgcagctttgctaacaagtgcacacctttgacagcggacaacatcttcatagtttcaaat ataaaatcggtcggccccaatatggtctcgagctgagattaatttcggatttcagttctgaatagataggtatctcaat tgttgttccatacgtataccatcctgcgcgattcagaagcttatagattcacaggggcgcgtggcttatccctttaactaa ggacagtttaaaccgattccagccacgcagggcgggttcgtggggtcctttcctatgcaagcaccgacggaggccca tctgtgtcttgagggctgttccgaccgggtaggaatttcccgttggatgcgtgtagggcgtgcaactcaatcctcgtcg gccacctattatacctcctgaaaagcatattgtgctagagtccccatagacttgctatgcactgcccagaagcatacat cgtcgtggccctggtgagcttcttcgagttcgagcaccgtggatcattgcgtttaagtattcttgccaatgttatctatag ggtccagaaaaatgcagcctatctgaggtcgtaggggcgagcaaaaattatacactatgaggcgttatatgcggact tcgcaatacctgctatccgatagactgggtcaagccctcgcgctttccatcgcgcgtgtacggctactggcatagcaca tatcagcagacgtgcacaatagcagcgtttgcccgtgcgtattcgactttgttcgaaccccaatcaggtgtttatgcta gcttgcacagatgaatgatccgtcgctctcagactacccagacttgcactca
Random 7	>random sequence 7 consisting of 1000 bases. gaccgcactggctagtctgctgaagggcgtgttaatttgttaccgcgatgcgacgccacgccgtcccatgctaccgag ccaaaagccatgcgtatatccagtactgtgccaagaacccgggttcagccgtctgggccacagggtctacgcctaag taaatgtgaaagtcaagcctcgtcccaatctacgaaactgtctgaatcagttgcatcctggcagaaacacttcccagt gcatataactattcgtacccttagtttcacctgagcttataagcctggttcagttataccaacgttggatagacaagtta gcgtcatgcgccttttacgttagcagactgactactcccccgtcccacattgcaagacgcacggacacgtatgcctggt

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Random 8	>random sequence 8 consisting of 1000 bases. cctgcctcgggccggatccgtttcatcagaaatcggacacatttctggcagcccaccctaatagacggtgttggcatg agtctgttgacattgcggaccgcgtcctcgggcgacgtacttcgggagccgctgtgtgcgcttgacatttgcgaggtat acgcaatcacatactggatacttcttccatatacgaagctctactggatacgtggggagcaactagctcataggattc cagttaccgtggatccctgggaacatttatatcggataatacctgtgacgcggtatcctcggaaagcaccctcgtacg cacgtgatcccgccttgcagttgcggtatacagcgggcacttttataggctagggtgtcatagtcttcccaagataaca cgcagtattgggttcggaagccctataggaatctatttagtcgaaggacataacctctggctaatcgcacataagagg tagtatacattcacggaacgattactcgagccgtactgagctattgtcgctgagcatccgtcttatcgcaccgagtctc acatacatgcgtaagagctctcgaaagcatgtataacctcattagtgatactgtcctccttttgcgacattcttgtcgta gcaagctagaataattttgcgttcgtatacgtagctaggaacaggggaccggatagtataacgctaccgtcaggaaa cctgccagcggcgagtgtgaaatgccaatgatgcgcctagtgcctccaggtctggtcgctcgccgcccgacagttatt atagtgctccatggggcaatccacatccttctgatgttgccacaacatctaacaccgacttaagcccgtaattatgccc acgtaaacctgggcgaggcaagccgatgaccttgaccagactcgaaacgctgcattagacgctttatcatctcttaag agttaccgccacatctgtataggcagttaccccgagttttcggtattaatgacattgca
Random 9	>random sequence 9 consisting of 1000 bases. ggattttatccacgttctgcaatgacacccccagcttatggtaataagcgctcagtaccaagctgaaggcacgcctgc ggcggggttgtatttagttgcaaatcgtttcagactcaggcaggttttaatgcgacgccgcaatctgaataatgcttat acccccatcagaggttggcaatgcaatctaggcctacacgttataggtaaagtaccaaaggtggtttgtctgccagat cggtccccatattgaaatcgggggctaggcccgaagtacgggagcccacctaaatgcatcctcaacgttggtctctcc ctatgttcaattcggtgttgcgttcagtttcttctaatccttagcggcagggggcatcagcacccaaactgagtcgaggt cattcttcagaagtaccacctatgggacgggctagcgcgtcagatcagtgtaagcgccggaccacctggcacgctgc tgtaaggtcgcagcagtaatgcacatgaaatcagatcggacatccacattatggcgtggagcgcgtgtggacaataa aaatctgttaccgggcttgaatagctgcgtgctagaaccgcccgacgtcaagattacaatttggtggctcgggtgatc aacacttctggtcacgatcactacacgtcaacgttttgtgtagcccgtgtgttgctaagcttttgtaggttattttaagtg tggccgtctcacggtccaccgttacttacgcccaaattagcaagcccctgaaccagcgtctacggcaatgtaaggatt aatctcagtttcggctttcttaaagaggattctagttgccccggaattcgtgatcaatggggtgcatttgaaaagcgta cctttcgcgccccgcaagtttatactaaacctcatccaatagcttcatccgtaacggaagaggtactctctagggtggc acgtacgaatgcaaacgccagccagttgtgggggggcggtatcgcgtgacggaactcga
Random 10	>random sequence 10 consisting of 1000 bases. caatacgatacttcacaacacgtttaaagttccacgtaactaacggcgcggtactttggcaggttacgtttgcgtaccc acgtatgtcgacctagaccctcccggacccgatttacggctcaatggttcgtggagcaaagttcaactcaagatttact attccttgttgaagcttatccatgatcgtaacagtagcatcctgtaaccgttaagatcaattcttggtaggaaagcattc agcctagccgcagggtagtcgtgacttagttgtttagcttccagaataccattaccgcatcatgaccgcgttgcgttag atttgtacgcttcaaattaataccggaaaatttagctccacaaaggctgtcgagcgtcacacgggagaccacgaaca gacctgagatacgctactagtagcctcgatcgattacgataagttctaatatataagcggacctcatctcgtgccttcc ttccgcacgggcagacacaccaagaaaacccgctaagaatcggacgagtgcatgggggcgaggttttagccctcca cgaaaccacggataatgggtacatacagcatgatgacgggaatacctgggcggagtataggaatgagccctcaatg actcgaagggttgataatgaggatgtggaaatgacggtcaatgctgcctggttcgctttagcgccgggtccttatgtgc gaagctacaccgtcgtacggcataccattgagcaggacgcatccccgtggtgagattgctacaagagtcacgctaag cgccgttcattgttgttaagtaacagtaatggacacggccctaacacatctatttatatccaattctgcgcggggtagc

	ttctcgactaaaatctacgagcggggacaccgtggctacgctatccgtctgtctgtatgtgaacgcctcatatagccta gggacaatatcccgcggagaaccaaaagcctgaaccctcgctccaagtattacttgggcca
Random 11	>random sequence 11 consisting of 1000 bases. cattcgtagcggagcctagcgctgggcgagatttggcggggacgggtccctaagcgaatgacaggtcttaaagattc agtgtataacgaacttttattgttcgtgtcctacggactgttgtatgtgcgacatatgccctgttgcttcatggagatga gatgtaatgtcgcggggaatccgcaaattattggggaagcgcatgtcctgacacgcagcgtccctctgatctcactca acatatcacaggtgataacttaaggactgatcggatggaagtggtataatcgaccccagacccgcgatcttagcccc atatagtagagcgtcttgtgtctgttactgaaccttctgatactaatcgtaatctgggaatcggaacctatatcccatgg gagacacggaggaactgttggagttttagtatcacatgtatttagaatggacgctggtatcagatacagagctccgaa agtggttccacgccaatttcacgtacgtgagacgatcataactatcatacgttacccacgtacacctgaggtagaacc atacggggtagccactcgccagtatcttcgtccctgcagatcaattcgcccgatacccgacttcaggattttctcagaa cttatgacacactgcgtgtacagttcgcggtgttatagacccagcgcgcccccaagtcagctattcaataggcattgta cctacacgatgattctcgccctgcgcttccagggccttggagtaaacggggcaatttaaaaggcacctatagtagtgc ggtaacacgcgatgaaacgccaggaaagcgcgaatcacgagctccggagcggcggctttgggcgcgcacgtaaca cgtctatctttattgatctcaaagcccacggacttaggctacagactcctctcacattagaataacatttggtgggggt aactagcatttgtggccggttcgagagagggcgacgttcccgtagcactttatttcgggatg
Random 12	>random sequence 12 consisting of 1000 bases. agcgttctttgttcaagaaagctccctcgtcgagtcgaagacactcgggccgcttttaatgaagccgttccaacaatta ctttatcgcaattgccgttataggatacctcatcgaagatattacatagggcatcttgcaacctcgtttattaacgccat actcgttttagaaggggtccgggatcacctggcaatttggagcaacgtagtagacaaaaccttgacatgtaatccacc ctgcgcaccgttagttttccttggagcgctcggctaacattatacaacgccattcaccttatatgaactacccgtataga caacgattgttgagcgttagtgtcggacccttcagatttccgctttggtgctacagagcaagcaggcaaggaacgagg ccgagcttgtgatgtaacccccatcacatactaaatcggcggcacctagctagccattttgcccataatccaaattgtg ttcgctccagtacctgatagtaatcaaaaccccctctatgccgaagcatacaaaggccctagctaaatgtgcctactac aatgactcttttatgattctatttagatccgcaagcccttgcggtttggggctaccgcggctaacttaacgacaatcatt cccccactcgcggtacgaagtagaatttgtagataactgtctgccttgaatgaacccgcgagacgtcaccaggtccgc ggggacgcagagtcaacgggaaggaattagcccgttaattctgcgtgcctctcgtaaccaaccaagcgcccgtggac cgcgatcgggttgacgactgccctgcacttaggtagtcgacgtgactaactttataagtcgctccctggtaggctcgga gagctcatgctagagcgcaatggtaaatgattaagcaccaatgcgagacttcgcaccgcaacttgtccgtctttaaat ggcatgagttctcatgcgttcccaggactttaccaaacgcaagatctttgccgagg
Random 13	>random sequence 13 consisting of 1000 bases. agggtgtcttgatggtggatctggtgctgggaatgcagtgctgtaactacctactggggatgtcccccatgtacaatca agttcatgtgaggagagcaacacggtgagtattccgaaccacgacttaagactaatagtaaaagaattaggttatcg ttgaacaggtcggccgcgatactgtctcatatctggttcgatagcgcattatcgagcaatagaacgcgtcagagagtt cacaactgttgttcaaaggtcacactttataaagtacctatgagttacgcaagtatgcaaagtagtaatgtttatcact ttaatttacacctgaggtccagtatttaaaatgtatgagttttgaacccatgccacgggtcttaaatcctactagttcag agattatcggacagttactacggctggggatgccgtcgaatcctctcggatacgctcgtttattatggctgatatcattg ccccggttagcactgcatcgggggcactgatgtgtggctcctcctcggtccgttccgctgcttgcaatggtaactggctt ttgtgttttcgtgcaatcaattggtgtcgttctatacggtttgcgatgttcgagacgttcgcgatgcggtgagagcgatt acgtgcaaatttcagggcgacagggaagttagatgccatgaacggggttttccgttattagtcctctgggtaggggtt cgcgacctcgtctcaagacaacggggtacaacttcatcccgcgatcccaacgaaattactgcgtattgcaatccggat ggggcctgagaaaaacaccttcggcctcctctatagcttaacctcctgtcttatcttaaactcaacgcacttcaccgac gtattctgcgccggggtaaacgcccaatccttgctaaaactatgctcaccccacaccgattctcataagcaactccttc tcttggactggacattgccgcggcacactttgggatcggcgccagggacggtt
Random 14	>random sequence 14 consisting of 1000 bases. agttaaagccatgagacggtgaaaattgggtagtactcctataaataaggttaacttctgtagctgccatcgaggtctt aatcaggaatgagtaattccgtgtgagggatacacagattccgactgaacatttttgtagggccggtaccggactaca tttcgcggctgactcaaacgaatggatcaccacaggtcaattagatccccaaccgcttactcctcacacgttatatcta

	aatcgcgccataaagcaattcctgttgaggatccagtcgcatcttggtctatacgtaaaccacatgctaaagcccacg ggagatccctatacctggttatcattccctaggagactctaggctaatcgtgatatgtcgccttttaaagggtaggtga taacacccctctctgtgtggtagcctggcaccctcaacgatgagctgcacgcgctccaggcggcataacagaataggg atcttgacgctttctagattctatagcccactatcgtctaacatacttataccggattgctgaaatcgttacggcctaatt gaccccgggcaactacgctgggtcaggtgttagtggttccgagaaaccaccgtggtggttgtagttattgactagacg aatggccccgatagtcgtctgtaggcaggtcacactggagatcgtatttcacgaggttaatagtgaattcagatatag atcgaaatgtactgctgcgtacatccgtgacgtaggctcgcctatctgaacaaggcagacgcctatttggacttcgcc cagatcaacttcgaatcattctcaggtggtggggatgattttatcgtttaggcagcgtccggacgtcaacgaatcacgt ggaagttgttacgaacaagtacgccagctcgcttactggctgaccggccgctttgacatacgtagtatggaaaatgta atctttacagcctttgcctgaggaagatatgggtgcaggctaccgtcctgtcactctt
Random 15	>random sequence 15 consisting of 1000 bases. ctccgcggtgagtcggtcgctcgcagtgcgggccacctgctagatgaggtcgtccattggttcgcgggtcacgacccg cacataaactgcgcaagagtttcgttccctggcggtcacgcgcttttcaaagggccatcatctcaacatcgtcggactt agaagatgtgctcggtaccggcacttaaggaacaacatgttaattacactttccaataacggacttgtagtagtgcca agaagtaatggttgatccggtcacggagtgaaccagtctcccgcacgtattcttcctcgatcagagcgaaaaaataccc ggaatagatgaggattagtgctccgccaagatagagcgaaggccgcgccacatggggacagatttctctatatgcta gttgttggttgcggagccgcgggggttagacaaccatgccgagcctaggtcccctagcgcccgcttcccctgtcttcag cgtattccgccttgtgatggccaccagctccctattgtactctcgctgtttcctagcgggtggatgatggtgaaattcgt ctactattgcgtagtgtacgatggaattgaccttctatttttctgaaacgcggcgggtaatatcgcaacgagttaaaac gtatatcaaataatcctgcagccgcaaggaacgtttttgcatggtacggcgaataccctctctttgacttgtgaaagtg cgcatacgtttggttgattaatcctcaagagtgtgatttcgttctgaataatctgaggcaacccccttcatagcttacat caccaacagtcatcatcggaacgccgcgacagacgacatctagtcatagtttttcgtagataggaacctcgtttcaat tgtcgctctcggaactggctttttcacggcatgatcagaagctatcttgcggccctaagtagggtaccccaattatgag agcgcaacgaacttctggactgtatccatcgaaacttcgcgcagtgcactctatat
Random 16	>random sequence 16 consisting of 1000 bases. cgagagtactgggtacttaagattcgtcacatctacgcctcgactcatttgtctggtcttaacgtcgtatacctctcttcg caaactcgcaacccggcgaggcacccgcccttaggccctatagttgagagcccagttaacgagtaggtagccgtttt agtcaggaccagcaggatagagtgcgccctcttaccaaactgccagtatatacgtctgtggtggaacgtacacgttcc catctggtcttactagggacaatcacttataggccactacctgggcaagcacgaccgaggtaacaaactgcttttaac ttctattgagcagaccaaagcgtgagaaagctcgaaaggccattgtcagtttggttacaacataatacttctatgtgtg tgggaaggtcatttcacgcgtataagtctgccctgtgagggcgtgccatgcaacctggcgaccaccgccctttggtgc tctgtccatctctccatctgggttcacaattagtctccagcctcaattaagcgttagctgtcagccatagaacaggggc gaagtagcggaccggcgctcattgtcgcgattcacgaagctgcgagatggactgattgaagaagcagctgatcttcg agacaaatgcttctatggtgcccgacacttggtcaagaaaggagctgggtgtattcatataaagtttactagttgagc ctgacgtcgccggagcatcttcatcacgataaagacacagccattcgctttaccctccctactaagacgaaaaaggc gcctgggggaggggggatacatcgacgtggttcgcatgtacgtacatagtaccaagcttgaggtgaacgctaatagtc ttctgaatggaaagacaatccatagaatgtcggctattcaacacttcgtatttggtttttgcgacgtcagtaagacaaa cccagtcagtttcactattgcattttatgggaacgtcaggctgtatatcacggtgggatta

Table S4

TFBS Enrichment results

matrix identifier	ratio	P-val
V$GC_01	1466667.75	2.42E-06
V$MAZR_01	1466667.75	2.42E-06
V$LBP1_Q6	1400001.00	4.35E-06
V$IRF1_01	1133334.37	4.57E-05
V$SP1_Q6	1000001.00	1.48E-04
V$ZIC2_01	933334.31	2.66E-04
V$PAX4_03	933334.31	2.66E-04
V$HFH4_01	866667.68	4.80E-04
V$MAZ_Q6	866667.68	4.80E-04
V$MYOGENIN_Q6	800001.00	8.64E-04
V$CREB_Q4	733334.37	1.55E-03
V$SP1_Q2_01	733334.37	1.55E-03
V$ELF1_Q6	666667.68	2.80E-03
V$PAX_Q6	666667.68	2.80E-03
P$Alfin1_Q2	666667.68	2.80E-03
V$COUP_DR1_Q6	666667.68	2.80E-03
V$GLI_Q2	666667.68	2.80E-03
V$E12_Q6	666667.68	2.80E-03
P$ABI4_01	600001.00	5.04E-03
V$HNF3B_01	600001.00	5.04E-03
I$BRCZ4_01	600001.00	5.04E-03
V$E2_Q6	600001.00	5.04E-03
V$TST1_01	600001.00	5.04E-03
F$FACBCA_Q2	600001.00	5.04E-03
V$HEB_Q6	600001.00	5.04E-03
V$SP1_Q4_01	600001.00	5.04E-03
V$E47_01	600001.00	5.04E-03
V$AP4_Q6_01	533334.37	9.07E-03
V$FOX_Q2	533334.37	9.07E-03
V$SPZ1_01	533334.37	9.07E-03
V$MINI20_B	533334.37	9.07E-03
V$CETS1P54_01	533334.37	9.07E-03
V$NFY_Q6	533334.37	9.07E-03
V$NGFIC_01	533334.37	9.07E-03
V$VJUN_01	533334.37	9.07E-03
I$ADF1_Q6	13.59	3.91E-04
I$HB_01	13.59	3.91E-04
V$HNF3ALPHA_Q6	13.59	3.91E-04

V$AP2_Q3	12.79	6.67E-04
V$MZF1_02	12.39	1.37E-06
V$FOXO4_01	11.19	6.66E-06
V$SP1_01	10.39	3.25E-03
V$EGR_Q6	10.39	3.25E-03
V$KROX_Q6	9.59	5.47E-03
V$MUSCLE_INI_B	9.59	5.47E-03
V$TFIII_Q6	9.11	3.52E-10
V$AR_Q2	8.79	9.16E-03
F$DDE1_B	8.79	9.16E-03
V$FOXO3_01	8.79	9.16E-03
V$NRF2_Q4	8.79	9.16E-03
V$NFAT_Q6	8.79	9.16E-03
F$STE11_02	8.79	9.16E-03
V$FOXD3_01	7.46	3.20E-05
V$HFH3_01	7.19	1.09E-03
V$FOXO1_01	7.19	5.23E-05
V$SRY_01	7.19	5.23E-05
N$DAF16_01	6.66	1.38E-04
V$ETF_Q6	6.49	6.13E-10
V$NFAT_Q4_01	6.39	2.88E-03
V$ETS_Q4	6.39	2.88E-03
V$ZIC3_01	6.39	2.88E-03
V$VDR_Q3	6.39	2.88E-03
V$PPAR_DR1_Q2	6.39	2.88E-03
V$HFH8_01	6.39	1.30E-07
I$TTK69_01	6.19	2.93E-03
V$CEBPGAMMA_Q6	5.99	4.64E-03
N$TRA1_01	5.19	7.81E-09
V$CIZ_01	5.06	5.99E-10
V$FOXO1_02	4.99	4.69E-04
V$HNF3_Q6	4.79	1.53E-04
V$DR1_Q3	4.79	3.24E-05
V$IRF7_01	4.39	1.77E-03
V$AP2ALPHA_02	4.31	5.66E-04
V$GCM_Q2	4.26	8.77E-03
V$MEF2_02	4.19	2.72E-03
V$RREB1_01	4.19	2.72E-03
V$FOXJ2_01	4.17	1.91E-08
V$ETS_Q6	4.15	8.68E-04
V$ETS2_B	3.99	4.17E-03
V$PU1_Q6	3.86	6.47E-04
V$LDSPOLYA_B	3.81	1.32E-08

V$AP2ALPHA_03	3.79	6.34E-03
F$RAP1_C	3.59	9.56E-03
I$GAGAFACTOR_Q6	3.59	9.56E-03
P$PCF2_01	3.59	9.56E-03
P$TGA1B_Q2	3.59	9.56E-03
V$AP2_Q6	3.52	1.42E-07
V$FOXO4_02	3.51	4.53E-03
V$AP4_Q5	3.35	1.25E-04
V$MAF_Q6_01	3.19	9.95E-03
V$LYF1_01	3.19	9.95E-03
V$MEF2_Q6_01	3.19	9.95E-03
P$RAV1_02	3.15	3.79E-07
V$FAC1_01	3.09	1.62E-03
V$MINI19_B	2.99	2.34E-03
P$MADSB_Q2	2.95	8.12E-04
V$ETS1_B	2.85	6.96E-03
V$SP3_Q3	2.85	3.38E-06
V$HNF4_Q6_01	2.79	2.04E-04
V$AP2ALPHA_01	2.76	4.09E-04
V$HELIOSA_02	2.73	8.20E-04
V$DR3_Q4	2.66	4.77E-03
I$BRCZ3_01	2.61	2.31E-03
V$MZF1_01	2.59	1.61E-03
V$NRF2_01	2.59	1.61E-03
F$STRE_B	2.58	2.00E-04
V$AP2GAMMA_01	2.55	1.65E-07
F$STRE_01	2.53	1.96E-04
F$GCR1_01	2.44	5.30E-04
V$GABP_B	2.39	5.11E-04
V$CETS168_Q6	2.32	2.35E-04
V$HAND1E47_01	2.30	1.35E-03
V$TBP_Q6	2.29	5.61E-08
V$FREAC7_01	2.26	8.07E-03
V$TATA_C	2.26	1.28E-03
P$AGL1_02	2.21	7.61E-03
V$HNF4_01	2.17	7.15E-03
V$IK1_01	2.10	2.90E-03
V$E2F_Q2	2.07	5.84E-03
V$COUPTF_Q6	2.05	8.30E-03
P$PBF_01	2.04	3.58E-03
I$EVE_Q6	2.03	2.37E-03
I$DL_02	2.02	7.71E-03
V$CP2_02	1.98	8.49E-04

V$HNF1_Q6_01	1.92	5.91E-04
I$E74A_01	1.89	1.05E-03
V$CREL_01	1.89	1.70E-03
V$GR_Q6	1.84	3.02E-03
V$HMGIY_Q3	1.77	1.73E-04
V$ELK1_02	1.72	2.86E-04
I$ANTP_Q6	1.70	1.47E-03
P$DOF3_01	1.63	3.13E-03
V$PEA3_Q6	1.63	3.72E-03
V$MTATA_B	1.60	8.62E-03
V$P300_01	1.60	9.41E-03
F$ADR1_01	1.58	5.24E-03
V$BARBIE_01	1.53	7.15E-03
V$SMAD4_Q6	1.52	7.88E-03
V$ZIC1_01	1.50	8.01E-03

Table S5. Acquisition parameters for the targeted detection of proteins potentially altered by H_2O_2 treatment and reverted to control condition by MOE. Protein entry number, peptide sequence, expected chromatographic retention time (min), normalized collision energy (NCE), *m/z* value of the precursor ion and *m/z* values of 7 precursor-to-product ion transitions of target peptides are listed in the table.

					Product ions (*m/z*)						
Protein entry (UniProtKb)	**Peptide sequence**	**RT (min)**	**NCE**	**Precursor (*m/z*)**	**Product 1**	**Product 2**	**Product 3**	**Product 4**	**Product 5**	**Product 6**	**Product 7**
sp|P46462|TERA_RAT	NAPAIIFIDELDAIAPK	23.4	25	604.336	971.5	614.4	315.2	244.2	186.1	467.3	580.3
sp|P46462|TERA_RAT	LEILQIHTK	13.8	16	365.557	739.4	626.4	498.3	385.2	248.2	243.1	356.2
sp|P37377|SYUA_RAT	EGVVHGVTTVAEK	9.5	19	442.574	804.4	648.4	547.3	446.3	347.2	276.2	187.1
sp|P37377|SYUA_RAT	TVEGAGNIAAATGFVK	15.3	26	753.402	1305.7	1176.6	1048.6	764.4	693.4	622.4	201.1
sp|P62138|PP1A_RAT	EIFLSQPILLELEAPLK	23.2	32	977.069	1235.8	799.5	670.4	428.3	357.2	243.1	390.2
sp|P62138|PP1A_RAT	AHQVVEDGYEFFAK	15.0	23	547.263	641.3	512.3	365.2	209.1	337.2	436.2	535.3
sp|P35565|CALX_RAT	GSLSGWILSK	17.2	19	524.295	903.5	790.4	703.4	646.4	588.3	701.4	814.4
sp|P35565|CALX_RAT	TSELNLDQFHDK	12.9	21	482.900	902.4	789.4	674.3	546.3	399.2	262.1	189.1
sp|Q63941|RAB3B_RAT	LQIWDTAGQER	14.4	23	658.833	1075.5	962.4	776.4	661.3	489.2	242.1	355.2
sp|Q63941|RAB3B_RAT	TITTAYYR	10.7	18	494.759	774.4	673.3	572.3	501.2	338.2	316.2	488.3
sp|P55161|NCKP1_RAT	AINQIAAALFTIHK	19.5	21	504.296	971.6	900.5	829.5	758.5	645.4	284.2	185.1
sp|P04692|TPM1_RAT	IQLVEEELDR	14.6	22	622.330	1002.5	889.4	790.4	661.3	532.3	242.1	355.2
sp|P04692|TPM1_RAT	SLEAQAEK	6.7	16	438.227	675.3	546.3	475.3	347.2	276.2	201.1	330.2
sp|P17764|THIL_RAT	DGLTDVYNK	11.5	18	512.751	739.4	638.3	523.3	424.2	261.2	173.1	286.1
sp|P17764|THIL_RAT	FANEITPITISVK	16.9	24	716.906	1100.7	971.6	858.5	757.5	219.1	333.2	462.2
tr|B2GV99|B2GV99_RAT	EAFQLFDR	16.5	18	513.256	825.4	678.4	550.3	437.2	290.1	201.1	476.2
tr|B2GV99|B2GV99_RAT	HVLVTLGEK	10.8	18	498.298	858.5	759.5	646.4	547.3	333.2	237.1	849.5
sp|P0C5X8|TTYH1_RAT	TELTTLEEVLSER	20.2	26	760.396	1289.7	1176.6	974.5	861.4	732.4	391.2	231.1

sp|P0C5X8|TTYH1_RAT	ALASIHSQLQGLER	13.5	22	508.283	930.5	843.5	715.4	602.3	474.3	304.2	185.1
sp|P86252|PURA_RAT	GPGLGSTQGQTIALPAQGLIEFR	20.0	32	771.085	1030.6	933.5	862.5	734.4	322.2	155.1	212.1
sp|P86252|PURA_RAT	FFFDVGSNK	17.0	19	530.759	913.4	766.4	619.3	504.3	405.2	295.1	914.4
sp|B2RYG6|OTUB1_RAT	LLTSGYLQR	13.0	19	525.801	937.5	723.4	579.3	416.3	303.2	227.2	328.2
sp|B2RYG6|OTUB1_RAT	FFEHFIEGGR	15.0	18	413.537	678.4	531.3	418.2	289.2	295.1	561.2	708.3
sp|P04906|GSTP1_RAT	EEVVTIDVWLQGSLK	20.5	29	858.464	645.4	532.3	358.2	457.2	558.3	1071.5	1184.6
sp|P04906|GSTP1_RAT	FEDGDLTLYQSNAILR	17.8	31	927.965	1178.7	1077.6	964.5	801.5	673.4	288.2	277.1
sp|P11661|NU5M_RAT	STSITQTQLSK	9.4	21	597.322	1005.6	918.5	805.4	704.4	576.3	234.1	189.1
sp|F1LQ48|HNRPL_RAT	TPASPVVHIR	10.0	16	359.545	720.5	524.3	425.3	199.1	270.1	357.2	553.3
sp|F1LQ48|HNRPL_RAT	QPPLLGDHPAEYGEGR	14.6	24	579.285	781.3	181.1	478.3	752.9	781.4	747.4	243.1
sp|P30904|MIF_RAT	IGGAQNR	3.7	14	358.196	602.3	545.3	488.3	417.2	289.2	171.1	228.1
sp|P30904|MIF_RAT	LHISPDR	8.0	16	419.233	724.4	587.3	474.2	251.2	364.2	451.3	663.3
sp|Q6PEC4|SKP1_RAT	TDDIPVWDQEFLK	16.9	23	535.931	664.4	536.3	407.3	260.2	445.2	542.2	641.3
sp|Q6PEC4|SKP1_RAT	ENQWCEEK	8.4	20	561.730	879.4	751.3	565.2	405.2	276.2	244.1	372.2
sp|P40307|PSB2_RAT	NGYELSPTAAANFTR	19.5	23	537.930	577.3	664.3	761.3	595.3	594.3	705.3	705.3
sp|P40307|PSB2_RAT	FILNLPTFSVR	18.3	23	653.880	706.4	361.2	175.1	410.2	374.2	601.4	670.4