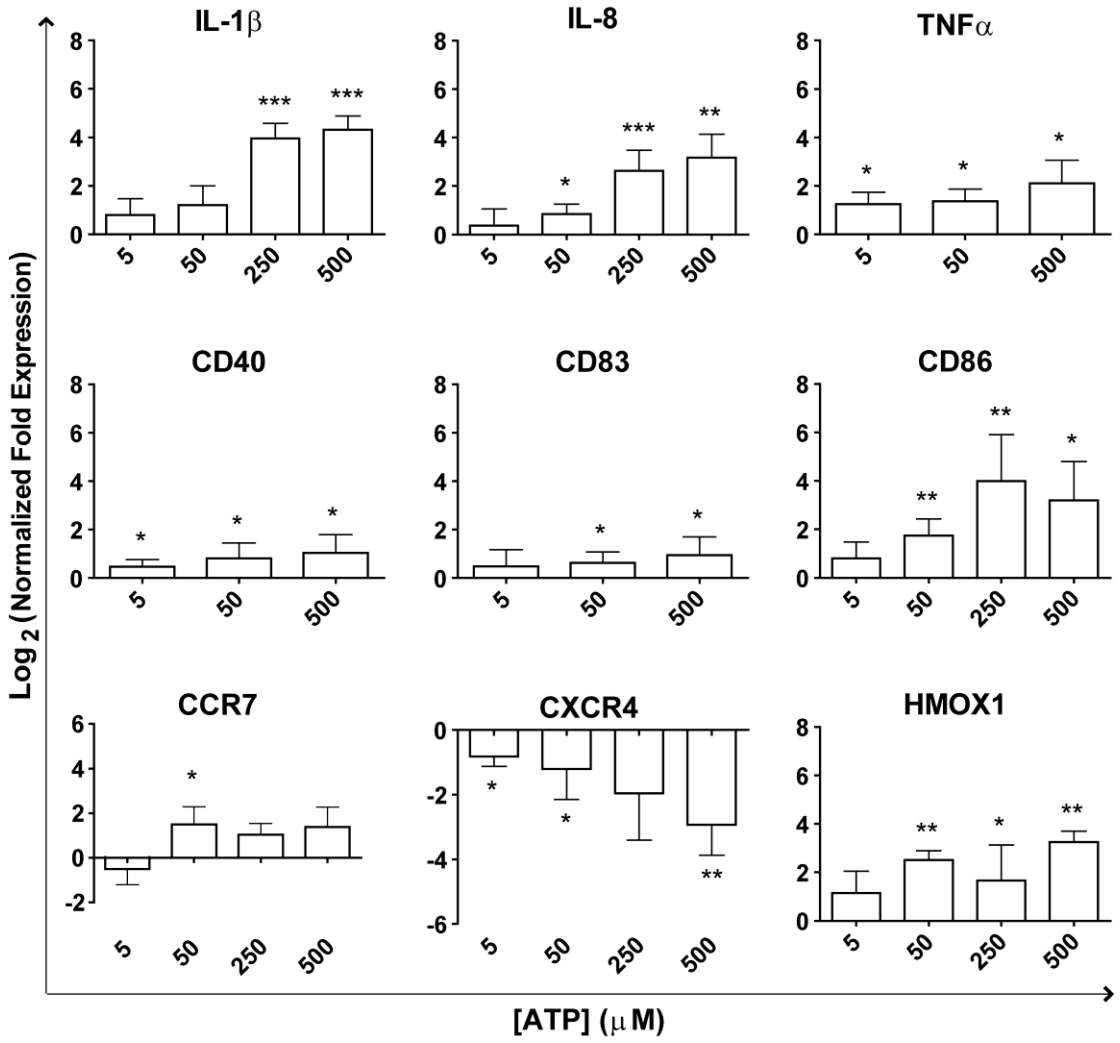
Electronic Supplementary Material (ESI) for Toxicology Research.

Supplementary Table 1 Primer sequences for studied genes

Gene Symbol	5' – 3' sequence F: Forward; R: Reverse	RefSeq ID
IL1B	F: GCTTGGTGATGTCTGGTC R: GCTGTAGAGTGGGCTTATC	NM_000576
IL8	F: CTTTCAGAGACAGCAGAG R: CTAAGTTCTTTAGCACTCC	NM_000584
TNF	F: AGAAGACCTCACCTAGAA R: TCTCAAGGAAGTCTGGAA	NM_000594
CD40	F: TGATAGTGAACAACTGGAA R: CCATAGGCAATATACATACATAA	NM_001250
CD83	F: ATTGAGTCATTATCCTTGCTAT R: GCTTCTTGGTAACCTTCTT	NM_004233
CD86	F: GAACCTAAGAAGATGAGT R: TCCAGAATACAGAAGATG	NM_175862
CCR7	F: GTGGCTCTCCTTGTCATT R: GGTGTTGTCTCCGATGTA	NM_001838
CXCR4	F: GAGGAGAGTTGTAGGATT R: GGTGTAGTTATCTGAAGTG	NM_001008540
HMOX1	F: CCTGAGTTTCAAGTATCC R: AACAACAGAACACAACAA	NM_002133
P2XR7	F: AACCACATTGCTATCTTA R: CTGAGAACATTAGAACCA	NM_002562
P2YR2	F: GCTCAGGATATTCACTCT R: CCCAACTTATACACACAAA	NM_176072
P2Y11	F: TCAGCAGATGAGCTTGAAC R: CTTTCCACCCACGTTTCC	NM_002566



Supplementary Fig. 1 Extracellular ATP induces alterations in THP1 cells mRNA profile. Cells were incubated for 6h with 5, 50, 250 and 500 μM ATP. The total RNA was extracted and retrotranscribed as described in material and methods. The mRNA levels of different cytokines (IL-1β, IL-8 and TNFα), maturation markers (CD40, CD83 and CD86), chemokine receptors (CCR7 and CXCR4) and of the electrophilic stress response enzyme HMOX1 are depicted as $\log_2$ of the normalized fold expression (see material and methods). GAPDH was used as reference gene. Mean values and standard deviation of at least 3 independent experiments are shown. One-way ANOVA with Tukey post-test was used to compare the results relatively to control (untreated cells; $\log_2=0$). * $p<0.05$; ** $p<0.01$; *** $p<0.001$.