1. Record Nr. TD18002410

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Titolo	GENE REGULATION BY MYC DURING B CELL ACTIVATION [Tesi di dottorato]
Editore	Università degli Studi di Milano, 2016-03-18
Lingua di pubblicazione	Inglese
Formato	Tesi di dottorato
Livello bibliografico	Monografia
Note	diritti: info:eu-repo/semantics/openAccess In relazione con info:eu-repo/semantics/altIdentifier/hdl/2434/363058
Sommario	c-Myc is a transcriptional regulator required for the cellular response to proliferative stimuli. The gene expression programs regulated by Myc in physiological settings remain to be clarified. Here, we provide a complete characterization of Myc-dependent regulatory events in primary mouse B cells following activation by bacterial lipopolysaccharide (LPS). Taking advantage of cells homozygous for a conditional knockout allele of c-myc, we induced deletion before LPS stimulation, followed by genome wide profiling of mRNA levels and Myc-DNA interactions. In contrast with previous studies, in which Myc was proposed to directly drive transcriptional amplification at all active loci (Nie et al. 2012, Lin et al. 2012), our study revealed that Myc is required for the up- and down-regulation of distinct subsets of genes early after stimulation, occurring prior to the global increase in RNA production. These gene expression programs where partially overlapping with those regulated by Myc upon oncogenic activation, a distinction made not only in B-cells, but also in fibroblasts (Sabò et al., 2014, Perna et al. 2012). Our data also show that Myc dependent regulation can occur at the level of RNA Polymerase II loading, as well as elongation. Altogether these data provide an extensive picture of Myc' s action in response to a mitogenic stimulus, highlighting the importance of Myc-target genes in the remodeling of

	cellular physiology and metabolism. Systematic work will be needed to unravel which, among all the Myc-regulated genes, are critical in mediating this chain of events.
Localizzazioni e accesso	http://memoria.depositolegale.it/*/http://hdl.handle.net/2434/363058