# OAS responsive repressor proteins linking sulfate metabolism and glucosinolate biosynthesis

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The *SDI1* and *SDI2* genes have been identified in early transcriptomics studies as being highly expressed in response to sulfate depletion in Arabidopsis and wheat. Later we linked their induction to the accumulation of *O*-acetyl-serine (OAS), which highly accumulates in response to reduced sulfate availability, but also in response to other stresses. Both genes belong to a cluster of OAS responsive genes. We identified that in Arabidopsis SDI1 (At5g48850) and SDI2 (At1g04770) are involved in down-regulating glucosinolate biosynthesis. Overexpression of both, *SDI1* and *SDI2*, result in a reduced accumulation of aliphatic and to a lesser extent indolic glucosinolates. We could show that this is achieved through a direct protein-protein interaction of SDI1 with the transcription factor MYB28. This complex prevents the transcription of genes controlled by MYB28, previously identified to play a role in controlling glucosinolate biosynthesis. SDI1 and SDI2, thus, down-regulate the expression of the glucosinolate pathway controlling transcription factors MYB29 and MYB76, and MYB28 itself and, hence, their downstream target genes. As glucosinolates provide a substantial sink for sulfate this regulatory step allows plants under sulfate starvation conditions to reduce or stop *de novo* glucosinolate biosynthesis in favor of plant primary metabolism.