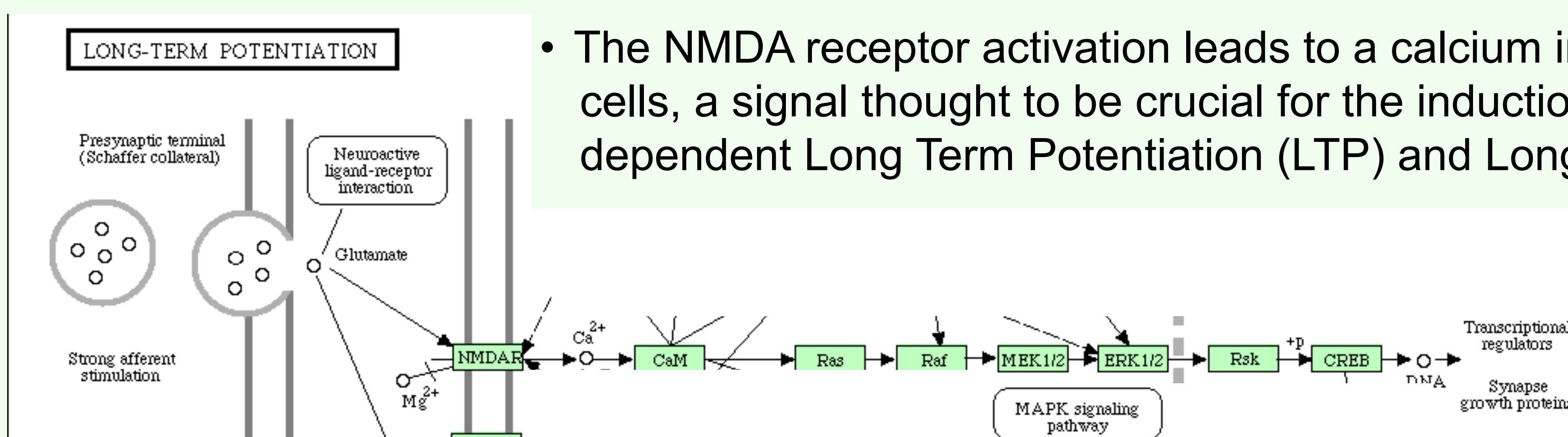


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INTRODUCTION:

- We had observed from a microarray study on the changes in gene expression in HepG2 cell line exposed to low levels of mercury that the Affymetrix probe set 213764_s_at mapped to chromosome 12p13.1-p12.3 was upregulated (PMID: 16823088).
- The protein-encoding gene Glutamate Receptor, Ionotropic, N-methyl D-aspartate (NMDA) 2B (GRIN2B) is also located on human chromosomal region 12p and has been prioritized in population-based studies as a candidate gene for predisposition to bipolar disorder (PMID: 16380905, 18007143).



- The NMDA receptor activation leads to a calcium influx into the post-synaptic cells, a signal thought to be crucial for the induction of NMDA-receptor dependent Long Term Potentiation (LTP) and Long Term Depression (LTD).

- Thus over-expression of these receptors can account for “excitotoxicity” of manic phases of bipolar diseases typical of Type I Bipolar Disorder.

OBJECTIVES OF STUDY:

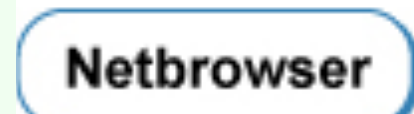
- Determine Medical Subject Heading (MeSH) qualifiers and protein interactions associated with GRIN2B.

METHODS:

- The NCIBI Gene2Mesh Tool (<http://gene2mesh.ncibi.org>) to determine MeSH terms significantly associated in PubMed abstracts.

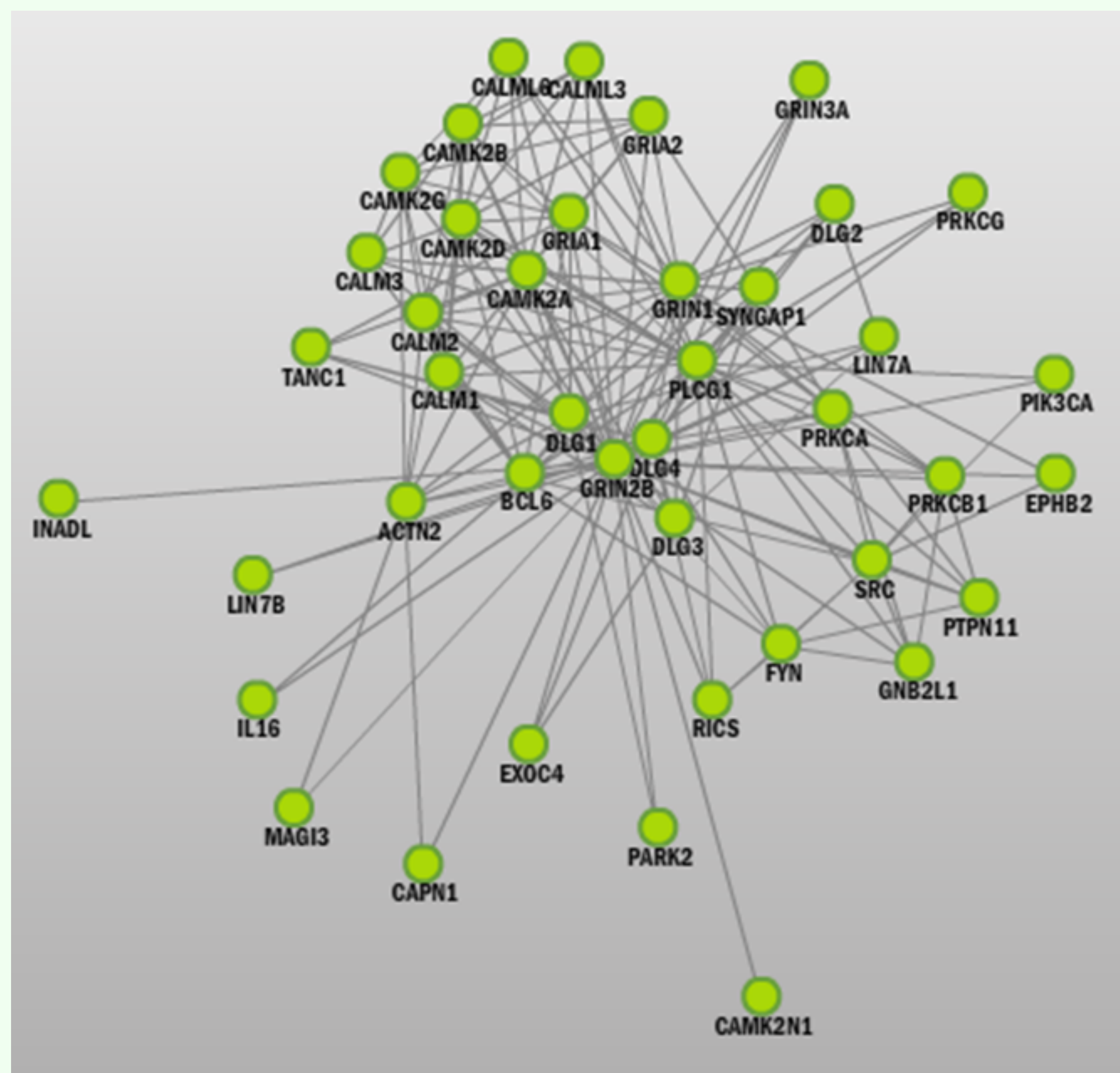


- The NCIBI NetBrowser Tool was used to visualize the interactions of proteins with GRIN2B available from the Michigan Molecular Interactions (MiMI).



RESULTS:

- A total of 49 significant MeSH headings were found matching the human gene symbol "GRIN2B". The associated MeSH Qualifiers were etiology, cytology, genetics, metabolism, pharmacology and physiology. Furthermore, the Gene2Mesh analysis revealed Alcoholism and Ethanol as significant MeSH Headings.
- Forty-two protein interactions were stored in MiMI for GRIN2B and we classified them based on the type of interaction information (bidirectional, in vitro and in vivo).



Netbrowser visualization of interactions of GRIN2B with other proteins

Classification of GRIN2B interaction by Interaction information in MiMI	bidirectional	In vitro	In vivo	Gene Symbol
GRIN2B_ACTN2	Green	Green	Green	GRIN2B_ACTN2
GRIN2B_BCL6	Green	Green	Green	GRIN2B_BCL6
GRIN2B_CALM1	Green	Green	Green	GRIN2B_CALM1
GRIN2B_CALM2	Green	Green	Green	GRIN2B_CALM2
GRIN2B_CALM3	Green	Green	Green	GRIN2B_CALM3
GRIN2B_CALML3	Green	Green	Green	GRIN2B_CALML3
GRIN2B_CALML6	Green	Green	Green	GRIN2B_CALML6
GRIN2B_CAMK2A	Green	Green	Green	GRIN2B_CAMK2A
GRIN2B_CAMK2B	Green	Green	Green	GRIN2B_CAMK2B
GRIN2B_CAMK2D	Green	Green	Green	GRIN2B_CAMK2D
GRIN2B_CAMK2G	Green	Green	Green	GRIN2B_CAMK2G
GRIN2B_CAMK2N1	Green	Green	Green	GRIN2B_CAMK2N1
GRIN2B_CAPN1	Green	Green	Green	GRIN2B_CAPN1
GRIN2B_DLG1	Green	Green	Green	GRIN2B_DLG1
GRIN2B_DLG2	Green	Green	Green	GRIN2B_DLG2
GRIN2B_DLG3	Green	Green	Green	GRIN2B_DLG3
GRIN2B_DLG4	Green	Green	Green	GRIN2B_DLG4
GRIN2B_EPHB2	Green	Green	Green	GRIN2B_EPHB2
GRIN2B_EXOC4	Green	Green	Green	GRIN2B_EXOC4
GRIN2B_FYN	Green	Green	Green	GRIN2B_FYN
GRIN2B_GNB2L1	Green	Green	Green	GRIN2B_GNB2L1
GRIN2B_GRIA1	Green	Green	Green	GRIN2B_GRIA1
GRIN2B_GRIA2	Green	Green	Green	GRIN2B_GRIA2
GRIN2B_GRIN1	Green	Green	Green	GRIN2B_GRIN1
GRIN2B_GRIN2B	Green	Green	Green	GRIN2B_GRIN2B
GRIN2B_GRIN3A	Green	Green	Green	GRIN2B_GRIN3A
GRIN2B_IL16	Green	Green	Green	GRIN2B_IL16
GRIN2B_INADL	Green	Green	Green	GRIN2B_INADL
GRIN2B_LIN7A	Green	Green	Green	GRIN2B_LIN7A
GRIN2B_LIN7B	Green	Green	Green	GRIN2B_LIN7B
GRIN2B_MAGI3	Green	Green	Green	GRIN2B_MAGI3
GRIN2B_PARK2	Green	Green	Green	GRIN2B_PARK2
GRIN2B_PIK3CA	Green	Green	Green	GRIN2B_PIK3CA
GRIN2B_PLCG1	Green	Green	Green	GRIN2B_PLCG1
GRIN2B_PRKCA	Green	Green	Green	GRIN2B_PRKCA
GRIN2B_PRKCB1	Green	Green	Green	GRIN2B_PRKCB1
GRIN2B_PRKCG	Green	Green	Green	GRIN2B_PRKCG
GRIN2B_PTPN11	Green	Green	Green	GRIN2B_PTPN11
GRIN2B_RICS	Green	Green	Green	GRIN2B_RICS
GRIN2B_SRC	Green	Green	Green	GRIN2B_SRC
GRIN2B_SYNGAP1	Green	Green	Green	GRIN2B_SYNGAP1
GRIN2B_TANC1	Green	Green	Green	GRIN2B_TANC1

- Twelve interactions with GRIN2B had annotation for the three interaction descriptors.

CONCLUSION:

- We have used NCIBI tools to extend our investigation on GRIN2B for understanding genetic predisposition to comorbid bipolar disorder and substance abuse.