

ALLERGY, GENETICS, SOFTWARE

# SNP BATCH ANNOTATION OF GWAS

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Genowatch ([paper|website](#)) is doing pretty well by annotating large SNP sets that would require otherwise numerous hours to map their position on genes, biological function and pathways.

The screenshot displays the GenoWatch web interface. On the left, a navigation menu includes 'Main Menu', 'Recent Results', 'Document', 'Presentation', 'Help', and 'Release Notes'. Below this is a 'Process Status' section with several progress indicators: 'Marker Info (NCBI)', 'SNP Risk Analysis', 'Gene List', 'Each Gene Info: LOC729324 (29/88)', 'Gene Structure: LINGO2 (38/88)', and 'PubMed Search: CHD1L (0) (29/88)'. The main content area is titled 'GenoWatch: a disease gene mining browser for association study' and lists the authors: Chen, Y.H., Liu, C.K., Chang, S.C., Lin, Y.J., Tsai, M.F., Chen, Y.T. and Yao, Adam (2008). It provides a 'Query by' dropdown menu set to 'Batch Query'. Below this is a 'Select region' section with 'Upstream(5\'' and 'Downstream(3\'' labels, an 'Upload a file example' button, and input fields for '50,000 (bp)' and 'd\x.txt' with a 'Durchsuchen...' button. A genomic track shows a red box around a SNP position with a 'Processing' button below it. An 'E-mail notification (Optional)' section has a 'To:' field. A yellow box displays 'Request ID: 12210564 (Valid for 30 days) You can copy this id to retrieve results later.'

A set of 60 SNPs took about 15 minutes to produce the following figure (which will be part of [my forthcoming presentation in Cernay](#)). Very nice - although the interpretation is getting really difficult.

