

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. At the top left, there is a navigation menu with options: Main Menu, Recent Results, Document, Presentation, Help, and Release Notes. The main heading is "GenoWatch: a disease gene mining browser for association study" with a citation: "Chen, Y.H., Liu, C.K., Chang, S.C., Lin, Y.J., Tsai, M.F., Chen, Y.T. and Yao, Adam (2008) GenoWatch: a disease gene mining browser for association study, Nucleic Acids Research, doi: 10.1093/nar/gkn214 Full Text". Below this is a "Query by" section with a dropdown menu set to "Batch Query". The "Select region" section includes "Upstream(5')", "Upload a file example", and "Downstream(3')". Input fields show "50,000 (bp)" for both upstream and downstream, with a file type "d'x.txt" and a "Durchsuchen..." button. A genomic track shows a red box around a gene, 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." On the left, a "Process Status" sidebar shows progress for "Marker Info (NCBI)", "SNP Risk Analysis", "Gene List", "Each Gene Info: LOC729324 (29/88)", "Gene Structure: LINGO2 (38/88)", "PubMed Search: CHD1L (0) (29/88)", and "Data Mining".

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.

