Lung toxicity and gene expression changes in response to whole-body inhalation exposure to cellulose nanocrystal in rats

Data Dictionary

Field Name	Field contents
Body weight (g)	Body weights of rats in grams
Total cells	Total number of cells in the bronchoalveolar lavage (BAL)
Macrophages	Number of macrophages in the BAL
PMN	Number of polymorphonuclear leukocytes in the BAL
LDH U/L)	Lactate dehydrogenase activity in the BAL fluid (U/L BAL fluid)
Binucleated AM	Number of binucleated macrophages in the BAL
PMA-Stimulated Chemiluminescence	Chemiluminescence counts/15 min/total number of BAL cells
Zymozan-stimulated Chemiluminescence	Chemiluminescence counts/15 min/total number of alveolar macrophages
IL-1β	Picogram IL-1β protein/ml BAL fluid
IL-10	Picogram IL-10 protein/ml BAL fluid
IL-12	Picogram IL-12 protein/ml BAL fluid
MCP-1	Picogram MCP-1 protein/ml BAL fluid
MIP-2	Picogram MIP-2 protein/ml BAL fluid
TNFα	Picogram TNFα protein/ml BAL fluid
Increased alveolar macrophages	Whether there was an increase in the number of alveolar macrophages in the lung by histopathological examination
Alveolitis	Whether there is any alveolitis in the lung section and its location by histopathological examination
Birefringent crystals in macrophages	Whether crystalline nanocellulose particles are detected in the lung macrophages by histopathological examination
Gene ID	Symbol for the gene detected
Count	Number of reads for the gene
Canonical pathway	Name of the canonical pathway significantly enriched in response to crystalline nanocellulose exposure
-log(p-value)	-log(p-value) of the canonical pathway enrichment
Molecules	Symbols for the genes belonging to the enriched canonical pathway, biological function, or disease category
Disease/Function Categories	Disease or function category significantly enriched in response to crystalline nanocellulose exposure
Diseases or Functions Annotation	Name of the enriched disease or function
p-value	p-value for the enrichment
#Molecules	Number of genes belonging to the enriched biological function or disease category
Upstream regulator	Name of the molecule that regulates the gene expression

Name of the molecule	Type of the molecule that regulates the gene expression
p-value of overlap	p-value for the involvement of the regulator in gene expression
Target molecule in dataset	Genes whose expressions are regulated by the up-stream regulator
RBC(M/uL)	Number of erythrocytes (million/µl blood)
HGB(g/dL)	Hemoglobin concentration (g/dL blood)
HCT(%)	Hematocrit value: erythrocyte ratio of total blood volume (%)
MCV(fL)	Mean erythrocyte volume in sample (fL)
MCH(pg)	Mean hemoglobin volume per red blood cell (RBC) count (pg)
MCHC(g/dL)	Mean hemoglobin concentration of erythrocytes (g/dL blood)
RDW-SD(fL)	The degree of variation in size of the erythrocyte population (fL)
RDW-CV(%)	The degree of variation in size of the erythrocyte population (%)
RET#(K/ul) -	Reticulocyte number (1000/ul blood)
PLT(K/ul)	Total number of platelets (1000/ul blood)
PDW(fL)	Platelet distribution width; the degree of variation in size of the platelet population (fL)
MPV(fL)	Mean platelet volume (fL)
P-LCR(%)	Platelet large cell ratio (%)
PCT(%)	Plateletcrit value (%)
WBC(K/uL)	Total number of leukocytes (1000/uL blood)
NEUT#(K/uL)	Neutrophil count (1000/uL blood)
LYMPH#(K/uL)	Lymphocyte count (1000/uL blood)
MONO#(K/uL)	Monocyte count (1000/uL blood)
EO#(K/uL)	Eosinophil count (1000/uL blood)
BASO#(K/uL)	Basophil count (1000/uL blood)
NEUT(%)	% Neutrophil in WBC
LYMPH(%)	% Lymphocyte in WBC
MONO(%)	% Monocyte in WBC
EO(%)	% Eosinophil in WBC
BASO(%)	% Basophil in WBC