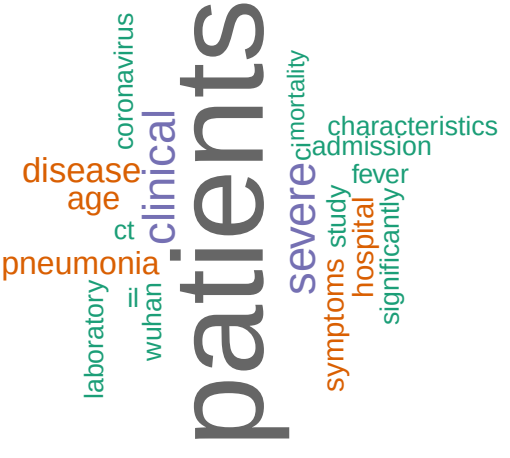
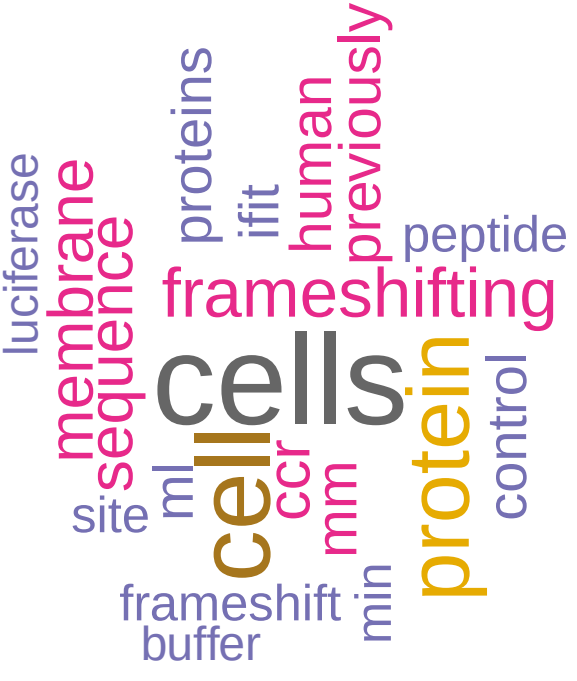
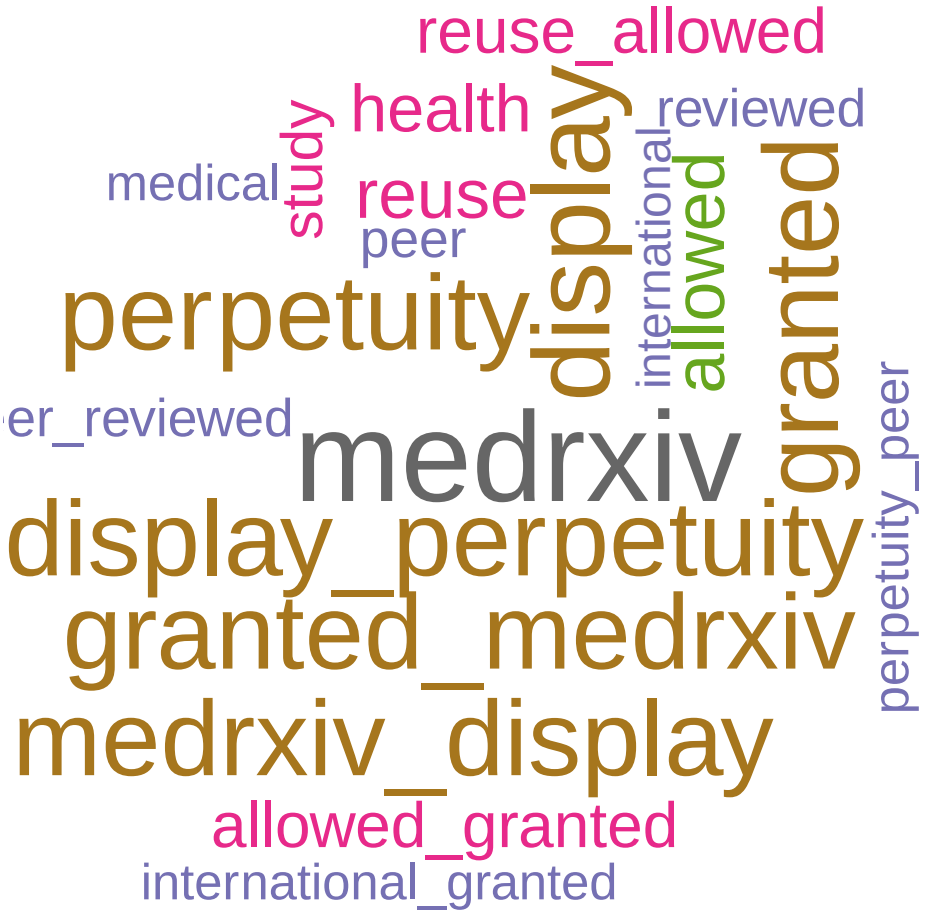
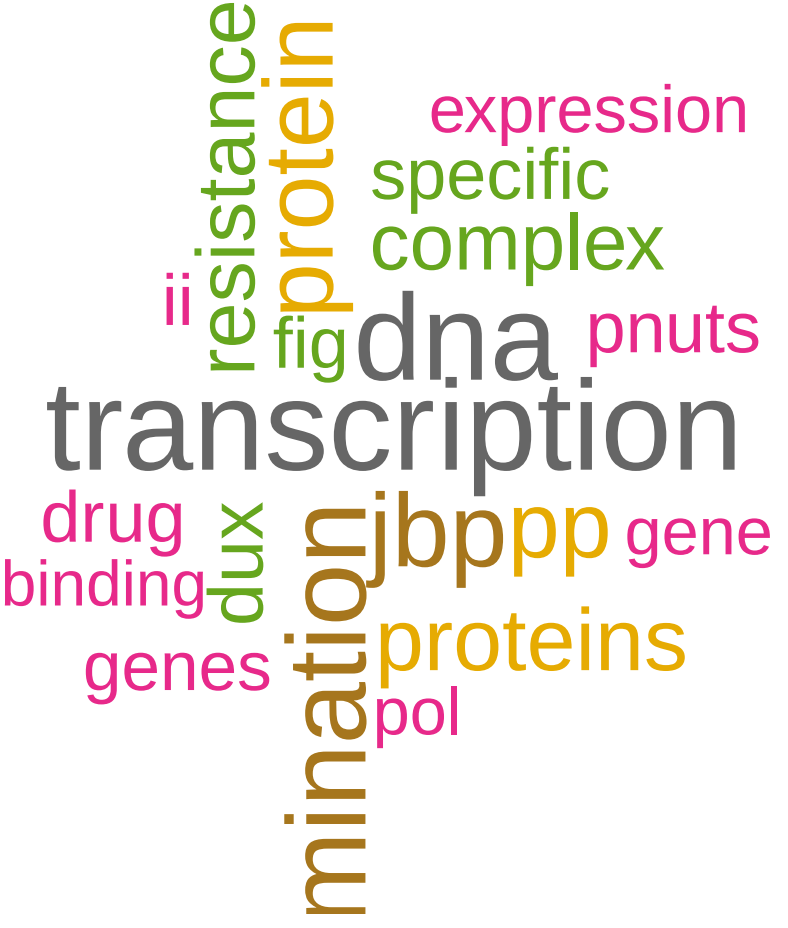
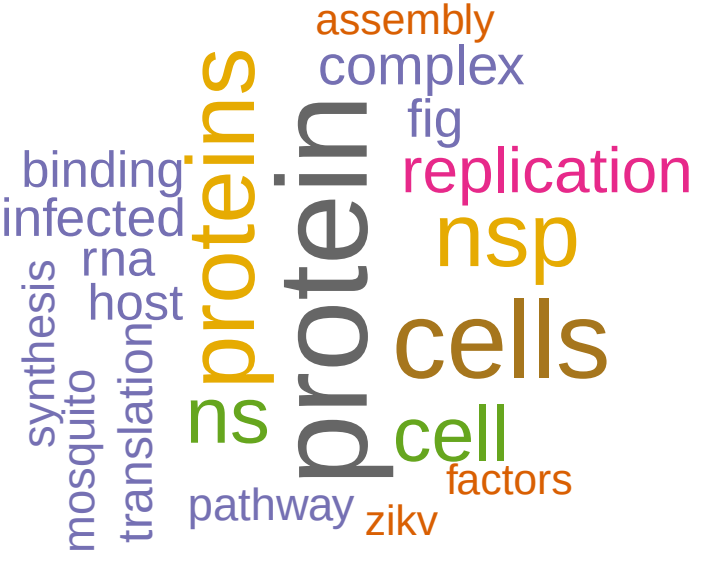

patients
severe
clinical
disease
pneumonia
age
ct
coronavirus
laboratory
wuhan
ii
mortality
characteristics
admission
fever
study
hospital
significantly
symptoms

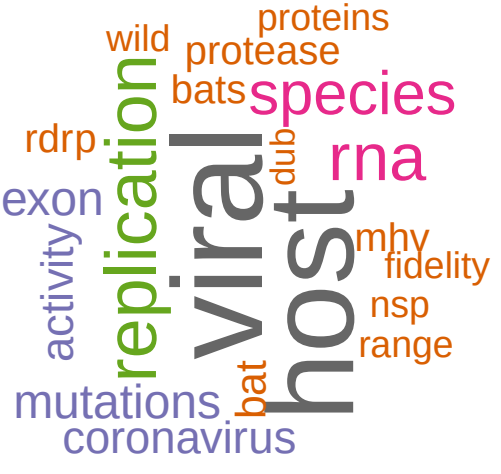

luciferase
membrane
sequence
proteins
ifit
human
previously
peptide
frameshifting
cells
protein
control
site
ml
cell
ccr
mm
min
frameshift
buffer


reuse_allowed
health
_reviewed
study
medical
reuse
peer
display
international
allowed
granted
perpetuity
er_reviewed
medrxiv
perpetuity_peer
display_perpetuity
granted_medrxiv
medrxiv_display
allowed_granted
international_granted

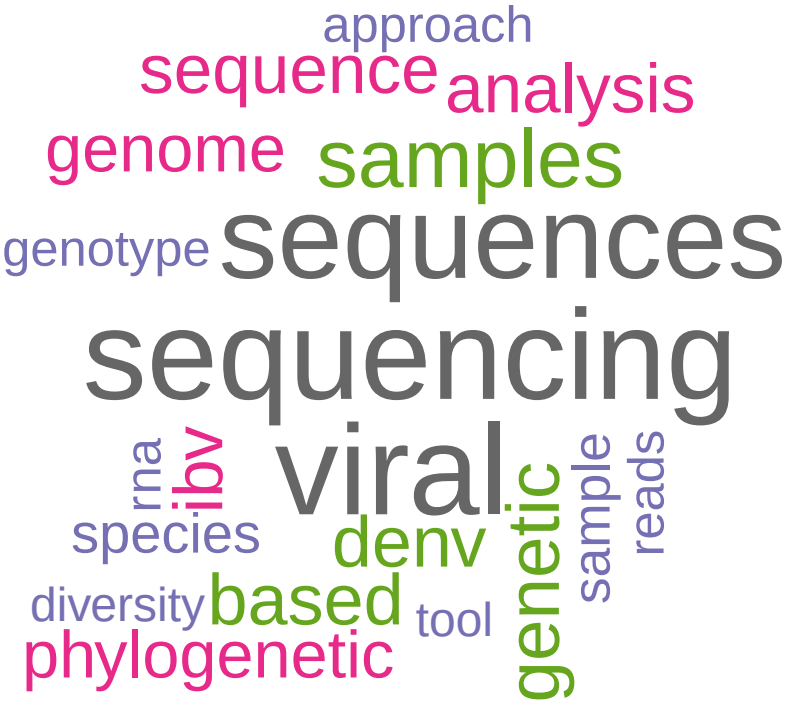

effects
colonies
levels
strains
pollen
nutritional
selection
rates
bees
viral
genetic
foragers
oney
fitness
evolution
immune
immunity
mutation
genes
differences


resistance
protein
expression
specific
complex
ii
fig
dna
pnuts
transcription
drug
dux
jbppp
gene
binding
proteins
genes
pol
mination

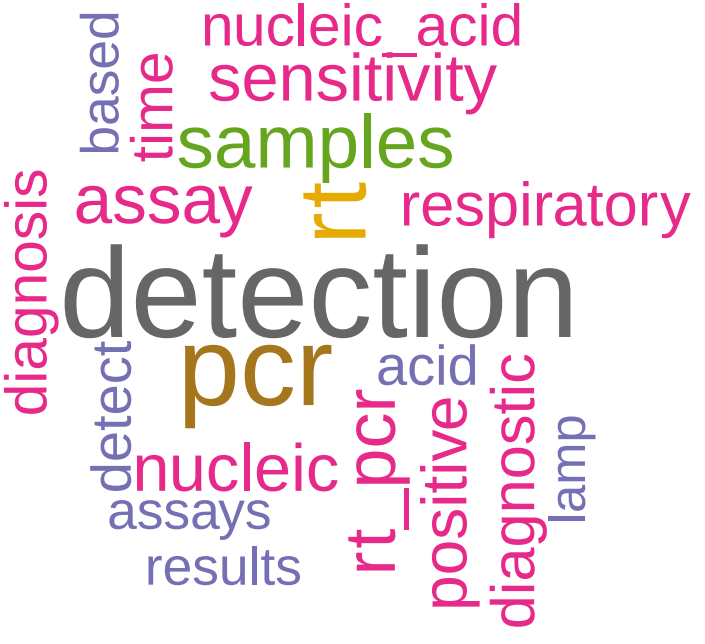

assembly
complex
fig
binding
replication
infected
nsp
rna
host
synthesis
cells
mosquito
translation
proteins
protein
ns
cell
factors
pathway
zikv


proteins
wild
protease
bats
species
rdrp
dub
rna
exon
viral
host
replication
activity
mhv
fidelity
nsp
range
bat
mutations
coronavirus

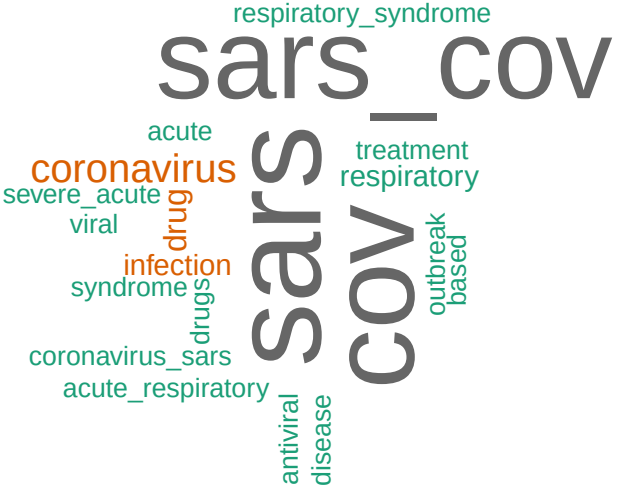

january
measures
rate
hubei
province
days
coronavirus
spread
epidemic
china
ci
control
wuhan
disease
outbreak
model
confirmed
time
ncov
estimated


approach
sequence
analysis
genome
samples
genotype
sequences
sequencing
viral
rna
ibv
species
denv
genetic
sample
reads
diversity
based
tool
phylogenetic


model
models
information
methods
based
studies
method
structure
molecular
behavior
infectious
results
approaches
learning
level
disease
network
predict
approach
prediction


nucleic_acid
sensitivity
based
time
samples
assay
rt
respiratory
diagnosis
detection
pcr
acid
detect
rt_pcr
positive
diagnostic
nucleic
lamp
assays
results


results
restricta
dsrna
epitopes
vaccine
antibody
immune
protein
zika
identified
fungal
study
viral
orf
cell
epitope
binding
amino
strains
antigen


respiratory_syndrome
sars_cov
acute
coronavirus
severe_acute
viral
drug
infection
syndrome
drugs
coronavirus_sars
acute_respiratory
sars
cov
treatment
respiratory
outbreak
based
antiviral
disease


susceptible
growth
outbreak
incidence
infected
estimate
rate
control
generation
disease
population
contact
estimates
epidemic
model
time
interval
transmission
reproduction
measures


including
zikv
gene_expression
cell
infection
cells
expression
antiviral
induced
human
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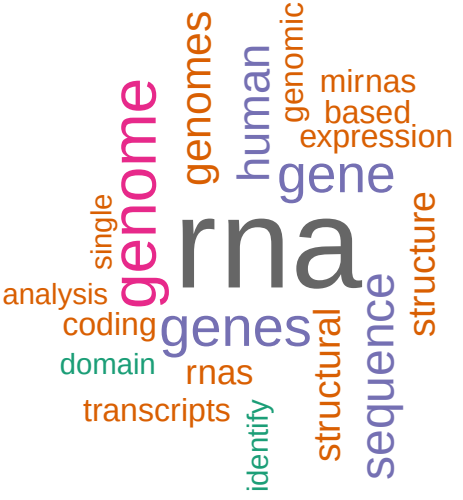
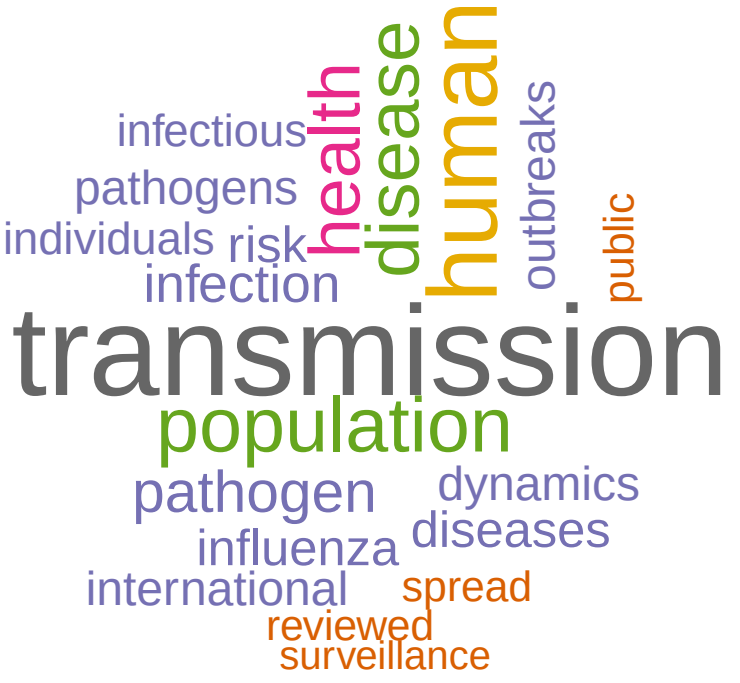
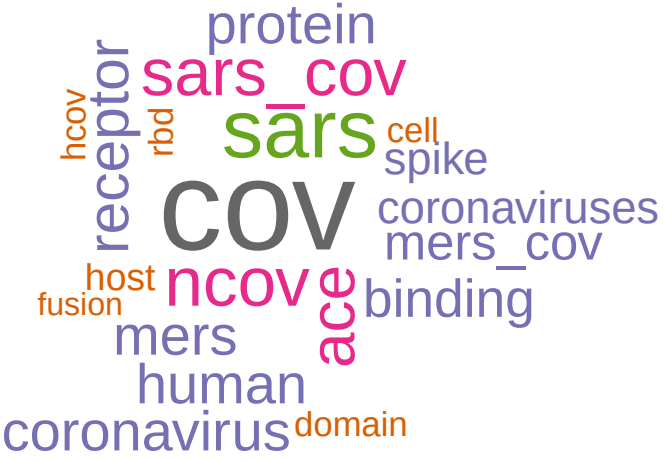
cellular
vivo
signaling
immune
activation
ibv
mice
type
response


rna
genome
genomes
human
genomic
mirnas
based
expression
gene
single
analysis
coding
genes
structure
sequence
structural
domain
rnas
transcripts
identify


infectious
health
disease
human
outbreaks
pathogens
public
individuals
risk
infection
transmission
population
pathogen
dynamics
diseases
influenza
international
spread
reviewed
surveillance


protein
sars_cov
receptor
hcov
rbd
sārs
cell
spike
cov
coronaviruses
mers_cov
host
ncov
ace
binding
fusion
mers
human
coronavirus
domain