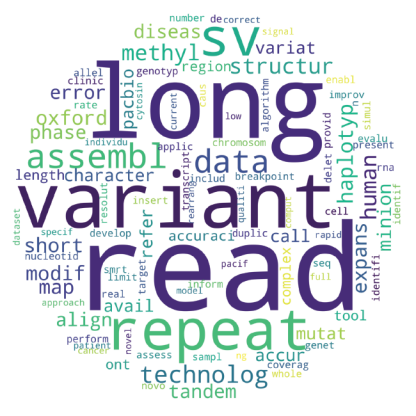
long
variant
read
repeat
assembl
data
sv
methyl
diseas
structur
variat
error
oxford
phase
haplotyp
human
minion
expans
short
modif
map
avail
align
accur
technolog
tandem
mutat
tool
call
accuraci
length
character
refer
pacbio
genotyp
region
algorithm
improv
evaluat
present
breakpoint
chromosom
delet
provid
cell
identifi
dataset
specif
develop
nucleotid
seq
complex
ont
novo
whole
genet
sampl
assess
novel
patient
cancer
coverag
signal
number
correct
clinic
allel
individu
applic
current
transcript
real
inform
model
pacif
rapid
approach
perform
insert
resolut
qualit
duplic
target
limit
sprt
full
low
rate
cytosin
bias
enabl
simul

oxford
technolog
minion
read
error
data
assembl
platform
long
new
approach
refer
clinic
align
devic
accuraci
applic
tool
perform
portabl
call
rapid
sampl
short
improv
accur
mutatrate
genet
produc
human
strain
novel
rna
hla
viru
map
real
requir
specif
quality
variant
achiev
enabl
identif
fist
next
pcr
region
microbi
provid
recent
field
resist
avail
commun
correct
cost
limit
challeng
basecall
identifiti
illumina
inform
coverag
complex
bacteri
current
potenti
pipelin
comput
throughput
multiplex
isol
consensu
research
target
metagenom
length
speci
characterist
make
pathogen
multiplex
compar
product
genomic
log
test

read
longspeci
complet
assembl
chromosom
pacbio
draft
strain
mb
qualiti
resourc
isol
technolog
contig
novo
de
illumina
data
plant
improv
obtain
genet
refer
size
level
scaffold
annot
hybrid
chloroplast
structur
compar
evolut
plasmid
mitochondri
repeat
mbp
dsm
protein
region
copi
fish
wide
insert
identifi
code
variat
approach
minion
platform
resist
oxford
pathogen
error
total
analys
element
bp
function
produc
highli
larg
length
contain
avail
famili
develop
report
combin
halomona
fragment
genomic
predict
naked
dna
include
copiedi
ko
plasmid
short
first
scale
breed
yeast
coverag
cell
bacteria
genome
multiplex
log
complex
pipelin
comput
throughput
isol
consensu
research
target
metagenom
length
speci
characterist
make
pathogen
multiplex
compar
product
genomic
log
test
bias
cytosin
genotyp
region
algorithm
improv
evaluat
present
breakpoint
chromosom
delet
provid
cell
identifi
dataset
specif
develop
nucleotid
seq
complex
ont
novo
whole
genet
sampl
assess
novel
patient
cancer
coverag
signal
number
correct
clinic
allel
individu
applic
current
transcript
real
inform
model
pacif
rapid
approach
perform
insert
resolut
qualit
duplic
target
limit
sprt
full
low
rate
cytosin
bias
enabl
simul