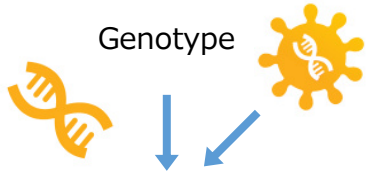

Genotype

???


Phenotype

1. Bacterial genome sequence from GenBank etc.

NCBI

```
ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA CACTGTAAATACCTGGGGGC
ATAACAACAACGCCGGAAAG GCAGGCTCCCTGTAAATATC GATCTGGGTCACACAATTAC TTTATCGTTTCAGCACCAAT
TGCAGCGATGCCTTTTTGCA AGCTGGGCAAACTAAGTATC TGACCCCGCATAAGGAATAG AACATGCTCCATCCGCGAGC CAGA
```

ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA CACTGTAAATACCTGGGGGC
ATAACAACAACGCCGGAAAG GCAGGCTCCCTGTAAATATC GATCTGGGTCACACAATTAC TTTATCGTTTCAGCACCAAT
TGCAGCGATGCCTTTTTGCA AGCTGGGCAAACTAAGTATC TGACCCCGCATAAGGAATAG AACATGCTCCATCCGCGAGC CAGA

2. Annotating genome (RegulonDB, Ecocyc Genbank etc.)

ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA CACTGTAAATACCTGGGGGC
ATAACAACAACGCCGGAAAG GCAGGCTCCCTGTAAATATC GATCTGGGTCACACAATTAC TTTATCGTTTCAGCACCAAT
TGCAGCGATGCCTTTTTGCA AGCTGGGCAAACTAAGTATC TGACCCCGCATAAGGAATAG AACATGCTCCATCCGCGAGC CAGA

3. Simulation of gene expression

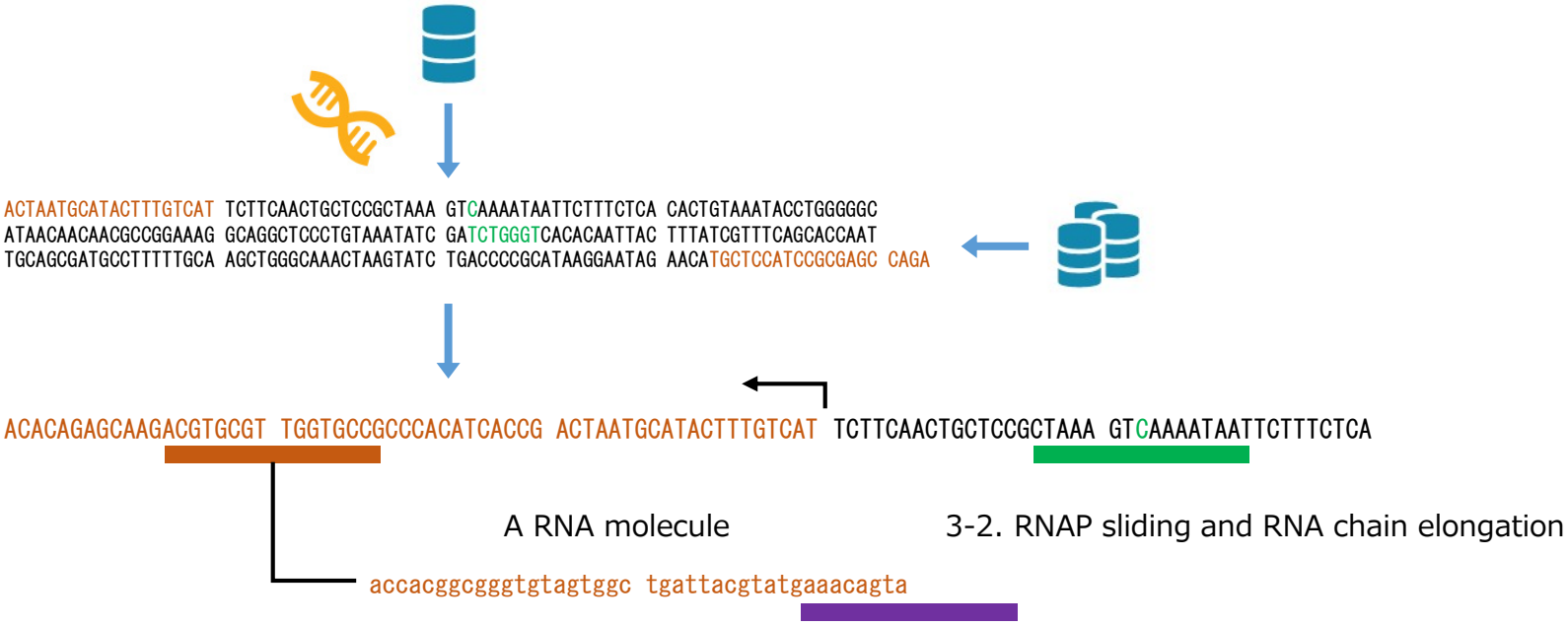
ACACAGAGCAAGACGTGCGT TGGTGCCGCCCACATCACCG ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA

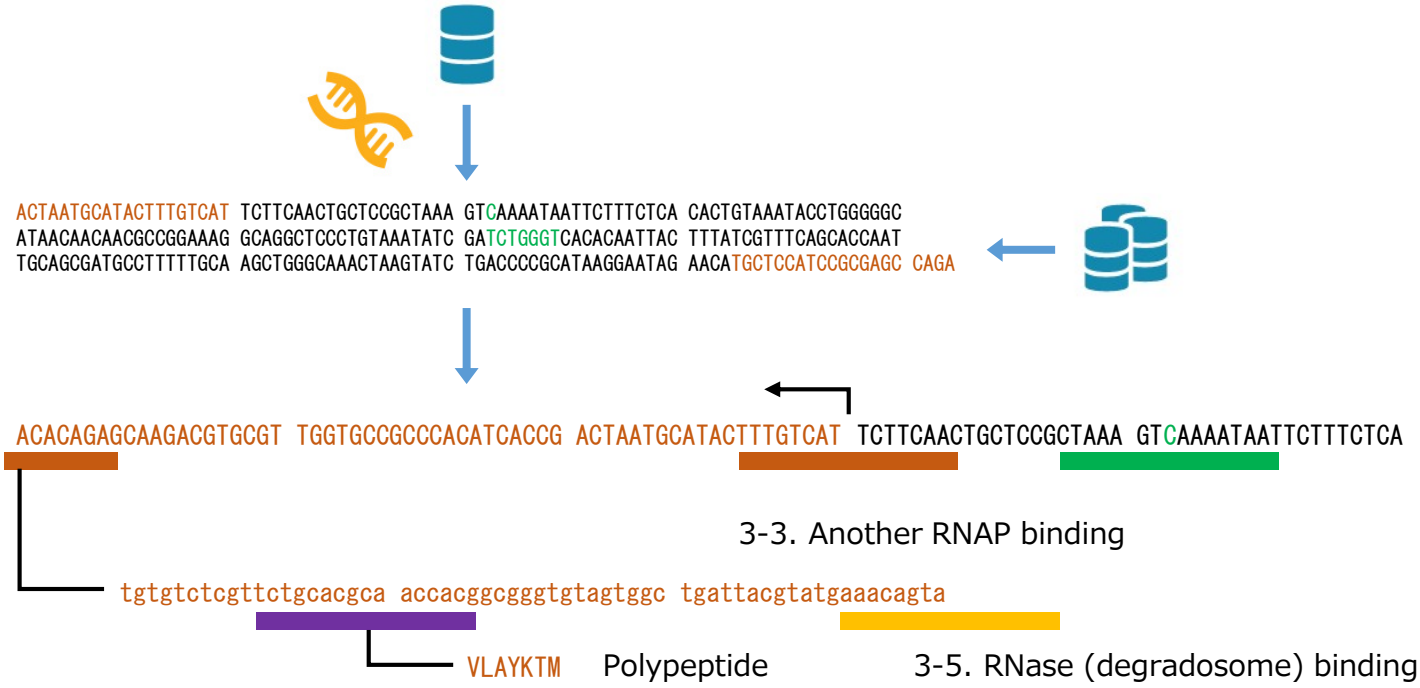
A DNA molecule

RNA polymerase

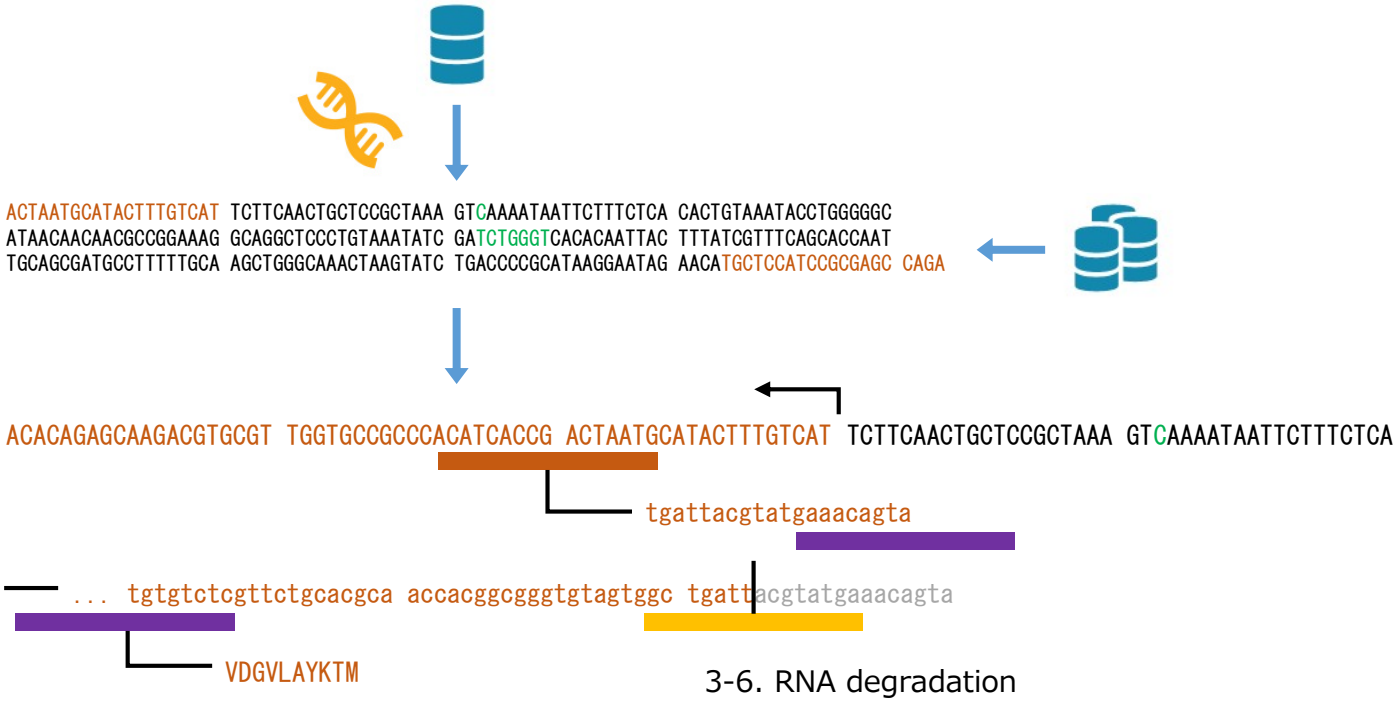
sigma70

3-1. Binding of Molecules on a DNA molecule

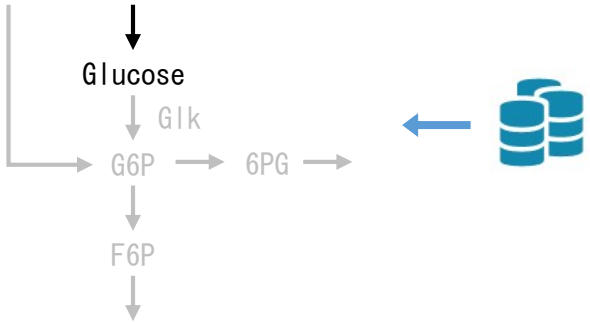

ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA CACTGTAAATACCTGGGGGC
ATAACAACAACGCCGGAAAG GCAGGCTCCCTGTAAATATC GATCTGGGTCACACAATTAC TTTATCGTTTCAGCACCAAT
TGCAGCGATGCCTTTTTGCA AGCTGGGCAAACTAAGTATC TGACCCCGCATAAGGAATAG AACATGCTCCATCCGCGAGC CAGA
ACACAGAGCAAGACGTGCGT TGGTGCCGCCCACATCACCG ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA
A RNA molecule
3-2. RNAP sliding and RNA chain elongation
accacggcgggtgtagtggc tgattacgtatgaaacagta
3-3. Ribosome binding

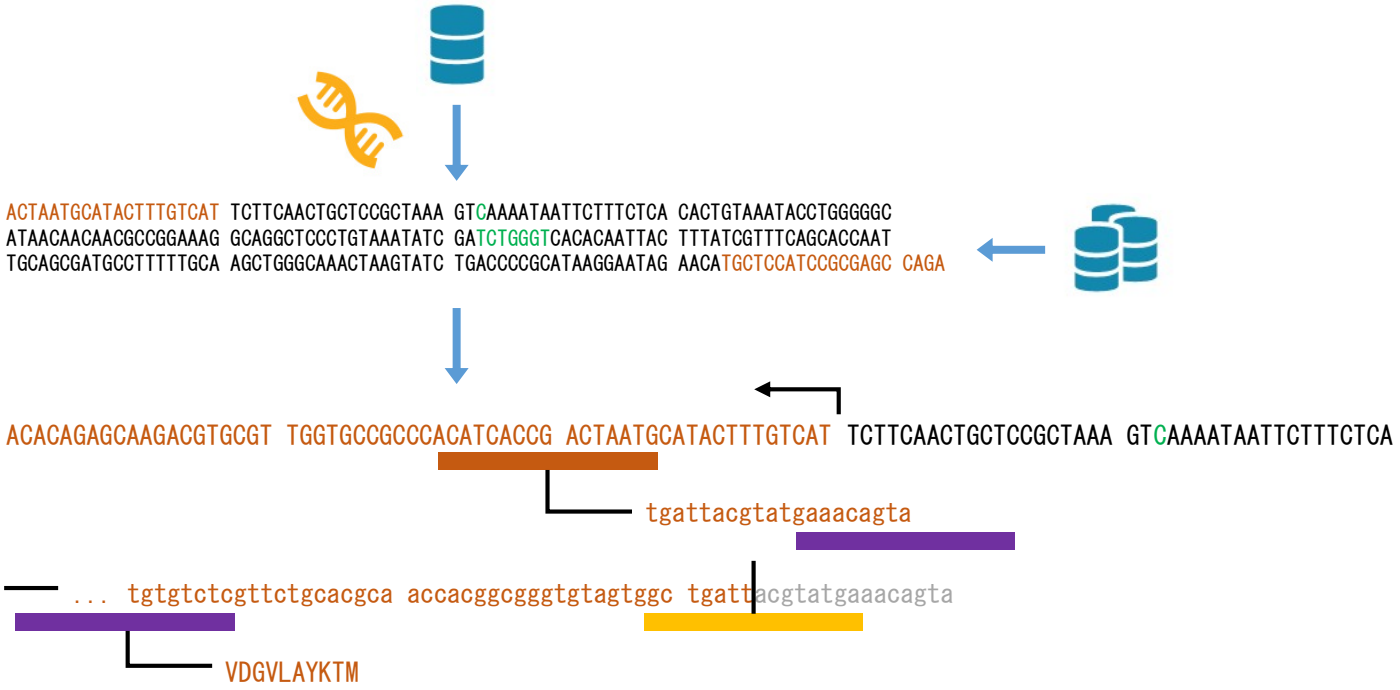


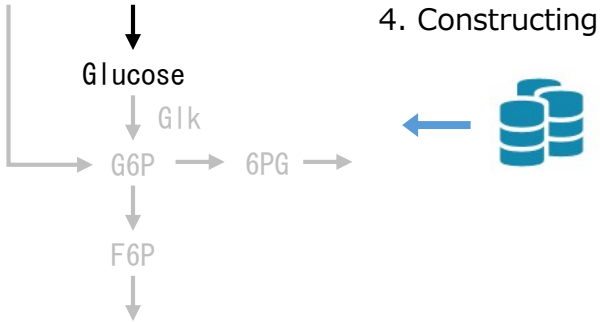
3-4. Ribosome Sliding and AA chain elongation



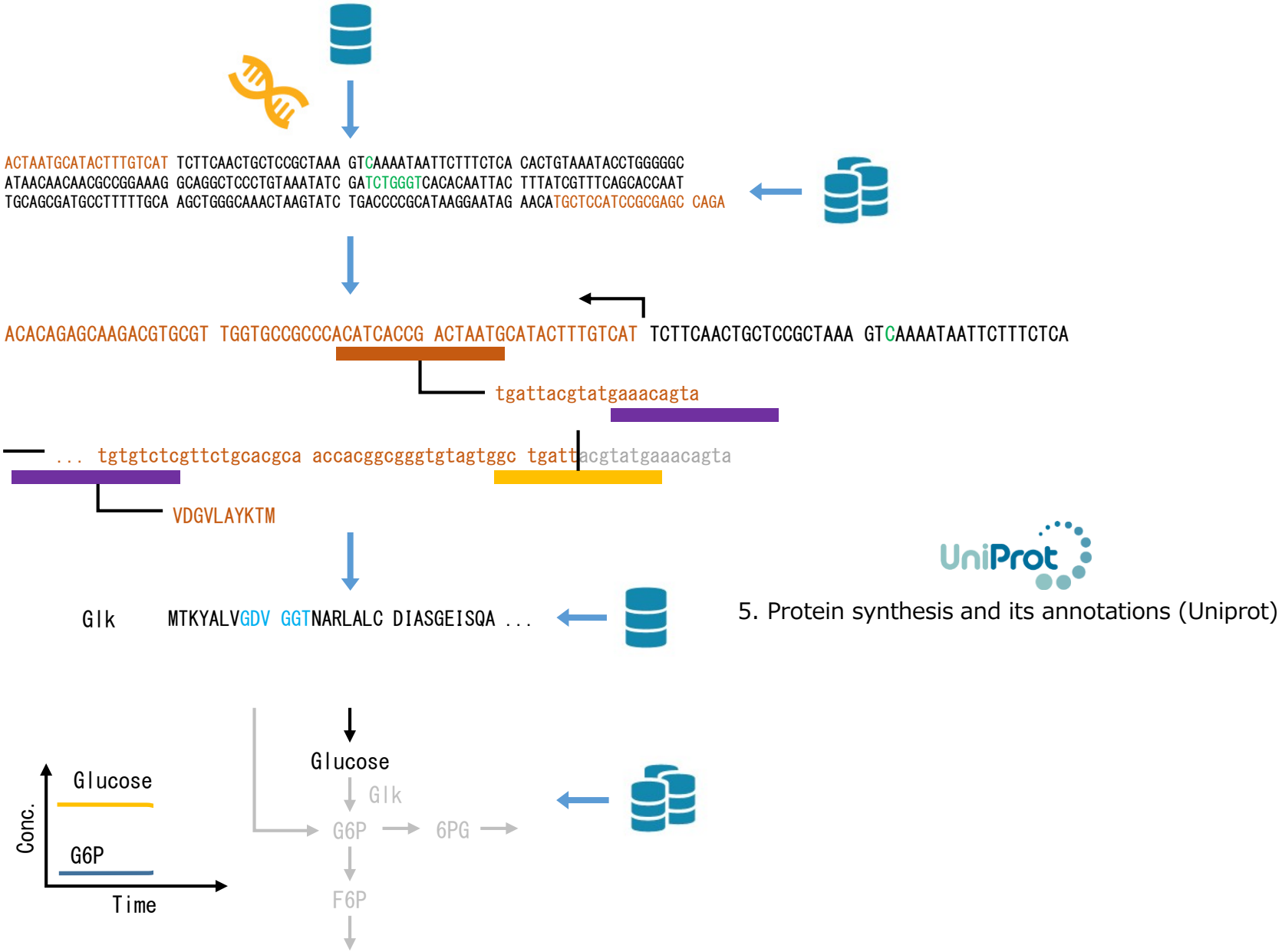
3-6. RNA degradation

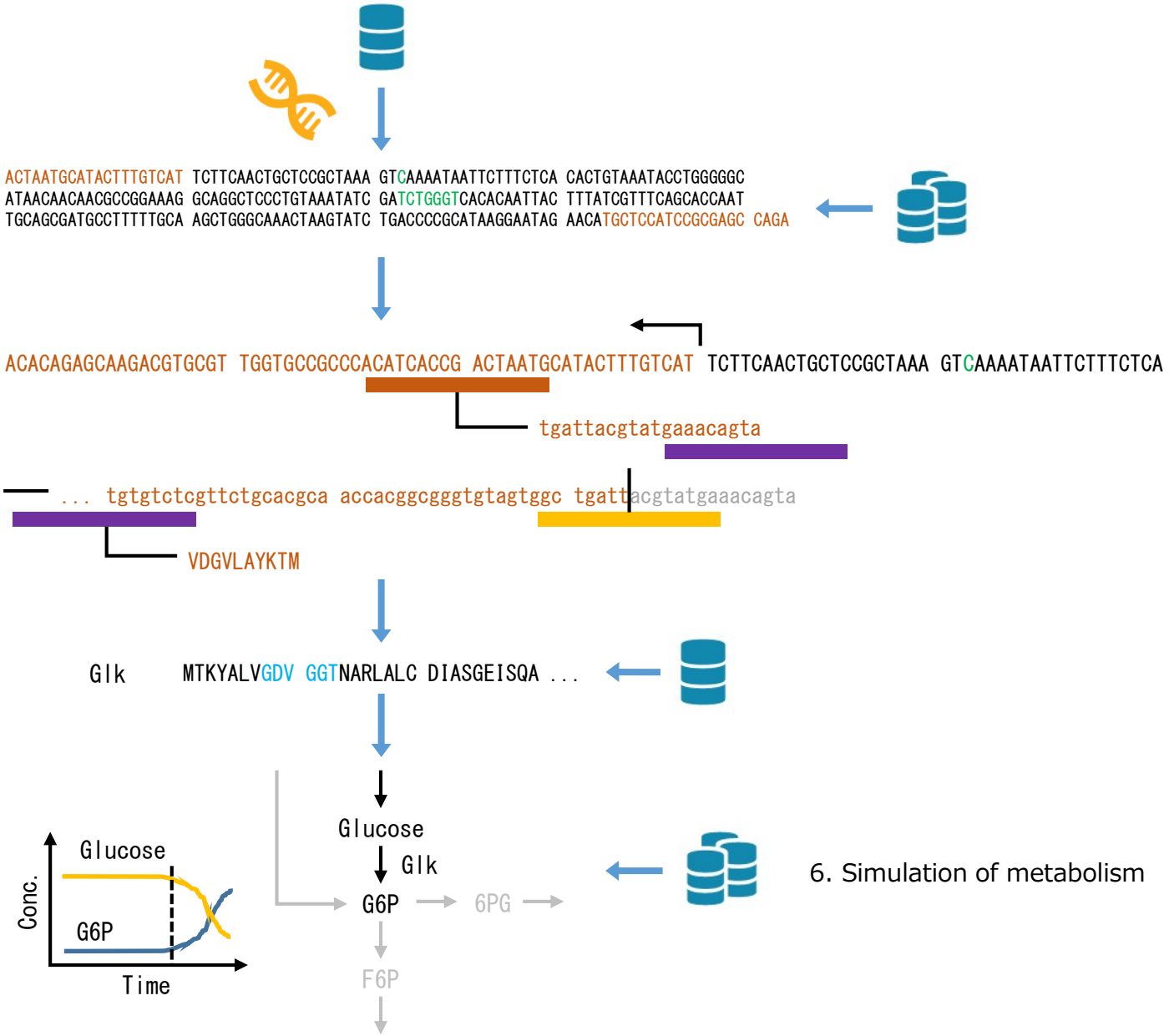




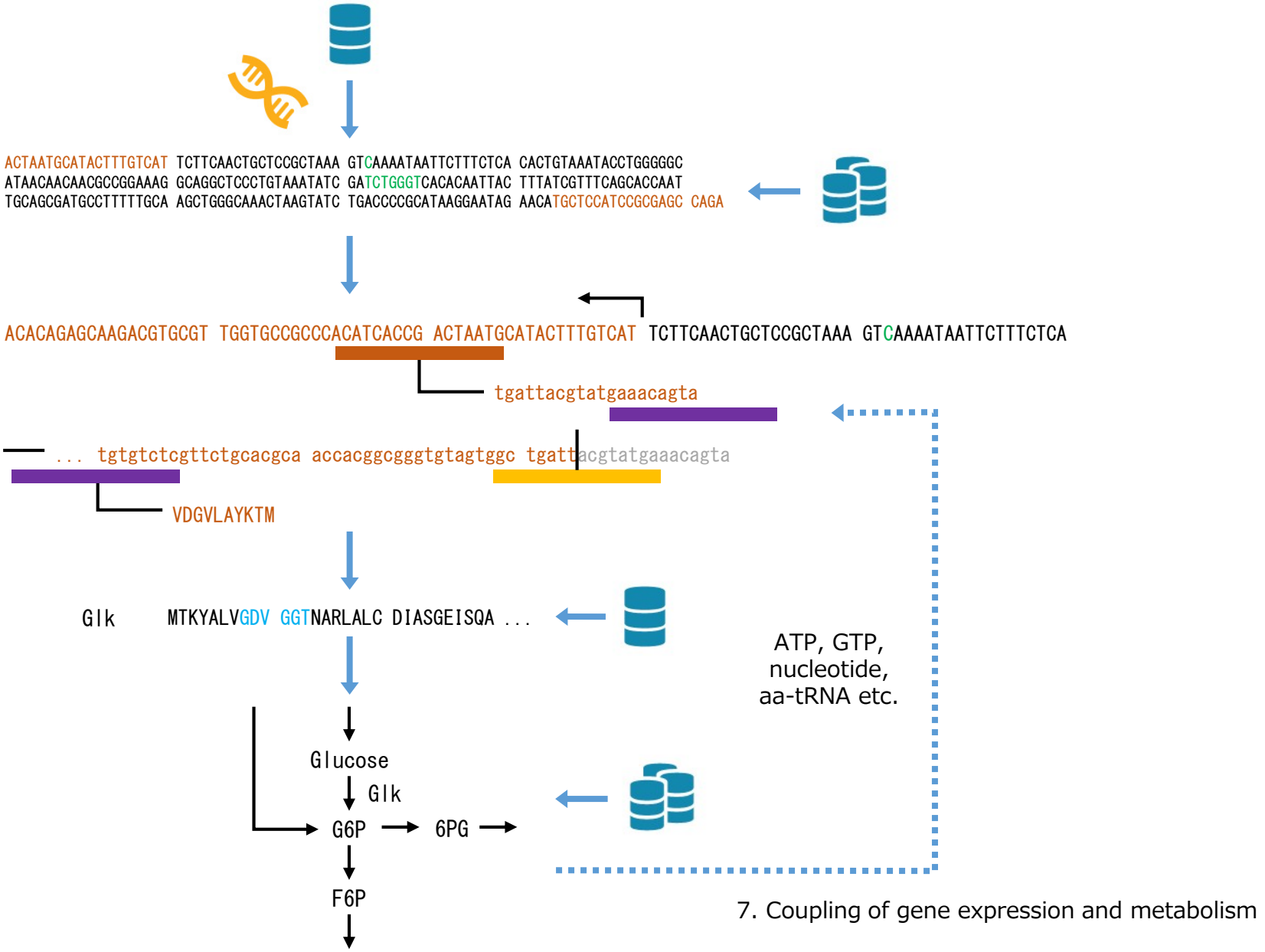


4. Constructing metabolic pathways (Ecocyc, KEGG, BRENDA etc.)

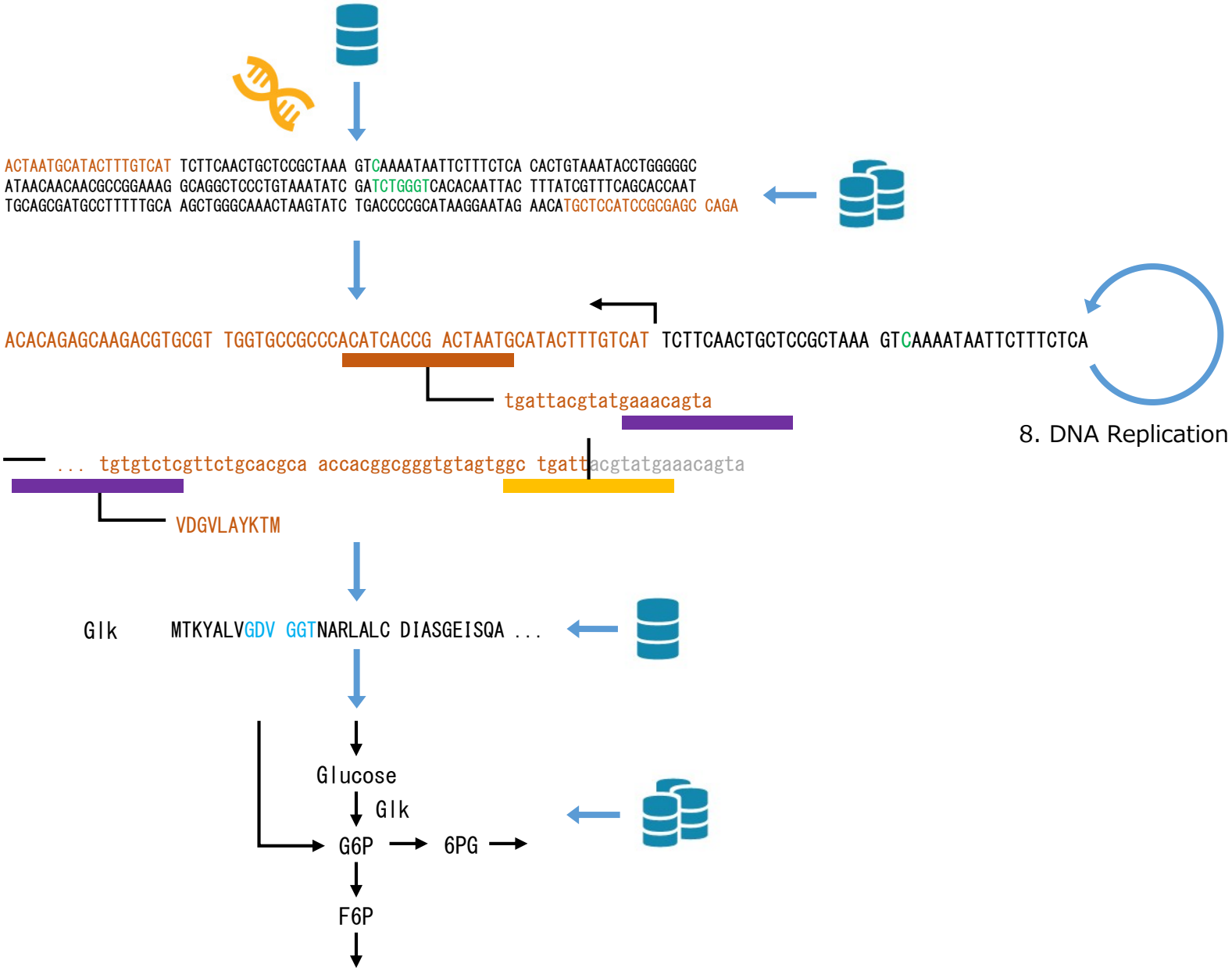

ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA CACTGTAAATACCTGGGGGC
ATAACAACAACGCCGGAAAG GCAGGCTCCCTGTAAATATC GATCTGGGTCACACAATTAC TTTATCGTTTCAGCACCAAT
TGCAGCGATGCCTTTTTGCA AGCTGGGCAAACTAAGTATC TGACCCCGCATAAGGAATAG AACATGCTCCATCCGCGAGC CAGA
ACACAGAGCAAGACGTGCGT TGGTGCCGCCCACATCACCG ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA
tgattacgtatgaaacagta
... tgtgtctcgttctgcacgca accacggcgggtgtagtggc tgattacgtatgaaacagta
VDGVLAYKTM
Glk MTKYALVGDV GGTNARLALC DIASGEISQA ...
UniProt
5. Protein synthesis and its annotations (Uniprot)
Glucose
G6P
Conc.
Time
Glucose
Glk
G6P
6PG
F6P

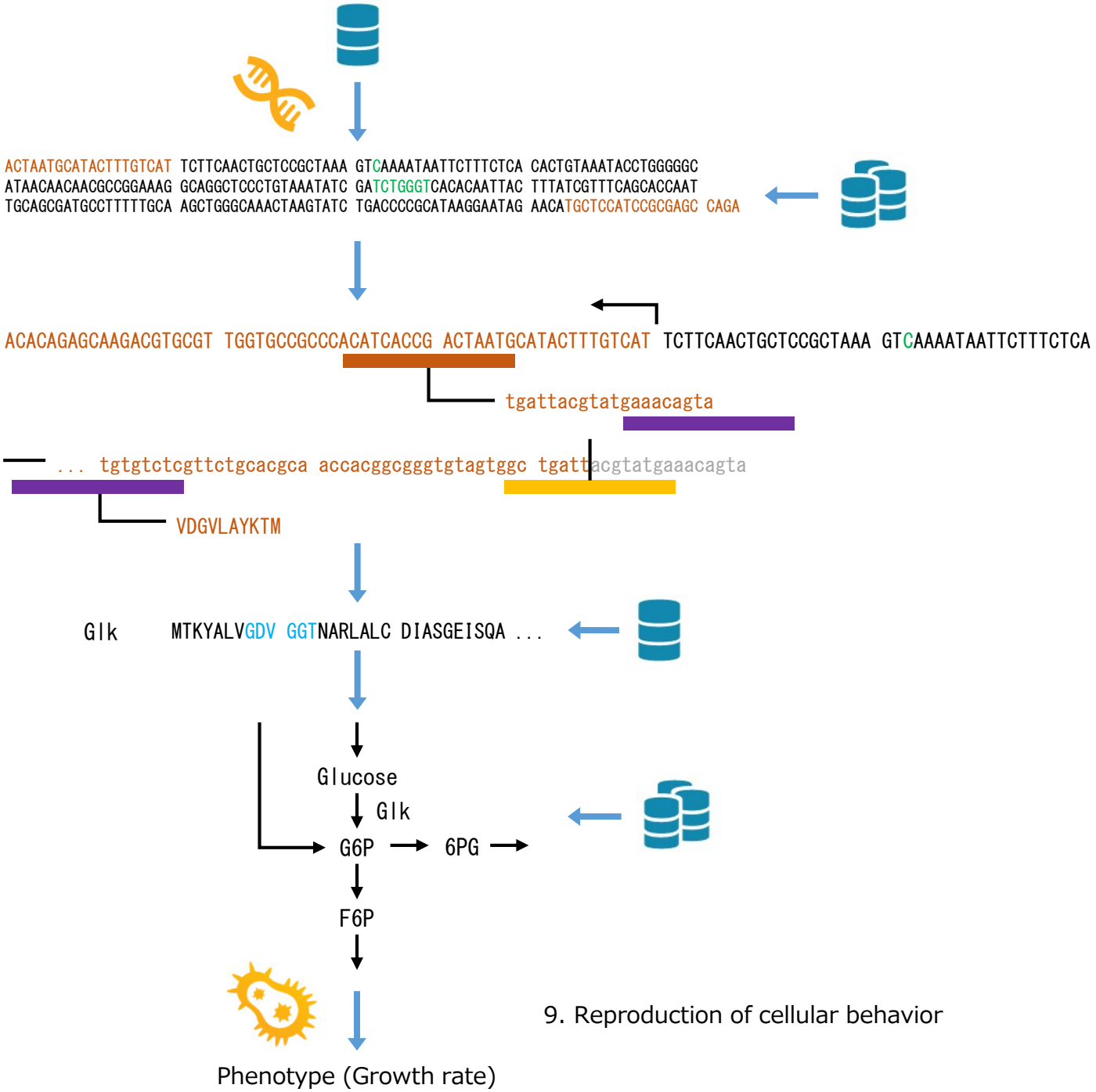


6. Simulation of metabolism

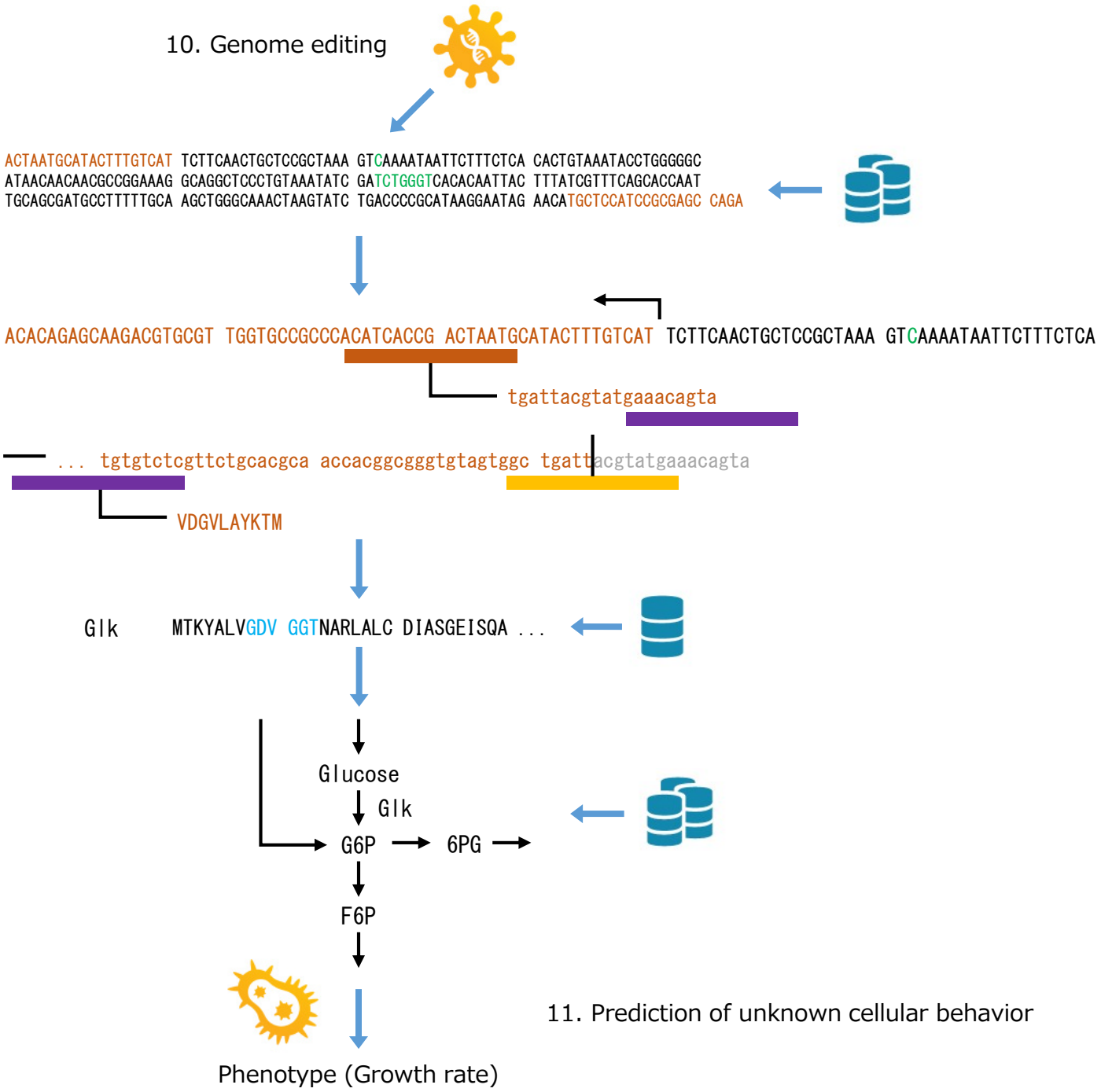


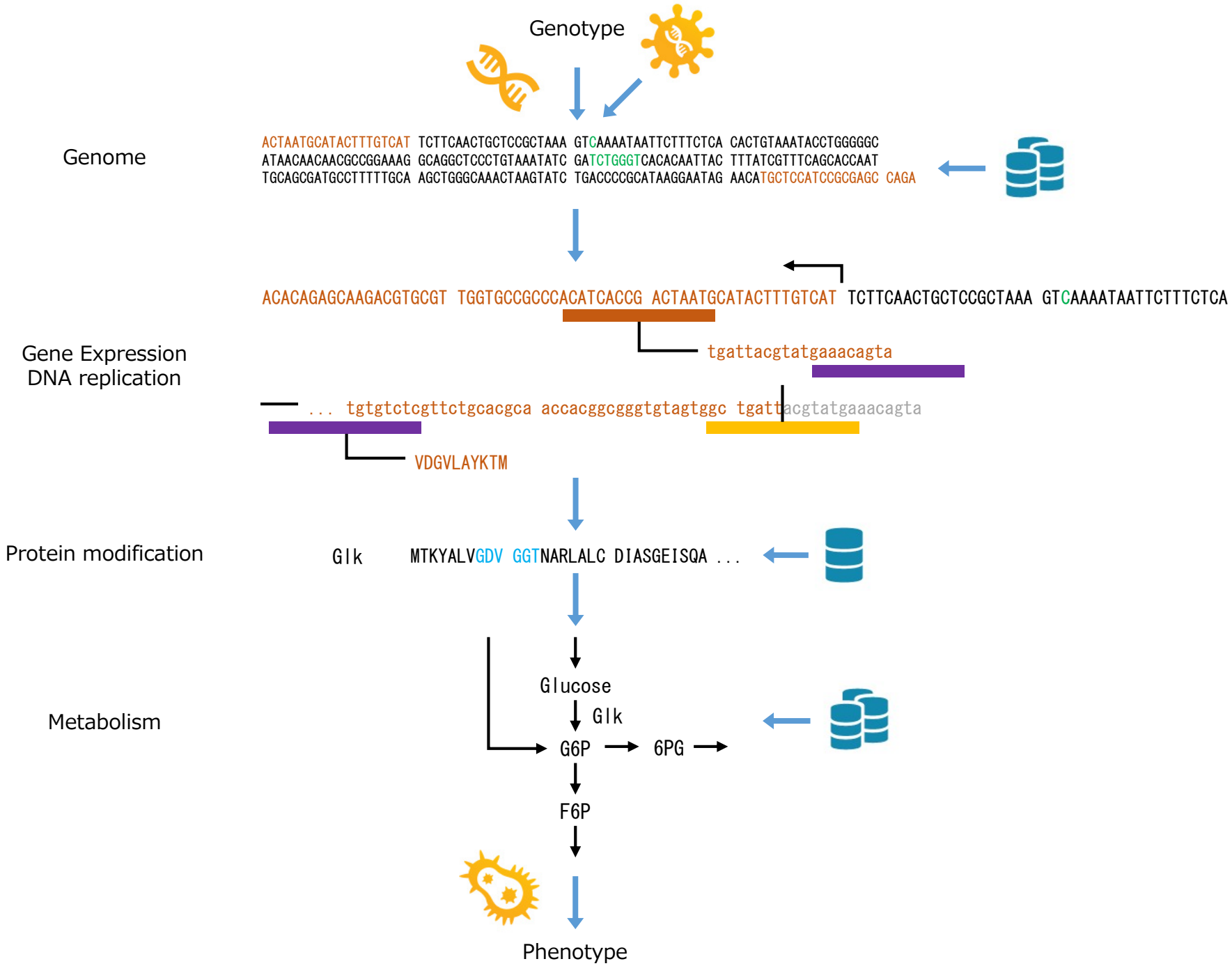
7. Coupling of gene expression and metabolism


ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA CACTGTAAATACCTGGGGGC
ATAACAACAACGCCGGAAAG GCAGGCTCCCTGTAAATATC GATCTGGGTCACACAATTAC TTTATCGTTTCAGCACCAAT
TGCAGCGATGCCTTTTTGCA AGCTGGGCAAACTAAGTATC TGACCCCGCATAAGGAATAG AACATGCTCCATCCGCGAGC CAGA
ACACAGAGCAAGACGTGCGT TGGTGCCGCCCACATCACCG ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA
tgattacgtatgaaacagta
8. DNA Replication
... tgtgtctcgttctgcacgca accacggcgggtgtagtggc tgattacgtatgaaacagta
VDGVLAYKTM
Glk MTKYALVGDV GGTNARLALC DIASGEISQA ...
Glucose
Glk
G6P
6PG
F6P

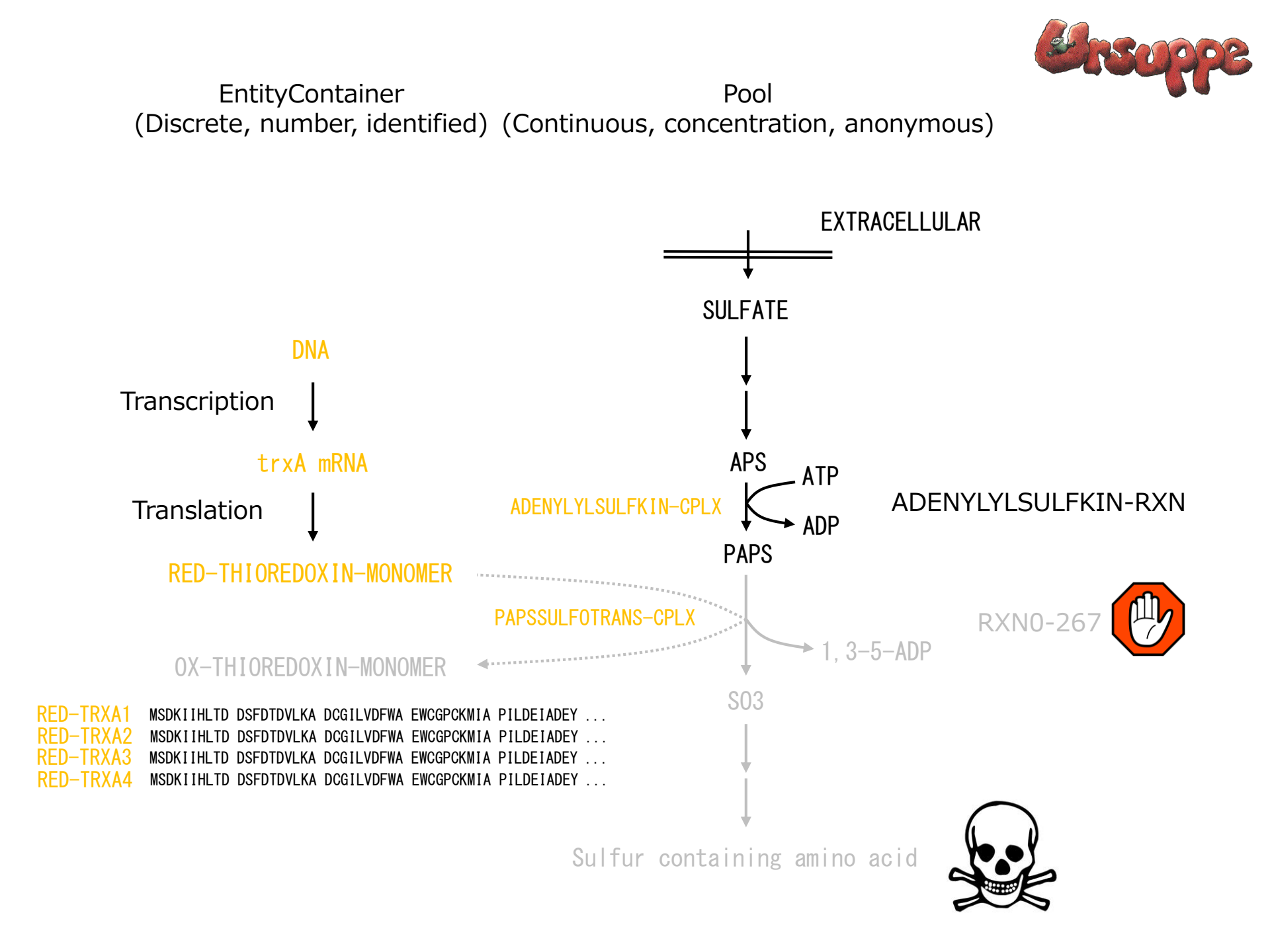


9. Reproduction of cellular behavior


10. Genome editing
ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA CACTGTAAATACCTGGGGGC
ATAACAACAACGCCGGAAAG GCAGGCTCCCTGTAAATATC GATCTGGGTCACACAATTAC TTTATCGTTTCAGCACCAAT
TGCAGCGATGCCTTTTTGCA AGCTGGGCAAACTAAGTATC TGACCCCGCATAAGGAATAG AACATGCTCCATCCGCGAGC CAGA
ACACAGAGCAAGACGTGCGT TGGTGCCGCCCACATCACCG ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA
tgattacgtatgaaacagta
... tgtgtctcgttctgcacgca accacggcgggtgtagtggc tgattacgtatgaaacagta
VDGVLAYKTM
Glk MTKYALVGDV GGTNARLALC DIASGEISQA ...
Glucose
Glk
G6P
6PG
F6P
Phenotype (Growth rate)
11. Prediction of unknown cellular behavior

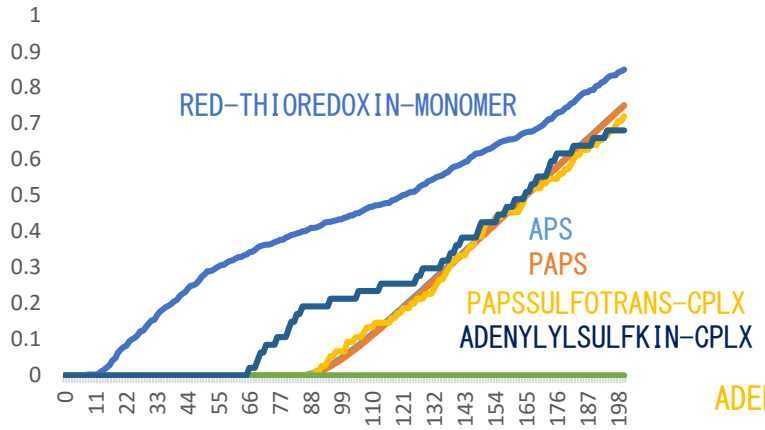

Genotype
Genome
ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA CACTGTAAATACCTGGGGGC
ATAACAACAACGCCGGAAAG GCAGGCTCCCTGTAAATATC GATCTGGGTCACACAATTAC TTTATCGTTTCAGCACCAAT
TGCAGCGATGCCTTTTTGCA AGCTGGGCAAACTAAGTATC TGACCCCGCATAAGGAATAG AACATGCTCCATCCGCGAGC CAGA
Gene Expression
DNA replication
ACACAGAGCAAGACGTGCGT TGGTGCCGCCCACATCACCG ACTAATGCATACTTTGTCAT TCTTCAACTGCTCCGCTAAA GTCAAAATAATTCTTTCTCA
tgattacgtatgaaacagta
... tgtgtctcgttctgcacgca accacggcgggtgtagtggc tgattacgtatgaaacagta
VDGVLAYKTM
Protein modification
Glk MTKYALVGDV GGTNARLALC DIASGEISQA ...
Metabolism
Glucose
Glk
G6P
6PG
F6P
Phenotype

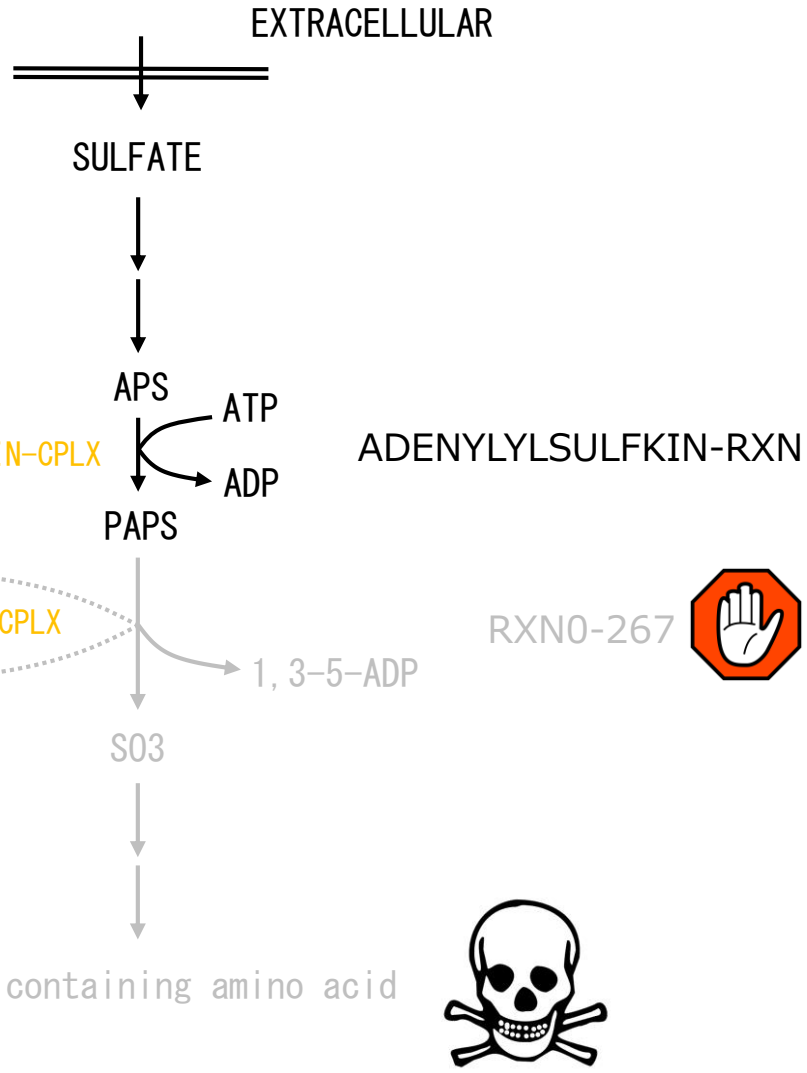
という説明スライドを作った。


EntityContainer
(Discrete, number, identified)
Pool
(Continuous, concentration, anonymous)
EXTRACELLULAR
SULFATE
DNA
Transcription
trxA mRNA
Translation
RED-THIOREDOXIN-MONOMER
APS
ATP
ADENYLYLSULFKIN-CPLX
ADP
ADENYLYLSULFKIN-RXN
PAPS
PAPSSULFOTRANS-CPLX
RXN0-267
1,3-5-ADP
OX-THIOREDOXIN-MONOMER
SO3
RED-TRXA1 MSDKIIHLTD DSFDTDVLKA DCGILVDFWA EWCGPCKMIA PILDEIADEY ...
RED-TRXA2 MSDKIIHLTD DSFDTDVLKA DCGILVDFWA EWCGPCKMIA PILDEIADEY ...
RED-TRXA3 MSDKIIHLTD DSFDTDVLKA DCGILVDFWA EWCGPCKMIA PILDEIADEY ...
RED-TRXA4 MSDKIIHLTD DSFDTDVLKA DCGILVDFWA EWCGPCKMIA PILDEIADEY ...
Sulfur containing amino acid

EntityContainer
(Discrete, number, identified)

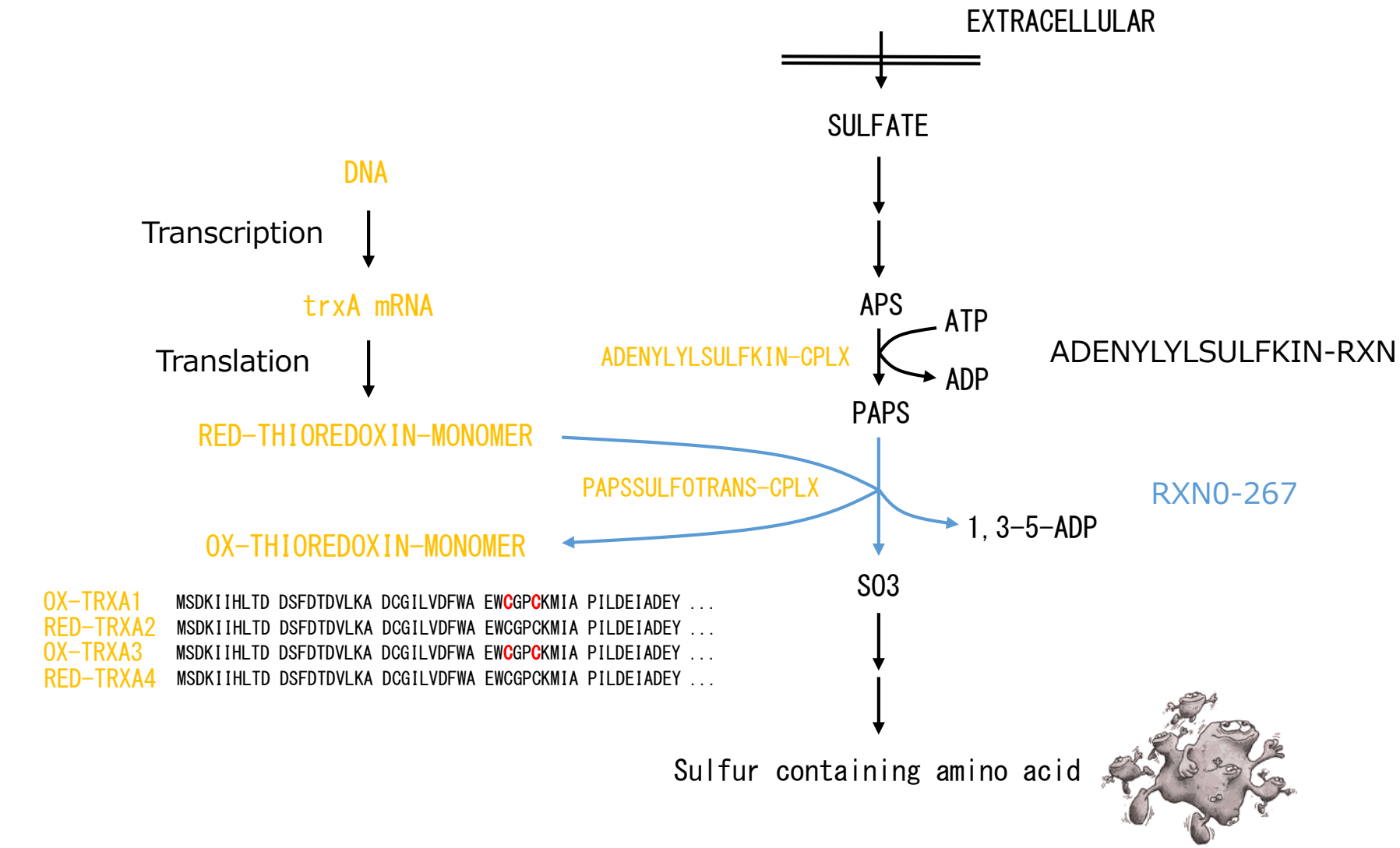
Pool
(Continuous, concentration, anonymous)





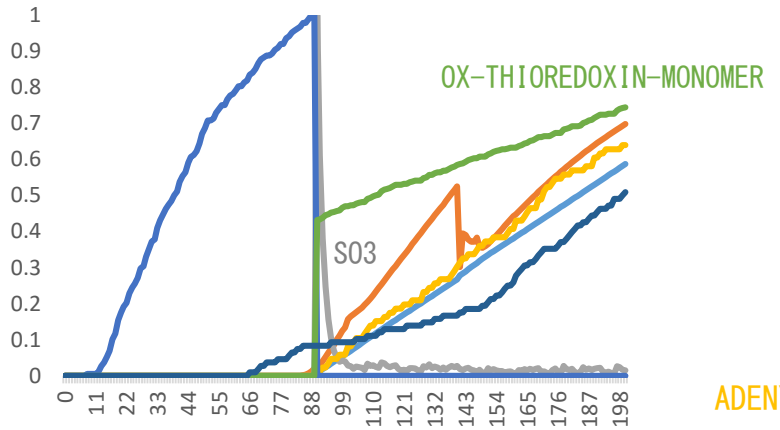
EntityContainer
(Discrete, number, identified)

Pool
(Continuous, concentration, anonymous)



EntityContainer
(Discrete, number, identified)

Pool
(Continuous, concentration, anonymous)



EXTRACELLULAR

SULFATE

APS

ATP

ADENYLYLSULFKIN-CPLX

ADP

ADENYLYLSULFKIN-RXN

PAPS

RED-THIOREDOXIN-MONOMER

PAPSSULFOTRANS-CPLX

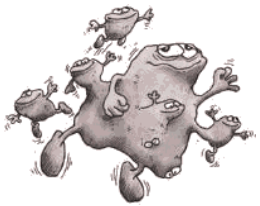
RXN0-267

OX-THIOREDOXIN-MONOMER

1,3-5-ADP

SO3

Sulfur containing amino acid



ハッカソンと言えば温泉♨である。

今回の参加者は20名程度になった。

時は来た！ 資金は…ない！