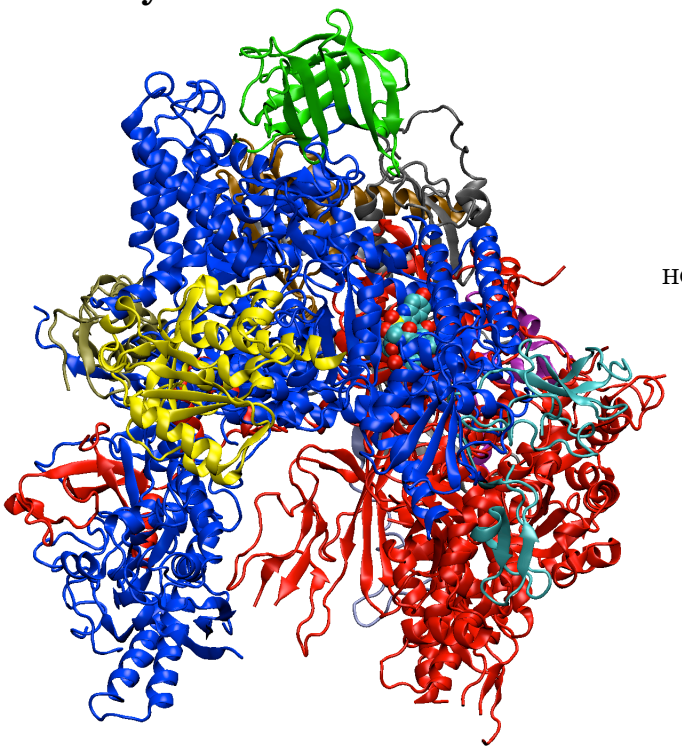
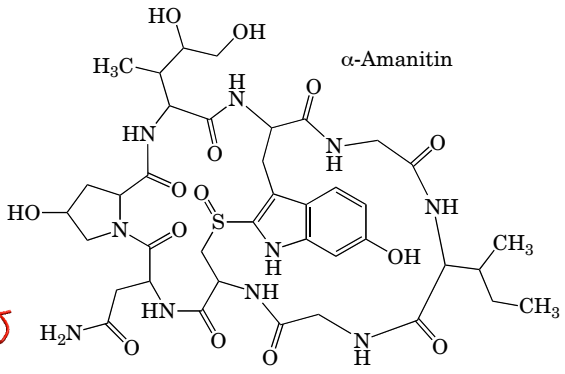
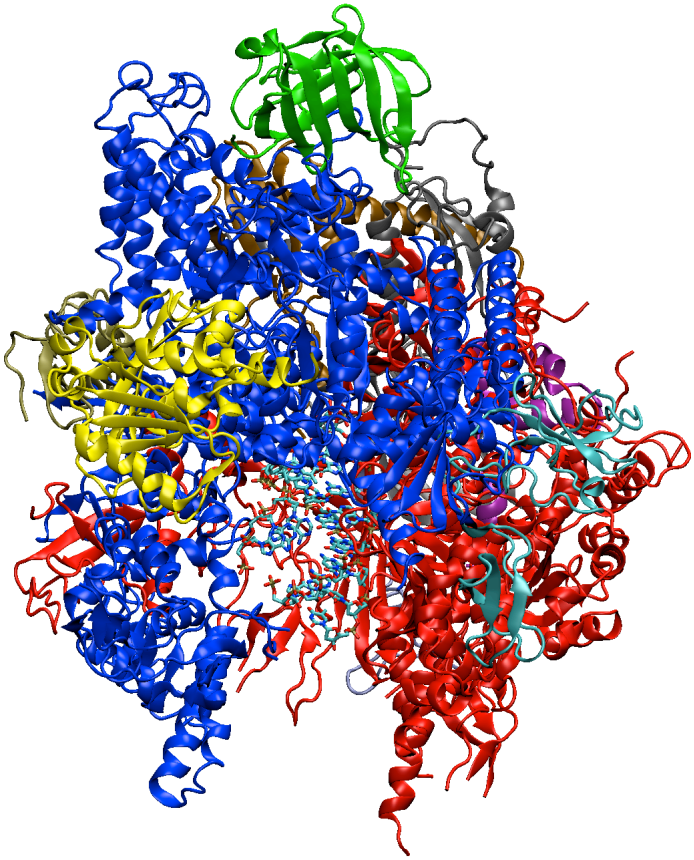
**RNA Polymerase**

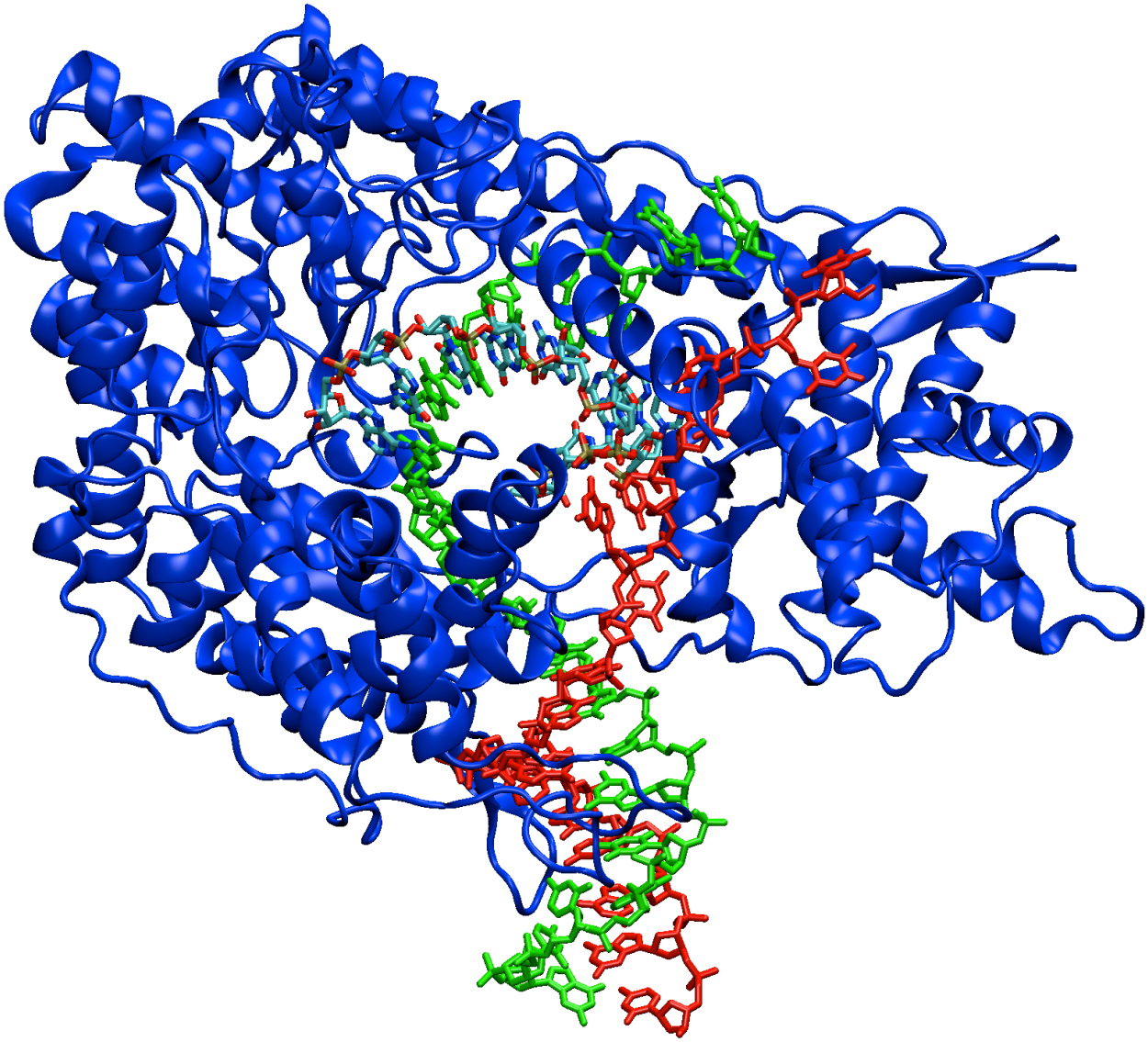




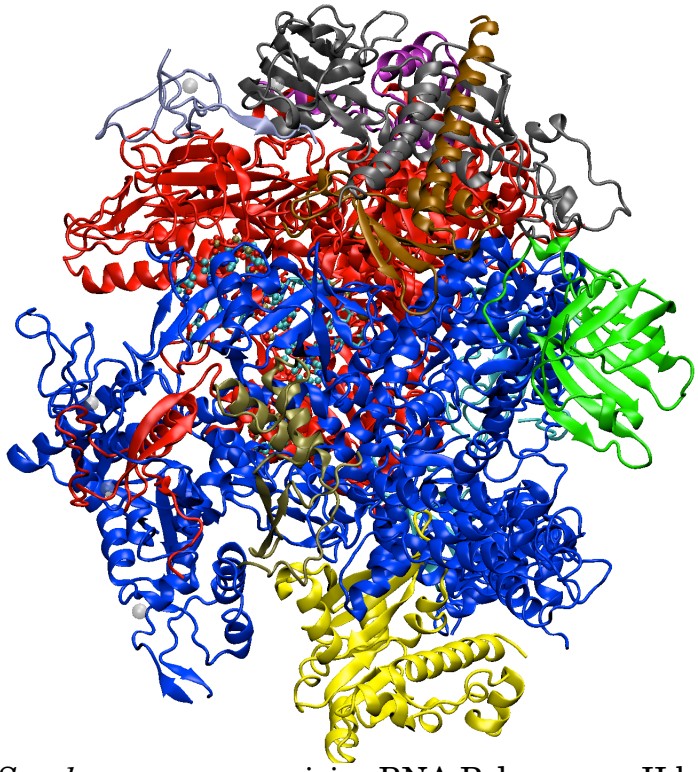

*Saccharomyces cerevisiae* RNA Polymerase II bound to α-amanitin pdb ID 1K83)



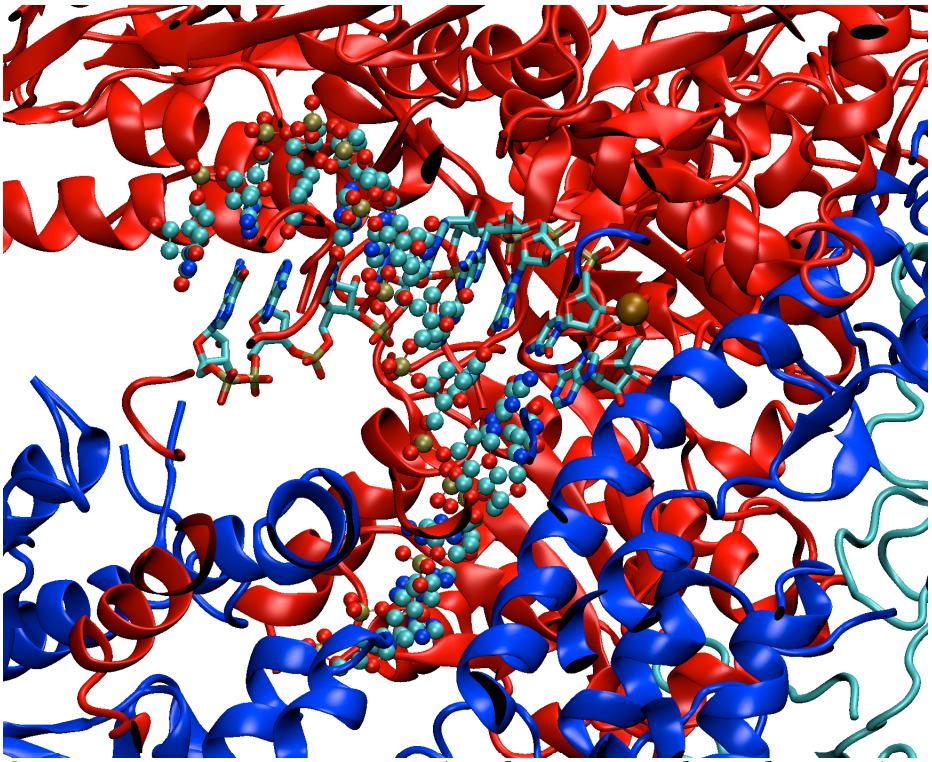
*Saccharomyces cerevisiae* RNA Polymerase II bound to RNA and DNA pdb ID 1I6H)



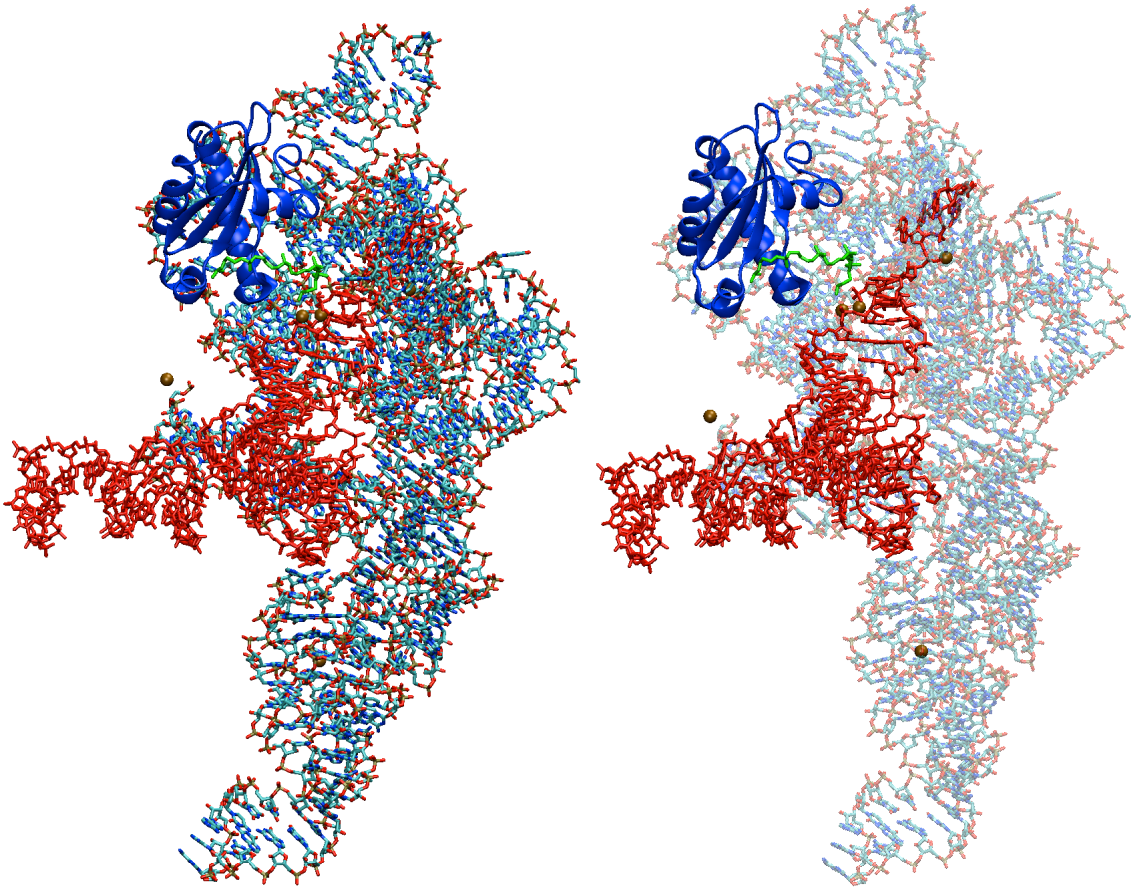
T7 RNA polymerase bound to DNA and RNA (pdb ID 1MSW)



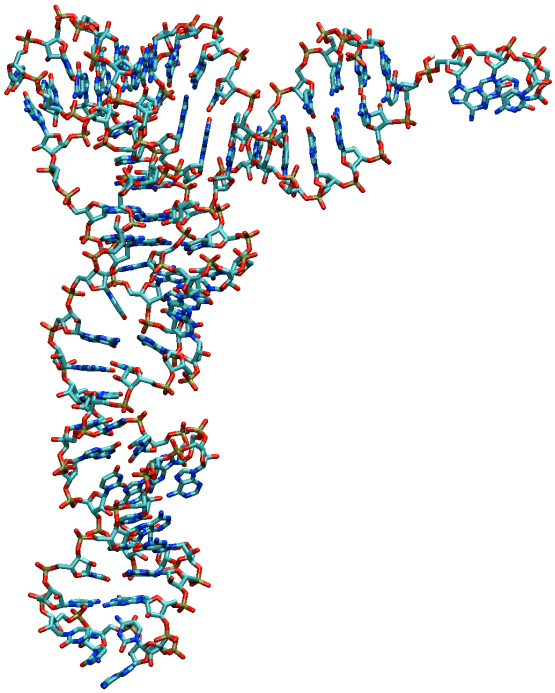
*Saccharomyces cerevisiae* RNA Polymerase II bound to RNA and DNA pdb ID 1I6H)



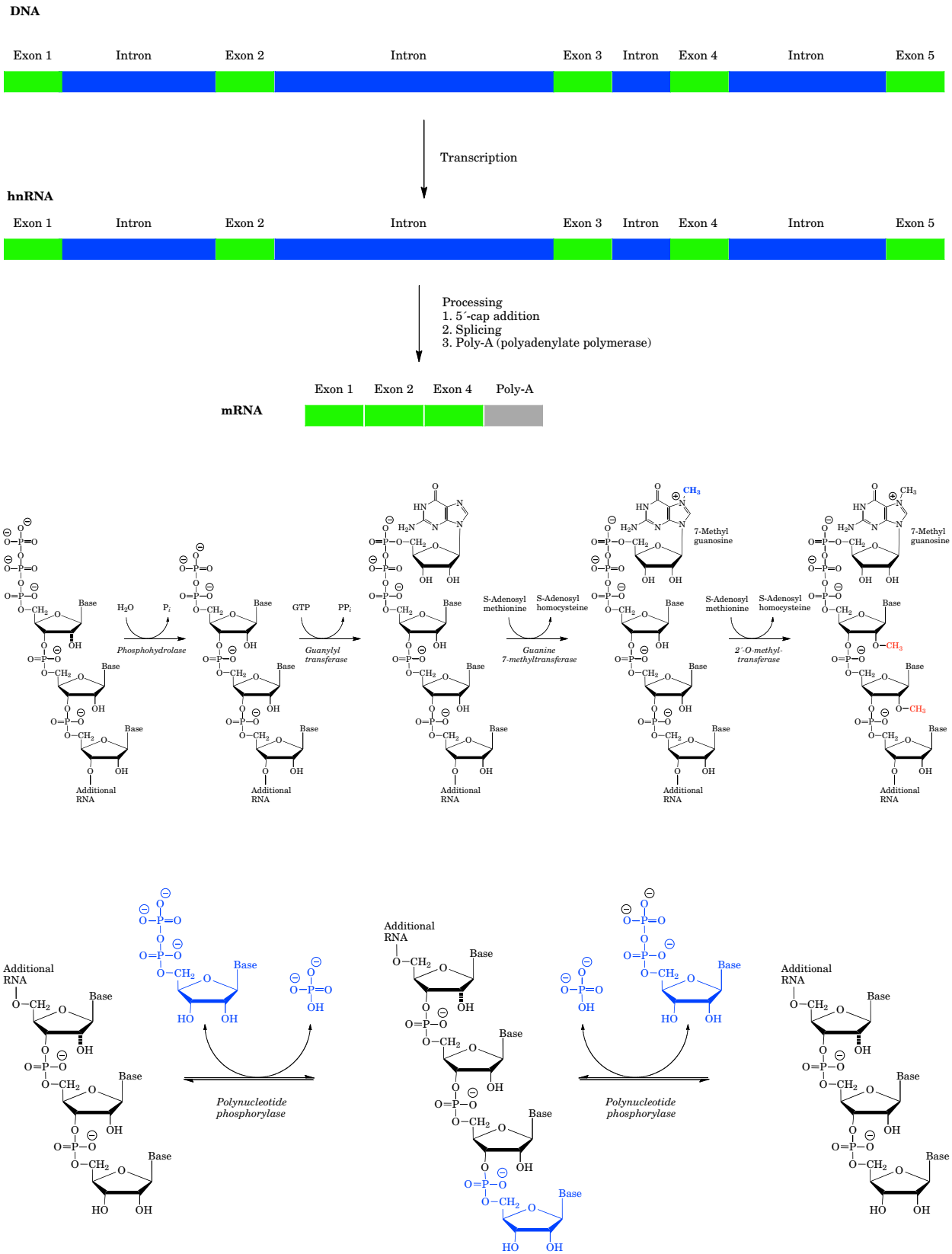
*Saccharomyces cerevisiae* RNA Polymerase II bound to RNA and DNA pdb ID 1I6H)

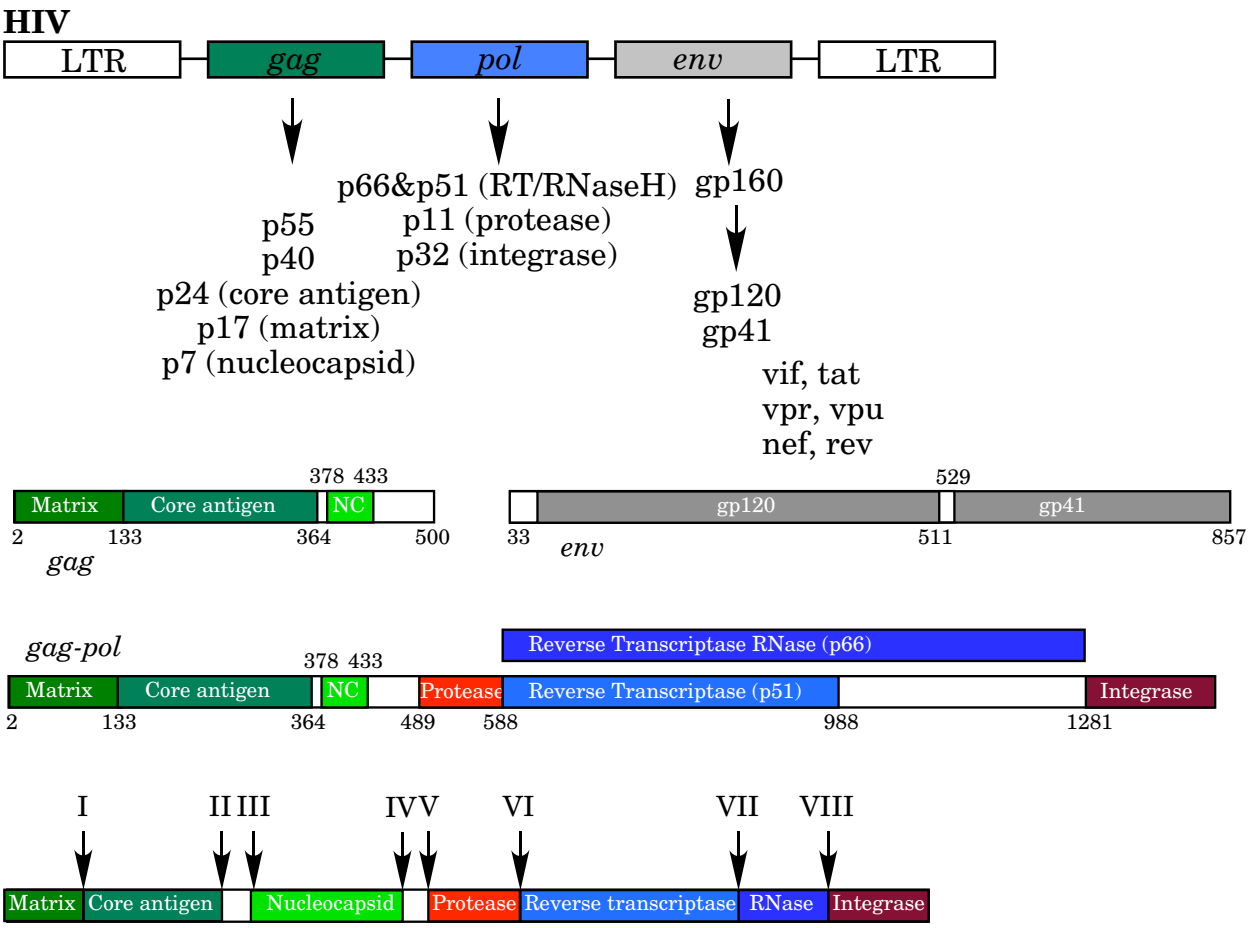


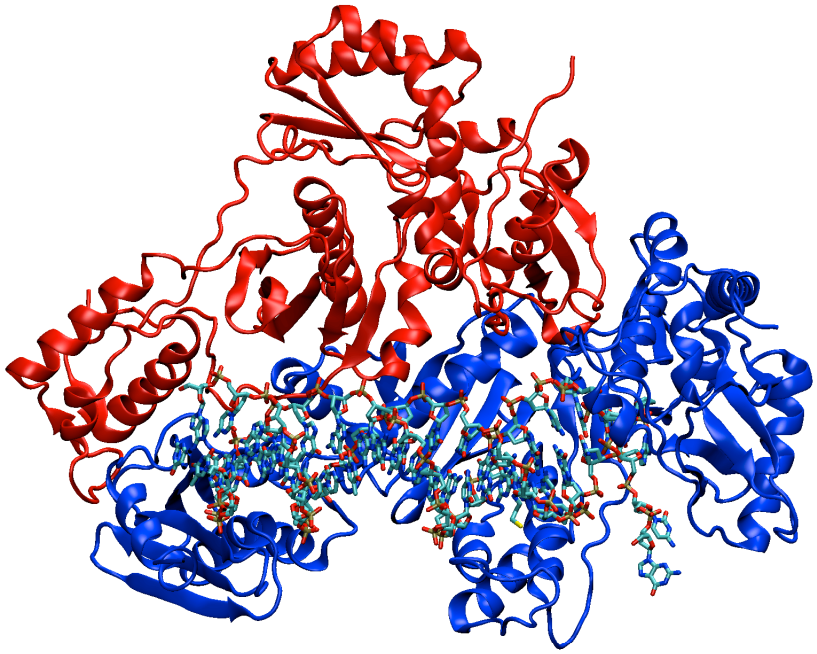
RNase P from *Thermotoga maritima* bound to $tRNA^{Phe}$ (pdb ID 3OKB)



RNA Modification Database
http://rna-mdb.cas.albany.edu/RNAmods/

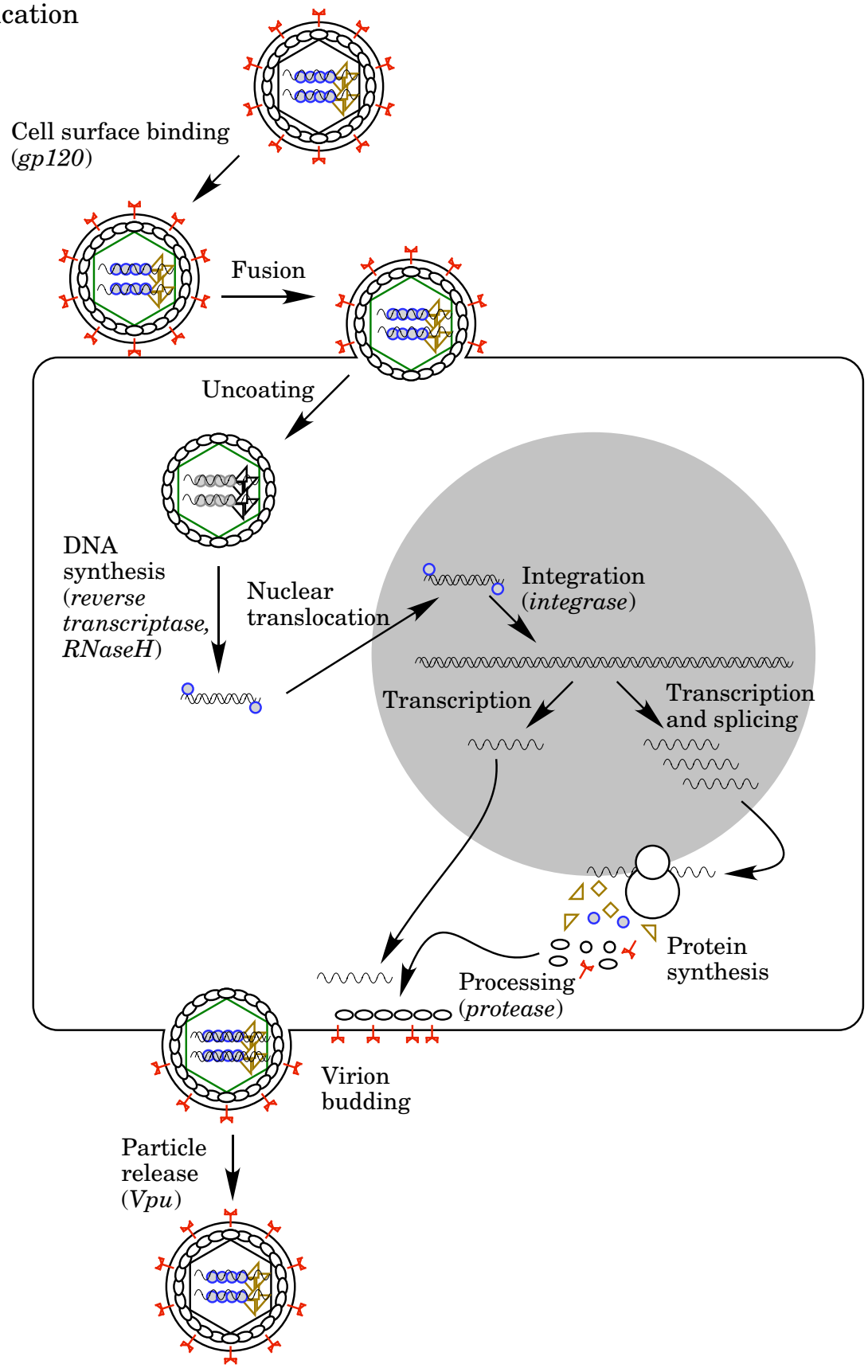

DNA
Exon 1
Intron
Exon 2
Intron
Exon 3
Intron
Exon 4
Intron
Exon 5
Transcription
hnRNA
Exon 1
Intron
Exon 2
Intron
Exon 3
Intron
Exon 4
Intron
Exon 5
Processing
1. 5´-cap addition
2. Splicing
3. Poly-A (polyadenylate polymerase)
mRNA
Exon 1
Exon 2
Exon 4
Poly-A
H2O
Pi
Phosphohydrolase
GTP
PPi
Guanylyl transferase
S-Adenosyl methionine
S-Adenosyl homocysteine
Guanine 7-methyltransferase
7-Methyl guanosine
2´-O-methyl-transferase
Additional RNA
Base
Polynucleotide phosphorylase



HIV Reverse Transcriptase (pdb ID 3KLE)

HIV Replication

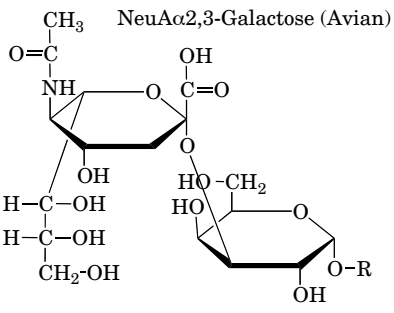


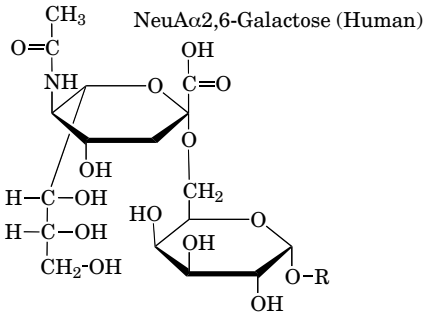
**Influenza**

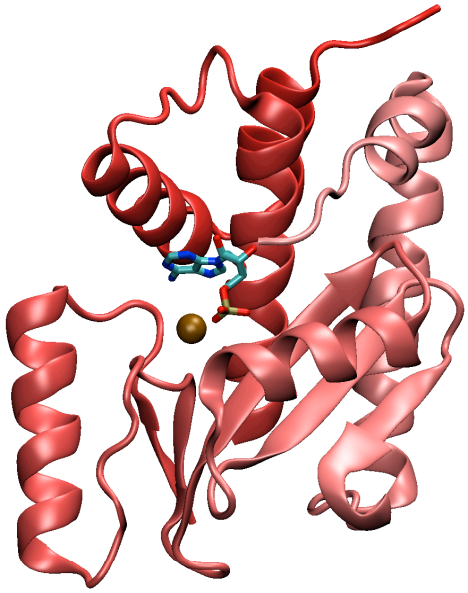
**RNA Molecules of Influenza A**

| RNA Molecule | Size (kb) | Gene Products |
|---|---|---|
| 1 | 2.3 | PB2 (Polymerase subunit) |
| 2 | 2.3 | PB1 (Polymerase subunit) and PB1-F2 (apoptosis induction) |
| 3 | 2.2 | PA (Polymerase subunit) |
| 4 | 1.8 | HA (Hemagglutinin); surface antigen, 16 types: H1, 2, 3, 5, 7, 9 affect humans, but only H1, 2, and 3 are human-human transmissible |
| 5 | 1.6 | NP (Nucleoprotein) |
| 6 | 1.4 | NA (Neuraminidase); surface antigen, 9 types: N1, N2 affect humans |
| 7 | 1.0 | M1 (matrix protein) and M2 (proton channel) |
| 8 | 0.9 | NS1 (non-structural protein) and NEP (nuclear export protein); some versions of NS1 have interferon and TNF-α antagonist activity |

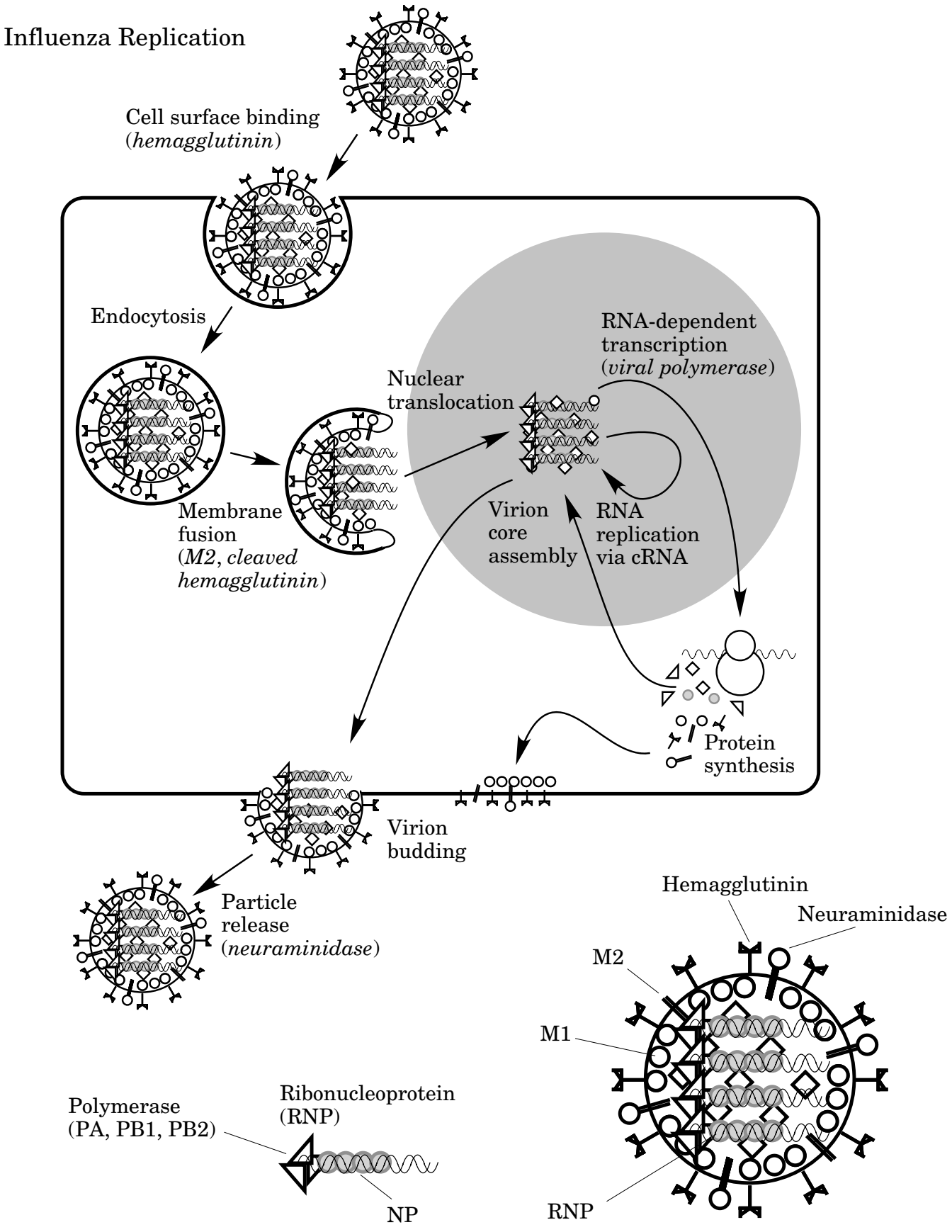
Receptors for Influenza



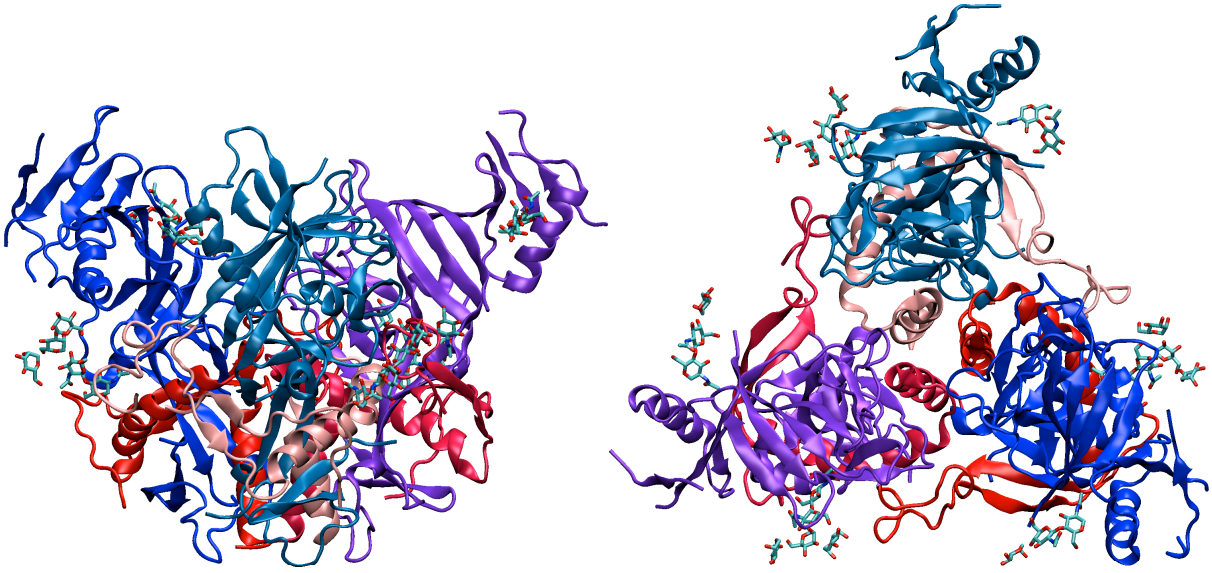
Avian Influenza Polymerase PA subunit endonuclease domain (pdb ID 3HW5)


Influenza Replication
Cell surface binding
(*hemagglutinin*)
Endocytosis
Membrane
fusion
(*M2*, *cleaved*
*hemagglutinin*)
Nuclear
translocation
RNA-dependent
transcription
(*viral polymerase*)
Virion
core
assembly
RNA
replication
via cRNA
Protein
synthesis
Virion
budding
Particle
release
(*neuraminidase*)
Hemagglutinin
Neuraminidase
M2
M1
RNP
Polymerase
(PA, PB1, PB2)
Ribonucleoprotein
(RNP)
NP

**Ebolavirus (Filoviridae)**
**Single-stranded RNA (negative strand) filamentous virus**

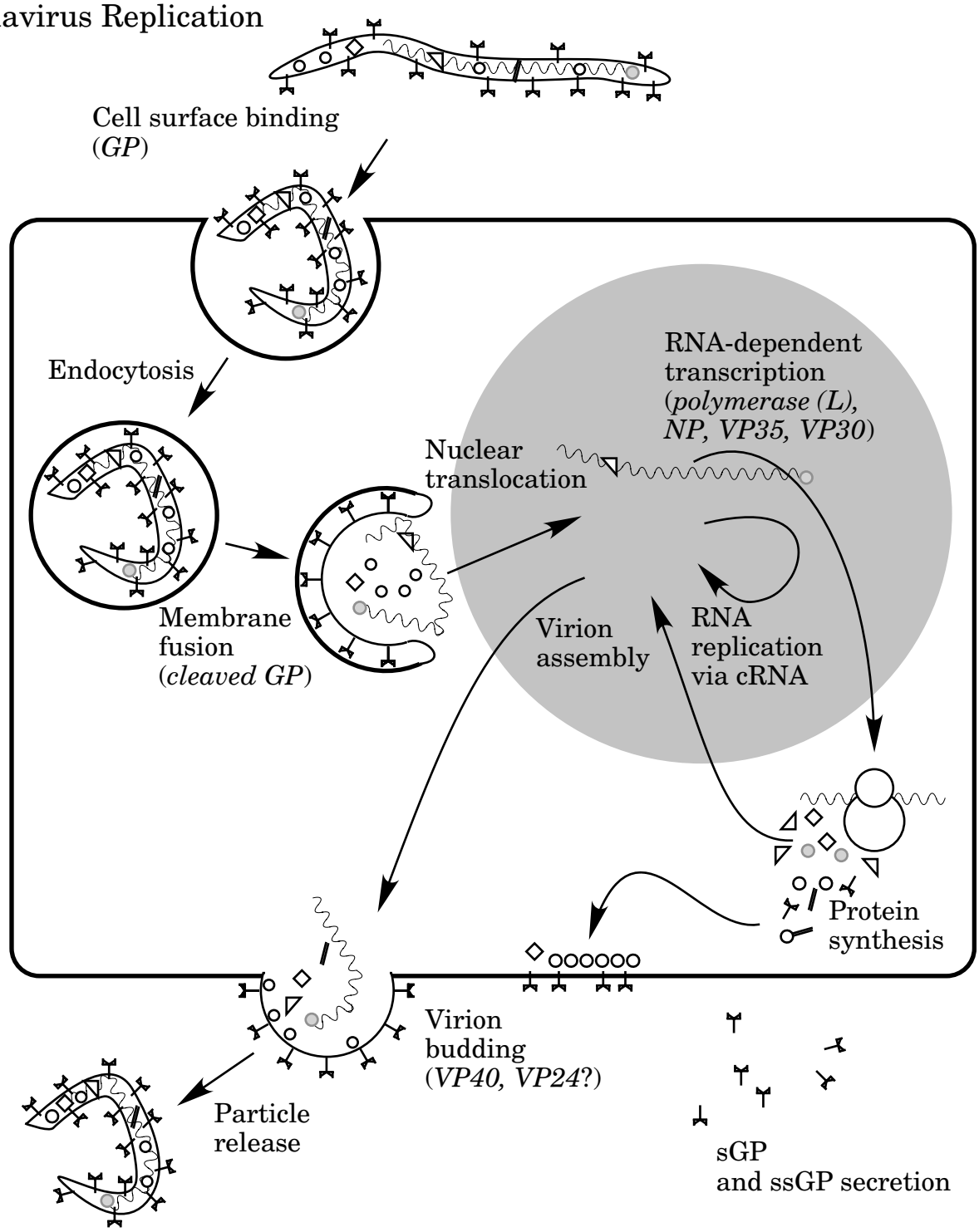
| Protein | Size (AA) | Function |
|---|---|---|
| NP | 739 | Nucleocapsid protein, RNA binding |
| VP35 | 340 | dsRNA binding, polymerase cofactor, interferon antagonist |
| VP40 | 326 | Matrix protein, virion budding |
| glycoprotein precursor | 676 | Receptor binding, membrane fusion<br>Precursor to secreted sGP and ssGP, toxic to infected cells (because of mucin domain?) |
| sGP | 364 | Dimeric secreted glycoprotein |
| ssGP | 297 | Monomeric secreted glycoprotein |
| VP30 | 288 | RNA binding, transcription initiation |
| VP24 | 251 | Membrane associated, interferon antagonist |
| L | 2212 | RNA Polymerase |

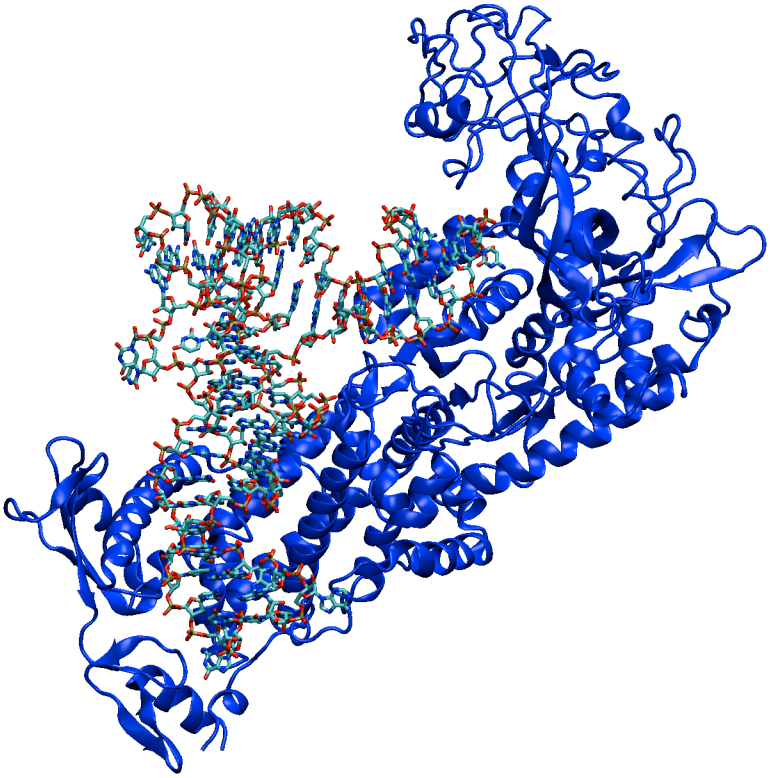
**Pathogenicity**
**Hemorrhagic fever, mortality ~70-90%**

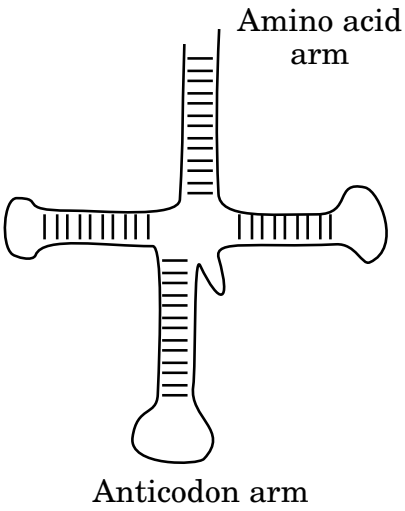


Ebolavirus GP trimer, cleaved, prefusion, without mucin and transmembrane domains (pdb ID 3CSY)

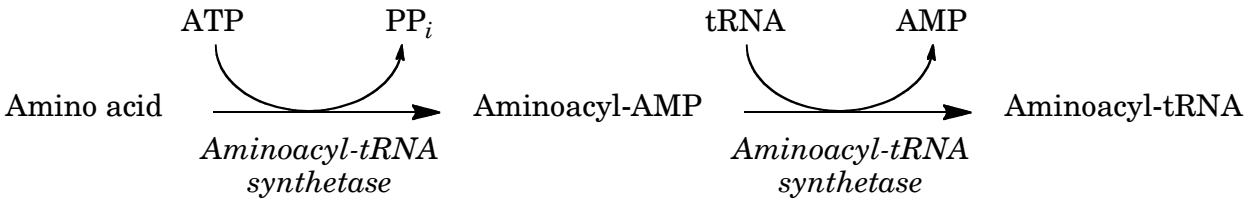
Ebolavirus Replication

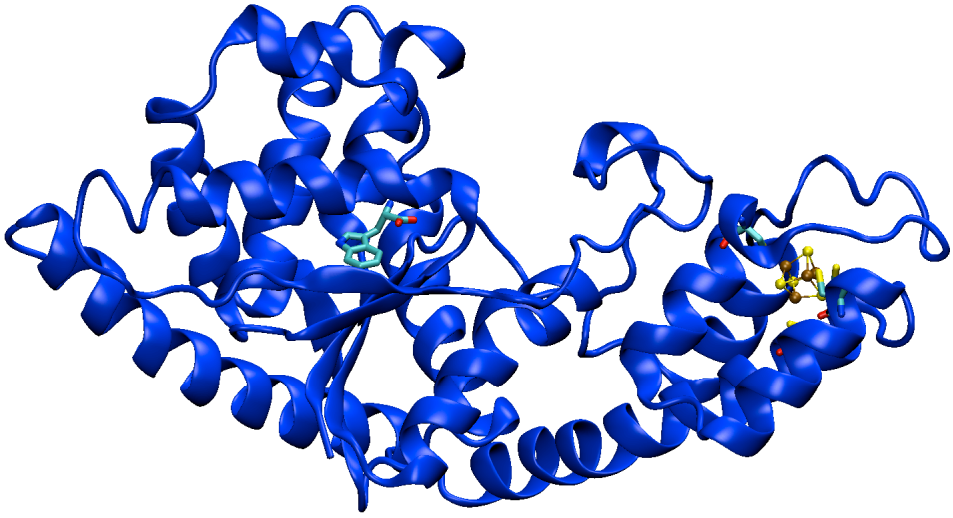







Isoleucinyl-tRNA synthetase from *Staphylococcus aureus* (pdb ID 1FFY)



Tryptophanyl-tRNA synthetase from *Thermotoga maritima* (pdb ID 2G36)

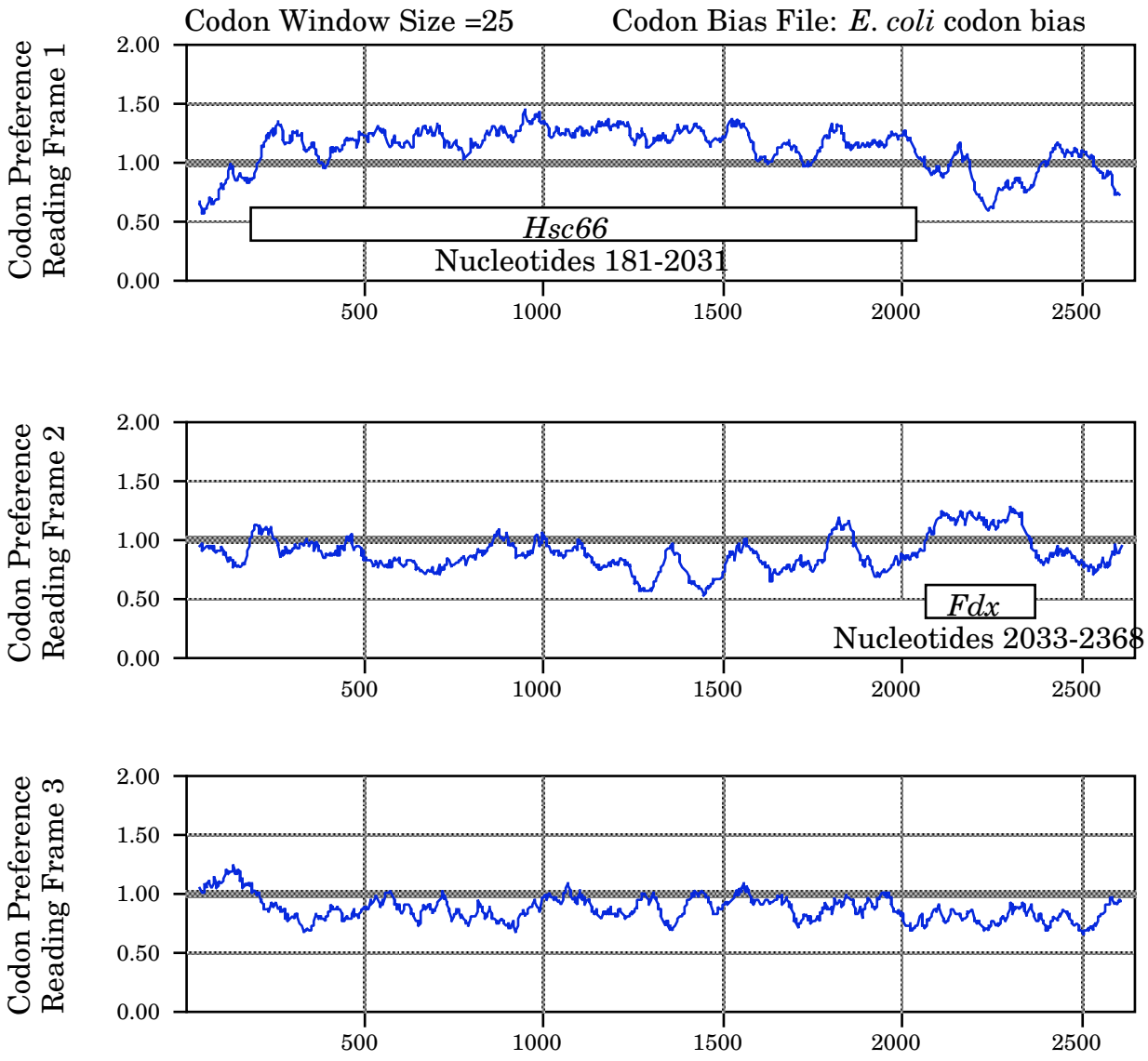
# Genetic Code

| First Position | Second Position T | | C | | A | | G | | Third Position |
|---|---|---|---|---|---|---|---|---|---|
| | TTT | Phe | *TCT* | *Ser* | TAT | Tyr | TGT | Cys | **T** |
| **T** | *TTC* | *Phe* | *TCC* | *Ser* | *TAC* | *Tyr* | TGC | Cys | **C** |
| | TTA | Leu | TCA | Ser | TAA | Stop | TGA | Stop | **A** |
| | TTG | Leu | TCG | Ser | TAG | Stop | TGG | Trp | **G** |
| | CTT | Leu | **CCT** | **Pro** | CAT | His | CGT | Arg | **T** |
| **C** | CTC | Leu | **CCC** | **Pro** | *CAC* | *His* | *CGC* | *Arg* | **C** |
| | **CTA** | **Leu** | CCA | Pro | CAA | Gln | **CGA** | **Arg** | **A** |
| | *CTG* | *Leu* | CCG | Pro | *CAG* | *Gln* | **CGG** | **Arg** | **G** |
| | ATT | Ile | *ACT* | *Thr* | AAT | Asn | AGT | Ser | **T** |
| **A** | *ATC* | *Ile* | *ACC* | *Thr* | *AAC* | *Asn* | AGC | Ser | **C** |
| | **ATA** | **Ile** | **ACA** | **Thr** | *AAA* | *Lys* | **AGA** | **Arg** | **A** |
| | ATG | Met | **ACG** | **Thr** | AAG | Lys | **AGG** | **Arg** | **G** |
| | *GTT* | *Val* | *GCT* | *Ala* | GAT | Asp | *GGT* | *Gly* | **T** |
| **G** | GTC | Val | GCC | Ala | GAC | Asp | *GGC* | *Gly* | **C** |
| | *GTA* | *Val* | *GCA* | *Ala* | *GAA* | *Glu* | **GGA** | **Gly** | **A** |
| | GTG | Val | GCG | Ala | GAG | Glu | **GGG** | **Gly** | **G** |

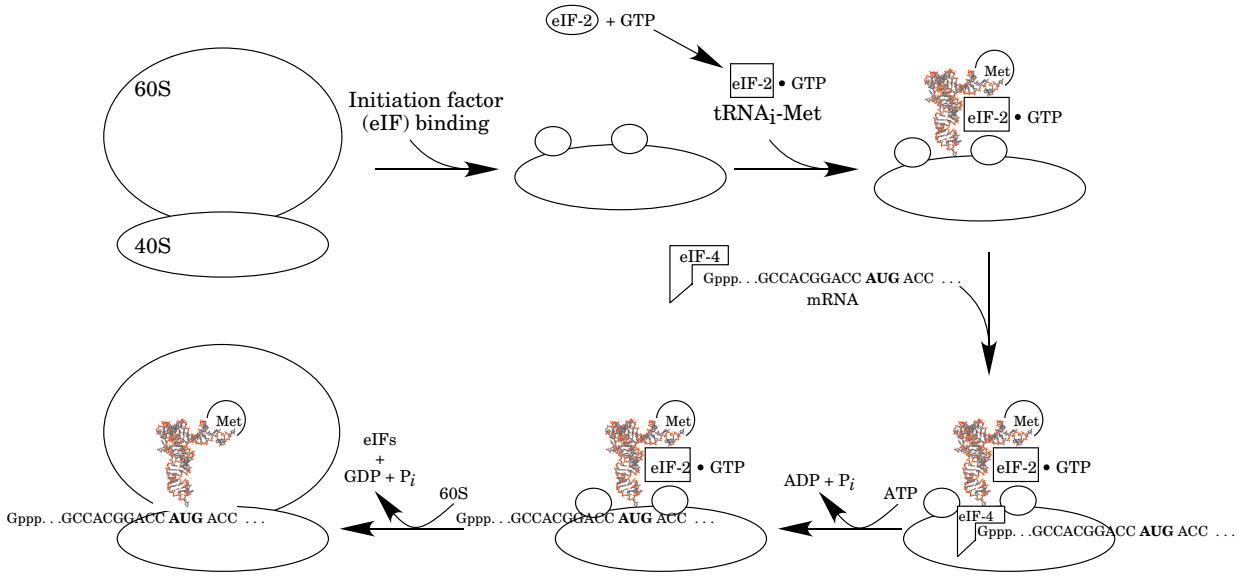
*Italics* indicates preferred tRNA in *E. coli*. **Bold** indicates minor tRNA in *E. coli*.

Adapted from: "Biased Codon Usage: An exploration of its role in optimization of translation." In: *Maximizing Gene Expression*, pp. 225-285, 1986.

Although the control elements (such as promoters) may differ markedly between species, nearly all organisms translate nucleic acid sequences into proteins using the same code, and therefore, foreign DNA expressed in an organism nearly always results in the same protein sequence as is found in the parent organism. However, all organisms do not use all codons with the same frequency. Some prokaryotes use tRNA availability as one method for regulating protein synthesis rates. Some foreign proteins are poorly expressed in *E. coli* due to large numbers of rare codons (*i.e.* having corresponding tRNAs that are produced in relatively small amounts). A rare codon frequency of 15% or less usually results in high expression, unless the rare codons are in close proximity to one another in the coding sequence.


Codon Window Size =25
Codon Bias File: E. coli codon bias
Codon Preference
Reading Frame 1
2.00
1.50
1.00
0.50
0.00
Hsc66
Nucleotides 181-2031
500
1000
1500
2000
2500
Codon Preference
Reading Frame 2
Fdx
Nucleotides 2033-2368
Codon Preference
Reading Frame 3

# Initiation

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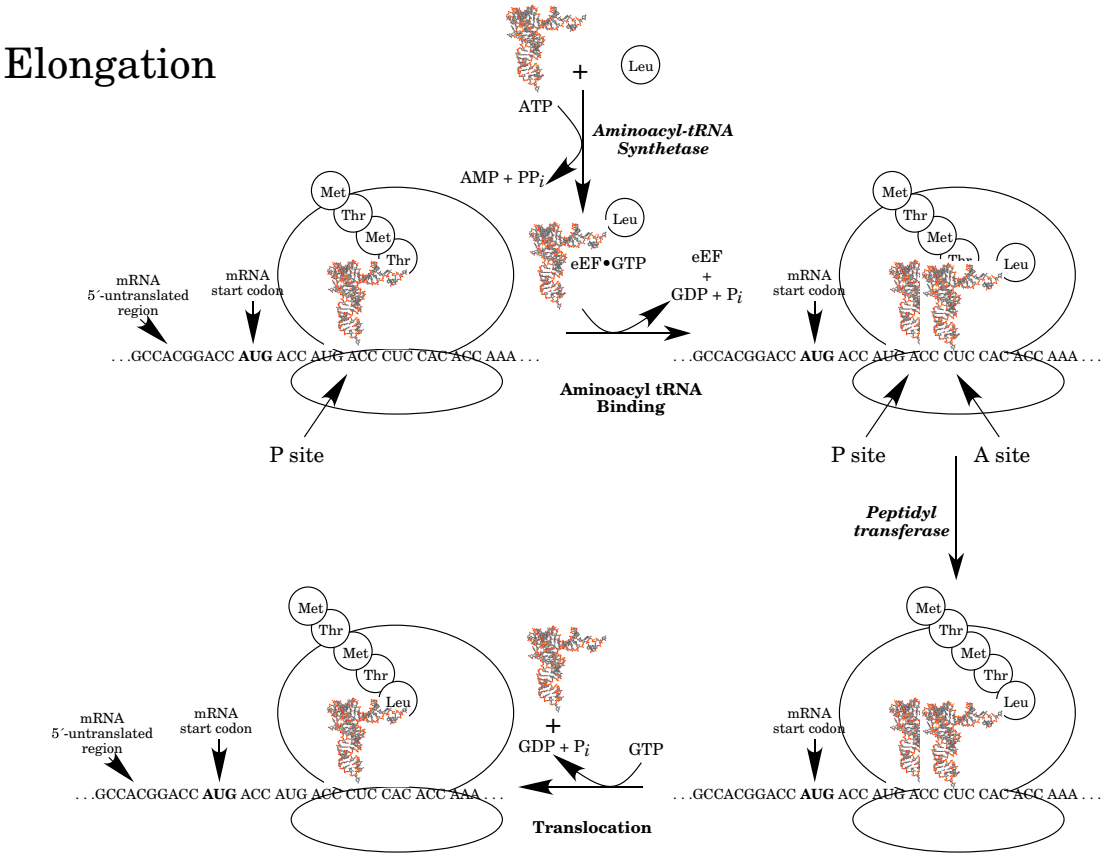
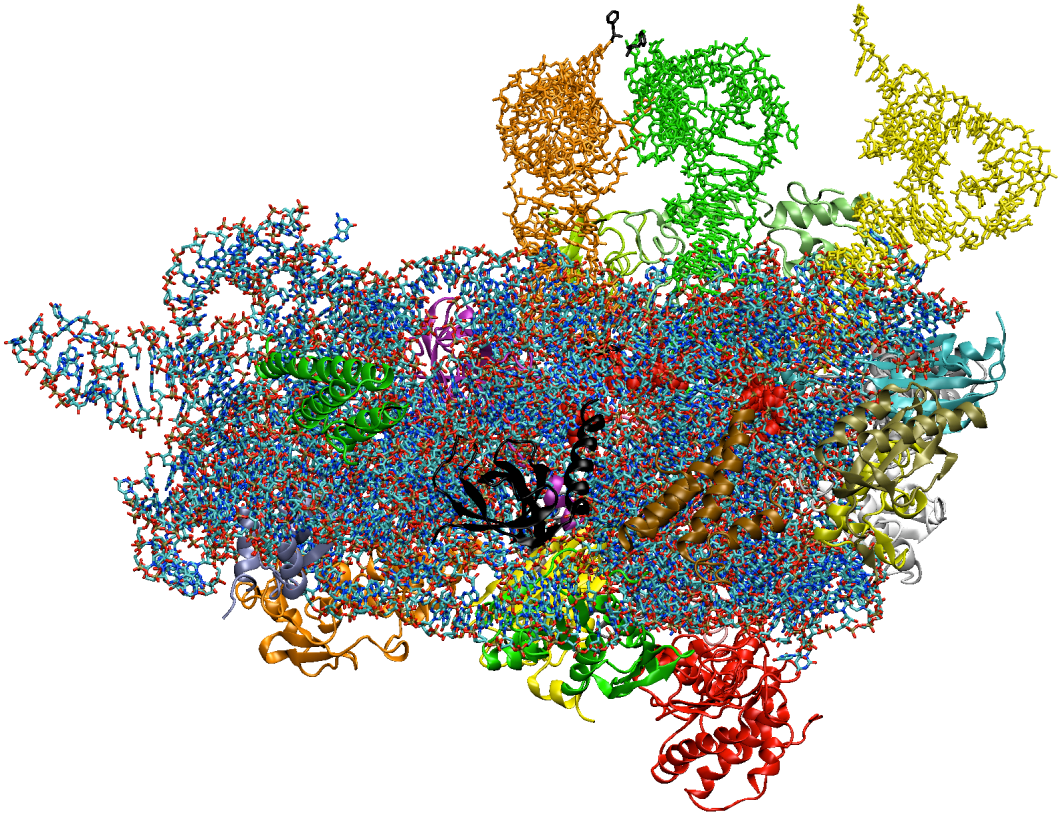
# Elongation





30 S subunit 2WDK