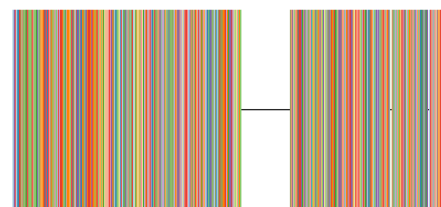
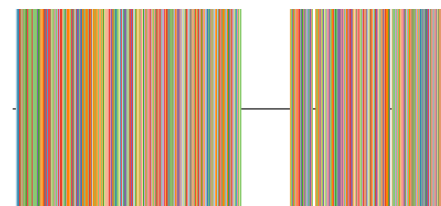
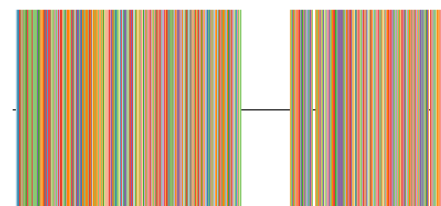
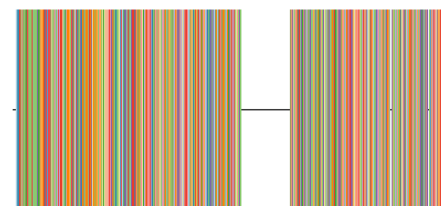
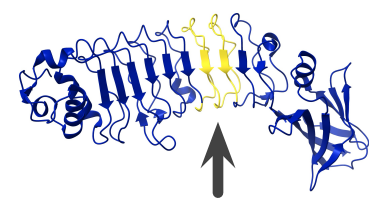
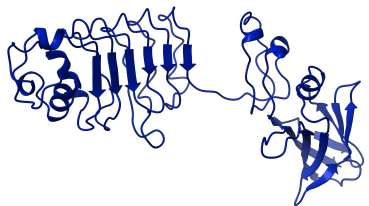
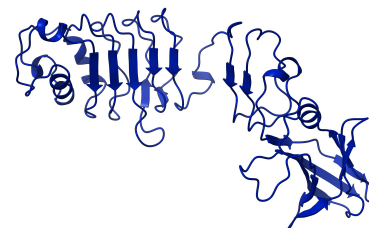
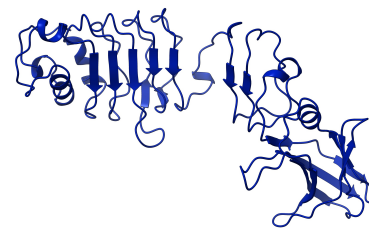
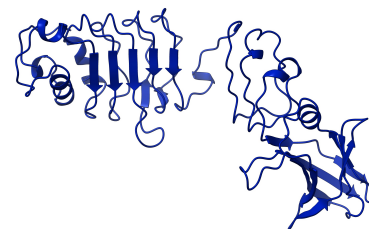
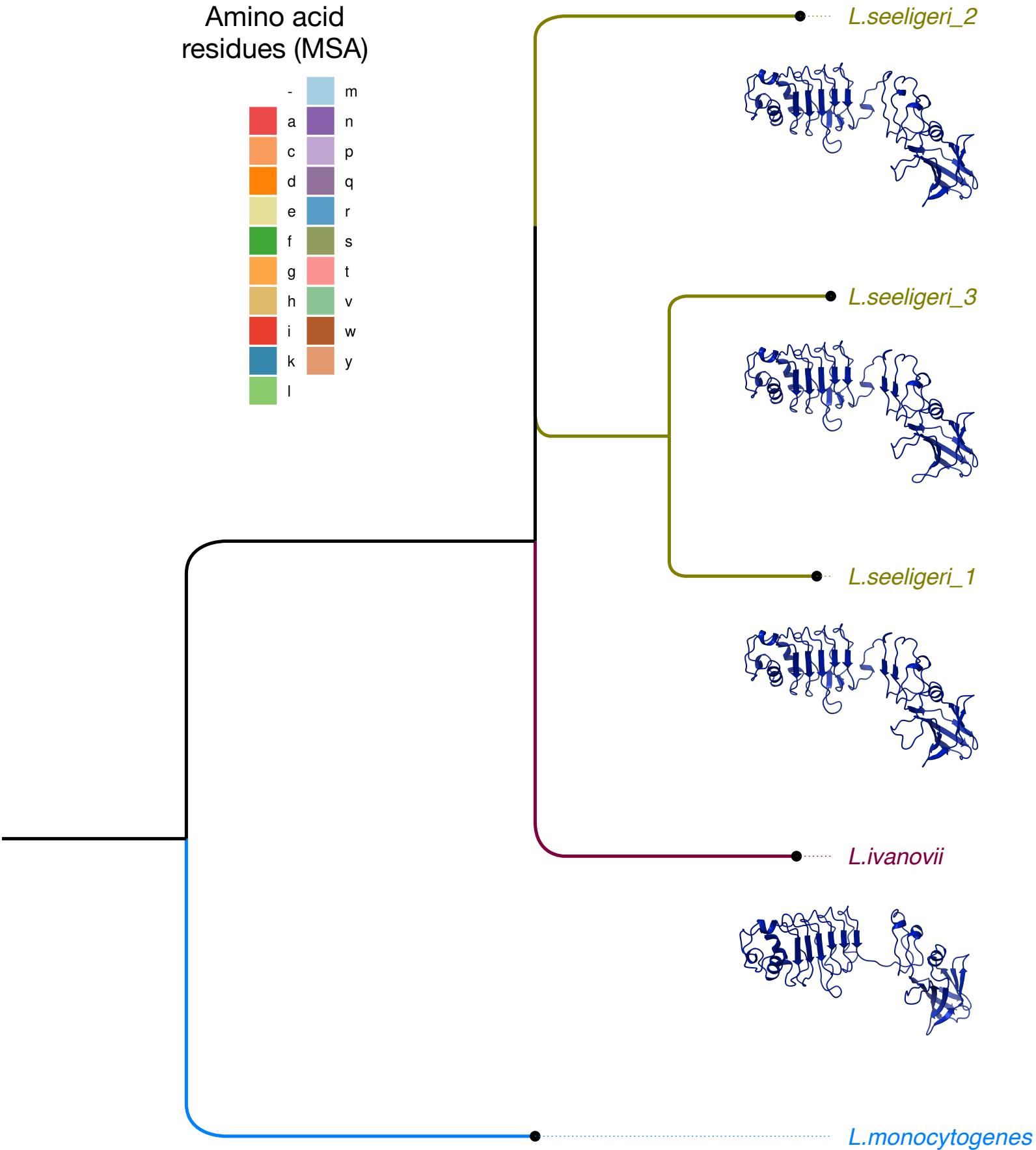


# Amino acid residues (MSA)

-	m
a	n
c	p
d	q
e	r
f	s
g	t
h	v
i	w
k	y
l	



Phylogenetic tree

Structural models

Multiple sequence alignment