

ChemicalSequence

commands

add (number)

remove (number)

bind_unit (first, last)

unbind_unit (first, last)

add_termination_site (termination site)

watch_site (binding site)

set_appariated_sequence (chemical sequence)

start_strand (position)

extend_strand (strand_id, position)

accessors

number_sites (first, last)

number_available_sites (first, last)

partial_strands ()

is_out_of_bounds (first, last)

is_termination_site (position, TS families)

length ()

sequence ()

sequence (first, last)

relative (absolute position)

appariated_sequence ()

complementary (position)