

Targeting DNA Topoisomerase II in Antifungal Chemotherapy

Kavya Kondaka and Iwona Gabriel *

Department of Pharmaceutical Technology and Biochemistry, Gdansk University of Technology, 80-233 Gdansk, Poland

* Correspondence: iwogabri@pg.edu.pl; Tel.: +48-58-348-6078; Fax: +48-58-347-1144

Table of contents:

1. ScTopo II catalytic cycle1
2. Three sequence alignment presented in yeast (ScTopo II) and human topo II isoforms2
3. Multiple sequence alignment of three different fungal species *Saccharomyces cerevisiae*, *Candida albicans* and *Candida glabrata* with human topo II isoforms.....3

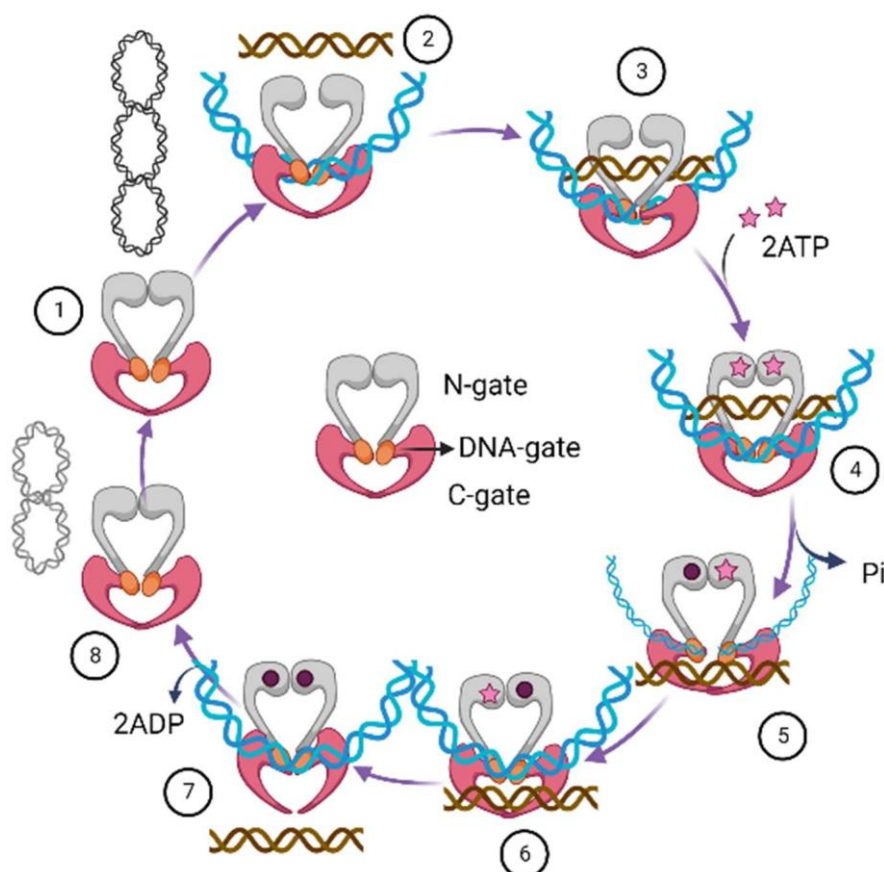


Figure S1. ScTopo II catalytic cycle (1) Enzyme and duplex DNA in relaxed state with $n+1$ linking number. Dimerization of subunits. (2) Binding and bending of G-segment. (3) Two molecules of ATP binding at closed N-gate. (4) ATP hydrolysis and capture of T-segment. (5) Transient DSB formation in G-segment of DNA-gate and passage of T-strand through it. (6) Re-ligation of G-segment. (7) Opening of C-gate and passage of T-segment and release of 2ADP. (8) Enzyme resetting and representation of duplex DNA with n linking number. Created with BioRender.com

msl-1

msl-2

msl-3

msl-4

msl-5

msl-6

msl-7

msl-8

msl-9

msl-10

msl-11

msl-12

msl-13

msl-14

msl-15

msl-16

msl-17

msl-18

msl-19

msl-20

msl-21

msl-22

msl-23

msl-24

msl-25

msl-26

msl-27

msl-28

msl-29

msl-30

msl-31

msl-32

msl-33

msl-34

msl-35

msl-36

msl-37

msl-38

msl-39

msl-40

msl-41

msl-42

msl-43

msl-44

msl-45

msl-46

msl-47

msl-48

msl-49

msl-50

msl-51

msl-52

msl-53

msl-54

msl-55

msl-56

msl-57

msl-58

msl-59

msl-60

msl-61

msl-62

msl-63

msl-64

msl-65

msl-66

msl-67

msl-68

msl-69

msl-70

msl-71

msl-72

msl-73

msl-74

msl-75

msl-76

msl-77

msl-78

msl-79

msl-80

msl-81

msl-82

msl-83

msl-84

msl-85

msl-86

msl-87

msl-88

msl-89

msl-90

msl-91

msl-92

msl-93

msl-94

msl-95

msl-96

msl-97

msl-98

msl-99

msl-100

msl-101

msl-102

msl-103

msl-104

msl-105

msl-106

msl-107

msl-108

msl-109

msl-110

msl-111

msl-112

msl-113

msl-114

msl-115

msl-116

msl-117

msl-118

msl-119

msl-120

msl-121

msl-122

msl-123

msl-124

msl-125

msl-126

msl-127

msl-128

msl-129

msl-130

msl-131

msl-132

msl-133

msl-134

msl-135

msl-136

msl-137

msl-138

msl-139

msl-140

msl-141

msl-142

msl-143

msl-144

msl-145

msl-146

msl-147

msl-148

msl-149

msl-150

msl-151

msl-152

msl-153

msl-154

msl-155

msl-156

msl-157

msl-158

msl-159

msl-160

msl-161

msl-162

msl-163

msl-164

msl-165

msl-166

msl-167

msl-168

msl-169

msl-170

msl-171

msl-172

msl-173

msl-174

msl-175

msl-176

msl-177

msl-178

msl-179

msl-180

msl-181

msl-182

msl-183

msl-184

msl-185

msl-186

msl-187

msl-188

msl-189

msl-190

msl-191

msl-192

msl-193

msl-194

msl-195

msl-196

msl-197

msl-198

msl-199

msl-200

msl-201

msl-202

msl-203

msl-204

msl-205

msl-206

msl-207

msl-208

msl-209

msl-210

msl-211

msl-212

msl-213

msl-214

msl-215

msl-216

msl-217

msl-218

msl-219

msl-220

msl-221

msl-222

msl-223

msl-224

msl-225

msl-226

msl-227

msl-228

msl-229

msl-230

msl-231

msl-232

msl-233

msl-234

msl-235

msl-236

msl-237

msl-238

msl-239

msl-240

msl-241

msl-242

msl-243

msl-244

msl-245

msl-246

msl-247

msl-248

msl-249

msl-250

msl-251

msl-252

msl-253

msl-254

msl-255

msl-256

msl-257

msl-258

msl-259

msl-260

msl-261

msl-262

msl-263

msl-264

msl-265

msl-266

msl-267

msl-268

msl-269

msl-270

msl-271

msl-272

msl-273

msl-274

msl-275

msl-276

msl-277

msl-278

msl-279

msl-280

msl-281

msl-282

msl-283

msl-284

msl-285

msl-286

msl-287

msl-288

msl-289

msl-290

msl-291

msl-292

msl-293

msl-294

msl-295

msl-296

msl-297

msl-298

msl-299

msl-300

msl-301

msl-302

msl-303

msl-304

msl-305

msl-306

msl-307

msl-308

msl-309

msl-310

msl-311

msl-312

msl-313

msl-314

msl-315

msl-316

msl-317

msl-318

msl-319

msl-320

msl-321

msl-322

msl-323

msl-324

msl-325

msl-326

msl-327

msl-328

msl-329

msl-330

msl-331

msl-332

msl-333

msl-334

msl-335

msl-336

msl-337

msl-338

msl-339

msl-340

msl-341

msl-342

msl-343

msl-344

msl-345

msl-346

msl-347

msl-348

msl-349

msl-350

msl-351

msl-352

msl-353

msl-354

msl-355

msl-356

msl-357

msl-358

msl-359

msl-360

msl-361

msl-362

msl-363

msl-364

msl-365

msl-366

msl-367

msl-368

msl-369

msl-370

msl-371

msl-372

msl-373

msl-374

msl-375

msl-376

msl-377

msl-378

msl-379

msl-380

msl-381

msl-382

Figure S3: Multiple sequence alignment of three different fungal species *Saccharomyces cerevisiae*, *Candida albicans* and *Candida glabrata* with human topo II isoforms is depicted. Uniprot ID mentioned in the left. The red rectangular bars indicate important consensus sequences like K-loop (333–338 residues), metal bound region (D from 526–528 residues), intercalator region (I at residue 833) and catalytic tyrosine (Y at 782 residue) with respect to *S. cerevisiae*. The differences are marked in blue rectangular bars.