Supplementary Table 1: Codon-optimized genes Sequence of the codon-optimized genes used in this study. The sequences of the His-tag and the cleavage site (blue) and the sequence of the gene (black) are shown.

Codon-	Sequence		
Optimised gene			
CsTop1	ATGAAACATCACCATCACCCCATGAGCGATTACGACATCCCCACTACTGAGAATCTTTATTTTCAGGGC GCCATGGTGAAATGGCGTACCCTGGTCCACAATGGTGTCGCACTGCCGCCGCCGTATCAACCGAAAGGTCTGTCA ATCAAAATCCGTGGTGAAACCGGTGAAACTGGATCCGCTGCAGGAAGAAATGGCGTATGCCTGGGCACTGAAAG GATACGCCGTACGTGCACGGATTTCCAGAAAACTTTCTGACAAAAGGCTCGAACGCCACTGAAA GCCGATAAGAAAACCGTTACCAATGGATTCCAGCAAGTCTACGAAATGGCGTAAACGCTGAACGCCAACTGAAA GCCGGATAAAGAATACCGTAACGATTTCCAGCGAAGTCTACGAATACGTGGAACGTGAACGCCAACTGAAA GCGGATAAAGAATACCGTAAGAAAATTTCTGCCGAACGTAAACGCCTGCGTGGAAGAACTGAAAGCGCGCCAACTGAA GCGGCCGAAATGGATGGTAAACGTTTCGAAAATGCGCGACGTAAACGCCGCGGGCATCTTTATGGGTCGT GGTAATCATCCGCGGGGGTGATTGCGAACGCGGTGCTTATGAAGAACACTTAACCGGGGCAACAACGGGGAAGAT GCCCGGTCCGCCGGGGTAATTGGGGTCGAGCCGCGCGCGC		
	GAACGTCTGGAAAAAGCAGAACTGAACCTGGATCTGGCAGTTAAAGTTCGTGATTACAATCTGGCGACCAGCCTG CGTAACTATATTGATCCGCGTGTGTATAAAGCATGGGGTCGTTATACCGGTTATGAATGGCGTAAAATCTATACC		
	GCAAGCCTGCGTAAATTCAAATGGGTTGAAAAAGCCAGCGTTAAACATGTGCTGCAGTATTTTGCCGAAAAA		
CsTOP1HsLinker-	ATGAAACATCACCATCACCCATCACCCCATGAGCGATTACGACATCCCCACTACTGAGAATCTTTATTTTCAGGGC		
Cter	GCCGTGAAATGGCGTACCCTGGTCCACAATGGTGTCGCACTGCCGCCGCCGTATCAACCGAAAGGTCTGTCAATC AAAATCCGTGGTGAAACCGTGAAACTGGATCCGCTGCAGGAGAAAAGGCGTATGCCTGGGCACTGAAGAAAGA		
	AAAGTGATGAAAGATGCGAAAACCCAAGAAAGTGGTTGAAAGCAAAAAGAAAG		

Supplementary Table 2: primer sequences Sequence of the DNA oligonucleotides used in this study.

Name	Sequence	Construct	
CsFL154R	5'-TAATCATCCGAAGCGTGGTCGTTG-3'	L154K point mutation in CsTop1	
CsRL154R	5'-CCACGACCCATAAAGATG-3'		
CsFL399RL402R	5'-CGCTTCAGCTGCTTTCCGGTTAGCCCGTT		
	TTGCGTAATAGAT-3'	L399R L402R point mutations in CsTop1	
CsRFL399L402R	5'-ATCTATTACGCAAAACGGGCTAACCGGA		
	AAGCAGCTGAAGCG-3'		
CsFHsCat	5' CTACTGGATCCGCGTGTGTATAAAG-3'	CsTOP1 ^{HsTyr} point mutations	
CRFHsCat	5' TTCAGTTTGCTGGTCGCCAAGATTGTA-3'		
Q5SDM 12/7/20	5'-GAAATGGTGGGAAGAAGAGCGCTATCCT		
16 F	GAAGGCATCGTGAAATGGCGTACCCTG-3'	CsTOP1 ^{HsNter} insertion	
Q5SDM 12/7/20	5'- CACTTCTGTTCCTCTTCTTCTTCGGCTTC		
16_R	TTTTTCTTGTGATGGTGATGGTGATG-3'		
Q5SDM 4/13/20	5'-CCCTAGCGCAGATATTAAACAGAAACG-		
19_F	3'	Hinge-1 point mutations (MLNPS)	
Q5SDM_4/13/20	5'-TTCAGCATCACATATTTTTTTTTTTCTTTACCGG-3'		
19_R			
Q5SDM_4/13/20	5'-CCTCCCGCAGATATTAAACAGAAACG-3'		
19_F		Hinge-2 point mutations (WLSPP)	
Q5SDM_4/13/20	5'-GCTCAGCCACACATATTTTTCTTTACC-3'		
19_R			
CsTop1WLSGGf	5'- AAAAATATGTGTGGGCTGAGCGGTGGCGC		
wd	AGATATTAAACAGAAACG-3'	Hinge-3 point mutations (WLSGG)	
CsTop1WLSGGr	5'- CGTTTCTGTTTAATATCTGCGCCACCGCT		
ev	CAGCCACACATATTTTT-3'		
CsTop1Y207Afw	5'- CTGACCGGTAAAGAAAAAGCTGTGTGG		
d	CTGAGCGATAC-3'	Y207A point mutation in CsTop1	
CsTop1Y207Arev	5'-GTATCGCTCAGCCACACAGCTTTTTCTTT		
	ACCGGTCAG-3'		



Supplementary Figure 1: CsTOP1 structure in one asymmetric unit.

Cartoon representation of the two CsTOP1 chains found in one asymmetric unit in SeMet CsTOP1 and native CsTOP1 crystals. The different subunits were further superposed. Coloring scheme is the same as Fig. 1.

Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	MVKWRTLVHNGVALPPPYQPKGLSIKIRGETVKLDPLQEEMAYAW MEEVAAAPQPQARIRWSSLVHRGVAFPPEHQPRGITISIKGEKVALNADQEELVYAW MKWKTLQHNGILFPPAFESQGIKIKVKGEKVSLDLLQEEMIYQW MTKIEQLIHNGVLSE-IPYLELSIEINGKVHKLSEKQEQMAIAW : * *.*: :. *. **:: *	ALK 48 AKK 60 AKK 47 VRK 47	
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	KDTPYVQDPVFQKNFLTDFLKTFNGRFQDVTINEIDFSEVVEYVERERQLKA KDTHYVQDPVFQSNFLLDLKPLLPEKFRKADLKISDFDFSQAFRLADEEKMMKEREK KDTPYAQDKVFQKNFTADFAKTLDPKFKGIYYEIDFSEFKVVDKEKDLKE LSTVYVEDPIFCKNYFKDFGEEIGDASLTDDNIDFSEVIAYVEKQKEIRD .* *.:* :* .*: :: .:.::***:.	100 ERI 120 99 97	CAP domain
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	DKEYRKKISAERKRLREELKARYGWAEMDGKRFEIANWMVEPPGIFMGRGNHPL KNLPREEKKKMAEAKKAERERLKALYGKAVVDGQEVDIANWLVEPPGLFMGRGQHPL -MMTKEEKKSLAAKRKELREKMKEKYGKAVMDGQEVEVANYMAEPPGIFIGRGEHPL -AKTKEQKKQEREERKVIREQLKEKYGTATLDGAQVEISNYTAEPSSIFMGRGEHPM :* :*. :* **.:* ** :**::*::*: .**	RGR 157 RGR 180 RGK 158 RGK 156 **:	
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	WKPRVYEEDITLNLGEDAPVPPGNWGQIVHDHDSMWLARWDDKLTGKEKYVWLSDTA WKPRVRPQDVTLNLGEDAPVPEGEWKEIVHDHTSTWLATWMENLTEKRKYVWLHDS WKKRVTPEDVILNLGKDAKVPPGKWGKIIHDQNSMWLASWMDDLTQKRKYVWLADTA WKEGPSKADIVLNLSPEAPRPEGEWLEIVWEPECLWIAKWTDKLSGKTKYVWLSDTT ** *: ***. :* * *: : *: * : *: * *: ***	DIK 217 ELR 240 GLK 218 PIK 216 ::	Hinge
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	QKRDKSKYDKAEMLENHIDRVREKIFKGLRSKEPKMREIALACYLIDRLAMRVGDEK QGNDKAKYDKALNLAQQLGKVEKEIMRKMKGSNDKAATAAYLIFKLAMRVGDEK QERDQAKYDKATKLAKEIEKIKNSIVKDMKSKDFKLSRIATACYLIYRTAMRVGDEK QDREIEKYDKANLVGDNLETIRNQIMSAISGSDKRNKKVATACYIIDHLNIRVGDEK * ***** : * *.*.*	DPD 277 DPD 297 DPD 278 DED 276 * *	
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	EADTVGATTLRVEHVKLLEDRIEFDFLGKDSVRWQKSIDLRNEP-PEVRQVFE EADTVGASTLRVEHIKFPQQNGKQYIEFNFLGKDSVPWQKTLEVNSEDTRALYDNLR EADTVGATTLRKEHIKLTGKAIEFDFLGKDSVRWQETVPAEGQD-KQFYDNLE EADTVGATTLRPEHIKINGSTVIFDFLGKDSVEWHKEREFPEIFVNSLQELIN ******* *** **: : : : : : : : : : : : :	ELL 332 NFM 357 KLI 333 EAN 332 :	CAT domain
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	EGKKEGDQIFQNINSRHVNRFLGKIVKGLTAKVFRTYIATKIVKDFLAAIPREKV KGKKPDQQIFDDINSRKVNAFFQTVMPGLTAKVFRTCIATKVVQQALVNPPIKVDRN ANKKPKDEIFDGITSRHVNAYYSSIVKGLTAKVFRTYLASTVVNSYLKNHDNVKS ESGNDKPQIFSDIGSRHVNAFFDEIVDGLTAKVFRTYHATTVVRNFLDESDVDPA .: :*** **:** : :: ******** *:*	TSQ 390 SQE 417 KSA 391 DPD 390	
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	EKFIYYAKLANLKAAEALNHKR <mark>APPKNWEQSIQKKEE SDKVYVAKSANLKAAIECNHKKGVDPKNPAAKKAAEKFEEAVAKRNQ NEKLYHAKMANLEAAKMCNHKRTIPKTYETALQKKKE FAKKEAAVMANREAAVECTHKKQEPKNWENRMQKYRERKLKGQERIE * ** ** ** ** **: : : : : : : : :</mark>	427 464 428 KAN 440	
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	RVKKLMQQL	436 475 437 KNA 500	Linker
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	KEARIAERLEKAELNL QEKRLKERLAKLKMQL QEKRLKERLAKLKMQL 	DLA 462 KLQ 501 DLS 461 KIS 560 .:	
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	VKVRDYNLATSLRNYIDPRVYKAWGRYTGYEWRKIYTASLLRKFKWVEKASVKHV QETRDYNLGTSLRNYIDPRVMKAWLNYVDLDWTKVYTATLQRKFKWVEGYKEKNY EKTKDYNLGTSLRNYIDPRVFKAWTDEVGAEWEKLYTAALQKKFLWVKSADVKWKDI KKTKTWNLGTSLKSYIDPRVYYDWGKEVDYDWRNYYSNALQRKFSWVERDADE ::::******************************	LQY 520 SRF 559 SQQ 521 613	C-terminal
Caldiarchaeum_subterraneum Nitrososphaera_viennensis Crenarchaeota_archaeon Heimdallarchaeota_archaeon	FAEKLAKDVDKGMQVKAAV 539 YP 561 Y 522 613		

Supplementary Figure 2: Alignment of archaeal TOP1 sequences.

Alignment of four archaeal TOP1 sequences from different phyla including *Caldiarchaeum* subtarreneum (Aigarchaeota), *Nitrososphaera viennensis* (Thaumarchaeota), *Crenarchaeota* archaeon (Crenarchaeota) and *Heimdallarchaeota* archaeon (Heimdallarchaeota, Asgard).



Supplementary Figure 3: Packing artifact of HsTOP1-DNA.

Cartoon representation of two complexes within the packing of HsTop1-DNA crystal structure (PDB 1K4T). The linker domain (yellow) of one TOP1 is pushed away from the DNA by the CAT domain (pink) of a neighboring TOP1 molecule. Coloring scheme is the same as Fig. 1.



Supplementary Figure 4: Relaxation of supercoiled DNA by mutated CsTop1.

a) Relaxation assay with CsTop1, CsTop1(Y207A) and CsTop1 (Hinge3, WLSGG). **b)** Relaxation assay with CsTop1 and CsTop1(HsTyr). The kinetics of relaxation is shown for each construct. Both experiments were done twice independently.