

Topo III

<i>Sulfolobus solfataricus</i>	Q97ZJ8	11	LIIAEKSKAAKK	314	GLISYPRTNS
<i>Nanoarchaeum equitans</i>	Q74N66	2	IIIAEKPSVAKR	289	GYISYPRTSS
<i>Methanosarcina mazei</i>	A0A0E3PWI6	4	VAFAEKNKAAQ	313	GFTSYPRSTET
<i>Methanosarcina mazei</i>	A0A0E3PXP2	3	LIVTEKNIAARR	313	GYISYPRTDN
<i>Thermoplasma volcanium</i>	Q97CT2	7	VIIAEKVDAGR	309	GLISYPRTDN
<i>Haloferax volcanii</i>	A0A384LCM2	7	LIITEKDNAARR	322	GYITYPRTDN
<i>Escherichia coli</i>	P14294	3	LFIAEKPSLARA	324	KLITYPRSDC
<i>Neisseria gonorrhoeae</i>	Q5EP76	3	LFLCEKPSQAKD	318	KITSYPRTPC
<i>Neisseria gonorrhoeae</i>	A0A7H9WG49	5	LIIAEKPDMAKS	297	KVLTYPRSDF
<i>Saccharomyces cerevisiae</i>	P13099	4	LCVAEKNSIAKA	352	GFISYPRTET
<i>Ustilago maydis</i>	A0A0D1C790	4	LCVAEKPSIAKS	342	GFLSYPRSTET
<i>Choanephora cucurbitarum</i>	A0A1C7N0U0	4	LCVAEKPSAAKK	327	GLISYPRTET
<i>Choanephora cucurbitarum</i>	A0A1C7NLX2	7	LMVAEKPSLAES	333	GYISYPRTET
<i>Trypanosoma brucei brucei</i>	Q383X7	5	LNVAEKPSVARE	320	GYISYPRTET
<i>Trypanosoma brucei brucei</i>	Q384B1	5	LMVAEKPSIAES	322	GYISYPRTES
<i>Giardia intestinalis</i>	V6TB71	6	LCVTEKNSVAAE	405	GLISYPRTET
<i>Giardia intestinalis</i>	V6TB61	3	LLIAEKPSIAEM	324	GYISYPRTES
<i>Arabidopsis thaliana</i>	Q9LVP1	12	LNVAEKPSVAKS	338	GFISYPRTET
<i>Arabidopsis thaliana</i>	F4ISQ7	8	LMVAEKPSIALS	327	GFISYPRTES
<i>Homo sapiens</i>	Q13472	37	LCVAEKNDAAKG	358	GYISYPRTET
<i>Homo sapiens</i>	O95985	5	LMVAEKPSLAQS	332	GYISYPRTET

Topo I

<i>Thermoplasmatales archaeon</i>	A0A2P6VYX4	6	LVIVESPAKVD	321	GHITYMRTDS
<i>Thermoplasmatales archaeon</i>	A0A2P6VTI6	4	VIVVESGAKTRT	300	ALITYMRTDS
<i>Thermotoga maritima</i>	P46799	8	YIVVESPAKAKT	284	AFITYMRTDS
<i>Mycobacterium tuberculosis</i>	P9WG49	20	LVIVESPTKARK	338	GYITYMRTDS
<i>Deinococcus radiodurans</i>	Q9RUL0	48	LVIVESPAKAKT	365	GYITYMRTDS
<i>Agrobacterium tumefaciens</i>	A9CJ93	3	VVVVESPAKAKT	299	GLITYMRTDG
<i>Caulobacter crescentus</i>	Q9A5J6	3	VVVVESPAKAKT	298	GLITYMRTDG
<i>Neisseria gonorrhoeae</i>	A0A7H9WPJ8	5	LLIVESPSKAKT	300	GLITYMRTDS
<i>Helicobacter pylori</i>	A0A402E4A0	4	LIIVESPAKAKT	293	GVITYMRTDS
<i>Helicobacter pylori</i>	A0A402E2T6	5	VIIIIESPNKVAK	290	GLITYIRTDA
<i>Helicobacter pylori</i>	A0A402E598	6	VFIIENPNKIAK	297	GLITYIRTDS
<i>Pseudomonas aeruginosa</i>	A0A431XC87	5	LVIVESPAKAKT	320	GYITYMRTDS
<i>Pseudomonas aeruginosa</i>	A0A431X2A2	3	LVIIIEAPGKLKK	294	GLITYHRTDN

Reverse gyrase

<i>Sulfolobus solfataricus</i>	Q97ZZ8	621	LFIVESPNKAKT	961	GLITYHRTDS
<i>Sulfolobus solfataricus</i>	Q97ZF5	583	LLIVESPTKAKT	899	GLITYHRTDS
<i>Nanoarchaeum equitans</i>	Q74MA4	43	LFIVESPNKART	348	GLITYHRTDS
<i>Methanopyrus kandleri</i>	Q49600	781	LMIVESPNKARM		
	Q8TYK7			74	GLITYHRTDS
<i>Pyrococcus abyssi</i>	Q9UZ86	641	LMIVESPNKART	951	GLCTYHRTDS
<i>Conexivisphaera calida</i>	A0A4P2VAE5	658	LLLIVESPTKART	986	GLITYHRTDS
<i>Thermotoga maritima</i>	O51934	544	LIIVESPTKAET	847	GFITYHRTDS

Mitochondrial Topo IA

<i>Trypanosoma brucei brucei</i>	Q38C52	12	LVIVESPNKVIK	358	GHITYPRTDS
<i>Arabidopsis thaliana</i>	F4JRX3	476	VIVVESMTKAKI	775	GLITYMRTDG

Figure S1. Alignment of type IA topoisomerase active site region residues. Residues around the first strictly conserved TOPRIM glutamate and the catalytic tyrosine for formation of the covalent intermediate are shown here. Archaeal sequences are highlighted in yellow. Residues conserved in all type IA topoisomerases are shown in red. A lysine that always follows the conserved TOPRIM glutamate in topo III sequences is shown in green.