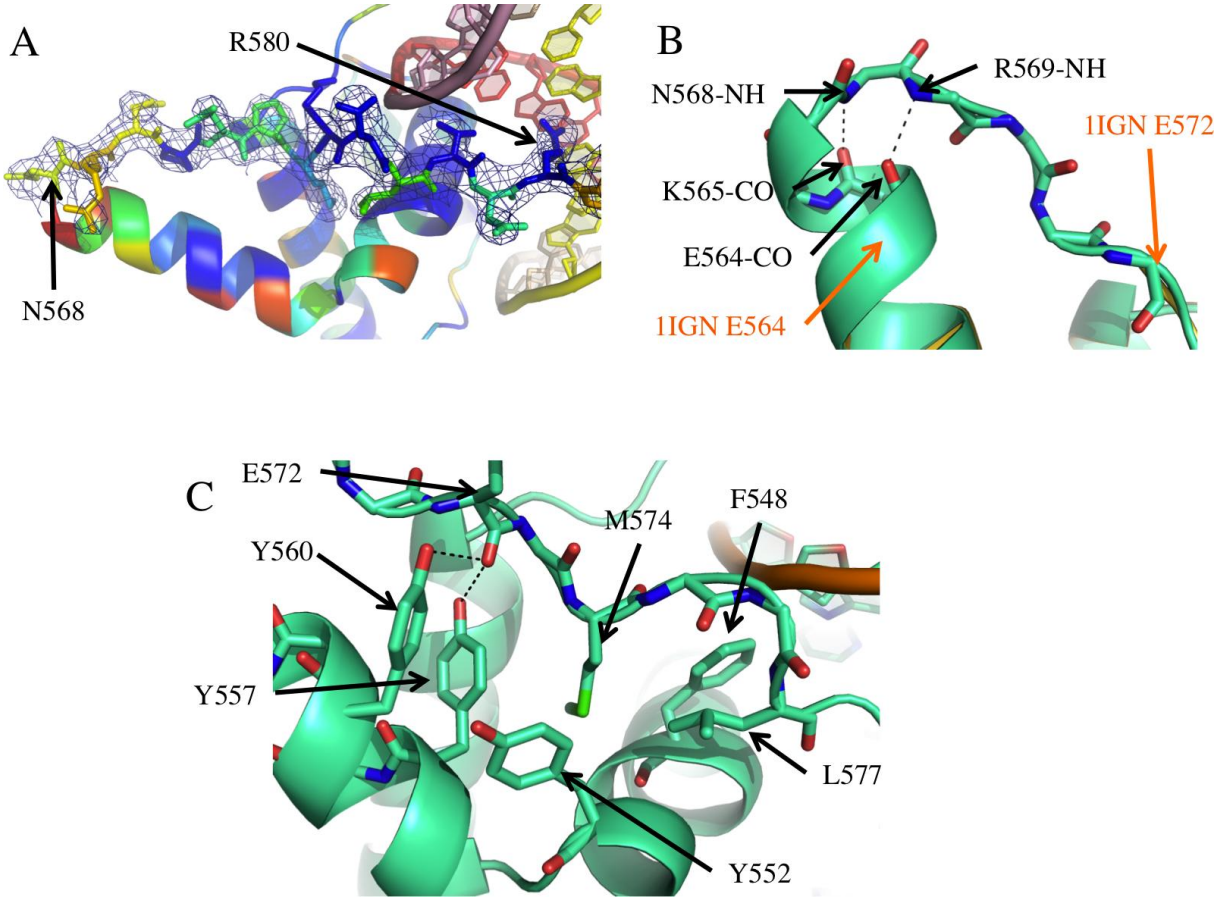
Supplementary Material



Supplementary Figure S1. A. Cartoon representation of SG19 structure region 565-580 in green cyan. The DNA C-rich and G-rich strands are coloured red and yellow, respectively, with the hemi-site in bright colours. The protein is coloured according to conservative scores from *CONSURF*. 2*F*o - *F*c electron-density map is also represented at 1σ contour level around 567-601 region. B. Enlargement of region 564-569, showing tight interaction involved in β-turn. The limits of the 1ign structure are also indicated in bright yellow. C. Polar interaction and hydrophobic network driving loop 565-580 towards the DNA major groove.

Supplementary Table S1

Referenced crystallization conditions used to calculate our protein/DNA specific screen.

REF	pH	Buffer	Prec	[Prec]	Add1	[Add1]	Add2	[Add2]
Ng et al., 2008	8.0	Tris	PEG4000	30%	$MgCl_2$	0.2M		
Genis et al., 2008	7.0	Tris	PEGmme550	15%	$MgCl_2$	5mM		
Pereira et al., 2008	6.0	Caco	PEG4000	15%	$MgCl_2$	0.1M		
Pereira et al., 2008			PEG3350	20%	K/Na tartrate	0.1M	$MgCl_2$	0.05M
Suwa et al., 2008	5-5.5	Caco	PEG3350	25%	MgAc	0.08M		
Redondo et al., 2007	4.5-5.5	Na Ac	PEG4000	5.6%	glycerol	30%		
Textor et al., 2007	9.0	Bis-Tris	PEG3350, PEG400	15%, 10%				
Shanmuganatham et al., 2007	5.7	Na Citrate	Amm Sulf, Eth glycol	1.4M, 21%	DTT	10mM		
Richardson et al., 2007	6.0	Na Citrate	KCl	0.2M	Amm Ac	0.1M	$MgCl_2$	5mM
Kapetaniou et al., 2007	8.5	Tris	PEG400	28-30%	$MgCl_2$	10mM	KCl	10mM
Watanabe et al., 2006	6.6-6.8	Bis-Tris	PEG10000	15%	Na/K tartrate	0.3M		
Vivian et al., 2006			PEG8000	13.5%	Li_2SO_4	0.45M	glycerol	10%
Vassylyeva et al., 2006	7.0	Hepes	PEGmme500	22.2%				
Sam et al., 2006	5.6-6.2	Na Citrate	PEG4000	30%	Amm Ac	0.2M		
Lu et al., 2006	8.5	Tris	PEG8000, PEG300	5%, 20%	glycerol	10%		
Imasaki et al., 2004	6.1	MES	PEG20000	13%	Na Ac	0.4M	6-aminocaproic acid	6%
Viadiu et al., 2003	4.6-5.0	Na Ac	MPD	32.5%	$CaCl_2$	5-10mM		
Sam et al., 2003	6.5	Imid	NaOAc	1M				
Aono et al ., 2003	8.5	Tris	PEG4000	20%	Li_2SO_4	0.1M		
Larivière et al., 2002			MPD	44%	t-but	4%	UDPglucose (with protein solution)	1mM
Pereira de Jesus et al., 2002	8.5	Tris	PEG4000	30%	Li_2SO_4 or $MgCl_2$	0.2M, 0.1M		
Hovde et al., 2002	5.6	Na Citrate	2-propanol, PEG4000	20%, 20%				
Tahirov et al., 2001	6.0	MES	PEG400	10%	KCl	0.1M	$MgCl_2$	10mM
Tahirov et al., 2001	6.5	Caco	PEG8000	10%	KCl	0.2M	MgAc	0.1M
Vivian et al., 2001	4.6	Na Ac	PEG4000	2-7%				
O'Loughlin et al., 2000	6.5	Mes	PEG8000, Glycerol	14%, 12%	$(NH_4)_2SO_4$	0.1M	$CaCl_2$	6mM
Horton et al., 1999	5.5	Na Citrate	PEG4000	20%	NaCl	0.12M		
Schwartz et al., 1999			Amm Sulf	1.8M	Glycerol	10%		
Tamulaitiene et al., 2004	6.5	Mes	PEG6000, NaCl	8-10%, 2M	Ethylene glycol	0-4%		
Escalante et al., 2002	6.5	Na Ac	PEG3000	15%	Glycerol	5%		
Viadiu et al., 2000	4.8	Na Ac	MPD	16-20%	$CaCl_2$	5mM		
Tan et al., 2000	5.2	Na Ac	PEG4000	6-10%	$NaNO_3$	0.2M	$Mg(NO_3)_2$, DTT	10mM, 10mM
Tan et al., 2000	5.5	Na Ac	PEG6000	7-10%	Amm Ac	0.1M	$CaCl_2$	10mM
Hirsch et al., 1997	6.0	Mes	Amm Sulf	2.2M	KCl	0.2M	Glycerol	5%
Pio et al., 1995	6.5	Caco	PEG600	10%	Zn Ac	0.2M		

Supplementary Table S2

Incomplete factorial screen calculated using SAmBA (Audic et al., 1997).

Prec1	pH	Prec2	Add1	Add2
Amm Sulf 2M	4,5	Glycerol 5%	Amm Ac 0.1M	Spermine 1mM
Amm Sulf 2M	5	ter-butanol 5%	MgCl2 0.1M1	0
Amm Sulf 2M	6	Propanol-2 5%	Amm Ac 0.1M	Co-hexamine 1mM
Glycerol 20%	4,5	Ethylene glycol 5%	CaCl2 0.1M	0
Glycerol 20%	5	ter-butanol 5%	MgCl2 0.1M1	Spermine 1mM
Glycerol 20%	6,5	0	Amm Ac 0.1M	Spermine 1mM
Glycerol 20%	7,5	Propanol-2 5%	0	0
Glycerol 20%	9	0	MgCl2 0.1M1	Co-hexamine 1mM
Li2SO4 1.5M	4,5	ter-butanol 5%	Amm Ac 0.1M	0
Li2SO4 1.5M	6,5	Ethylene glycol 5%	Amm Ac 0.1M	0
Li2SO4 1.5M	9	Glycerol 5%	0	Spermine 1mM
MPD 30%	6	0	CaCl2 0.1M	Spermine 1mM
MPD 30%	7	Glycerol 5%	MgCl2 0.1M1	Co-hexamine 1mM
MPD 30%	7,5	0	CaCl2 0.1M	Co-hexamine 1mM
PEG8000 10%	5,5	Glycerol 5%	Amm Ac 0.1M	Co-hexamine 1mM
PEG8000 10%	7	0	MgCl2 0.1M1	0
PEG8000 20%	4,5	0	MgCl2 0.1M1	Co-hexamine 1mM
PEG8000 20%	5	Ethylene glycol 5%	Amm Ac 0.1M	0
PEG8000 20%	6	Propanol-2 5%	CaCl2 0.1M	0
PEG8000 20%	6,5	Glycerol 5%	0	Co-hexamine 1mM
PEG8000 20%	7	Propanol-2 5%	0	Spermine 1mM
PEG8000 20%	8	Ethylene glycol 5%	MgCl2 0.1M1	Spermine 1mM
PEG3350 15%	4,5	ter-butanol 5%	0	Co-hexamine 1mM
PEG3350 15%	6	0	MgCl2 0.1M1	0
PEG3350 15%	6,5	ter-butanol 5%	MgCl2 0.1M1	Co-hexamine 1mM
PEG3350 15%	9	Propanol-2 5%	0	Spermine 1mM
PEG3350 25%	5,5	ter-butanol 5%	MgCl2 0.1M1	0
PEG3350 25%	7	Ethylene glycol 5%	Amm Ac 0.1M	Co-hexamine 1mM
PEG3350 25%	7,5	ter-butanol 5%	CaCl2 0.1M	Spermine 1mM
PEG400 20%	4,5	Glycerol 5%	MgCl2 0.1M1	Spermine 1mM
PEG400 20%	7,5	Ethylene glycol 5%	0	Spermine 1mM
PEG400 20%	8	0	CaCl2 0.1M	Co-hexamine 1mM
PEG400 30%	5	Glycerol 5%	0	0
PEG400 30%	6	ter-butanol 5%	0	Co-hexamine 1mM
PEG400 30%	7	0	CaCl2 0.1M	0
PEG400 30%	9	0	MgCl2 0.1M1	Spermine 1mM
PEGmme-550 20%	5	Propanol-2 5%	0	Co-hexamine 1mM
PEGmme-550 20%	5,5	Glycerol 5%	Amm Ac 0.1M	0
PEGmme-550 20%	6	Ethylene glycol 5%	MgCl2 0.1M1	Spermine 1mM
PEGmme-550 20%	7,5	0	MgCl2 0.1M1	Spermine 1mM
PEGmme-550 20%	8	Glycerol 5%	CaCl2 0.1M	0
PEGmme-550 30%	5	Glycerol 5%	CaCl2 0.1M	Spermine 1mM
PEGmme-550 30%	5,5	0	0	0
PEGmme-550 30%	9	Ethylene glycol 5%	MgCl2 0.1M1	0
Propanol-2 20%	4,5	Propanol-2 5%	MgCl2 0.1M1	Spermine 1mM
Propanol-2 20%	5	0	0	Spermine 1mM
Propanol-2 20%	8	0	Amm Ac 0.1M	0

Supplementary Table S3

Protein sequences used for conservation analysis from T-coffee alignment.

Rap1-Saccaromycescerevisiae	KASFTDEEDEFILDVVRKNPTRRTTHTLYDEISHY--VPNHTGNSIRHRFRVYLSKRLEY
Rap1-Saccharomycesdairenensis	KSSFTETEDEFILDVVRKNPTRRTTHTLYDEISHY--VPNHTGNSIRHRFRVYLSKRLDF
Rap1-Zygosaccharomycesrouxii	KASFTEQEDEFILDVVRKNPTRRTTHTLYDEISHY--VPNHTGNSIRHRFRVYLSKRLEY
Rap1-Lachanceathermotolerans]	KSSFTEEEDEFILDVVRKNPTRRTTHTLFDEISHY--VPKHTGNSIRHRYRVYLAKRLNF
Hypo-Vanderwaltozymapolyspora	KTSFTEEEDEFILDVVRKNPTRRTTHTLFDEISHY--VPNHTGNSIRHRYRVYLSKRLEF
Rap1-Naumoviacastellii	KASFTEAEDEFILDVVRKNPTRRTTHTLYDEISHY--VPNHTGNSIRHRFRVYLSKRLDY
hypo-Candidaglabrata	KTSFTEEEDEFILDVVRKNPMRRTTHTLFDEISHY--VPNHTGNSIRHRFRVHLSKRLDF
Hypo-Kluyveromyceslactis	KSSFTKEEDEFILDVVRKNPTKRTTHTLYDEISHY--VPNHTGNSIRHRFRVYLSKRLEF
Hypo-Ashbyagossypii	KSSFTEEEDEFILDVVRKNPTRRTTHTLFDEISHY--VPNHTGNSIRHRYRVYLSKRLNY
Hypo-Meyerozymaguilliermondii	--RFNKVKDDYILKQVRMHPKYRNSHKFFDDLANHPQLEGHTGNSIRSRFRTHLEPKLDW
Hypo-Pichiaguilliermondii	--RFNKVKDDYILKQVRMHPKYRNSHKFFDDLANHPQLEGHTGNSIRSRFRTHLEPKLDW
Hypo-Clavisporalusitaniae	-TKFTPEADKYILEQVRLKPRFRTSHKFFEELSHHELLRGHTGNSVRSRFRAHLEHRLDY
Rap1-Saccaromycescerevisiae	VYEVDK-FGKLVRDDDGNLIKTKV--LPPSIKRKFSADEDYTLAIAVKKQFYRD-LF-QI
Rap1-Saccharomycesdairenensis	VYEVDK-YGKLVRDEDGNLIKTKL--LPPSIKKKFTADEDYALAVSVKKQFYRD-LY-QI
Rap1-Zygosaccharomycesrouxii	VYEVDK-DGKLIRDANGNLVHTKV--LPPSIKKKFTAEEDYQLAIGIKKQFYRD-LY-QI
Rap1-Lachanceathermotolerans]	VYQVDS-TGKLVRDDNGDLIKTTV--LPKSLKNKFTASEDYALSVEVKKQFYRD-IY-QM
Hypo-Vanderwaltozymapolyspora	VYQVDS-SGKLVRDENGNLVKTKV--LPPSIKKKFTAEDDYNLAMGIKKQFYRD-LY-QV
Rap1-Naumoviacastellii	VYQVDS-YGKLVRDENGNLIKTKT--LPPSIKKKFTADEDYILALAVKKQFYRD-LY-QI
hypo-Candidaglabrata	VYQVDQ-YGKLVRDENGNLIKTKV--LPPSIKKKFTADEDYELAIAIKQQFYKD-IY-QL
Hypo-Kluyveromyceslactis	VYQVDE-DGKLVRDQDGNLIKTDI--LPNGLKRKFTSEEDYNLAVAVKKQFYRD-AF-QR
Hypo-Ashbyagossypii	VYKVDE-NGKLLRDEKGEFIKTDV--LPQGLKRKFTADEDYQLALNIKKQFYKD-IY-QV
Hypo-Meyerozymaguilliermondii	VYKTAS-DGSLIKDEHGQLIRDTLDNLPKTLKNRFTAEEDYELCQAIVD-FNRAR-FFGA
Hypo-Pichiaguilliermondii	VYKTAS-DGSLIKDEHGQLIRDTLDNLPKTLKNRFTAEEDYELCQAIVD-FNRAR-FFGA
Hypo-Clavisporalusitaniae	VWKTDE-YDNLVLDHEGRQIAIPT-NSAKTIKNRFTAEDDYNLCRDIID-HVLAN---QD
Rap1-Saccaromycescerevisiae	DPDTGRS----------PNHVPGSEPNFAAYRTQSRRGPIAREFFKH
Rap1-Saccharomycesdairenensis	DPDSGQSLISAQD-S-PTAIARRN--MTMDPNHIPGSEPGFKEYKVNDRKGPIAREFFKS
Rap1-Zygosaccharomycesrouxii	DPDTGVSLISDED-S-PTAIAKRN--MTMDPNHVPGTEPNFQDYRVSDRRGPIAREFFKH
Rap1-Lachanceathermotolerans]	DPDTGESLIKDIN-A-PDGNLKGS--FGAGSDERQNPGPSFKDFRVGERRGPVPREFFKK
Hypo-Vanderwaltozymapolyspora	DPDTGESLILEDD-S-PVAIAKRK--MTMMPNHIPGTEPNFQEYKVNERRGPLAREFFKQ
Rap1-Naumoviacastellii	DPDTGTNLISNED-S-PTAIARRN--MTMDPNHVPGNEPSFNDFRVNDRRGPVAREFFKS
hypo-Candidaglabrata	DPVTGQSLISDND-P-PARVAKRQ--MMMDPNVQRGSEPPFSKYRVGTRRGPIAREFFKQ
Hypo-Kluyveromyceslactis	DPDTGASLIAEDD-E-PNIVAKRQ--LVMNTEIDPSEVPSFEKYTVNDRRGPLSREFFKL
Hypo-Ashbyagossypii	DPDTGESLIRDDD-E-PSTVAKRK--MVMDPTFIPGKEPSFQDYNVGDRRGPLSREFFKT
Hypo-Meyerozymaguilliermondii	ADEHG--IVRDETGKPK-------EF---------------DLY--GQLTVPIS--FFST
Hypo-Pichiaguilliermondii	ADEHG--IVRDETGKPK-------EF---------------DLY--GQLTVPIS--FFST
Hypo-Clavisporalusitaniae	ADQL-K-VTDGSY-----------------------------EYPLNENKFSVSIVFFDE
Rap1-Saccaromycescerevisiae	FAEEHAAHTENAWRDRFRKFLLAYGIDDYISYYEAEKAQNREPEPMKNLTNRPKR-PGVP
Rap1-Saccharomycesdairenensis	FADENPTHTENAWRDRYRKFLLTFGVDAYIAYYEIERASGREPKPMKNLTNRPKR-VNAP
Rap1-Zygosaccharomycesrouxii	FGESHPTHTENAWRDRFRKFLLSYGIDNYIYYYERELGHGNDPEPMKNLTNRVKR-PGIP
Rap1-Lachanceathermotolerans]	YADENPNHTENAWRDRFRKFLLTFGIDRYIEYYENEIAQSRVPQAMKNMTNRPKR-PGVP
Hypo-Vanderwaltozymapolyspora	FGEHYPSHTENAWRDRFRKFLLSYGIDNYITYYETEKENGNEPEPMKNFTTRPKR-SALS
Rap1-Naumoviacastellii	FADANVSHSENAWRDRFRKFLLTFGVDHYIEYFEQETNAGRKPEPMKNLTNRPRR-KAGI
hypo-Candidaglabrata	FTENHPTHTESAWRDRFRKFLLEYGVDKYIEYYETQKANNDEPEAMKNLTIRTKR-DNFP
Hypo-Kluyveromyceslactis	FALEVPTHSENAWRDRFRKFILPYGIDSYISYYEKCMEEGIEPESIKNMTNRPKR-EG-P
Hypo-Ashbyagossypii	YGEKYPSHTENAWRDRFRKFLLNYGIDEYIAYYENEQAHNRVPEPMKNMTNRVKR-PG-P
Hypo-Meyerozymaguilliermondii	LAKTNPMHTPNSWRDRYRKFVSRYGAKKYIDYYDKVTASGGVPEPIKGDSPSTAKAIK--
Hypo-Pichiaguilliermondii	LAKTNPMHTPNSWRDRYRKFVSRYGAKKYIDYYDKVTASGGVPEPIKGDSPSTAKAIKQL
Hypo-Clavisporalusitaniae	YARLHPQHSSSSWRDRYRKFARVYGLQKYRDYYLREKDSKEGPQPMKNLTSRASK-EKKK
Rap1-Saccaromycescerevisiae	TPGNYNSAAKRARN-
Rap1-Saccharomycesdairenensis	TPGNYNSSVKRAR--
Rap1-Zygosaccharomycesrouxii	TPGNYNSA-KK----
Rap1-Lachanceathermotolerans]	TPGNYNSFAKKVK--
Hypo-Vanderwaltozymapolyspora	APGNYGSYVKKLK--
Rap1-Naumoviacastellii	TPGNYNSAIKRQR--
hypo-Candidaglabrata	TPGNYGNAAKRQK--
Hypo-Kluyveromyceslactis	SPGNYNTTLKKSK--
Hypo-Ashbyagossypii	APGNYNN-AKK----
Hypo-Meyerozymaguilliermondii	----------Q-
Hypo-Pichiaguilliermondii	IGSNY----RKDTQS
Hypo-Clavisporalusitaniae	IENNV----RRMKK-

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