### **Supplementary Information**

# Insights into the mechanism of action of the arbitrium communication system present in SPbeta phages

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**Supplementary Fig. 1. AimR**<sup>kat</sup> **is a dimeric protein.** Size exclusion chromatographymulti-angle light scattering (SEC-MALS) chromatograms of **a** AimR<sup>kat</sup> and **b** AimR<sup>kat</sup>-N273A in absence (black) and presence (red) of AimP<sup>kat</sup> peptide (GIVRGA). Chromatograms show the readings from the light scattering (dashed line) and refractive index (continuous line) detectors. The vertical axis represents the molecular mass. The horizontal curves represent the calculated molecular masses. In all cases the molecular weight calculated corresponds to a dimer (90kDa).



**Supplementary Fig. 2. AimR reported structures.** The structures for AimR<sup>kat,</sup> AimR<sup>SPβ</sup> and AimR<sup>Phi</sup> in their apo and AimP-bound are shown in cartoon rendering with protomers colored in blue and pink. Dimerization Interfaces are highlighted with brighter or darkest tones the slipping surface or capping helices, respectively. DNA recognition helices  $\alpha$ 3 are highlighted in green. For each structure its PDB code, space group, cell size and the presence of tags in the crystallized protein as well as the crystallization conditions are indicated. Depending on the use of one or two dimerization surfaces, the structures are classified as presenting open or closed conformation, respectively.



Supplementary Fig. 3. Comparison of AimR receptors in the Apo state. On the left is shown the pairwise comparison of AimR<sup>kat</sup> (blue tones), AimR<sup>SPβ</sup>-I (yellow-orange shades; PDB 6HP3) and AimR<sup>SPβ</sup>-II (green shades; PDB 6IPX) receptors in apo state by superimposing a protomer (left) of these dimers. While the second protomer is packed closed for the AimR<sup>kat</sup> and AimR<sup>SPβ</sup>-I dimers, showing both a very similar dimeric organization, in AimR<sup>SPβ</sup>-II the second protmer moves away (more than 30 Å with respect to the apposition of the second protomer in the other structures) showing an open conformation. Superimposition of the individual protomers (right) shows an almost identical conformation in all the structures with only small displacements in the capping helices used by AimRs to dimerize that, in the case of AimR<sup>SPβ</sup>-II, includes the extra His-tag. 5



**Supplementary Fig. 4. Two dimerization surfaces allow AimP-induced rearrangements to AimR receptors.** Cartoon rendering with helices as cylinders of AimR<sup>kat</sup> dimers in apo (left; in yellow-orange tones) and AimP-bound (*right*, blue tones) states. The two dimerization areas presented in the dimer are highlighted with more intense tones and the structural elements participating in the interactions are labelled. While the C-terminal dimerization area, including the capping-helix, maintains identical contacts in both structures, the N-terminal area acts as a slipping surface changing the interactions between structures.

a					
		No peptide	AimP <sup>Kat</sup> GIVRGA	<mark>AimP<sup>SPβ</sup></mark> GMPRGA	AimP <sup>Phi</sup> SAIRGA
	Tm (°C)	41	61	43	43



**Figure 5. Thermal shift assay for AimR**<sup>Kat</sup> and AimR<sup>SPβ</sup>. **a** The denaturation Tm of AimR<sup>Kat</sup> in its apo form (black line) shows and increment in the presence of GIVRGA peptide (blue line), its AimP, but not in the presence of GMPRGA peptide (red line) or SAIRGA peptide (green line), the AimPs from SPβ and Phi3T phages, respectively. All peptides were assayed at 0.5mM concentration. **b** AimR<sup>SPβ</sup> stability decreases by the presence of C-terminal His-tag how confirms denaturation curves of AimR<sup>SPβ</sup> with (AimR<sup>SPβ</sup>-II; red curve) and without (AimR<sup>SPβ</sup>-I; blue curve) this tag. Source data are provided as a Source Data file.



Supplementary Fig. 6. AimP-induced conformational changes in AimR receptors. Structural comparison of AimR<sup>kat</sup>, AimR<sup>SPβ</sup>-I and AimR<sup>SPβ</sup>-II receptors in their apo (blue tones) and AimP-bound (yellow-orange tones) states. The structural superimposition shows how AimP binding induces in the protomer (right) a closure movement that brings together TPR<sup>N-ter</sup> and TPR<sup>C-ter</sup> domains for the AimR<sup>kat</sup> and AimR<sup>SPβ</sup>-I structures. These conformational changes translate to the dimers (left) in the reduction of the distance between  $\alpha$ 3 helices. On de contrary, AimP does not induce any changes for AimR<sup>SPβ</sup>-II whose protomers present identical conformations in both states and, consequently, the corresponding dimers are structurally identical. 8



Supplementary Fig. 7. AimR<sup>kat</sup> in its apo state presents a DNA-binding competent conformation. The superposition of AimR<sup>kat</sup> in its apo stated (yellow-orange tones) on the DNA-bound AimR<sup>SPβ</sup> structure (PDB 6pH7; blue-cyan tones) shows that the DBD domains and the  $\alpha$ 3 helices (darker tones) occupy identical positions in both structures and, therefore, the helices are prefect positioned for the DNA boxes (highlighted in magenta) read-out. Two orthogonal views are shown with the AimRs rendered in cartoon and the DNA in backbone.

	АРО	PEPTIDE	DNA
AimR <sup>kat</sup>	88Å	64Å	89Å
	6571	657L	7QUN
<b>AimR<sup>spβ</sup></b>	80-89Å	75Å	89Å
	6HP3	6HP5	6HP7
AimR <sup>spβ</sup> -II	98Å	Aee	Â0e
	6JG5	6JG9	6JG8
AimR <sup>phi</sup>	85Å 5ZVV		

Supplementary Fig. 8. Distances between DNA binding helices in AimR reported structures. The structures for AimR<sup>kat,</sup> AimR<sup>SPβ</sup> and AimR<sup>Phi</sup> in their apo (colored in blue tones), AimP-bound (colored in pink tones) and DNA-bound (colored in yellow tones with DNA in green) are shown in cartoon rendering, with protomer A in darker tones. Dimerization slipping Interfaces are shown with cylindrical helices. DNA recognition helices  $\alpha$ 3 are highlighted in red, with distances between  $\alpha$ 3 helices of protomers A and B indicated in each case. C-terminal His-tag C are shown in sticks and coloured in light green in those structures where they are present. For each structure its PDB code is indicated.



**Supplementary Fig. 9. Structural comparison of AimR receptors in their AimP-bound state.** The superposition of AimR<sup>kat</sup>, AimR<sup>SPβ</sup>-I and AimR<sup>SPβ</sup>-II receptors bound to their cognate AimPs shows that the individual protomers (*right*) present identical conformation. However, the organization of the dimers (*left*) is quite different, changing the relative disposition of the second protomer, which is surprising in the comparison of AimR<sup>SPβ</sup>-I with AimR<sup>SPβ</sup>-II since both structures correspond to the same protein in complex with the same peptide.

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Name	Strain	Genome ID	AimR NCBI Ref	AimP NCBI Ref
SPbeta	Bacillus subtilis	NC_001884.1	WP_009968986.1	WP_009967508.1
Katmira	Bacillus subtilis	JMEF01000083.1	WP_033885437.1	WP_134819006.1
SRCM102756	Bacillus subtilis	NZ_CP028218.1	WP_160244980.1	WP_160243822.1
NMTD54	Bacillus atrophaeus	NZ_PVQN01000007.1	WP_106034888.1	WP_142394717.1
Phi3T	Bacillus subtilis	KY030782.1	WP_153256842.1	WP_134982144
JNUCC	Bacillus subtilis	NZ_VPFB0.000001	WP_147772092.1	WP_147772091.1
B4073	Bacillus subtilis	NZ_JXHP0.000037	WP_041338585.1	WP_142350264.1
SMRC103612	Bacillus subtilis	CP035406.1	WP_059293807.1	WP_139236146.1

b		DBD	Helix α3	Unconserved 0123	<mark>4 5 6 7 8 9 10</mark>	Conserve	ed	OBD	Helix a3		
	SPbeta MELIR	IAMER DIENDNSIMN KWATVAGIN	0	50 F S S	Phi 3T			20	0 40		1
	Katmira MELIR SRCM102756MELIR	IAMKE DLENDNSLMN EWATVAGLE Iamke Dlendnslmn ewatvagle	PNPLYDFLNH D KTFNI PNPLYDFLNH D KTFNI	E 755	JNUCC B4073	MIKNEO	EKDN QLAARLAKL	A GYEKVNGFI	FVNTPEKEME FVNTPEKEME	N IEGLINIVK NLGGLIKIVK	
	NMTD54 NELIR Consistency	KAMRK DLENDKTLMS KWATVAGLE 5 • 8 • • • • • 77 • • 7 • • • • • • • •	PNPLYDFLNH D SKTFN		SRCM10361: Consistency	L I K N E (	EKDN QLAARLAKL	A GYERVNGF1	FVNTPEREME	NIEGLINIVE 84**:6***	
		60 TPR1 70	0TPR2.90	100				70	0 <b>TPR2</b> .90	10	00
	Katmira IVNIV	KSQYP DREYELMKDY CLELDVKTKA	ARSALEYADA NMFFEII		_Phi3T JNUCC	N LF P D S S LF P D N	EEQL LSEYFLELD	P NKKCAROSVI P NKKCAROSVI	YSDINQWD <mark>T</mark> L YADINQWDDL	TD KII INLCN TD EII INLCN	
	SRCM102756LVNIV NMTD54 LVNIV	KSQYP DREYELMKDY CLELDVKTKA KSQY <mark>S DREYEFMKDY CLELDVKTK</mark> A	ARSALEYADA NMEFEII ARSALEYADA NKEDEI	EDVL IDTL	B4073 SRCM103612	S L F S E P	RECL LSEYFLOLD	P NKKCAROSVI	YSDINGWDSL YSDINGWDEL	TD KIILNLCN	
	Consistency 8	**** <mark>6 *****7**** **</mark> ****	6 5	6 = 5 =	Consistency	7 • 68	5 7 8		8 8 4	68 4 7	
	SPbeta IDSMI	110 120 1 S <mark>CSNM KSKEYG</mark> K <mark>VYK IHRELS<mark>N</mark>SVI</mark>	30	150 PEMN	Phi2m			120	30		50
	Katmira IDSMI SRCM102756 IDSMV	SCSNM KSKEYGKVYK IHRELSKGEI	DVFEASANIG KORIKT		JNUCC	S K N S T S	QENG KVYSIHRKL	N RRELSLTEAT		PEMLFFSNAM	
	NMTD54 LERMV	NCTNN KSKEYGQVYK IHKSLTDGEI	EFFDASNNLG RLKLKT	EMN	B4073 SRCM103612	SKNATS	SQEWG NIYSIHRKL SREWG QIYSIHRRL	N KSELGLNDA N KSEITLNDA	RETGRCKIKT	PEMELFESNAM PEMELESNIL	
	Consistency 8 8 6 9	7 7 6 7 7 7 7 7 7 7 6 8 7 7 7 7 6 8		200	Consistency	• 6 • 8 6 ·	7	5 8 <mark>5 7 8 1</mark>	7 <mark>5</mark> 8 7	6 * * 7 7 * * * 6 8	
	SPbeta SFSRL	LLLYH YLSTGNFSPM AQLIKQIDLS	EISENMYIRN TYQTRV		_Phi3T	LHYAYI	160	170I	180190 <b>IKESFKSRVS</b>	MLEANISLNE	00
	SRCM102756 IFSKM	LLMYD CLNKGNFAPH MLLFKOIDLS	EIKENRILKN SFETRI	N VII L	JNUCC B4073	LMY <mark>G</mark> YI LMYEYI	L <mark>SIGE FGLMKSTSK</mark> NIGE FGLMKSTAK	L LDFDELPQGY	IKDLYTSRVS IKDSYASRVA	LLKANISFNE LLKANIYLND	
	NMTD54 IFSKI Consistency 6 87	LTLYH YINTSDFAPM KSIDDIDLS • 68 • 5 4 • 7577 • 8 • • 44 • 65 • • • • 7	DLKENQFIKD SFQTRI 887 - 58885 787 - 9	Y VII K 4 T S	SRCM103612	INYEYI	KIGE FGLMKSTSQ	FLDIEELPDGS	INECYYGRIE		
			30	250	Consistency		5				-
	SPbeta SNIKL Katmira SNIYL	NENSL EECREYSKKA LESTNILREG	VESTITIONS LIFSNY	LAQ	_Phi3T	N S <mark>L</mark> L E J	ROHS NRATENSNU	N RICFFATLT	GNTLIFEDYD	EAKKAYIKGQ	50
	SRCM102756 SNIYL	NENNL DLCREYAQKA ISSTDTORFI	VFSYLTIGTS YIFSDF	DLSK	JNUCC B4073	N N <mark>L Q K J</mark> N D <mark>L E K S</mark>	REYC LDAIEKNSI SRYYS EEVITNTDI	D RICFFAYLT	GNSLIFESYD GNTLIFESYD	RAEHS YIKGK KAKES YELGR	
	Consistency B 4	7 83 8746 86 654	8 6 58 77	5686	SRCM103612 Consistency	YELED 55 <b>54</b> 56	RIHC QKVIESTNN 6 265 346 65555	N RLIVEGYLEN	GNTFIFEDYE	EAKLCYEKGM 6 * * 2 5 * 4 6 * 4	
			80	300			260	270	280		00
	SPbeta ENFLK Katmira QNYL	GLSIS VONENYNMIF QQALCFLNN Glkfa kg <mark>npgfeeff</mark> krnlsflnn	WRKENKWINF ESDSIM WNKENEWINY DSD <mark>A</mark> VT		_Phi3T	KYARNI OYARNI	-VHQ EMLDGALCE	L SNIWKKENQI	VNYNSDNIKY VNETSODTKY	LOLKAFYYIN	
	SRCM102756 ONYLI NMTD54 SSYMK	GLKFA KGNPGFEEFF KRNLSFLNNF Glnas knnkmfaeyf krnlsflsnv	WNKENKWINY ESDAVT WNKENEWLNF NSDDIT	D I Q E	B4073	TFARTS	THHO YKLRLALCE		VDFNSNLVAD	QIEVAYYYTN	
	Consistency 67884	547 64 438465 776 6 7 5	7 7 7 8 7 6 596	2	Consistency	4 8 * * 5 4	0463 45853 ***	• <b>5</b> • 6 • <b>4</b> • 8 • 7	9685 52643	5443 8 56	
	SPbeta QAHCF		30		Dhi 27			320	330		50
	Katmira VIFEL SRCM102756VIFEL	INHKE LSKALQLLNK LEERDQNENE	LGFHYYLKGL ITNEKE	A F F K	JNUCC	QGELI	KANTI LDDLSKREQ	D DNELGFYFY	RGLLSLDKSD	FYKSIAY FKK	
	NMTD54 VAHFF	INKKE DIKAGHLLQL LETKDQNDNE	LGFHYYLKGL FEQNID	Y FYD	B4073 SRCM103612	MKELE	KAISV ISSLEKRDL K <mark>ası iek</mark> iekln <mark>v</mark>	L DDDLGFLNH	KGLIYQEKSY KGLLYDDVS <mark>P</mark>	FYESTAKLKK FHE <mark>SIKK</mark> FKK	
		360 370 3	80		Consistency	54554	7 3 5 9 8 6 4 8 6 7 6 6 4	2 34 76 752 7	5 8 <b>• •</b> 8 <b>4</b> 3 8 6 7 3	877 6547 **	•
	SPbeta SIEYF	KKSND KFLIRLPLLE LOKMGENOKI	LELLL		_Phi3T		IQLP LLQLERMGA	370			
	SRCM102756 SVEYF	KSSQD KLFIKMPLIQ LEKMGENPRI	LQIISM		JNUCC B4073	SEDKY: SGDKMI	SLQLP LVQLEKLGA FINLP LGKLRKMGC	D LDLLSLISL D ENLLELILI			
	Consistency 9 88	*5*7* *64*88**85 *876*6*48*	68848		SRCM103612 Consistency	SGDKLO	CLNLP LIELKKRGY	T DEILNLISL			
С						,					
	SPbeta	ATCACTTAAATATTAGGTTTT	ATAACATCTAGTGAT		Phi3T	1	AAGTTCCAGAAA	TTCAAAAATO	CAAAAAATAAG	AACAT	
	Katmira	ATCACTTAAATATTAAGTTTT	TATAACATCTAGTGAT		JNUCC		AAGTTCCAGGAA	TTCTAAAAT	I'GAAAAATGAG	AACAT	
	NMTD54	ATCACGAGATAAATTTAAGTTTT	GCATAACATCTAGIGAI		SMRC103	3612	AAGTTCCAGAAA	TTCTAAAAAC	GAAAAATGA	AACAT	
Ы											
ä	CDhota	MUUT THAT UTLOAT CREVTON	- CCTOON CONFUN	MDDCA	Dhi 2m	,	MERCIPECT UTT T	AT A TOPULAC	000000000000000000000000000000000000000		DOP
	Katmira	MKKFIMAITIAAVI.SISFVGA	ASSNEOASGDIEVAG	IVRGA	JNUCC	1	MKKVIYGIMITA	ALAVSEVAG	OSVSTASASL	EISVASAT	RGA
	SRCM102756	MKKFIMAIAIAAVLSISFVGA	ASSNEQASGDYEVAG	VVRGA	B4073	i	MKKVLYSLIIVI	ALAVGFVGG	KSMETASVDO	PIKVASPS	RGA
	NMTD54	MKKVIMSALIVSAVALAFVGS	INKSNEASEEYNVAG	MVRGA	SMRC103	8612 i	MKKIYFGLVILL	ALAVGFVSG	QSVETASC	DVTVASAS	RGA

AimR receptors chimerity. a Arbitirum system compared showing similarities to those of SP $\beta$  (green background) or Phi3T (blue background). **b-d** Alignments of AimR receptors (**b**), DNA operators (**c**) and AimPs peptides (**c**) for systems showing chimerity trails with SP $\beta$  (*left*) and Phi3T (*right*). AimR alignments in **b** were performed with PRALINE (matrix BLOSUM62) server and are colored according to relative conservation. The location of DBD, helix  $\alpha$ 3, TPR1 and TPR2 are highlighted in boxes and labelled. Palindromic sequences for the DNA operators are highlighted in (**c**), as well as mature peptides (**d**)

## **Supplementary Tables**

## Supplementary Table 1. Data collection and refinement statistics

	AimR <sup>Kat</sup>	AimR-AimP <sup>Kat</sup>	AimR <sup>Kat</sup> -DNA
Data collection			
Space group	$P2_{1}2_{1}2_{1}$	C222 <sub>1</sub>	P2 <sub>1</sub>
Cell dimensions			
a, b, c (Å)	77.58, 98.30,	69.70, 209.76,	132.72, 39.87,
	144.35	140.25	143.01
$\alpha, \beta, \gamma$ (°)	90, 90, 90	90, 90, 90	90, 100.49, 90
Resolution (Å)	72.2-2.4 (2.46-	144.1-2.6 (2.77-	65.3-2.5
	2.4)*	2.7)	(2.57-2.5)
R <sub>pym</sub>	0.03 (0.40)	0.05 (0.61)	0.04 (0.73)
Ι / σΙ	13.5 (1.9)	9.5 (1.2)	10.6 (1.0)
Completeness (%)	99.7 (100)	99.8 (99.9)	96.4 (75.8)
Redundancy	12.6 (13.5)	4.7 (5.0)	6.4 (5.3)
Pofinoment			
Resolution $(Å)$	21	26	25
No reflections	43780(4329)	28616 (2830)	50316 (3867)
Runt / Run	0.22(0.33)/	0.18 (0.31)/	0.20(0.40)/
WORK / Tree	0.25(0.37)	0.22(0.31)	0.25(0.39)
	( )		
No. atoms			
Macromolecules	6455	6434	8226
Ligand/ion	20	12	35
Water	67	11	49
B-factors			
Macromolecules	60.70	66.50	91.05
Ligand/ion	114.20	96.00	141.80
Water	65.80	67.30	70.90
R.m.s. deviations		/ /	
Bond lengths (A)	0.014	0.014	0.016
Bond angles (°)	1.734	1.760	1.93

\*Values in parentheses are for highest-resolution shell.

## Supplementary Table 2. Strains and plasmids used in this study.

Strain or plasmid	Genotype	Reference
Strains		
B. subtilis strain 168	trpC2	1
B. subtilis ∆6	<i>trpC2;</i> $\Delta SP\beta$ ; sublancin 168-sensitive; $\Delta skin$ ;	2
	∆PBSX; ∆prophage1; pks::Cm; ∆prophage 3; Cmr	
B. subtilis subsp.		3
KATMIRA 1933		
BKK20860	trpC2 Δ <i>vop</i> K::kan	4
	s	
JP19877	Δ6 lysogenic SPbeta	This work
JP19936	Δ6 ΔaimR <sub>SPB</sub>	This work
JP19982	JP19877 amyE::P <sub>spank</sub>	This work
JP20009	JP19877 amyE::P <sub>spank</sub> -aimR <sub>SPβ</sub>	This work
JP19944	$\Delta 6 amy E:: P_{spank}-aim R_{SP\beta}$	This work
JP20222	JP19936 amyE::P <sub>spank</sub>	This work
JP20223	JP19936 amyE::P <sub>spank</sub> -aimR <sub>SPβ</sub>	This work
JP20224	JP19936 amyE::P <sub>spank</sub> -aimR <sub>Kat</sub>	This work
JP20147	JP19936 <i>amyE</i> :: <i>P<sub>spank</sub>-aim</i> R <sub>SPβ 6xHis Ct</sub>	This work
Plasmids		
pDR244	B. subtilis temperature-sensitive plasmid with	4
	constitutively expressed Cre recombinase	
pMiniMAD2	B. subtilis temperature-sensitive plasmid with	5
	erythromycin resistance	
pDR110	B. subtilis amyE integration vector containing IPTG-	6
	inducible P <sub>snank</sub> promoter	
pJP2340	pDR100 aimR <sub>SPB</sub>	This work
pJP2341	pDR100 aimR <sub>SPKat</sub>	This work
pJP2342	pDR100 <i>aim</i> R <sub>SPβ 6xHis Ct</sub>	This work
pLIC-SGC1	pET expression vector with N-terminal His <sub>6</sub> and TEV	Addgene
	protease cleavage site. Includes sites for LIC	plasmid # 39187
	cloning.	
pLIC-AimRKat33	pLIC containing <i>aim</i> R <sup>kat</sup> cloned	This work
pLIC-	pLIC containing <i>aim</i> R <sup>kat</sup> with mutation N273A cloned	This work
AimRKat33 <sup>N273A</sup>		
pLIC-AimR <sup>SPβ</sup>	pLIC containing <i>aim</i> R <sup>SPβ</sup> cloned	7
PET21b	pET expression vector	Novagene
pET-AimR <sup>SPβ</sup> -II	pET21b containing <i>aim</i> R <sup>SPβ</sup> cloned	This work

Supplementary Table 3. Oligonucleotides used in this study.

Oligo	Sequence			
Cloning in pDR110 plasmid				
AimR_pDR110_FW		CCCAAGCTTGACTCGTAATGTGATCTATAG		
AimR <sup>SPβ</sup> _pDR110_RV		ACGCGTCGACCATTGTCTCACCTCCTTTAAAGTAAAAG		
AimR <sup>Kat</sup> _pDR11	)_RV	ACGCGTCGACCACCTCCTTTCATTATTAAGTTTACATAG		
AimR <sup>SPβ</sup> 6xHis -		ACGCGTCGACCATTGTCTCACCTCCTTTAGTGGTGGTGGTGG		
pDR110_RV		TGGTGTTCAAGAAGTAAAAGTAATTCTAAAAGTTTTTGATTTTC		
		ACCC		
Cloning in pLic	SGC1 p	lasmid		
Kat33Plic_FW		ACTTCCAATCCATGGAGTTAATAAGGATAGCTATGAAGAAAG		
Kat33Plic_RV		TATCCACCTTTACTGTTACATAGTAATAATCTTTAGTAATCTTG		
		GATTTTC		
Cloning in pET	21b plas	smid		
SPbCter_FW		CAGTGGTGGTGGTGGTGGTGCTCAAGTAAAGTAATTCTAAAA		
		GTTTTTG		
SPbCter_RV		GAGATATACATATGGCTAGCATGGAGTTAATAAGGATAGC		
pet21_FW		CACCACCACCACCAC		
pet21_RV		GCTAGCCATATGTATATCTCCTTCTTAAAGTTAAAC		
AimR mutants				
Kat33 <sup>N273A</sup> _FW		TTTAAGTTTTTTAAACAATTTTTGGAAC		
Kat33 <sup>N273A</sup> _RV		GCTCTTTGAAAAACTCCTCAAACC		
Double strande	d DNA j	probes for EMSA		
DNA_kat	NA_kat GTTGATCACTTAAATATTAAGTTTTTATAACATCTAGTGATGGCC			
DNA_SPβ	SPβ GTTGATCACTTAAATATTAGGTTTTAATAACATCTAGTGATGGCC			
DNA_Phi3T	3T GTTGATGTTCCAGAAATTCAAAAATCAAAAAATAAGAACATGGCC			
Biotinylated double stranded probes for Biolaver Interferometry				
DNA_SPβ_b	GTTG	ATCACTTAAATATTAGGTTTTAATAACATCTAGTGATGGCC		
DNA_Phi3T_b	GGGA	AAGTTCCAGAAATTCAAAAATCAAAAAATAAGAACATGGGG		
DNA_Kat_b GTTGATCACTTAAATATTAAGTTTTTATAACATCTAGTGATGGCC				

#### References

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