## Mutations in conservative sites

### wbkA, G225V

	N lerlleaya+lpealr+dyplvia <mark>G</mark> gkgWk+e+learvarlglaghvrltgyvdda
	1 2 4 6 8 10 12 14 16 18 20 22 24 <mark>26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 57</mark>
	N L I R L L E A Y A N L P E C V R N N F L L V V A <mark>G</mark> G K <mark>G W</mark> N L G D I G K T I N R L G I A E Y T R L T <mark>G Y V</mark> T D S
_	N L V G L L E A F S R A R R A A C A D W R <mark>L V</mark> I A <mark>G</mark> G D <mark>G W</mark> R D S A I R Q A L D P L L A A G H V R L A <mark>G R V</mark> D D P
	N L V R L L D A F T R S R A A A R A D W T L A L A <mark>G</mark> G Q <mark>G W</mark> K D E A I R A R L A P L I S A G H V R V L <mark>G Y V</mark> S D S
	N L G N L I K A Y G L L P Q S A R S R C D L V I V <mark>G</mark> G K <mark>G W</mark> K Q T G L A D D V R D G A L G T N I K F T <mark>G</mark> F V D D A
A0A0Q8LIF9_9HYPH	N L G N L I K A Y G L L P A G I R S G C D L V I V <mark>G G T G W</mark> K Q T G L A D K V R A G G L E A N I K F T <mark>G F V</mark> D D M
R7UP24_CAPTE	N L N R L L Q A Y A T L D E P L K Q K H Q <mark>L V</mark> I A <mark>G</mark> G K <mark>G W</mark> G A V E V D S L V T Q Y G L A N Y V L K L <mark>G Y V</mark> S E G
A0A081NAL7_9GAMM	N L N R L L Q A Y A I L D E D L K Q K Y P L V I V <mark>G</mark> G K <mark>G W</mark> G G V N V E N L I T R Y G L S N H V R K L <mark>G</mark> Y V S E D
A0A7U3YJU0_DESPD	N L D R L L A A F A T L P E N L R A E T L <mark>L V I A G G</mark> K <mark>G W</mark> G G V N I S S L L Q Q Y D L E R N V L V T <mark>G Y V</mark> N D A
	N L H <mark>R L</mark> L K <mark>A Y A R L</mark> P A S L R Q N T Q F <mark>V</mark> L V <mark>G</mark> A K <mark>G W</mark> G G V D V A Q L V S Q L G V A R D V V L P <mark>G</mark> Y V D D A
	N L P Q <mark>L</mark> L R <mark>A Y</mark> A L Q P P A V R A T C M <mark>L</mark> A I I <mark>G</mark> G S <mark>G W</mark> R S S G L P T I I T E L G L S E D V K L I <mark>G</mark> Y V S E G
	N L P N <mark>L</mark> L E <mark>A Y</mark> A R L P G R V R E G L A <mark>L V</mark> I A <mark>G G</mark> Q <mark>G W</mark> R L G D L R Q Q I A R L G I E P F V R L T <mark>G Y</mark> V P D D
K0Q4Q3_9HYPH	N L N G <mark>L</mark> L E <mark>A</mark> F A A L P E S I R T G L L <mark>L V I A G G</mark> Q <mark>G W</mark> G L G D L E A E I T R L K L N A S V R L T <mark>G</mark> F V S D A
A0A1V0B5R5_9PSED	N L L R L L E <mark>A Y</mark> S C <mark>L</mark> P S K I K D N Y P <mark>L V</mark> L <mark>A G G H G W</mark> K L - S L E E M I M R A G L T D H T T V L <mark>G</mark> A I S N E
A0A5P9EV63_9GAMM	N L K <mark>R L</mark> L E <mark>A</mark> Y S L Y R E R V T D P L P <mark>L</mark> K I C <mark>G G</mark> K <mark>G W</mark> G M P E L K G K V Q E L D L E E S V E I L <mark>G Y</mark> I T D D
	N L N R <mark>L</mark> L L S Y K Q Y L D K T P E P L P <mark>L</mark> K I A <mark>G</mark> G S <mark>G W</mark> G G V S I E S V I A Q H G I S A H V S L L <mark>G</mark> Q V T D Q
	N Y S R I I H S L A E L R A Q - G M D L C <mark>L V I A G G</mark> K <mark>G W</mark> L Q D E M H Q T I K H T H M E D A V K L I <mark>G Y</mark> A D D A
	N V E R L I E A F G K L P A E - L R S Q P L V I G <mark>G</mark> K R <mark>G W</mark> L A E P I Y A A V Q R Y G L A Q S V I F L <u>D F</u> V S D S
A5G833_GEOUR	N L D G L M R A Y A Q L C A R P D F S H T L V I A <mark>G</mark> G S <mark>G W</mark> K N E G L K E L I R T L G L G E K V H F T <mark>G Y V</mark> D E T
_	N I S R L L Q A F A A L C D N P S F K H R <mark>L V</mark> I S <mark>G</mark> A Y <mark>G W</mark> K N K D V Y S S I A G L G I T D R V S F T <mark>G Y V</mark> A Q G
	N I P T L L R A F Y L L K K K - G I Q H R <mark>L V</mark> I A <mark>G G K G W</mark> K Y K S V Y K T V N E L N L Q K E V I F T <mark>G Y</mark> I P S E
	N I I R L I S A Y S K L I T I N P N A P N L V L A G R K G W M Y E E I F R K V Q Q E N I E D R V K F I G Y V A P D
U2QYN1_9FUSO	N I E R T I K A F I K Y K K E V K D D L K F <mark>V</mark> I V <mark>G G</mark> K <mark>G W</mark> K Y D N I M K L I E S M G T D I I L T <mark>G Y</mark> I D E E
A0A510JQX4_9FUSO	N I E R I V K S F K R Y K Q E I N D D L K <mark>L V</mark> I V <mark>G</mark> K K <mark>G W</mark> K Y D N I M K L I E S M G T D I I I T <mark>G Y</mark> I D E E
	N I G R I I D A Y A K Y Q Q Q A K D D I S L V L A <mark>G</mark> K K <mark>G W</mark> M Y Q E I F D K V K E H S L E D K V V F T <mark>G Y V</mark> N E I
A0A419T4A5_9FIRM	N I S T I I K <mark>A Y</mark> Q N L L K K Y D T N I Y <mark>L V</mark> I A <mark>G</mark> K K <mark>G W</mark> M Y K E I F K K V K D Y G I E K K V I F T <mark>G Y V</mark> D E E
A0A6S6Y108_9PROT	N L E R I I D A H Q S L P L P V R N S F P <mark>L V</mark> I A <mark>G</mark> R H <mark>G W</mark> G G E A L V A R L R Q L E A K G T V R W L N <u>Y V</u> T N E
Q1H1U6_METFK	N V G R V I E <mark>A Y</mark> R S <mark>L</mark> P Q G I R N E V P <mark>L V</mark> I V <mark>G</mark> R A <mark>G W</mark> R C E D V V E M L T S S S G N S L R W L <u>K H L</u> P D A
I0I600_CALAS	N I A R L L Q A Y Q S L S R D G G V A W D <mark>L V</mark> L A <mark>G</mark> A S <mark>G W</mark> Q S E G F D E Q V A G M G L S R S V R W L <mark>G Y V</mark> P D E
A0A540VBM9_9CHLR	N L A R L V E A Y A R L W Q Q P V P W D <mark>L V</mark> L A <mark>G G E G W</mark> L H R E L Q R L V E R A G L A G H I H L T <mark>G Y V P</mark> Q A
	N L E R <mark>L</mark> I E <mark>A</mark> F A A L G E A E R A G A R <mark>L A I A G</mark> K L <mark>G W</mark> L T Q A I E Q K A A A L G V A E H I R F L <mark>G Y V</mark> P D A
	N L Q R V L E <mark>A</mark> F A A V E R E - Q P S A R <mark>L V</mark> I V <mark>G</mark> G A R <mark>W</mark> Q A T P I V E R A K G M R N V R L T <mark>G F V</mark> S D A
	N L R R L L R A F R E Y L N L T A D P H P L V L A <mark>G</mark> G K <mark>G W</mark> M E G D L E N F I G E L G L N D H V R L T <mark>G</mark> Y V S D E
A0A6V8LR73_9DELT	N Q E R L F E A L A R L G G K R P <mark>L V</mark> L A <mark>G G R G W</mark> L M D E M G R K V N A L G L A S R V K L T <mark>G Y V</mark> D D A
G7Q4B5_9DELT	N H E R <mark>L</mark> F A <mark>A Y A</mark> A W R R D T G G D M P <mark>L V</mark> L A <mark>G G K G W</mark> L M D D V A R T V K E L G I A D H L V F T <mark>G Y V</mark> T D A
D0KY26_HALNC	N L E R L L N A Y G A L P E G V R R D Y P <mark>L V</mark> L <mark>A G G G G W</mark> N D S D L Q R Q I Q Q M E R R G E <b>V</b> I R T <b>G Y</b> L P R S
A0A191ZIB0_9GAMM	N L I R <mark>L</mark> I D <mark>A Y A R L</mark> P S T L R S A Y P <mark>L V</mark> L V <mark>G G</mark> V <mark>G W</mark> Q N A D L L T R V Q A M E S A G E L I R T <mark>G Y</mark> L P Q A
	N L P R L L A A Y A I A R R - K G L S Q K L L I G <mark>G</mark> A K <mark>G W</mark> R L S S L A A V V D E Y T L Q D H V V F L <mark>G Y V</mark> A D E
F9ZQ63_ACICS	N I G R L L A A Y A A L P D R L R K E H P <mark>L</mark> Y L A <mark>G</mark> S F <mark>G W</mark> R E A E F S D V L K R L V E I G E A R I L <mark>G F V</mark> P D P
A0A8J7UJF0_9HYPH	N L V R <mark>L</mark> L D <mark>A</mark> F E Q L P Q T L R Q R Y P <mark>L V L A G</mark> Y K <mark>G W</mark> N N T A I L E R L H R A E T Q G W A R Y L <mark>G Y V P</mark> D E
A0A160DXY1_9GAMM	N L V R <mark>L</mark> V R <mark>A Y A </mark> L L P A A L R A A Y P <mark>L V I V G</mark> A R <mark>G W</mark> L N R E L E R V L G P L E A A G V A R R L <mark>G Y V</mark> D E A
	N
A0A4R2NEZ4_9BURK	N I D R L L S A Y E G L P P A L R Q R Y P <mark>L V</mark> L A <mark>G G T G W</mark> H S E H T H A H M A R A A A A G W L H Y L R <mark>Y</mark> V P Q A
A0A363RQF1_9BURK	N L D R L V Q <mark>A Y A L L P</mark> E E M R R A C P <mark>L V V A G G</mark> Q <mark>G W</mark> N S E S V H A R M A K A Q E Q G W L R Y M S F <b>V</b> D Q R
A0A4S8F5W6_9BURK	<mark>N</mark> V E R <mark>L</mark> I E <mark>A Y A L L P V D L R R E W P <mark>L V I A G G K G W</mark> N S E A V H A R M A K A Q A E G W L R Y L S F <mark>V</mark> D Q R</mark>
A0A1Y0ESC7_9BURK	N I A R L I E A Y A R L S R D L R L T W P L V L V <mark>G G</mark> P <mark>G W</mark> H S E A I H A R M A Q A Q A E G W L R Y L S F I D Q R

Supplemental Figure 1. The multiple alignment of bacterial glycosyltransferases from UniProt database which are homologous to the wbkA protein of Brucella abortus (Q2YMN5\_BRUA2). The site of substitution G255V observed in KB 17/100 strain is indicated by red rectangle. The intensity of blue color corresponds to conservation level.

wboA, W219L

Glycosyl transferase domain (InterPro entry IPR001296)

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	+	+	k	ер	+	р	Υ	f	W	t	t	N a	s	р	Н	ΚN	N h	+	n	a	l +	ΑI	s	i	Уγ	/ e	r	Ιç	g	+	Ιk	С	ı	i 1	G	٧	n t	е	+	LT
	1	2		4	6		8	1	0	12	_	4	16		18	2	0	22	2	24	26	2	8	30	3	2	34	3	6	38	40	)	42	4	4	46	48	3	50	52
Q2YQ89_BRUA2	٧	S	K١	V K	Έ	Р	ΥI	FL	١,	P	ΤI	N P	N	Α	Н	K١	۱H	Α	K	A F	- Q	A L	D	L	ΥY	<b>/</b> G	Κ	Lk	G	K	ΙK	Τ.	K	I۱	/ G	V	SS	V	R I	M D
A0A1M7Y499_9FIRM	W	L	S I	D I	G	Ε	ΥI	F ]	M	S	Т	N P	S	٧	Н	K١	۱H	I	F	ΑL	N	A L	I	Κ	ΥY	/ E	-	S	G	K	L K	С	I	I	G	Α	D T	Е	М	FΚ
A0A7H0GDY0_9SPHN	F	K	۷۱	E R	R	G	ΥI	FL	. W	/V	TI	N A	S	Α	Н	K١	۱H	٧	A	A F	R	A L	R	Н	ΥY	/ E	S	LO	G	Q	L K	С	L	Ι (	G	Р	V T	D	М	LI
A0A6G7ZKL4_9SPHN	٧	Т	۷	E P	G	Κ	ΥI	FΙ	ı۷	<b>/</b>  V	Т	N A	A	Α	н	K١	١H	٧	N A	A L	R	A L	R	Н	ΥY	/ E	G	LO	G	Е	L T	С	LI	4 (	G	Р	V T	D	М	LI
A0A5N7MSI5_9HYPH	G	L	Ε (	G R	S	N	ΥI	F۱	/W	P	Т	N A	A	P	Н	K١	١H	L	М -	Τl	E	A L	s	R	ΥY	/ Q	V	Q C	Q G	Α	L C	С	н١	<b>/</b> 1	G	٧	N S	Q	L	L D
A0A0W0Y5L5_9GAMM	W	Р	I	РЕ	Е	Р	ΥI	FL	ı۷	T	Т	٧ĸ	ά	L	н	K١	<b>I</b> L	Ε	N A	A L	. т	A L	Υ	Ι	ΥY	/ T	R	LD	G	K	FΑ	С	н١	<b>/</b> 1	G	٧	N A	Q	D	ΙL
A0A2V1HCZ0_9GAMM	Р	K	Т	Q G	S	Q	ΥI	FΙ	ı۷	T	Т	N S	D	Р	н	K١	<b>I</b> L	D	K	I F	E	A L	K	Ι	ΥY	/ E	Т	ΗΝ	١G	S	L K	С	L	I	G	٧	N T	Α	S	ΙL
F9U6Z1_9GAMM	Q	N	K	ĒΡ	E	Р	ΥI	F I	W	T	Т	N A	S	Р	Н	K١	۱Н	L	N A	Α ]	ΙΙ	A L	R	М	ΥY	/ D	Е	LO	G	s	L R	С	K١	<b>/</b> 1	G	L	LS	S	D١	ΝL
A0KMA1_AERHH	Q	Н	ΚI	D L	. C	D	ΥI	F 1	W	T	ΤΙ	N L	S	Р	Н	K١	VН	L	N A	Α١	/ K	A L	D	Ι	ΥY	/ N	Q	L A	G	s	L K	С	F	ΙĪ	G	٧	N T	Q	N	ΙM
A0A0X1T5Z6_PSEAA	R	D	Р (	QΑ	Р	Α	ΥI	FL	. W	/T	S	N L	. A	М	Н	K١	VН	Ε	N A	A L	K	A L	K	Ι	ΥY	/ E	Е	МС	Q G	Е	Lν	С	F	L٦	/ G	٧	ΕТ	Ε	K	LL
A4J979_DESRM	Κ	Р	Т	G N	ΙP	R	ΥI	FL	. W	/T	Т	N L	. A	Р	Н	ΚN	۱н	٧	N A	A F	K	A L	L	Ι	ΥY	/ E	Е	Y	G	R	L E	С	С	Ι 9	G	٧	N T	E	N	ΙL
A0A1I7JB27_9BURK	٧	K	K S	s c	G	Н	ΥI	FL	. W	/T	Т	N A	A	Р	н	ΚN	۱н	Κ	N A	Α١	/ Q	A L	E	Ι	ΥY	/ E	Е	LD	G	R١	N C	С	K	I	G	Α	N T	K	G	ΙL
A0A081NW49_9BACL	S	Q	L	F P	F	Р	ΥI	F I	Y	Р	Α	V T	S	Р	н	ΚN	۱н	Υ	N	LL	L	A Y	s '	R	F S	S R	R	s c	γ	-	- S	L	L	LĪ	G	Υ	N T	Н	L	L R
A0A1I1U7H8_9BACL	Α	Α	K	L P	Р	Е	Υ	ΙI	Y	Р	S	V T	S	Р	н	K١	۱H	Υ	N	LL	. I	A L	S	Q	F A	A D	R	Κk	( Y	-	- P	L	V	LI	G	Υ	s T	Ε	L	L R
A0A0Q4QNI5_9BACL	Α	Α	R	I P	S	Κ	Υ	I	Y	Р	S	N T	S	Р	Н	K۱	N H	N	N	LL	. E	A L	S	н	W F	( G	R	Tk	C	-	- P	L	V	L 1	G	Υ	L T	Е	Т	L R
A0A7X3AC50_9BACL	Α	Α	Α	L P	K	Е	Υ	I	Y	Р	S	N T	S	P	Н	K۱	۱ H	S	N	L	L	A L	Α	K	Y	( H	R	Κk	КН	-	- P	L	٧	L I	G	Υ	LT	Ε	K	L R

Supplemental Figure 2. The multiple alignment of bacterial glycosyltransferases from UniProt database which are homologous to the wboA protein of Brucella abortus (Q2YQ89\_BRUA2). The site of substitution W219L observed in strains 75/79-AB and 82 is indicated by red rectangle. The intensity of blue color corresponds to conservation level.

# Mutations in semi-conservative sites

#### Pmm, N255K

Alpha-D-phosphohexomutase, alpha/beta/alpha domain III (InterPro entry IPR005846)

	ldaivstdgDaDRPliadetG+wl <mark>r</mark> GDvlGiltarflgadtvvtPvssnt
	1 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50
Q2YMR0_BRUA2	L D A V V S T D G D G D R P L V I D D Q G R Q V N G D T L G I L T A R Y F R A K T V V T P L S T T S
A0A1I4T0J3_9HYPH	L D A V V S T D G D G D R P L V I D E A G R Q V N G D V L G I L T A R R L G A K T V V T P I S S T S
A0A657LZT3_9HYPH	L D A V V S T D G D G D R P L V I D D T G R Q I <mark>H</mark> G D V L G M L T A R A <u>I</u> G A K T V V T P L S S T G
A0A1N6TVL7_9HYPH	L
G4RGW7_PELHB	F
A0A1G7RWX0_9HYPH	C D A V V S T D G D G D R P L L L S E Y G A Q V <mark>N</mark> G D I I G A L A A R A L G A K T I V T P L T S T S
J2VYK2_9HYPH	L D A L V S T D G D A D R P L V A D E T G A F I <mark>R</mark> G D S L G L L T A H F L N A D A V V T P V T S N T
A0A2P7B2G2_9HYPH	L D A L V S T D G D A D R P L I A D E Q G V F L <mark>R</mark> G D S V G L L T A C F L Q A D A V V T P V T S N T
A0A2N9VVF2_9HYPH	L D A L V S T D G D A D R P L V A D E H G V F L <mark>R</mark> G D S V G L L T A R F L N A D A V V T P V T S N T
J1JWF1_9HYPH	L
A0A1R0FAI8_9HYPH	L D A L V S T D G D A D R P L I A G S D G I F L <mark>K G D V V G M L T A K Y L F A</mark> D A <b>V V T P V</b> T S T S
A0A0F5FVT4_9HYPH	L D A I V S A D G D G D R P L V M D G Q G Q F V <mark>R</mark> G D V L G L L T A R F L G A D A V V T P V T S N S
A0A7W6H9Q2_9HYPH	F D A I V S T D G D A D R P L M A D E R G T L L <mark>R</mark> G D L I G L L T A R H L G L T T I V T P V T S S A
A0A0Q4XSH8_9HYPH	F
B1M2U5_METRJ	F D A L V T T D G D A D R P L V A D G T G C I V <mark>R</mark> G D V L G L I T A R F L G A D T V V V P V T A G S
A0A0F7KE05_9PROT	L D A L L S T D G D A D R P L I G N E T G R W L <mark>R</mark> G D V V G L L C <u>A</u> Q Y L D A H T V V T P V S S <u>T</u> T
A0A2Z6GD46_9PROT	L D A I I S T D G D G D R P L I G D E T G D W L <mark>R G D V V G L L C S H F L G A D T V V T P V S C N T</mark>
A0A126T637_9GAMM	L D A L I S T D G D G D R P L I G D E T G E W L <mark>R</mark> G D I V G L L C A K F L G A D T V V T P V S C N T
A0A172U5V4_9GAMM	L D A L I S T D G D G D R P L I G D E S G E W L <mark>R</mark> G D I V G L L C A K F L G A D T V V T P V S C N T
A0A1S1Y295_9GAMM	L D A I I S T D G D G D R P L I G D E T G E W L <mark>R</mark> G D I V G L L C A K F L G A D T V V T P V S C N T
G3J1H3_METTV	L D A I I S T D G D G D R P L I A D E T G N W L R G D I V G L L C A R F L D A D T V V T P V S C N T
A0A7T0JKA9_9GAMM	L D A I I S T D G D G D R P L I A D E T G T W L <mark>R</mark> G D I V G L L C A H F L G A D T V V T P V S C N T
A0A2W2BDZ4_9HYPH	L
A0A501WZ83_9RHOB	L D A V V S T D G D G D R P L I G D E T G A F L <mark>R G D V V G V L A A R Y L G A D A V A T P V</mark> S S N S
A0A858QWU1_9GAMM	
A0A7Y6YBB3_9GAMM	F D L I V S T D G D A D R P L I G D E Q G N W L <mark>R</mark> G D V V G V L C A R A L G <u>V</u> E T V V T P V S S N T
C6WVI2_METML	F D A I I S T D G D A D R P L I G D E H G N W L <mark>R</mark> G D V V G V L C A K F L S A E T V V T P V S S N T
A0A533U0R7_CHLSQ	F
A0A0B0HCL1_SOVGS	F
A0A7Z2VX60_9BURK	F D A I V S T D G D A D R P L I G D E R G T W L <mark>R G D I V G I L C G Q Y L G A D F V V T P V</mark> S S N T
A0A1T1AUG9_RHOFE	F D A I L S T D G D A D R P L L G D E R G Q W L <mark>R</mark> G D V V G I L C A Q F L R A Q V V V T P V S S N T
A0A1H0VMD5_9BURK	F D A L L S T D G D A D R P L I G D E N G E W L <mark>R G D V V G I L C A K Y L Q A Q V V V T P V</mark> S S N T
F9ZL11_ACICS	L D A L V S T D G D A D R P M L A D E C G N W W R G D L L G L V S A R I L A A D A V V T P V S S N T
A0A543Q831_ACITH	L D A L L T T D G D A D R P M I A D T T G R W W <mark>R</mark> G D V L G V L T A R A L G A Q T V V T P V S S N T
G0JU90_9PROT	L D A L L T T D G D A D R P M I A D H E G H W W R G D V L G I L T A H A L G A H T V V T P V S S N T
F8XNG1_9PROT	D A D R P M I A D H E G R W W R G D V L G I L T A H A L G A H T V V T P V S S N T
B7J7C0_ACIF2	L D A L L T T D G D A D R P M I A D H E G R W W <mark>R</mark> G D V L G I L T A H A L G A H T V V T P V S S N T
A0A4R1HBW8_9GAMM	
W6K842_MAGSQ	L D A I V S T D G D A D R P L L A D E T G T W F <mark>R</mark> G D V A G I L C A R F L G A K Q V V T P V S S N S
A0A0S2TGX0_9GAMM	F D C L V S A D G D G D R P L V S D A G G H W L R G D V A G I L T A R Y L G A R A V A T P V S S N S
A0A2K8L3L4_9PROT	L D C I V S T D G D G D R P L V S D E H G E W L <mark>R</mark> G D V A G I L T A R Y L A A T H V V T P V S S N S
A0A498DI78_9PROT	F
A0A5R9GPL8_9PROT	F D C I I S A D G D G D R P L I S D E H G N W L R G D V A G V L C A R Y L A A T H V V T P V S S N S
A0A0G9MZJ0_9SPHN	F D A I V S T D G D S D R P L L A D E S G E W L <mark>R</mark> G D V L G V I C A R H L G A D R V V T P V S S N T
A0A0N1AEQ4_9SPHN	L D A I L S T D G D S D R P L L A D E T G A W L R G D V L G I L C A R A L E L A A V A T P V S S N S
A0A0D6MM92_9PROT	L
A0A252AL26_9PROT	L D A I L T T D G D S D R P L L A D G K G E W L <mark>R</mark> G D V L G I V A A R Y L A A K A I T T P V S S N T
A0A2Z5ZJS1_9PROT	F D A I L T T D G D S D R P L L A D K N G T W L <mark>R</mark> G D V L G I L A A Q T L G A G S V A T P V S S N T
G6XLV3_9PROT	Y H A I L T T D G D S D R P L L A D H Q G N W L <mark>R</mark> G D V L G I L S A R F L D A A S V S T P V S S N T
A9H070_GLUDA	L D A I L T T D G D S D R P L L A D R A G N W L <mark>R</mark> G D V L G I L A A R F L N A A A V T T P V S S N T
A0A7W4PQE0_9PROT	L D A I L T T D G D S D R P L L A D A R G N W L R G D V L G I L A A R F L G A A S V T T P V S S N T

Supplemental Figure 3. The multiple alignment of bacterial phosphomannomutases from UniProt database which are homologous to the pmm protein of Brucella abortus (Q2YMR0\_BRUA2). The site of substitution N255K observed in strain KB 17/100 is indicated by red rectangle. The intensity of blue color corresponds to conservation level.

#### wbkA, A321E

Glycosyl transferase family 1 domain (IPR001296)

										l													B		
	SS	Ιp	e v	a g	d a	a I	Ιv	d p	Ιd	v d	e i	i a c	i a	Ιa	r	Ιe	d e	e a	l r	a r	Ιa	+ a c	j   +	- r a	arf
	1 2	4	6	8	10	12	14	16	18	20	2	2 2	4	26	28	30	32	34	36	38	40	42	44	46	48 50
Q2YMN5_BRUA2	SSI	M P I	E V	A G	D A	ΑI	LV	D P	LN	V A	E ]	I S N	ΙA	LY	RI	ΑΤ	DN	IKI	L W	QR	K S	LLA	\ L Q	N I	ERF
A0A4R0P988_9HYPH																									RRF
A0A085EZA8_9HYPH	G S	L P I	ΕI	A G	A G	G L	A V	D P	F D	ΕQ	Qι	_ G L	_Α	LA	RL	F S	DD	TI	L R	A G	LS	SAA	H A	N A	RRF
L0KQH0_MESAW	SSI	ΜРΙ	ΕV	A G	NN	A V	LV	D P	E D	РΑ	A ]	I A A	١А	F S	R L	. C T	DA	E	FR	NG	I A	A D A	KK	(NA	GRF
A0A0Q8LIF9_9HYPH	SSI	ΜРΙ	E V	A G	DN	A V	LV	D P	N D	PV	A ]	I A A	١А	FΗ	R L	C V	DA	E	F R	NG	I A	A G A	\ K R	LN A	ERF
R7UP24_CAPTE																									RF-
A0A081NAL7_9GAMM	SSI	ΜРΙ	ΕV	A G	DA	GΙ	L I	D P	Y S	ΙR	SI	I A S	G	L R	TN	1 M D	SK	QF	R D	LL.	ΑА	RAK	( N N	I A T	RF-
A0A7U3YJU0_DESPD																									ARF
A0A844U0W6_9BORD	SSI	ΜРΙ	ΕV	АА	DA	G F	F V	D P	L D	ΕV	S I	I A D	G	LA	RL	LA	ED	AI	L R	Q S	LA	SRA	RC	I A	SRY
Q1YMA8_AURMS																									DRF
A0A135HYQ6_9HYPH	SSI	ΜРΙ	E V	A G	DA	A L	LI	D P	A D	V Q	SI	I A D	G	LA	RL	. A T	D D	VI	LY	R E	LS	SRT	R A	N A	GRF
K0Q4Q3_9HYPH	SSI	ΜРΙ	ΕV	G G	D A	V L	LV	E P	s s	νQ	S N	4 T N	ΙG	LA	RL	. A T	D V	' S I	LY	s ĸ	L C	SAA	RA	N A	ERF
A0A1V0B5R5_9PSED																									KKF
A0A5P9EV63_9GAMM																									GEF
A0A1X9NBG1_9GAMM																	-				_				QKY
A0A3T1DE52_9BACL																									EKF
A0A3N6NH46_9BURK																									GRF
D8FF99_9DELT																									KQF
A0A6V8LR73_9DELT																									ARF
G7Q4B5_9DELT																									GLF
A0A6S6Y108_9PROT									-			_				_									QQF
Q1H1U6_METFK								_																	LAY
A0A318S9V7_9DEIO															_		_								TLF
A0A3P4B2T6_9BURK																									AQF
D0KY26 HALNC																									QAF
A0A191ZIB0_9GAMM																									QLF
A0A7Y7NMV3_9DELT																									ALF
A0A0Q8QXT3_9BURK																									ESF
F9ZQ63_ACICS																									SLY
A0A2S0P9G8_9NEIS																									АТҮ
A0A8J7UJF0_9HYPH																									AGF
A0A160DXY1_9GAMM																									RAF
A0A4R2KKA1_9GAMM																									AER
A0A4R2NEZ4_9BURK	SS	L P I	E V	V G	SA	A L	QΙ	D P	Q D	ΤQ	ΑL	L R N	ΙA	LΕ	Q	S L Q	DE	A V	۷R	IΗ	АН	RAG	LA	RA	CQF
A0A363RQF1_9BURK	SCI	ΜРΙ	E V	A G	G A	A Y	LV	N P	R D	V D	D I	I R F	l G	LΕ	НС	LS	DE	A V	۷Q.	A D	AR.	AKG	LA	RA	AQL
A0A4S8F5W6_9BURK																									SQL
A0A1Y0ESC7_9BURK	SCI	ΜРΙ	ΕV	A G	G A	ΑН	LV	D P	L D	VΕ	DΙ	AH	l G	LA	RC	LE	D E	ΑV	N L	V Q	A R	TQG	LA	RA	AAL
A5G833_GEOUR	s c	L P I	ΕV	A G	D S	A L	LV	ΥP	H S	V E	D I	I A A	١G	ΙΑ	RL	LG	DE	AI	L R	R T	СI	ERG	RE	RA	KLF
A0A0F3GZM7_9BACT																									RKF
A0A1F2P8Y2_9EURY																									KMF
A0A839K073_9FIRM	A S	L P I	ΕV	V G	DA	A V	LV	D P	LS	V D	SI	I R E	G	ΙA	SL	LH	I N E	KI	L R	FΕ	LS	QKG	I E	RA	QTF
A0A2K2TX08_9CLOT																									QKY
A0A1M7Y4E9_9FIRM	SS	L P I	E V	A G	DA	ΑI	LV	N P	ΥC	S D	E ]	I C N	ΙA	МН	NL	LA	DN	ΙΙF	F R	QΚ	LI	LAG	N E	R V	KQF
U2QYN1_9FUSO																									KKF
A0A510JQX4_9FUSO																									KKF
A0A4R8HGG0_9FIRM																									AKF
A0A419T4A5_9FIRM																									KKF
I0I600_CALAS																									KRF
A0A540VBM9_9CHLR																									RRF
A9WBD1_CHLAA																									HLF
_																									

Supplemental Figure 4. The multiple alignment of bacterial glycosyltransferases from UniProt database which are homologous to the wbkA protein of Brucella abortus (Q2YMN5\_BRUA2). The site of substitution A321E observed in strain KB 17/100 is indicated by red rectangle. The intensity of blue color corresponds to conservation level.