

	Protein	Strain	Species	Acc. No.	Position	Signature
A	CcrA1	NCTC10442	<i>S. aureus</i>	BAA86648	7-15:	YLRQST tkQ
	CcrA1	STU33	<i>S. saprophyticus</i>	BAG24390	7-15:	YLRQST lkQ
	CcrA1	JCSC6943	<i>S. aureus</i>	BAK53058	7-15:	YLRQST tkQ
	CcrA1	JCSC6945	<i>S. aureus</i>	BAK53158	7-15:	YLRQST tkQ
	CcrA1	LGA251	<i>S. aureus</i>	CCC86806	7-15:	YLRQST lkQ
	CcrA2	N315	<i>S. aureus</i>	BAA82194	7-15:	YLRQST mkQ
	CcrA2	MW2	<i>S. aureus</i>	NP_644854	7-15:	YLRQST mkQ
	CcrA2	SE50	<i>S. epidermidis</i>	ABF59120	7-15:	YLRQST mkQ
	CcrA3	85/2082	<i>S. aureus</i>	BAA88754	7-15:	YLRQST tkQ
	CcrA3	KM1381	<i>S. pseudintermedius</i>	CAP17736	7-15:	YLRQST tkQ
	CcrA4	HDE288	<i>S. aureus</i>	AAL85204	7-15:	YVRQST lkQ
	CcrA4	CHE482(4-1)	<i>S. aureus</i>	ABL75417	7-15:	YVRQST lkQ
	CcrA4	CHE482(4-2)	<i>S. aureus</i>	ABL75419	7-15:	YVRQST lkQ
	CcrA4	ATCC 12228	<i>S. epidermidis</i>	NP_763612	7-15:	YVRQST lkQ
	CcrA5	KM241	<i>S. pseudintermedius</i>	CAP17701	7-15:	YLRQST tkQ
	CcrB1	GIFU12263	<i>S. hominis</i>	BAB83487	12-20:	YTRVST erQ
	CcrB1	MSSA476	<i>S. aureus</i>	YP_042165	12-20:	YTRVST erQ
	CcrB1	JCSC6943	<i>S. aureus</i>	BAK53057	12-20:	YTRVST ekQ
	CcrB2	N315	<i>S. aureus</i>	BAA82196	12-20:	YVRVST emQ
	CcrB2	CA05	<i>S. aureus</i>	BAB72109	12-20:	YVRVST emQ
	CcrB2	ATCC12228	<i>S. epidermidis</i>	NP_763591	12-20:	YVRVST emQ
	CcrB2	DM35	<i>S. warneri</i>	ABB52797	12-20:	YVRVST emQ
	CcrB3	LAG251	<i>S. aureus</i>	CCC86805	12-20:	YVRVST emQ
	CcrB3	KM241	<i>S. pseudintermedius</i>	CAP17702	12-20:	YVRVST emQ
	CcrB3	KM1381	<i>S. pseudintermedius</i>	CAP17737	12-20:	YVRVST eiQ
	CcrB3	RP62A	<i>S. epidermidis</i>	YP_190041	12-20:	YVRVST emQ
	CcrB3	TSU33	<i>S. saprophyticus</i>	BAG24389	12-20:	YVRVST eiQ
	CcrB4	HDE288	<i>S. aureus</i>	AAL85205	12-20:	YARVST emQ
	CcrB4	ATCC12228	<i>S. epidermidis</i>	NP_763611	12-20:	YARVST emQ
	CcrB4	M06/0171	<i>S. aureus</i>	CCK74160	12-20:	YARVST etQ
CcrB6	JCSC6945	<i>S. aureus</i>	BAK53157	12-20:	YTRVST erQ	
CcrC	JCSC6082	<i>S. aureus</i>	BAG71445	8-16:	YSRVST seQ	
CcrC	ZH47	<i>S. aureus</i>	CAL22883	8-16:	YSRVST seQ	
CcrC	WIS	<i>S. aureus</i>	BAD24834	8-16:	YSRVST seQ	
CcrC	TSGH17	<i>S. aureus</i>	AAY60816	8-16:	YSRVST seQ	
CcrC	85/2082	<i>S. aureus</i>	BAB47672	8-16:	YSRVST seQ	
CcrC	PM1	<i>S. aureus</i>	BAG06191	8-16:	YSRVST seQ	
CcrC	M06/0171	<i>S. aureus</i>	CCK74167	8-16:	YSRVST seQ	
CcrC	JCSC1435	<i>S. haemolyticus</i>	BAE03365	8-16:	YSRVST seQ	
CcrC	25-60	<i>S. haemolyticus</i>	ABP68832	8-16:	YSRVST seQ	
CcrC	13-48	<i>S. epidermidis</i>	ABP68833	8-16:	YSRVST seQ	
CcrC	ATCC15305	<i>S. saprophyticus</i>	YP_300136	8-16:	YSRVST seQ	
B	pLG2 resolvase	57395	<i>S. pseudintermedius</i>	100% to AEF32572	6-14:	YARVST asQ
	Tn552 resolvase	57395	<i>S. pseudintermedius</i>	100% to ADX77603	5-13:	YARVST glQ

FIG. S1. A. Alignment of the site-specific recombinase motif of selected representatives of the Ccr serine recombinase family. The motif is defined as: Y-[LIVACST]-R-[VAQ]-S-[ST]-x(2)-Q, with the catalytic serine residue indicated in bold, amino acids (aa) acceptable for one given position listed between square brackets and x for any aa followed by the possible repetition range between the parentheses. This pattern is a modified version of the Prosite entry PS00397. Invariant aa are shaded black, highly conserved aa dark grey, and less conserved positions light grey. B. Two positive hits were obtained in the sequence of MRSP 57395 with this site-specific recombinase motif. Both showed site-specific recombinases with a serine in the active site, but were unrelated with mobilization of SCCmec.