Supplementary materials

Table S1. Strains used in this study.

Strains	Description	Reference
BL21-AI	F^{-} *ompT hsdSB* (r_B^- m_B^-) *gal dcm araB*::T7RNAP-*tetA*	Invitrogen
KD604	BL21-AI_ΔCRISPR carrying *Pseudomonas aeruginosa* CRISPR array with a single spacer: ACGCAGTTGCTGAGTGTGATCGATGCCATCAG	This study
KD606	BL21-AI_ΔCRISPR carrying *Pseudomonas aeruginosa* CRISPR array with a single spacer: ACCGGACCTTCAATCGGCCCTTCGCTGATGGC	This study
KD628	BL21-AI_ΔCRISPR carrying *Pseudomonas aeruginosa* CRISPR array with a single repeat	This study
KD675	The same as KD604 but it contains a protospacer with a mismatch at position +1 (**T**CGCAGTTGCTGAGTGTGATCGATGCCATCAG) preceded by a functional GG PAM introduced in it's genome into *ompL/yihN* intergenic region corresponding to the positions 4372171-4372261 of NC_012947	This study
ED1a	*E. coli* ED1a strain with native I-F CRISPR-Cas system	Touchon, M., and Rocha, E. P. C., 2010

To construct *E. coli* strains carrying *Pseudomonas aeruginosa* CRISPR arrays, the *E. coli* BL21-AI strain (Invitrogen) lacking endogenous *cas* genes and carrying the T7 RNAP gene under the control of the arabinose-inducible *araBAD* promoter was used. The resident CRISPR1 array in the *E. coli* BL21-AI cells (corresponding to the positions 1002803-1003730 of NC_012947) was replaced by a DNA fragment containing *P. aeruginosa* CRISPR leader followed by a repeat-spacer-repeat array (or only leader-repeat fragment for KD628) flanked by upstream T7 RNAP promoter and *lacO*, and downstream T7 terminator sequences. *E. coli* genomic modifications were performed using a technique based on the previously described method of Datsenko and Wanner, 2000.

Table S2. Statistics for reads corresponding to spacers derived from various plasmids in the course of adaptation by the *P. aeruginosa* CRISPR-Cas system (for results shown in Fig. 5).

	pCas	pCsy	pACYC	pSPA	pSPAmut
Plasmid-derived spacers	474318	166866	1018	3756	116066
Strand bias, %	35.56	38.67	51.57	90.07	66.06
GG PAM frequency, %	97.58	97.90	94.30	99.41	95.46
Derived spacers (shifters), %	1.20	1.10	1.77	0.24	3.46
Derived spacers (flippers), %	0.63	0.46	3.54	0.16	1.00
Strand bias corrected, %	35.48	38.67	48.62	90.23	66.23
GG PAM frequency corrected, %	99.41	99.46	99.61	99.81	99.92

"Derived spacers" refers to spacers that originate from recognition of protospacers with correct GG PAM but are produced either by short shifts in the upstream or downstream direction ("shifters") or are inserted in an inverted orientation in the CRISPR array ("flippers'0.

Table S3. Statistics for reads corresponding to spacers derived from the genome of *E. coli* KD675 cells carrying a self-targeting spacer (for results shown in Fig. 6).

KD675 genome-derived spacers	37616
Strand bias, %	50.57
GG PAM frequency, %	91.44
Derived spacers (shifters), %	5.01
Derived spacers (flippers), %	0.93
Strand bias corrected, %	50.12
GG PAM frequency corrected, %	97.38

Table S4. Statistics for reads corresponding to spacers derived from the protospacer plasmid pSEDmut by the type I-F CRISPR-Cas system from *E. coli* ED1a (for results shown in Fig. 7).

pSEDmut-derived spacers	1587038
Strand bias, %	35.72
GG PAM frequency, %	88.77
Derived spacers (shifters), %	8.53
Derived spacers (flippers), %	2.56
Strand bias corrected, %	34.83
GG PAM frequency corrected, %	99.86