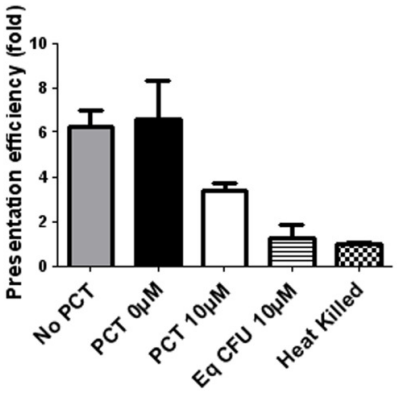
Supplementarydata

Supplementary Figure 1.KBMA *P. aeruginosa* deliver OVA to BMDCs, where the antigen is loaded into the MHC class I pathway.BMDCs were incubated for 3 h with *P. aeruginosa* expressing S54-OVA without PCT or with PCT plus 0 or 10 µM of amotosalen. Ten bacteria/ml of HK S54-OVA bacteria was used as a control. DCs were then incubated with gentamicin (250µg/ml) to eliminate the bacteria. Presentation of the SIINFEKL epitope on MHC class I molecules was examined by co-incubation with B3Z T cell hybridomas and measurement of β-galactosidase production after 16 h. The absorbance of HK S54-OVA was set to 1. The vertical axis shows the relative value per pEiS54-OVA bacterium (5 x 10^5 bacteria). The results are presented as the means + s.d. of triplicate wells. This experiment was repeated twice with similar results.



Supplementary Table 1.Bacterial strains, plasmids, cell lines and mice used in this study.

Name	Relevant characteristics/sequence	Source or reference
Bacterial Strains		
CHA	Wild type, mucoid CF isolate from CHU Grenoble	44
OST	Deleted for Exotoxins S and T	21, 37
OSTABGmlox	OST *ΔuvrA::lox ΔuvrB::Gmlox,* Gm^Rsusceptible to photochemical treatment	This work
OSTAB	OST *ΔuvrA::lox ΔuvrB::lox,* susceptible to photochemical treatment	This work
OSTAB*ΔpopBD*	OSTAB *ΔpopBD::Gmlox*	This work
OST S54-OVA	OST transformed with pEiS54 $OVA_{248-376}$, Cb^R	10
OSTAB S54-OVA	OSTAB transformed with pEiS54 $OVA_{248-376}$, Cb^R	This work
OSTAB S54-M1	OSTAB transformed with pEiS54 M_1-K_{252}, Cb^R	This work
OSTAB S54-Ei	OSTAB transformed with empty pEiS54	This work
Plasmids		
pEiS54		9
pEiS54-OVA	Chicken Ovalbumin (D_{248}-A_{376})fused to $ExoS_{1-54}$	10
pEiS54-M1	M1 Flu Puerto Rico Full length (M_1-K_{252}) fused to $ExoS_{1-54}$	This work
pEiS0-OVA	Chicken Ovalbumin (D_{248}-A_{376})without secretion tag	16
pEX100TUvrA::Gm	*uvrA* up and down fragment amplified with primers F and R	This work
pEX100TUvrB::Gm	*uvrB* up and down fragment amplified with primers F and R	This work

Supplementary Table 2. Primers used in this study.

Primer name	Sequence 5' to 3'	Restriction site
Deletion of *uvrA*		
UvrA Up-F	CTGAATTCGGCCCCCCTCGTGCACCAGT	*Eco*RI
UvrA Up-R	GTAAGCTTGCGCCCCACGAATCAGGATC	*Hind*III
UvrA Down-F	GTAAGCTTGCCGAGATGCCCCAGTCGCA	*Hind*III
UvrA Down-R	CTGAATTCGGCGGACCACTGG	*Eco*RI
Deletion of *uvrB*		
UvrB Up-F	GAATTCGCGCAGCGTCGGATCT	*Eco*RI
UvrB Up-R	AAGCTTCATCGAGCAGGTGGTGCG	*Hind*III
UvrB Down-F	AAGCTTGTTGTTGTTGCGCAGGTA	*Hind*III
UvrB Down-R	GGATCCTTGGCGTCACAGCTCC	*Bam*HI
External primer		
UvrA-F	CCTCATGGAAGAAACCGCTG	
UvrA-R	GATCACATAAGCACCAAGCG	
UvrB-F	AGGGTAGTCACCAGCACCC	
UvrB-R	GATGTGATCGACATCTTCCC	
Influenza M1 (M_1-K_{252}) cloning		
M1 *Age*I-F	CCACCGGTAGTCTTCTAACCGAGGTCGAAA	*Age*I
M1 *SphI*-R	CTTGCATGCTCACTTGAACCGTTGCATCT	*Sph*I

Supplementary Table 3. The *in vivo* toxicity of KBMA *P. aeruginosa.* Mortality of C57BL/6J mice after s.c. injection of 5 x 10^6, 5 x 10^7, 5 x 10^8 or 5 x 10^9 bacteria.

Strain	Dose	Mortality
OST	**5 x 10^6**	**0/3**
	5 x 10^7	**3/3**
OSTAB	**5 x 10^6**	**0/3**
	5 x 10^7	**3/3**
KBMA OSTAB	**5 x 10^7**	**0/3**
	5 x 10^8	**1/3**
	5 x 10^9	**3/3**

Supplementary Table 4.Analysis of systemic response by xMAP technology.

Cytokines (pg/ml)	Mean ± Std error			Mann-Whitney test		
	PBS group	OST group	KBMA group	OST vs PBS	KBMA vs PBS	OST vs KBMA
IL-1α	42 ± 5	1842 ± 333	91 ±10	P = 0.0495	P = 0.0495	P = 0.0495
IL-1β	375 ± 34	10691 ± 2731	383 ± 46	P = 0.0495	NS	P = 0.0495
IL-2	28 ± 3	100 ± 20	21 ± 2	P = 0.0495	NS	P = 0.0495
IL-3	12 ± 1.3	43 ± 3.5	9 ± 1	P = 0.0495	NS	P = 0.0495
IL-5	53 ± 3	64 ± 2	53 ± 4	P = 0.0495	NS	P = 0.0495
IL-6	41 ± 9	>15000	70 ± 6	ND	NS	ND
Kc	77 ± 4	>15000	258 ± 8	ND	P = 0.0495	ND
IL-9	300 ± 51	1621 ± 191	274 ± 14	P = 0.0495	NS	P = 0.0495
IL-10	219 ± 15	6259 ± 592	270 ± 19	P = 0.0495	P = 0.0495	P = 0.0495
IL-12p40	175 ± 11	5182 ± 884	182 ± 14	P = 0.0495	NS	P = 0.0495
IL-12p70	197 ± 13	607 ± 22	158 ± 16	P = 0.0495	NS	P = 0.0495
IL-13	1138 ± 80	2052 ± 149	1457 ± 88	P = 0.0495	P = 0.0495	P = 0.0495
IL-17	105 ± 6	1621 ± 528	63 ± 4	P = 0.0495	P = 0.0495	P = 0.0495
Eotaxin	970 ± 109	8991 ± 936	1111 ± 102	P = 0.0495	NS	P = 0.0495
GCS-F	156 ± 12	>40000	8869 ± 1522	ND	P = 0.0495	ND
GM-CSF	125 ± 11	339 ± 14	152 ± 7	P = 0.0495	NS	P = 0.0495
INF-γ	315 ± 24	1459 ± 577	296 ± 25	P = 0.0495	NS	P = 0.0495
MCP-1	487 ± 27	>12000	537 ± 31	ND	NS	ND
MIP-1α	36 ± 2	1258 ± 132	60 ± 7	P = 0.0495	P = 0.0495	P = 0.0495
MIP-1β	186 ± 13	566 ± 77	172 ± 16	P = 0.0495	NS	P = 0.0495
RANTES	54 ± 5	1255 ± 124	128 ± 15	P = 0.0495	P = 0.0495	P = 0.0495
TNF-α	936 ± 62	2154 ± 582	825 ± 82	P = 0.0495	NS	P = 0.0495

Data are expressed as the means ± s.d. in pg/ml with n=3. Abbreviations: IL = interleukin; NS = not significant; ND = not determined. P values for the Mann-Whitney U test are represented. Statistical significance is indicated when P< 0.05.