

SUPPLEMENTARY INFORMATION

Unraveling the contributions of hydrogen-bonding interactions to the activity of native and non-native ligands in the quorum-sensing receptor LasR

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Table S1. Catalog of LasR mutants generated in this study and selected previously reported data for LuxR-type proteins with related mutations.

<i>This study</i>	<i>Previous studies</i>			
LasR mutation	LuxR-type protein	Mutation	Effect on activity with native ligand	Reference
Y56F	LasR	Y56C	present in QS-deficient clinical isolate	1
	LasR	Y56F	no change	2
	LuxR	Y62F	significant decrease in sensitivity	3
	TraR	Y53F	moderate decrease in sensitivity	4
	TraR	Y53S	inactive or major decrease in sensitivity	4
W60F	LasR	W60F	moderate decrease in sensitivity	2
	LuxR	W66H	inactive	3
	TraR	W57F	inactive or major decrease in sensitivity	4
R61M	TraR	W57Y	inactive or major decrease in sensitivity	4
	LasR	R61M	moderate decrease in sensitivity	5
D73L	LuxR	R67M	inactive or major decrease in sensitivity	5
	LasR	D73E	loss in activity (sensitivity not reported)	6
T75V W88F	LasR	D73N	not determined	7
	LuxR	D79N	inactive	3, 8
	TraR	D70E	inactive	9
	TraR	D70N	inactive	9
	TraR	D70S	inactive or major decrease in sensitivity	4
	TraR	D70V	inactive or major decrease in sensitivity	4
	RhlR	D81E	did not bind native ligand <i>in vitro</i>	10
	LasR	T75K	present in QS-deficient clinical isolate	1
	LasR	W88Y	loss in activity (sensitivity not reported)	6
	LasR	W88C	not determined	11
Y93F T115V	LuxR	W94D	inactive	3
	LuxR	W94Q	could not be stably expressed	12
S129A	none			
	LasR	T115I	isolated PAO1 mutant had major deficiencies in producing OdDHL, BHL, elastase, and nucleoside hydrolase	13-14
	TraR	T115I	significant decrease in sensitivity	4
	TraR	T129S	no change	4
	TraR	T129A	inactive or major decrease in sensitivity	4
	TraR	T129V	significant decrease in sensitivity	4
	TraR	T129L	inactive or major decrease in sensitivity	4
	TraR	T129I	inactive or major decrease in sensitivity	4
N/A*	TraR	T129F	inactive or major decrease in sensitivity	4
	CviR	M89A	moderate decrease in sensitivity	15
	CviR	M89S	moderate decrease in sensitivity	15
	CviR	M89L	no change	15
	CviR	M89F	no change	15
N/A*	CviR'	S89M/ N77Y	maximum activity substantially decreased	15
	QscR	S56G	moderate decrease in sensitivity	16
	QscR	S56T	slight decrease in sensitivity	16

* Nearby residues in CviR and QscR not examined in this study; data included here to be comprehensive.

Table S2. Bacterial strains and plasmids used in this study.

Strain or plasmid	Description*	Reference
<i>E. coli</i>		
DH5a	F ⁻ , j80d/lacZDM15D(lacZYA-argF)U169 deoR recA1 endA1 hsdR17(rk ⁻ , mk ⁺) phoA supE44 λ ⁻ thi-1 gyrA96 relA1	Invitrogen
<i>Plasmids</i>		
pJN105L	Arabinose-inducible expression plasmid for <i>lasR</i> ; Gm ^R	17
pSC11	<i>lasI-lacZ</i> transcriptional fusion reporter plasmid; Ap ^R	18
pJG002	Y56F mutant analog of pJN105L	19
pJG005	W88F mutant analog of pJN105L	19
pJG008	W60F mutant analog of pJN105L	19
pJG009	R61M mutant analog of pJN105L	19
pJG010	D73L mutant analog of pJN105L	19
pJG011	T75V mutant analog of pJN105L	19
pJG012	Y93F mutant analog of pJN105L	This study
pJG0013	T115V mutant analog of pJN105L	19
pJG014	S129A mutant analog of pJN105L	19

*Abbreviations: Gm^R, gentamicin resistance; Ap^R, ampicillin resistance

Table S3. Primers for site-directed mutagenesis.

Mutation	Forward primer sequence ^a	Reverse primer sequence ^a
flanking primers	CGATTAGAAATTCCTTAAGAAGAACGTAGCGCTATG	CCACGCTCTAGAGGCAAGA
Y56F (TAC→TTC)	TCGGCAACT TTC CCGGCCGC	GCGGCCGG GAA GTTGCCGA
W60F (TGG→TTC)	GGCCGCC TTC CGCGAGCATT	AATGCTCGCG GAG GCGGCC
R61M (CGC→ATG)	GGCCGCCTGG ATG GAGCATTACG	CGTAATGCTC CAT CCAGGCGGCC
D73L (GAC→CTC)	GCGGGT CCTC CCGACGGTCA	TGACCGTCGG GAG GACCCGC
T75V (ACG→GTG)	GGTCGACCCG GTG TCAGTCACT	AGTGACTGAC CAC CGGGTCGACC
W88F (TGG→TTC)	GCCGATTTTC TTC GAACCGTCCA	TGGACGGTTC GAA GAAAAATCGGC
Y93F (TAC→TTC)	ACCGTCCATC TTC CAGACGCGAA	TTCGCGTCTG GAA GATGGACGGT
T115V (ACC→GTC)	GTATGGGCTG GTC ATGCCGCTGC	GCAGCGGCAT GAC CAGCCCATAC
S129A (AGC→GCC)	GCGCGCTG GCC TCAGCGT	ACGCTGAG GGC CAGCGCGC

^a**Bold** = mutated codon

Table S4. Sequence alignment of 100 LasR homologs.

Boxed residues are those mutated in this study.

	1	10	20	30	40	50	60	70	80	90	100	110	120	125
LasR(aag04819.1)	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001747665	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001991323	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_569310	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002232821	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_624828	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002158591	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002265247	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_855658	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_776923	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002955225	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002537872	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002871035	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
NP_106527	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001242900	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001203095	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001927660	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002547516	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003558208	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_777789	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003749681	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001715477	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001083200	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003734010	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002911505	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003978623	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002947664	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003750859	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
NP_521406	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003744152	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001117674	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_623508	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001583946	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_105961	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002909041	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002907673	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003910271	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001888024	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003608086	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001860599	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003847232	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001167907	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001043640	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001758389	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_486928	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001603072	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_003262848	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_002911546	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001815695	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
YP_001115608	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	1	10	20	30	40	50	60	70	80	90	100	110	120	125
YP_002874841	-----MLNWRNTRLPKL-EGENEITSVFEMVINQTYELGFOYCSFKMSSQ													
YP_001437405	-----MKESDFFNWRREMTTRF-QEIQDSSDIYSLKKTETQNMEDYDFALCVRHP													
YP_003941366	-----MRDIDFFSWRRDVLQKF-QLASSEEEIYSLQQQTEMLEWDYALCVRHP													
YP_003530769	-----MTSENYFIWRADIKSAY-EKGGIDHITRLIEQQLRALDELDFYSLFIRHP													
YP_002649216	-----MTSENYFIWRADIKSAY-EKGGGIVHITRIEQQLRELELDFYSLFIRHP													
YP_001908006	-----MTSENYFIWRADLKSAY-DNGSGIAHITRVEQQLKELELDFYSLFIRHP													
YP_003519711	-----MTSENYFSWRTETENHF-QALATTQQLKGLLDYIQLSGFDYFAFFIQHR													
YP_206883	-----MNIKNINANE--KIIDKIKTCNNKNDINQCLSEIAKIIHCEYYLFAIYIP													
YP_001143989	-----MYMFNDAIWEHIDRFTKAKTSEIQOQLERFSHQMGFDYFRLLIIFP													
YP_003267496	-----MSSKRD-----EFDCVERIFNLPSDVDANEHAQSILQDTLATYGFDFP													
YP_003450678	-----MPPSVVSVSDHTDPGCTLMGQEPPTAWEGGMROGKFRILSRSGRLPRQDSVLYCRFMSKDKSH													
YP_002910942	-----MTGGETSKASPSIRLGEDPSLAVLIEHLPAEIDCPFAY-----													
YP_001022984	-----MLLGSFQSVLEARNRDEFRGEVVRFAKRLGFETVS-----													
YP_001898047	-----MVSPLYTFEGLLTAGSHAETAAFMERHAGNLGYGRFFYSPLLVA													
YP_528967	-----MEQLDYAELCSALCEATDEETLKEKLCFKCELVGFEFYIFGLISS													
YP_659944	-----MMQVEEFYELLESVDESSSIDALKETCERFCQLIDIPFYLLGVIGQ													
YP_106048	-----MFEGLSIGSFNEILNATCKKSLFEQTAYHVRQLGFKNFAYRQISG													
YP_106160	-----MLSAALPESRDVRTLVETFRQAALQIQYQHHAIVELS-													
YP_001777917	MAVIWRQATTLAFCTAHRASSETRATAIAMHCTTSNSNDARTATAPCSSARSSCERAPVDRVCQRGAGDTPVPSQLTSSLAGRWAPLATAFLNTVDLSLLKLFQDVSASLGFPPFAISRVS													
YP_972129	-----MILRDFIQRANQALTQTELLACFEQAVLLLYGQHFSLCYVQL													
YP_004012994	-----MDRFATERFIEDANAAKSSKEVSALFGKALAVFGYDRYCYSLIT-													
NP_768520	-----MPLASSRRESRGPDLFSFIECAIQTRSI AALFDLLVNFASNEGFDFKVAYGALSC													
YP_567541	-----MSADEGNQWRRALEFVDAADR-LDGPSLIRQFETHIASGFSAYIMAGLP-													
YP_484040	-----MLAGESHLWRRALEFVDAADR-LDAPSLVRQFESHASAGFSAYIMAAP-													
YP_002966880	-----MYDDCAARALDFVEGLDDCHDHDQVAHSVERILAEFGFEHFVITGLP-													
YP_781245	-----MLTGDLTGDYGDALTFVEELSTLTTISAAIDFIEKGFCAYGFEITIVTGIP-													
YP_002495629	-----MSGMEDFFLRETFALIDALDEVDRPFEAQTRIFEHIQHVGFSTFTIRLP-													
YP_001776815	-----MAG--ALSIRQTAFDIVHRLRRAS'TD'VDVYSELRRSGAIFGYDVFLIAGLPR													
YP_001641953	-----MSR-----KSLDLTLEILKSLDRAHSREDILRAIMPRNLALGIEYVISAMIPL													
YP_002497059	-----MSS-----KSLDLSRELLQSIHRTATPENVRDQLLKKLAGVGEHVLLATLRI													
YP_001240084	-----MEQYGFPCFAYLSFAP													
NP_106660	-----MQLVFETLLEQLSLSVDEVDFHNALASAAGAFDIPAFAYLSLVS													
YP_003259225	-----MSVFCSDNEIINNTIKTYLSRKLKQYGDLYKAYMIMNK													
YP_003017024	-----MSVFCSDNEIINNTIKSYLGRKLKQYGDLYKAYMIMNK													
YP_003331714	-----MSISFSNVDFINSTIQNYLNRKLKSYGDLKAYAYLIMNK													
YP_003885142	-----MSISFSNVDFINSTIQSYLNRKLKSYGDKPYAYLIMNK													
YP_003002472	-----MSISFSNVDFINSTIQNFIDRKLKSYGDLKAYAYLIMNK													
YP_002985768	-----MVVSLPEVDFIRAAIQNHRLARNLQCYSGLYKAYAYLIMNK													
YP_001005891	-----MIIDYFDNESINEDIKNYIQRRIKAYGDLRYSYLVMNK													
YP_003019697	-----MSPLFTDSEIISRVIKKHFNKNLDRYDGIKFSFMVLNK													
YP_003261727	-----MSQLFYNNETISRIKKSQFDMALSHYGDIKYAYMVLNK													
YP_002934275	-----MFADNESLTREIKQFIDRSLVAYGHIQFAYALLNK													
NP_670674	-----MHSVFNRSNEVIETLRDYIDRKLTIYDSPRYTYMVINK													
YP_003520251	-----MFSFFLENQITITDLQTYIQRKLSGSPPEYAYTVVSK													
YP_001906896	-----MEPEDNINDIISKQLEAALSDELGEFIWAYVVLSK													
YP_003941575	-----MLKEYEENVDVIIKNQLETTLNTLGDLSWAYVVLSK													
YP_003729882	-----MKDYYNDQKINSLIKDELDAFFEDYQGVIIYAYAIMNK													
YP_002924396	-----MFFKNELINKKVKYLEENMLKNHKNKFGYLVYIHK													
YP_001832058	-----MCAAKNGSALLKPTTLRSPASWAANASTENVAITQLLDLEANLSERTLEEFVFIQKY													
YP_001669935	-----													
YP_001748729	-----													

	126	130	140	150	160	170	180	190	200	210	220	230	240	250					
LasR	-----	LFGLLP	-----	KDSQYENAFIVGN	YPAARE	HYDRAGYARV	DFTV	SHCTQSVLP	IFW	PSIYQ	TR	-----	KQHEFFEEASAAGL	-VYGI	TMPLHGARGELGAI	SL	SVEAENRAEAN		
YP_001747665	L	-----	AAQAPKLYLYSN	YPLAWI	ERYQRDEFYK	QDFA	AALSHTS	TEPVLW	TEDE	LYSEAP	-----	DFREQACKHGL	-RHGWT	OSLHDLRHNETQV	S	VARFPFKD	IHE		
YP_001991323	P	-----	GTSAKEQIANVLLH	QWPDV	WRRYFSKGYIFT	DA	AIRRVTS	SMVPPF	S	WTELEW	-DH	-----	DSPAGHRILGEEAEFGL	-KEGHT	VMVTL	DGHSAGI	S	IAGAMTELP	
YP_569310	P	-----	GTSAKEQIANVLLH	QWPDV	WRRYFSKGYIFT	DA	AIRRVTS	SMVPPF	S	WTELEW	-DH	-----	DSPAGHRILGEEAEFGL	-KEGHT	VMVTL	DGHSAGI	S	IAGAMTELP	
YP_002232821	L	-----	PLARPDQIVGN	HPRWE	HRYVKFGYVT	ID	IKRVAS	QRPV	WNA	FDPEGDT	-----	AFWHDAACFCGM	-RYGWS	HGGYDRAGNLGVI	T	LV	RD	TPLDADE	
YP_624828	L	-----	PLARPDQIVGN	HPRWE	HRYVKFGYVT	ID	IKRVAS	QRPV	WNA	FDPEGDT	-----	AFWHDAACFCGM	-RYGWS	HGGYDRAGNLGVI	T	LV	RD	TPLDADE	
YP_002158591	H	-----	SMVKS	DISILD	NYPKWR	QYDDANLIK	YD	IVDYS	NSNHSP	IN	W	IFENNA	NAVNK	KSP	-----	NVIEEAKISGL	-YSGFS	FP	IHTKDG
YP_002265247	K	-----	TMIKSDIKILD	NYPL	WRNYDEANLIK	YD	IVDYS	FSHHSP	IN	W	IFENNA	NAVNK	KSP	-----	NVIEEAKISGL	-YSGFS	FP	IHTKDG	
YP_855658	S	-----	TIQRPDV	IIFN	GCPOAV	DTYTS	SGFFA	ID	IVK	CAMT	KSTPI	WAD	VN	DEER	CDE	Q	REMMQLANE	YGI	-CDG
YP_776923	-----	CYQEYR	-----	MSGGTLK	NCR	TLN	YPA	WLS	LYR	DRAYL	T	D	IA	QHAL	SS	LMPL	W	DR	I
YP_002955225	-----	TSLAKL	SSD	GAVES	YELANIN	Y	PV	W	L	QTY	KE	KN	F	S	G	I	D	IV	K
YP_002537872	-----	VFGIA	QIG	TNGLI	QTY	D	V	M	N	I	S	Y	P	E	W	L	I	T	Y
YP_002871035	-----	LLSLGP	-----	STHDP	FN	R	I	M	T	Y	P	S	D	W	L	K	R	Y	K
NP_106527	A	-----	QKVLK	PAQ	ADSAI	M	L	N	Y	P	N	W	K	E	R	Y	F	K	M
YP_001242900	-----	APGQ	S	L	Q	H	T	L	A	N	G	W	P	S	E	F	D	L	Y
YP_001203095	-----	APGQ	S	L	Q	H	T	L	A	N	G	W	P	S	E	F	D	L	Y
YP_001927660	K	-----	RLPART	Q	K	N	F	I	E	N	T	S	D	E	W	R	L	Y	F
YP_002547516	PV	-----	LNAT	N	E	R	H	T	F	G	I	N	N	Y	P	E	W	R	Y
YP_003558208	HSIN	-----	I	E	R	V	V	S	S	G	F	G	F	E	A	K	S	A	H
YP_777789	W	-----	PLSR	K	V	L	V	F	S	N	F	P	E	E	W	R	R	Y	F
YP_003749681	L	-----	PLSE	P	K	I	L	L	N	N	Y	P	O	A	W	R	E	R	Y
YP_001715477	L	-----	SI	A	E	P	K	T	I	M	L	N	N	Y	P	E	A	W	K
YP_001083200	L	-----	SI	A	E	P	K	T	I	M	L	N	N	Y	P	E	A	W	K
YP_003734010	L	-----	SI	A	E	P	K	T	I	M	L	N	N	Y	P	E	A	W	K
YP_002911503	W	-----	PV	S	R	P	K	I	L	L	N	N	Y	P	O	A	W	R	Y
YP_003978623	-----	P	T	N	P	Q	F	M	S	I	D	Y	P	I	A	W	Q	E	R
YP_002947664	V	-----	P	T	R	P	K	L	V	M	S	T	Y	D	E	R	S	R	Y
YP_003750859	L	-----	PV	S	K	P	A	V	A	I	F	D	T	Y	P	A	Q	W	H
NP_521406	L	-----	PV	S	K	P	A	V	A	I	F	D	T	Y	P	A	Q	W	H
YP_003744152	L	-----	PV	S	K	P	A	V	A	I	F	D	T	Y	P	A	Q	W	H
YP_001117674	L	-----	PV	S	K	P	A	V	A	I	F	D	T	Y	P	A	Q	W	H
YP_623508	L	-----	PV	S	K	P	A	V	A	I	F	D	T	Y	P	A	Q	W	H
YP_001583946	L	-----	PV	S	K	P	A	V	A	I	F	D	T	Y	P	A	Q	W	H
YP_105961	L	-----	P	I	S	K	P	V	V	A	I	F	D	T	Y	P	N	G	W
YP_002909041	Q	-----	P	G	S	Q	L	V	E	I	F	D	T	Y	P	Q	W	H	A
YP_002907673	L	-----	P	V	G	E	S	V	K	V	F	D	N	Y	P	E	W	R	Y
YP_003910271	-----	LI	AM	L	P	-----	R	P	T	M	R	E	D	A	Y	I	R	S	T
YP_001888024	-----	LI	AM	L	P	-----	R	P	T	M	R	E	D	A	Y	I	R	S	T
YP_003608086	-----	LV	AM	L	P	-----	R	P	T	M	R	E	D	A	Y	I	R	S	T
YP_001860599	-----	LV	AM	L	P	-----	R	P	T	M	R	E	D	A	Y	I	R	S	T
YP_003847232	-----	RL	AI	L	P	-----	D	P	R	AP	I	E	A	E	H	A	F	Q	S
YP_001167907	-----	Y	A	T	T	S	P	-----	T	G	A	V	Q	G	Y	A	N	Y	P
YP_001043640	-----	Y	A	T	T	S	P	-----	T	G	A	V	Q	G	Y	A	N	Y	P
YP_001758389	P	-----	GL	P	K	R	R	H	A	G	F	V	L	A	S	T	M	P	E
YP_486928	P	-----	RT	S	V	K	Q	I	A	N	V	L	H	R	W	L	P	L	S
YP_001603072	-----	G	A	P	N	A	E	T	A	L	V	Y	P	D	A	L	K	H	Y
YP_003262848	L	-----	N	I	T	N	Q	V	M	M	N	N	Y	S	O	N	W	K	R
YP_002911546	L	-----	P	L	S	N	P	P	S	L	T	V	S	N	Y	P	A	W	Q
YP_001815695	I	-----	P	I	T	R	P	A	I	M	G	W	S	N	Y	P	E	A	W
YP_001115608	I	-----	P	I	T	R	P	A	S	M	E	W	N	N	Y	P	O	A	W

126 130 140 150 160 170 180 190 200 210 220 230 240 250
YP_002874841 V-----SENQTNPIEFTNYPKHWTFFVYNOARYFDVDDVYKHCKRCVLPVWEGTLPKADAP-----SLWSLAQTLNV-NVAWTOAVHDFQGVFMSMLTLRGTDDVSPVPE
YP_001437405 V-----PFRPKLTLHTTYPEAWLHEHYQAEINYVYIDVLPKPNANYLVGPLSWNDALFAGAAE-----ELWNAARDHGL-KVGVTOCVIAPNRAQGFLSYVSGTSPRGSMA
YP_003941366 V-----PFRPKIALQTYTPRAWIAQYQAEINYFTIDVLPKPNYRHGYLEWDRLEFD-----EFWDAARDHGL-RKGVTOCLILPNRALGFLSYVSGTSPRGSMA
YP_003530769 V-----PFRPKTFLYSNYPQWLWHYWRGEFYQLDVLKMCSSSPGKIWLWDDKTIIS-AGL-----EFWEHARNYGI-FHGISCSVMSASNRVAVGIIISGSKRPFTTGSR
YP_002649216 V-----PFRPKTFLYSNYPEDWLEHYFREDFYQLDVLKMCSSSPGKIWLWDDKTIIS-SGV-----RVFENARNYGI-FHGISCSVMSASNRVAVGIIISGSKRPFTTGSR
YP_001908006 V-----PFRPKTFLYSNYPQWLWHYWRGEFYQLDVLKMCSSSPGKIWLWDDKTIIS-SGV-----RVFDDARIHGI-YHGISCSVMSASNRVAVGIIISGSKRPFTTGSR
YP_003519711 V-----PFRPRVYLHDTYPKLWIKWIKRYEQNYAIDVVLQCLRSRSGKGVHWTPPELFS-SAK-----EMWQDACNFGL-LSGFSCSAMASNRVAVGIIISGSKRPFTTGSR
YP_206883 H-----SIIKPDVSIIDNYPEKRWKRYDDAGLLEYDWDYDKSHHSPINWVFKKTIKKESP--NVIKEAQESGL-ITGFSPPIHTASNGFGMISFAHSDKD-IYTD
YP_001143989 I-----SMQKSHVALFNKCPSTWFPEAYSERHYLTDVVFVFLGLKQTOPIRWKLDLDCSPWLPSASREVNMNLAADFVGRNGVSPPLHTPQGEHGIIISFISEKKSNDLDM
YP_003267496 -----CFAIYGAPRGAIAIDNYHLLLNAYPNAWADRYYEKHYWYSDVLAHCGRSPTPIDWTTVONQPAQP-ASAEQVMREAEHEDL-CSGVTTVTRDVSGRGLGIIISLATRDVYSAELR
YP_003450678 FLSRIIDSVGPFNVYFTGTCTSSDRHVNLLTITSEKWRMRYFDRRYENIDVLSAARRATPVVDWDLKFDSDG-----VEDFIADALCYGIRLQGVTFSLRDMHQRLAIVISLQSNDDPAVWRV
YP_002910942 -----VMIDKNS---LELGCFLSSYPIHLOQEYRRRALHRVDVYLHAIQSVAPFSWAEAFRQQRVPD---PSEFDALRREFGLHDGYVTFVHDHPYQYVGMISFFNRG-GRPEFR
YP_001022984 -----AITVVDHPVGDTEFVAIDNADDAYKDAIEDPKAGQIDVMOHCKROSVPPIWOSTYVVSAGO-----GSMWEAQARFGFRGTGICLALHMPGRRHFVIGVDRDQ-ALPKDR
YP_001898047 GDARHFFK-----DDHNVAEEMLYTKNIFSTYPAWIRRYQEAGHVAADVVKLITTSNLPITHWDA-----DDLQAARSPVDFEAREHGL-ATGITPPIHNGFDHTRALFSVTSQAPERSQR
YP_528967 -----ASSLSPTTISTISNYPDFWKNYFEEGMQRHDDVRYCMQNTSAIKWRQLMDLEHYVDIAIEKIMIRASESGL-CDGLSIPKAPSGEIAIFSLASNR-EEGLNQ
YP_659944 -----TSSYS-PTIRVISNYPEKLEFYFKESEQNDVVKYIFEKQSPIRWDLKVEVDQFSSTKGLLVFEKAAAYGL-YNGISIPIRSTSENIAVFSVAIDE-RSDANR
YP_106048 -----AASSR---CMLDGFPAWRRLRYDAADYLSIDVYQHCRCRTVPLIWHD---DLWTTSRAKLRMRDEAKSYGL-VYGISCPVHDRSGAISMSMATDPPFEHDAS
YP_106160 -----GASHPAS-IDVVS LHYSEWVEHYTRNDYFADVHRAAFRYSTPFSWNVDA-TA---NLRRERHLLMEAEADAGL-DNGISIPPLHQPLGRVLLVLSLGS-TAPTHDAD
YP_001777917 RH-----AGNGRAMS-VETLCARYPDHVVHAYARDYGPVDVVRMAFARATPYRWAIDR-GL---NRIEQRVLGEARDAGL-TSGVSIPLREANGDILLVNLAS-PSPEIKTE
YP_972129 RQ-----DGGSTSPPIGVLSHNYPSFVSHYIARNYLEDVVRHAPQAMSPYKWDVVS-AQ---GDREAHIMDEATDAGL-ADGIGLPIHEPGGRIFLATYASHQQLTLGND
YP_004012994 -----DHPSLGLNAGHGLVCNYPDDWMEHYLRNLYEKKIDVPOYGISASRPPTWASVV-AQRKWHPDQMKVMHEAEEARL-CDGIAVPCVGVNGLAGEGIIASSHGGVSPDR
NP_768520 S-----NERRLPEYLPPPTTIFPSSWCQRYAEQEQYQADVVRRTAMLPRPPIWDELTI-SRYELQAPRELRLVREAKEAGL-KHGMISVPLFGSQGRSAFVSFASPFDDADP-Q
YP_567541 -----SPGAGLADLLFANGWPRGWFELYVGRNYMAVDVPRHGAATVQPFVSDAP-YDRKRDRAAHQVMTDAAEFGL-VRGYCIPLHYDDG-GAMISMAGEAPDLDPPTA
YP_484040 -----APGAGLAELTLANGWPRGWFELYVGRNYMAVDVPRHGAATVQPFVSDAP-YDRKRDRAAHQVMTDAAEFGL-VRGYCIPLHYDDG-GAMISMAGEAPDLDPPTA
YP_002966880 -----NPNDRLDQVLLIRRLPAGWFELYARHNYMYLDDVFRNCRATSPFPWGEAF-YDPETEPGAIEVMQRATDFGM-ARGHVSPIHHPGEGCEAFSMSGRNPDLTGRT
YP_781245 -----NHKQFSQMVMAKRWDEWFKLYTQNNYHRDDVVRHLRKSFNPFVSDAP-YDRKRDRAAHQVMTDAAEFGL-VRGYCIPLHYDDG-GAMISMAGEAPDLDPPTA
YP_002495629 -----RPSDRLGNMIFNMWPKDWLPHYDRVGHYRFDVVRQCYRTPTEPFVSDAP-YDRKRDRAAHQVMTDAAEFGL-VRGYCIPLHYDDG-GAMISMAGEAPDLDPPTA
YP_001776815 -----APHENLYDCSLISGWPPHWRGRYQERRHMHVDVVRHIRIRGTTPDFLWQEA-VDAQVTPEGMVMVEEARAFSL-NEGHCVPFPHQDGTGAEVSGFSGGQVRLSQDE
YP_001641953 K-----RLPARTQKNYLILENTSDEWNRLYFSKGYMYTDDVVOATLSSTTGFVWSEIE-PAGVLDPRSQRVMNEAGEFGL-GDGFITPLATLEEERGGITFAGPQLDISPGQ
YP_002497059 C-----DAVPCDRRPTVFIGTYDWARRYARNYLHDDVVRGVAERASGFATDDP-LIASDDREARRVLEDEAGEFGL-HEGTLPLLLTLEGGTAGVSVFVGERLDLSPAV
YP_001240084 R-----GDEDDALAITITPYSAWVEQYRANRYDRIDVVIARSVATTLPPFAWSTDC--FDALNNRQKWFLLEAESEFEI-RHGVITPIHDROGKVATIILAACEARSAFEA
NP_106660 -----DRVTKPRLLISNYSWGTSHYLRHQYERIDVVIEWARCSECPFWGPGI-GHAGISTRQQLFDEAAEFGI-CCGITPLVDRRGGVAAMTFADRLDPTFLR
YP_003259225 K-----NPSQVVIISNYPQWVNTYKKNYQHIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDDNNLNLAALSIMFEEHSPTDIE
YP_003017024 K-----NPSQVVIISNYPQWVNTYKKNYQHIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDDNNLNLAALSIMFEEHSPTDIE
YP_003331714 K-----KPTDVVVIISNYPSEWVEIYRNNNYQHIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_003885142 K-----KPTDVVVIISNYPTEWVFIYRNNNYQHIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_003002472 K-----KPTDVVVIISNYPTEWVFIYRNNNYQHIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_002985768 R-----FPTDMVIISNYPSEWVNTYKKNYNSIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_001005891 K-----TPLHPTIISNYPDLWVKYKKNYSYHLIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_003019697 K-----NPSQMIISNYPDEWVNVLYKENKYQHIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_003261727 K-----KPTTEILIISNHHDEWREIYQANNYQHIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_002934275 K-----NPSDIIISNYPDEWVNTYKKNYNSIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
NP_670674 -----NPGDIFIVTSPNWAELIYNNYQHIDVILTAINKVSPFSEWEDNIVNSKL--KFSKIFNLSKEYDI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_003520251 K-----NPSNVLIISSYPDEWVLYRANNFQITDVIITAFKRTSPFADENITMSDL--RFTKIFSLSKQYNI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_001906896 K-----DMSCIFGVNTYPSGHWKQYREKGLQYTDVITSLNRLTPFAWENITLMSDL--RFTKIFSLSKQYNI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_003941575 K-----DMSCIFGVNTYPSGHWKQYREKGLQYTDVITSLNRLTPFAWENITLMSDL--RFTKIFSLSKQYNI-VNGYTFVLHDPANNLTIISFMFEENRSGELE
YP_003729882 K-----DPSQMQIINNMP-AWFDVYLERKYQFIDVVIIRGLRCVEDYEWENEVILSEGY--NLTRIFNESFYQNI-YRGTTFPLHDYLNLLVVISV-IGK---KEFD
YP_002924396 K-----DFHHICIIISNCP-EWFDIYLEFNHQLIDVVIKALSVEDYEWENEVILSEGY--NLTRIFNESFYQNI-YRGTTFPLHDYLNLLVVISV-IGK---KEFD
YP_001832058 YELKN-----IFYICPSLPGRTITDPTYILGTYSQEWIHYRERNYVNLDDVIVNGARSLLPIDWAKLRPSPK---IQKFFGEATDFGVGRQGLTIPVRGPTNLWALFCMTTDDTQAEWQ
YP_001669935 -----
YP_001748729 -----


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251      260      270      280      290      300      310      320      330      340      350      360      370      376
LasR    RFMESVLPFLWMLKDYALQSGAGLA-----FEHP-VSKPVVLTSTREKEVLQWCAIGKTSWEISVINCSEANVNFMHGNIRRRKFGVTSRRVAAIMAVNLGLITL-----
YP_001747665 L--YDKAGVQVQLCHTLHDTICEHH-----LAKLSS--PLKMSDRELEVWKWSAAGKTAADVACILSLSQSTVNFHIRSVITKTASNKAGAVA IAMMRGLIDQ-----
YP_001991323 RGPVQMMAIYSFARAHLRERP-----PAPVTLTIREADVHLHWIAEAGKTDWEIARILQVSEHLVDKVARQIKSKFQVNVNRVQAVVQAMRAGVIH-----
YP_569310   RGPVQMMAIYSFARAHLRERP-----PAPVTLTIREADVHLHWIAEAGKTDWEIARILQVSEHLVDKVARQIKSKFQVNVNRVQAVVQAMRAGVIH-----
YP_002232821 I--SRLRAPCASLSHAAHAYLMPRL-----ADPIAPVGTG-LTLREREVLAWTADGKTAYEIGMIFGIAERTVKFHLQNAVVKLDAMNKTHAATKAAMLGGLP-----
YP_624828   I--SRLRAPCASLAHAHAYLMPRL-----ADPIAPVGTG-LTLREREVLAWTADGKTAYEIGMIFGIAERTVKFHLQNAVVKLDAMNKTHAATKAAMLGGLP-----
YP_002158591 S--LFLHACMNPI LIVPSLVDNYRK-----INIANNKSNNDLTKREKECLAWACEGKSSWDISKILGCSERTVTFHLTNAQMKLNTNRCQISKAILTGAIDCPYFKN-----
YP_002265247 N--LFLNACMSVPLILPELLDSNQR-----ITKEDQOVHTKLTREKECELIWSCEGKSRWEISKILGCSERTVTFHLANSQKLGANNRCQISKAILTRAMNPLY-----
YP_855658   L--SAVVPFI SWLSMHIFEAVARVCL-----AG---LSPHDALSLRELEVCRWAAEGKQVSDIAQILGIPRTVTFHLNNAVSKLGASSKQAI SWALKQCMQVRLNEMALVANVDEKQ-----
YP_776923   MPCDVPS-WGALVANMLDACCRRLE-----AVQSDAPCLS--TRELEILKWAEBGKSTWDI SRIVSLTEHGVLHHRISIMKKFDVPTRRQAVLMASRFGLL-----
YP_002955225 KYDPTVIAILOTIVPHLHLASSRII-----ESRLIQHNKLLSGREREVLSWLHGKSSWDISTILQISECTVNYHIYNI IKKLDVQNRPAQAVAVATHLGLDDP-----
YP_002537872 N--HPREKFI IENLTPHLHTAFTTYL-----SKTKAPVN-FELSKREIEVLNWWKGGKSSWDISVILAI SVRTVKFHVENIMVKNLNAVSRTHAVAILASAGVIDID-----
YP_002871035 DDNLGPLGMLFMLIPFLLEGSQKHL-----KTVG--EPPSSLTLRESEVLKWTGVGKTTWEMSCILGCSERTINFHIANASRKLGSFSRRQAVGVALAQGLISL-----
YP_001242900 RTVTYQLAALHFHVRVTKGT-----SNA-LKQVQDLSLREKECLLWIARGKSSWEI GKILGISGNTVNFHLKNAMRKLDTASRTVAAIKATSLGIVEV-----
YP_001203095 RGALHLISIFTH-SRLRALARATSG-----G-----QSRRLSRIEAEVLSWAARGKTAWETARILGVSENRVNRWHLEEAQRKLETKNKTATVATALVNGEITI-----
YP_001220765 RGALHLISIFTH-SRLRALARATAG-----N-----PGRRLSRIEAEVLSWAARGKTAWETARILGVSENRVNRWHLEEAQRKLETKNKTATVATALVNGEISI-----
YP_001927660 RGMFLTIASVYVVGQTLLIDNGPSE-----RRMG-LTPRERESLQWVAEGKTDWEI GELMGISRHGVDFHLRSARVKGCVSRVQAVAEGRFRGLIV-----
YP_002547516 EAHLIHIISQFFHSCALPVVMEEHL-----IGSY-RRRRSFLSAREKETVIWVSKGKSSWEIAKILGISSEKSVFYMESVKKRLEAVNRTQAVVKAIMLGLIQTDRFQSGDGRKATMAMPSRA-----
YP_003558208 Q-----LATLELINTVSAQAMTRLT-----NPVEELTKREREILAWSSEGKSSWEIGMICSITERTVKFHLKNIYKKNLVQNRAQAI VCAIROGLI-----
YP_777789   L--QQEELKMRWLVNAAHLAITRAV-----LPKLSPEGDIELTDREVEVLKWAADGKTAESAEMILISVYTVNFHVKNVADGFKLNTSNATAAVARAAMLGLLI-----
YP_003749681 L--ADNTRRMQWLTHMAHLALSRL-----RADLAGDSDSLTGREVEVMKWTADGKSAQDIADILAI SKNTVDFHVKNNAVKKLQAVNKTAAVRAAMLGYLF-----
YP_001715477 Q--KAQYTNMYWLTQTVHSSIAKIV-----NDVEFAKFNLYLTNREKEALRWTAEGKTSAEIAQILGVTERTVNFHLSNSMQKLVNWNKI SAAIRAVMLGLL-----
YP_001083200 Q--KAQYTNMYWLTQTVHSSIAKIV-----NDVEFAKFNLYLTNREKEALRWTAEGKTSAEIAQILGVTERTVNFHLSNSMQKLVNWNKI SAAIRAVMLGLL-----
YP_003734010 Q--KAQYTNMFWSLQTVHSSIAKIV-----NETEFAQFNLYLTNREKEALRWTAEGKTSAEIAQILGVTERTVNFHLSNSMQKLVNWNKI SAAIRAVMLGIL-----
YP_002911505 L--ERNEFRMRWLVTTHLAMTRVL-----MPKLPMPDTERGLTDREVEVLKWAADGKTSAGEISTILRISVDTVNFHVKNNAVAKLKT VNKTSAVVRAAMLGLLS-----
YP_003978623 L--LSKELRMRWLVTAAHLAFSKVL-----LPRFKLAPNVPLTRRETEILKWAADGKTSDDVSEI LAIAESTVRFHTKNAISKLGARNRTAAVARAALLGLLS-----
YP_002947664 M--RAKDLLFQGLVKNKAHAFRCRL-----GGPLAG--IEPLTKRQVEVLRWTDGKTSDEIAAAILCISKPTVDFHLRNAMARLGATKSSAAAFASRLGLLN-----
YP_003750859 L--DRLSATTNWLANLAHTLMS PFL-----MPKLVPESSNAVLTAREREVL CWTGEGKTAYEIGQILRISERTVNFHVNNVLLKLAATNKVQAVVKAIVIGLI-----
NP_521406   L--EQLSATTNWLANLAHALMS PFL-----MPKLVPESSAALTAREREVL CWTGEGKTAYEIGQILRISERTVNFHVNNVLLKLAATNKVQAVVKAIAIAGLI-----
YP_003744152 L--GQLSIATHWLANLAHTLMS PFL-----VPKLVPESSNAVLTAREREVL CWTGEGKTAYEIGQILRISERTVNFHVNNVLLKLAATNKVQAVVKAIAIATGLI-----
YP_001117674 I--NMLTLQTNWLANLSHSLMSRFM-----LPKLSPAAGVTLTAREREVL CWTGEGKTACEIGQILSISERTVNFHVNNILEKLAATNKVQAVVKAIAAGLIDTP-----
YP_623508   I--NMLTLQTNWLANLSHSLMSRFM-----VPKLSPAAGVTLTAREREVL CWTGEGKTACEIGQILSISERTVNFHVNNILEKLGATNKVQAVVKAISAGLIETP-----
YP_001583946 I--NMLTLQTNWLANLSHSLMSRFM-----VPKLSPEARVALTAREREVL CWTGEGKTACEIGQILSISERTVNFHVNNILEKLGATNKVQAVVKAISAGLIDTP-----
YP_105961   I--NHLTLQANWLANMSHSLMSRF-----VPKLAPESGVALTHREREVL CWTGEGKTACEIGQILSISERTVNFHVNNILDKLGATNKVQAVVKAIAMGLIDAP-----
YP_002909041 I--NSLTLQANWLANLSHSLMGRFL-----VPKLSPAASISLTKREREVL SWTSEGRTASEIGEQLNISERTVTFPHINNILAKLGAANKVQAVVKAIGMGLIQAP-----
YP_002907673 L--KRLSLQLSWITNAVHSAMTAHV-----FDSLGLGAAISLTEREQVLRWTEGLNADFISEKLNISVSTVNWHIGKVLAKFGATNKVQAAARAVALNLL-----
YP_003910271 RHIDVVL PNLVLLRDLVIDTSQRHL-----HTHAQSLLPK-LTPRERECLQWTARGKSTWEI SHILNCSEAVNVFMHKNIRTKLGVNSRRAAAVIATQLGLIDPG-----
YP_001888024 RHINVALPNLVLLRDLVIDTSQRHL-----NTHAQTL LPK-LTPRERECLKWTARGKSTWEI SHILNCSEAVNVFMHKNIRTKFVNSRRAAAVIAAQLGLIDPG-----
YP_003608086 RHNVAALPNLVLLRDLVIDTSKQHL-----DSHAQSLMPK-LTPRERECLKWTARGKSTWEI SHILSCSEAVNVFMHKNIRAKFGVNSRRAAAVIAAQLGLIDPG-----
YP_001860599 RHLDVVL PNLVLLRDLVIDTSQPHL-----NHTQALVPK-LTPRERECLKWTARGKSTWEI SHILNCSEAVNVFHLKNIRTKFVNSRRAAAVIATQLGLIDPG-----
YP_003847232 RDANHHLP ELACFRDFILESSLQFM-----KPSRQVENPISVTHRELECKLWASAGKSSWEIGHILNCTEATVNFHFSNIRRKFFSTSRQQAIVKAI SLGLIHPN-----
YP_001167907 KLKRAAIGDLQVAAVHLHDVAMRSD-----VISR-ALRQPRLSTREIEVLQWVAAGKSQMDIGDILGISHRTVEVHLRSAREKGLTSTVQAVGRAIGLGLVYPR-----
YP_001043640 KHKRAVIGELQVAAVHLHDVAMRSD-----VISR-ALRQPRLSTREIEVLQWVAAGKSQTDIGDILGISHRTVEVHLRSAREKGLTSTVQAVGRAIGLGLVYPR-----
YP_001758389 RVAVNLVATYAVGQLL MNSRPAA-----PAPARLSPREREALQWAAEGKTDVEIGMVMGITAGVVDYHLRSARAKLDTVNRHTVAQALRSGLIT-----
YP_486928   RGMVQLVAMYAFLRSLKLGKPK-----TPAITLTKREADVHLHWIAEAGKTDWEISKILRVSEHLVDKMARQIRTKLGAVNRIQAVALAMRSGIIR-----
YP_001603072 LVALGFINSQYYET--LSKLSEAE-----PG-----PVPTFSRREKECLLWVSRGKTTWEDISVILGISENTINAYLKNVILKLGCSGRQAVLRAIDLNLISP-----
YP_003262848 L--KELQYRLTWLTQISHHCMEII-----TTKKMPETMITLTMREKVDLRTWTAAGKTSGETSTIMNITERTVNFHIANSMQKLNCKINKTSATVRAAMLGLLD-----
YP_002911546 R--DRNEFI VHWLANVAHAALAPFL-----P--AAGEPEANLTSRETDV LKWTADGKTAYEISRLSISESTVNFHVKNIMSKLGTSTNKI QAVAKAALTGML-----
YP_001815695 L--RRTEPEMIWFCQFVHATMSNLI-----VSDVMPGAMRSLREKEVLHWTAEAGKTAEEVAAILQLTERNVGFHIQNAIDKLDANKTHATVKAAMGLIPVRC-----
YP_001115608 L--RRTEPEMIWLCQFVHATMSNLI-----VSDVMPGAMRSLREKEVLHWTAEAGKTAEEVAAILQLTERNVGFHIQNAIDKLDANKTHATVKAAMGLIPVRC-----

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251 | 260 | 270 | 280 | 290 | 300 | 310 | 320 | 330 | 340 | 350 | 360 | 370 | 376

YP_002874841 | L--YEKAGHVWLWCHAMHAVVAQKY-----AGKPSALPPSKLTPRETEILKWSAMGKTASDIATILCLSSERTVGFHISSTFFKGLGVNKKIAAVLCASKAGLF-----

YP_001437405 | D--DELALRLQHLVEQSLVTMMRLE-----DPAATVL--EMKLSKREKEILQWTAEGKTSAEIAIILSISENTVNFHQKNMQKFFNAPNKTQIACYAAAIIGLI-----

YP_003941366 | E--DETQMRLOMLAEFSTTALLRLD-----DSAILTP--EMKFSKRELEILKWTAEAGKTSAEIISILSISENTVNFHQKNMQKFFNAPNKTQIACYAVATGLI-----

YP_0030530769 | T--TETELKIQYVLEAEGSMAALININ-----DISMATT--KLFDSKRELEILKWTAEAGKTSAEIISILSISENTVNFHQKNMQKFFNAPNKTQIASYAAAIIGLI-----

YP_002649216 | T--PVMELKIQYISELSMASLIKIN-----DISMATT--KLDLSQRELEILKWTAEAGKTSAEIISILSISENTVNFHQKNMQKFFNAPNKTQIASYAAAIIGLI-----

YP_001908006 | T--PEIEELKIQYISELTMAALIDIN-----DISMATT--KLDLSERELEVLKWTAEAGKTSAEIISILSISENTVNFHQKNMQKFFNAPNKTQIASYAAAIIGLI-----

YP_003519711 | R--VELEVKLHFLAEQSLSLERLN-----DEALMVQ--GNDFSQRELEILRWTAEGKTSQEISLILSISEHTVNFYQKNMKKRFNVSNKTQIACYAAAIIGLI-----

YP_0206883 | S--LFLHASTNVPLMLPSLVDNYQK-----INTTRKKSIDSILTKREKECLAWASEGKSTWDISKILGCSERTVTFHLLTNTQMKLNTNRCQSIKAILTGAINCPYLKN-----

YP_001143989 | F--ENVPLLSFCASYIFNSALQLIK-----SRPDLMKHHLTELSDRKECLFWASEGKTSWEIATILGISERTVNFHLLNQVNTKTDKSNRNRQAIKSISSGIIVPSLDDVTTITNLRLS-----

YP_003267496 | DRIRHAIPIAQFVLSHLVEKLEAHF-----HVRLEDLQRYKLSERERECLRWAAGKTSWEIGHILGIAERTAI FHLNNAMKKGAVNRSHAVARALQHGVIAL-----

YP_003450678 | RRPRIIPDFIHFSLALHSAMVSSEP-----DD--AEEVPCKLSPREREVLDWASRGKTSWETGMVLGLSEKTVNFYLRNACQKMNAAATKVQAAAQAVREGLI-----

YP_002910942 | AEIERVKGAMQLALVLFHSRINAKP-----PDSR--HRVES--LTLRERTVLKWAAMGKSYSEIADICGIRERTVKYHMANVVQKLDVSTAKQAVIVASRLGLAALSEG-----

YP_001022984 | GEVTRLVADLQLFVAVHAQDTAMRVL-----VPERLQLERPKLTPRELDLSLRWTMDGKTAWEVGSIIMGISERTAVLHINNAMHKLACTNKHQAVLKALRLGLLR-----

YP_001898047 | HTDAISGLAVLTALHLHEAVRRLDA-----SMSN--AP--IPSLTSREKECLQWAAAGKTSWEIARILSVSERTVIFHIGNATKKGATNRRQAVARAISRLRIAP-----

YP_528967 | RINACLPPAQSFQTQVFCYSALML-----KLAQ--NK--QTHLTAREKESLFWACEGKTTWEISKILDVSEKTVIFHLLSATS KLGAVNRQHAVAKAILSGLIKPTL-----

YP_659944 | VLDNAQMFCHTFATHLFFERYVLEI-----SASD--ETDRRELTKRELECLFWACEGKTAWEISQIINVSEKTVIFHLLGNSNTKLGAINRQHAVALAIKGGIIPKNI-----

YP_106048 | DILRLLSLQLLASFVHAAMHELDD-----CRLR--ROGSCDLTARERESLQWAGRGKTAWEISKILGISERTVNFHLSNAARKIGANNRAQAVVIASARGLI-----

YP_106160 | AKWRNAYLLGMQFNLFQSMRTPCR-----P--IPPSVHLTDREQMCLTWWARGKSSWVIANMLDISKYTVDFHIE NAMEKLNTRSRTPAAVKATROGLIFP-----

YP_001777917 | VHMRLASLIGALFHQELHRLMKPH-----R--PEPALELSPROQECLAWVARGKSSWIAAIVGISPHTVDYHIAEAMKILGINSRTAAAVHAVTTGLIQV-----

YP_972129 | RCVRYYALVTFAFHALYTRMFATEQT-----Q--IPPAVKLTSREAECLTWVYAGKSSWEIGRIMRISSEHTVNFHLLKNMAKFDTSASRVTAAVRAANLGLISIP-----

YP_004012994 | TLLHKVQALAIQPHLAFTELEKIET-----PLTE--NLAEVYLTEREKEIMSWAAEGKSDSVIAEILGVSHSTVRFHMNNVFKKLNANERTLATVKAIRHGLILPSFIG-----

NP_768520 | DRMAHLTTLASAFHNAVAQITPPL-----DES--CEDPIPTPRETECEILYVWAEKSAWVIGQLVNVTDNTVNFHMKNVIRKLGAAANRTNAVAKATRRGII-----

YP_567541 | KGAMQLIGVYAH--NRIRSLHRPKP-----QRRLLTSRECEILWAAHAGKTAWEISIIHLIAERTVKFHLIEASKLNNAVNRTAATAVAKALAFGLIKL-----

YP_484040 | KGAMQLIGVYAH--NRLRSLNRPKP-----QRRLLTSRECEILSWAAQKTAWEISIMILRIERTVKFHLIEASRKLNAVNRTAATAVAKALSLGLIRL-----

YP_002966880 | KPAVHMIIAMYAF--ERARQVGRRPAPK-----P-----PSNPLTQREQEVLTWAAALGKSSRDTAEIMQITERTALAHAVNATHKLGAAANRTQAVVRAMQSKFIRV-----

YP_781245 | KPALHLMAMYAF--DRIRSLVS--PAN-----D-----APRRLTHRECTLNWTAAQKSAWEIGEILQIAQRTAEHLATAARKLGAVNKTHAVAIARQKLIAP-----

YP_002495629 | RRGLHMLGLYAWGAATRTTEDRRRS-----E-----PGRLLSARERDVLSWAAMGRREEIATILGVSHETVATHLKSARIKIGARNRTTQTVVEALRKRITL-----

YP_001776815 | RAALHLVAIYAM--STAKAIARRRGL-----SEDD--GTPPSPLTGREAECLKWSSTGKSAWEIGVILSISRTVEHHLGSAVRRKLSVTRTQAVAEALRRHIIID-----

YP_001641953 | RGMLTLLASVYVVGQTLIDNGPSE-----RRMG--LTPRERESLQWVAEGKTDWEIGELMGISRHGVDFHLRSARVKLGCVSRTPQAVAEGRFRGLII-----

YP_002497059 | RGMLTLVGTVALGQVLLANGQAE-----ALSEPLSPRERESLQWADGKSDWEIGEAMGISEHGAIRHLRAVRRKLGTTSRHAVALGLRLGIIIS-----

YP_001240084 | QISKYRHELHLIAIYLYARLDVTP-----TP--A--SPLRPLCTQREICLQWAAARGKSSALDTAEIINVSRRTVVFHTQNAKRKLGAVTVQQAQAVAKGLAYDIIGM-----

NP_106660 | VAEQYEQALEIMAMCFHIGVRRKLA-----RG--L--AVDGVSLTPREYECLEWTAAGKSAWEIGCILGKERTAAFHLDNAKKKLGVRTKNQAVTLLASSRSSIL-----

YP_003259225 | NIVEKNKDKLQMLLIVIEHEKITTTLY--KEIT--QTPQSKQDKEIFSQRENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGVLEQLIKP--EPL-----

YP_003017024 | SIVEENKDKLQMLLITVHEKITTTLY--KEMT--QSTQSRKQGDKEIFSQRENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGVLEQLIKP--EPS-----

YP_003331714 | EIVQNNKEKLQMLLISAEKLTSLY--REMS--KNNRNSKSEQEADLFSQRENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGVEMNLIKPVEPVKARS-----

YP_003885142 | EIQNNKDKLQMLLISAEKLTSLY--REMS--RNRNNSKSEQEADLFSQRENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGVEMNLIKPVEPVKARS-----

YP_003002472 | EIQNNRDKLQMLLISAEKLTSLH--REMS--RNRHNSKQEQEADIFSQRENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGVEMNLIKPVEPVKARS-----

YP_002985768 | NMIHGNQEKLQMLLIATHEKLTSLY--RELA--ESRQHR--SNDMLFSERENDILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRMGIEMNLIIRRV-----

YP_001005891 | ESIEINKEKIQMLLILTHEKMLGLY--QSNDSKNENRNPKIERDIFSPRENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGIELKLIKPI-----

YP_003019697 | KFIEEKDTPQMLLIDAYEKIISLCL--REMIESKK--QLNNKE--MFSQRENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGVLEQLIKPVQ-----

YP_003261727 | DVIESNKDKLQMLTMTIHAETISLY--REMIRNKEDERSNDKD--IFSQRENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGIELQIRIPVQS-----

YP_002934275 | ---RNRGVLQMLLIDAHERFINGQ--RQITAQRHCSNKEPIENIFSTRENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGVLEQLIKPIEG-----

NP_670674 | SRVLNDRDLQMLLIEHMKLTLQQRNMNIQERQKGMGPKAIIISPRENEVLYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGVLEQLIKPILA-----

YP_003520251 | QRLASEQGTQMLLIDFNEQMYRLAGAEAEAPTVNQNAD--KTFISSRENEVLYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGVLEQLIKPASAAR-----

YP_001906896 | ETFIKNKGEISLLASVHETYTLT--SLSEKNASRSRENASRFTERENEILYWASMGKTYPEIAILDILDKISTVKFPHIGNVVKLGVLNAKHAIRLGMELQLIKPV-----

YP_003941575 | ELLIQHGDISLLASVHETYTLT--SLSEKDT--DKHSQPTPRENEILHWTSLGKTYQETGMILGIVRTVKFPHMSNIVKMGVANARHARLGVLEQLIKPVE-----

YP_003729882 | FDIDKHRKFMFLIHLHQKTLNLY-----SQHQQ--KKNAPLSPRERQILKWSVDGKTYAEIAIILSIAERTVKFPHMGNVKMLGVNNAARHAIKLGAEELLEN-----

YP_002924396 | FFDID--REKMYLLVKTQKLLSLY-----EKFEIPTKKNIGLSKRENEILHWSIGKTYQETSKITGICEKSIKFKMKNITNKLGAINSRHAIKLAYELKLLKQISYAF-----

YP_001832058 | ARHYELIRDMVHVVAHFIQORAFEMH-----HQDEGIDINTTKREIEALSWSAEGKTFLEDISVLMRISQETVKAHLDARSYKLGALNRIHAVAIAIRAGLRI-----

YP_001669935 | -----MTDNARYS-----QPPADAPVRLTPRERQVLLWCAYGKSSWEIGRILDKCESTVNFHVSNIILRKFVDPTRVVAVIKAIRYGLLAEQ-----

YP_001748729 | -----MKANTQOI-----EDSQADTPIRLTPREQVLLWCAYGKSSWEIGQILQCQESTVNFHVNILRKFVDPTRVAVIKAIRYGLLAEQ-----

Accession Number-to-Species Key for **Table S4**.

Accession Number	Species & Strain	Accession Number	Species & Strain
YP_001747665	<i>Pseudomonas putida</i> W619	YP_001437405	<i>Cronobacter sakazakii</i> ATCC BAA-894
YP_001991323	<i>Rhodopseudomonas palustris</i> TIE-1	YP_003941366	<i>Enterobacter lignolyticus</i> SCF1
YP_569310	<i>Rhodopseudomonas palustris</i> BisB5	YP_003530769	<i>Erwinia amylovora</i> CFBP1430
YP_002232821	<i>Burkholderia cenocepacia</i> J2315	YP_002649216	<i>Erwinia pyrifoliae</i> Ep1/96
YP_624828	<i>Burkholderia cenocepacia</i> AU 1054	YP_001908006	<i>Erwinia tasmaniensis</i> Et1/99
YP_002158591	<i>Vibrio fischeri</i> MJ11	YP_003519711	<i>Pantoea ananatis</i> LMG 20103
YP_002265247	<i>Aliivibrio salmonicida</i> LF11238	YP_206883	<i>Vibrio fischeri</i> ES114
YP_855658	<i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i> ATCC 7966	YP_001143989	<i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> A449
YP_776923	<i>Burkholderia ambifaria</i> AMMD	YP_003267496	<i>Haliangium ochraceum</i> DSM 14365
YP_002955225	<i>Desulfovibrio magneticus</i> RS-1	YP_003450678	<i>Azospirillum</i> sp. B510
YP_002537872	<i>Geobacter daltonii</i> FRC-32	YP_002910942	<i>Burkholderia glumae</i> BGR1
YP_002871035	<i>Pseudomonas fluorescens</i> SBW25	YP_001022984	<i>Methylibium petroleiphilum</i> PM1
NP_106527	<i>Mesorhizobium loti</i> MAFF303099	YP_001898047	<i>Ralstonia pickettii</i> 12J
YP_001242900	<i>Bradyrhizobium</i> sp. BTAi1	YP_528967	<i>Saccharophagus degradans</i> 2-40
YP_001203095	<i>Bradyrhizobium</i> sp. ORS278	YP_659944	<i>Pseudoalteromonas atlantica</i> T6c
YP_001927660	<i>Methylobacterium populi</i> BJ001	YP_106048	<i>Burkholderia mallei</i> ATCC 23344
YP_002547516	<i>Agrobacterium vitis</i> S4	YP_106160	<i>Burkholderia mallei</i> ATCC 23344
YP_003558208	<i>Shewanella violacea</i> DSS12	YP_001777917	<i>Burkholderia cenocepacia</i> MC0-3
YP_777789	<i>Burkholderia ambifaria</i> AMMD	YP_972129	<i>Acidovorax citrulli</i> AAC00-1
YP_003749681	<i>Ralstonia solanacearum</i> PSI07	YP_004012994	<i>Rhodomicrobium vannielii</i> ATCC 17100
YP_001715477	<i>Acinetobacter baumannii</i> AYE	NP_768520	<i>Bradyrhizobium diazoefficiens</i> USDA 110
YP_001083200	<i>Acinetobacter baumannii</i> ATCC 17978	YP_567541	<i>Rhodopseudomonas palustris</i> BisB5
YP_003734010	<i>Acinetobacter oleivorans</i> DR1	YP_484040	<i>Rhodopseudomonas palustris</i> HaA2
YP_002911505	<i>Burkholderia glumae</i> BGR1	YP_002966880	<i>Methylobacterium extorquens</i> AM1
YP_003978623	<i>Achromobacter xylosoxidans</i> A8	YP_781245	<i>Rhodopseudomonas palustris</i> BisA53
YP_002947664	<i>Variovorax paradoxus</i> S110	YP_002495629	<i>Methylobacterium nodulans</i> ORS 2060
YP_003750859	<i>Ralstonia solanacearum</i> PSI07	YP_001776815	<i>Methylobacterium radiotolerans</i> JCM 2831
NP_521406	<i>Ralstonia solanacearum</i> GMI1000	YP_001641953	<i>Methylobacterium extorquens</i> PA1
YP_003744152	<i>Ralstonia solanacearum</i> CFBP2957	YP_002497059	<i>Methylobacterium nodulans</i> ORS 2060
YP_001117674	<i>Burkholderia vietnamiensis</i> G4	NP_001240084	<i>Bradyrhizobium</i> sp. BTAi1
YP_623508	<i>Burkholderia cenocepacia</i> AU 1054	NP_106660	<i>Mesorhizobium loti</i> MAFF303099
YP_001583946	<i>Burkholderia multivorans</i> ATCC 17616	YP_003259225	<i>Pectobacterium wasabiae</i> WPP163
YP_105961	<i>Burkholderia mallei</i> ATCC 23344	YP_003017024	<i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> PC1
YP_002909041	<i>Burkholderia glumae</i> BGR1	YP_003331714	<i>Dickeya dadantii</i> Ech586
YP_002907673	<i>Burkholderia glumae</i> BGR1	YP_003885142	<i>Dickeya dadantii</i> 3937
YP_003910271	<i>Burkholderia</i> sp. CCGE1003	YP_003002472	<i>Dickeya zeae</i> Ech1591
YP_001888024	<i>Burkholderia phytofirmans</i> PsJN	YP_002985768	<i>Dickeya dadantii</i> Ech703
YP_003608086	<i>Burkholderia</i> sp. CCGE1002	YP_001005891	<i>Yersinia enterocolitica</i> subsp. <i>enterocolitica</i> 8081
YP_001860599	<i>Burkholderia phymatum</i> STM815	YP_003019697	<i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> PC1
YP_003847232	<i>Gallionella capsiferiformans</i> ES-2	YP_003261727	<i>Pectobacterium wasabiae</i> WPP163
YP_001167907	<i>Rhodobacter sphaeroides</i> ATCC 17025	YP_002934275	<i>Edwardsiella ictaluri</i> 93-146
YP_001043640	<i>Rhodobacter sphaeroides</i> ATCC 17029	NP_670674	<i>Yersinia pestis</i> KIM10+
YP_001758389	<i>Methylobacterium radiotolerans</i> JCM 2831	YP_003520251	<i>Pantoea ananatis</i> LMG 20103
YP_486928	<i>Rhodopseudomonas palustris</i> HaA2	YP_001906896	<i>Erwinia tasmaniensis</i> Et1/99
YP_001603072	<i>Gluconacetobacter diazotrophicus</i> PA1 5	YP_003941575	<i>Enterobacter lignolyticus</i> SCF1
YP_003262848	<i>Halothiobacillus neapolitanus</i> c2	YP_003729882	<i>Pantoea vagans</i> C9-1
YP_002911546	<i>Burkholderia glumae</i> BGR1	YP_002924396	<i>Candidatus Hamiltonella defensa</i> 5AT (<i>Acyrtosiphon pisum</i>)
YP_001815695	<i>Burkholderia ambifaria</i> MC40-6	YP_001832058	<i>Beijerinckia indica</i> subsp. <i>indica</i> ATCC 9039
YP_001115608	<i>Burkholderia vietnamiensis</i> G4	YP_001669935	<i>Pseudomonas putida</i> GB-1
YP_002874841	<i>Pseudomonas fluorescens</i> SBW25	YP_001748729	<i>Pseudomonas putida</i> W619

Table S5. Conservation among 100 LasR homologs at mutated sites in this study.

residue	Y56		W60		R61		D73		T75		W88		Y93F		T115		S129	
	Freq	%	Freq	%	Freq	%	Freq	%	Freq	%	Freq	%	Freq	%	Freq	%	Freq	%
A	1	1.0	0	0.0	4	4.0	0	0.0	3	3.0	0	0.0	5	6.8	16	16.2	0	0.0
C	3	3.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	1.4	7	7.1	5	5.1
D	0	0.0	0	0.0	0	0.0	99	100.0	0	0.0	0	0.0	3	4.1	0	0.0	0	0.0
E	0	0.0	0	0.0	2	2.0	0	0.0	0	0.0	0	0.0	4	5.5	0	0.0	0	0.0
F	4	4.0	0	0.0	10	10.0	0	0.0	0	0.0	0	0.0	15	15.2	0	0.0	1	1.0
G	0	0.0	0	0.0	2	2.0	0	0.0	0	0.0	0	0.0	0	0.0	1	1.0	2	2.0
H	3	3.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
I	0	0.0	0	0.0	5	5.1	0	0.0	15	15.2	0	0.0	3	4.0	1	1.0	0	0.0
K	1	1.0	0	0.0	6	6.1	0	0.0	0	0.0	0	0.0	6	8.0	0	0.0	0	0.0
L	1	1.0	1	1.0	12	12.0	0	0.0	1	1.0	0	0.0	8	8.0	0	0.0	2	2.0
M	1	1.0	0	0.0	10	10.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
N	1	1.0	0	0.0	2	2.0	0	0.0	0	0.0	0	0.0	4	5.5	0	0.0	4	4.0
P	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Q	0	0.0	0	0.0	7	7.1	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
R	0	0.0	0	0.0	14	14.0	0	0.0	0	0.0	0	0.0	9	9.0	0	0.0	0	0.0
S	0	0.0	0	0.0	4	4.0	0	0.0	1	1.0	0	0.0	1	1.4	28	28.3	65	65.7
T	2	2.0	0	0.0	2	2.0	0	0.0	26	26.3	0	0.0	3	4.1	45	45.5	20	20.2
V	0	0.0	0	0.0	18	18.0	0	0.0	53	53.5	0	0.0	8	8.0	1	1.0	0	0.0
W	10	10.0	97	97.0	0	0.0	0	0.0	0	0.0	99	99.0	0	0.0	0	0.0	0	0.0
Y	72	72.0	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	3	4.1	0	0.0	0	0.0
Gap	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	26	26.0	0	0.0	0	0.0

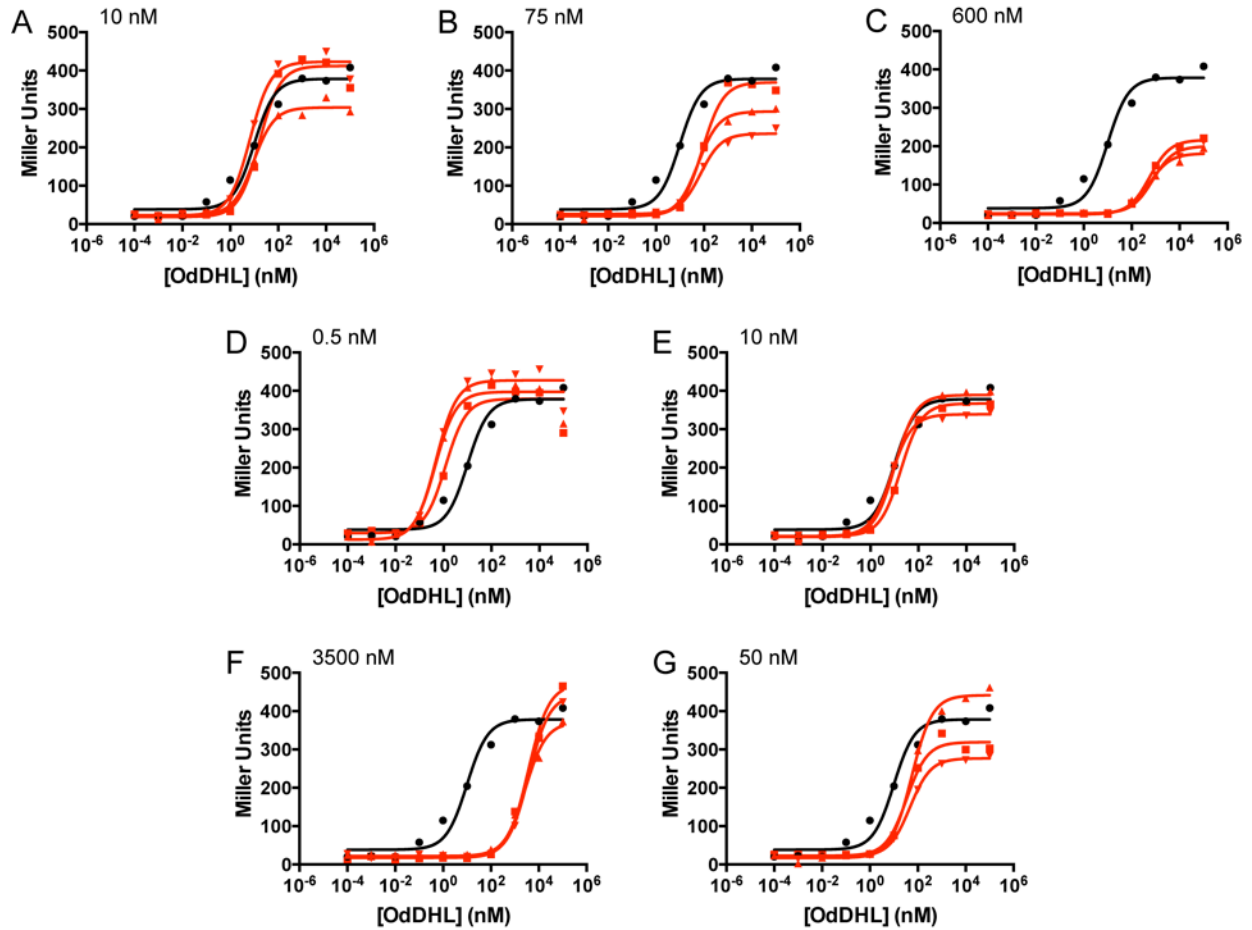


Figure S1. Dose-response curves for mutant LasRs with OdDHL. OdDHL dose-response curves used to calculate EC₅₀ values for OdDHL in each LasR mutant: (A) Y56F, (B) W60F, (C) R61M, (D) T75V, (E) Y93F, (F) T115V, and (G) S129A. For each plot, the three red curves compose a biological triplicate of data for OdDHL in the mutant, and the black curve is a representative replicate for OdDHL in wild-type LasR for comparison. The geometric mean of each EC₅₀ value is displayed on each plot and in **Table 1** in the main text.

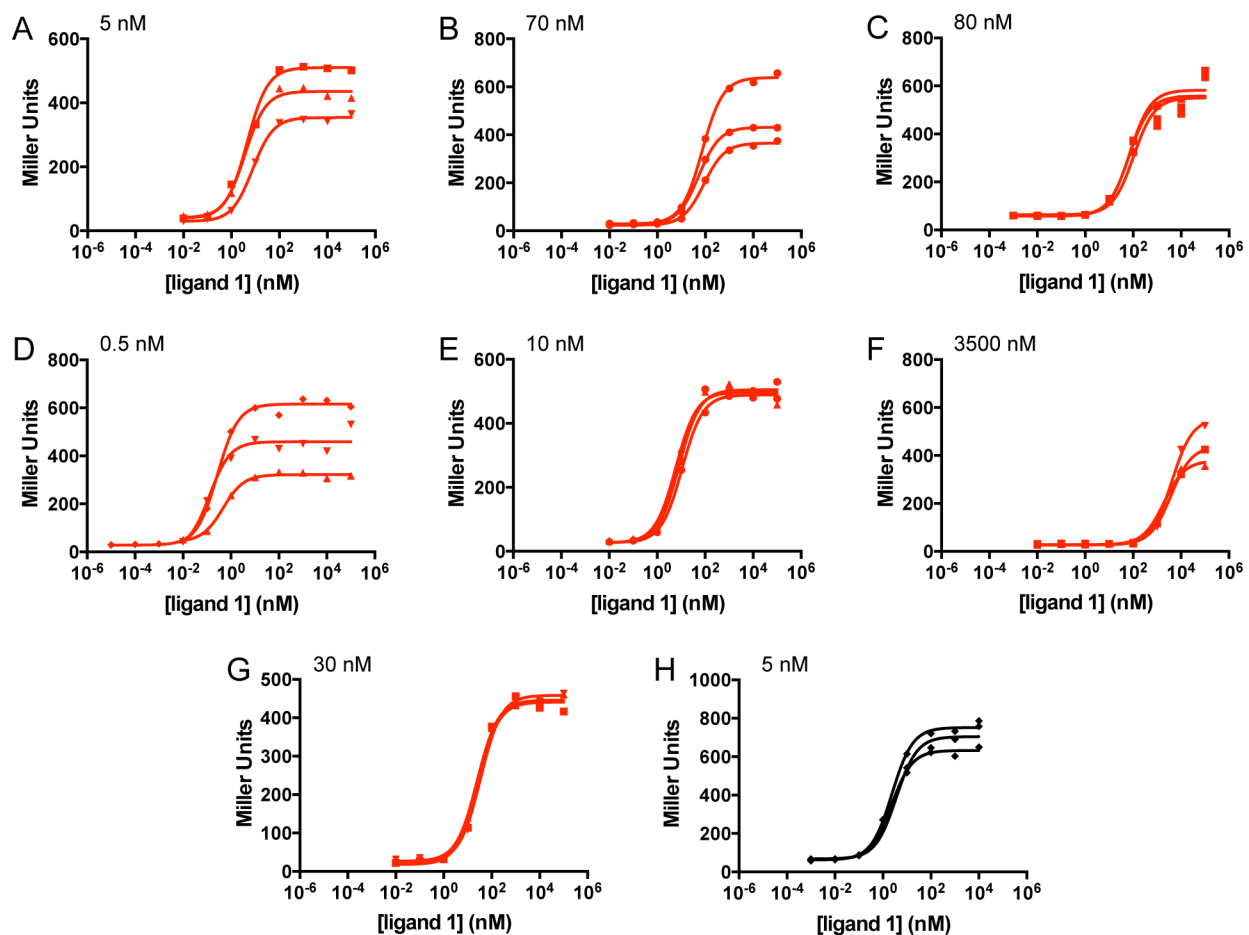


Figure S2. Dose-response curves for mutant LasRs with ligand 1. Ligand 1 dose-response curves used to calculate EC_{50} values for **1** in each LasR mutant: (A) Y56F, (B) W60F, (C) R61M, (D) T75V, (E) Y93F, (F) T115V, and (G) S129A. Panel (H) shows the dose-response curve for **1** in wild-type LasR. For each plot, the three curves compose a biological triplicate of data for **1**. The geometric mean of each EC_{50} value is displayed on each plot and in **Table 2** in the main text.

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