The *Pseudomonas aeruginosa* LasR quorum-sensing receptor balances ligand selectivity and sensitivity

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Abstract

Bacteria use a cell-cell communication process called quorum sensing to orchestrate collective behaviors. Quorum sensing relies on group-wide detection of and response to extracellular signal molecules called autoinducers. Autoinducers are often structurally similar, raising questions concerning if and how bacteria distinguish between them. We use the *Pseudomonas aeruginosa* LasR quorum-sensing receptor to explore receptor selectivity and sensitivity. We find that LasR responds to homoserine lactone autoinducers harboring different acyl tails. Alteration of LasR amino acid S129 increases ligand selectivity and decreases ligand sensitivity. Conversely, the L130F mutation enhances LasR sensitivity while reducing selectivity. We solve crystal structures of LasR ligand binding domains complexed with non-cognate autoinducers. Comparison to the existing structure of the LasR ligand binding domain bound to the cognate autoinducer shows that ligand selectivity/sensitivity is mediated by a flexible loop adjacent to the ligand binding site. We show that *P. aeruginosa* harboring LasR variants with modified selectivity or sensitivity exhibit altered quorum-sensing responses. We suggest that an evolutionary trade-off between ligand selectivity and sensitivity enables LasR to optimally regulate quorum-sensing traits.

Introduction

Quorum sensing is a cell-cell communication process that enables bacteria to collectively control behavior (reviewed in Papenfort & Bassler, 2016). Quorum sensing relies on the production, release, and detection of extracellular signal molecules called

autoinducers (Albus et al., 1997, Engebrecht et al., 1983, Latifi et al., 1995). At low cell density, autoinducer concentration is low, and bacteria act as individuals. As cell density increases, autoinducer concentration also rises. Under this condition, autoinducers bind to cognate receptors, initiating the population-wide regulation of genes underlying collective behaviors.

Many species of Gram-negative bacteria use acylated homoserine lactones [HSLs] as autoinducers (Brint & Ohman, 1995, Cao & Meighen, 1989, Eberhard et al., 1981, Hanzelka et al., 1999, Pearson et al., 1994). HSL autoinducers possess identical lactone head groups, but they vary in acyl tail length and decoration. The tail modifications promote specificity between particular HSL autoinducers and partner receptors (Churchill & Chen, 2011). There are two kinds of HSL autoinducer receptors. First, there are LuxR-type receptors, which are cytoplasmic HSL-binding transcription factors that possess variable ligand binding domains [LBD] and well-conserved helix-turn-helix DNA binding domains [DBD] (Nasser & Reverchon, 2007, Vannini et al., 2002). There are also LuxN-type receptors, which are membrane-spanning two-component signaling proteins that bind HSL ligands in their periplasmic regions and transduce information regarding ligand occupancy internally by phosphorylation/dephosphorylation cascades (Bassler et al., 1993, Freeman et al., 2000, and reviewed in Papenfort & Bassler, 2016).

Ligand sensitivity and selectivity has been examined in the founding member of the LuxN receptor family from *Vibrio harveyi* (Ke et al., 2015). LuxN is exquisitely selective for its cognate autoinducer $3OHC_4HSL$. Specific amino acids were identified in the predicted LuxN transmembrane spanning region that confer selectivity for tail length and

for tail decoration. Longer HSLs competitively inhibit LuxN, suggesting that, in mixed-species consortia, *V. harveyi* monitors the vicinity for competing species, and in response to their presence, exploits LuxN antagonism to delay the launch of its quorum-sensing behaviors, thus avoiding loss of expensive public goods to non-kin.

Some analyses of ligand preference in LuxR-type receptors have been performed. TraR from *Agrobacterium tumefaciens* excludes non-native HSLs (Hawver et al., 2016, Vannini et al., 2002, You et al., 2006, Zhu & Winans, 2001), LasR from *Pseudomonas aeruginosa* detects several long chain HSLs (Gerdt et al., 2017), and SdiA from *Escherichia coli* is highly promiscuous and avidly responds to HSLs with variable chain lengths (Michael et al., 2001, Nguyen et al., 2015, Sitnikov et al., 1996). Comparison of structures of the LasR and TraR LBDs suggests that increased hydrogen bonding to the ligand in TraR, compared to LasR, accounts for the selectivity difference (Gerdt et al., 2017). Here, we systematically explore the LasR response to $3OC_{12}HSL$ and non-native HSLs with respect to selectivity and sensitivity. We use mutagenesis to establish the amino acid determinants that enable LasR to discriminate between HSLs. We identify LasR S129 as the amino acid residue that, when altered, improves LasR selectivity for HSLs by restricting the set of HSLs capable of activation. Mutations at LasR S129, however, reduce overall affinity for HSL ligands. In contrast, we find that LasR L130F exhibits diminished ligand selectivity, responding to a broader set of HSLs than wildtype LasR, with enhanced sensitivity. Altering LasR sensitivity or selectivity affects the timing and strength of quorum-sensing control of *P. aeruginosa* behaviors. Finally, we solve crystal structures of the LasR LBD L130F bound to non-native autoinducers to establish

the structural basis underlying ligand selectivity and sensitivity. We find that a flexible loop located near the ligand binding pocket promotes ligand promiscuity in the wildtype protein. This loop exists in SdiA, which is promiscuous, but not in TraR which is highly specific for its cognate ligand. We propose that there is a trade-off between ligand selectivity and sensitivity in LasR and evolution has established a balance between ligand discrimination and ligand sensitivity. Because LasR requires higher concentrations of non-cognate autoinducers than its cognate autoinducer for activation, this tradeoff could allow LasR to robustly respond to its own signal molecule, even in the presence of other bacteria that are producing HSL autoinducers. Nonetheless, *P. aeruginosa* would be capable of reacting to the presence of these other bacteria when it is outnumbered.

Results

LasR responds to multiple HSL autoinducers

To investigate the preference LasR displays for different HSLs, we employed a plasmid reporter system in which transcription from a LasR-controlled promoter fused to luciferase (p*lasB-lux*) was assessed in *E. coli*. Arabinose-inducible *lasR* was cloned on a second plasmid (Paczkowski et al., 2017, Pearson et al., 1997). A set of HSLs differing in both carbon chain length and in functionality at the C-3 carbon were synthesized using a modification of a previously reported method (Chhabra et al., 2003) (see Appendix). Figure 1A shows reporter output following addition of 100 nM of the cognate autoinducer, $3OC_{12}HSL$, and four other HSLs ($3OC_{14}HSL$, $3OC_{10}HSL$, $3OC_{8}HSL$, and $3OC_{6}HSL$). All

five HSLs activated LasR, but to differing levels. $3OC_{12}HSL$, $3OC_{14}HSL$, and $3OC_{10}HSL$ elicited maximal LasR activity, and $3OC_8HSL$ and $3OC_6HSL$ stimulated 7-fold and 18-fold less activity, respectively. We examined 8 other HSLs harboring different functionalities on the C-3 carbon in combination with the various tail lengths. Using dose-response analyses, we obtained EC_{50} values for the compounds (Table 1 and Table EV1). $3OC_{12}HSL$ was the most potent ligand, with an EC_{50} of approximately 2.8 nM. $3OC_{14}HSL$ was half as potent with an EC_{50} of 5.6 nM. From there, the EC_{50} values followed the order $3OC_{10}HSL < 3OC_8HSL < 3OC_6HSL$. Table EV1 shows the remainder of the data and that the ketone versions of the molecules are the most potent for every chain length. For this reason, we used the five HSLs shown in Table 1 for much of the remainder of this work. We measured *in vivo* LasR activity in response to the test HSLs using an elastase assay (Gambello & Iglewski, 1991). Elastase is encoded by *lasB*, and as a reminder, we employed the *lasB* promoter in the *E. coli* reporter assay. For the elastase analyses, we used a Δ*lasI P. aeruginosa* strain that makes no endogenous $3OC_{12}HSL$. When supplied at 100 nM, all of the test compounds elicited some elastase activity, but $3OC_{12}HSL$ stimulated the highest elastase production (Fig 1B). We do note that in *P. aeruginosa*, $3OC_{14}HSL$ and $3OC_8HSL$ stimulated lower activity than expected based on their EC_{50} values in *E. coli.* Indeed, as shown below, these two molecules had reduced activity in all assays in all *P. aeruginosa* strains used here. While we do not know the underlying molecular mechanism, we suspect that perhaps there is reduced permeability into *P. aeruginosa* and/or there is a factor in *P. aeruginosa* that does not exist in *E. coli* that binds and titrates out these two molecules. Nonetheless, our results indicate that, at least

with respect to the HSLs we tested, *in vivo,* LasR is most active in response to its cognate autoinducer $3OC_{12}HSL$, but non-cognate HSLs can induce production of the quorum-sensing product elastase, and presumably other quorum-sensing regulated outputs.

LasR and most other LuxR-type receptors fold around their cognate HSL ligands. Thus, they are only soluble, capable of dimerizing, and binding DNA when ligand is present (Bottomley et al., 2007, Zhu & Winans, 2001). The results in Figure 1A and 1B suggest that LasR can fold around HSLs in addition to $3OC_{12}HSL$. To verify this notion, we tested whether LasR could be solubilized by non-native HSLs. To do this, we grew *E. coli* producing the LasR LBD in the presence of the 13 HSL compounds (Fig 1C shows the five test compounds and Figure EV1A shows the eight other compounds in the collection). Consistent with previous results, in the absence of any ligand (DMSO control), the LasR LBD is present in the whole cell lysate, but not in the soluble fraction indicating that the protein is insoluble (O'Loughlin et al., 2013, Schuster et al., 2004). All five of the HSL test compounds except for $3OC_6HSL$ solubilized the LasR LBD (Fig 1C). Nonetheless, we could only purify to homogeneity the LasR LBD bound to the ligands containing the longer acyl tails: $3OC_{12}HSL$, $3OC_{14}HSL$, and $3OC_{10}HSL$. Together, the results in Figure 1 suggest that although $3OC_8HSL$ and $3OC_6HSL$ can bind to and activate LasR, their interactions must be more transient than ligands with longer acyl tails. To garner evidence for this idea, we performed thermal shift analyses on LasR LBD-ligand complexes without and with the addition of either the same or a different HSL. The LasR LBD bound to $3OC_{10}HSL$, $3OC_{12}HSL$, and $3OC_{14}HSL$ had melting temperatures of 42.3 ^{o}C, 49.1 ^{o}C, and 50.5 ^{o}C, respectively (Fig 2, black lines) showing that LasR stability

increases with increasing ligand tail length. Notably, the LasR LBD is more stable when bound to the non-cognate ligand $3OC_{14}HSL$ than when bound to the cognate ligand $3OC_{12}HSL$. The discrepancy between the enhanced stability of purified LasR LBD:$3OC_{14}HSL$ relative to $3OC_{12}HSL$ in the thermal shift assay and the higher EC_{50} for $3OC_{14}HSL$ compared to $3OC_{12}HSL$ could result from increased hydrophobic interactions in the stably purified complex that do not drive activation and affinity of LasR for a particular ligand.

Exogenously supplied autoinducers can shift the melting temperature of an existing receptor-ligand complex if the added ligand has the ability to stabilize the unfolding protein as it releases the pre-bound ligand. Importantly, exogenously supplied HSLs can only stabilize the LasR LBD if they have affinities that are equal to or higher than the originally bound ligand (Paczkowski et al., 2017). In the case of the LasR LBD:$3OC_{10}HSL$ complex, when added exogenously, the ligands $3OC_{10}HSL$, $3OC_{12}HSL$, and $3OC_{14}HSL$ stabilize the LasR LBD, increasing the melting temperature 3.4 ^{o}C, 6.4 ^{o}C, and 5.5 ^{o}C, respectively (Fig 2). By contrast, the LasR LBD:$3OC_{12}HSL$ and the LasR LBD:$3OC_{14}HSL$ complexes could only be further stabilized by exogenously supplied $3OC_{12}HSL$ and $3OC_{14}HSL$, but not by $3OC_{10}HSL$, indicating that the association rate of $3OC_{10}HSL$ for the LasR LBD is slower than that of $3OC_{12}HSL$ and $3OC_{14}HSL$ (Fig 2). While the short acyl chain HSLs were capable of activation of LasR with high micromolar EC_{50} values in the p*lasB-lux* reporter assay, $3OC_{6}HSL$ and $3OC_{8}HSL$ did not stabilize the LasR LBD protein sufficiently in *E. coli*, presumably due to their low affinities (Fig 1C and Table 1). Thus, they could not be tested in the traditional thermal shift assay. They also

did not enhance the stabilization of the LasR LBD pre-bound with other ligands, analogous to the inability of $3OC_{10}HSL$ to stabilize the LasR LBD:$3OC_{12}HSL$ complex as it melted (Fig 2). Together, our results indicate that in an environment containing a mixture of HSL autoinducers, LasR will preferentially detect long chain HSLs, with superior preference for its own autoinducer $3OC_{12}HSL$, followed closely by $3OC_{14}HSL$.

LasR S129 drives ligand selectivity and sensitivity.

To understand how LasR selects HSL ligands with which to interact, we performed site directed mutagenesis guided by the existing crystal structure of the LasR LBD bound to $3OC_{12}HSL$ (Bottomley et al., 2007). We first focused on residue S129. Previous work has demonstrated that alteration of serine to alanine at this site enables some synthetic LasR activators to transform into inhibitors and vice-versa (Gerdt et al., 2015, Gerdt et al., 2014). Moreover, the LasR LBD structure suggests that S129 is part of the network that interacts with the ligand acyl tail (Bottomley et al., 2007). For these reasons, we predicted that S129 could contribute to LasR selectivity. We constructed LasR S129C, S129W, S129F, S129T, and S129M and examined their activities in the *E. coli* p*lasB-lux* reporter system. Table 1 shows the EC_{50} values for all of the mutants and the five test compounds. The EC_{50} values follow the order: wildtype < LasR S129C < LasR S129W < LasR S129F < LasR S129T < LasR S129M. We note there are three exceptions to this trend among the low affinity interactions (Table 1). However, in those cases, the EC_{50} values are high and we suspect that the differences are not meaningful. The most severe mutation, LasR S129M responded exclusively to $3OC_{12}HSL$ but it was the least sensitive

of all the mutants to this ligand. Conversely, among the mutants, LasR S129C responded to the largest range of HSL varieties and it was the most sensitive. In Figure 3A, we provide the assay results for LasR S129F with the five test HSLs. We chose LasR S129F as the representative mutant for in-depth analysis because it had intermediate EC_{50} values among those obtained for this set of mutants. We assayed LasR S129F at 10 μM of each compound, because increased ligand concentration was required to activate LasR S129F compared to wildtype LasR (see Table 1 and Fig 1). At 10 μM ligand, wildtype LasR and LasR S129F maximally responded to $3OC_{12}HSL$ and $3OC_{14}HSL$. However, compared to wildtype LasR, LasR S129F was 7-fold less responsive to $3OC_{10}HSL$, 13-fold less responsive to $3OC_{6}HSL$ and showed almost no response to $3OC_{8}HSL$. In the Δ*lasI P. aeruginosa* strain (Fig 3B), LasR S129F displayed a similar pattern. Together, our data indicate that alteration of LasR S129 restricts the set of HSLs that can activate LasR but also increases the EC_{50} values of activating HSLs. We conclude that LasR S129 drives selectivity. While the LasR S129 variants improve selectivity, they diminish sensitivity. This finding suggests that a trade-off exists between selectivity and EC_{50}.

LasR L130F drives ligand sensitivity

Because LasR S129F improves ligand selectivity and reduces sensitivity, we suspected that other residues in the vicinity could also affect ligand selectivity. For this reason, we exchanged L128 and L130 for phenylalanine. As above, we tested their responses to the set of representative HSLs using the *E. coli* p*lasB-lux* reporter assay.

Table 1 shows that, surprisingly, LasR L130F exhibited a lower EC_{50} for every autoinducer tested. LasR L128F also conferred improved sensitivity to some short chain HSLs (Table EV1), but its phenotype was less pronounced than that of LasR L130F, so we further analyzed the LasR L130F mutant here. Figure 3C shows the wildtype LasR and the LasR L130F responses to a low concentration (50 nM) of the test HSLs. At this concentration, LasR L130F was roughly equivalent to wildtype LasR with respect to the response to $3OC_{12}HSL$, $3OC_{14}HSL$, and $3OC_{10}HSL$. However, LasR L130F was approximately 5-fold more responsive to $3OC_8HSL$ than wildtype LasR and it was modestly more responsive to $3OC_6HSL$. When we performed the *P. aeruginosa* elastase assay at 50 nM test compound (Fig 3D), wildtype LasR only responded to $3OC_{12}HSL$, whereas LasR L130F responded to $3OC_{14}HSL$, $3OC_{10}HSL$, and $3OC_8HSL$ in addition to $3OC_{12}HSL$. Collectively, these results show that LasR L130F is more sensitive to HSLs than wildtype LasR but it is less selective.

We used thermal shift analyses to explore the mechanism underlying the increased sensitivity of the LasR L130F mutant for HSLs. We used $3OC_{12}HSL$ and $3OC_{14}HSL$ as our test ligands. Compared to the wildtype LasR LBD, the LasR LBD L130F is more stable when bound to each ligand (Fig 4A), suggesting that the L130F alteration increases the overall stability of the LasR protein. We exploited this feature to successfully purify the LasR LBD L130F bound to $3OC_8HSL$. As mentioned above, we could not purify the wildtype LasR LBD bound to $3OC_8HSL$. We performed thermal shift analyses on the LasR LBD L130F bound to $3OC_8HSL$, $3OC_{10}HSL$, $3OC_{12}HSL$, and $3OC_{14}HSL$ to which we added different HSLs. Similar to the wildtype LasR LBD, exogenous addition of HSLs

with long acyl chains further enhanced the stability of the LasR LBD L130F:HSL complexes compared to when HSLs with shorter acyl chains were added (Fig 2 and 4B). For instance, the LasR LBD L130F:3OC$_8$HSL stability was enhanced by the addition of 3OC$_8$HSL, 3OC$_{10}$HSL, 3OC$_{12}$HSL, and 3OC$_{14}$HSL but not 3OC$_6$HSL (Fig 4B). Protein solubility analyses track with these findings; long acyl chain ligands solubilize the LasR LBD L130F protein whereas short chain ligands do not (Fig 4C, EV1B). Consistent with our EC$_{50}$ values, chain length appears to be the most important factor driving protein solubility and stabilization for both the LasR LBD and the LasR LBD L130F (FigEV1B and 4B, respectively).

LasR ligand selectivity and sensitivity influence the timing of quorum-sensing-controlled traits

We have shown that LasR L130F detects and responds to HSLs at lower concentrations than does wildtype LasR, whereas LasR S129F requires higher concentrations. Thus, we predicted that introducing these alleles into *P. aeruginosa* should influence its quorum-sensing responses in opposing manners. To test this prediction, we assayed pyocyanin production over time as the quorum-sensing readout in response to 3OC$_{12}$HSL, 3OC$_{14}$HSL, and 3OC$_8$HSL in a Δ*lasI P. aeruginosa* strain containing wildtype *lasR*, *lasR S129F*, or *lasR L130F*. Guided by the EC$_{50}$ values for each HSL, we tested appropriate low and high concentrations of each HSL to set windows that would enable us to observe responses from the wildtype and each mutant. Consistent with their relative EC$_{50}$ values, when a low concentration of 3OC$_{12}$HSL (50 nM) was

added, the strain with LasR L130F made more pyocyanin than the strain with wildtype LasR at every time point (Fig 5A). At this HSL concentration, the strain carrying LasR S129F never activated pyocyanin production, presumably because the concentration of $3OC_{12}HSL$ was far below the EC_{50} for LasR S129F (Fig 5A). When the same assay was performed with 1μM $3OC_{12}HSL$, rapid and maximal pyocyanin output occurred for *P. aeruginosa* carrying both wildtype LasR and LasR L130F. Furthermore, this high ligand concentration reveals that LasR S129F can drive pyocyanin production in response to $3OC_{12}HSL$, albeit weakly and only after 5.5 hours (Fig 5B). A similar pattern was observed for the low concentration of $3OC_{14}HSL$. Specifically, LasR L130F activated pyocyanin production earlier than wildtype LasR, and LasR S129F failed to activate pyocyanin production (Fig 5C). At the high concentration of $3OC_{14}HSL$, LasR S129F did activate pyocyanin production, however later and less strongly than wildtype LasR and LasR L130F (Fig 5D). With respect to $3OC_8HSL$, at both low and high concentrations, all of the responses were considerably weaker than with the longer chain HSLs, nonetheless, in each case, LasR L130F more strongly activated pyocyanin production than wildtype LasR (Fig 5E, F). LasR S129F showed no response in the $3OC_8HSL$ assays (Fig 5E, F).

We note one curious finding with 10 μM $3OC_{14}HSL$ in Figure 5D. At this concentration, wildtype LasR activated pyocyanin earlier and more strongly than LasR L130F, which does not track with the EC_{50} values and all of our above companion analyses. We propose that this phenotype is due to RsaL accumulation. RsaL is a quorum-sensing regulator whose expression is activated by LasR (Rampioni et al., 2007, Schuster & Greenberg, 2007). RsaL represses pyocyanin production genes (Cabeen,

2014, Schuster & Greenberg, 2007). We propose that because LasR L130F is more active than wildtype LasR, at high autoinducer concentration, LasR L130F possesses increased activity relative to wildtype LasR, and so LasR L130F stimulates higher RsaL production than does wildtype LasR. As a consequence, partial pyocyanin inhibition occurs. This logic suggests that, at high autoinducer concentration, wildtype LasR would activate sufficient RsaL production to cause pyocyanin inhibition. Indeed, addition of 100 μM $3OC_{12}HSL$ to the Δ*lasI* strain carrying wildtype LasR induced less pyocyanin production than when 1 μM $3OC_{12}HSL$ was added (Fig EV2). We show that RsaL is responsible for this phenotype by deleting the *rsaL* gene. As expected, the Δ*lasI* Δ*rsaL* strain produced increased overall pyocyanin relative to the Δ*lasI* strain. Importantly, however, unlike the Δ*lasI* strain, the Δ*lasI* Δ*rsaL* double mutant does not produce more pyocyanin in response to 1 μM $3OC_{12}HSL$ than in response to 100 μM $3OC_{12}HSL$ (Fig EV2). We never observed pyocyanin reductions in the strains carrying any of the LasR alleles when $3OC_8HSL$ was added, even at 100 μM. We suspect this is because $3OC_8HSL$ is such a poor agonist that there is not enough LasR activity at any concentration to stimulate high level RsaL accumulation.

Structural basis underlying LasR ligand preferences

To determine the molecular basis enabling LasR to accommodate non-native autoinducers, we determined the structures of the LasR LBD L130F bound to $3OC_{10}HSL$ and $3OC_{14}HSL$. As mentioned, the wildtype LasR LBD structure bound to the native autoinducer, $3OC_{12}HSL$ already exists (Bottomley et al., 2007). Our rationale for using

the LasR LBD L130F mutant for these studies was that, its inherently enhanced stability, as judged by the thermal shift data (Fig 4A), suggested that it would be ideal for crystallographic studies that are not possible with the wildtype LasR LBD. Indeed, we could determine the structures of LasR LBD L130F:3OC$_{10}$HSL and LasR LBD L130F:3OC$_{14}$HSL to 2.1 Å and 1.9 Å, respectively (Table A1). This resolution is sufficient to observe ligand occupancy and to compare with the LasR LBD:3OC$_{12}$HSL structure (Fig 6A). The L130F residue is buried in a hydrophobic pocket distal to the ligand binding pocket (Fig EV3A). Phenylalanine, rather than leucine at this position, provides increased hydrophobic interactions with amino acid residues L23, L30, F32, I35, L114, L118, L128, L151, and L154. We suggest that this arrangement increases the overall stability of the LasR protein, which in turn, allows it to accommodate an expanded set of HSLs compared to wildtype LasR.

To understand how LasR can accommodate multiple long chain HSL ligands in its binding site, we used the crystal structures to examine the key residues and regions of the binding pocket that interact with the different ligands. In all the structures, the lactone head groups have the exact same placement, likely due to strong hydrogen bonding between the lactone ring carbonyl moiety and residue W60 (Fig 6B, displayed in brown). The lactone head group and the ketone moiety on carbon 3 are further stabilized by an extensive hydrogen bonding network comprised of residues Y56, K61, D73, T75, W88, Y93, S129, and S131 (Fig 6B, displayed in brown). In the three structures, the C$_{10}$, C$_{12}$, and C$_{14}$ tails take similar paths, until carbon 6, where C$_{10}$ and C$_{14}$ diverge from the path taken by the C$_{12}$ tail in the original structure. Remarkably, this departure in tail path

enables both the shorter and longer tails to occupy a similar hydrodynamic volume as the tail on 3OC$_{12}$HSL (Fig EV3B). The volume constraint is likely established by hydrophobic interactions with residues G38, L40, A50, I52, A70, V76, L125, and A127 (Fig 6B, displayed in pink). These same residues are also responsible for stabilizing 3OC$_{10}$HSL in the ligand binding pocket. However, because the C$_{10}$ tail is two carbons shorter than that of the native ligand, the terminal carbons in 3OC$_{10}$HSL have higher intrinsic flexibility at the ligand-protein interface. The measured B-factors suggest increased flexibility stems from less stable hydrophobic interactions (Fig 6C).

We next investigated whether there were any structural rearrangements in the crystals that could account for the expanded HSL binding capabilities of LasR L130F compared to wildtype LasR. An ~2 Å shift occurs in the loop corresponding to residues 40-52 (highlighted by asterisks in Fig 6A) in the LasR LBD L130F:3OC$_{14}$HSL structure compared to the LasR LBD L130F protein complexed with 3OC$_{10}$HSL and the wildtype LasR LBD complexed with 3OC$_{12}$HSL (Fig 6A and 6C). This loop corresponds to a region with above average B-factor, as depicted by magenta coloring in Figure 6C. The alteration in the positioning of the loop indicates that it could be important for accommodating different HSLs. To test this possibility, we mutated LasR residue Y47 in this loop. We chose Y47 because it is the residue that shifts the most among the different structures. LasR Y47S and LasR Y47R displayed decreased sensitivity to both 3OC$_{12}$HSL and 3OC$_{14}$HSL in the *E. coli* reporter assay (Fig EV4) suggesting that the loop provides interactions with the ligand tails that foster increased protein stability, allowing LasR to be activated.

To understand the structural basis underlying specificity and promiscuity in this family of proteins, we compared the structures of SdiA LBD:3OC$_8$HSL, CviR LBD:C$_6$HSL, and TraR LBD:3OC$_8$HSL to LasR LBD L130F:3OC$_{14}$HSL (Fig 7A). We chose these particular structures because the receptors display a range of ligand selection preferences – from strict to promiscuous. Similar to what we show here for LasR, SdiA is promiscuous with respect to ligand selectivity (Michael et al., 2001, Nguyen et al., 2015, Sitnikov et al., 1996). Conversely, CviR and TraR display strict specificity for their native autoinducers (Chen et al., 2011, Vannini et al., 2002, Zhang et al., 2002, Zhu & Winans, 2001). In terms of overall tertiary structure, a loop similar to the one we pinpoint in Figure 6A as critical for LasR to accommodate different ligands, exists in the SdiA LBD (Fig 7A). No such loop exists in the CviR and TraR LBD structures (Fig 7A). This result is consistent with the idea that this flexible loop confers ligand promiscuity.

In addition to the differences in the overall structures of the receptors, we noted different conformations for the acyl chains in the LasR LBD structures compared to those in the other LuxR-type receptors. The autoinducer acyl chains in the CviR, TraR, and SdiA LBD structures have similar conformations within the ligand binding pockets terminating between residues Y88 and M89 for CviR, Y61 and F62 for TraR, and Y71 and Q72 for SdiA. By contrast, the acyl chains of the different ligands in the LasR LBD L130F structures orient their terminal carbons toward the opposing face of the ligand binding pocket (Fig 7B). These different paths appear to be driven by the hydrophobic interactions we described above for the different LasR ligands (Fig 6B). We identified eight hydrophobic residues (G38, L40, A50, I52, A70, V76, L126, and A127) that dictate the

shape of the ligand binding pocket in LasR. Indeed, these residues have generally hydrophobic characteristics in all LuxR-type proteins, but the size of each sidechain varies (Fig 7B). For example, A127 in LasR corresponds to F132 in SdiA. The smaller residue in LasR accommodates the altered path taken by its autoinducer, allowing the terminal carbon of the acyl chain to bind proximal to residue A127. A bulkier residue at this position, as in SdiA, sterically hinders this path for the ligand, forcing the acyl chain to bend in the opposite direction. Thus, in SdiA, F132 forces the terminal carbon of $3OC_8HSL$ to bind distally. Indeed, the I153 residue in CviR and the M127 residue in TraR appear to perform roles analogous to F132 in SdiA in dictating the distal orientations of their ligands.

Our crystal structures suggest that LasR G38 could also be important for allowing HSL tails to adopt a conformation different from those in SdiA, TraR, and CviR and, in so doing, possibly affect LasR ligand selection (Fig 7B). SdiA, TraR, and CviR all contain larger amino acid sidechains (C45, L45, and A59, respectively) at this position (Fig 7B). LasR G38 lies proximal to carbons 9 and 10 in the acyl chains of all the ligands in all the LasR LBD structures. Presumably, a bulkier side chain would sterically hinder the preferred tail paths for $3OC_{12}HSL$ or $3OC_{14}HSL$, but might enhance the binding of short chain HSLs, such as $3OC_6HSL$, due to increased hydrophobic interactions. To test this prediction, we mutated G38 in LasR to bulkier amino acids: leucine, isoleucine, and alanine. We tested these alleles in our *E. coli* p*lasB-lux* reporter in response to both a short ($3OC_6HSL$) and a long ($3OC_{12}HSL$) chain HSL (Fig 7C). LasR G38I produced low p*lasB-lux* activity with both molecules suggesting that isoleucine is too bulky to

accommodate any HSL well. Consistent with this interpretation, the EC_{50} values for LasR G38I were 498 nM for $3OC_{12}HSL$ and ~66 μM for $3OC_6HSL$. By contrast, LasR G38A and LasR G38L fully activated the reporter in response to both test ligands (Fig 7C). The EC_{50} values for wildtype LasR, LasR L130F, LasR G38A, and LasR G38L were equivalent for $3OC_{12}HSL$ (2.8 nM, 2.0 nM, 2.3 nM, and 2.1 nM, respectively, Fig 7C, top panel). However, the EC_{50} values for LasR G38A and LasR G38L were lower (1.3 μM and 1.6 μM, respectively) than that of wildtype LasR (2.4 μM) for $3OC_6HSL$ (Fig 7C, bottom panel). These values are comparable to that of LasR L130F for $3OC_6HSL$ (1.4 μM, Fig 7C, bottom panel). Given that we have established that LasR L130F is more stable than wildtype LasR, irrespective of ligand chain length, we suggest that the findings in Figure 7 support the hypothesis that larger amino acid residues at G38 improve the LasR affinity for shorter chain HSLs by forming more stable protein-ligand complexes.

Discussion

P. aeruginosa can live in environments in which it encounters other bacterial species that produce HSL autoinducers (Tashiro et al., 2013). Our results show that LasR can, with reduced affinity, detect non-native HSLs and in response, activate transcription of quorum-sensing target genes. We suggest that determining the mechanisms that promote or restrict ligand access to LasR is important for understanding how the *P. aeruginosa* quorum-sensing response could be naturally or synthetically manipulated. Here, we identified mutations that alter the selectivity and sensitivity of LasR. We found

that LasR L130F improves LasR sensitivity, but at the cost of decreased selectivity. In contrast, we find that alterations at LasR S129 can increase selectivity for autoinducer recognition but, that feature is offset by a reduction in sensitivity. Our findings suggest that LasR balances ligand sensitivity with selectivity. The LasR S129 mutants show that decreasing the LasR sensitivity to ligands dampens and delays the quorum-sensing response (Fig 3B and 5). We presume that inadequate activation decreases the potency of *P. aeruginosa* virulence. By contrast, the more sensitive LasR L130F allele causes higher and premature activation of quorum sensing (Fig 3D and 5). In this case, the release of expensive public goods before the population is at a sufficient cell density to optimally use those goods could promote cheating. LasR L130F may also negatively influence virulence at high autoinducer concentration by stimulating overproduction of RsaL (Fig 5D).

We investigated the published sequences of hundreds of clinical isolates of *P. aeruginosa* and we did not find any strain that possessed a mutation at either S129 or L130 (Feltner et al., 2016). We conclude that it is detrimental for LasR to become either more sensitive to or less selective for ligands. Perhaps, striking the ideal balance between selectivity and sensitivity in LasR means that detection of some non-native HSLs must be tolerated, although, importantly, only at higher concentrations relative to the native autoinducer.

We propose that LasR promiscuity could serve an important function in the environment (i.e., soil) and in eukaryotic hosts where *P. aeruginosa* encounters other species of bacteria. We suggest that LasR detection of non-native HSLs enables it to

“eavesdrop” on its competitors. However, our finding that 3OC$_{12}$HSL is the most potent agonist indicates that *P. aeruginosa* prioritizes detecting its own autoinducer over those of other species. Amongst our set of test compounds, 3OC$_{14}$HSL is the second best LasR agonist and it is also highly potent, indicating that the LasR receptor has not optimized against detection of longer chain HSLs. Possibly, *P. aeruginosa* readily interacts with 3OC$_{14}$HSL-producing bacteria. Alternatively, *P. aeruginosa* might not encounter 3OC$_{14}$HSL in its natural surroundings as, presently, scant evidence exists for natural production of 3OC$_{14}$HSL by bacteria. There are two preliminary reports of soil-dwelling nitrogen-fixing bacteria that are capable of making 3OC$_{14}$HSL, 3OHC$_{14}$HSL and/or C$_{14}$HSL (Gao et al., 2014, Mellbye et al., 2017), but if, when, and how much they do remains mysterious. Specifically, mass spectrometry and bioassay show that *Nitrosospira briensis* produces 3OHC$_{14}$HSL, but only at concentrations of 1 nM (Mellbye et al., 2017), too low for detection by wildtype LasR. Second, *Nitrospira multiformis* has a LuxI-type synthase (NmuI) that produces 3OC$_{14}$HSL and C$_{14}$HSL in recombinant *E. coli*. However, neither of these molecules solubilized the putative receptor, NmuR, and no conditions were identified under which *Nitrospira multiformis* produced the molecules (Gao et al., 2014). Future study will be necessary to determine the prevalence of HSLs longer than C$_{12}$ in nature and whether *P. aeruginosa* encounters such molecules.

With the one exception of 3OC$_{14}$HSL, wildtype LasR detects 3OC$_{12}$HSL far more efficiently than other HSLs. Therefore, it is likely that, in mixed-species consortia, 3OC$_{12}$HSL out-competes all other autoinducers. This finding suggests that while LasR is capable of detecting non-cognate autoinducers, it does not do so when *P. aeruginosa* is

the majority species. However, we propose that there could exist conditions under which low-affinity "eavesdropping" would benefit *P. aeruginosa.* First, when *P. aeruginosa* is at low cell density, provision of non-cognate ligands made by other bacterial species that are at higher cell density could induce *P. aeruginosa* to activate its quorum-sensing behaviors prematurely relative to when it is at low cell density in mono-species culture. If so, *P. aeruginosa* could synthesize toxic defensive products such as pyocyanin and rhamnolipids that endow it with an advantage over competing species (Baron & Rowe, 1981, Smalley et al., 2015). Beyond defensive products, perhaps some of the quorum-sensing-controlled products produced under such conditions can be used exclusively by *P. aeruginosa* and not by competing species. If so, LasR promiscuity could grant *P. aeruginosa* a "last ditch" opportunity to survive in environments in which it is vastly outnumbered by competing species.

Our combined genetic, biochemical, and structural work revealed the molecular basis for non-native autoinducer recognition by LasR. There exists a key flexible loop that, if present (LasR, SdiA), endows particular LuxR-type receptors with the ability to bind to multiple HSL ligands, but if absent (TraR, CviR), the LuxR-type receptor is highly specific for a particular HSL ligand. Indeed, this structure-function analysis could explain why a competitive inhibitor of CviR, chlorolactone (CL), behaves as an agonist in *P. aeruginosa* (O'Loughlin et al., 2013). These findings are particularly enlightening when considering attempts to design inhibitors that specifically target different LuxR-type receptors. The flexible loop and hydrophobic residues in LasR near the acyl chain binding site that we pinpoint here will need to be taken into account when developing small

molecule inhibitors that target LasR or other LuxR-type proteins that possess this feature. Designing molecules that target the flexibility of the loop region and/or that destabilize the protein could be explored for promiscuous receptors, such as LasR. By contrast, targeted screening around molecules that resemble CL could yield inhibitors for LuxR-type proteins that display strict specificity for their cognate autoinducers, such as CviR.

Materials and Methods

Site directed mutagenesis:

Mutations in *lasR* were constructed on the pBAD-A-*lasR* plasmid (Paczkowski et al., 2017). Primers were designed using the Agilent Quikchange primer design tool and PCR with pFUltra polymerase (Agilent). PCR reactions were treated with DpnI to eliminate parental plasmid DNA and the plasmids with the mutant *lasR* genes were transformed into One Shot TOP10 chemically competent *E. coli* cells (Invitrogen). Reactions were plated on LB agar plates containing ampicillin (50 μg/mL) and individual mutants were verified via sequencing with primers for the *lasR* gene (ARM203 and ARM204). Primers and strains used in this work are listed in Table A2 and Table A3, respectively.

P. aeruginosa strain construction:

In-frame, marker-less *lasR* mutations were engineered onto the chromosome of *P. aeruginosa* PA14 using pEXG2-suicide constructs with gentamicin selection and *sacB*

counter selection (Borlee et al., 2010, Kukavica-Ibrulj et al., 2008). The *lasR* gene and 500 bp of flanking regions were cloned into pUCP18 (Schweizer, 1991). Site directed mutagenesis was performed as described above to construct point mutations in plasmid-borne *lasR*. The DNA carrying the mutant *lasR* genes was obtained from pUCP18 by restriction enzyme digestion with BamHI and EcoRI (NEB), and subsequently, the fragments were ligated into pEXG2. The recombinant pEXG2 plasmids were transformed into *E. coli* SM10λ*pir* and, from there, the plasmids were mobilized into *P. aeruginosa* PA14 via biparental mating (Mukherjee et al., 2017, Simon et al., 1983). Exconjugants were selected on LB plates containing 30 μg/mL gentamicin and 100 μg/mL irgasan after overnight growth at 37° C. After recovery, 5% sucrose was used to select for loss of the plasmid. Candidate mutants were patched onto LB plates and LB plates containing 30 μg/mL gentamicin to select against the resistance marker. Colony PCR was performed on gentamicin sensitive patches with primers that annealed 500 bp [base pairs] upstream and downstream of *lasR* (ARM455 and ARM456). These PCR products were sequenced with *lasR* forward and reverse primers (ARM203 and ARM204).

<u>*E. coli* p*lasB-lux* reporter assay for LasR activity</u>:

The development of an assay that reports on LasR activity in response to exogenous ligands using luciferase as the readout has been described previously (Paczkowski et al., 2017). In brief, 2 μL of overnight cultures containing p*lasB-luxCDABE* and pBAD-A with either wildtype *lasR* or mutant *lasR* alleles were back diluted into 200 μL LB medium and placed into clear-bottom 96-well plates (Corning). The plates were shaken at 30° C for 4

h and 0.1% arabinose was added to each well along with a test HSL at the concentrations designated in the text and figures. To perform dose response analyses, 1 mM of each HSL was serially diluted 3-fold 10 times, and 2 μL of each dilution was added to the wells. Higher or lower HSL concentrations were assayed when EC_{50} values did not fall into this range. Plates were shaken at 30° C for 4 h. Bioluminescence and OD_{600} were measured using a Perkin Elmer Envision Multimode plate reader. Relative light units were calculated by dividing the bioluminescence measurement by the OD_{600} nm measurement. Non-linear regression was performed in Graphpad Prism6 to obtain EC_{50} values.

Elastase Assay:

The *P. aeruginosa* PA14 Δ*lasI* strains carrying either wildtype or mutant *lasR* genes were grown overnight with shaking at 37° C in LB medium. Cultures were back diluted 1:50 in 3 mL of LB and grown for an additional 8 h with shaking at 37° C. Strains were back diluted 1:1000 into 3 mL of LB medium and test HSLs or an equivalent volume of DMSO were added to each culture. These cultures were grown overnight at 37° C with shaking. 1 mL of each culture was removed and the cells were pelleted by centrifugation at 16,100 x g. The supernatant was removed and filtered through a .22 μm filter (Millipore) and 100 μL of supernatant was added to 900 μL of 10 mM Na_2HPO_4 containing 10 mg of elastin-Congo red substrate (Sigma-Aldrich). These preparations were incubated at 37° C for 2 h. The mixtures were subjected to centrifugation at 16,100 x g for 10 min. The resulting supernatants were removed and OD_{495} nm measured with a Beckman Coulter DU730 spectrophotometer against a blank of H_2O.

Thermal shift assay:

Thermal shift analyses of 6xHis-LasR LBD and 6xHisLasR L130F LBD bound to HSLs were performed as previously described (Paczkowski et al., 2017). In short, ligand-bound protein was diluted to 5 μM in reaction buffer (20 mM Tris-HCL pH 8, 200 mM NaCl, and 1 mM DTT [dithiothreitol]) containing DMSO or 10 μM HSL test compound in 18 μL total volume. The mixtures were incubated at room temperature for 15 min. 5000x SYPRO Orange (Thermo-Fisher) in DMSO was diluted to 200x in reaction buffer and used at 20x final concentration. 2 μL of 200x SYPRO Orange was added to the 18 μL sample immediately prior to analysis. Samples were subjected to a linear heat gradient of 0.05 ^{o}C/s, from 25 ^{o}C to 99 ^{o}C in a Quant Studio 6 Flex System (Applied Biosystems) using the melting curve setting. Fluorescence was measured using the ROX reporter setting.

Pyocyanin Time Course:

Overnight cultures of the *P. aeruginosa* Δ*lasI*, Δ*lasI lasR S129F*, Δ*lasI lasR L130F*, and Δ*lasI* Δ*rsaL* strains were grown in LB medium with shaking at 37° C. 1.5 mL of each culture was diluted into 50 mL of fresh LB medium. HSLs were added at the concentrations described in the text and figures and the cultures were shaken at 37° C for an additional 3 h. From there forward, 1 mL aliquots were removed every 30 min for 300 min and cell density (OD_{600} nm) was measured immediately using a Beckman Coulter DU730 Spectrophotometer. The aliquots were subjected to centrifugation at 16,100 x g for 2 min and the clarified supernatants were removed. The OD_{695} nm of the supernatants

were measured. Pyocyanin activity was determined by plotting the OD_{695} nm/OD_{600} nm over time for each strain.

Protein production, purification, and crystallography:

Recombinant 6xHis-LasR LBD and 6xHis-LasR LBD L130F proteins bound to $3OC_8HSL$, $3OC_{10}HSL$, $3OC_{12}HSL$, or $3OC_{14}HSL$ were purified as previously described for LasR LBD:$3OC_{12}HSL$ using Ni-NTA affinity columns followed by size exclusion chromatography (Paczkowski et al., 2017). 6xHis-LasR LBD bound to $3OC_{10}HSL$ and 6xHis-LasR LBD bound to $3OC_{14}HSL$ were crystallized by the hanging drop diffusion method. Diffraction data were processed using the HKL-3000 software package (Minor et al., 2006). The structures were solved using Phaser in Phenix (Adams et al., 2011, Afonine et al., 2012) by molecular replacement, with the structure of LasR LBD:$3OC_{12}HSL$ used as the search model (Bottomley et al., 2007). Model building was performed using Coot (Emsley & Cowtan, 2004, Emsley et al., 2010) and further refinement was accomplished using Phenix (Adams et al., 2011). Images of the structures were generated with PyMOL (DeLano, 2009). When we describe specific amino acid or amino acid-ligand interactions, we provide the image for the best resolved example in the asymmetric unit.

Protein solubility assay:

E. coli BL21 DE3 (Invitrogen) containing plasmid-borne 6xHis-LasR LBD or 6xHis-LasR LBD L130F were grown overnight and back diluted 1:500 in 20 mL of LB medium

containing ampicillin (100 μg/mL). Cultures were grown to OD_{600} of 0.5 and protein production was induced with 1 mM IPTG [Isopropyl β-D-1-thiogalactopyranoside]. Upon addition of IPTG, the desired test HSL was also added at a final concentration of 10 μM, and the cultures were incubated at 25 ^{o}C with shaking for 4 h. Cells were harvested at 3,000 x g and resuspended in lysis buffer (500 mM NaCl, 20 mM Tris-HCL pH 8, 20 mM imidazole, 5% glycerol, 1 mM EDTA, and 1 mM DTT). The cells were lysed using sonication (1 s pulses for 15 s with a 50% duty cycle). The fraction we call the whole cell lysate was harvested after sonication. The soluble fraction was isolated by centrifugation at 32,000 x g. Samples were subjected to electrophoresis on SDS-PAGE gels (Biorad) and imaged with an Image Quant LAS4000 gel dock using the trans-illumination setting (GE Healthcare).

Statistical Methods:

In all experiments, all values are the average of 3 biological replicates. Error bars represent standard deviations of the means. 2-tailed T-tests were performed to compare experimental groups. P values: *<.05, **<.01, ***<.0001

Accession Number

The coordinates and structure factors will be deposited in the Protein Data Bank upon acceptance of the manuscript.

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Author Contributions

A.R.M. performed the experiments and interpreted the data in Figures 1, 3, 5, 7, EV2, EV4 and Tables 1 and EV1. J.E.P. performed the experiments and interpreted the data in Figures 2, 4, 6, 7, EV1, and EV3. B.R.H designed the synthesis for all the homoserine lactones used. B.L.B., A.R.M., and J.E.P conceived of the study. B.L.B coordinated the study and helped with interpretation of results. All of the authors contributed to the writing of the manuscript.

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Figure Legends

Figure 1. *LasR is activated by multiple homoserine lactone autoinducers.* A) LasR-dependent bioluminescence was measured in *E. coli*. Arabinose-inducible LasR was produced from one plasmid and the p*lasB-lux* reporter construct was carried on a second plasmid. 0.1% arabinose was used for LasR induction. B) Elastase activity was measured from Δ*lasI P. aeruginosa* using elastin-Congo red as the substrate. In A and B, 100 nM of the designated HSLs were tested. Each bar represents the average of 3 biological replicates. Error bars denote standard deviations of the mean. Paired 2-tailed t-tests were performed comparing each compound to the DMSO control. P-values: * <.05, ** <.01, *** <.0001. In panels A and B, we have separated the DMSO control and the results with the cognate autoinducer $3OC_{12}HSL$ by the dotted vertical line. C) Comparison of LasR LBD protein levels in whole cell lysates (WCL) and in the soluble fractions (S) of *E. coli* cells that harbor the DNA encoding the LasR LBD on a plasmid. 1 mM IPTG was used for

LasR LBD induction and either 1% DMSO or 10 μM of the indicated HSL was supplied. In all lanes, protein from .05 OD of cells was loaded. Results are representative of 3 trials.

Figure 2. *LasR is stable when bound to long chain HSLs.* Thermal shift analyses of purified LasR LBD bound to $3OC_{10}HSL$ (top), $3OC_{12}HSL$ (middle), and $3OC_{14}HSL$ (bottom) without (designated DMSO) and following supplementation with an additional 10 μM of the indicated HSLs. Each line represents the average of 3 replicates.

Figure 3. *LasR S129F and LasR L130F alter LasR sensitivity to HSL autoinducers*. A) Wildtype LasR and LasR S129F-driven bioluminescence from the *E. coli* p*lasB-lux* reporter (see Fig 1, panel A for detail). B) Wildtype LasR and LasR S129F-driven elastase activity in Δ*lasI P. aeruginosa* (see Fig 1, panel B for detail). In A and B, 10 μM of the indicated HSLs were provided. C and D) As in panels A and B, respectively, with wildtype LasR and LasR L130F and 50 nM of the indicated HSLs. Black bars, wildtype LasR; white bars, LasR S129F; gray bars, LasR L130F. The average of 3 biological replicates are shown. Error bars denote standard deviations of the mean. Unpaired 2-tailed T-tests were performed comparing WT LasR to the mutant LasR for each compound. p-values: * < .05, *** <.001. In all panels, we have separated the DMSO control and the results with the cognate autoinducer $3OC_{12}HSL$ by the dotted vertical line.

Figure 4. *The LasR LBD L130F is more stable than the wildtype LasR LBD.* A) Thermal shift analyses of purified LasR LBD (solid lines) and LasR LBD L130F (dotted lines) bound

to $3OC_{12}HSL$ (orange) or $3OC_{14}HSL$ (green). Each line represents the average of 3 replicates. B) Thermal shift analyses of purified LasR LBD L130F bound to $3OC_8HSL$ (top left), $3OC_{10}HSL$ (bottom left), $3OC_{12}HSL$ (top right), and $3OC_{14}HSL$ (bottom right) without (designated DMSO) and following supplementation with an additional 10 μM of the indicated HSLs. C) Comparison of LasR L130F levels in the whole cell lysates (WCL) and the soluble fractions (S) of *E. coli* cells harboring the DNA encoding LasR LBD L130F on a plasmid (see Fig 1, panel C for details). Either 1% DMSO or 10 μM of the indicated HSL molecule was added.

Figure 5. *Wildtype LasR, LasR S129F, and LasR L130F display distinct pyocyanin production phenotypes in response to different HSL autoinducers.* Pyocyanin production was measured spectophotometrically in Δ*lasI P. aeruginosa* over the growth curve. Y-axis "Pyocyanin" is the amount of pyocyanin pigment (OD_{695} nm) over cell density (OD_{600} nm). Designations are: red, DMSO control; blue, wildtype LasR; purple, LasR L130F; green, LasR S129F. Data show the mean of 3 biological replicates. Error bars denote standard deviations of the mean. Concentrations and ligands used are: A) 50 nM $3OC_{12}HSL$, B) 1 μM $3OC_{12}HSL$, C) 100 nM $3OC_{14}HSL$, D) 10 μM $3OC_{14}HSL$, E) 10 μM $3OC_8HSL$, and F) 100 μM $3OC_8HSL$

Figure 6. *Crystal structures of LasR LBD L130F bound to $3OC_{10}HSL$ and $3OC_{14}HSL$.* A) Crystal structures of LasR LBD L130F:$3OC_{10}HSL$ (gold) and LasR LBD L130F:$3OC_{14}HSL$ (magenta) compared to the wildtype LasR LBD:$3OC_{12}HSL$ structure (blue, modified from

Bottomley et al. 2007, PBD: 2UVO). The bottom images show 90-degree rotations of the crystal structures relative to the images above. In the top right-most 2 structures, the asterisks highlight the LasR loop region that includes residues 40-52 and that undergoes a conformational shift when 3OC$_{14}$HSL is bound. B) LasR LBD L130F:3OC$_{14}$HSL crystal structure (protein: magenta, ligand: green). Amino acids drawn in stick format show important residues for lactone head binding (Y56, W60, K61, D73, T75, W88, Y93, S129, and S131, all colored in brown) and acyl tail binding (G38, L40, A50, I52, A70, V76, L125, and A127, all colored in pink). C) Comparison of the average B-factors for LasR LBD L130F bound to 3OC$_{10}$HSL and bound to 3OC$_{14}$HSL. The structures are colored from gold to magenta with gold representing the lowest average B-factor and magenta representing the highest average B-factor.

Figure 7. *A conserved flexible loop region confers promiscuity to LuxR-type receptors.* A) Top images: structural comparison of the LuxR-type receptors LasR LBD L130F:3OC$_{14}$HSL (magenta) and SdiA LBD:3OC$_{8}$HSL (green, modified from Nguyen et al., 2015, PDB: AY17) that exhibit promiscuity with respect to ligand binding. Bottom images: structural comparison of the LuxR-type receptors CviR LBD:C$_{6}$HSL (pink, modified from Chen et al., 2011, PDB: 3QP1) and TraR LBD:3OC$_{8}$HSL (silver, modified from Zhang et al., 2002, PDB: 1L3L) that display strict ligand specificity. B) Structural comparison of the protein:ligand interfaces for LasR LBD L130F:3OC$_{14}$HSL (top left, magenta), SdiA LBD:3OC$_{8}$HSL (top right, green), CviR LBD:C$_{6}$HSL (bottom left, pink), and TraR LBD:3OC$_{8}$HSL (bottom right, silver). Residues that make important

hydrophobic sidechain interactions in each protein:ligand complex are shown in stick format and named. C) Dose response curves from the *E. coli* p*lasB-lux* reporter assay (see Fig 1, panel A) were used to determine EC_{50} values for $3OC_{12}HSL$ (top panel) and $3OC_6HSL$ (bottom panel) for wildtype LasR (blue), LasR G38A (dark red), LasR G38I (orange), LasR G38L (dark green), and LasR L130F (magenta). Data represent the mean of 3 biological replicates. Error bars denote standard deviations of the mean.

Table 1. EC_{50} (nM) values for LasR and HSL compounds in the *plasB-lux* assay

LasR Allele

	WT	S129C	S129W	S129F	S129T	S129M	L130F
$3OC_{12}HSL$	2.8	5.9	77	177	870	6570	2.0
$3OC_{14}HSL$	5.6	11.8	9.8	41.2	4070	NR	5.3
$3OC_{10}HSL$	8.0	31.5	1300	5540	4510	NR	5.4
$3OC_{8}HSL$	885	2860	2290	NR	NR	NR	80.7
$3OC_{6}HSL$	2360	4660	NR	55500	71700	NR	1390

NR denotes non-responsive

Expanded View Figure Legends

Figure EV1. *Long acyl chain HSLs solubilize the LasR LBD and the LasR LBD L130F.* Comparison of wildtype LasR LBD protein levels in whole cell lysates (WCL) and in the soluble fractions (S) of *E. coli* cells harboring the DNA encoding the LasR LBD on a plasmid. B) As in panel A with LasR LBD L130F. In both panels, 1 mM IPTG was used for LasR induction and either 1% DMSO or 10 μM of the indicated HSL was added. See Figure 1, panel C of the main text for details.

Figure EV2. *RsaL is required for inhibition of pyocyanin production by high HSL concentrations in P. aeruginosa.* Pyocyanin production was measured

spectophotometrically from *P. aeruginosa* Δ*lasI* and Δ*lasI* Δ*rsaL* strains over the growth curve following addition of DMSO, 1 μM $3OC_{12}HSL$, or 100 μM $3OC_{12}HSL$ as indicated. Y-axis "Pyocyanin" is the amount of pyocyanin pigment (OD_{695} nm) over cell density (OD_{600} nm). Data show the mean of 3 biological replicates. Error bars denote standard deviations of the mean.

Figure EV3. *Electron density for LasR LBD L130F near residue F130 and the $3OC_{14}HSL$ ligand.* A) A simulated annealing omit map, contoured at 1σ, shows the electron density around LasR residue F130 and the surrounding hydrophobic residues. F130 interacts with L23, L30, F32, I35, L114, L118, L128, L151, and L154 in the LasR LBD L130F:$3OC_{14}HSL$ structure. The panel depicts the perspective highlighting the F130 interactions with L23, F32, I35, L128, and L154, and these residues are labeled. B) A simulated annealing omit map, contoured at 1σ, shows the electron density around the HSLs in the LasR LBD bound to $3OC_{10}HSL$ (green), $3OC_{14}HSL$ (red), or $3OC_{12}HSL$ (blue, from data in Bottomley *et al*., 2007).

Figure EV4. *LasR Y47R and LasR Y47S have lower affinities for $3OC_{12}HSL$ and $3OC_{14}HSL$ than wildtype LasR.* Bioluminescence from the p*lasB-lux* reporter driven by wildtype LasR (blue), LasR Y47R (red), and LasR Y47S (green) (See Fig 1, panel A of the main text for details). $3OC_{12}HSL$ (A) or $3OC_{14}HSL$ (B) were added at the designated concentrations. The data show the average of 3 biological replicates. Error bars depict standard deviations of the mean.

Figure 1.

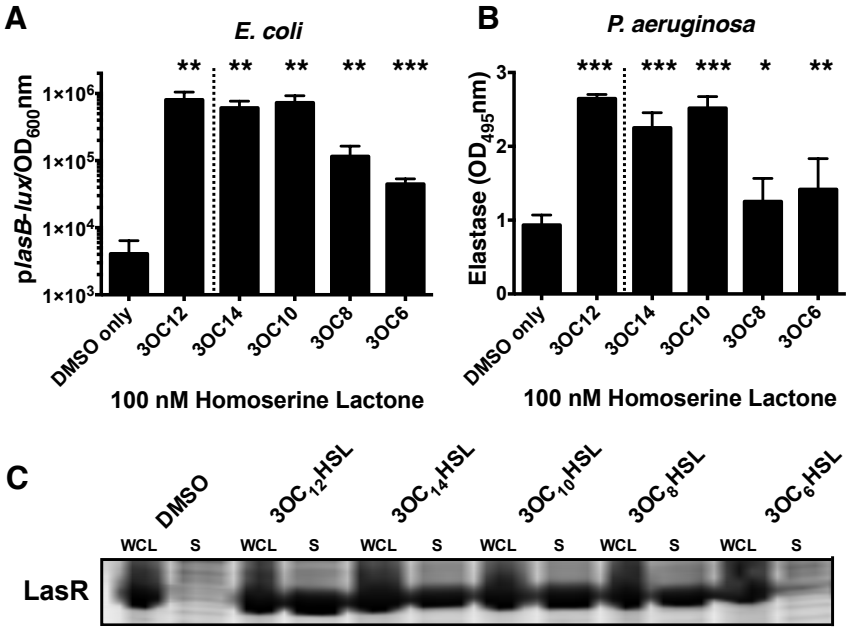

A
E. coli
p*lasB*-*lux*/OD600nm
1×10^6
1×10^5
1×10^4
1×10^3
**
**
**
**
***
DMSO only
3OC12
3OC14
3OC10
3OC8
3OC6
100 nM Homoserine Lactone
B
P. aeruginosa
Elastase (OD495nm)
3
2
1
0
***
***
***
*
**
DMSO only
3OC12
3OC14
3OC10
3OC8
3OC6
100 nM Homoserine Lactone
C
DMSO
3OC12HSL
3OC14HSL
3OC10HSL
3OC8HSL
3OC6HSL
WCL
S
LasR

Figure 2.

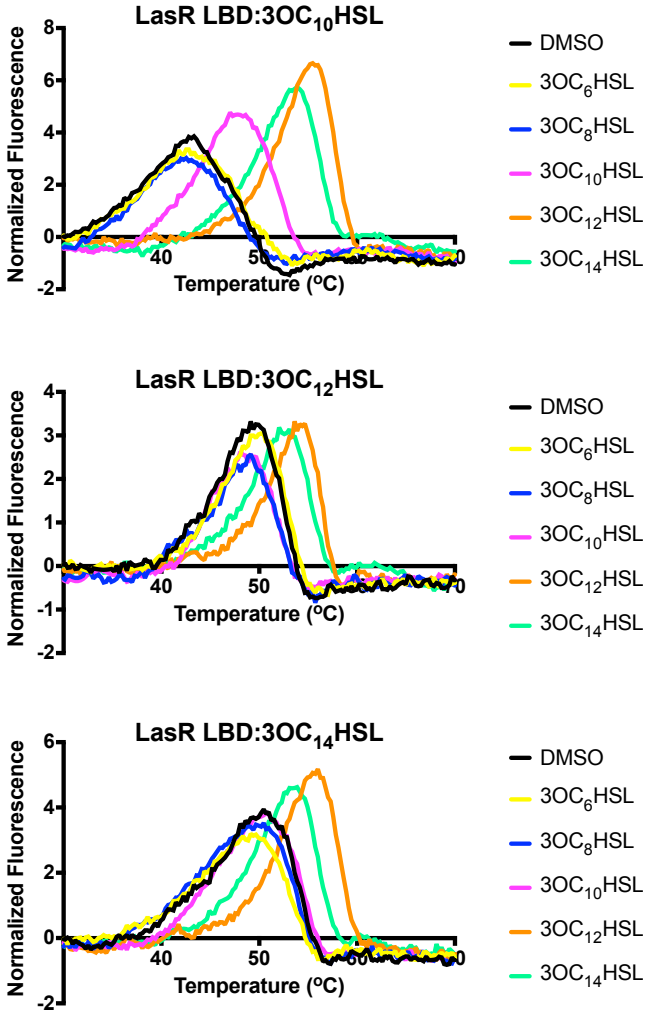

LasR LBD:3OC10HSL
Normalized Fluorescence
Temperature (ºC)
LasR LBD:3OC12HSL
Normalized Fluorescence
Temperature (ºC)
LasR LBD:3OC14HSL
Normalized Fluorescence
Temperature (ºC)
DMSO
3OC6HSL
3OC8HSL
3OC10HSL
3OC12HSL
3OC14HSL

Figure 3.

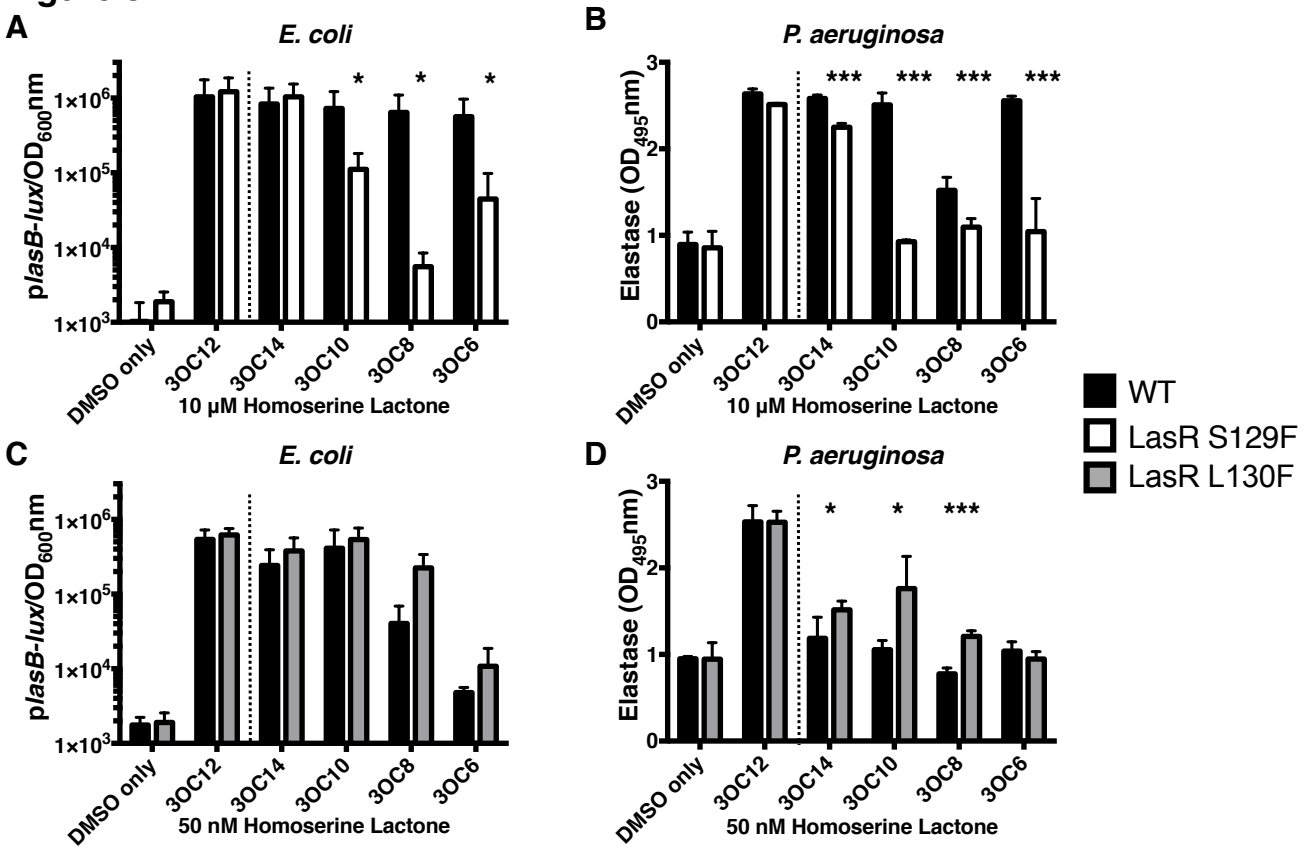

A
E. coli
plasB-lux/OD600nm
1×10^6
1×10^5
1×10^4
1×10^3
*
*
*
DMSO only
3OC12
3OC14
3OC10
3OC8
3OC6
10 μM Homoserine Lactone
B
P. aeruginosa
Elastase (OD495nm)
3
2
1
0
***
***
***
***
DMSO only
3OC12
3OC14
3OC10
3OC8
3OC6
10 μM Homoserine Lactone
C
E. coli
plasB-lux/OD600nm
1×10^6
1×10^5
1×10^4
1×10^3
DMSO only
3OC12
3OC14
3OC10
3OC8
3OC6
50 nM Homoserine Lactone
D
P. aeruginosa
Elastase (OD495nm)
3
2
1
0
*
*
***
DMSO only
3OC12
3OC14
3OC10
3OC8
3OC6
50 nM Homoserine Lactone
WT
LasR S129F
LasR L130F

Figure 4

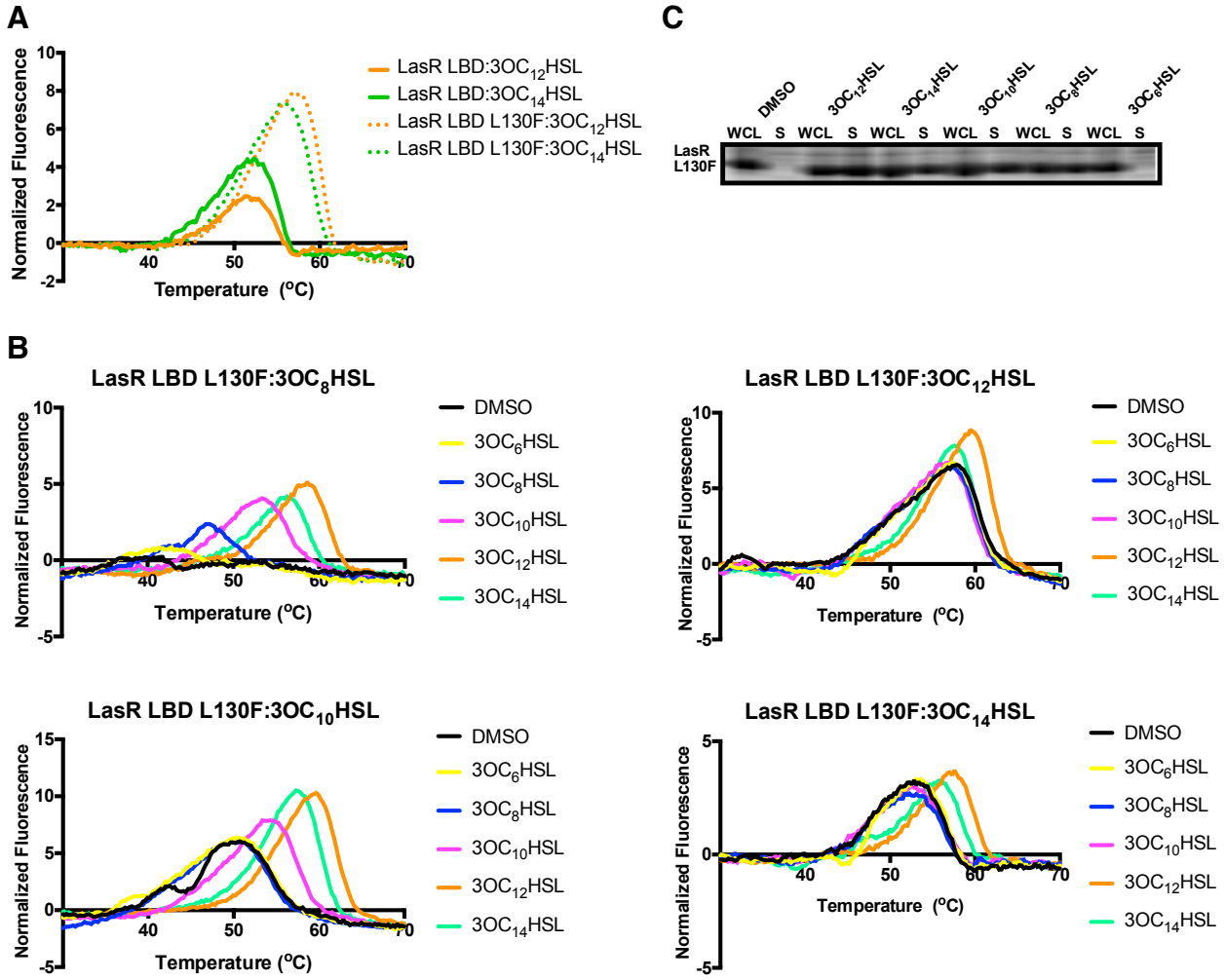

A
Normalized Fluorescence
Temperature (°C)
LasR LBD:3OC12HSL
LasR LBD:3OC14HSL
LasR LBD L130F:3OC12HSL
LasR LBD L130F:3OC14HSL
C
DMSO
3OC12HSL
3OC14HSL
3OC10HSL
3OC8HSL
3OC6HSL
WCL S WCL S WCL S WCL S WCL S WCL S
LasR L130F
B
LasR LBD L130F:3OC8HSL
LasR LBD L130F:3OC12HSL
LasR LBD L130F:3OC10HSL
LasR LBD L130F:3OC14HSL
DMSO
3OC6HSL
3OC8HSL
3OC10HSL
3OC12HSL
3OC14HSL

Figure 5.

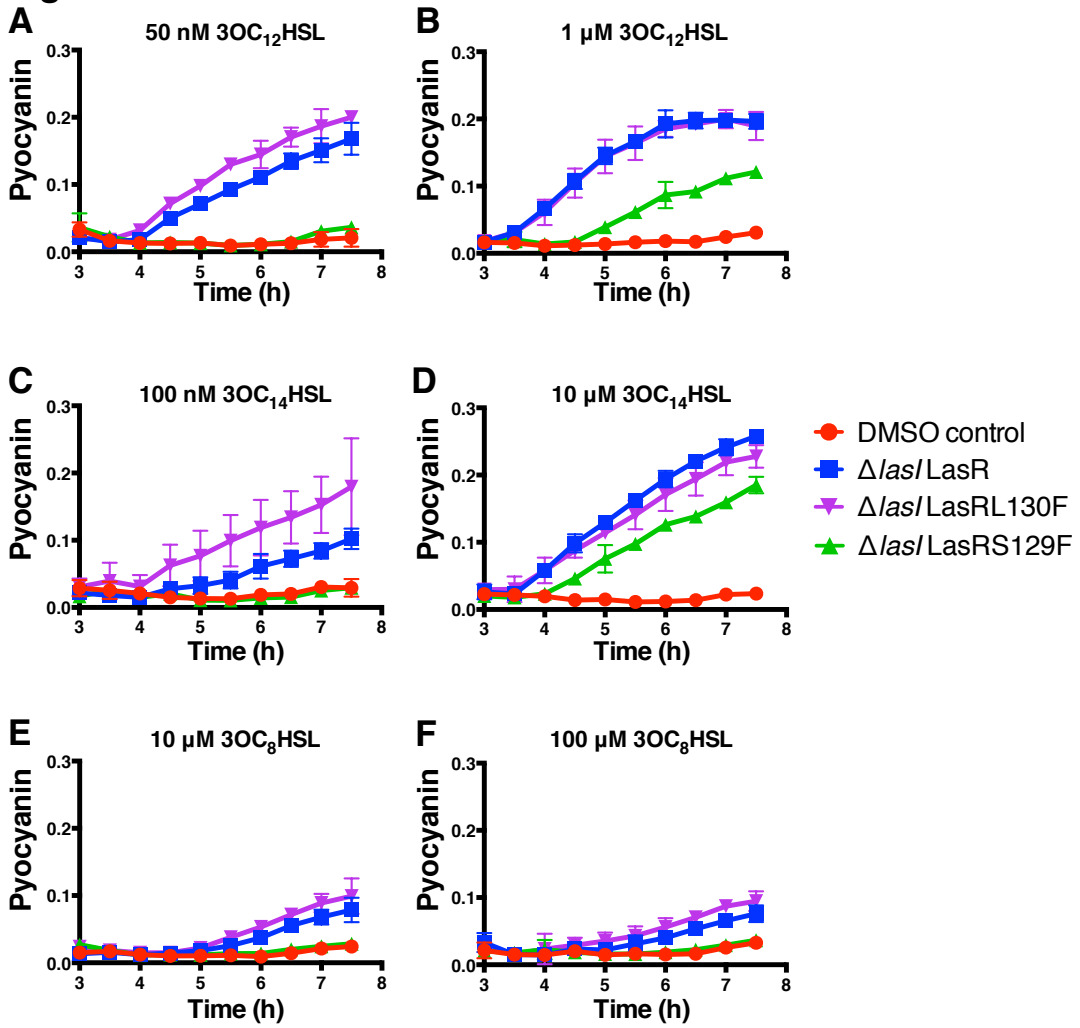

A
50 nM 3OC12HSL
B
1 μM 3OC12HSL
C
100 nM 3OC14HSL
D
10 μM 3OC14HSL
E
10 μM 3OC8HSL
F
100 μM 3OC8HSL
Pyocyanin
Time (h)
0.0
0.1
0.2
0.3
3
4
5
6
7
8
DMSO control
Δ*las*/LasR
Δ*las*/LasRL130F
Δ*las*/LasRS129F

Figure 6.

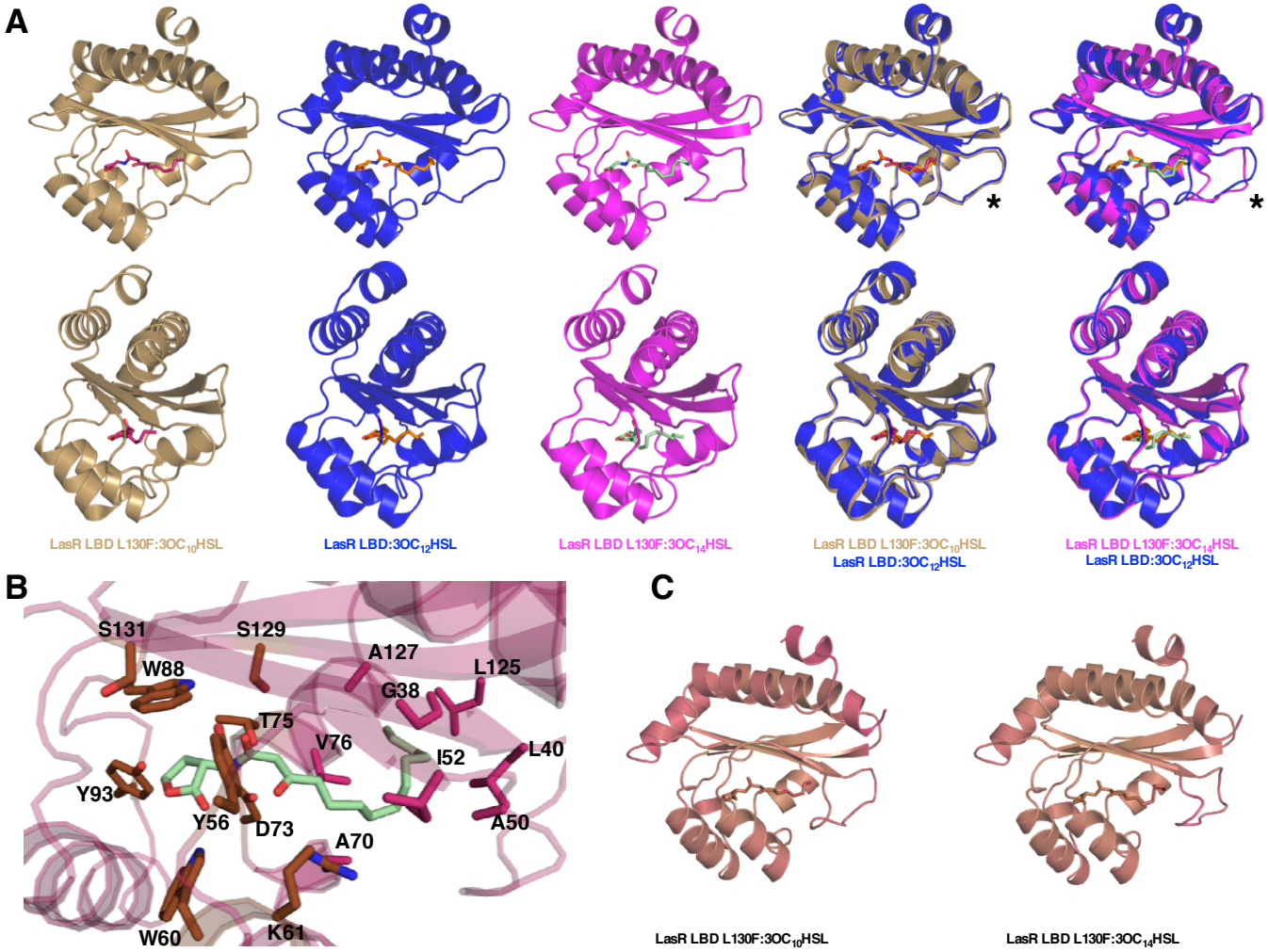
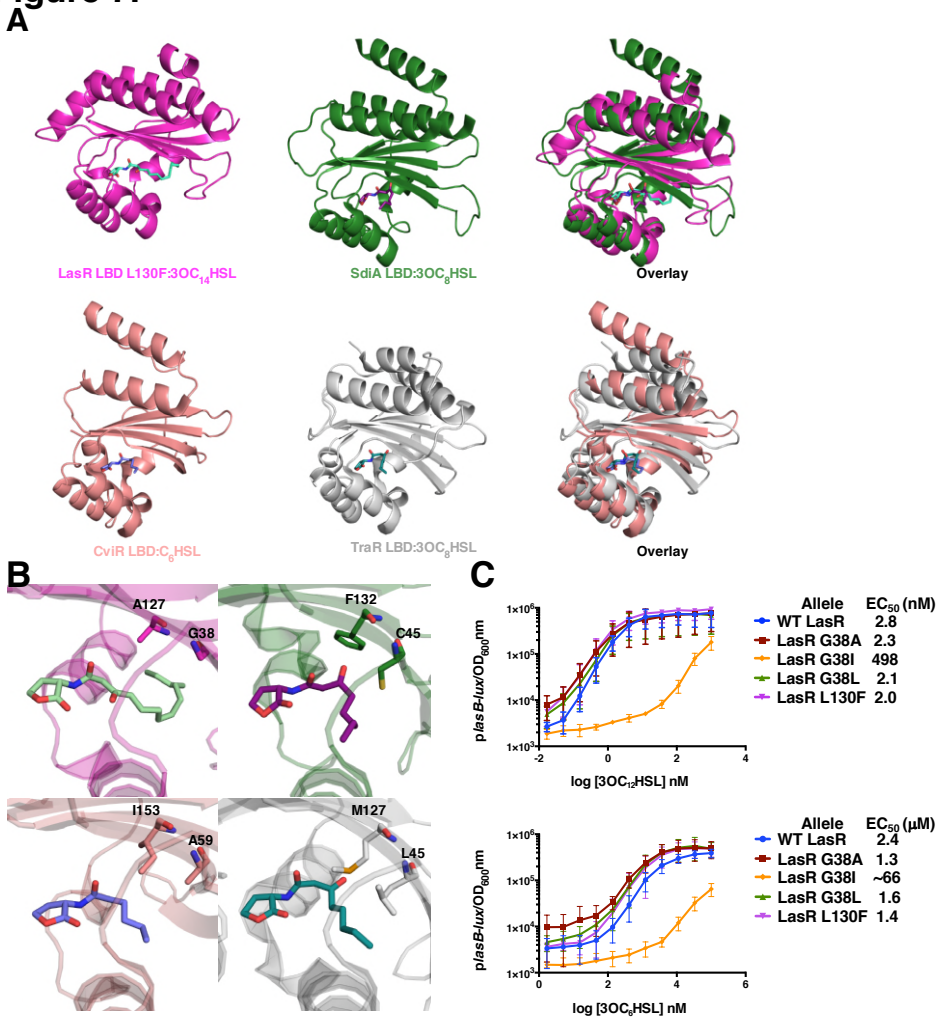

A
*
*
LasR LBD L130F:3OC10HSL
LasR LBD:3OC12HSL
LasR LBD L130F:3OC14HSL
LasR LBD L130F:3OC10HSL
LasR LBD:3OC12HSL
LasR LBD L130F:3OC14HSL
LasR LBD:3OC12HSL
B
S131
S129
W88
A127
L125
G38
T75
V76
I52
L40
Y93
Y56
D73
A50
A70
W60
K61
C
LasR LBD L130F:3OC10HSL
LasR LBD L130F:3OC14HSL

Figure 7.


A
LasR LBD L130F:3OC14HSL
SdiA LBD:3OC8HSL
Overlay
CviR LBD:C6HSL
TraR LBD:3OC8HSL
Overlay
B
A127
G38
F132
C45
I153
A59
M127
L45
C
Allele EC50 (nM)
WT LasR 2.8
LasR G38A 2.3
LasR G38I 498
LasR G38L 2.1
LasR L130F 2.0
pIasB-lux/OD600nm
log [3OC12HSL] nM
Allele EC50 (μM)
WT LasR 2.4
LasR G38A 1.3
LasR G38I ~66
LasR G38L 1.6
LasR L130F 1.4
log [3OC8HSL] nM