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Riboswitch Dynamics and Their Expanding Biotechnological Applications

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Received: 6 June 2025; Revised: 27 June 2025; Accepted: 23 July 2025; Published: 13 August 2025

Abstract: Riboswitches are natural RNA regulatory elements that control gene expression through ligand-induced conformational changes. These dynamic RNA sensors modulate downstream gene activity by influencing transcription or translation. Recent advances in riboswitch engineering have expanded their utility in biotechnology and synthetic biology. This review highlights key insights into the structural and functional dynamics of riboswitches and discusses emerging strategies for their application as programmable biological tools.

Keywords: RNA; riboswitch; dynamics; applications

1. Introduction

RNAs play central roles in cells not only as messenger RNA (mRNA) but also through their regulatory functions as noncoding RNAs [1]. Regulatory RNAs are broadly classified into two categories: *cis*-acting and *trans*-acting elements [2–4]. *Trans*-acting regulators, such as small RNAs (sRNAs), typically bind to target mRNAs to inhibit translation or promote mRNA degradation [5–7]. In contrast, *cis*-acting RNA elements directly sense intracellular stimuli—including ions, metabolites, and temperature—to modulate downstream gene expression [7–10]. These regulated genes are involved in essential cellular processes, such as metabolism, signal transduction, and stress response [11–13].

Among *cis*-acting regulators, riboswitches are highly conserved RNA motifs located in the 5'-untranslated region (5'-UTR) of mRNAs, where they control fundamental metabolic pathways (e.g., coenzyme and amino acid biosynthesis) [14–16]. Structurally, riboswitches comprise two functional domains: an aptamer for ligand sensing and an expression platform for gene regulation [17,18]. Upon ligand binding, the aptamer undergoes conformational changes that alter the expression platform's activity, enabling precise modulation of downstream genes. Advances in dynamic studies have enabled the clarification of the intricate mechanisms underlying riboswitch-mediated ligand response and gene regulation, facilitating their engineering for *in vitro* and *in vivo* applications [19,20]. Given their programmable gene-regulatory capabilities, riboswitches hold significant promise as tools in synthetic biology and as potential antibiotic targets [21–23]. This review highlights recent insights into riboswitch dynamics and explores their emerging applications in biotechnology.

2. Dynamic Studies of Riboswitches

Structural studies of riboswitches have primarily focused on determining high-resolution structures of aptamer-ligand complexes to elucidate their atomic-level architecture [24–26]. Key structural motifs—such as kissing loops (KL), pseudoknots (PK), and helical regions—play pivotal roles in the global folding of riboswitches, ultimately governing their gene regulatory functions. These structural insights are essential for identifying the precise interactions between riboswitches and their cognate ligands [27]. However, riboswitches are highly dynamic molecules that undergo conformational switching upon ligand binding. As depicted in Figure 1a, ligand binding can induce terminator formation, prompting RNA polymerase (RNAP) dissociation and transcription termination [28]. Alternatively, riboswitches may regulate gene expression at the translational level by modulating ribosome binding site (RBS) accessibility, thereby activating or suppressing translation [29] (Figure 1a). A unique example is the glucosamine-6-phosphate riboswitch, where ligand binding triggers ribozyme activity to influence RNA stability [30].



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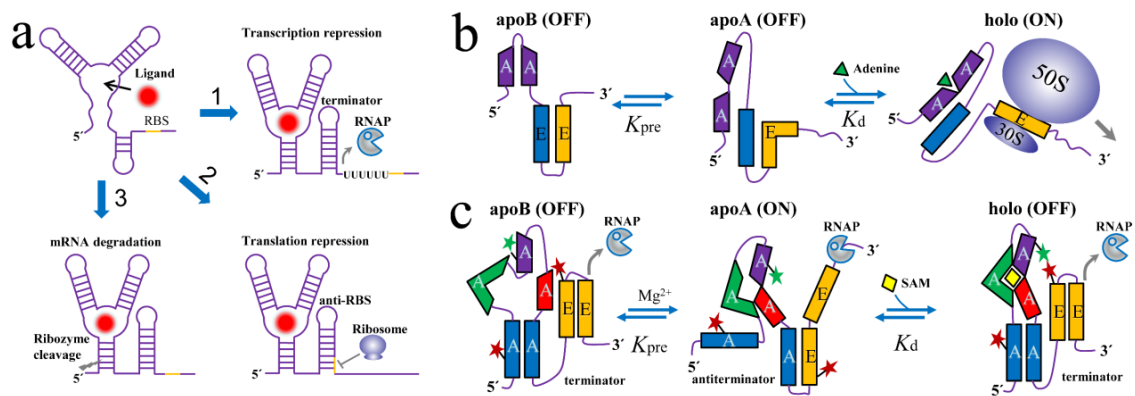


Figure 1. Dynamic structure folding of riboswitches. (a) riboswitch adopts three approaches to influence the transcriptional level, the translational level, and the mRNA stability to modulate gene expression under ligands binding. NMR (Nuclear magnetic resonance spectroscopy) and FRET (Förster resonance energy transfer) show the powerful ability to reveal the multiple states of adenine riboswitch [31]. (b) and SAM-I riboswitch [32]. (c) respectively. Abbreviation: RNAP (RNA polymerase), RBS (Ribosome binding site), A (Aptamer domain), and E (Expression platform).

Traditionally, riboswitch dynamics were described using a simplified two-state model [33]. Yet, advanced structural techniques have revealed far greater complexity in their conformational landscapes. For instance, the *Vibrio vulnificus* adenine riboswitch exhibits three distinct states: an inactive *apoB* conformation, an active *apoA* state, and a ligand-bound *holo* state (Figure 1b). In this system, RBS refolding into a single-stranded form enables ribosome engagement for translation initiation. Further evidence from X-ray free electron laser (XFEL) studies identified a third conformation—a ligand-bound intermediate—supporting a three-state mechanistic model for metabolite sensing and signal transmission [34] (Figure 2b).

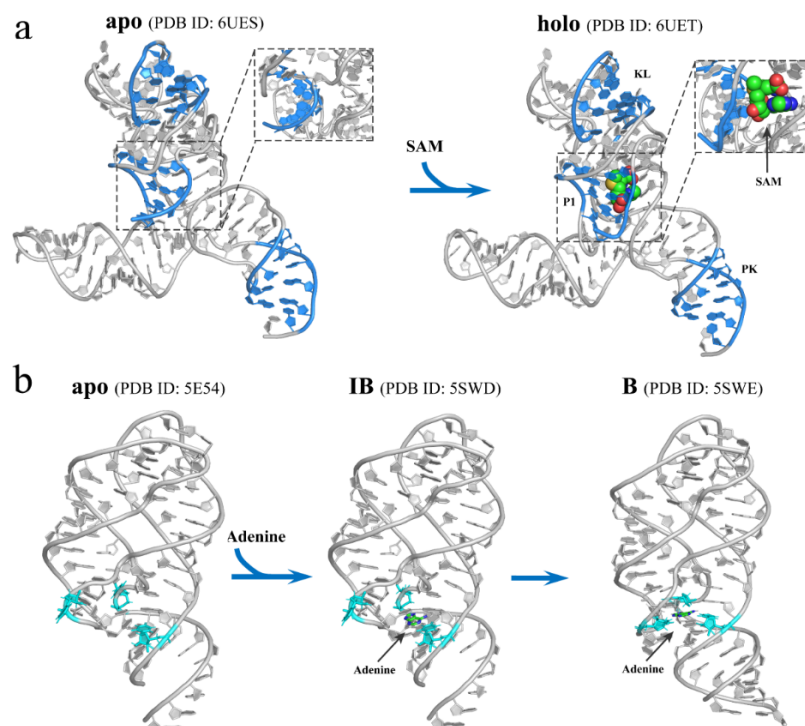


Figure 2. Dynamic folding of riboswitches. Cryo-EM and XFEL have been applied to obtain the high-resolution dynamic folding of SAM-IV (a) and adenine riboswitches (b). SAM and adenine molecules are shown with spheres and sticks, respectively. Adenine interacting bases are displayed with cyan sticks. Abbreviation: KL (Kissing loop), PK (Pseudoknot), IB (Intermediate-bound state), B (Bound state).

The *Bacillus subtilis* S-adenosyl-L-methionine-I (SAM-I) riboswitch regulates gene expression through the formation of a transcriptional terminator upon SAM binding. Single-molecule Förster resonance energy transfer

(single-molecule FRET, or smFRET) studies have mapped the conformational energy landscape of this riboswitch (Figure 1c), demonstrating its transition from a transcriptionally inactive *apoB* state to an active *apoA* state that facilitates SAM binding. Cryo-electron microscopy (cryo-EM) has emerged as a powerful tool for investigating RNA conformational dynamics. Recent structural determination of the SAM-IV riboswitch (50 kDa) by cryo-EM revealed that both *apo* and *holo* conformations, providing mechanistic insights into its regulatory function [35] (Figure 2a). Complementary to high-resolution techniques, small-angle X-ray scattering (SAXS) has been extensively employed to monitor global structural changes in various riboswitches, including TPP (Thiamine pyrophosphate), SAM-II, and c-di-GMP (Cyclic diguanosine monophosphate) riboswitches, under ligand-free and ligand-bound conditions [36–39]. These lower-resolution studies have significantly contributed to our understanding of riboswitch structure-function relationships from a dynamic perspective.

3. Applications of Riboswitches as Antibiotic Targets

Riboswitches are small molecule-sensing RNA widely distributed in both Gram-positive and Gram-negative bacteria, with rare occurrences in eukaryotes and absence in mammalian cells. The flavin mononucleotide (FMN) riboswitch, which regulates genes involved in flavin metabolism, has been identified in numerous pathogenic bacterial species [40,41]. FMN serves as a crucial coenzyme for flavoproteins and as a biosynthetic precursor for flavin adenine dinucleotide (FAD). Natural and synthetic compounds targeting FMN riboswitches have emerged as potential antibacterial agents. Roseoflavin, a naturally occurring FMN analog, exhibits antibacterial activity against Gram-positive bacteria by binding to FMN riboswitches and suppressing expression of riboflavin transporters, thereby inhibiting bacterial growth [42,43]. However, Gram-negative bacteria demonstrate intrinsic resistance to roseoflavin. Through systematic screening, ribocil was identified as an FMN riboswitch-binding compound effective against Gram-negative pathogens [44,45]. Structural studies revealed that ribocil exists as two enantiomers, *R*-ribocil and *S*-ribocil, with the *S*-form exhibiting high binding affinity and antibacterial activity (Figure 3a). Further optimization promoted the development of ribocil-C, an *S*-ribocil derivative demonstrating potent activity against *Escherichia coli* strains [44].

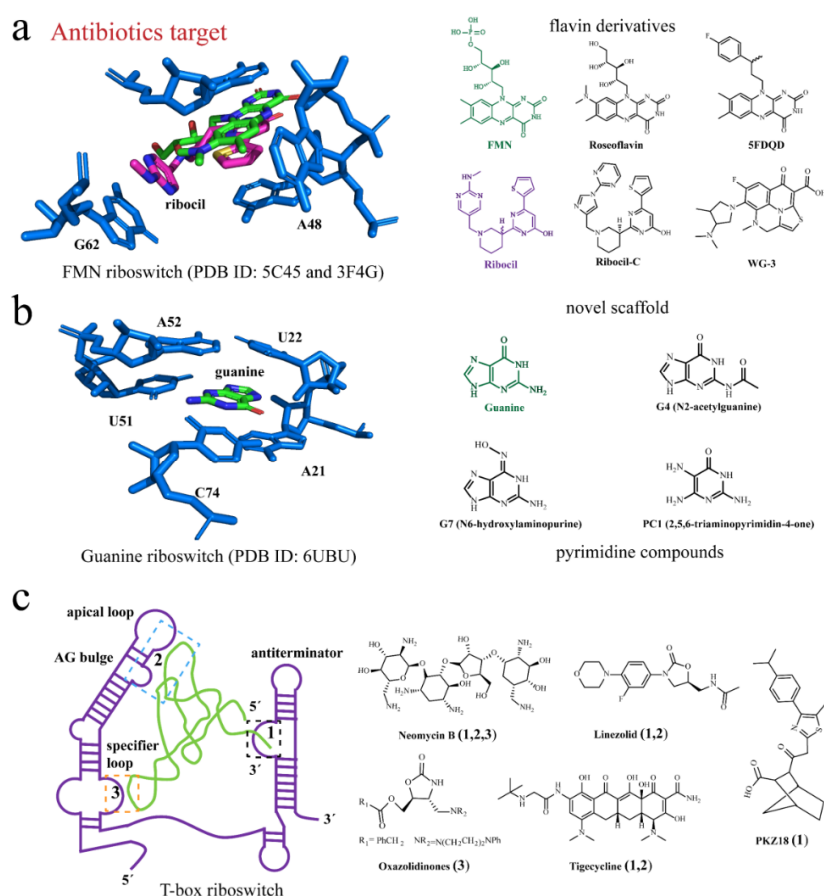


Figure 3. Riboswitch-based biotechnology contains the novel antibiotics discovery using the ligand-binding mechanisms of FMN (a), guanine (b), and T-box riboswitch (c). FMN and the antibiotic Ribocil are shown with green and purple sticks, respectively.

The guanine riboswitch in *Bacillus subtilis* serves as a key regulatory element for genes involved in purine transport and de novo biosynthesis [46]. Leveraging structural insights from high-resolution crystal structures, researchers have developed two pyrimidine analogs (G4, N2-acetylguanine and G7, N6-hydroxylaminopurine) that effectively target this riboswitch. These compounds demonstrate significant growth inhibition of *B. subtilis* in culture medium (Figure 3b), highlighting their potential as antibacterial drugs [47–49]. Similarly, T-box riboswitches have emerged as promising therapeutic targets due to their essential role in regulating amino acid metabolism and transport genes [50–55]. These riboswitches can be disrupted by small molecules including oxazolidinones and neomycin B, which competitively inhibit tRNA binding [56,57] (Figure 3c). Such interference with T-box riboswitch function leads to bacterial cell death, demonstrating the therapeutic potential of targeting these RNA regulatory elements.

4. Riboswitches' Applications as Biosensors

Riboswitch functionality can be characterized through reporter gene fusion assays, where riboswitches are coupled with genes encoding β -galactosidase or green fluorescent protein (GFP), enabling quantitative assessment of ligand-dependent regulatory activity via reporter protein expression levels [20,58,59]. For example, this approach has been instrumental in elucidating the roles of various transporters in maintaining vitamin B12 homeostasis, where reporter constructs were employed to monitor B12-dependent regulation (Figure 4). As an essential cofactor in numerous biochemical reactions, vitamin B12 serves as a key ligand for these regulatory studies [60]. Similarly, riboswitch-based reporter systems have proven to be valuable for monitoring intracellular signaling molecules. The second messenger c-di-GMP, which regulates critical physiological processes including motility, biofilm formation, and virulence, has been effectively quantified in vivo using engineered c-di-GMP riboswitch constructs [61] (Figure 4).

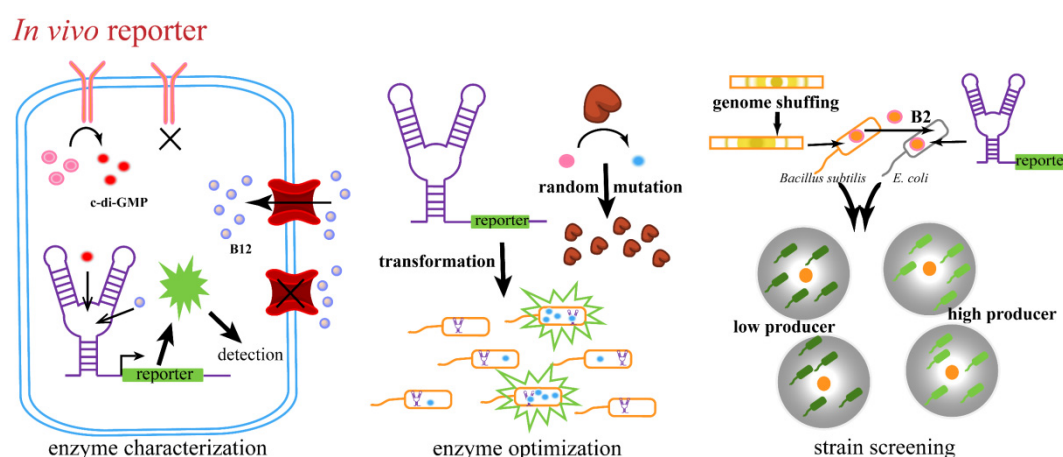


Figure 4. Riboswitch as in vivo reporter for enzyme function characterization, enzyme activity optimization, and high-yield strain screening.

Beyond their native regulatory roles, riboswitches have been developed as powerful tools for enzyme evolution and metabolic engineering. High-throughput screening platforms leveraging lysine and synthetic theophylline riboswitches have successfully identified enzyme variants with enhanced catalytic activity, including theophylline synthase from monooxygenase libraries and improved aspartate kinase mutants [62,63]. Furthermore, riboswitch-based reporters enable sensitive selection of microbial strains with optimized production of target metabolites [20,64], demonstrating their versatility in metabolic engineering applications. Traditional approaches for real-time biomolecule detection in living systems have predominantly employed protein-based biosensors, such as fluorescent proteins [65]. However, riboswitch-based biosensors offer several distinct advantages that make them an attractive alternative. First, their production through in vitro transcription bypasses the complexities of protein expression systems, significantly accelerating biosensor development. Second, riboswitches inherently possess high ligand specificity and undergo conformational changes upon binding, enabling direct signal transduction. These unique properties have been exploited to develop aptamer-based biosensors for monitoring diverse cellular metabolites, including fundamental cofactors (e.g., TPP), second messengers, and industrially relevant compounds (e.g., caprolactam) [66–69]. A notable example is the Spinach RNA aptamer system, where integration with a TPP riboswitch creates a fluorescent reporter that activates upon simultaneous binding of TPP

and the fluorogen DFHBI (3,5-Difluoro-4-hydroxybenzylidene imadazolinone) [66] (Figure 5a). This design principle has been successfully extended to monitor various signaling molecules, including adenine, SAM, c-di-GMP, c-di-AMP, and c-AMP-GMP, through their respective riboswitch-Spinach fusions [70,71] (Figure 5a). Beyond fluorescent activation, riboswitches can also employ quenching mechanisms. The cobalamin riboswitch, for instance, functions as an RNA tag that exhibits fluorescence enhancement upon cobalamin binding due to relief of intrinsic quenching [72–74] (Figure 5b). Furthermore, riboswitches responsive to toxic ligands (e.g., fluoride and guanidine) have been repurposed as biosensors in cell-free systems for environmental xenobiotic detection (Figure 5c), demonstrating their versatility across diverse applications [75–79].

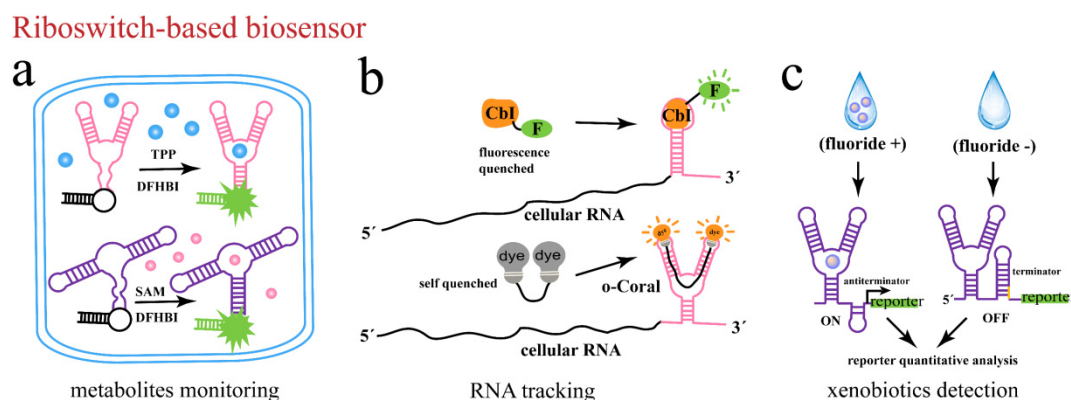


Figure 5. Riboswitches as biosensors for monitoring cellular metabolites, RNA imaging, and detection of environmental xenobiotics. **(a)** Riboswitches detect small molecules and then activate the DFHBI fluorescence by binding to a fused fluorescent RNA aptamer. **(b)** Self-quenching fluorescent molecule specifically binds to cellular RNA containing riboswitch aptamer, thereby endowing non-covalent RNA labeling for the assistance of RNA tracking. **(c)** Fluoride and other xenobiotic riboswitches regulate reporter gene expression to detect target molecule concentrations.

5. Conclusions

Riboswitches play a pivotal role in metabolic regulation by modulating gene expression in response to cellular metabolites. These structured RNA elements undergo ligand-induced conformational changes that precisely control downstream gene expression at transcriptional, translational, and post-transcriptional levels. Emerging evidence suggests that riboswitch dynamics are far more complex than the traditional two-state model, involving intricate conformational transitions that remain poorly understood. Current limitations in characterizing the structural dynamics of both aptamer domains and expression platforms upon ligand binding have significantly impeded progress in several key areas: (1) mechanistic understanding of riboswitch structure-function, (2) rational design of synthetic riboswitches, (3) component engineering for improved performance, and (4) de novo construction of ligand-specific variants. A comprehensive elucidation of riboswitch structural dynamics is essential for developing next-generation RNA-based regulators that offer precise gene expression control and expanded application potential. Such fundamental insights will provide critical guidelines for the rational design of functional RNA elements tailored to specific biotechnological and therapeutic applications.

Riboswitches serve as sophisticated molecular regulators that orchestrate metabolic processes through precise structural transitions. These naturally evolved RNA elements and their synthetic counterparts have emerged as versatile platforms for biotechnological innovation. Their unique gene-regulatory capabilities enable diverse applications spanning both in vivo and in vitro systems, particularly as promising antibiotic targets and highly specific biosensors (Figure 6). The functional repertoire of riboswitches can be substantially expanded through engineering approaches. Natural tandem riboswitch architectures provide blueprints for developing, including modular RNA systems integrating multiple regulatory functions, complex genetic circuits employing tandem riboswitch logic gates, and chimeric constructs combining distinct functional motifs. Notable advances include the successful implementation of riboswitch-riboswitch and riboswitch-ribozyme arrays in living systems. Furthermore, the strategic fusion of riboswitches with CRISPR guide RNAs has significantly enhanced the precision and tunability of CRISPR technologies [80,81]. In future, the integration of protein-binding RNA aptamers with riboswitches functionality promises to yield next-generation tools for real-time metabolic monitoring, precision genome engineering, and advanced diagnostic platforms [82].

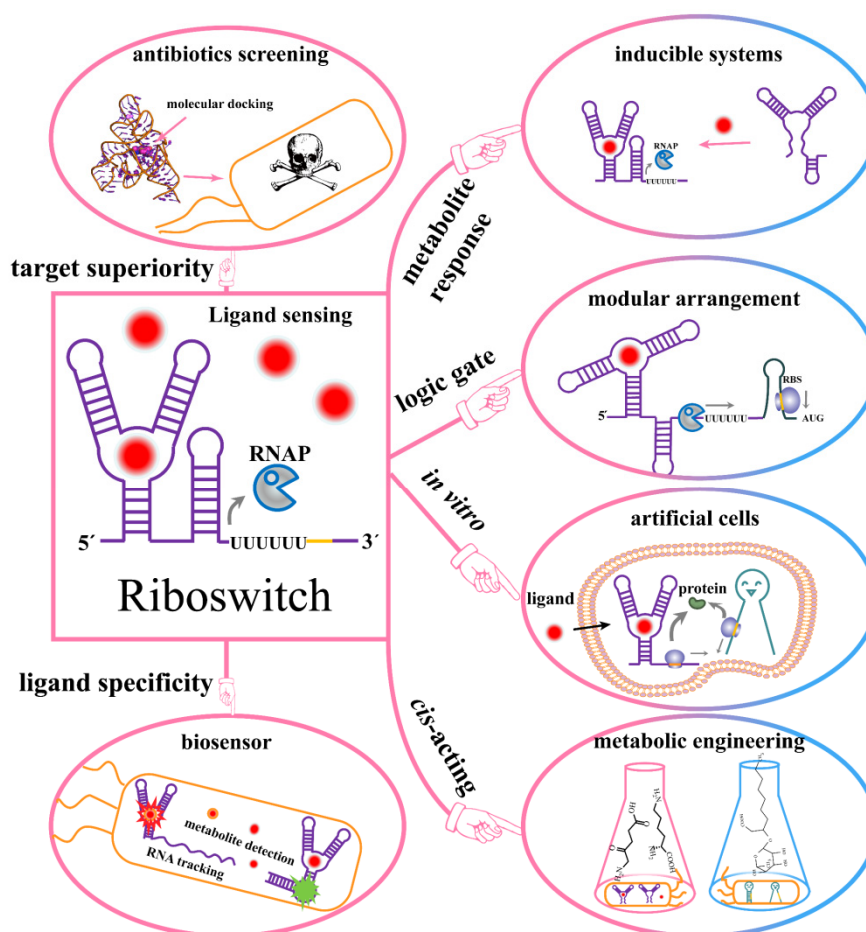


Figure 6. Schematic of riboswitches' applications in biotechnology.

Despite their potential, riboswitch applications in synthetic biology and biotechnology face several limitations. Their functionality depends on ligand-induced conformational changes, yet the underlying dynamic switching mechanisms—particularly at the single-molecule level—remain poorly characterized, constraining both natural riboswitch utilization and engineering efforts. While SELEX (Systematic Evolution of Ligands by Exponential Enrichment) has enabled expansion of RNA aptamer libraries, achieving optimal dynamic range (e.g., high ON/OFF ratios) and sensitivity (e.g., activation at physiological ligand concentrations) remains challenging. Computational approaches, including energy-based rational design and machine learning-assisted de novo design (utilizing reverse folding algorithms and RNA large language models), may offer solutions to these limitations. Additional challenges arise in biosensor development: riboswitch-based detectors currently rely on either transcriptional/translational regulation (reporter systems) or fluorescent RNA aptamers. Reporter systems lack real-time sensing capability, while fluorescent aptamers typically exhibit high background noise, low fluorescence intensity, and poor signal-to-noise ratios. Integration with smart signal output platforms, such as wireless devices or nanotechnology systems, may improve riboswitch biosensor performance. Although riboswitch-targeted antibiotics represent a novel mechanism of action, no FDA-approved drugs targeting riboswitches have been developed to date. Ribocil, currently in preclinical and early clinical studies, exhibits potential off-target effects in human cells due to structural similarities in the riboflavin pathway. However, combination therapies with conventional antibiotics may help the development of riboswitch-targeted antibiotics.

Author Contributions: D.C. and Y.L. wrote the manuscript. All authors have read and agreed to the published version of the manuscript.

Funding: This work was supported by the National Natural Science Foundation of China (grant 32471342).

Data Availability Statement: Not applicable.

Conflicts of Interest: The authors declare no competing interests.

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