**Reinforcement learning for retrosynthesis with chemoenzymatic reactions and type I polyketide synthases**

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# **Abstract**

Retrosynthetic planning tools have traditionally relied on either organic chemistry or monofunctional enzymatic catalysis to decompose target molecules into simpler precursors, leaving a third powerful synthesis modality, multifunctional type I polyketide synthases (PKSs), largely untapped. Here we present TridentSynthRL, a hierarchical multi-agent reinforcement learning framework, built upon the Monte Carlo tree search (MCTS) algorithm, that unifies all three synthesis routes within a single computational platform to explore a broad chemical space of small-molecule targets. Given a target molecule, TridentSynthRL first employs a chemoenzymatic MCTS agent to retrosynthetically fragments this target using our previously published chemical and enzymatic reaction templates. When this search produces an intermediate identified as a polyketide, a separate MCTS agent is subsequently spawned to design chimeric PKS assembly lines capable of synthesizing this intermediate in the forward direction from simple acyl-CoA building blocks. The identification of polyketide intermediates is enabled by a supervised graph neural network classifier trained on approximately one million synthetically generated polyketides and two million structurally similar chemoenzymatically modified variants. The chemoenzymatic MCTS search is further guided by our previously published enzymatic reaction feasibility classifier, DORA-XGB, and by reaction enthalpy estimates for synthetic chemistry transformations, thereby enabling prioritization of thermodynamically favorable pathways. We deployed TridentSynthRL on the kavalactone family from Piper methysticum, designing retrosynthetic pathways to all fifteen members, each accessible via at least one PKS-containing route. We further demonstrate a more efficient hybrid chemoenzymatic pathway to the natural product cryptofolione, improving upon our prior work that combined only mono- and multifunctional enzymes without synthetic chemistry.

# **Introduction**

The scalable synthesis of structurally complex molecules at high titers, rates, and yields is a foundational problem in biological and chemical manufacturing. Natural products and their derivatives, for instance, are particularly valuable manufacturing targets given their widespread use as small-molecule therapeutics, agrochemicals, and commodity chemicals. Yet, their structural diversity and precise stereochemistry make large-scale manufacturing exceptionally difficult. Retrosynthesis, the systematic decomposition of target molecules into simpler, readily available precursors, has long provided a strategic framework for designing synthetic pathways to such complex molecules for eventual scale-up. Over the past several years, computational retrosynthesis tools have advanced rapidly, driven by both automatically-extracted and expert-curated reaction templates, template-free language models, and increasingly, machine learned heuristics and scores. Template-based methods apply explicit reaction rules encoded as SMARTS patterns to recursively deconstruct targets, as exemplified by tools such as ASKCOS, RetroPath, RetroRules, and our group’s own DORAnet, amongst others. Template-free approaches instead use transformer architectures trained on previously published reactions in the literature to predict retrosynthetic transformations without predefined rules. Among the various search algorithms employed to navigate the combinatorial space of multi-step retrosynthesis, Monte Carlo tree search (MCTS) has emerged as a particularly effective strategy, owing to its ability to balance the exploration of novel routes with the exploitation of promising intermediates. First applied to retrosynthetic planning by Segler et al., MCTS draws on the same principled exploration–exploitation trade-off that underpins AlphaGo and AlphaZero, where it was instrumental in achieving superhuman performance in the board game Go.

Despite these algorithmic advances, most retrosynthesis tools have thus far focused exclusively on either synthetic organic chemistry or monofunctional enzymatic transformations to propose and evaluate routes to valuable small molecules. Recognizing the complementary strengths of chemical and enzymatic catalysis, several recent computational platforms have begun integrating both modalities, enabling the exploration of a broader chemical space than would be accessible through either approach alone.

Monofunctional enzymes, defined here as enzymes that catalyze single chemical transformations, such as alcohol dehydrogenases, aminotransferases, or decarboxylases, are highly effective at regio- and stereoselectively modifying specific functional groups on a substrate’s carbon backbone (Figure 1). However, enzymatic catalysis alone cannot support the full range of transformations required for small-molecule synthesis. Enzymes typically operate within narrow ranges of temperature, pressure, and solvent conditions and often lose activity outside physiological environments, thereby limiting the diversity of reactions that can be performed biologically. In contrast, synthetic chemistry can access a wider suite of transformations through either transition-metal catalysis or reaction conditions that fall outside common physiological limits. Examples include palladium- or nickel-catalyzed carbon–carbon bond-forming reactions such as Suzuki, Heck, and Liebeskind–Srogl cross-couplings, as well as olefin metathesis reactions used to construct or remodel carbon scaffolds. These transformations often require non-physiological conditions, metal catalysts that are cytotoxic to cells, and/ or involve intermediates, such as aldehydes, radicals, or long-chain hydrophobic metabolites that are typically unstable or poorly soluble in aqueous environments (Figure 1). Collectively, these constraints highlight the value of integrated retrosynthetic approaches that jointly consider chemical and enzymatic transformations within a single planning framework.

To this end, our group recently released **DORAnet**, a synthesis planning tool that recursively applies 386 synthetic chemistry and 3,604 enzymatic chemistry reaction templates to a given target molecule for a predetermined number of enzymatic and synthetic chemistry steps. Earlier efforts to merge chemistry and biology include the dual-network framework developed by Levin et al., which maintains separate machine learning models trained on chemical and enzymatic reactions and combines their output probability scores during search to balance both modalities. Sankaranarayanan and Jensen similarly coupled ASKCOS with an enzymatic reaction search module using RetroBioCat to support multistep chemoenzymatic pathway design, while Kreutter and Reymond employed transformer models in an iterative loop to propose multistep chemoenzymatic pathways.

While integrating synthetic chemistry and monofunctional enzymatic transformations expands accessible chemical space, incorporating multifunctional enzyme systems such as polyketide synthases (PKSs) can broaden this space even further (Figure 1). Here, we define multifunctional enzymes as enzyme assemblies capable of catalyzing multiple distinct transformations within a single coordinated complex, in contrast to monofunctional enzymes that catalyze individual reactions only. Type I PKSs are modular megaenzymes that function as molecular assembly lines composed of multiple catalytic domains operating in concert to iteratively construct elongated carbon backbones from simple acyl-coenzyme A (acyl-CoA) building blocks (Figure 1). Central to this process is the ketosynthase (KS) domain, which catalyzes iterative carbon–carbon bond-forming Claisen condensation reactions that extend the growing polyketide chain and enable the construction of complex carbon scaffolds with defined stereochemistry. Since these successive reactions occur within the same multienzyme complex, PKSs and related systems can generate complex scaffolds without isolating intermediates after each transformation, potentially reducing downstream separation and purification requirements relative to stepwise chemical or monofunctional enzymatic synthesis.

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| **Figure 1.** TridentSynthRL leverages the complementary strengths of synthetic chemistry as well as mono- and multi-functional enzymes to access a wide chemical space of molecular targets. Monofunctional enzymes, which catalyze a single reaction, excel at regioselectively and stereoselectively performing small modifications on a substrate’s carbon backbone. Meanwhile, multifunctional enzymes, which catalyze multiple reactions, can construct such carbon backbones through the iterative catalysis of acyl-CoA substrates, as in the case of polyketide synthases (PKSs). Despite their ability to catalyze reactions in a controlled and selective manner, enzymes cannot function under temperatures and pressures outside of typical physiological conditions, nor can their host cells survive cytotoxic intermediates, such as aldehydes or long-chain alcohols. Consequently, the suite of functional group transformations biology can catalyze is relatively narrow, thereby providing an opportunity to couple both forms of enzymatic chemistry with synthetic chemistry to ultimately synthesize more targets than would be possible with either route alone. |

In biological systems, PKSs are encoded within biosynthetic gene clusters and are responsible for the production of numerous therapeutically valuable natural products that are difficult to access through synthetic chemistry alone. Recent advances in PKS engineering and heterologous expression have demonstrated that these assembly lines can be reconfigured to produce not only natural product analogues but also a range of commodity and specialty chemicals, underscoring their potential as a programmable biosynthetic platform for manufacturing. **In our prior work, we developed a computational PKS-based forward-synthesis planning platform that combined mono- and multifunctional enzymatic transformations in a breadth-first-search approach to propose pathways toward both commodity chemicals and structurally complex natural products, such as cryptofolione.**

Here, we have built upon our previous work and harnessed reinforcement learning (RL) to efficiently integrate all three synthesis modalities, i.e., synthetic chemistry, monofunctional enzymatic transformations, and multifunctional enzyme systems within a single unified framework, TridentSynthRL. To the best of our knowledge, this represents the first computational retrosynthesis platform to simultaneously leverage all three synthesis routes. TridentSynthRL employs a hierarchical search strategy based on the Monte Carlo tree search (MCTS) algorithm to navigate the vast combinatorial design space that emerges when these synthesis routes are considered simultaneously. Given a target molecule, a chemoenzymatic MCTS agent first uses chemical and monofunctional enzymatic reaction templates to iteratively fragment this target into simpler upstream intermediates. When a candidate polyketide is detected among these intermediates, a secondary forward-synthesis MCTS agent is invoked to evaluate whether this fragment can be synthesized by assembling modular PKS architectures from simple acyl-coenzyme A building blocks. In order to efficiently detect polyketides, we trained a supervised graph neural network (GNN) classifier on approximately one million synthetically generated polyketides and two million structurally related chemoenzymatically modified molecules. To prioritize experimentally viable routes, TridentSynthRL also incorporates reaction thermodynamic estimates and machine-learning–based enzymatic reaction feasibility scores directly into the search policy, thereby biasing the algorithm towards feasible and thermodynamically favorable pathways. We demonstrate the capabilities of TridentSynthRL through two representative case studies. First, we applied TridentSynthRL to the kavalactone family of natural products from Piper methysticum, a class of polyketide-derived lactones whose structural complexity present challenges for traditional synthetic chemistry-based routes. In this study, TridentSynthRL identified pathways to all fifteen kavalactones, with each target accessible through at least one route incorporating a PKS-derived intermediate. We further applied TridentSynthRL to the structurally complex natural product cryptofolione, for which a hybrid chemoenzymatic–PKS synthesis strategy was found that reduces the number of required PKS modules relative to our previously proposed designs, thereby improving experimental feasibility since shorter PKS chimeras are easier to express heterologously in microbial cell factories. Together, these case studies illustrate how integrating synthetic chemistry, monofunctional enzymes, and multifunctional PKS assembly within a unified search architecture enables the identification of experimentally plausible routes various targets that may be difficult to access using any single synthesis modality alone.

**Results**

### **Formulating chemoenzymatic retrosynthesis as a Markov Decision Process**

In building TridentSynthRL, we formulated the chemoenzymatic retrosynthesis problem as a Markov decision process (MDP) and addressed it using the Monte Carlo tree search (MCTS) algorithm. In RL, an MDP provides a mathematical framework for sequential decision making in which an agent transitions between states by selecting actions and receives rewards that guide it towards desirable outcomes. Within this MDP framework, retrosynthetic planning can be viewed as a sequence of decisions, each corresponding to the application of a reaction template, that recursively transform an input small-molecule target, which defines the initial state, into simpler precursor molecules, which represent subsequent states.

In our implementation, each node (or state) in our search tree represents a molecule encoded as an RDKit Mol object, with the root node corresponding to the target molecule. Child nodes are then generated by applying both chemical and enzymatic reaction templates with DORAnet (available at <https://github.com/wsprague-nu/doranet>) in the retrosynthetic direction, thus producing upstream intermediates. In this way, the search tree expands outward from the target towards simpler building blocks (Figure 2). The objective of our search is to identify sequences of transformations that can convert the target molecule into commercially available or biologically accessible building blocks while maximizing pathway feasibility.

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| **Figure 2.** Overview of the TridentSynthRL multi-agent Monte Carlo tree search (MCTS) framework for retrosynthetic planning**.** The algorithm proceeds through three iterative phases. (1) Selection: The chemoenzymatic agent traverses the search tree from the target molecule, selecting a leaf node (red circle) for expansion based on learned value estimates. (2) Chemoenzymatic Expansion: The selected node is expanded by applying chemical (blue arrows) and enzymatic (green arrows) retrosynthetic transformations to generate precursor nodes. Expansion terminates when all precursors resolve to commercially available building blocks (blue squares), biological building blocks (green squares), or known polyketide intermediates (orange squares), yielding a terminal state *S*\_T. When a predicted or known polyketide intermediate is encountered during expansion, a specialized PKS agent is launched to explore polyketide synthase assembly line configurations (orange arrows) for that substructure. (3) Update: Upon reaching a terminal state, rewards are backpropagated (red dashed arrows) from the terminal node up to the root, updating value estimates along the traversed path to guide future iterations toward higher-quality retrosynthetic routes. |

Classical Monte Carlo tree search (MCTS) proceeds through four stages during each iteration: 1) selection, 2) expansion, 3) simulation (rollout), and 4) update. In the simulation phase, the MCTS algorithm typically performs a fast forward rollout from a newly expanded node to estimate the long-term value of that state by randomly sampling possible future trajectories. In retrosynthetic planning, such rollouts would entail repeatedly applying reaction templates for many additional steps to determine whether a pathway ultimately reaches viable starting materials. However, realistic synthetic routes may span numerous reaction steps, and the branching factor of chemical reaction networks is large. As a result, rollout simulations over long retrosynthetic horizons can be computationally expensive and prone to accumulating chemically infeasible or unrealistic transformations, introducing noise into node value estimates. To avoid this cost while maintaining efficient search, we omit the rollout phase in TridentSynthRL and instead rely on heuristic reaction feasibility and thermodynamic scores to provide immediate feedback to the search process during node expansion and backpropagation.

Consequently, within TridentSynthRL, each iteration consists of three steps: 1) selection, 2) expansion and 3) update. During the selection step, the existing retrosynthesis tree is traversed beginning from the root node (target molecule) until a leaf node is reached (Figure 2). This selection is guided by the widely-applied upper confidence bound 1 (UCB1) selection policy (see Methods), which balances the exploration of under-visited nodes with the exploitation of promising intermediates. In the expansion step, the selected leaf node is expanded (Figure 2) by applying all 386 chemical and 3604 enzymatic reaction templates within DORAnet in the retrosynthetic direction, generating upstream precursor states (compounds) that are then added to the existing tree as new child nodes. Finally, during the update step, the rewards associated with these newly generated nodes are propagated back through the tree (Figure 2) to update each node’s visit counts and value estimates. Within this framework, the state space of the chemoenzymatic agent consists of individual molecular compounds encountered during retrosynthetic decomposition while the action space comprises the full set of 3990 reaction templates within DORAnet. Each action corresponds to applying one template retrosynthetically to the current molecule to generate precursor fragments, which are then added to the tree as upstream intermediates. Prior to running TridentSynthRL, users can specify both the maximum number of search iterations and the maximum tree depth for which to execute the retrosynthetic search and TridentSynthRL terminates when either of the two stopping criterion is reached. After termination, the ensuing retrosynthesis tree is traversed one final time to extract pathways between the initial root node and any terminal leaf nodes.

A node is considered terminal if it satisfies one of three criteria: (1) it corresponds to a commercially available chemical building block drawn from the Enamine catalog (~278,000 compounds), (2) it matches a biological building block from a curated set of common metabolites across multiple organisms, or (3) it is identified as a polyketide intermediate for which a chimeric PKS design has been successfully generated. Nodes corresponding to prohibited or hazardous compounds (~652 entries) are immediately pruned from the search.

Within RL algorithms, designing reward functions is crucial to attaining good solutions. Here, to guide the retrosynthetic search toward experimentally feasible routes, we employ a modular reward policy that accounts for both the identity of individual intermediate molecules that are encountered and the feasibility of the pathway taken to reach them. At the node level, compounds corresponding to terminal states, i.e., commercial or biological building blocks, or polyketide intermediates verified to be PKS-synthesizable receive a fixed base reward of . For non-terminal intermediates, a dense reward signal is provided using a rescaled synthetic accessibility (SA) score derived from RDKit, which is linearly transformed (see Methods) so that molecules that are more synthetically accessible receive higher rewards.

Path-level feasibility is subsequently incorporated through reaction-level scores derived from both machine learning and thermodynamic estimates. For enzymatic steps, feasibility is evaluated using our previously published DORA-XGB reaction feasibility classifier, which produces dimensionless scores ranging from 0 to 1, with higher scores representing more feasible reactions. For synthetic chemistry transformations, reaction enthalpies are computed using our previously released open-sourced thermodynamics calculator PAthermo (available at <https://github.com/dmdqy/pathermo>). Since reaction enthalpies from PAthermo are in kcal/mol, these are first converted to the same numerical scale as DORA-XGB scores using a sigmoidal transformation that penalizes highly endergonic steps while preserving favorable or near-thermoneutral reactions (see Methods). This normalization ensures that feasibility metrics for chemical and enzymatic reactions are directly comparable and bounded between 0 and 1.

For a given pathway, the cumulative feasibility is computed as the geometric mean of the per-step feasibility scores along that route. Using the geometric mean allows pathways of different lengths to be compared fairly, since it avoids systematically penalizing longer but otherwise plausible sequences. The final reward assigned to a node is then calculated as the product of the state-level reward (e.g., terminal-state or synthetic accessibility score) and this path-level feasibility factor, allowing the search to preferentially expand pathways that are both synthetically accessible and chemically or biologically feasible. During the update phase of TridentSynthRL, these normalized rewards are propagated back through the tree

A distinguishing feature of TridentSynthRL is its hierarchical multi-agent design. When the expansion step produces an intermediate predicted to be compatible with PKS biosynthesis, a specialized MCTS agent is launched in the forward-synthesis direction to evaluate whether the fragment can indeed be constructed by a PKS assembly line. If the PKS agent successfully identifies a chimeric PKS design that yields the target fragment, a terminal reward of +1.0 is assigned and propagated back through the chemoenzymatic search tree. If no PKS design is found, the intermediate instead receives its scaled SA score. This hierarchical coupling enables the coordinated exploration of hybrid pathways that combine chemical, enzymatic, and PKS-based transformations and is described in detail in the following section.

### **Formulating chimeric polyketide synthase design as a Markov Decision Process**

When the chemoenzymatic MCTS agent identifies an intermediate predicted to be a polyketide, TridentSynthRL spawns a second, specialized MCTS agent that operates in the forward-synthesis direction to evaluate whether a chimeric type I PKS assembly line can be designed to produce that fragment from simple acyl-CoA building blocks. We formulated this chimeric PKS design problem as a separate MDP in which the sequential decisions correspond to the iterative addition of extension modules to a growing polyketide chain, mirroring the modular biosynthetic logic of type I PKSs.

In this MDP, each state represents a PKS intermediate defined by three components: (1) the chemical structure of the polyketide product bound to the synthase via a thioester linkage to the acyl carrier protein (ACP), encoded as an RDKit Mol object, (2) the complete PKS module architecture specifying the ordered sequence of catalytic domains selected thus far, and (3) the current depth in the search tree, corresponding to the number of extension modules that have been appended. The root state of this MDP corresponds to an empty PKS design with no modules, from which the search builds outward by iteratively adding extension modules in the forward biosynthetic direction.

The action space of the PKS agent comprises the set of possible extension modules that can be appended at each step. Each action corresponds to adding a single extension module to the growing assembly line, where the module is defined by the choice of extender unit, i.e., the acyl-CoA substrate loaded by the acyltransferase (AT) domain (e.g., malonyl-CoA, methylmalonyl-CoA, or ethylmalonyl-CoA), and the combination of optional tailoring domains that determine the reduction state of the newly incorporated ketide unit. Specifically, each extension module minimally contains a ketosynthase (KS) domain, which catalyzes the Claisen condensation that extends the polyketide chain by two carbon units, and an ACP domain, which tethers the growing intermediate. In addition, each module may optionally include a ketoreductase (KR) domain that reduces the β-keto group to a hydroxyl, a dehydratase (DH) domain that eliminates water to form an enoyl intermediate, and an enoylreductase (ER) domain that fully saturates the carbon–carbon double bond. This combinatorial selection of extender units and domain architectures gives rise to four possible reduction states per extension module: no reduction (KS-AT-ACP), partial reduction (KS-AT-KR-ACP), partial reduction with dehydration (KS-AT-KR-DH-ACP), and full reduction (KS-AT-KR-DH-ER-ACP). The first module in the assembly line additionally specifies the loading module, which determines the starter unit (e.g., acetyl-CoA, benzoyl-CoA, or propionyl-CoA, among others) that initiates chain biosynthesis. At each expansion step, our previously released PKS design tool RetroTide enumerates the set of feasible one-step extensions given the current PKS architecture and the target polyketide fragment, returning up to 25 candidate designs ranked by structural similarity to the target.

Like the chemoenzymatic agent, the PKS agent proceeds through three iterative stages per MCTS iteration: selection, expansion, and update. During selection, the agent traverses the existing PKS design tree from the root using a modified UCB1 policy that incorporates subgraph-guided pruning to focus the search on chemically promising branches. Specifically, when evaluating unvisited child nodes, the agent checks whether the polyketide product at that node is a subgraph of the target fragment using RDKit’s substructure matching routines. Children whose products are confirmed subgraphs of the target receive maximal selection priority, forcing their immediate exploration, while children whose products fail the subgraph test are assigned minimal priority and are effectively pruned from the search. This structural filtering ensures that the agent only expands PKS designs whose growing intermediates remain consistent with the target’s carbon skeleton, thereby avoiding wasted iterations on assembly line configurations that have already diverged from the desired product. For previously visited children, standard UCB1 scoring is applied, balancing exploitation of high-value nodes with exploration of under-visited alternatives.

During expansion, the selected leaf node is expanded by calling RetroTide’s one-step PKS design function, which extends the current assembly line by a single module. RetroTide evaluates the set of possible extender units and domain architectures and returns up to 25 candidate designs, each representing a distinct next module choice. These candidates are added to the tree as new child nodes, with each child inheriting the parent’s PKS architecture augmented by the newly appended module.

Following expansion, a simulation is performed to estimate the long-term value of the newly expanded node. Unlike the chemoenzymatic agent, which omits rollouts entirely, the PKS agent performs a forward simulation by invoking RetroTide’s full multi-step design function from the current node’s PKS architecture, generating up to 15 complete assembly line designs that extend to completion. The best resulting design is then evaluated for target matching by simulating product release through two thioesterase (TE)-catalyzed mechanisms: thiolysis, which cleaves the thioester bond to yield a linear carboxylic acid, and lactonization, which performs an intramolecular cyclization to generate a macrolactone or lactone. If the released product from either mechanism is isomorphic to the target fragment, as determined by RDKit graph isomorphism, a terminal reward of +1.0 is assigned. If no exact match is found, a partial reward is computed using the maximum common substructure (MCS) similarity between the best released product and the target, defined as the ratio of atoms in the MCS to the total atom count of the union of the query and reference molecules. This scoring scheme provides a dense reward signal that guides the search toward increasingly target-like intermediates even before an exact match is achieved.

During the update step, the reward obtained from simulation is backpropagated from the expanded leaf node up through all ancestors to the root, incrementing each node’s visit count and accumulating its total reward. These statistics are subsequently used by the UCB1 selection policy in future iterations to compute the average value and exploration bonus for each node, thereby directing the search toward PKS architectures that have historically yielded high-similarity intermediates.

The PKS MCTS search terminates when any of three conditions is met: (1) the maximum tree depth is reached, which corresponds to the maximum number of extension modules permitted in the chimeric assembly line (default: 15 modules), (2) an exact target match is identified through either thiolysis or lactonization release, or (3) no valid child nodes remain after subgraph pruning, indicating that all possible extensions have diverged from the target structure. Upon termination, if the PKS agent has identified at least one successful chimeric design, a terminal reward of +1.0 is returned to the parent chemoenzymatic agent and backpropagated through the retrosynthetic search tree, thereby reinforcing the pathway that led to the polyketide intermediate. If no successful design is found, the intermediate instead receives its rescaled synthetic accessibility score, as described in the preceding section. This hierarchical coupling between the two agents enables TridentSynthRL to coordinate the exploration of hybrid pathways that combine retrosynthetic fragmentation via chemical and monofunctional enzymatic transformations with forward biosynthetic verification via PKS assembly.

### **Training a supervised classifier to detect polyketides**

A critical component of TridentSynthRL is the mechanism by which polyketide intermediates are detected during the chemoenzymatic MCTS expansion, thereby triggering the spawning of PKS agents. While a static database lookup against a precomputed library of ~106,000 PKS products provides a deterministic baseline, this approach cannot generalize to novel polyketide scaffolds not explicitly enumerated. Moreover, the synthetic accessibility (SA) score, while useful as a dense reward signal for guiding the chemoenzymatic search, is inherently biased toward the commercial chemical building blocks on which it was trained. It tends to assign low (favorable) synthesizability scores to compounds resembling entries in chemical catalogs, while assigning higher (unfavorable) scores to biomolecules, metabolites, and polyketide natural products—precisely the compounds that TridentSynthRL should recognize as biologically accessible. We therefore developed a learned classifier that generalizes from a representative training set to recognize the structural hallmarks of polyketide backbones.

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| **Figure 3.** Polyketide libraries and their chemoenzymatically-modified counterparts were synthetically generated to build a training set for a supervised polyketide classification model. Our previously released PKS design tool, RetroTide, was used to build an initial database of polyketide scaffolds by combinatorially assembling chimeric type I PKS designs *in silico* with 1) a single loading module, 2) up to 3 extension modules (each with all possible domain architectures, i.e., KS, AT, ACP, and optional KR, DH, and ER domains), and a 3) terminal thioesterase domain allowing for both thiolysis and lactonization offloading reactions, yielding approximately 1 million core polyketide structures (labelled 1) for training. These structures were then modified further via DORAnet for a single step using all synthetic chemistry and enzymatic chemistry reaction templates. For each polyketide, the most chemically similar product from the synthetic chemistry modified set as well as that from the from the enzymatic chemistry modified set was selected, yielding approximately 2 million polyketide variants (labelled 0) to be added to the training set. |

We constructed the training set through a two-step synthetic data generation pipeline. In the first step, RetroTide was used to combinatorially assemble chimeric type I PKS designs *in silico*, comprising a single loading module (29 possible starter units), up to three extension modules (each enumerating all four possible domain architectures: KS-AT-ACP, KS-AT-KR-ACP, KS-AT-KR-DH-ACP, and KS-AT-KR-DH-ER-ACP—crossed with 6 extender units), and a terminal thioesterase domain allowing both thiolysis and lactonization offloading at all possible ring sizes. This enumeration yielded approximately one million core polyketide scaffolds, each labelled as class 1 (polyketide). Limiting enumeration to three extension modules also biases the library toward shorter PKS assembly lines, which are more readily expressed in heterologous hosts.

In the second step, each polyketide was subjected to a single step of DORAnet chemoenzymatic expansion using all 3,604 enzymatic and all 386 synthetic reaction templates. For each polyketide, the most structurally similar product from the enzymatic modification set and the most structurally similar product from the synthetic modification set were selected based on molecular similarity, yielding approximately two million chemoenzymatically modified polyketide variants, each labelled as class 0 (non-polyketide). These serve as hard negatives—molecules that are structurally close to polyketides but have undergone at least one non-PKS transformation—forcing the classifier to learn the precise structural features that distinguish PKS products from their chemoenzymatic derivatives rather than relying on superficial chemical dissimilarity.

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| **Figure 4.** Architecture of supervised GNN. Input SMILES strings are parsed with RDKit into molecular graphs in which atoms are represented as nodes and bonds as edges. Each atom is encoded as a 40-dimensional one-hot feature vector capturing atomic number, degree, formal charge, hydrogen count, hybridization, aromaticity, and ring membership, while each bond is encoded as a 5-dimensional one-hot vector indicating bond type or self-loop. Node features are projected into a 256-dimensional hidden space via a learned linear transformation, and edge features are incorporated directly at the attention computation step. The backbone consists of 3 stacked graph attention layers, each with 4 multi-head attention heads, residual connections, LayerNorm, ELU activation, and dropout (*p* = 0.1). After the final attention layer, node embeddings are mean-pooled to produce a single graph-level representation, which is passed through a two-layer classification head with sigmoid activation to yield the predicted probability of the input molecule being a polyketide synthase (PKS) product. |

Input SMILES strings are parsed via RDKit into molecular graphs. Each atom is encoded as a 40-dimensional feature vector comprising one-hot encodings of atomic number (13 dim), total degree (7 dim), formal charge (6 dim), total hydrogen count (6 dim), and hybridization state (6 dim), plus binary indicators for aromaticity (1 dim) and ring membership (1 dim). Each bond is encoded as a 5-dimensional feature vector: a one-hot encoding of bond type (single, double, triple, aromatic; 4 dim) plus a self-loop indicator (1 dim). Node features are projected into a 256-dimensional hidden space via a learned linear transformation. The backbone consists of three stacked graph attention (GAT) layers, each with four multi-head attention heads that incorporate edge features directly into the attention computation. Each layer applies the attention mechanism followed by LayerNorm, ELU activation, and dropout (*p* = 0.1), with a residual connection bypassing the entire block. After the final attention layer, node embeddings are mean-pooled to produce a single 256-dimensional graph-level embedding, which is passed through a two-layer classification head (256 → 128 with ReLU → 1 with sigmoid) to yield the predicted polyketide synthesizability probability.

The model is trained with binary cross-entropy loss (pos\_weight = 2.0 to compensate for the 2:1 class imbalance of negatives to positives) using AdamW optimization (learning rate = 3×10–4, weight decay = 1×10–4) with gradient clipping at norm 1.0. An optional cosine annealing learning rate schedule with linear warmup (first 5% of epochs) is supported. Performance is evaluated by area under the precision-recall curve (AUPRC). The model supports distributed multi-GPU training via PyTorch DistributedDataParallel.

During MCTS deployment, the trained GNN replaces or supplements the static database lookup as the polyketide detection mechanism. When a new child node is created during chemoenzymatic expansion, its SMILES is fed through the GNN; if the predicted probability exceeds 0.5, the node is flagged as a polyketide and the RetroTide PKS agent is spawned. Users retain the option of using database lookup for deterministic matching, which is useful for validation and benchmarking. The GNN approach, however, generalizes to novel polyketide scaffolds not present in any precomputed library, providing a critical advantage as the accessible polyketide chemical space far exceeds what can be exhaustively enumerated.

## **Deploying TridentSynthRL on the Kavalactone Family**

We deployed TridentSynthRL on the family of kavalactones from *Piper methysticum* (kava), a collection of 15 structurally related natural products with demonstrated anxiolytic, analgesic, and neuroprotective properties (Figure 5). All 15 kavalactones share a core α-pyrone (six-membered lactone) scaffold but differ in their aromatic substitutions, degree of backbone saturation, and patterns of hydroxylation and methoxylation. This structural diversity within a common scaffold makes the kavalactone family an ideal test set for TridentSynthRL: the shared α-pyrone core is a natural candidate for PKS biosynthesis via thioesterase-mediated lactonization, while the varied peripheral modifications require the full flexibility of chemoenzymatic reactions.

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| **Figure 5.** Chemical structures of the kavalactone family from *Piper methysticum* (kava) for which TridentSynthRL was tested against. The six major kavalactones, i.e., kavain, 7,8-dihydrokavain, yangonin, Desmethoxyyangonin, Methysticin, and 7,8-dihydromethysticin are shown, along with their related structural analogs. These compounds share a core -pyrone scaffold and vary in their aromatic substitutions, degrees of saturation, and hydroxylation/ methoxylation patterns, all of which contribute to their various pharmacological effects, including their anxiolytic, analgesic, and neuroprotective properties. TridentSynthRL was able to find thermodynamically feasible pathways to all members of the kavalactone family with at least one pathway for each structure involving a type I PKS. Users also have the option to tune the total number of pathways enumerated by running TridentSynthRL for fewer or more iterations. |

TridentSynthRL successfully identified thermodynamically feasible retrosynthetic pathways to all 15 members of the kavalactone family. For every compound, at least one pathway involves a type I PKS to construct the core carbon backbone, demonstrating the value of integrating PKS biosynthesis into the retrosynthetic search. Complete pathway details for all 15 kavalactones are provided in the Supporting Information. Below we highlight three representative pathways that illustrate different strengths of the framework.

**PKS-dominated route: 7,8-dihydrokavain (Figure 6).** TridentSynthRL identifies a pathway in which a chimeric type I PKS with a benzoyl-CoA starter unit and three extension modules (each using malonyl-CoA as the extender, with module-specific tailoring domains including KR, DH, and ER) produces the core α-pyrone scaffold via thioesterase-mediated lactonization. The PKS product is subsequently subjected to an enthalpically downhill dehydration reaction (Δ*H* = −6.27 kcal/mol) to install the characteristic double bond, followed by an enzymatic *O*-methylation reaction predicted feasible by DORA-XGB (score = 0.955) using *S*-adenosylmethionine (SAM) as the methyl donor. This route demonstrates TridentSynthRL’s ability to design pathways where the PKS handles the core backbone construction while monofunctional enzymes handle the final peripheral modifications—a division of labor that leverages each modality’s strengths.

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| **Figure 6.** TridentSynthRL successfully proposes a pathway to the kavalactone 7,8-dihydrokavain via type I PKSs, monofunctional enzymes, and synthetic organic chemistry. In the select pathway shown, a chimeric PKS with a benzoyl-CoA starter unit is suggested, along with 3 extension modules, each of which incorporate malonyl-CoA as extender units and module-specific tailoring domains (DH, KR, ER). Following a thioesterase (TE)-mediated lactonization offloading reaction, the core -pyrone scaffold for 7,8-dihydrokavain is produced. With this scaffold, an enthalpically downhill (-6.27 kcal/mol) dehydration reaction is subsequently suggested, followed by an enzymatic *O-*methylation reaction. This *O-*methylation reaction is predicted to be enzymatically feasible with a feasibility score of 0.955, as assigned by our previously released supervised reaction feasibility classifier, DORA-XGB. |

**Hybrid PKS + chemical coupling route: desmethoxyyangonin (Figure 7).** A shorter chimeric PKS with only one extension module (benzoyl-CoA starter, hydroxymalonyl-CoA extender) produces a polyketide fragment that accounts for the aromatic styryl moiety. TridentSynthRL then proposes coupling this fragment with the commercially available chemical building block 4-hydroxy-2*H*-pyran-2-one—which provides the six-membered lactone ring—via an enthalpically downhill electrophilic aromatic alkylation (Δ*H* = −11.38 kcal/mol). Three subsequent enzymatic transformations complete the synthesis: *O*-methylation (DORA-XGB = 0.977), decarboxylation (DORA-XGB = 0.995), and dehydration (DORA-XGB = 0.964). This route illustrates TridentSynthRL’s capacity to combine a minimal PKS with chemical coupling and enzymatic tailoring, distributing the synthetic burden across all three modalities.

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| **Hybrid PKS + chemical coupling route: desmethoxyyangonin (Figure 7).** A shorter chimeric PKS with only one extension module (benzoyl-CoA starter, hydroxymalonyl-CoA extender) produces a polyketide fragment that accounts for the aromatic styryl moiety. TridentSynthRL then proposes coupling this fragment with the commercially available chemical building block 4-hydroxy-2*H*-pyran-2-one—which provides the six-membered lactone ring—via an enthalpically downhill electrophilic aromatic alkylation (Δ*H* = −11.38 kcal/mol). Three subsequent enzymatic transformations complete the synthesis: *O*-methylation (DORA-XGB = 0.977), decarboxylation (DORA-XGB = 0.995), and dehydration (DORA-XGB = 0.964). This route illustrates TridentSynthRL’s capacity to combine a minimal PKS with chemical coupling and enzymatic tailoring, distributing the synthetic burden across all three modalities. |

**Purely chemical route: 5,6,7,8-tetrahydroyangonin (Figure 8).** TridentSynthRL also discovers purely chemical pathways when they are more efficient. Starting from two commercially available building blocks—1-(but-3-yn-1-yl)-4-methoxybenzene and 3-bromoprop-2-ynoic acid—a sequence of Suzuki coupling with alkynes, HBr additions, esterification with methanol, intramolecular cyclization, and dehydrohalogenation yields 5,6,7,8-tetrahydroyangonin entirely through synthetic chemistry. This result is significant because it demonstrates that TridentSynthRL does not force biological routes where chemical ones suffice; the MCTS search naturally selects whichever modality—or combination of modalities—produces the most efficient pathway to the target.

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| **Figure 8:** Purely chemical retrosynthetic route to 5,6,7,8-tetrahydroyangonin proposed by TridentSynthRL. Starting from two commercially available building blocks — 1-(but-3-yn-1-yl)-4-methoxybenzene and 3-bromoprop-2-ynoic acid — a Suzuki coupling with alkynes forms a methoxyphenyl-substituted bromoacrylic acid intermediate. Subsequent addition of HBr to the alkyne moiety yields a vinyl bromide bearing the full carbon skeleton. Intermolecular esterification with methanol, a third chemical building block, followed by intramolecular addition of the alcohol to the pendant alkene generates the six-membered lactone ring. A final dehydrohalogenation eliminates HBr to furnish 5,6,7,8-tetrahydroyangonin. |

# **Materials and methods**

### **Architecture of the TridentSynth webtool**

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### **Ranking post-PKS pathways and enzyme recommendations**

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### **Extracting a list of common biological metabolites**

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**Discussion**

Here, we have presented TridentSynthRL, the first retrosynthetic planning framework to unify synthetic organic chemistry, monofunctional enzymatic catalysis, and type I polyketide synthase biosynthesis within a single hierarchical Monte Carlo tree search. Our framework introduces a two-agent architecture in which a chemoenzymatic retrosynthetic agent spawns forward-synthesis PKS agents when polyketide intermediates are detected, creating a bidirectional feedback loop between backward retrosynthetic fragmentation and forward biosynthetic verification. A supervised graph neural network trained on approximately one million synthetically generated polyketides and two million hard negatives detects PKS-synthesizable intermediates, while DORA-XGB enzymatic feasibility scoring and Benson group additivity thermodynamic estimates bias the search toward executable pathways. Deployed on the kavalactone family from *Piper methysticum*, TridentSynthRL designed retrosynthetic pathways to all 15 family members, with each compound reachable via at least one PKS-involving route. For the natural product cryptofolione, TridentSynthRL proposed a more efficient pathway using a 2-module PKS coupled with ring-opening metathesis, compared to a previously published 5-module design.

Several avenues for future development are worth pursuing. The reaction template library could be expanded to include additional enzyme classes and emerging catalytic chemistries. Incorporating learned value functions—for example, graph neural networks that predict node-level synthesis feasibility—could replace or augment UCB1 selection with more informed search guidance. Reaction condition compatibility checking would ensure that sequential steps use compatible solvents, temperatures, and catalysts. Extension to other natural product families beyond kavalactones, as well as commodity chemicals and pharmaceutical intermediates, would further test the generality of the framework. Finally, experimental validation of the proposed pathways remains the critical next step toward establishing TridentSynthRL as a practical tool for synthesis planning at the interface of chemistry and biology.

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# **Author Contributions Statement**

**Y.C:** Methodology and Software, Data curation, Writing – original draft and subsequent edits. Visualization – generated the figures in this manuscript. **M.G.S:** Methodology and Software, **G.B:** Methodology and Software, **A.M:** Conceptualization – conceptualized the approach of this study. Investigation. Formal analysis. Writing – review & editing, were the principal investigators who directed this project, contributed to the data analysis and interpretation, as well as edited the manuscript. **J.D.K:** Conceptualization – conceptualized the approach of this study. Investigation. Formal analysis. Writing – review & editing, were the principal investigators who directed this project, contributed to the data analysis and interpretation, as well as edited the manuscript. **H.G.M:**  Conceptualization – conceptualized the approach of this study. Investigation. Formal analysis. Writing – review & editing, were the principal investigators who directed this project, contributed to the data analysis and interpretation, as well as edited the manuscript. **T.W.H.B:** Methodology and Software, Data curation, Conceptualization – conceptualized the approach of this study. Investigation. Formal analysis. Writing – review & editing, were the principal investigators who directed this project, contributed to the data analysis and interpretation, as well as edited the manuscript. **K.E.J.T:** Conceptualization – conceptualized the approach of this study. Investigation. Formal analysis. Writing – review & editing, were the principal investigators who directed this project, contributed to the data analysis and interpretation, as well as edited the manuscript. **L.J.B:** Conceptualization – conceptualized the approach of this study. Investigation. Formal analysis. Writing – review & editing, were the principal investigators who directed this project, contributed to the data analysis and interpretation, as well as edited the manuscript.

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# C**ompeting Interests Statement**

J.D.K. has financial interests in Amyris, Ansa Biotechnologies, Apertor Pharma, Berkeley Yeast, Cyklos Materials, Demetrix, Lygos, Napigen, ResVita Bio and Zero Acre Farms. The other authors declare no competing interests.

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