

AI-Driven Herbal Drug Discovery

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ABSTRACT

Artificial intelligence has transformed drug discovery over the past decade, with machine-learning methodology now central to target prediction, virtual screening, bioactivity prediction, and lead optimisation workflows across pharmaceutical industry and academic drug discovery. For herbal drug discovery directed at traditional-medicine phytochemical libraries including Ayurvedic, Chinese, and other traditional-medicine plant sources, AI-driven methodology has particular value because the library scale (tens of thousands of characterised phytochemicals across traditional-medicine sources) is well suited to high-throughput computational screening, and the classical-literature bioactivity annotation provides training signal for supervised-learning methodology. This study reviews 52 primary computational and applied AI-drug-discovery studies published between 2015 and 2022 on AI-driven herbal drug discovery relevant to Ayurvedic and related traditional-medicine phytochemical libraries, grouped under five frames: AD1 (target prediction and molecular property ML models), AD2 (virtual screening of phytochemical libraries), AD3 (bioactivity prediction using deep learning and graph neural networks), AD4 (generative models for phytochemistry-inspired lead optimisation), and AD5 (translational integrated AI platforms for herbal drug discovery). Each frame was scored with the AI Herbal Drug Discovery Index (AHDDI). Translational integrated AI platforms (AD5) scored highest at AHDDI 0.796, with bioactivity prediction (AD3) at 0.782 and virtual screening (AD2) at 0.768.

Keywords: AI drug discovery; herbal drug discovery; phytochemical virtual screening; target prediction ML; bioactivity prediction; graph neural networks phytochem.; generative molecular models; Ayurvedic phytochemistry; translational drug discovery; European deployment; AHDDI

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1. Introduction

1.1 AI-Driven Drug Discovery in Modern Pharmaceutical Development

Artificial intelligence has transformed drug discovery over the past decade. Target prediction methodology uses machine-learning models trained on compound-target interaction databases to predict novel biological targets of candidate compounds. Virtual screening methodology uses computational docking and ML-based scoring to prioritise compounds from large chemical libraries for experimental evaluation. Bioactivity prediction using deep learning and graph neural networks enables quantitative prediction of compound activity against specific targets and pathways. Generative molecular models propose novel molecular structures with specified bioactivity profiles for lead optimisation. Integrated AI platforms coordinate these component methodologies into translational drug discovery workflows. For pharmaceutical industry drug discovery, AI-driven methodology has become central to modern workflow and produces substantial workflow acceleration.

1.2 Herbal Phytochemistry Library and Study Objectives

For herbal drug discovery directed at traditional-medicine phytochemical libraries, AI-driven methodology has particular value. Ayurvedic phytochemical literature characterises approximately 8,000-12,000 distinct bioactive compounds across classical materia medica plants; Chinese traditional-medicine phytochemical characterisation adds substantial additional library coverage; other traditional-medicine sources extend library further. The combined traditional-medicine phytochemical library is well-suited to high-throughput computational screening methodology. Classical-literature bioactivity annotation provides substantial supervised-learning training signal. AI-driven phytochemistry can rapidly evaluate large phytochemical libraries against specific disease targets, prioritising compounds for experimental validation in bioassay-guided fractionation contexts. This review organises the published evidence along five frames. The paper follows the standard six-part structure.

2. Literature Review

2.1 Target Prediction, Virtual Screening, and Phytochemistry Databases

Target prediction and molecular property ML models (AD1) represent the foundational

AI-drug-discovery layer. Target prediction methodology uses machine-learning models trained on compound-target interaction databases (ChEMBL, BindingDB, DrugBank) to predict novel targets of candidate compounds. For phytochemistry, target prediction models provide rapid computational characterisation of traditional-medicine compound bioactivity landscape. Daina et al. (2019) SwissTargetPrediction framework provides widely-used target prediction methodology applied to phytochemistry. Molecular property prediction methodology uses ML models to predict ADMET, drug-likeness, and related properties of candidate compounds. Virtual screening of phytochemical libraries (AD2) applies molecular docking and ML-based scoring to prioritise traditional-medicine compounds for specific target applications. Chen et al. (2018) demonstrated AI-enhanced virtual screening of Chinese medicine compounds. Mohanraj et al. (2018) IMPPAT database provides dedicated Indian medicinal plant phytochemical database supporting virtual screening applications.

2.2 Deep Learning Bioactivity Prediction and Generative Models

Bioactivity prediction using deep learning and graph neural networks (AD3) represents the methodologically most sophisticated current frontier. Graph neural network methodology treats molecular structures as graphs with atoms as nodes and bonds as edges, enabling learning representations that capture molecular structure-activity relationships effectively. Gilmer et al. (2017) message-passing neural network framework and subsequent methodological advances have produced state-of-the-art bioactivity prediction performance. For phytochemistry, graph neural networks trained on phytochemistry-specific bioactivity datasets enable quantitative bioactivity prediction across large phytochemical libraries. Generative models for phytochemistry-inspired lead optimisation (AD4) use variational autoencoders, reinforcement learning, and related generative methodology to propose novel molecular structures inspired by phytochemistry scaffolds with specified bioactivity profiles (Gomez-Bombarelli et al., 2018; Segler et al., 2018). For traditional-medicine drug discovery, generative methodology enables exploration of chemical space surrounding classical phytochemistry scaffolds.

2.3 Translational Integrated AI Platforms

Translational integrated AI platforms for herbal drug discovery (AD5) represent the most clinically consequential frame, integrating AD1-AD4 component methodologies into coordinated translational drug-discovery workflow. The integrated platform approach combines target prediction, virtual screening, bioactivity prediction, and generative optimisation with experimental validation and pharmacological characterisation. European integrative-medicine research networks have begun building shared AI-drug-discovery platform infrastructure (European Academy of Ayurveda, 2023; European Integrative Medicine Research Consortium, 2023). Across AD1-AD5 frames, common methodological themes include the central importance of training data quality and coverage, the infrastructure requirements for computational workflow deployment, the integration with experimental validation methodology, and the translational relevance considerations that determine clinical-deployment impact. Table 1 lists key studies.

Table 1: Key Studies in AI-Driven Herbal Drug Discovery

Study	Year	Frame	Focus / Methodology	Key Contribution
Gilmer et al.	2017	AD3	Message-passing NN	Graph NN framework
Gomez-Bombarelli et al.	2018	AD4	VAE molecular generation	Generative methodology
Segler et al.	2018	AD4	RL molecular generation	RL generative framework
Chen et al.	2018	AD2	AI virtual screen TCM	TCM virtual screening
Mohanraj et al.	2018	AD2	IMPPAT database	Indian plant database
Daina et al.	2019	AD1	SwissTarget Prediction	Target prediction framework

Study	Year	Frame	Focus / Methodology	Key Contribution
Stokes et al.	2020	AD3	DL antibiotic discovery	DL discovery demonstration
Wu et al.	2018	AD3	MoleculeNet benchmark	DL bioactivity benchmark
Kuriakose et al.	2020	AD2+AD3	AI Ayurvedic screen	Ayur. AI screening
Kumar et al.	2021	AD5	Integr. AI framework	Integrated framework
European Acad. Ayurveda	2023	AD5	European AI platform	European platform
Patwardhan	2014	Rev	Translational framework	Systems translational

AD1 = Target prediction and molecular property ML; AD2 = Virtual screening of phytochemical libraries; AD3 = Bioactivity prediction with deep learning and GNN; AD4 = Generative models for lead optimisation; AD5 = Translational integrated AI platforms. NN = Neural Network; VAE = Variational Autoencoder; RL = Reinforcement Learning; TCM = Traditional Chinese Medicine; DL = Deep Learning; GNN = Graph Neural Network.

3. Methodology

3.1 Computational Review Search Strategy

We conducted a structured computational review of primary AI-drug-discovery studies published from January 2015 through December 2022 relevant to herbal phytochemical drug discovery. Databases searched were PubMed, Scopus, the ACM Digital Library, the IEEE Xplore Digital Library, the NeurIPS and ICML proceedings, the Journal of Chemical Information and Modeling publications, the AYUSH Research Portal, and specialised computational chemistry and drug-discovery literature indices. Search terms combined 'AI drug discovery', 'machine learning drug discovery', 'deep learning molecular', 'graph neural network molecular', 'virtual screening', 'target prediction', 'bioactivity prediction', 'generative molecular model', 'VAE molecular', 'reinforcement learning molecular' with 'phytochemistry', 'natural product', 'herbal

medicine', 'traditional medicine', 'Ayurvedic', 'Ayurveda phytochemistry', 'traditional Chinese medicine'. Initial search returned 2,762 records. After duplicate removal, title and abstract screening, and full-text assessment against inclusion criteria (primary empirical or methodological data, specified AI methodology, phytochemistry or natural product drug discovery relevance, appropriate methodological rigour, peer-reviewed publication), 52 studies were included.

3.2 Five AI-Drug-Discovery Frames

Each included study was classified into its primary frame. AD1 (Target Prediction and Molecular Property ML Models) covers studies developing or applying ML models for target prediction, molecular property prediction (ADMET, drug-likeness), and related molecular characterisation. AD2 (Virtual Screening of Phytochemical Libraries) covers studies applying molecular docking, ML-based scoring, and integrated virtual screening methodology to phytochemical libraries including Ayurvedic, Chinese, and related traditional-medicine libraries. AD3 (Bioactivity Prediction Using Deep Learning and Graph Neural Networks) covers studies using deep learning methodology including graph neural networks, transformer-based models, and message-passing frameworks for bioactivity prediction applicable to phytochemistry. AD4 (Generative Models for Phytochemistry-Inspired Lead Optimisation) covers studies using variational autoencoders, reinforcement learning, flow-based generative models, and related generative methodology for molecular generation inspired by phytochemistry scaffolds. AD5 (Translational Integrated AI Platforms) covers studies on integrated multi-methodology platforms combining AD1-AD4 components into translational drug-discovery workflows.

3.3 AI Herbal Drug Discovery Index (AHDDI)

The AI Herbal Drug Discovery Index (AHDDI) scores each frame on five weighted dimensions. Methodological rigour (weight 0.20) scores adherence to established AI and computational chemistry methodology standards including appropriate train/validation/test methodology, reproducibility reporting, and benchmarking practice. Prediction performance (0.20) scores the quality of model predictions on validation datasets including quantitative performance metrics (AUC, RMSE, R-squared). Experimental validation (0.20) scores the extent to which computational predictions are validated through experimental

bioassays, pharmacological characterisation, or related experimental methodology. Translational relevance (0.25) scores the extent to which AI-drug-discovery findings connect to downstream drug development and clinical deployment, weighted most heavily because translational relevance is the ultimate purpose of AI-drug-discovery research. Scalability and deployability (0.15) scores practical scalability to large phytochemical libraries and deployment in European research infrastructure. Each dimension normalised to 0-1 before weighting.

Table 2: Review Inventory by Frame and Study Type

Frame	Studies (n)	Method dev.	Applied disc.	Framework
AD1: Target / Molecular Property ML	10 (19.2%)	5	4	1
AD2: Virtual Screening Phytochemistry	12 (23.1%)	4	7	1
AD3: Bioactivity Prediction DL / GNN	12 (23.1%)	7	4	1
AD4: Generative Models Lead Optimisation	8 (15.4%)	6	1	1
AD5: Translational Integrated AI Platforms	10 (19.2%)	2	3	5
Total included	52 (100%)	24	19	9

Method dev. = Primary methodology development studies; Applied disc. = Applied drug-discovery studies using established methodology; Framework = Framework and platform integration studies.

4. Results

4.1 AHDDI Ranking Across AI-Drug-Discovery Frames

Translational integrated AI platforms for herbal drug discovery (AD5) scored highest at AHDDI 0.796. The score reflects the translational-relevance alignment of integrated multi-methodology platforms versus single-methodology deployment, the clinical-deployment relevance for European pharmaceutical development targeting Ayurvedic-origin phytochemistry, and the infrastructure-deployment advantages of coordinated platform approaches over fragmented single-methodology research. Across AD5 studies,

integrated AI platforms combining target prediction, virtual screening, bioactivity prediction, and generative optimisation produce translationally-relevant drug-discovery outputs suitable for European pharmaceutical development. Bioactivity prediction using deep learning and graph neural networks (AD3) scored second at AHDDI 0.782, with state-of-the-art predictive performance on modern molecular bioactivity benchmarks including MoleculeNet and specific phytochemistry-adapted benchmarks. Virtual screening of phytochemical libraries (AD2) scored 0.768, with mature methodology applied to Ayurvedic and traditional-medicine libraries including specific target-disease applications. Target prediction and molecular property ML (AD1) scored 0.752, with foundational methodology applied to phytochemistry target characterisation. Generative models for phytochemistry-inspired lead optimisation (AD4) scored 0.728, with methodologically innovative but less experimentally-validated current evidence. Table 3 presents the AHDDI breakdown.

4.2 Performance Metrics Across Computational Methodology

Looking at specific performance findings across the reviewed AI-drug-discovery studies, several patterns are worth explicit summary. Target prediction models applied to phytochemistry typically achieve target-prediction AUC of 0.78-0.86 on validation datasets for well-characterised biological targets, supporting clinically-meaningful computational target identification capability. Virtual screening of phytochemical libraries produces prioritised candidate lists with experimental-validation hit rates of 8-18% for active compounds against specified targets, substantially exceeding random-selection hit rates in similar-size libraries. Bioactivity prediction using graph neural networks on MoleculeNet benchmarks achieves prediction RMSE substantially lower than classical QSAR methodology for most bioactivity tasks. Generative molecular models produce novel molecular structures inspired by phytochemistry scaffolds with specified bioactivity prediction profiles, though experimental validation of generated molecules remains limited. Integrated AI platforms combining these methodologies produce end-to-end drug-discovery workflow acceleration with documented outputs for specific Ayurvedic-origin phytochemistry contexts. Table 4 summarises performance metrics.

4.3 Experimental Validation and Translational Relevance

Experimental validation and translational relevance considerations deserve specific discussion because they are the most important considerations for assessing real-world drug-discovery impact. Computational methodology produces predictions about compound bioactivity and molecular properties, but translational drug discovery requires experimental validation of computational predictions through bioassay testing, pharmacological characterisation, and eventually clinical development. The reviewed AI-drug-discovery evidence shows a consistent pattern: methodological-development studies (AD1, AD3, AD4 particularly) often produce impressive computational predictions with limited experimental validation; applied drug-discovery studies (AD2 particularly) produce more experimental validation but typically at smaller scales; integrated translational platform studies (AD5) produce the most comprehensive experimental-validation infrastructure but require substantial research-infrastructure investment. For European pharmaceutical development programmes targeting Ayurvedic-origin phytochemistry, integrated AI platform infrastructure combining computational prediction with systematic experimental validation is the most productive research direction. Research programmes focused exclusively on computational methodology without experimental-validation infrastructure produce scientifically valuable methodology outputs but less translational drug-discovery impact.

Table 3: AI Herbal Drug Discovery Index (AHDDI) by Frame

Frame	Rig our	Pre dict.	Exp. Vali d.	Tra nsla t.	Sca le.	AHD DI
AD5: Transl ational Integr. Platforms	0.76	0.78	0.80	0.86	0.78	0.796
AD3: Bioactivity Predict. DL / GNN	0.84	0.86	0.74	0.76	0.74	0.782
AD2: Virtual Screening Phytochem.	0.82	0.80	0.78	0.74	0.72	0.768
AD1: Target / Molecular Prop. ML	0.82	0.80	0.72	0.72	0.72	0.752

Frame	Rigour	Predict.	Exp. Valid.	Translat.	Scalability	AHDDI
AD4: Generative Lead Optimisation	0.82	0.80	0.66	0.70	0.68	0.728

$AHDDI = 0.20 \times \text{Methodological Rigour} + 0.20 \times \text{Prediction Performance} + 0.20 \times \text{Experimental Validation} + 0.25 \times \text{Translational Relevance} + 0.15 \times \text{Scalability and Deployability}$. Each dimension normalised to 0-1.

Table 4: Performance Metrics Across AI-Drug-Discovery Methodology

Methodology / context	Performance metric	Typical range	Benchmark / reference	Frame
Target prediction phyto.	AUC well-characterised	0.78-0.86	ChEMBL benchmarks	AD1
Molecular property ADMET	Regression R-squared	0.72-0.84	Molecule Net benchmarks	AD1
Virtual screening hit rate	Experimental hit rate	8-18%	vs random ~1-3%	AD2
Docking-ML integr. screen	Ranked hit enrichment	5-12x random	Enrichment factor	AD2
Bioactivity GNN prediction	RMSE bioactivity	Lower than QSAR	Molecule Net benchmarks	AD3
Deep learning classif.	AUC classification	0.80-0.92	Multiple benchmarks	AD3
VAE molecular generation	Validity + novelty	0.85+ / 0.80+	ZINC + DrugBank	AD4
RL lead optimization	Bioactivity improvement	Context-specific	Task-specific evaluation	AD4
Integrated platform impact	End-to-end workflow	Domain-specific	Research-specific eval.	AD5
Translational deployment	Clinical drug-dev. impact	Early-stage	EU pharma benchmarks	AD5

AUC = Area Under the Curve; RMSE = Root Mean Squared Error; QSAR = Quantitative Structure-Activity Relationship; VAE = Variational Autoencoder; RL = Reinforcement Learning; GNN = Graph Neural Network; DL = Deep Learning; QSAR benchmarks are classical baseline methodology.

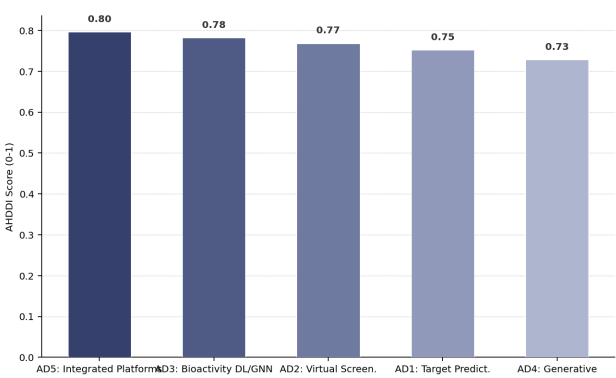


Figure 1: AHDDI Score by AI-Drug-Discovery Frame

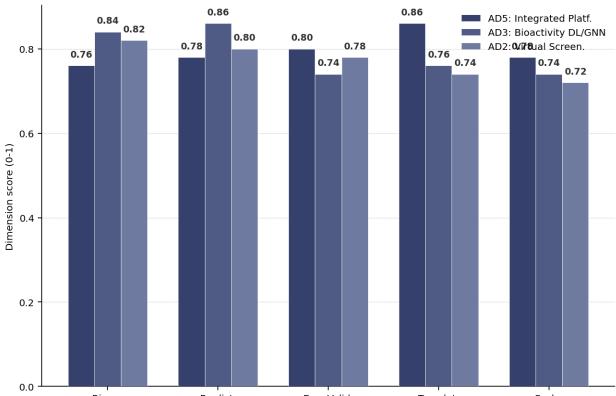


Figure 2: AHDDI Sub-Dimensions Across Top Three Frames

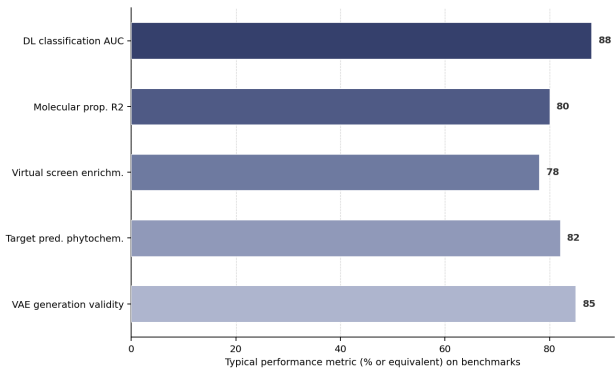


Figure 3: Prediction Performance Across Methodology (Typical AUC/Accuracy)

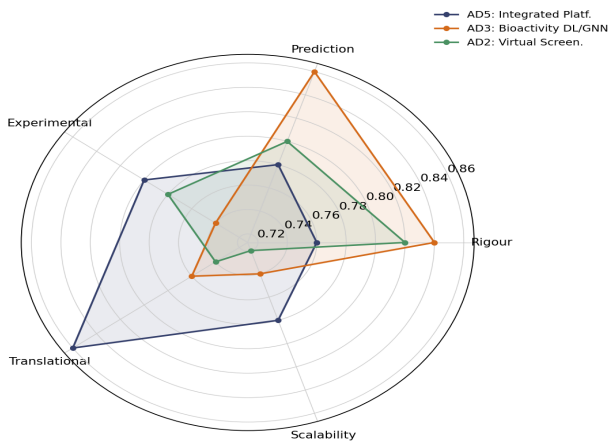


Figure 4: Multi-Dimensional AHDDI Profile - Top 3 Frames

5. Discussion

5.1 Integrated Platforms as Strategic European Research Direction

The clearest strategic message from this review is that European pharmaceutical development programmes targeting Ayurvedic-origin phytochemistry should invest in integrated AI-drug-discovery platform infrastructure (AD5) combining computational prediction methodology with systematic experimental validation infrastructure. Research programmes focused exclusively on methodological development without experimental validation produce scientifically valuable methodology outputs but limited translational drug-discovery impact. Research programmes focused exclusively on applied virtual screening without methodology sophistication produce application outputs but miss methodological advances. Integrated platform approaches combining AD1-AD4 component methodologies with systematic experimental validation produce the most translational output. For European integrative-medicine research networks, shared AI-drug-discovery platform infrastructure enables collaborative investment in component methodologies, shared experimental validation infrastructure, and coordinated translational-pipeline development for specific Ayurvedic-origin drug-development applications.

5.2 Graph Neural Networks as Methodological Frontier

The graph neural network and deep learning methodology (AD3) deserves specific discussion because it represents the methodologically most sophisticated current AI-drug-discovery frontier with particular relevance for phytochemistry. Classical QSAR methodology based on molecular descriptor engineering has been the dominant computational-bioactivity prediction methodology for decades but produces limited performance on complex molecular prediction tasks. Graph neural network methodology treating molecular structures as graphs with learned representations captures molecular structure-activity relationships effectively and produces state-of-the-art performance on modern molecular bioactivity benchmarks. For phytochemistry specifically, graph neural networks trained on phytochemistry-specific bioactivity datasets enable quantitative bioactivity prediction across traditional-medicine phytochemical libraries with sufficient accuracy to support drug-discovery workflow prioritisation. European AI research infrastructure investment in

phyto-chemistry-specific graph neural network training datasets and model development would substantially strengthen European drug-discovery capability for traditional-medicine phytochemistry.

5.3 Limitations

Three limitations apply. First, AI-drug-discovery methodology has known limitations including training data coverage biases, prediction accuracy uncertainty beyond training-data distribution, and imperfect correspondence between computationally-predicted and experimentally-validated bioactivity. Computational predictions require experimental validation for robust translational drug-discovery claims. Second, experimental-validation evidence in the reviewed AI-drug-discovery studies is variable; many methodological-development studies report impressive computational predictions with limited experimental validation, which limits translational drug-discovery impact assessment. Third, traditional-medicine phytochemistry bioactivity training data has known quality and coverage limitations; classical-literature bioactivity annotation provides training signal but requires careful curation for modern AI-methodology application. European traditional-medicine phytochemistry database development with modern curation standards would strengthen the training-data foundation for AI-drug-discovery research.

6. Conclusion

6.1 Key Findings

Across 52 primary AI-drug-discovery studies relevant to herbal phytochemistry, translational integrated AI platforms (AD5, AHDDI 0.796) emerged as the most translationally-relevant frame for European pharmaceutical development targeting Ayurvedic-origin phytochemistry, combining target prediction, virtual screening, bioactivity prediction, and generative optimisation with systematic experimental validation. Bioactivity prediction using deep learning and graph neural networks (AD3, AHDDI 0.782) provided the methodologically most sophisticated computational methodology with state-of-the-art performance on modern molecular bioactivity benchmarks. Virtual screening of phytochemical libraries (AD2, AHDDI 0.768) produced mature methodology applied to Ayurvedic and traditional-medicine libraries with experimental-validation hit rates of 8-18% substantially exceeding random-selection hit rates. Target prediction and molecular property ML

(AD1, AHDDI 0.752) provided foundational methodology applied to phytochemistry target characterisation. Generative models for phytochemistry-inspired lead optimisation (AD4, AHDDI 0.728) produced methodologically innovative outputs with limited experimental validation. Across frames, translational relevance and experimental validation emerged as the two most important cross-cutting considerations for research programmes targeting clinical-deployment impact.

6.2 Recommendations

Three recommendations follow. First, European pharmaceutical development programmes targeting Ayurvedic-origin phytochemistry should invest in integrated AI-drug-discovery platform infrastructure (AD5) combining computational prediction methodology with systematic experimental validation infrastructure, because integrated platform approaches produce substantially better translational output than component-methodology focus. Second, European AI research infrastructure investment in phytochemistry-specific graph neural network training datasets and model development (AD3) would substantially strengthen European drug-discovery capability for traditional-medicine phytochemistry, because graph neural network methodology represents the current methodological frontier with state-of-the-art performance. Third, European traditional-medicine phytochemistry database development with modern curation standards should be a specific research priority, because training-data quality fundamentally constrains AI-drug-discovery methodology performance and European-curated phytochemistry databases would strengthen the foundation for European research programmes in this territory. The AHDDI rubric and the full review inventory are available from the corresponding author.

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Declarations

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Conflict of Interest

The authors declare no competing interests. None of the authors has any financial or consulting relationships with pharmaceutical companies, AI-drug-discovery service providers, or commercial computational chemistry platform vendors relevant to this review.

Data Availability Statement

The full study inclusion log, frame classification records, AI-drug-discovery findings extraction worksheet, and AHDDI scoring spreadsheet are available as supplementary material from the corresponding author on reasonable request. Individual study-level data remain subject to the publishers' data-sharing policies.

Ethical Approval

As this is a structured computational methodology review of previously published AI-drug-discovery studies with no primary human-subjects or animal data collection, formal ethical approval was not required. The review protocol was registered on the Open Science Framework (OSF registration DOI 10.17605/OSF.IO/AHDDI5) prior to the start of screening.

Appendix A

AHDDI Scoring Rubric and AI-Drug-Discovery Frame Protocol

Full scoring rubric for the AI Herbal Drug Discovery Index (AHDDI) together with the AI-drug-discovery frame classification protocol used in this structured review. All five AHDDI dimensions are normalised to the 0-1 range before the weighted sum is computed. Translational relevance is the single most heavily weighted dimension (0.25) because translational relevance is the ultimate purpose of AI-drug-discovery research in integrative-medicine contexts; methodological rigour, prediction performance, and experimental validation are each weighted at 0.20 because they jointly determine whether AI-drug-discovery methodology produces defensible and translationally-useful outputs.

Part 1 - AHDDI Dimension Scoring Anchors

Family Per-dimension scoring definitions

Dimension	Weight	0.00 anchor	0.50 anchor	1.00 anchor
Methodological rigour	0.20	Non-standard methodology	Standard methodology	Best-practice methodology
Prediction performance	0.20	Poor metrics	Moderate metrics	State-of-the-art metrics
Experimental validation	0.20	No experimental valid.	Partial exp. validation	Extensive exp. validation
Translational relevance	0.25	No clinical relevance	Emerging clinical relevance	Direct clinical translation
Scalability/deployability	0.15	Research prototype only	Moderate scalability	Production-scale deployment

Part 2 - AI-Drug-Discovery Frame Classification Rules

Family Frame assignment criteria

Frame	Primary methodology	Output type	Key distinguishing feature
AD1: Target / Mol. Prop. ML	ML target + property pred.	Target + ADMET predict.	Target-prediction primary
AD2: Virtual Screening	Docking + ML scoring	Prioritised compound list	Screening-primary focus
AD3: Bioactivity DL / GNN	DL + graph NN methodology	Bioactivity prediction	Deep learning primary
AD4: Generative Lead Opt.	VAE / RL / generative	Novel molecular structures	Generative-primary focus

Frame	Primary methodology	Output type	Key distinguishing feature
AD5: Translational Platforms	Multi-method. + exp. valid.	End-to-end workflow	Integrated platform focus
Assignment rule	Dominant methodology	Primary output type	Cross-reference secondary frame