
AI-Driven Proxy-Based Screening of Degradation Risk in Blue OLED Emitters

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Abstract

1 The operational lifetime of deep-blue organic light-emitting diodes (OLEDs) re-
2 mains a critical technological bottleneck due to intrinsic high-energy exciton-
3 driven degradation. In this study, we present an AI-assisted virtual screening
4 framework to quantitatively rank degradation risks of blue emitter candidates us-
5 ing experimentally motivated physical proxies. A curated set of representative
6 blue emitters was analyzed using RDKit- and DeepChem-based molecular rep-
7 resentations to extract descriptors related to charge-transfer localization, exciton-
8 exciton interaction propensity, and excitation energy. These proxies were inte-
9 grated into a composite degradation risk score to emulate early-stage industrial
10 screening prior to costly quantum chemical calculations or device fabrication.
11 Structural similarity analysis further revealed chemically similar emitters exhib-
12 iting substantially different predicted degradation risks, emphasizing the role of
13 charge localization and exciton interaction pathways. The proposed framework
14 demonstrates how AI tools can be used as virtual experimental instruments to
15 guide risk-aware material down-selection and early-stage design of blue OLED
16 emitters.

17

1 Introduction

18 Write your introduction here. Introduction Deep-blue organic light-emitting diodes (OLEDs) are
19 essential for high-color-gamut display technologies; however, their operational lifetime remains a
20 fundamental bottleneck. Unlike green and red emitters, blue emitters operate at intrinsically high
21 excitation energies, which accelerate chemical bond cleavage, charge-induced reactions, and ex-
22 citon-exciton interaction pathways. As a result, blue OLED materials exhibit significantly faster
23 degradation, limiting device lifetime and commercial reliability. Conventional approaches to life-
24 time evaluation primarily rely on device-level stress testing or high-level quantum chemical calcu-
25 lations to assess bond dissociation energies and excited-state stability. While these methods pro-
26 vide valuable mechanistic insights, they are costly, time-consuming, and impractical for large-scale
27 early-stage material screening. Consequently, a substantial gap exists between molecular design
28 and experimental lifetime validation, making it difficult to rapidly down-select degradation-prone
29 candidates before device fabrication. Recent material strategies, including thermally activated de-
30 layed fluorescence (TADF), multi-resonance TADF (MR-TADF), and hyperfluorescence architec-
31 tures, have significantly improved internal quantum efficiency and color purity. Nevertheless, these
32 advances have not fundamentally resolved the lifetime limitations of deep-blue emitters, as degra-
33 dation remains governed by high-energy exciton physics, charge-transfer localization, and exci-
34 ton-exciton interaction processes such as singlet-singlet annihilation (SSA) and triplet-polaron an-
35 nihilation (TPA). To address this gap, we propose an AI-assisted virtual screening framework that
36 emulates early-stage industrial material filtering by integrating experimentally motivated physical
37 degradation proxies with molecular representations. Rather than developing a black-box predic-

38 tive model, we employ AI tools as virtual experimental instruments to extract descriptors related to
 39 charge-transfer propensity, exciton interaction likelihood, and excitation energy. These descriptors
 40 are combined into a composite degradation risk score to quantitatively rank blue emitter candidates
 41 prior to costly quantum chemical calculations or device fabrication. Using a curated set of represen-
 42 tative blue OLED emitters, we demonstrate that structurally similar molecules can exhibit substan-
 43 tially different predicted degradation risks, underscoring the importance of charge localization and
 44 exciton interaction pathways beyond simple structural similarity. The proposed framework provides
 45 a practical methodology for risk-aware material down-selection and early-stage design guidance in
 46 blue OLED materials research.

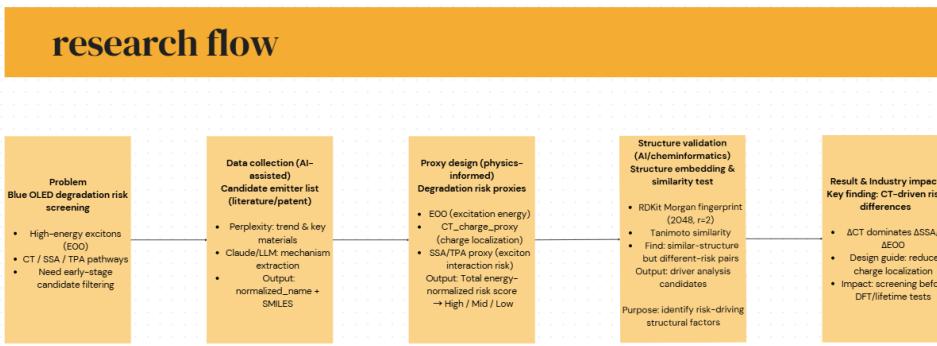


Figure 1: Overall workflow for physics-informed, AI-assisted screening of blue OLED degradation risk.

47 The framework integrates literature- and LLM-assisted data collection, physics-informed proxy de-
 48 sign for excitation energy (E00), CT charge localization, and SSA/TPA interaction risk, followed by
 49 structure-based validation using RDKit Morgan fingerprints and Tanimoto similarity.

50 2 Methods

51 Method

52 2.1 Literature-Driven Candidate Collection Using AI Tools

53 2.1 Literature-Driven Candidate Collection Using AI Tools Blue OLED emitter candidates were
 54 collected using a combination of AI-assisted literature search and manual curation. Perplexity AI
 55 was used to identify recent review and primary research articles related to deep-blue OLED emitters,
 56 including TADF, MR-TADF, hyperfluorescence, phosphorescent emitters, and host materials. These
 57 searches were guided by keywords such as deep-blue OLED stability, TADF blue lifetime, and MR-
 58 TADF degradation.

59 2.2 Dataset Standardization and SMILES Acquisition

60 For each selected emitter, a standardized molecular representation was generated using canonical
 61 SMILES strings. SMILES were obtained from published supplementary information, public chem-
 62 ical databases, or manually curated based on reported chemical structures. All molecules were stan-
 63 dardized using RDKit to ensure consistent valence, aromaticity perception, and hydrogen handling.
 64 This standardization step ensures reproducibility and eliminates representation-dependent artifacts
 65 in downstream descriptor and fingerprint calculations.

66 2.3 RDKit-Based Structural Descriptor Generation

67 Physicochemical and structural descriptors were computed using RDKit (version 2025.09.4). Cal-
 68 culated descriptors included molecular weight, ring counts, heteroatom counts, topological polar

69 surface area (TPSA), hydrogen bond donors/acceptors, and carbon sp³ fraction. These descriptors
70 provide a baseline structural characterization and were additionally used to support interpretation
71 of proxy trends. RDKit Morgan fingerprints (radius = 2, 2048 bits) were generated for structural
72 similarity analysis.

73 **2.4 DeepChem-Based Molecular Representation**

74 DeepChem (version 2.8.0) was used to generate machine-readable molecular representations to sup-
75 port feature extraction and downstream analysis. Due to the absence of GPU acceleration and deep
76 learning backends, DeepChem was used in a lightweight descriptor and featurization mode with-
77 out training neural network models. This ensured compatibility with CPU-only environments while
78 enabling standardized molecular feature handling.

79 **2.5 Definition of Physically Motivated Degradation Proxies**

80 Three physically motivated degradation risk proxies were defined to capture key mechanisms
81 known to govern blue OLED operational instability: (i) charge-transfer localization propensity, (ii)
82 excitation-energy-weighted charge localization risk, and (iii) excitation-energy-weighted exciton-
83 exciton interaction risk (SSA/TPA). These proxies were designed to reflect experimentally and the-
84oretically established degradation pathways, including polaron-induced bond cleavage, localized
85 high-energy excitons, and exciton-exciton annihilation processes.

86 **2.6 Composite Degradation Ranking**

87 Individual proxy values were combined to generate a composite degradation risk score. Each proxy
88 was normalized to a common scale prior to aggregation. The composite risk score was designed to
89 emulate early-stage industrial screening practices by prioritizing emitters with multiple concurrent
90 degradation risk factors rather than reliance on a single structural or energetic metric.

91 **2.7 Structural Similarity Analysis**

92 Structural similarity between emitters was quantified using Tanimoto similarity computed from RD-
93 Kit Morgan fingerprints. For selected representative molecular pairs, similarity values were com-
94 compared against differences in composite degradation risk scores. This analysis was used to identify
95 cases where structurally similar molecules exhibit significantly different predicted degradation sus-
96 ceptibilities, highlighting the decoupling between structural similarity and degradation risk.

97 **2.8 Proxy Definition and Total Energy-Normalized Degradation Risk Formulation**

Figure S1. Proxy components and total energy-normalized risk scores for all candidate blue emitters

normalized_name	CT_charge_proxy	E00_weighted_charge_risk	E00_weighted_SSA_TPA_risk	Total_energy_normalized_risk	Group (High/Mid/Low)
SDPS-4PhCz	2.932	3.139	10.751	6.945	High
V-DABNA	2.656	2.629	7.221	4.925	High
5CzBN	2.571	2.456	7.052	4.754	High
BDpyInCz	2.737	2.454	5.732	4.093	Mid
DPAVBI	3.724	3.801	3.555	3.678	Mid
BmPAC	3.524	3.444	3.38	3.412	Mid
DABNA	3.009	3.004	2.889	2.947	Low
DMAC-TRZ	2.571	2.385	3.29	2.838	Low
MS2	1.904	1.901	2.183	2.042	Low

Figure 2: To enable physics-informed early-stage screening of blue OLED emitters, we defined a set of degradation risk proxies capturing charge localization and exciton-exciton interaction mechanisms. These proxies were combined with excitation energy to construct an integrated, energy-normalized degradation risk score..

98 The charge-transfer localization proxy was defined as:

$$R_{CT} = f_{CT}(charge\ localization\ descriptors) \quad (1)$$

99 The excitation-energy-weighted charge risk was defined as:

$$R_{charge}^{E_{00}} = E_{00} \times R_{CT} \quad (2)$$

100 The excitation-energy-weighted SSA/TPA interaction risk was defined as:

$$R_{SSA/TPA}^{E_{00}} = E_{00} \times R_{SSA/TPA} \quad (3)$$

101 The total energy-normalized degradation risk score was then computed as:

$$R_{total} = w_1 R_{CT} + w_2 R_{charge}^{E_{00}} + w_3 R_{SSA/TPA}^{E_{00}} \quad (4)$$

102 where w_1 , w_2 , and w_3 are weighting coefficients set to unity in this study for equal contribution.
103 This formulation emphasizes the amplified degradation susceptibility associated with high excitation
104 energies in blue emitters. All computational parameters, library versions, and descriptor definitions
105 are provided to ensure full reproducibility of the reported results.

106 **2.9 Implementation Details**

107 All computations were performed in a Python 3.11.14 environment using RDKit (2025.09.4),
108 DeepChem (2.8.0), NumPy (2.4.1), and pandas (2.3.3). Calculations were executed on a CPU-
109 only system equipped with an Intel i5 processor and 16 GB RAM, without GPU acceleration. This
110 lightweight computational setup demonstrates that the proposed framework is accessible and repro-
111ducible in resource-limited research environments.

112 **2.10 Computational Workflow and Reproducibility**

113 The complete computational workflow consists of: (i) literature-driven candidate selection, (ii)
114 SMILES standardization, (iii) RDKit descriptor and fingerprint generation, (iv) proxy calculation,
115 (v) composite risk aggregation, and (vi) similarity-based comparative analysis. All scripts were ex-
116 ecuted in a modular pipeline to facilitate stepwise validation and reproducibility. This workflow
117 enables independent researchers to replicate the analysis and extend the framework to larger molec-
118 ular libraries or alternative blue emitter families.

119 **3 Result**

120 **3.1 Composite Degradation Risk Ranking of Blue Emitters**

121 3.1 Composite Degradation Risk Ranking of Blue Emitters Using the proposed composite degra-
122 dation risk scoring framework, a representative set of blue OLED emitters was quantitatively ranked
123 according to their predicted degradation susceptibility. Figure 2 summarizes the normalized proxy
124 values (CT charge proxy, SSA/TPA proxy, and excitation energy E) and the resulting composite risk
125 scores.

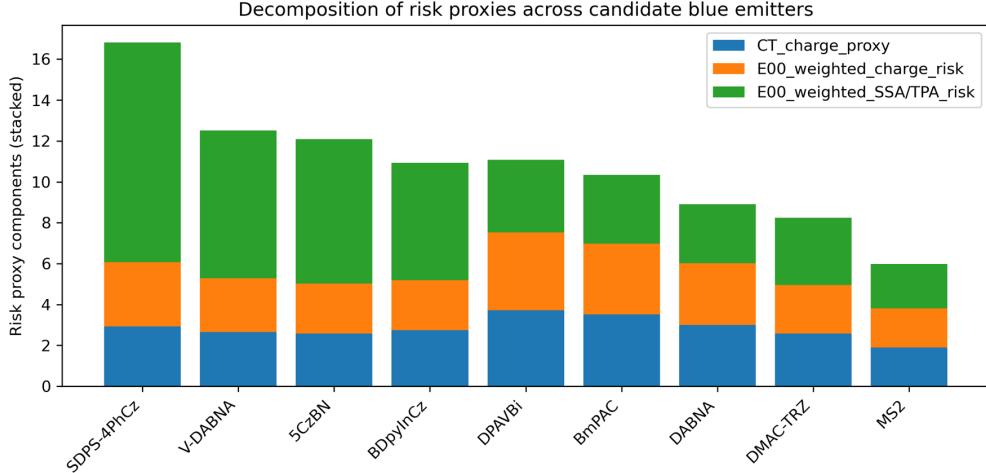


Figure 3: Decomposition of degradation risk proxies across candidate blue emitters. The total degradation risk is decomposed into three physics-informed components. This result demonstrates that structural similarity alone is insufficient for predicting degradation risk and highlights the necessity of incorporating physics-informed degradation proxies.

126 CT charge localization proxy, E00-weighted charge-related risk, and E00-weighted SSA/TPA interaction
 127 risk. High-risk emitters (e.g., SDPS-4PhCz and V-DABNA) exhibit dominant SSA/TPA and
 128 CT-related contributions, whereas low-risk emitters (e.g., DABNA, DMAC-TRZ, and MS2) show
 129 systematically reduced contributions across all proxies. This decomposition reveals that CT-driven
 130 and exciton-interaction mechanisms jointly govern early-stage degradation susceptibility. Based on
 131 this ranking, nine representative emitters were selected for detailed analysis: SDPS-4PhCz, DMAC-
 132 TRZ, V-DABNA, 5CzBN, BDpyInCz, DPAVBi, BmPAC, DABNA, and MS2. These molecules
 133 were chosen to span a broad range of predicted degradation risks and molecular design strategies,
 134 including conventional TADF, MR-TADF, and phosphorescent architectures. As shown in Figure
 135 2 and Table 1, SDPS-4PhCz exhibits one of the highest composite risk scores, driven by simulta-
 136 neously high CT charge proxy and elevated SSA/TPA proxy values, together with a relatively
 137 high excitation energy. In contrast, DMAC-TRZ shows a low composite risk score, characterized
 138 by a relatively low CT charge proxy, moderate SSA/TPA proxy, and lower E, indicating reduced
 139 susceptibility to charge localization and exciton-induced degradation.

140 3.2 Mechanism-Specific Contributions to Degradation Risk

141 3.2 Mechanism-Specific Contributions to Degradation Risk Decomposition of the composite score
 142 reveals distinct degradation drivers across different emitters. For MR-TADF materials such as
 143 DABNA and V-DABNA, elevated SSA/TPA proxy values indicate a higher likelihood of exci-
 144 ton-exciton interaction-driven degradation, despite moderate excitation energies. This suggests that
 145 excitonic interaction pathways may dominate degradation even when excitation energy alone is not
 146 extreme. For conventional TADF emitters such as 5CzBN and BDpyInCz, the CT charge proxy indi-
 147 cates relatively favorable charge delocalization; however, moderate-to-high SSA/TPA proxy values
 148 combined with deep-blue excitation energies contribute to non-negligible degradation risk. In par-
 149 ticular, 5CzBN shows elevated composite risk due to the combined effect of high exciton interaction
 150 propensity and high excitation energy. In contrast, phosphorescent emitter MS2 exhibits a relatively
 151 low CT charge proxy and moderate SSA/TPA proxy, resulting in a comparatively low composite
 152 degradation risk despite its high excitation energy. This highlights that charge localization and exci-
 153 ton interaction pathways can partially mitigate or exacerbate degradation independently of excitation
 154 energy.

155 **3.3 Structural Similarity versus Degradation Risk**

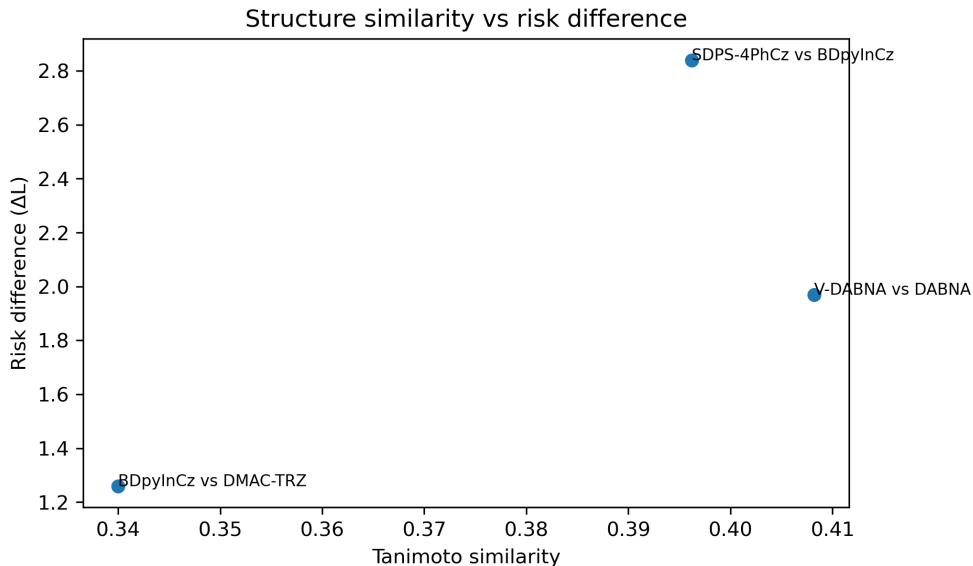


Figure 4: Structure similarity versus degradation risk difference for representative emitter pairs. Tanimoto similarity was computed using RDKit Morgan fingerprints (2048 bits, radius = 2), while the degradation risk difference (L) represents the absolute difference in total risk score, demonstrating structure–risk decoupling in selected molecular pairs.

156 **3.3 Structural Similarity versus Degradation Risk** Tanimoto similarity was computed using RDKit
157 Morgan fingerprints (2048 bits, radius = 2), while the degradation risk difference (L) represents the
158 absolute difference in total risk score, demonstrating structure–risk decoupling in selected molecu-
159 lar pairs. Structural similarity analysis (Figure 3) reveals multiple cases in which chemically simi-
160 lar emitters exhibit substantially different predicted degradation risks. For example, DABNA and
161 V-DABNA share closely related multi-resonance frameworks, yet differ in composite risk due to
162 variations in CT charge proxy and SSA/TPA proxy values. Similarly, 5CzBN and BDpyInCz, both
163 based on TADF architectures, show distinct risk profiles arising from differences in exciton interac-
164 tion and charge localization proxies. These results demonstrate that simple structural similarity is
165 insufficient to predict degradation susceptibility. Instead, electronic and excitonic features captured
166 by the AI-derived proxies play a critical role in determining relative degradation risk.

167 **3.4 Rationale for Representative Candidate Selection**

168 **3.4 Rationale for Representative Candidate Selection** The nine representative emitters were selected
169 to illustrate distinct degradation regimes: (i) high-risk CT- and exciton-driven materials (e.g., SDPS-
170 4PhCz), (ii) low-risk, charge-delocalized TADF materials (e.g., DMAC-TRZ), (iii) MR-TADF ma-
171 terials dominated by exciton interaction pathways (e.g., DABNA, V-DABNA), and (iv) phospho-
172 rescent emitters with relatively suppressed charge localization (e.g., MS2). This selection enables
173 mechanistic interpretation of degradation trends across major blue OLED material classes and sup-
174 ports the use of the composite risk score as a practical early-stage screening metric. Robustness and
175 sensitivity analysis. To assess the robustness of the proxy-based risk classification, we performed
176 a sensitivity analysis by perturbing the weighting factors of the excitation-energy normalization by
177 $\pm 20\%$

178 **4 Conclusion**

179 **4. Conclusion** In this study, we presented a physics-informed, AI-assisted virtual screening frame-
180 work for assessing degradation risk in deep-blue OLED emitters at the molecular design stage. By

181 integrating experimentally motivated degradation proxies with molecular representations derived
182 from RDKit and DeepChem, we constructed a composite degradation risk score that enables rapid,
183 cost-effective ranking of candidate emitters prior to device fabrication or high-level quantum chem-
184 ical calculations.

185 Our results demonstrate that chemically and structurally similar emitters can exhibit substantially
186 different predicted degradation risks, highlighting the critical role of charge localization, exciton
187 interaction pathways, and excitation energy in governing early-stage material stability. These find-
188 ings emphasize that structural similarity alone is insufficient for reliable lifetime screening and that
189 physics-informed descriptors provide essential complementary information for degradation-aware
190 material selection.

191 Beyond the specific set of blue emitters analyzed in this work, the proposed framework offers a
192 generalizable paradigm for AI-driven, proxy-based risk assessment in organic electronic materials.
193 By serving as a virtual experimental instrument, this approach can significantly lower the cost and
194 time barriers associated with early-stage materials discovery, enabling individual researchers and
195 small research groups to perform industry-relevant screening without access to extensive laboratory
196 infrastructure.

197 Looking forward, this framework can be extended by incorporating larger and more diverse emitter
198 datasets, additional physically motivated degradation proxies, and hybrid integration with device-
199 level lifetime data. Such extensions would further enhance predictive reliability and support the
200 development of next-generation blue OLED materials with improved operational stability, thereby
201 accelerating the translation of molecular design insights into practical, long-lifetime device tech-
202 nologies.

203 Acknowledgments

204 Acknowledgments The authors acknowledge the use of AI-assisted tools and open-source software
205 in enabling this study to be conducted with limited experimental resources. The integration of chem-
206 informatics libraries and large language model-assisted literature exploration significantly reduced
207 the cost and time required for early-stage materials screening. This work highlights how individual
208 researchers and small teams can perform meaningful, industry-relevant research through AI-driven
209 computational experimentation, lowering traditional barriers associated with extensive laboratory
210 infrastructure and long-term device testing. The authors also acknowledge the broader open-source
211 and research communities for providing accessible tools and datasets that made this work possible.

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241 **5 AI Co-Scientist Challenge Korea Paper Checklist**

242 **1. Claims**

243 Question: Do the main claims made in the abstract and introduction accurately reflect the
244 paper’s contributions and scope?

245 Answer: [Yes]

246 Justification: The claims in the abstract and introduction are consistent with the presented
247 methodology and results, including physics-informed proxy design and structure-based val-
248 idation using RDKit similarity analysis. The reported conclusions directly follow from the
249 quantitative proxy analysis and structure–risk comparisons.

250 **2. Limitations**

251 Question: Do the main claims made in the abstract and introduction accurately reflect the
252 paper’s contributions and scope?

253 Answer: [Yes]

254 Justification: This work explicitly discusses several limitations. First, the study is based on
255 a relatively small curated set of nine representative blue emitters, which limits the statisti-
256 cal generalizability of the results. Second, the degradation risk is estimated using physics-
257 informed proxy metrics rather than direct device lifetime measurements, and therefore the
258 reported rankings reflect relative risk tendencies rather than absolute operational lifetimes.
259 Third, the proxy definitions rely on simplified descriptors of charge localization and exci-
260 ton–exciton interaction propensity, which may not fully capture all degradation pathways
261 present in real device architectures. Finally, the structural similarity analysis is limited to
262 fingerprint-based Tanimoto similarity, which may not fully reflect three-dimensional pack-
263 ing or solid-state effects. These limitations are discussed in the main text and indicate that
264 the framework is intended for early-stage screening rather than final device-level lifetime
265 prediction.

266 **3. Theory Assumptions and Proofs**

267 Question: For each theoretical result, does the paper provide the full set of assumptions and
268 a complete (and correct) proof?

269 Answer: [N/A]

270 Justification: This paper does not introduce new mathematical theorems, lemmas, or formal
271 analytical proofs. Instead, the methodology is based on empirically and physically moti-
272 vated proxy definitions derived from established concepts in charge-transfer localization,
273 exciton–exciton interaction mechanisms, and excitation-energy scaling. All core formula-
274 tions (e.g., proxy definitions and composite risk score formulation) are explicitly stated in
275 the Methods section, and the underlying assumptions are discussed in the context of their
276 physical interpretation. Since the work relies on computational descriptor extraction and
277 heuristic proxy-based ranking rather than formal theoretical derivations, no formal proofs
278 are applicable.

279 **4. Experimental Result Reproducibility**

280 Question: Does the paper fully disclose all the information needed to reproduce the main
281 experimental results of the paper to the extent that it affects the main claims and/or conclu-
282 sions of the paper (regardless of whether the code and data are provided or not)?

283 Answer: [Yes]

284 Justification: All results in this paper are generated through a fully specified and deter-
285 ministic computational pipeline. The full workflow, including literature-driven candidate
286 collection, dataset standardization, SMILES acquisition, RDKit-based descriptor genera-
287 tion, DeepChem-based molecular representations, proxy calculations, energy-weighted
288 risk formulation, and structural similarity analysis, is described in detail in the Methods
289 section. The versions of key software packages (e.g., RDKit, DeepChem, NumPy, pandas,
290 and Python) and the computational environment are explicitly reported. Input molecular
291 structures (SMILES), intermediate processed datasets, and final proxy calculation tables
292 are provided as supplementary files, enabling independent reproduction of all reported fig-
293 ures and rankings on a standard CPU-based system. Together, these details allow other
294 researchers to reproduce and verify the main experimental results without access to propri-
295 etary software or specialized hardware.

296 **5. Open access to data and code**

297 Question: Does the paper provide open access to the data and code, with sufficient instruc-
298 tions to faithfully reproduce the main experimental results, as described in supplemental
299 material?

300 Answer: [Yes]

301 Justification: The data and code required to reproduce the main experimental results are
302 provided in the supplementary materials associated with this submission. These include
303 input molecular structures (SMILES files), curated candidate lists, RDKit-generated struc-
304 tural descriptors, DeepChem-based molecular representations, proxy calculation scripts,
305 and final tabulated results used to generate all figures and rankings. Detailed instructions
306 for running the computational workflow, including required software versions, environ-
307 ment configuration, and execution order of scripts, are described in the Methods and Re-
308 producibility sections. To preserve anonymity during the review process, public repository
309 links are not included in the main paper; however, all necessary files and scripts are pack-
310 aged with the submission to enable reviewers to reproduce the reported results on a standard
311 CPU-based system.

312 **6. Experimental Setting/Details**

313 Question: Does the paper specify all the training and test details (e.g., data splits, hyper
314 parameters, how they were chosen, type of optimizer, etc.) necessary to understand the
315 results?

316 Answer: [Yes]

317 Justification: The experimental setting is fully specified in the Methods and Reproducibility
318 sections. This study does not involve supervised model training, train/test splits, or hyper-
319 parameter optimization. Instead, all results are based on deterministic, rule-based com-
320 putational workflows using RDKit and DeepChem to generate molecular descriptors and
321 representations, followed by physically motivated proxy calculations. The exact software
322 versions (Python, RDKit, DeepChem, NumPy, Pandas), hardware configuration (CPU-only
323 system), and execution order of scripts are explicitly documented. Input molecular struc-
324 tures (SMILES), descriptor definitions, proxy formulation equations, and normalization
325 procedures are provided to ensure that all reported rankings and figures can be reproduced
326 without stochastic components or hidden parameters.

327 **7. Experiment Statistical Significance**

328 Question: Does the paper report error bars suitably and correctly defined or other appropri-
329 ate information about the statistical significance of the experiments?

330 Answer: [NA]

331 Justification: This study employs a fully deterministic computational pipeline without
332 stochastic training, random sampling, or repeated experimental trials. All molecular de-

333 scriptors, proxy calculations, and ranking procedures are deterministically defined, and
334 therefore conventional statistical significance testing and error bars are not applicable. In-
335 stead, robustness is assessed through cross-proxy consistency and structure–risk decou-
336 pling analysis.

337 **8. Experiments Compute Resources**

338 Question: For each experiment, does the paper provide sufficient information on the com-
339 puter resources (type of compute workers, memory, time of execution) needed to reproduce
340 the experiments?

341 Answer: [Yes]

342 Justification: All experiments were executed on a local desktop workstation using CPU-
343 only resources. The system configuration consisted of an Intel Core i5-class CPU, 16
344 GB RAM, and no GPU acceleration. The computational workflow included RDKit-based
345 molecular descriptor generation, DeepChem-based molecular representation extraction,
346 proxy calculations, normalization, and plotting scripts. Each full experimental run required
347 less than approximately 10 minutes of wall-clock time, and total compute usage for the
348 entire study was well within a few CPU-hours. No internal clusters, cloud computing ser-
349 vices, or GPU resources were used. Storage requirements were minimal (on the order of
350 tens of megabytes) and consisted primarily of CSV/Excel files and generated figures. All
351 reported experiments correspond directly to the full set of computations performed for this
352 study.

353 **9. Code Of Ethics**

354 Question: Does the research conducted in the paper conform, in every respect, with the
355 NeurIPS Code of Ethics <https://nips.cc/public/EthicsGuidelines>?

356 Answer: [Yes]

357 Justification: The authors have reviewed and complied with the NeurIPS Code of Ethics.
358 This work does not involve human subjects, personal data, or sensitive information. All
359 datasets consist of molecular structures and physicochemical descriptors derived from pub-
360 licly available literature and standard cheminformatics tools. The study does not raise
361 privacy, consent, or human subject concerns. The computational methods and results are
362 reported transparently to support reproducibility and responsible scientific conduct. No
363 ethical deviations or special regulatory considerations apply to this research.

364 **10. Broader Impacts**

365 Question: Does the paper discuss both potential positive societal impacts and negative so-
366 cietal impacts of the work performed?

367 Answer: [Yes]

368 Justification: This work discusses both potential positive and potential negative societal im-
369 pacts of the proposed AI-assisted, physics-informed virtual screening framework for blue
370 OLED materials. On the positive side, the approach can significantly lower the cost and
371 time barriers associated with early-stage materials discovery by reducing reliance on ex-
372 tensive laboratory infrastructure and long-term device lifetime testing. This can broaden
373 access to advanced materials research for smaller research groups, students, and institu-
374 tions with limited experimental resources, thereby promoting more inclusive and democra-
375 tized research and development. The framework may also contribute to improved energy-
376 efficient display technologies by accelerating the development of more stable blue OLED
377 emitters, which can have downstream benefits in consumer electronics and energy con-
378 sumption. On the potential negative side, the methodology could be misused or over-relied
379 upon if proxy-based predictions are treated as definitive lifetime or reliability guarantees
380 without sufficient experimental validation. This could lead to inappropriate material se-
381 lection or premature deployment decisions in industrial settings. There is also a general
382 risk that automated screening tools may obscure underlying physical assumptions if users
383 do not critically assess the limitations of the proxy models. To mitigate these risks, the
384 paper explicitly emphasizes that the proposed framework is intended as a pre-screening
385 and prioritization tool rather than a replacement for experimental validation. The study
386 highlights the limitations of proxy-based risk estimation and encourages responsible use of

387 the framework in conjunction with experimental verification and domain expertise. No pri-
388 vacy, surveillance, or fairness concerns apply, as the work does not involve human subjects,
389 personal data, or decision-making systems affecting individuals or groups.

390 **11. Safeguards**

391 Question: Does the paper describe safeguards that have been put in place for responsible
392 release of data or models that have a high risk for misuse (e.g., pretrained language models,
393 image generators, or scraped datasets)?

394 Answer: [NA]

395 Justification: The paper does not release trained models, deployable prediction services, or
396 datasets that pose a high risk for misuse or dual-use. The proposed framework is a research-
397 oriented, proxy-based virtual screening methodology applied to small, curated molecular
398 datasets for blue OLED materials. It does not involve generative models, user-facing AI
399 systems, or large-scale web-scraped datasets. No sensitive, unsafe, or user-generated con-
400 tent is collected or released. Accordingly, no special safeguards such as access restrictions,
401 safety filters, or controlled model release mechanisms are required. The work is intended
402 solely for academic and industrial research purposes in materials science, and the paper
403 emphasizes responsible use of proxy predictions in conjunction with experimental valida-
404 tion.

405 **12. Licenses for existing assets**

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407 the paper, properly credited and are the license and terms of use explicitly mentioned and
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409 Answer: [Yes]

410 Justification: properly cited and used in accordance with their respective licenses. Specifi-
411 cally, RDKit (used for molecular featurization and descriptor generation) is licensed under
412 the BSD license, and DeepChem (used for molecular representations) is licensed under the
413 MIT License. NumPy and pandas, used for data processing and analysis, are also licensed
414 under permissive open-source licenses (BSD-style licenses). Publicly available literature-
415 reported molecular structures and materials data were collected from peer-reviewed pub-
416 lications and publicly accessible chemical databases. These sources are cited in the Ref-
417 erences section. No proprietary, restricted, or license-violating datasets were used. No
418 web-scraped datasets subject to restrictive terms of service were included. All software
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421 **13. New Assets**

422 Question: Are new assets introduced in the paper well documented and is the documenta-
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429 under permissive open-source licenses (BSD-style licenses). Publicly available literature-
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431 lications and publicly accessible chemical databases. These sources are cited in the Ref-
432 erences section. No proprietary, restricted, or license-violating datasets were used. No
433 web-scraped datasets subject to restrictive terms of service were included. All software
434 tools and external assets are used in compliance with their original licenses, and proper
435 attribution is provided in the manuscript.

436 **14. Crowdsourcing and Research with Human Subjects**

437 Question: For crowdsourcing experiments and research with human subjects, does the pa-
438 per include the full text of instructions given to participants and screenshots, if applicable,
439 as well as details about compensation (if any)?

440 Justification: [N/A]

441 This study does not involve crowdsourcing, human participants, or any form of research
442 with human subjects. All analyses are based exclusively on computational modeling,
443 literature-derived molecular data, and in silico descriptor calculations. No human-provided
444 data, annotations, surveys, or participant interactions were conducted.

445 **15. Institutional Review Board (IRB) Approvals or Equivalent for Research with Human
446 Subjects**

447 Question: Does the paper describe potential risks incurred by study participants, whether
448 such risks were disclosed to the subjects, and whether Institutional Review Board (IRB)
449 approvals (or an equivalent approval/review based on the requirements of your country or
450 institution) were obtained?

451 Answer: [N/A]

452 Justification: This research does not involve human subjects, human data, or any interaction
453 with human participants. Therefore, Institutional Review Board (IRB) approval or
454 equivalent ethical review is not required for this study.

455 **A Appendix/supplemental material**

456 Computational setup The analyses were conducted on a local workstation equipped with an Intel i5 CPU and 16 GB RAM, without GPU acceleration. The software environment consisted of
457 Python 3.11.14, RDKit 2025.09.4, DeepChem 2.8.0, NumPy 2.4.1, and pandas 2.3.3. No stochastic
458 model training was performed; therefore, all results are deterministic given the provided input
459 files. Pipeline The reproducibility pipeline consists of the following steps: (i) collection of candidate
460 emitter structures and literature-reported PL/EL peak data, (ii) generation of molecular fingerprints
461 and descriptors using RDKit, (iii) computation of CT charge localization proxies, (iv) calculation
462 of SSA/TPA interaction proxies, (v) excitation-energy (E00) normalization, and (vi) aggregation
463 into a total energy-normalized degradation risk score. All intermediate results are stored as CSV
464 files, and all figures are generated directly from these processed data tables. Data and Code Availability
465 The datasets and code used in this study are available to support reproducibility of the re-
466 ported results. Input molecular structures, processed descriptor tables, proxy calculation outputs,
467 and figure-generation scripts are provided in a structured repository. All intermediate CSV files
468 used to generate the figures and tables in this manuscript are included. The computational workflow
469 is implemented in Python and can be executed on a standard CPU-based system without GPU re-
470 quirements. Access instructions and file organization details are provided in the repository to enable
471 independent verification and reuse.

473 **A.1 Candidate Emitter Structures and Property Sources**

474 Structural and basic molecular property information for the nine candidate blue emitters (SDPS-
475 4PhCz, V-DABNA, 5CzBN, BDpylCz, DPAVBi, BmPAC, DABNA, DMAC-TRZ, MS2) were col-
476 lected from publicly available chemical databases and primary literature sources.

477 Primary data sources include:

- 478 • PubChem Compound Database: <https://pubchem.ncbi.nlm.nih.gov>
479 • ChemSpider: <https://www.chemspider.com>
480 • Original peer-reviewed publications for each emitter (DOI-based retrieval)

481 **A.2 Researcher-Generated Data and Scripts**

482 The following datasets and scripts were generated in this study and used for proxy calculation,
483 ranking, and structural similarity analysis:

- 484 • deepchem_check_9.xlsx: Curated dataset for DeepChem molecular representations
485 • step3_rdkit_output: RDKit-based structural descriptor outputs

- 486 • step4A1_ssa_tpa_proxies: SSA/TPA-related proxy calculations
- 487 • step4A2_ct_charge_proxies: Charge-transfer localization proxy calculations
- 488 • step6_structure_sim_but_risk_diff: Structural similarity vs. risk difference analysis
- 489 • step6_top_similarity_pairs: Top similarity pair listings
- 490 • figure2_stacked.png: Proxy composition stacked bar visualization
- 491 • Figure3_similarity_vs_riskdiff.png: Similarity versus degradation risk difference plot