

Supplementary Materials

Supplementary Fig. S1 Chord diagram depicting cell type-eGene-PD associations. Each arc represents an immune-cell-specific eGene significantly associated with PD. The diagram illustrates both shared and distinct eGene-cell-trait connections across prioritized candidates.

Supplementary Fig. S2 Forest plot of MR results for four eGenes using sc-eQTL data obtained from the DICE project.

Supplementary Fig. S3 Identification and annotation of major immune cell types in peripheral blood scRNA-seq data. (A) Dot plot showing the expression patterns of canonical marker genes across the nine major immune cell types. (B) UMAP feature plots displaying the expression of representative marker genes used for cell-type annotation.

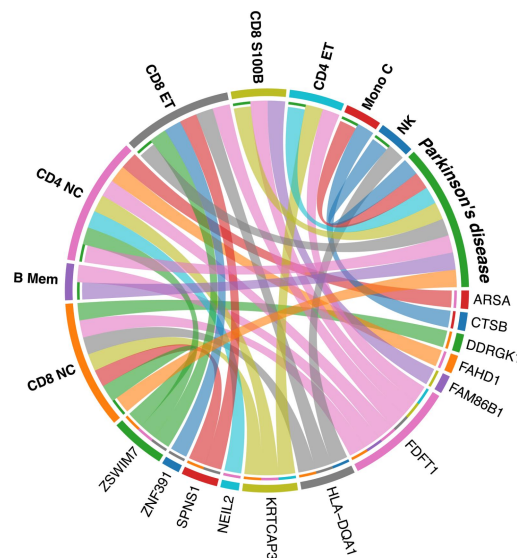
Supplementary Fig. S4 BBB permeability prediction of amodiaquine using SwissADME.

Supplementary Fig. S5 BBB permeability prediction of alprazolam using SwissADME.

Supplementary Fig. S6 BBB permeability prediction of methadone hydrochloride using SwissADME.

Supplementary Fig. S7 BBB permeability prediction of felodipine using SwissADME.

Supplementary Fig. S8 Molecular docking interactions between candidate drugs and target proteins. (A) Leupeptin and CTSB. (B) DNQX and CTSB. (C) β -Solamarine and CTSB. (D) 4-Amino-1,8-naphthalimide and ARSA. (E) Gambierol and FAHD1. (F) 3,5-Dinitrocatechol and ARSA. Left: protein-ligand complex; center: close-up of binding site; right: 2D interaction map highlighting key residues and binding types.

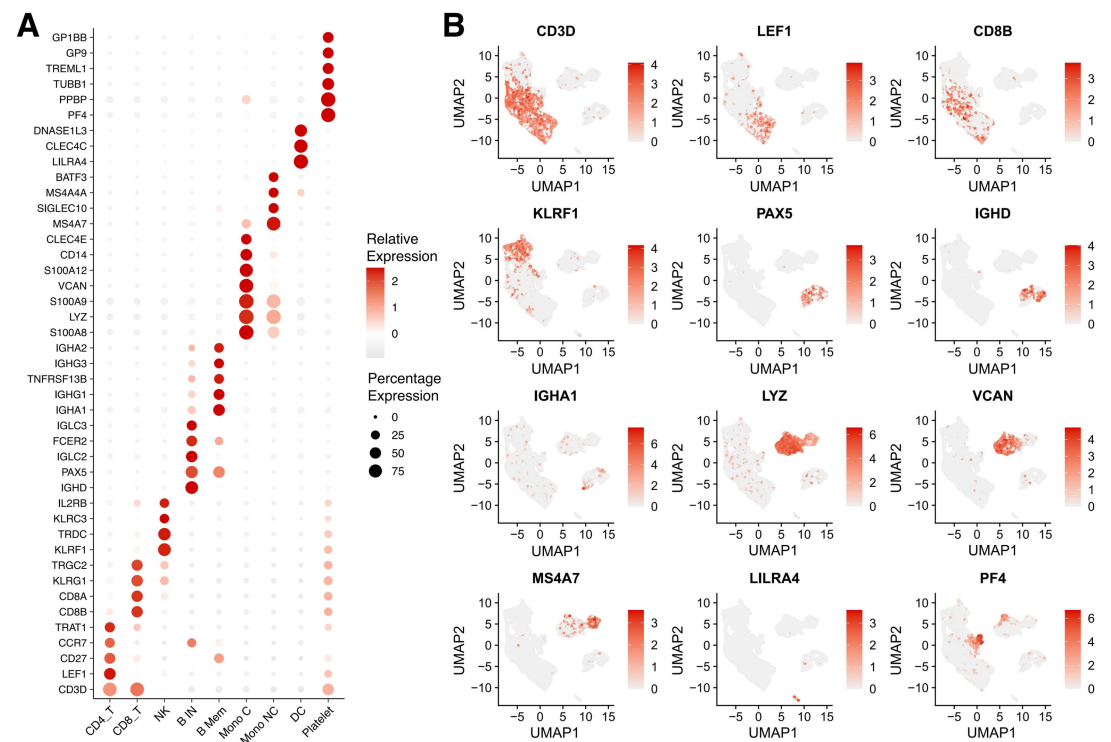


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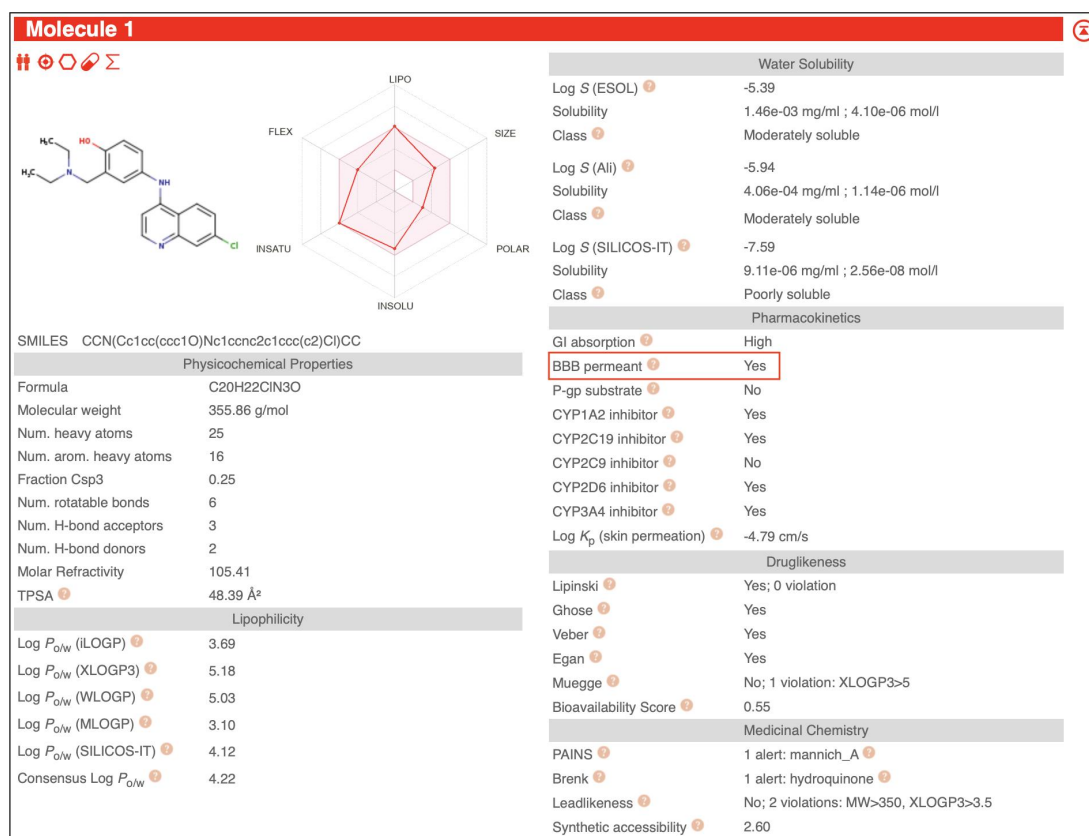
Cell type	eGene	Outcome	Method	OR (95%CI)	P-value
CD8+ Naïve	KRTCAP3	PD	Wald ratio	1.100 (1.044–1.158)	3.20E–04
CD4+ Naïve	ZSWIM7	PD	Wald ratio	0.891 (0.854–0.930)	1.42E–07
CD4+ Naïve	FAHD1	PD	Wald ratio	0.943 (0.910–0.977)	1.12E–03
CD4+ Naïve	NEIL2	PD	Wald ratio	0.993 (0.945–1.043)	7.71E–01

Sc-eQTL data from DICE

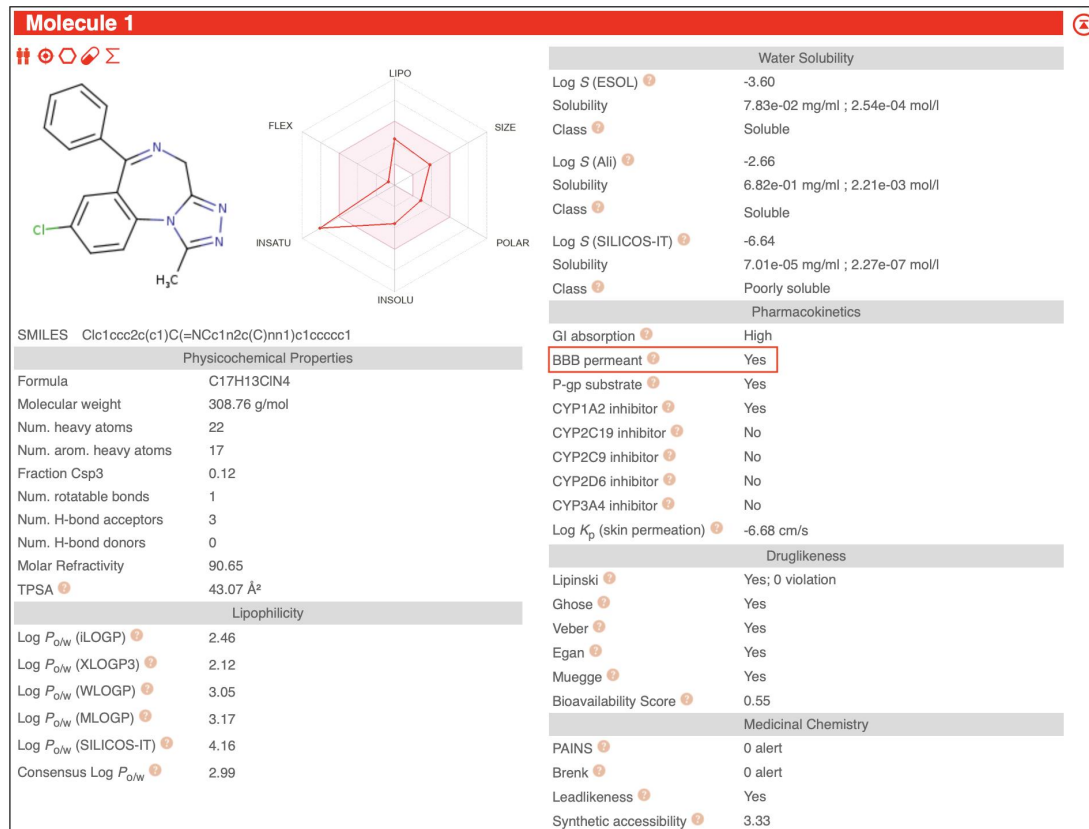
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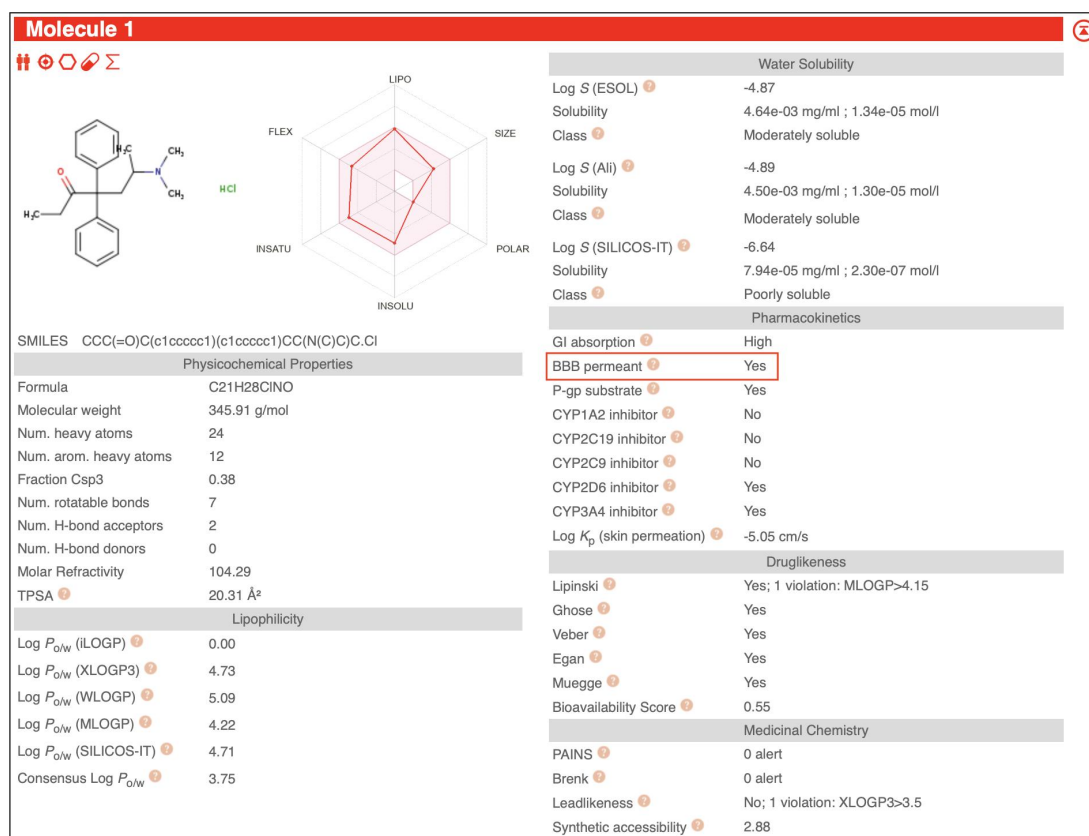
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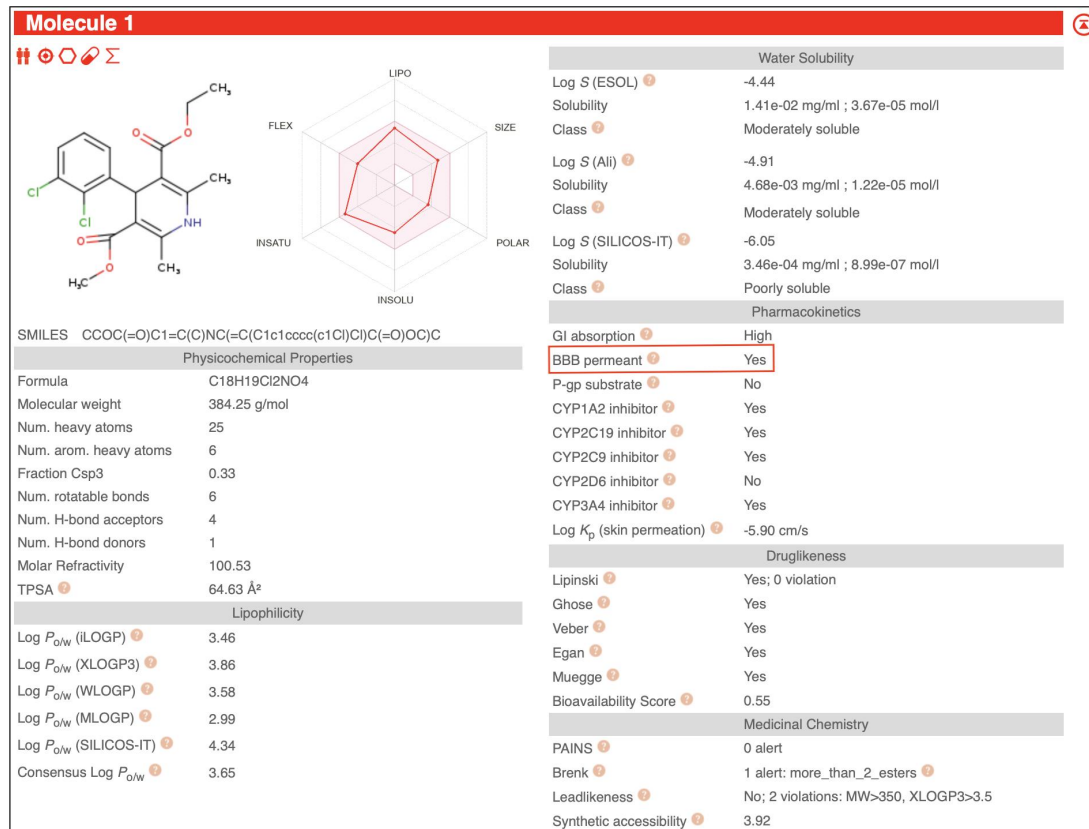
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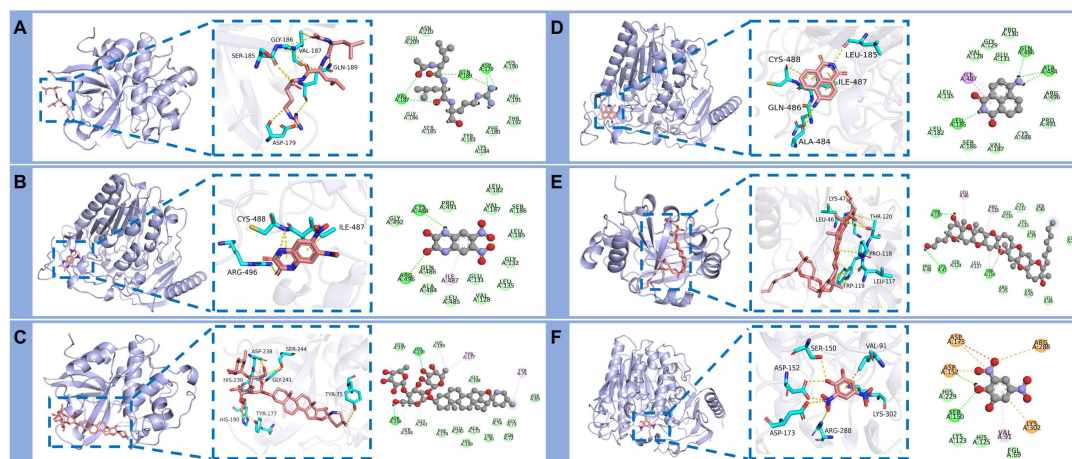
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