

HIV NNRTI

BI-2540

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Summary

BI-2540 is a potent inhibitor of HIV non-nucleoside reverse transcriptase (NNRT) and cross-reactive against clinically relevant mutants of reverse transcriptase.

Chemical Structure

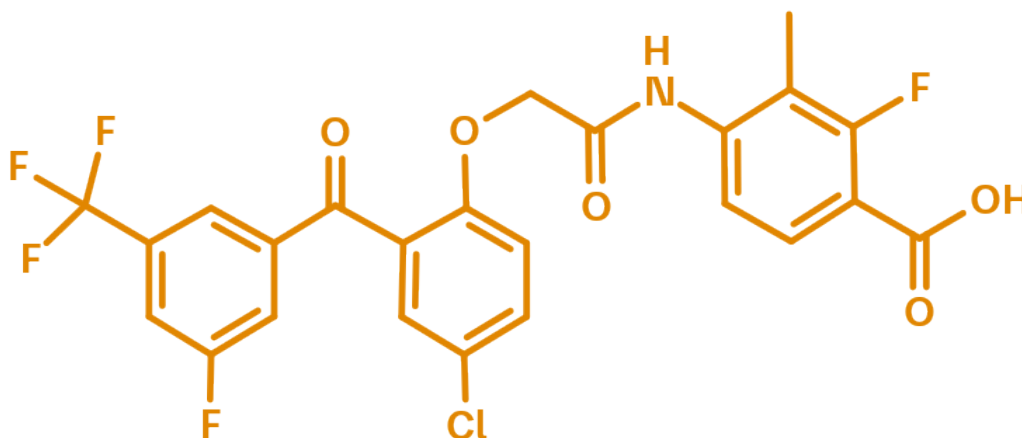


Figure 1: 2D structure of BI-2540, a non-nucleoside reverse transcriptase inhibitor (NNRTI)

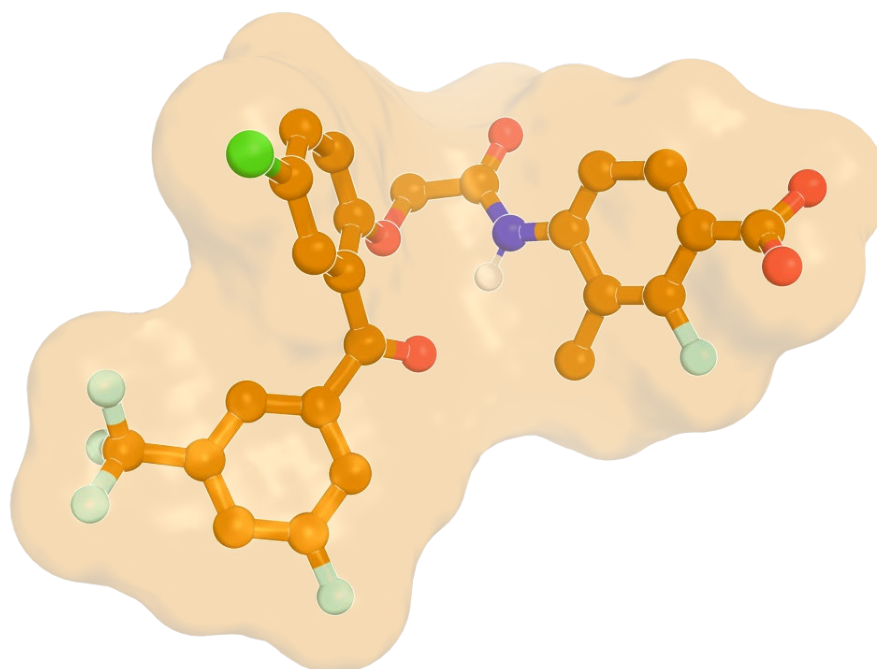


Figure 2: BI-2540, 3D conformation.

Highlights

BI-2540 is a potent inhibitor of the HIV non-nucleoside reverse transcriptase (NNRT). This compound is also cross-reactive against clinically relevant mutants of reverse transcriptase. BI-2540 is suitable for both *in vitro* and *in vivo* experiments. In rats, it has shown a low clearance and good bioavailability upon oral administration.

Target information

Description of the protein: The human immunodeficiency virus (HIV-1) reverse transcriptase (RT) enzyme performs the retrotranscription of the viral single-stranded RNA into double-stranded linear DNA. The viral genomic retrotranscription arises from the cooperative effect of two enzymatic functions of RT: a DNA polymerase activity (copy of the RNA/DNA template) and ribonuclease H activity (cleavage of RNA when part of a RNA/DNA duplex).

Protein domain structure: RT of HIV-1 is a heterodimer composed of subunit p66 (560 AA) and p51 (440 AA). The larger subunit p66 contains both active sites responsible for RT enzymatic functions (DNA polymerase and RNase H activities)¹.

Molecular mechanism: there are two different classes for RT inhibitors: nucleoside RT inhibitors (NRTI) and non-nucleoside RT inhibitors (NNRTI). NNRTI bind to an allosteric site adjacent to the polymerase active site (~10 Å). Binding of NNRTI interferes with the chemical step of DNA synthesis by affecting the alignment of the primer terminus with the polymerase active site. Thus, NNRTIs efficacy stems from the structural rearrangement in the p66 subunit which precludes viral DNA synthesis.

Biology: HIV-1 largely infects CD4-positive T lymphocytes and macrophage cells, thus destroying the immune system. Lymphoid organs are a major reservoir of ongoing HIV-1 replication. HIV life cycle consists of seven steps: 1) binding, 2) fusion, 3) reverse transcription, 4) integration, 5) replication, 6) assembly, and 7) budding.

Disease link: HIV-1 infects >30 million people worldwide. Infected patients cannot be cured; therefore a “triple drug cocktail” of antiretroviral therapy (ART) must be continuously administered. Combination drug therapies suppress viral load by blocking viral replication and improving efficacy to overcome resistant variants^{1,2}.



Figure 3: HIV NNRTI in complex with related structure GW564511 (PDB code: 3DLG)

***In vitro* activity**

BI-2540 is a potent HIV non-nucleoside reverse transcriptase (NNRT) inhibitor. For cellular efficacy against RT mutants please refer to the selectivity section.

PROBE NAME / NEGATIVE CONTROL	BI-2540	BI-2439
MW [Da, free base] ^a	527.8	475.9
HIV1-RT Pico, WT (IC ₅₀) ^b [nM]	12	5053
HIV replicon ELISA, WT (EC ₅₀) ^c [nM]	0.76	n.a.
HIV replicon LUC, WT (EC ₅₀) ^d [nM]	2.6	n.a.

^a For the salt form you will get, please refer to the label on the vial and for the molecular weight of the salt, please refer to the FAQs

Cellular efficacy against RT mutants: HIV-1 luciferase assays: C8166 cells, 72 h incubation at 37°C; readout: RLU of luciferase, Steady Glo

MUTATIONS	BI-2549	X-FOLD VS. WT
Wild type (WT) EC ₅₀ [nM]	2.58	--
A98G EC ₅₀ [nM]	3.94	1.5
K103N EC ₅₀ [nM]	2.36	0.9
V106A EC ₅₀ [nM]	12.8	5.0
V106I EC ₅₀ [nM]	4.19	1.6
E138K EC ₅₀ [nM]	15.0	5.8
Y181C EC ₅₀ [nM]	2.44	0.9
Y188C EC ₅₀ [nM]	0.38	0.1
Y188L EC ₅₀ [nM]	39.1	15
G190A EC ₅₀ [nM]	3.10	1.2
P236L EC ₅₀ [nM]	7.53	2.9
L100I/K103N EC ₅₀ [nM]	3.18	1.2
K103N/G190A EC ₅₀ [nM]	8.16	3.2

K103N/V108I EC ₅₀ [nM]	4.82	1.9
K103N/Y181C EC ₅₀ [nM]	6.54	2.5
K103N/P225H EC ₅₀ [nM]	4.77	1.8
V106A/E138K EC ₅₀ [nM]	119	46
V106A/P236L EC ₅₀ [nM]	199	77
V106I/E138K EC ₅₀ [nM]	38.1	15
V106I/P236L EC ₅₀ [nM]	36.1	14
E138K/P236L EC ₅₀ [nM]	60.3	23

***In vitro* DMPK and CMC parameters**

PROBE NAME / NEGATIVE CONTROL	BI-2540	BI-2439
LogD @ pH 11	2.7	1.3
Solubility @ pH 7.0 [µg/mL]	>52	n.a.
Caco-2 permeability AB @ pH 7.4 [$\times 10^{-6}$ cm/s]	23	12
Caco-2 efflux ratio	0.1	1.4
Microsomal stability [% Q _H] (human)	<24	n.a.
Plasma Protein Binding [%] (human)	99.5	99.8
CYP 3A4 (IC ₅₀) [µM]	18	>50
CYP 2C9 (IC ₅₀) [µM]	>30	8.5
CYP 1A2 (IC ₅₀) [µM]	>30	>50

CYP 2C19 (IC ₅₀) [μM]	>30	>50
CYP 2D6 (IC ₅₀) [μM]	>30	>50

In vivo DMPK parameters

BI-2540 shows a low clearance and good bioavailability upon *p.o.* dosing in rats.

BI-2540	RAT
Clearance [% Q _H] ^a	2.9
V _{ss} [L/kg] ^a	2.26
Mean residence time after <i>i.v.</i> dose [h] ^a	12.8
t _{max} [h] ^b	1.0
C _{max} [μM] ^b	11860
AUC [μM*h] ^b	125620
F [%] ^b	53

^a *i.v.* dose: 1 mg/kg

^b *p.o.* dose: 2.6 mg/kg

In vivo pharmacology

No data available.

Negative control

BI-2439 is a relatively close analog of BI-2540 with significantly lower activity (420-fold) in the HIV-RT Picogreen Fluorescence assay ($IC_{50} = 5 \mu M$) and is therefore offered as an *in vitro* negative control.

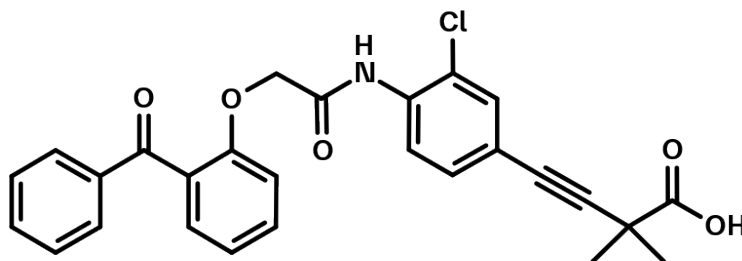


Figure 4: BI-2439 which serves as a negative control

Selectivity

SELECTIVITY DATA AVAILABLE	BI-2540	BI-2439
SafetyScreen44™ with kind support of  eurofins	Yes	Yes
Invitrogen®	No	No
DiscoverX®	No	No
Dundee	No	No

Co-crystal structure of the Boehringer Ingelheim probe compound and the target protein.

No X-ray available.

Reference molecule(s)

Commercially available NNRTIs: Nevirapine, Delavirdine, Efavirenz, Dapivirine, Etravirine, Rilpivirine².

Supplementary data

Selectivity data can be downloaded free of charge from [opnMe](#).

References

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2. Usach I., Melis V., Peris J.-E. Non-nucleoside reverse transcriptase inhibitors: A review on pharmacokinetics, pharmacodynamics, safety and tolerability *J Int AIDS Soc* **2013**, 16(1), 1–14. DOI: [10.7448/IAS.16.1.18567](#), PubMed: [24008177](#).
3. Wang X., Zhang L., Sun X., Lee H., Krishnamurthy D., O'Meara J. A., Landry S., Yoakim C., Simoneau B., Yee N. K., Senanayake C. H. Practical Synthesis of A Benzophenone-Based NNRT Inhibitor of HIV-1 *Org. Process Res. Dev.* **2012**, 16(4), 561–566. DOI: [10.1021/op200301h](#).