

MLKL inhibitor | BI-8925

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MLKL inhibitor | BI-8925

Summary

BI-8925 is the first covalent tool compound for the necroptosis effector protein MLKL with a structurally understood mode of action.

Chemical Structure

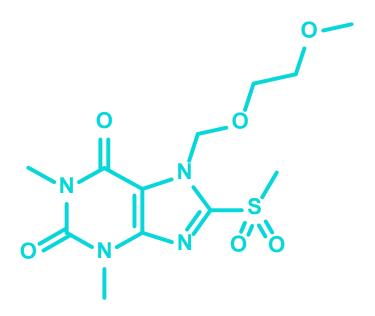


Figure 1: 2-D structure of BI-8925, a MLKL inhibitor

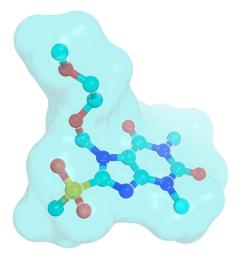


Figure 2: BI-8925, 3D conformation based on the complex with MLKL as solved by X-ray crystallography (PDB code: 6ZZ1)

Highlights

BI-8925 is a covalent inhibitor targeting Cys86 in the N-terminal executioner domain of the necroptosis effector protein mixed lineage kinase domain-like protein (MLKL). MLKL is locked in its auto-inhibited monomeric state by the packing of α -helix 6 against its four-helix bundle in the N-terminal executioner domain. Upon activation through phosphorylation in its C-terminal pseudokinase domain α -helix 6 unfolds and the N-terminal executioner domain can multimerize and integrate into the membrane, which finally leads to Necroptosis. BI-8925 stabilizes the auto inhibited state by a π - π interaction between its xanthine core and Phe148 located in the auto-inhibitory α -helix 6. Consequently, unfolding of α -helix 6 and multimerization of the MLKL executioner domain is prevented. BI-8925 inhibits necroptosis in Jurkat and U937 cells with an IC50 of 541 and 271 nM, respectively.

Target information

Mixed lineage kinase domain-like protein (MLKL) is the effector protein in the signal pathway leading to Necroptosis. MLKL is comprised of two domains. The C-terminal pseudokinase domain is connected via two brace helices to the N-terminal four helix bundle domain. The N-terminal executioner domain is locked in its inactive state by the auto-inhibitory first brace helix (α -helix 6). Upon TNF signalling in the absence of caspase activity MLKL becomes activated via the kinases RIPK1 and RIPK3 through phosphorylation in its pseudokinase domain. Upon activation the auto-inhibitory brace helix unfolds and the N-terminal executioner domain of MLKL multimerizes and integrates into the membrane, which then leads to membrane rupture and necroptosis.



Figure 3: Complex of BI-8925 with MLKL, as solved by X-ray crystallography (PDB code: 6ZZ1). The structure was also solved by NMR spectroscopy (PDB code: 6ZPR). Both structures show a very high level of agreement⁶

In vitro activity

BI-8925 displays nM activity in two different cellular necroptosis assays.

PROBE NAME / NEGATIVE CONTROL	BI-8925	BI-8762
MW [Da]	346.36	240.28
Assay A (IC ₅₀) [nM] ^a	541	>100000
Assay B (IC ₅₀) [nM] ^a	271	>100000

^a see reference 6

Assay A: Stimulation of Jurkat FADD-/- cells was achieved with huTNF α and subsequent cell viability analysis was carried out with Cell Titer Glo $^{\circ}$ Luminescent Cell Viability Assay

Assay B: U937 cells were treated with the caspase inhibitor zVAD-fmk and stimulated with huTNF α ; cell viability analysis was performed with Cell Titer Glo $^{\circ}$ Luminescent Cell Viability Assay.

In vitro DMPK and CMC parameters

PROBE NAME / NEGATIVE CONTROL	BI-8925	BI-8762
logD pH2/pH11	1/0.5	-
Solubility @ pH 6.8 [μg/ml]	75	59
CACO permeability @ pH 7.4 [*10 ⁻⁶ cm/s]	17	53
CACO efflux ratio	0.7	0.8

Negative control

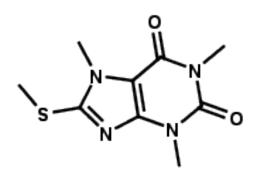


Figure 4: BI-8762 which serves as a negative control

Selectivity

SELECTIVITY DATA AVAILABLE	BI-8925	BI-8762
SafetyScreen44™ with kind of support of curofins	data in progress - will be added soon	data in progress - will be added soon
Invitrogen®	No	No
DiscoverX®	No	No
Dundee	No	No

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

The Xray crystal structure of the target without ligand is available (PDB code: 6ZVO)

The Xray crystal structure of the target in complex with BI-8925 is available (PDB code: 6ZZ1)

See figure 3

The NMR structure of the target without ligand is available (PDB code: 6ZLE)

The NMR structure of the target in complex with BI-8925 is available (PDB code: 6ZPR)

Reference molecule(s)

Necrosulfonamide (NSA)

Summary

BI-8925 is a covalent inhibitor of MLKL with a structurally and functionally characterized mode of action and good activity in cells ($IC_{50} = 541 \text{ nM}$).

Supplementary data

2-D structure files can be downloaded free of charge from opnMe.

References

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