Progresses in the Field of Aldehyde Dehydrogenase Inhibitors: Novel Imidazo[1,2-*a*]pyridines Against the 1A Family.

Luca Quattrini, Edoardo Luigi Maria Gelardi, Giovanni Petrarolo, Giorgia Colombo, Davide Maria Ferraris, Francesca Picarazzi, Menico Rizzi, Silvia Garavaglia, Concettina La Motta.

Table of Contents

Table 1-SI. Data collection and refinement statistics of the human ALDH1A3 model.

Figure 1-SI. Conformational stability of 3f-ALDH1A3 complex in MD simulations.

Figure 2-SI. Overlap of the binding mode of the crystallized compound **3c** and the representative poses of compound **3f**, extrapolated from MD trajectories.

Figure 3-SI. Anti-proliferative activity of compounds 3c against U87-MG cell line.

Table 2-SI. Physio-chemical and spectral data of compounds 2b,c.

 Table 3-SI. Physio-chemical and spectral data of compounds 3a-t.

Experimental procedures of biochemical and cell viability assays.

Experimental procedures of crystallization studies and structure determination.

Experimental procedures of computational studies.

References.

Table 1-SI. Data collection and refinement	nt statistics of the human ALDH1A3 model.
--	---

DATA COLLECTION	
	3c
Space group	P21221
Cell dimensions	
a, b, c (Å)	81.3 89.2 159.2
α, β, γ (°)	90 90 90
Resolution (Å)	47.96 - 2.9
R _{pim} / R _{merge}	0.061 (0.40)/0.117(0.80)
Mean(I) / sd(I)	2.3 (2.1)
Completeness (%)	98.5 (98.95)
Redundancy	10.6 (4.6)
<u>REFINEMENT</u>	
Resolution (Å)	2.9
No. reflections	25959 (2556)
R _{work} / R _{free}	0.19 / 0.26(0.30 / 0.35)
No. atoms	
Protein	7408
Solvent	11
Ligands	138
Mean B-factors	
$\frac{\text{Protein}(A^2)}{W_1 + (A^2)}$	60.9
Water (A^2)	44.5
P m s deviations	/9.4
Bond lengths (Å)	0.017
Angles (°)	1 57
	1.07
Ramachandran outliers (%)	0.1

Figure 1-SI. All-atom root mean square deviation (RMSD) of compound **3f** (red) and **3f**-ALDH1A3 complex (black) along MD trajectory.



Figure 2-SI. Overlap of the binding mode of the crystallized compound **3c** (aquamarine sticks) and the representative poses of compound **3f** (green sticks), extrapolated from MD trajectories.



Figure 3-SI. Anti-proliferative activity of compound 3c against U87-MG cell line.



Table 2-SI. Physio-chemical and spectral data of compounds 2b,c.

8-Bromo-2-(4-methylphenyl)imidazo[1,2-a]pyridine, 2b. White solid. M.p. 258-260 °C. Cryst. solvent: Acetonitrile. Yield: 55%. ¹H-NMR (δ, ppm): 8.953 (d, 1H, J=1.20 Hz), 8.603 (s, 1H), 8.321 (d, 2H, J = 8.88 Hz), 8.242 (d, 2H, J = 8.88 Hz), 7.638 (d, 1H, J = 9.60 Hz), 7.445 (dd, 1H, J = 9.60 Hz, J= 1.71 Hz).

8-Bromo-2-(4-methoxyphenyl)imidazo[1,2-a]pyridine, 2c. White solid. M.p. 232-234 °C. Cryst. solvent: EtOH. Yield: 76%. ¹H-NMR (δ, ppm): 9.189 (s, 1H), 8.678 (s, 1H), 7.928 (d, 1H, J = 9.28 Hz), 7.853 (d, 1H, J = 9.44 Hz), 7.557 (s, 1H), 7.550 (d, 1H, J = 7.95 Hz), 7.499 (t, J = 8.09 Hz, 1H), 7.091 (d, 1H, J = 7.92 Hz), 3.867 (s, 3H).

 Table 3-SI. Physio-chemical and spectroscopic data of compounds 3a-t.

2,8-Diphenylimidazo[**1,2**-*a*]**pyridine**, **3a**. M.p. 86-89°C. Cryst. solvent: Methanol. Yield: 16%. ¹H-NMR (δ, ppm): 8.558 (d, 1H, J = 6.70 Hz), 8.507 (s, 1H), 8.224 (d, 2H, J = 7.82 Hz), 8.000 (d, 2H, J = 7.70 Hz), 7.547 (t, 2H, J = 7.11 Hz), 7.471 (m, 5H), 7.337 (t, 1H, J = 7.37 Hz), 7.022 (t, 1H, J = 6.91 Hz). ¹³C-NMR (δ, ppm): 144.75, 143.84, 136.61, 134.31, 129.19, 129.12, 128.78, 128.59, 128.21, 126.60, 126.11, 123.51, 113.03, 110.19. HRMS (ESI, m/z): calcd for C₁₉H₁₄N₂ 270.11515, found [M+H]⁺ 271.12297.

8-(4-Fluorophenyl)-2-phenylimidazo[1,2-*a***]pyridine, 3b**. M.p. 129-132°C. Cryst. solvent: Methanol. Yield: 32%. ¹H-NMR (δ, ppm): 8.559 (d, 1H, J = 6.70 Hz), 8.509 (s, 1H), 8.319 (dd, 2H, J = 6.17 Hz, J = 4.52 Hz), 8.003 (d, 2H, J = 7.74 Hz), 7.485 (m, 3H), 7.365 (m, 3H), 7,021 (t, 1H, J = 6.94 Hz). ¹³C-NMR (δ, ppm): 163.72, 144.77, 134.27, 132.94, 131.18, 129.17, 128.23, 127.38, 126.65, 126.13, 123.38, 115.72, 115.51, 112.99, 110.25. HRMS (ESI, m/z): calcd for C₁₉H₁₃FN₂ 288.10573, found [M+H]⁺ 289.11355.

8-(4-Chlorophenyl)-2-phenylimidazo[1,2-*a***]pyridine, 3c.** M.p. 150-153°C. Cryst. solvent: Methanol. Yield: 42%. ¹H-NMR (δ, ppm): 8.578 (d, 1H, J = 6.73 Hz), 8.518 (s, 1H), 8.304 (d, 2H, J = 8.64 Hz), 8.004 (d, 2H, J = 7.12 Hz), 7.615 (d, 2H, J = 8.64 Hz), 7.552 (d, 1H, J = 6.70 Hz), 7.167 (t, 2H, J = 7.64 Hz), 7.343 (t, 1H, J = 7.37 Hz), 7.030 (t, 1H, J = 6.95 Hz). ¹³C-NMR (δ, ppm): 144.80, 143.58, 135.34, 134.22, 133.27, 130.81, 129.18,128.29, 128.27, 127.08,126.97, 126.14, 123.61, 112.98, 110.29. HRMS (ESI, m/z): calcd for C₁₉H₁₃ClN₂ 304.07618, found [M+H]⁺ 305.08400.

8-(4-Isobutylphenyl)-2-phenylimidazo[1,2-*a***]pyridine, 3d.** M.p. 83-85°C. Cryst. solvent: Ethanol. Yield: 43%. ¹H-NMR (δ, ppm): 8.531 (d, 1H, J = 6.68 Hz), 8.494 (s, 1H), 8.159 (d, 2H, J = 8.2 Hz), 7.998 (d, 2H, J = 7.00 Hz), 7.492-7.446 (m, 3H), 7.375-7.322 (m, 3H), 7.005 (t, 1H, J = 6.96 Hz), 3.309 (s, 3H), 2.569 (d, 2H, J = 7.24 Hz), 1.967-1.900 (m, 1H), 0.936 (d, 6H, J = 6.6 Hz). ¹³C-NMR (δ, ppm): 144.66, 143.87, 141.70, 134.34, 134.03, 129.36, 129.18, 128.85, 128.54, 128.18, 126.30, 126.11, 123.08, 113.05, 110.14, 44.87, 30.09, 22.73. HRMS (ESI, m/z): calcd for C₂₃H₂₂N₂ 326.17775, found [M+H]⁺ 327.18558.

1-Phenyl-2-(4-(2-phenylimidazo[1,2-*a***]pyridin-8-yl)phenoxy)ethan-1-one, 3e**. M.p. 82-85°C. Cryst. solvent: Ethanol. Yield: 10%. ¹H-NMR (δ , ppm): 8.480 (dd, 1H, J = 7.35 Hz, J = 1.23 Hz), 8.260 (s, 1H), 8.140 (d, 2H, J = 7.27 Hz), 8.030 (d, 2H, J = 7.25 Hz), 7.680 (t, 1H, J = 7.00 Hz), 7.570 (d, 2H, J = 7.15 Hz), 7.500 (t, 3H, J = 7.20 Hz), 7.300 (d, 2H, J = 7.10 Hz), 7.210 (dd, 1H, J = 7.15 Hz, J = 1.20 Hz), 6.980 (d, 2H, J = 7.00 Hz), 6.860 (t, 1H, J = 7.20 Hz), 5.70 (s, 2H). ¹³C-NMR (δ , ppm): 194.53, 147.21, 143.88, 139.59, 134.83, 134.30, 129.34, 129.11, 128.39, 128.04, 125.95, 120.34, 112.62, 110.40, 104.34, 71.38. HRMS (ESI, m/z): calcd for C₂₁H₁₆N₂O₂ 328.12063, found [M+H]⁺ 329.12845.

Methyl 4-(2-phenylimidazo[**1**,**2**-*a*]**pyridin-8-yl)benzoate**, **3f**. M.p. 190 °C. Cryst. solvent: Ethanol. Yield: 39%. ¹H-NMR (δ, ppm): 8.619 (d, 1H, J = 6.16 Hz), 8.539 (s, 1H), 8.423 (d, 2H, J = 8.57 Hz), 8.128 (d, 2H, J = 8.52 Hz), 8.017 (d, 2H, J = 7.74 Hz), 7.634 (dd, 1H, J = 0.96 Hz, J = 7.04 Hz), 7.473 (t, 2H, J = 7.40 Hz), 7.349 (t, 1H, J = 7.40 Hz), 7.064 (t, 1H, J = 6.92 Hz), 2.664 (s, 3H). ¹³C-NMR (δ, ppm): 198.10, 144.90, 143.56, 141.06, 136.51, 134.16, 129.23, 129.20, 128.68, 128.32, 127.44, 127.23, 126.16, 124.35, 112.98, 110.32, 49.07. HRMS (ESI, m/z): calcd for C₂₁H₁₆N₂O₂ 328.12120, found [M+H]⁺ 329.12817.

8-([1,1'-Biphenyl]-4-yl)-2-phenylimidazo[1,2-*a***]pyridine**, **3g**. M.p. 204-205°C. Cryst. solvent: Ethanol. Yield: 34%. ¹H-NMR (δ , ppm): 8.577 (d, 1H, J = 6.25 Hz), 8.526 (s, 1H), 8.373 (d, 2H, J = 8.40 Hz), 8.026 (d, 2H, J = 7.12 Hz), 7.866 (d, 2H, J = 8.48 Hz), 7.800 (d, 2H, J = 7.21 Hz), 7.588 (d, 1H, J = 7.92 Hz), 7.544-7,458 (m, 4H), 7.414 (t, 1H, J = 7.33 Hz), 7.348 (t, 1H, J = 4.40 Hz), 7.048 (t, 1H, J = 6,96 Hz). ¹³C-NMR (400 MHz, DMSO-d6) (δ , ppm): 144.22, 143.29, 139.61, 135.11, 133.78, 129.09, 128.96, 128.66, 127.70, 127.55, 126.58, 126.47, 126.13, 125.61, 122.84, 112.54, 109.70. HRMS (ESI, m/z): calcd for C₂₅H₁₈N₂ 346.14645, found [M+H]⁺ 347.15428. **8-Phenyl-2-(p-tolyl)imidazo[1,2-***a***]pyridine, 3h**. M.p. 40°C. Cryst. solvent: Methanol. Yield: 40%. ¹H-NMR (δ, ppm): 8.537 (d, 1H, J = 5.20 Hz), 8.450 (s, 1H), 8.111 (d, 2H, J = 7.78 Hz), 7.882 (d, 2H, J = 8.09 Hz), 7.543 (t, 2H, J = 7.54 Hz), 7.478 (dd, 1H, J = 7.12 Hz, J = 1.04 Hz), 7,444 (t, 1H, J = 7.36 Hz), 7.267 (d, 2H, J = 7.93 Hz), 7.004 (t, 1H, J = 6.90 Hz), 2.344 (s, 3H). ¹³C-NMR (δ, ppm): 144.38, 143.25, 136.98, 136.17, 131.05, 129.25, 128.62, 128.27, 128.04, 127.99, 126.02, 125.55, 122.86, 112.41, 109.24, 20.86. HRMS (ESI, m/z): calcd for C₂₀H₁₆N₂ 284.13080, found [M+H]⁺ 285.13862.

8-(4-Fluorophenyl)-2-(p-tolyl)imidazo[1,2-*a***]pyridine, 3i**. M.p. 125-128°C. Cryst. solvent: Ethanol. Yield: 31%. ¹H-NMR (δ , ppm): 8.544 (d, 1H, J = 6.66 Hz), 8.460 (s, 1H), 8.301 (dd, 2H, J = 8.84 Hz, J = 5.64 Hz), 7.888 (d, 2H, J = 8.09 Hz), 7.499 (d, 1H, J = 6.33 Hz), 7.385 (t, 2H, J = 8.96 Hz), 7.273 (d, 2H, J = 7.88 Hz), 7.012 (t, 1H, J = 6.92 Hz), 2.348 (s, 3H). ¹³C-NMR (δ , ppm): 144.88, 143.62, 137.53, 132.98, 131.48, 131.18, 129.76, 127.26, 126.57, 126.05, 123.28, 115.73, 115.51, 112.90, 109.81, 21.36. HRMS (ESI, m/z): calcd for C₂₀H₁₅FN₂ 302.12138, found [M+H]⁺ 303.12920.

8-(4-Chlorophenyl)-2-(p-tolyl)imidazo[1,2-*a***]pyridine, 3j**. M.p. 178-180°C. Cryst. solvent: Methanol. Yield: 40%. ¹H-NMR (δ, ppm): 8.559 (d, 1H, J = 6.68 Hz), 8.463 (s, 1H), 8.294 (d, 2H, J = 6.72 Hz), 7.890 (d, 2H, J = 8.09 Hz), 7.613 (d, 2H, J = 6.70 Hz), 7.533 (dd, 1H, J = 7.16 Hz, J = 1.04 Hz,), 7.273 (d, 2H, J = 7.89 Hz), 7.015 (t, 1H, J = 6.92 Hz), 2.349 (s, 3H). ¹³C-NMR (δ, ppm): 145.48, 145.10, 138.60, 137.47, 136.67, 134.75, 129.62, 129.37, 128.02, 126.08, 125.70, 113.44, 112.68, 107.60, 21.36. HRMS (ESI, m/z): calcd for C₂₀H₁₅ClN₂ 318.09183, found [M+H]⁺ 319.09965.

8-(4-Fluorophenyl)-2-(4-methoxyphenyl)imidazo[1,2-*a***]pyridine, 3k. M.p. 167°C. Cryst. solvent: Ethanol. Yield: 41%. ¹H-NMR (δ, ppm): 8.549 (dd, 1H, J = 1.08 Hz, J = 7.16 Hz), 8.404 (s, 1H), 8.296 (dd, 2H, J = 2.00 Hz, J = 6.64 Hz), 7.924 (dd, 2H, J = 2.04 Hz, J = 6.72 Hz), 7.606 (dd, 2H, J = 2.00 Hz, J = 6.64 Hz), 7.521 (dd, 1H, J = 1.08 Hz, J = 7.16 Hz), 7.048-6.985 (m, 3H),**

3.808 (s, 3H). ¹³C-NMR (δ, ppm): 159.58, 144.87, 143.46, 135.42, 133.20, 130.80, 128.78, 127.47, 126.81, 123.36, 115.70, 115.49, 114.62, 112.78, 109.22, 55.63. HRMS (ESI, m/z): calcd for C₂₀H₁₅FN₂O 318.11629, found [M+H]⁺ 319.12412.

8-(4-Chlorophenyl)-2-(4-methoxyphenyl)imidazo[1,2-*a***]pyridine**, **3l**. M.p. 167°C. Cryst. solvent: Ethanol. Yield: 20%. ¹H-NMR (δ , ppm): 8.549 (dd, 1H, J = 1.00 Hz, J = 7,12 Hz), 8.403 (s, 1H), 8.298 (d, 2H, J = 8.642 Hz), 7.926 (d, 2H, J = 8.803 Hz), 7.606 (d, 2H, J = 8.683 Hz), 7,523 (dd, 1H, J = 7.12 Hz, J = 1.00 Hz), 7.043-6.986 (m, 3H), 3.810 (s, 3H). ¹³C-NMR (δ , ppm): 159.58, 144.87, 143.46, 135.42, 133.20, 130.80, 128.77, 126.82, 126.80, 123.36, 114.61, 112.77, 109.21, 55.62. HRMS (ESI, m/z): calcd for C₂₀H₁₅ClN₂O 334.08674, found [M+H]⁺ 335.09457.

8-(3,5-Dimethoxyphenyl)-2-(4-methoxyphenyl)imidazo[1,2-*a***]pyridine, 3m. M.p. 122-125 °C. Cryst. solvent: Methanol. Yield: 36%. ¹H-NMR (δ, ppm): 8.529 (d, 1H, J = 5.92 Hz), 8.388 (s, 1H), 7.924 (d, 2H, J = 8.76 Hz), 7.548 (d, 1H, J = 6.36 Hz), 7.040 (d, 2H, J = 8.76 Hz), 6.970 (t, 1H, J = 6.92 Hz), 6.590 (s, 1H), 3.854 (s, 3H), 3.808 (s, 6H). ¹³C-NMR (δ, ppm): 160.22, 159.08, 144.23, 143.18, 137.91, 127.39, 126.88, 126.46, 126.12, 122.83, 114.21, 112.22, 108.60, 106.78, 100.11, 55.26, 55.14. HRMS (ESI, m/z): calcd for C₂₂H₂₀N₂O₃ 360.14684, found [M+H]⁺ 361.15467.**

2-(4-Methoxyphenyl)-8-(3,4,5-trimethoxyphenyl)imidazo[1,2-*a***]pyridine, 3n**. M.p. 145-146 °C. Cryst. solvent: Methanol. Yield: 36%. ¹H-NMR (δ, ppm): 8.515 (d, 1H, J = 5.76 Hz), 8.391 (s, 1H), 7.943 (d, 2H, J = 8.84 Hz), 7.699 (s, 2H), 7.585 (dd, 1H, J = 7.28 Hz, J = 1.00 Hz), 7.037 (d, 2H, J = 8.84 Hz), 6.994 (t, 1H, J = 6.92 Hz), 3.924 (s, 6H), 3.832 (s, 3H), 3.758 (s, 3H). ¹³C-NMR (δ, ppm): 159.56, 153.09, 145.57, 144.22, 138.33, 132.62, 131.87, 127.28, 126.64, 124.39, 122.14, 114.08, 112.33, 107.62, 106.47, 60.94, 56.28, 55.32. HRMS (ESI, m/z): calcd for C₂₃H₂₂N₂O₄ 390.15741, found [M+H]⁺ 391.16523.

Methyl 4-(2-(4-methoxyphenyl)imidazo[1,2-*a***]pyridin-8-yl)benzoate, 30**. M.p. 130°C. Cryst. solvent: Methanol. Yield: 38%. ¹H-NMR (δ, ppm): 8.591 (d, 1H, J = 6.48 Hz), 8.425-8.404 (m, 3H), 8.121 (d, 2H, J = 8.49 Hz), 7.938 (d, 2H, J = 8.80 Hz), 7.605 (d, 1H, J = 6.48 Hz), 7.054-7.019

(m, 3H), 3.812 (s, 3H), 3,337 (s, 3H). ¹³C-NMR (δ, ppm): 198.08, 159.60, 144.97, 143.45, 141.17, 136.47, 129.23, 128.68, 127.49, 127.30, 126.97, 126,77, 124.1, 114.63, 112.78, 109.25, 55.63, 27.30. HRMS (ESI, m/z): calcd for C₂₂H₁₈N₂O₃ 342.13628, found [M+H]⁺ 343.14410.

8-([1,1'-Biphenyl]-4-yl)-2-(4-methoxyphenyl)imidazo[1,2-*a***]pyridine, 3p**. M.p. 208-210°C. Cryst. solvent: Methanol. Yield: 46%. ¹H-NMR (δ , ppm): 8.548 (d, 1H, J = 6,72 Hz), 8,411 (s, 1H), 8.364 (d, 2H, J = 8.48 Hz), 7.946 (d, 2H, J = 8.80 Hz), 7.858 (d, 2H, J = 7.20 Hz), 7.796 (d, 2H, J = 7.20 Hz), 7.5663-7.5039 (m, 3H), 7.413 (t, 1H, J = 7.33 Hz), 7.053-7.003 (m, 3H), 3.815 (s, 3H). ¹³C-NMR (δ , ppm): 159.55, 144.84, 143.70, 140.14, 135.74, 129.61, 129.49, 128.07, 127.72, 127.46, 127.11, 126.99, 126.93, 126.5, 123.12, 114.63, 112.86, 109.16, 55.63. HRMS (ESI, m/z): calcd for C₂₆H₂₀N₂O 376.15701, found [M+H]⁺ 377.16484.

8-(4-Fluorophenyl)-2-(3-methoxyphenyl)imidazo[1,2-*a***]pyridine, 3q**. M.p. 110-113°C. Cryst. solvent: Ethanol. Yield: 53%. ¹H-NMR (δ, ppm): 8.546 (dd, 1H, J = 6.66 Hz, J = 1.02 Hz), 8.529 (s, 1H), 8.316 (dd, 2H, J = 7.86 Hz, J = 4.54 Hz), 7.548 (m, 3H), 7.385 (m, 3H), 7.020 (t, 1H, J = 9.07 Hz), 6.922 (dd, 1H, J = 7.82 Hz, J = 2.18 Hz), 3.836 (s, 3H). ¹³C-NMR (δ, ppm): 159.59, 144.10, 135.16, 132.40, 130.68, 129.79, 126.86, 126.14, 122.91, 118.06, 115.24, 115.02, 113.13, 112.54, 111.18, 110.06, 55.07. HRMS (ESI, m/z): calcd for C₂₀H₁₅FN₂O 318.11629, found [M+H]⁺ 319.12412.

8-(4-Chlorophenyl)-2-(3-methoxyphenyl)imidazo[1,2-*a***]pyridine, 3r**. M.p. 122-124°C. Cryst. solvent: Ethanol. Yield: 23%. ¹H-NMR (δ , ppm): 8.565 (dd, 1H, J = 6.72 Hz, J = 1.08 Hz), 8.536 (s, 1H), 8.302 (d, 2H, J = 7.58 Hz), 7.617 (d, 2H, J = 8.72 Hz), 7.585 (d, 1H, J = 7.57 Hz), 7,552 (m, 2H), 7.381 (t, 1H, J = 7.82 Hz), 7.030 (t, 1H, J = 6.96 Hz), 6.923 (dd, 1H, J = 8.26 Hz, J = 1.68 Hz), 3.838 (s, 3H). ¹³C-NMR (δ , ppm): 160.11, 144.65, 143.48, 135.63, 135.31, 133.28, 130.81,128.80, 127.08, 126.95, 123.62, 118.60, 113.71, 113.02, 111.68, 110.59, 55.59. HRMS (ESI, m/z): calcd for C₂₀H₁₅ClN₂O 334.08674, found [M+H]⁺ 335.09457.

2-(3-Methoxyphenyl)-8-(3,4,5-trimethoxyphenyl)imidazo[1,2-*a***]pyridine, 3s. M.p. 119-121°C. Cryst. solvent: Methanol. Yield: 20%. ¹H-NMR (δ, ppm): 8.540-8.538 (m, 2H), 7.744 (s, 2H), 7.643-7.573 (m, 3H), 7.395 (t, 1H, J = 7.92 Hz), 7.030 (t, 1H, J = 6.88 Hz), 7.390 (dd, 1H, J = 8.16 Hz, J = 1.88 Hz), 3.924 (s, 6H), 3.832 (s, 3H), 3.830 (s, 3H). ¹³C-NMR (δ, ppm): 160.10, 153.04, 144.34, 143.66, 138.05, 135.75, 131.68, 130.34, 127.87, 126.39, 123.06, 118.35, 114.17, 113.00, 110.88, 110.39, 106.63, 60,58 56.34. HRMS (ESI, m/z): calcd for C₂₃H₂₂N₂O₄ 390.15741, found [M+H]⁺ 391.16523.**

8-([1,1'-Biphenyl]-4-yl)-2-(3-methoxyphenyl)imidazo[1,2-*a***]pyridine, 3t.** M.p. 165°C. Cryst. solvent: Ethanol. Yield: 37%. ¹H-NMR (δ , ppm): 8.563 (d, 1H, J = 5.76 Hz), 8.543 (s, 1H), 8.372 (d, 2H, J = 8.44 Hz), 7.860 (d, 2H, J = 8.44 Hz), 7.800 (d, 2H, J = 7.25 Hz), 7.616-7.579 (m, 3H), 7.520 (t, 3H, J = 7.48 Hz), 7.431-7.370 (m, 2H), 7.047 (t, 1H, J = 6.92 Hz), 6.927 (dd, 1H, J = 8.04 Hz, J = 0.72 Hz), 3,843 (s, 3H). ¹³C-NMR (δ , ppm): 159.96, 145.20, 143.99, 142,68, 141.18, 140.86, 139.61, 135.08, 129.65, 129.40, 128.80, 127.39, 127.23, 127.17, 123.29, 118.86, 113.85, 112.96, 111.76, 109.01, 55.42. HRMS (ESI, m/z): calcd for C₂₆H₂₀N₂O 376.15701, found [M+H]⁺ 377.16484.

Experimental procedures of biochemical and cell viability assays.

Expression and purification of human ALDHs. Large amounts of pure recombinant human ALDH1A1, ALDH1A2 and ALDH1A3 isoenzymes were obtained as previously described.¹ Briefly, induced cells, collected by centrifugation, were re-suspended in an appropriate volume of lysis buffer (50 mM Na₂HPO₄, 300 mM NaCl, 1 mM β -mercaptoethanol, 20 mM imidazole, pH 7.5) added of benzonase nuclease (250 U/ μ L) and Protease inhibitor cocktail from SIGMA. After ultracentrifugation, the clarified sample was purified by a His-tag affinity chromatography followed by size-exclusion chromatography, using an AKTA FPLC system, at 4 °C. To evaluate the purity and homogeneity of the protein, after each purification step, eluted fractions were analyzed by SDS-PAGE and the protein quantification was always determined by Bradford protein assay. This procedure allowed us to obtain about 20 mg of pure and active human ALDH1A3, ALDH1A2 and ALDH1A1 used for all crystallization trials and kinetic analyses.

Medium-throughput screening to determine the inhibitory efficacy of imidazo[1,2-*a*]pyridine derivatives. A medium throughput screening campaign was performed for enzymes ALDH1A3, ALDH1A1 and ALDH1A2, using the previously reported continuous spectrometric assay for ALDH1A3 optimized to suit Greiner Bio-One® 96-wells UV-Transparent Microplate² and following a selection strategy for hit identification of various chemical nature that proved successful in other campaigns carried out in our laboratory against various targets.³⁻⁵ Tests were carried out by using 200 µl of reaction mixture, containing 20 mM Tris HCl pH 8.0, 1 mM β-mercaptoethanol, 150 mM KCl, 15% DMSO, 500 µM NAD⁺ and 2,6 µM of pure recombinant isoenzymes. Reactions were started by the addition of 20 mM acetaldehyde. Change in absorbance at 340 nm (ε_{NADH}=6220 M⁻¹ cm⁻¹) was monitored for 30 min in a Tecan® Sunrise at 25 °C. The activity of each enzymes was tested in the presence of each synthesized compound at 25 µM concentration, in triplicates.

Enzyme kinetic analysis to calculate IC₅₀ values of the most promising compound. Selected compounds showing the best inhibitory activity at 25 μ M were further investigated for their inhibitory efficacy, to calculate their IC₅₀ values. The enzymatic inhibition assays were performed in a total volume of 200 μ l of 20 mM Tris HCl pH 8.0, 1 mM β -mercaptoethanol, 150 mM KCl, 15% DMSO, 500 μ M NAD⁺, 2,6 μ M of pure recombinant isoenzymes in the presence of different inhibitors concentrations from 100 μ M to 0.78125 μ M and pre-incubated for 5 minutes. Reactions were started by the addition of 20 mM acetaldehyde. The kinetic parameters were determined by fitting the measured data to a Michaelis-Menten curve,⁶ by using SigmaPlot.⁷

Enzyme kinetic analysis to calculate the K_i values of 3c and 3f. The enzymatic inhibition assays were performed in a total volume of 200 µl of 20 mM Tris HCl pH 8.0, 1 mM β-mercaptoethanol, 150 mM KCl, 15% DMSO, 500 µM NAD⁺, 2,6 µM of pure recombinant isoenzymes in the presence of different inhibitors concentrations. For the complex **3c**-ALDH1A3 the inhibitor was tested at 50, 25, 10, 5, 2.5, 1 and 0.5 µM. For the complex **3f**-ALDH1A3 the inhibitor was tested at 50, 5, 0.5, 0.05 and 0.005 µM. Reactions were started by the addition of different concentration of acetaldehyde, from 1 mM to 20 mM, after 5 minutes of pre-incubation. The kinetic parameters were determined by fitting the measured data to a Michaelis-Menten curve,⁶ by using SigmaPlot.⁷

Cell viability assay. 10 x 10^5 U87-MG human glioblastoma cells were plated in Eagle's Minimum Essential Medium (MEM) and treated for 72 hours with the test compound, **3c**, solubilized in DMSO (in a final concentration of 10%). Cells viability was measured using the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium assay as described elsewhere.⁸

Experimental procedures of crystallization studies and structure determination.

Crystals of ALDH1A3 in complex with **3c** were obtained by using the vapour-diffusion technique in sitting drop and applying a spare-matrix-based strategy with a crystallization robot (Oryx4, Douglas Instruments). The best crystals were grown by mixing 0.5 µl of protein solution at a concentration of 8 mg/mL, pre-incubated with 1 mM NAD⁺ and 300 µM MF13, with an equal volume of a reservoir solution containing 2.4 M sodium malonate, pH 7.0, and equilibrated against 50 µl of the reservoir solution, at 20 °C in about 30 days. For X-ray data collection, crystals were quickly equilibrated in a solution containing the crystallization buffer and 12.5% glycerol as cryo-protectant and flash frozen at 100 K in liquid nitrogen. Data up to 3.2 Å resolution were collected at the beamline ID29 European Synchrotron Radiation Facility (ESRF, Grenoble, France). Analysis of the diffraction data set allowed us to assign the crystal to the orthorhombic $P2_122_1$ space group with cell dimensions of a = 81.56 Å, b = 89.36 Å, c = 159.04 Å and $\alpha = \beta = \gamma = 90^{\circ}$, containing four molecules per asymmetric unit with a corresponding solvent content of 52.3%. Data were processed using the program package XDS⁹ and the CCP4 suite of programs¹⁰ was used for scaling. The structure determination of ALDH1A3 was carried out by means of the molecular replacement technique using the coordinates of the tetramer of human ALDH1A3 as the search model (Protein Data Bank ID code 5FHZ²). PHASER¹¹ was used to automatically determine the ALDH1A3 structure in complex with 3c. The initial model was subjected to iterative cycles of crystallographic refinement with the programs REFMAC5¹² and PHENIX.REFINE,¹³ alternated with manual graphic session for model building using the program Coot.¹⁴ 5% of randomly chosen reflections were excluded from refinement of the structure and used for the Free R factor calculation.¹⁵ The program ARP/wARP¹⁶ was used for adding solvent molecules. Refinement was continued until convergence to R-factor and free R-factor values of 0.1962 and 0.2601 respectively, with ideal geometry. Data collection and refinement statistics are given in Table 1-SI (Supporting Information). The atomic coordinates and structure factors of human ALDH1A3 in complex with GA11 have been deposited with the Protein Data Bank (www.rcsb.org) with the accession code 6TRY. Figures were generated using the program PyMOL.¹⁷

Experimental procedures of computational studies.

Docking calculations were performed with the Gold program,¹⁸ using the CHEMPLP fitness function. The crystallographic structure of ALDH1A3 in complex with **3c** molecule was used as rigid receptor in molecular docking simulations. The structure of **3f** was sketched in 2D format using Picto (OpenEye) version 4.4.0.4, converted in 3D coordinates by OMEGA (OpenEye) version 3.1.0.3¹⁹ and then energy minimized using the MMFF94S force field.²⁰ GOLD default parameters were used, while docking efficiency was increase to the maximum value.

MD simulations were carried out on docking complexes using Amber18.²¹ The ff14SB force field²² was used to parameterize the protein and the GAFF force field²³ was used for compound **3f**. Docking complexes were solvated in a rectilinear box of explicit TIP3P water molecules. First, energy minimization was carried out only on water molecules for 5000 steps in which the first 1500 used the steepest descent algorithm (SDA), and the last 3500 the conjugate gradient algorithm (CGA). Then, whole systems were energy minimized for 10000 steps in which the first 1500 with the SDA, and the last 8500 with the CGA. Temperature was gradually raised at constant volume (NVT ensemble) from 0 K to 300 K over 1 ns by the Langevin thermostat. Density equilibration was carried out at constant pressure (NPT ensemble) by the Beredensen barostat, for 1 ns with periodic boundaries conditions. Finally, after an equilibration of 50 ns (NPT ensemble), MD trajectories were produced for of 300 ns (NPT ensemble). Then, the Cpptraj software was used to analyze the MD trajectories.²⁴

References

(1) Quattrini, L.; Gelardi, E. L. M.; Coviello, V.; Sartini, S.; Ferraris, D. M.; Mori, M.; Nakano, I.; Garavaglia, S. La Motta, C. Imidazo[1,2-a]pyridine Derivatives as Aldehyde Dehydrogenase Inhibitors: Novel Chemotypes to Target Glioblastoma Stem Cells. *J Med Chem*. Manuscript under revision.

(2) Moretti A, Li J, Donini S, Sobol RW, Rizzi M, Garavaglia S. Crystal structure of human aldehyde dehydrogenase 1A3 complexed with NAD+ and retinoic acid. *Sci Rep.* **2016**, *19*, 3571.

(3) Sahu, N. U.; Singh, V.; Ferraris, D. M.; Rizzi, M.; Kharkar, P. S. Hit discovery of Mycobacterium tuberculosis inosine 5'-monophosphate dehydrogenase, GuaB2, inhibitors. *Bioorg Med Chem Lett.* **2018**, *28*, 1714-1718.

(4) Lahiri, S.; Rizzi, M.; Rossi, F.; Miggiano, R. Mycobacterium tuberculosis UvrB forms dimers in solution and interacts with UvrA in the absence of ligands. *Proteins*. **2018**, *86*, 98-109.

(5) Ferraris, D. M.; Spallek, R.; Oehlmann, W.; Singh, M.; Rizzi, M. Crystal structure of the Mycobacterium tuberculosis phosphate binding protein PstS3. *Proteins*. **2014**, *82*, 2268-2274.

(6) Michaelis, L.; Menten, M. L. Die Kinetik der Invertinwirkung. *Biochemische Zeitschrift*. 1913, 49, 333-369.

(7) SigmaPlot Extract Graphs and Data Analysis (StatSys v12.3).

(8) Travelli, C.; Aprile, S.; Rahimian, R.; Grolla, A. A.; Rogati, F.; Bertolotti, M.; Malagnino, F.; Di Paola, R.; Impellizzeri, D.; Fusco, R. Identification of novel triazole-based Nicotinamide phosphoribosyltransferase (NAMPT) inhibitors endowed with antiproliferative and anti-inflammatory activity. *J Med Chem.* **2017**, *60*, 1768-1792.

(9) Kabsch, W. XDS. Acta Crystallogr D Biol Crystallogr. 2010, 66, 125-132.

(10) Collaborative Computational Project, Number 4. (1994) The CCP4 suite: programs for protein crystallography. *Acta Crystallogr D Biol Crystallogr*. **1994**, *50*, 760-763.

(11) McCoy, A. J.; Grosse-Kunstleve, R. W.; Adams, P. D.; Winn, M. D.; Storoni, L. C.; Read, R. J. Phaser crystallographic software. *J. Appl. Crystallogr.* 2007, *40*, 658-674.

(12) Murshudov, G. N.; Vagin, A. A.; Dodson, E. J. Refinement of macromolecular structures by the maximum-likelihood method. *Acta Crystallogr.* **1997**, *D53*, 240-255.

(13) Afonine, P. V.; Grosse-Kunstleve, R. W.; Echols, N.; Headd, J. J.; Moriarty, N. W.; Mustyakimov, M.; Terwilliger, T. C.; Urzhumtsev, A.; Zwart, P. H.; Adams, P. D. Towards automated crystallographic structure refinement with phenix.refine. *Acta Crystallogr D Biol Crystallogr.* 2012, *68*, 352-67.

(14) Emsley, P.; Lohkamp, B.; Scott, W. G.; Cowtan K. Features and development of Coot. *Acta Crystallogr D Biol Crystallogr.* **2010**, *66*, 486-501.

(15) Brunger, A. T Free R value: a novel statistic quantity for assessing the accuracy of crystal structures. *Nature*. **1992**, *355*, 472-475.

(16) Perrakis, A.; Harkiolaki, M.; Wilson, K. S.; Lamzin, V. S. ARP/wARP and molecular replacement. *Acta Crystallogr D Biol Crystallogr*. **2001**, *57*, 1445-1450.

(17) Schrödinger LLC (2010) The PyMOL Molecular Graphics System, version 1.3

(18) Jones, G.; Willett, P.; Glen, R. C.; Leach, A. R.; Taylor R. Development and validation of a genetic algorithm for flexible docking. *J. Mol. Biol.* **1997**, *267*, 727-748.

(19) Hawkins, P. C. D.; Skillman, A. G.; Warren, G. L.; Ellingson, B. A. Stahl, M. T. Conformer gneration with OMEGA: algorithm and validation using high quality structures from the protein databank and the Cambridge Structural Database. *J. Chem. Inf. Model.* **2010**, *50*, 572-584.

(20) SZYBKI 1.10.0.3: OpenEye Scientific Software, Santa Fe, NM. http://www.eyesopen.com.

(21) Case, D. A.; Ben-Shalom, I. Y.; Brozell, S. R.; Cerutti, D. S.; Cheatham, T. E. III; Cruzeiro,

V. W. D.; Darden, T. A.; Duke, R. E.; Ghoreishi, D.; Gilson, M. K.; Gohlke, H.; Goetz, A. W.;

Greene, D.; Harris, R.; Homeyer, N.; Izadi, S.; Kovalenko, A.; Kurtzman, T.; Lee, T. S.; LeGrand,

S.; Li, P.; Lin, C.; Liu, J.; Luchko, T.; Luo, R.; Mermelstein, D. J.; Merz, K. M.; Miao, Y.; Monard,

G.; Nguyen, C.; Nguyen, H.; Omelyan, I.; Onufriev, A.; Pan, F.; Qi, R.; Roe, D. R.; Roitberg, A.;

Sagui, C.; Schott-Verdugo, S.; Shen, J.; Simmerling, C. L.; Smith, J.; Salomon-Ferrer, R.; Swails,

J.; Walker, R. C;. Wang, J.; Wei, H.; Wolf, R. M.; Wu, X.; Xiao, L.; York, D. M.; Kollman, P. A. AMBER 2018, 2018 University of California, San Francisco.

(22) Maier, A.; Martinez, C.; Kasavajhala, K.; Wickstrom, L.; Hauser, K. E.; Simmerling, C. ff14SB: Improving the accuracy of protein side chain and backbone parameters from ff99SB. *J Chem Theory Comput.* **2015**, *11*, 3696-3713.

(23) Case, D. A.; Wang, J.; Wolf, R. M.; Caldwell, J. W.; Kollman, P. A. Development and testing of a general amber force field. *J Comput. Chem.* **2004**, *25*, 1157-1174.

(24) Roe, D. R.; Cheatham, T. E. III. PTRAJ and CPPTRAJ: software for processing and analysis of molecular dynamics trajectory data. *J Chem Theory Comput.* **2013**, *9*, 3084-3095.