SUPPORTING INFORMATION

Crystal Structure of Aldehyde Dehydrogenase 16 Reveals Trans Hierarchical Structural Similarity and a New Dimer

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Beamline	ALS 4.2.2
Space group	P2
Unit cell parameters (Å, °)	a = 97.9,
	b = 63.1,
	c = 134.1,
	$\beta = 108.9^{\circ}$
Wavelength (Å)	1.000
Resolution (Å)	63.08-2.95 (3.11-2.95)
Observations	116172 (15801)
Unique reflections	32443 (4706)
$R_{\text{merge}}(I)$	0.088 (0.627)
$R_{\rm meas}(I)$	0.122 (0.856)
$R_{\rm pim}(I)$	0.083 (0.580)
Mean <i>I</i> / σ	10.5 (1.7)
Mean $CC_{1/2}$	0.996 (0.631)
Completeness (%)	98.4 (98.6)
Multiplicity	3.6 (3.4)

 Table S1. Data Collection Statistics for LaALDH16^a

^aValues for the outer resolution shell of data are given in parentheses.



Fig. S1. Model of the nonfunctional NAD⁺-binding site of HsALDH16A1. This figure shows a superposition of the crystal structure of LsALDH16-NAD⁺ (gray with pink NAD⁺) and a model of HsALDH16A1 generated with SWISS-MODEL (blue). Residues are labeled as LsALDH16/HsALDH16A1.



Fig. S2. Catalytic activity of ALDH16 monitored by the progress curve of NADH production using hexanal as the substrate in the presence of the cofactor NAD⁺. (A) LsALDH16 displays ALDH activity. (B) HsALDH16A1 does not display ALDH activity.