Supplementary Materials for:

Homology modeling, molecular dynamics, and site-directed mutagenesis study of AlkB human homolog 1 (ALKBH1) Pavel Silvestrov^a, Tina A. Müller^b, Kristen N. Clark^b, Robert P. Hausinger^b, G. Andrés Cisneros^{a,*}

Supplementary Table S1

Primers and plasmids used to create ABH1 variants.

Plasmid	Variant	Primers	Based on
nADU175	11112 4		plasmid pDAD67
равп1/3	ппза	1015 CAUGITACCAUTOUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU	рвако/
	C119A		"DAD(7
равнізо	CII8A		рВАК0/
	C120.4		"DAD(7
	C129A	10F5 CUCAGAAACCIAAIGIAGCGAACCIGGACAAACAACAIG5	рВАК0/
			mDAD67
равнія	H134A	10F5 GIAIGIAAUUIGGAUAAAGUGAIGIUIAAAGAAGAGAUUU 5	рВАК0/
			"DAD(7
равнія	H303A		рВАК0/
	C2044		
равнізя	C304A		pBAR6/
	0271 4		
pABH142	C3/1A	INFO CATCAGIACAGAAGGIIICGCGCAAAACCTTCTCTACTCATC 3	pBAR6/
	112724		DAD(7
рАВН192	H3/2A		pBAR6/
	11112A/C120A		
	H113A/C129A		pABH137
	G118A/G120A		
pABH188	C118A/C129A		pABH136
A D11102			A DI1175
pABH193	H113A/C118A	TOP 5' GGGCGIGGGGGGGAAACAGGCGCGTCTTTCACCCACCCCCC 2	pABH1/5
4.01110.4	C120 A /11124 A		A DI1127
pABH194	C129A/H134A		pABH13/
4.01105			4.011120
pABH195	H303A/C304A	for 5' GAAGGGGAAGGCC1GCC1GCGGGGGCGC1AGAGGCACC1C1C 3'	pABH139
		rev 5' GAGAGGTGCCTCTAGCGCCGCAGGCAGGCCTTCCCCTTC 3'	
pABH189	C304A/C3/1A	for 5' CATCAGTACAGAAGGTTTCGCGCATCTGGATGACCAGAATAG 3'	pABH139
		rev 5' CTATICIGGICAICCAGAIGCGCGAAACCIICIGIACIGAIG 3'	4 DUI 40
pABH196	C3/1A/H3/2A	for 5' GTACAGAAGGTTTCGCGGCGCTGGATGACCAGAATAG 3'	pABH142
		rev 5' CTATICIGGICATCCAGCGCCGCGAAACCTICIGIAC 3'	
pABH203	H113A/C129A/H134A	tor 5' CAGGTTACCAGTGGGCGTGGGGGGGGGAAACAGTGC 3'	pABH194
		rev 5' GUAUIGIIIUACUUAUGUUAUIGGIAAUUIG 3'	4.011000
pABH204	H113A/C118A/C129A	tor 5' GGGCGTGGGTGAAACAGGCGCTTAAGTTATATTCCC 3'	pABH203
	/H134A	rev 5' GGGAATATAACTTAAGCGCCTGTTTCACCCACGCCC 3'	

Supplementary Figure S1. Sequence alignments (a) between AlkB and the AlkB part of ALKBH1 (b) between DBL and the DBL part of ALKBH1. The residues introduced to the sequences and the overlapping regions are underlined.





Potential Energy, ALKBH1 without Disulfide Bridges



Supplementary Figure S3. Dynamics of distances between lysines and serines throughout the 100ns simulation with disulfide bridges are shown for the three pairs: (a) K133 and S136 (b) K154 and S147 (c) K182 and S181.



Supplementary Figure S4. Residues in proximity to K25. Shown are a snapshot at the 100th ns of the simulation with disulfide bridges and the dynamics of distances between the nitrogen of the amino group of K25 and the atoms in nearby residues.

