Stractures	Nativo		SeMet	
Data collection	Native		Semet	
	ר ר רח		2 2 2	
Space group	$PZ_1Z_1Z_1$		$PZ_1Z_1Z_1$	
Cell dimensions				
a, b, c (A)	54.91, 103.05, 108.93		55.12, 103.12, 110.99	
α, β, γ (°)	90.0, 90.0, 90.0		90.0, 90.0, 90.0	
		Peak	Inflection	Remote
Wavelength		0.9805	0.9808	0.9537
Resolution (Å)	103 14-2 10	110 43-2 75	110 99-2 75	110 43-2 75
Resolution (II)	(2.21, 2.10)	$(2.00_{-}2.75)$	$(2.90_{-}2.75)$	$(200_{-}275)$
D	$(2.21^{-}2.10)$	(2.70-2.75)	$(2.70^{-}2.75)$	$(2.70^{-}2.75)$
Λmerge	0.0(29.1)	9.7 (30.3)	9.5 (52.6)	9.5 (54.0)
	11.9 (3.4)	8.8 (4.0)	9.2 (4.1)	9.2 (3.9)
Completeness (%)	98.9 (95.3)	99.6 (99.8)	99.7 (99.8)	99.7 (99.8)
Redundancy	3.6 (3.3)	3.3 (3.4)	3.3 (3.4)	3.3 (3.4)
Refinement				
Resolution (Å)	2.10			
No. reflections	34537			
Rwork / Rfroo	195/224			
No atoms	3504			
Drotoin	3375			
Water	120			
V alei D factore	129			
D-lactors	264			
Protein	36.4			
Water	40.1			
R.m.s deviations				
Bond lengths (Å)	0.016			
Bond angles (°)	1.699			

Supplementary Table 1. Data collection, phasing and refinement statistics for MAD (SeMet) structures

*Values in parentheses are for highest-resolution shell.

Supplementary Table 2. NMR constraints and structural statistics				
Total NOE distance constraints	2781			
Short Range (i, i-1)	1283			
Medium Range (i, i- < 5)	651			
Long Range (i, i- ≥ 5)	847			
Total dihedral angle constraints	166			
ψ	83			
Φ	83			
Average Cyana target function	2.18 ± 0.34			
Violations				
Maximum distance violation (Å)	0.49			
Maximum van der Waals violation (Å)	0.28			
Maximum dihedral angle violation (°)	4.97			
RMS deviations from mean structure*				
Backbone atoms (Ν, Cα, C') (Å)	0.86 ± 0.2			
All heavy atoms (Å)	1.29 ± 0.19			
Ramachandran plot				
Residues in most favourable regions (%)	75.9			
Residues in additionally allowed regions	21.8			
(%)				
Residues in generously allowed regions (%)	1.9			
Residues in disallowed regions (%)	0.5**			

Supplementary Table 2. NMR constraints and structural statistics

*residues 199-315 (residues that showed medium range or longer NOEs) ** These residues, apart from M258, had no chemical shift assignments.

Protein ID	Peptide sequence	Mascot Ion score
TDIF1_HUMAN	AVLQPSINEEIQTVFNK	114
TDIF1_HUMAN	DLAASDDYR	28.8
TDIF1_HUMAN	DNVGEEVDAEQLIQEA <mark>C</mark> R	97.7
TDIF1_HUMAN	GGLELGDAGAAGQLVLTNPWNI <mark>M</mark> IK	66.2
TDIF1_HUMAN	GGLELGDAGAAGQLVLTNPWNIMIK	93.8
TDIF1_HUMAN	GRPPGHILSSDR	28.8
TDIF1_HUMAN	HWLAEQHHMR	31.9
TDIF1_HUMAN	KGRPPGHILSSDR	37
TDIF1_HUMAN	KYMETLR	36.2
TDIF1_HUMAN	LNESTTFVLGSR	96.2
TDIF1_HUMAN	MAYLLIEEDIRDLAASDDYR	49
TDIF1_HUMAN	SQMTTSFTDPAIS <mark>M</mark> DLLR	103
TDIF1_HUMAN	SQMTTSFTDPAISMDLLR	123
TDIF1_HUMAN	YAADPQDKHWLAEQHHMR	61.3
CN043_HUMAN	IPGTDAQAQAED <mark>M</mark> NVK	43.1
CN043_HUMAN	KEGEEEVPEIQEKEEQEEGR	24.9
CN043_HUMAN	SAQEEVEVDIK	43
CN043_HUMAN	SHESNAPGSAGGQASEKPR	42.1
CN043_HUMAN	WPNSVMAPGR	33.5
HDAC1_HUMAN	SFNLPMLMLGGGGYTIR	62.0
HDAC1_HUMAN	VKTEDEKEKDPEEK	18.6

Supplementary Table 3. Mass spectrometry data for FLAG tagged DNTTIP1

Modified amino-acids shown in red



A stable complex of HDAC1, DNTTIP1 and MIDEAS. Small scale co-transfection of HEK293F cells and purification of FLAG tagged constructs of MIDEAS and DNTTIP1 with DNTTIP1, MIDEAS and HDAC1 as indicated.



Circular dichroism experiments on the dimerisation domain of DNTTIP1.

(A) Melting curves of DNTTIP1 (56-147) as it is thermally denatured, slow cooled and then denatured again. The circular dichroism was monitored at 222 nm. (B) Circular dichroism spectra of DNTTIP1 (56-147) at 5°C before, after slow cooling and after snap cooling together with spectra at 95°C after both rounds of thermal denaturation.



15N-HSQC spectra of the DNA titration with DNTTIP1.

A) 0.2mM DNTTIP1 with no DNA, B) with 0.25 molar equivalents of DNA, C) with 1.0 molar equivalents of DNA, D) with 5 molar equivalents of DNA. Red peaks are arginine sidechain NE resonances folded from ~ 70ppm.



SEC-MALS profile of the complex with full-length HDAC1, full-length DNTTIP1 and MIDEAS (717-887).

The measured molecular weight is 455.9 kDa +/-14 kDa. The calculated molecular weight for a tetramer containing four copies of each protein is 448 kDa.



Superdex S-200 gel filtration purification of the full length HDAC1, full length DNTTIP1 and MIDEAS(650-887) complex.