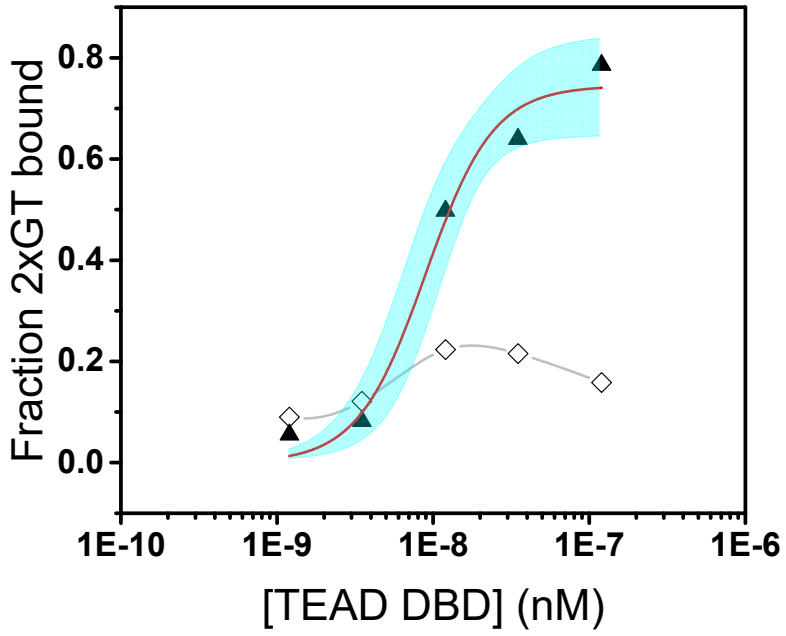
Supplementary Materials:

Fig S1. Analysis of EMSA data of TEAD DBD binding to tandemly duplicated DNA. Band intensities were determined using Image J from data shown in Fig 6A (top, right in Anbanandam et al., 2006). Open diamonds correspond to one TEAD bound per 2xGT double stranded DNA. Closed triangles correspond to two molecules of bound TEAD per molecule of 2xGT DNA. Red curve is the fit derived from non-linear curve fitting routine to the Hill equation, $y = [Ymax * x^n]/[(Kd)^n + x^n]$, using Levenberg-Marquardt algorithm. Area shaded in cyan represents the 95% confidence interval.



Results of curvefit:

Reduced Chi-Sqr	0.00203	
Adj. R-Square	0.98221	
	Value	Standard Error
Ymax	0.74478	0.03571
Kd	8.94497E-9	1.23305E-9
n	2 (fixed)	0

Fig. S2. Organization of ΔL1 dimers in the crystal lattice: TEA domain fold is made of domain-swapped chains. Shown here in cartoon form, is an assembly of three domain-swapped dimers from two adjacent cells.

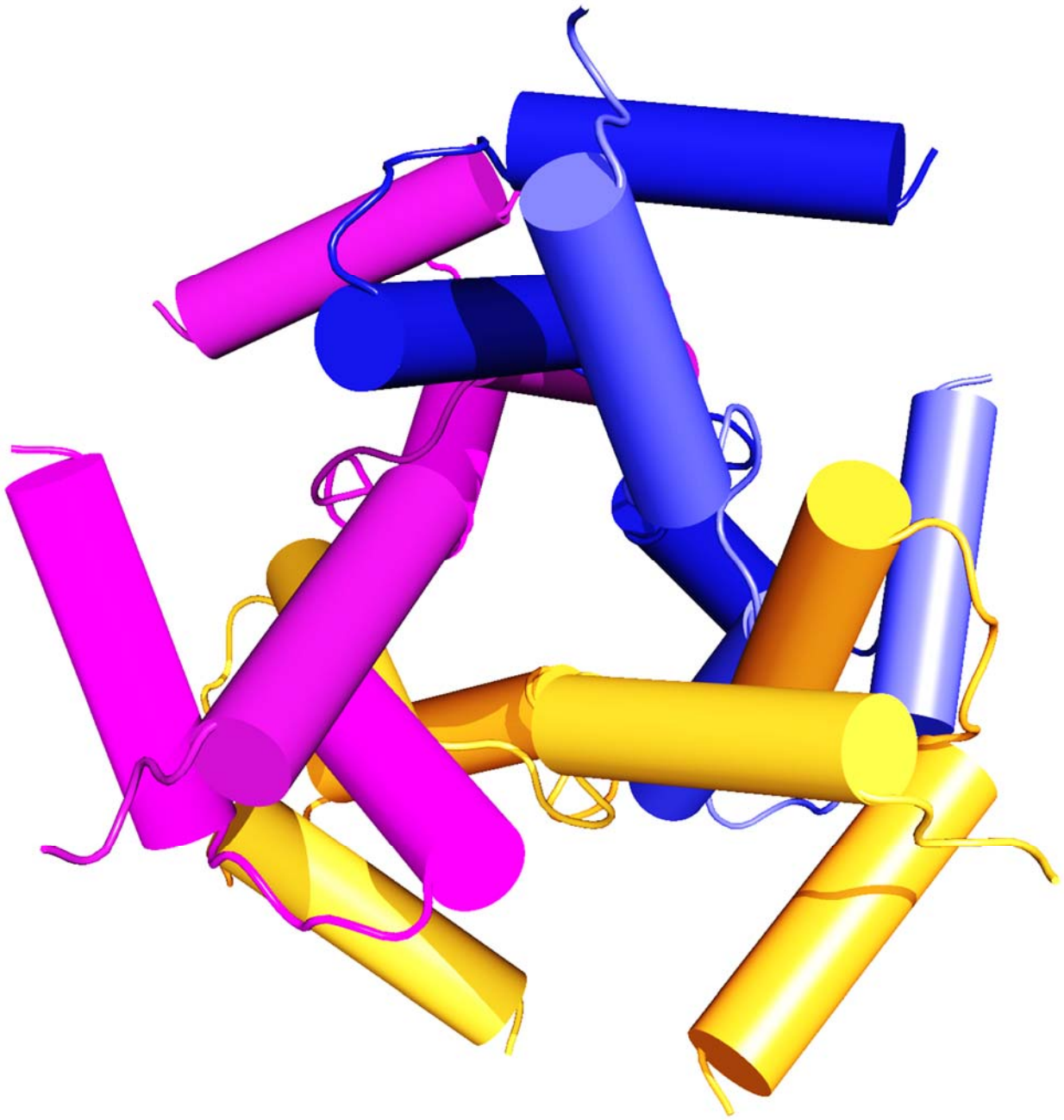
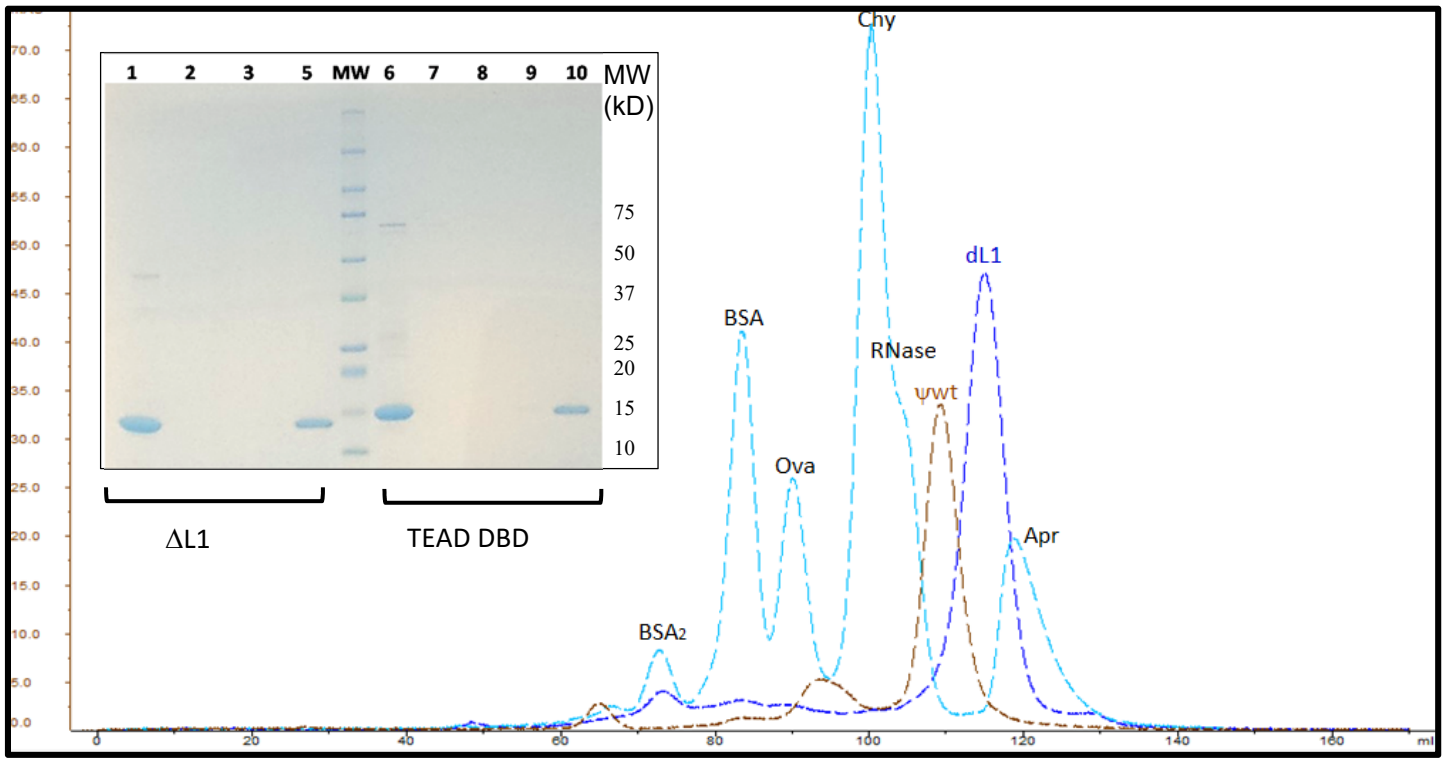


Fig. S3. Sephacryl S200 XK 16/60 elution profile of ΔL1 TEAD DBD (blue trace) and TEAD DBD (brown trace) is shown with molecular weight calibration proteins (cyan trace). Molecular weight calibration proteins: BSA=bovine serum albumin (runs as monomer and dimer), Ova=ovalbumin, Chy=chymotrypsinogen, RNase=Ribonuclease, Apr=aprotinin.

Buffer: 50mM Hepes, pH 8.0, 250mM NaCl, 0.01% NaN3; flow rate: 0.25mL/min, 1.8mL/fraction. 4-7 mg of each protein was injected.



Inset: SDS-PAGE of SEC peak fractions. TGX 4-20% gradient gel electrophoresis.

Lanes 1-5: ΔL1 TEAD DBD

1: Ni-NTA purified ΔL1 protein- sample injected into column; ***2*****:** F#41; ***3*****:** F#46; ***4*****:** F#50

5**:** F#64

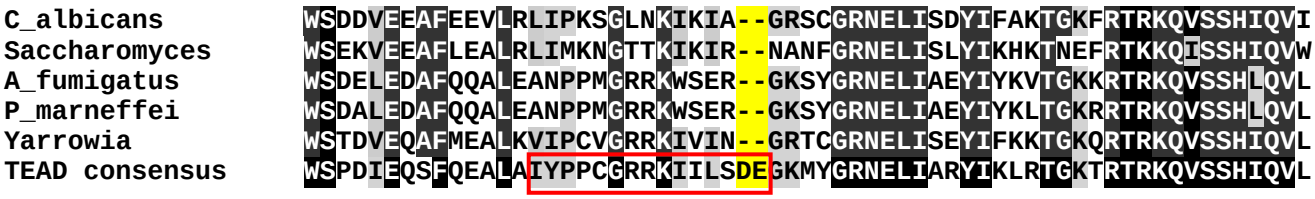
MW: MW markers

Lanes 6-10: C27S TEAD DBD

6: Ni-NTA purified C27S protein- sample injected into column; ***7:*** F#36; ***8:*** F#46; ***9:*** F#52

10: F#61

Fig. S4. Fungal Tec1 DBD amino acid sequence alignment.



A shortening of the L1 loop in nature: The amino acids 'DE' (AspGlu) within the L1 loop of TEAD consensus sequence are absent in fungal TEC1. L1 loop residues that are missing in ΔL1 TEAD DBD are boxed in red.

Table S.1. Domain swapping contacts for ΔL1 TEAD DBD

Chain/residue	Atom	Chain/residue	Atom	Distance (Å)
***L1 loop H-bonds**:*				
B0041-MET	N	C0039-GLY	O	2.84
B0044-ARG	NE	C0037-TYR	O	2.71
B0044-ARG	NH2	C0037-TYR	O	2.88
***H1 H-bonds**:*				
B0051-TYR	OH	C0032-GLU	OE1	2.77
B0058-LYS	NZ	C0025-ASP	OD2	2.8
B0060-ARG	NE	C0021-VAL	O	2.81
B0060-ARG	NH2	C0021-VAL	O	2.99
B0068-HIS	NE2	C0027-GLU	OE1	2.67
***Non-bonded L1 contacts**:*				
C0039-GLY	C	B0041-MET	N	3.8
C0039-GLY	O	B0041-MET	N	2.84
C0039-GLY	O	B0041-MET	CA	3.73
C0038-PRO	O	B0041-MET	CB	3.3
C0039-GLY	O	B0041-MET	CB	3.64
C0038-PRO	O	B0041-MET	CG	3.77
C0038-PRO	O	B0041-MET	SD	3.22
C0038-PRO	O	B0044-ARG	CG	3.6
C0037-TYR	O	B0044-ARG	CD	3.88
C0038-PRO	O	B0044-ARG	CD	3.58
C0037-TYR	C	B0044-ARG	NE	3.67
C0037-TYR	O	B0044-ARG	NE	2.71
C0038-PRO	C	B0044-ARG	NE	3.51
C0038-PRO	O	B0044-ARG	NE	3.4
C0039-GLY	N	B0044-ARG	NE	3.75
C0034-LEU	CD1	B0044-ARG	CZ	3.85
C0037-TYR	O	B0044-ARG	CZ	3.19
C0038-PRO	C	B0044-ARG	CZ	3.84
C0039-GLY	N	B0044-ARG	CZ	3.7
C0034-LEU	O	B0044-ARG	NH2	3.37
C0034-LEU	CG	B0044-ARG	NH2	3.89
C0034-LEU	CD1	B0044-ARG	NH2	3.52
C0037-TYR	O	B0044-ARG	NH2	2.88

C0033-ALA	CB	B0048-ILE	CG1	3.87
C0030-PHE	CD1	B0048-ILE	CG2	3.74
C0033-ALA	CB	B0048-ILE	CG2	3.79
C0034-LEU	CD1	B0048-ILE	CD1	3.79
C0029-SER	O	B0051-TYR	CD2	3.53
C0033-ALA	CB	B0051-TYR	CD2	3.67
C0036-ILE	CD1	B0051-TYR	CE1	3.62
C0029-SER	O	B0051-TYR	CE2	3.44
C0032-GLU	CB	B0051-TYR	CE2	3.86
C0032-GLU	OE1	B0051-TYR	CE2	3.69
C0032-GLU	OE1	B0051-TYR	CZ	3.7
C0036-ILE	CD1	B0051-TYR	CZ	3.9
C0032-GLU	CB	B0051-TYR	OH	3.55
C0032-GLU	CD	B0051-TYR	OH	3.78
C0032-GLU	OE1	B0051-TYR	OH	2.77
C0029-SER	OG	B0055-ARG	CB	3.72
C0025-ASP	O	B0056-THR	CG2	3.67
C0029-SER	OG	B0056-THR	CG2	3.33
C0025-ASP	OD2	B0058-LYS	CD	3.76
C0026-ILE	CG1	B0058-LYS	CD	3.78
C0026-ILE	CD1	B0058-LYS	CD	3.52
C0025-ASP	OD2	B0058-LYS	CE	3.45
C0023-SER	OG	B0058-LYS	NZ	3.61
C0025-ASP	CG	B0058-LYS	NZ	3.27
C0025-ASP	OD1	B0058-LYS	NZ	3
C0025-ASP	OD2	B0058-LYS	NZ	2.8
C0022-TRP	CZ3	B0060-ARG	CG	3.83
C0021-VAL	C	B0060-ARG	NE	3.69
C0021-VAL	O	B0060-ARG	NE	2.81
C0021-VAL	CG1	B0060-ARG	NE	3.72
C0021-VAL	CG2	B0060-ARG	NE	3.86
C0026-ILE	CD1	B0060-ARG	NE	3.59
C0021-VAL	O	B0060-ARG	CZ	3.32
C0026-ILE	CD1	B0060-ARG	CZ	3.37
C0021-VAL	C	B0060-ARG	NH2	3.84
C0021-VAL	O	B0060-ARG	NH2	2.99
C0026-ILE	CD1	B0060-ARG	NH2	3.05
C0022-TRP	CZ2	B0064-GLN	C	3.53
C0022-TRP	CZ2	B0064-GLN	O	3.22
C0021-VAL	CG1	B0064-GLN	NE2	3.26
C0021-VAL	CG2	B0064-GLN	NE2	3.44
C0022-TRP	CE2	B0068-HIS	CB	3.87
C0022-TRP	CZ2	B0068-HIS	CB	3.57

C0022-TRP	CE2	B0068-HIS	CG	3.71
C0022-TRP	CE2	B0068-HIS	CG	3.72
C0022-TRP	NE1	B0068-HIS	CG	3.87
C0022-TRP	CZ2	B0068-HIS	CG	3.85
C0022-TRP	CD1	B0068-HIS	CD2	3.71
C0022-TRP	CE2	B0068-HIS	CD2	3.32
C0022-TRP	NE1	B0068-HIS	CD2	3.08
C0022-TRP	CZ2	B0068-HIS	CD2	3.66
C0027-GLU	OE1	B0068-HIS	CD2	3.59
C0030-PHE	CD2	B0068-HIS	CD2	3.66
C0030-PHE	CE2	B0068-HIS	CD2	3.43
C0030-PHE	CZ	B0068-HIS	CD2	3.62
C0022-TRP	CD1	B0068-HIS	ND1	3.84
C0022-TRP	CE2	B0068-HIS	ND1	3.76
C0022-TRP	NE1	B0068-HIS	ND1	3.71
C0022-TRP	CG	B0068-HIS	CE1	3.88
C0022-TRP	CG	B0068-HIS	CE1	3.71
C0022-TRP	CD1	B0068-HIS	CE1	3.49
C0022-TRP	NE1	B0068-HIS	CE1	3.69
C0027-GLU	OE1	B0068-HIS	CE1	3.62
C0022-TRP	CG	B0068-HIS	NE2	3.75
C0022-TRP	CD1	B0068-HIS	NE2	3.11
C0022-TRP	CE2	B0068-HIS	NE2	3.6
C0022-TRP	NE1	B0068-HIS	NE2	2.96
C0027-GLU	CD	B0068-HIS	NE2	3.71
C0027-GLU	OE1	B0068-HIS	NE2	2.67
C0030-PHE	CE1	B0069-ILE	CG1	3.67
C0030-PHE	CZ	B0069-ILE	CG1	3.54
C0034-LEU	CD1	B0069-ILE	CG1	3.87
C0027-GLU	OE2	B0072-LEU	CD2	3.7
C0030-PHE	CE2	B0072-LEU	CD2	3.69