SUPPLEMENTAL DATA

Radzimanowski *et al.*:

The structure of the human FE65-PTB1 domain

Supplemental tables

Table S1: Data collection statistics for phosphate bound H3 crystals

Space group	H3
Unit cell ($Å^3$)	146.0 x 146.0 x 78.3
Wavelength (Å)	1.000
Resolution (Å)[1]	50.0 – 2.7 (2.77-2.70)
Unique reflections	17113
Completeness (%)[1]	100 (100)
Multiplicity[1]	3.8 (3.8)
R_{sym} (%)[1,2]	7.7 (34.1)
Mean I/σ_I[1]	12.9 (3.0)

[1]Values in parenthesis correspond to the highest resolution shell.
[2]$R_{sym} = \Sigma \, ||F_{obs}|-|F_{calc}|| \, / \, \Sigma \, |F_{obs}|$

Table S2: Closest structural homologues of Fe65-PTB1

The DALI (1) search for structural homologues was performed on the basis of the structure derived from the $P2_12_12_1$ space group lacking redidues Tyr402 to Glu418 (α2/β2 loop). For each protein (Z score > 12), the number of aligned residues (Cα), the rmsd for the aligned Cα atoms, the sequence identity after structural alignment and the PDB entry codes are tabulated. The identified PTB-domains belong all to the Dab-like PTB domain sub-family.

Protein	**Cα**	**Rmsd (Å)**	**Identity (%)**	**PDB code**
APPL1-PTB domain	114	1.9	22	2ela (2)
X11-PTB domain	114	2.0	19	1x11 (3)
Dab1 PTB domain	113	2.0	14	1ntv (4)
Fe65L1 (APBB2) C-terminal PTB domain	108	1.8	25	1wgu (unpublished)
Epidermal growth factor receptor pathway substrate-8 (EPS8) PTB domain	112	2.5	18	2cy4 (unpublished)
Tensin 1 PTB domain	106	2.8	16	1wvh (unpublished)

References

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