

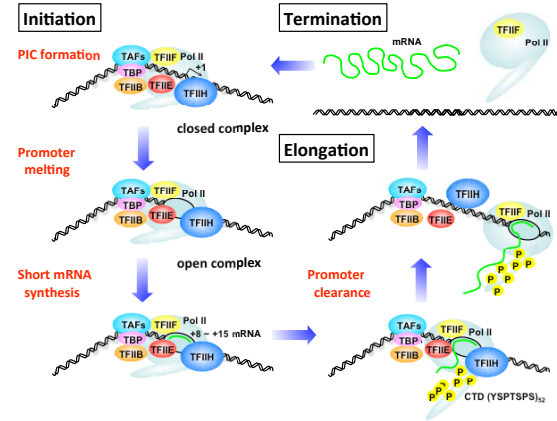
# “クロマチン上での基本転写因子、転写制御因子、ヒストン修飾因子の構造生物学”

## ～ヒト基本転写因子TFIIEとTFIIHとの相互作用に対する構造生物学的洞察～

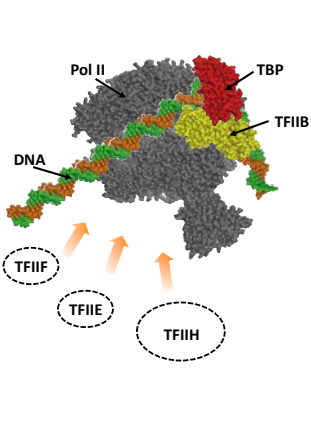
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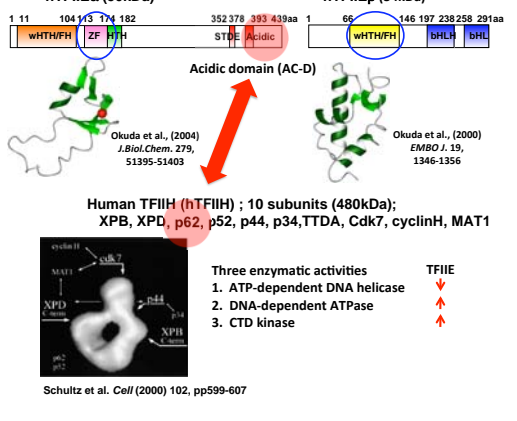
### 1 Transcription in eucaryote



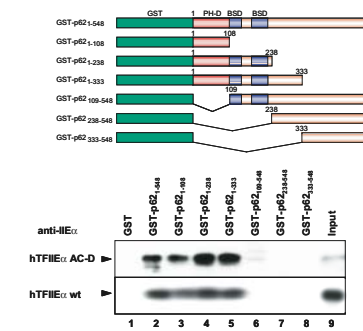
### 2 Structural model for the TBP-DNA-TFIIB-Pol II complex



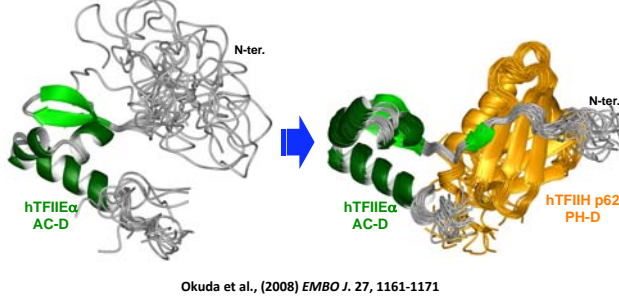
### 3 Human TFIIE (hTFIIE); Heterodimer (84kDa)



### 4 hTFIIeα AC-D specifically binds to PH-D of hTFIIF p62



### 5 Flexible N-terminal acidic tail from hTFIIeα AC-D wraps around PH-D of p62

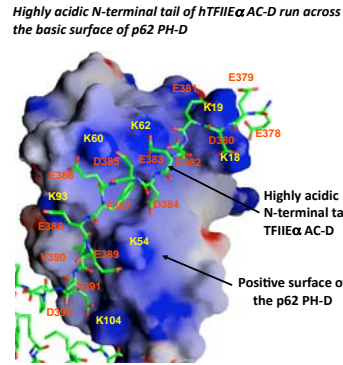


### 6 Structural statistics for the 20 best structures of hTFIIeα AC-D and its complex with hTFIIF p62 PH-D

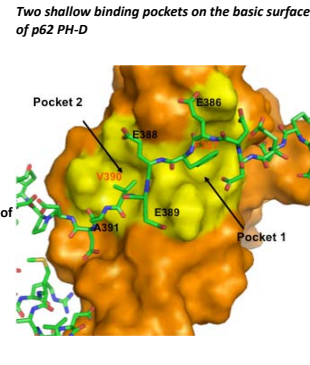
	Free hTFIIeα AC-D	Complex hTFIIeα AC-D / hTFIIF p62 PH-D
Statistics for structure calculations		
R.m.s. deviations from experimental restraints <sup>a</sup>		
Distance (Å)	0.030 ± 0.000	0.014 ± 0.000
Dihedral (°)	0.080 ± 0.026	0.47 ± 0.03
R.m.s. deviations from idealized covalent geometry		
Bonds (Å)	0.0020 ± 0.0001	0.0020 ± 0.0000
Angles (°)	0.53 ± 0.00	0.55 ± 0.00
Improp (°)	0.40 ± 0.01	0.44 ± 0.01
Final energies		
E total (kcal mol <sup>-1</sup> )	100.5 ± 0.6	347.8 ± 4.2
E bond (kcal mol <sup>-1</sup> )	3.2 ± 0.5	11.1 ± 0.4
E angle (kcal mol <sup>-1</sup> )	75.3 ± 0.6	230.4 ± 1.9
E van der Waals (kcal mol <sup>-1</sup> )	3.1 ± 0.4	20.6 ± 1.7
E NOE (kcal mol <sup>-1</sup> )	6.5 ± 0.5	41.2 ± 2.8
E dihedral (kcal mol <sup>-1</sup> )	0.0 ± 0.0	3.6 ± 0.5
E improper (kcal mol <sup>-1</sup> )	12.4 ± 0.6	40.6 ± 1.1
Coordinate precision		
Backbone atoms (Å)	0.24 ± 0.08 <sup>b</sup>	0.20 ± 0.04 <sup>b</sup> 0.44 ± 0.08 <sup>b</sup> 0.58 ± 0.11 <sup>b</sup>
Heavy atoms (Å)	0.70 ± 0.07 <sup>b</sup>	0.68 ± 0.05 <sup>b</sup> 0.85 ± 0.10 <sup>b</sup> 0.55 ± 0.10 <sup>b</sup>
Ramachandran plot statistics		
Most favoured regions (%)	82.9 <sup>c</sup>	79.4 <sup>c</sup>
Additional allowed regions (%)	17.1 <sup>c</sup>	16.9 <sup>c</sup>
Generously allowed regions (%)	0.0 <sup>c</sup>	2.5 <sup>c</sup>
Disallowed regions (%)	0.0 <sup>c</sup>	0.7 <sup>c</sup>

<sup>a</sup> None of the structures exhibited distance violations > 0.5 Å, dihedral angle violations > 5°.  
<sup>b</sup> The value was calculated over residues 383-433 of hTFIIeα AC-D of the free form or in the complex.  
<sup>c</sup> The value was calculated over residues 7-104 of hTFIIF p62 PH-D in the complex.  
<sup>d</sup> The value was calculated over residues 383-433 of hTFIIeα AC-D and residues 7-104 of hTFIIF p62 PH-D in the complex.

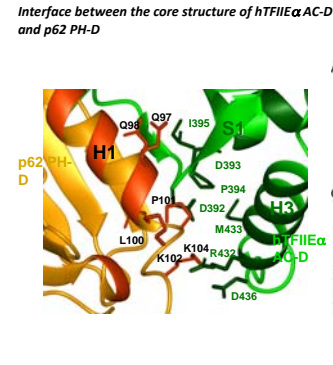
### 7 Highly acidic N-terminal tail of hTFIIeα AC-D run across the basic surface of p62 PH-D



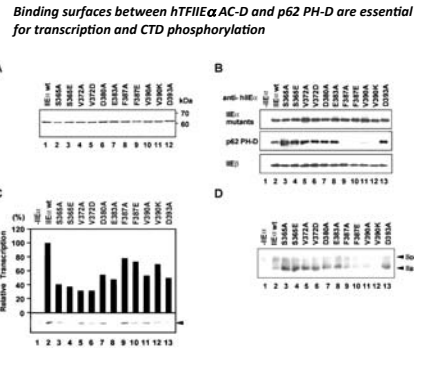
### 8 Two shallow binding pockets on the basic surface of p62 PH-D



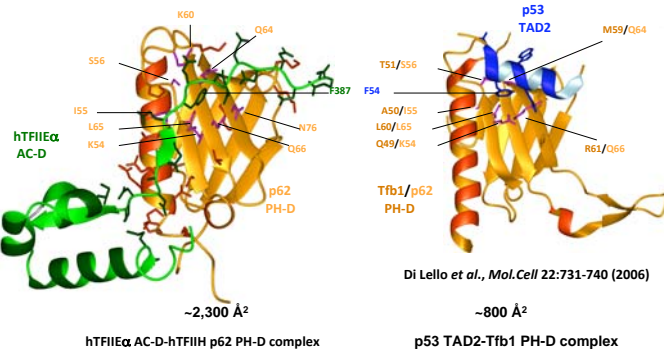
### 9 Interface between the core structure of hTFIIeα AC-D and p62 PH-D



### 10 Binding surfaces between hTFIIeα AC-D and p62 PH-D are essential for transcription and CTD phosphorylation



### 11 hTFIIeα AC-D shares the p62 PH-D binding surface with p53 TAD2



### 12 Interaction between hTFIIeα AC-D and p62 PH-D could be a switch to replace p53 with TFIIE on TFIIF in transcription

