

# **β-Sheet mimetics that Target the Transcriptional Coactivator β-Catenin**

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#### https://doi.org/10.17952/37EPS.2024.P1254



Protein complexes are defined by the three-dimensional structure of participating binding partners. Knowledge about these structures can facilitate the design of peptidomimetics which have been applied for example, as inhibitors of protein–protein interactions (PPIs). Even though β-sheets participate widely in PPIs, they have only rarely served as the basis for peptidomimetic PPI inhibitors, in particular when addressing intracellular targets. Here, we present the structure-based design of  $\beta$ -sheet mimetics targeting the intracellular protein β-catenin, acentral component of the Wnt signaling pathway. Based on aprotein binding partner of β-catenin, a macrocyclic peptide was designed and its crystal structure in complex with β-catenin obtained. The presented design strategy can support the development of inhibitors for other  $\beta$ -sheet-mediated PPIs.

# **1 TCF Derived Tracer Peptide**

A	Site 3 binding	Site 2 binding	
Lef-1 (01-63)	MPQLSGGGGGGDPELCATDEMIPFKDEGDPQKEKI	IFAEISHPEEEGDLADIKSSLVNESEIIP	
TCF3 (01-61)	MPQLNSGGGDELGANDELIRFKDEGEQEEKS-	PGEGSAEGDLADVKSSLVNESENHSSDSDS	
TCF4 (01-53)	MPQLNGGGGDDLGANDELISFKDEGEQEEKS-	SENSSAERDLADVKSSLVNESE	
TCF4-L	DELISFKDEGEQE	- BA - BA ERDLADVKSSLVN	
TCF4(35)	DELISFKDEGEQEEKS-	SENSSAERDLADVKSSLVN	



(A) Sequence alignment of the CBD's of Lef-1 (PDB ID 3ouw), TCF3 (PDB ID 1g3j), TCF4 (PDB ID 2gI7) and TCF4-L and TCF4(35). In green the resolved residues by X-ray. Framed the crucial residues for binding. (B) FP-binding assay of TCF4-L and TCF4(35) towards  $\beta$ -catenin. K<sub>p</sub>values were obtained from FP measurements (n=3, ± std. error). (C) FP competition assay with TCF4-derived tracer peptides c = 10 nM) and full-length  $\beta$ -catenin (c = 250 nM). Competitor concentration was varied (c = 1.6 x 10<sup>-4</sup>-375  $\mu$ M, n=2, ± std. error)

# 3 A Cyclic Peptide Inhibits the $\beta$ -Catenin/TCF4 Interaction

#### **2 E-Cadherin-Derived Peptides**





(A) Chemical structure of the macrocycle 12. Amino acids of $\beta$ -strands $\beta$ 1 and $\beta$ 2 are highlighted in blue. (B) FP competition assay with TCF-
4-derived tracer peptide c = 10 nM) and full-length $\beta$ -catenin (c = 250 nM). Competitor concentration was varied (c = 7.9 x 10 <sup>-3</sup> -188 $\mu$ M, n=3,
± std. error). (C) Crystal structure of β-catenin (grey, surface representation) in complex with peptide 12 (blue, cartoon representation, PDB
ID 7ar4). The hot spot residues as well as βA-βAand the DP-LP turn are shown in stick representation (blue). 12 is superimposed with the
CBD of E-cadherin (orange, cartoon representation, PDB ID 1i7x). Residues L676 and D674 are shown explicitly.

		45 aa	
11	>5	14 aa	

(A) Top: Crystal structure (PDB ID 2gI7) of β-catenin (grey) in complex with the CBD of TCF-4 (green) and superimposed with the CBD of Ecadherin (orange, PDB ID 1i7x, chain B). Bottom: Close-up of indicated region with b-catenin in surface representation (grey). Hot-spot amino acids of E-CBD (D665, I657, Y643, D674, L676) and TCF (D16, E17) are shown as stick. Terminal amino acids of peptides E-CBD, 1, 2 and 3 are indicated. Position where sequence of E-CBD was opened to generate peptide 6 is indicated. (B) Peptide affinities and lengths are shown including the visualization of involved peptide regions. K<sub>p</sub>-values were obtained from FP measurements (n=3, ± std. error). (C) Table shows peptides derived from 6. The  $\beta$ -alanine loop ( $\beta$ A- $\beta$ A) is highlighted in black. Measurements in analogy to Figure 1b..

### 4 Conclusions

– This is the first crystal structure of a synthetic ligand bound to this site of  $\beta$ -catenin.

- A derivative peptide of **12** showed activity in Wnt reporter gene assay.
- Outlook is to improve cellular uptake further.

#### References

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Boehringer

#### **Financial Support**



AstraZeneca





Bayer CropScience