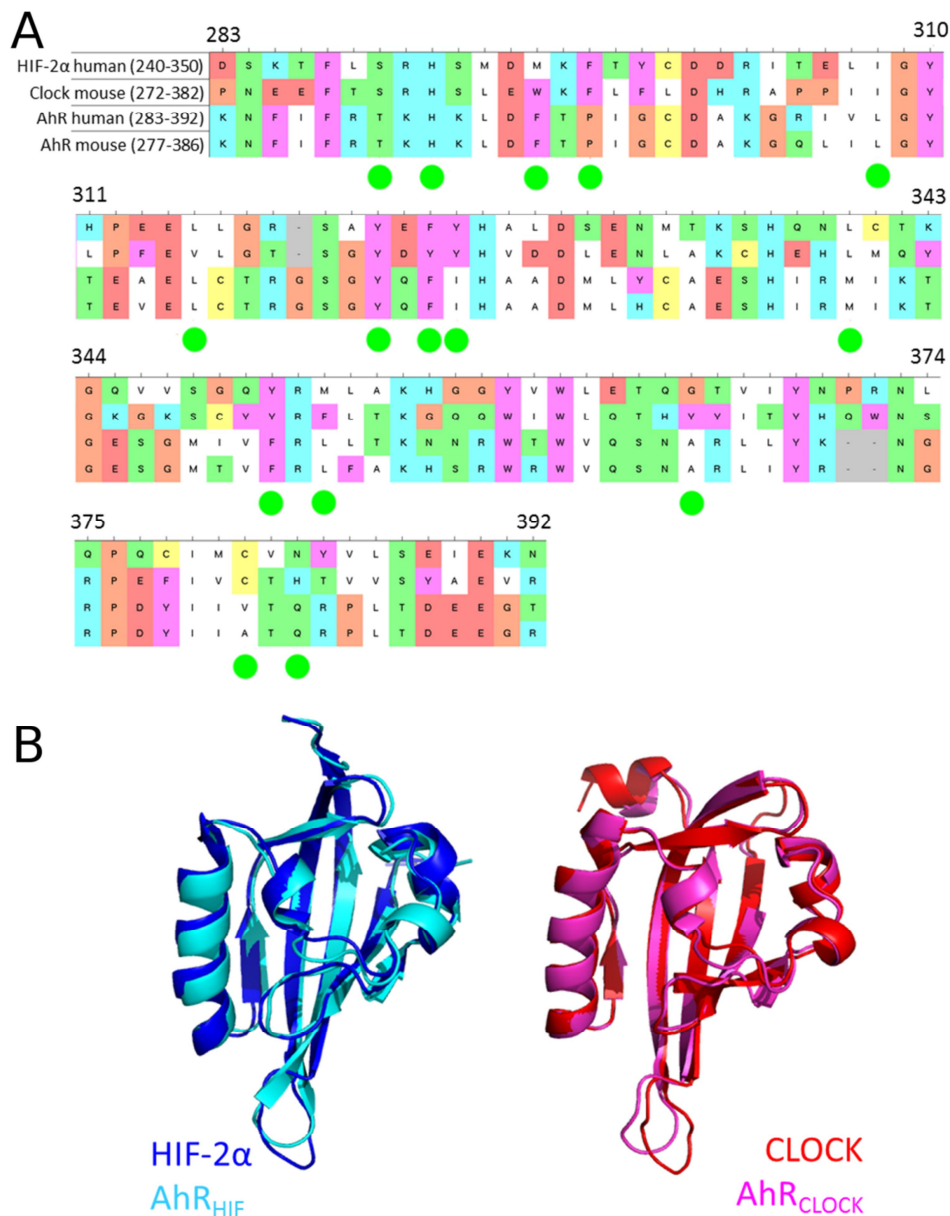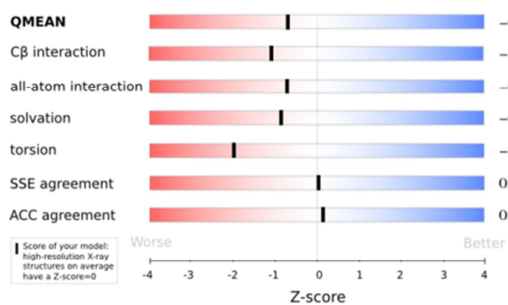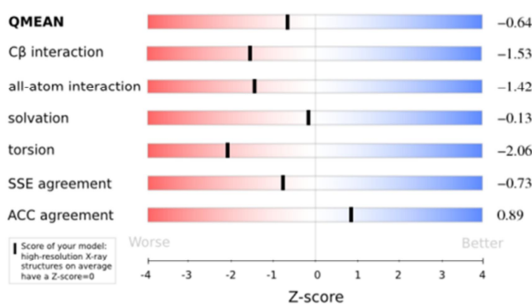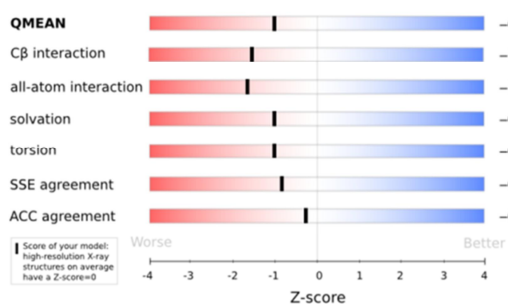**S1 Fig. Homology modeling of AhR PAS-B.** A: Sequence alignment of HIF-2α, CLOCK, human AhR and mouse AhR PAS-B sequences was generated by ClustalW. Sequence numbering corresponds to the human AhR sequence. Green circles indicate amino acids taking part in TCDD binding, which was determined in mutational experiments for the mouse AhR by Pandini *et al.* [1]. B: The best homology models display an RMSD of 0.711 Å and 0.525 Å after structural alignment to their templates for AhR_HIF and AhR_CLOCK, respectively (HIF-2α, CLOCK, AhR_HIF and AhR_CLOCK). C: Model quality was also estimated by the QMEAN server (http://swissmodel.expasy.org/qmean/cgi/index.cgi; [2]) beside ProSA [3] and ProCheck [4]. The estimated quality by QMEAN is slightly lower for the generated structures compared to that of the experimental structures.

C

CLOCK (PDBID: 4F3L)

		Z-score
QMEAN		−0.67
Cβ interaction		−1.07
all-atom interaction		−0.68
solvation		−0.84
torsion		−1.95
SSE agreement		0.06
ACC agreement		0.17

Score of your model; high-resolution X-ray structures on average have a Z-score=0

Worse — Better

HIF2α (PDBID: 1P97)

		Z-score
QMEAN		−0.64
Cβ interaction		−1.53
all-atom interaction		−1.42
solvation		−0.13
torsion		−2.06
SSE agreement		−0.73
ACC agreement		0.89

Score of your model; high-resolution X-ray structures on average have a Z-score=0

Worse — Better

AhR_CLOCK (Modeller)

		Z-score
QMEAN		−0.98
Cβ interaction		−1.52
all-atom interaction		−1.62
solvation		−0.99
torsion		−0.99
SSE agreement		−0.82
ACC agreement		−0.24

Score of your model; high-resolution X-ray structures on average have a Z-score=0

Worse — Better

AhR_HIF (Modeller)

		Z-score
QMEAN		−1.08
Cβ interaction		−1.97
all-atom interaction		−1.88
solvation		−1.31
torsion		−2.12
SSE agreement		−0.33
ACC agreement		0.04

Score of your model; high-resolution X-ray structures on average have a Z-score=0

Worse — Better