Supporting Information

Yu et al. 10.1073/pnas.1216890110

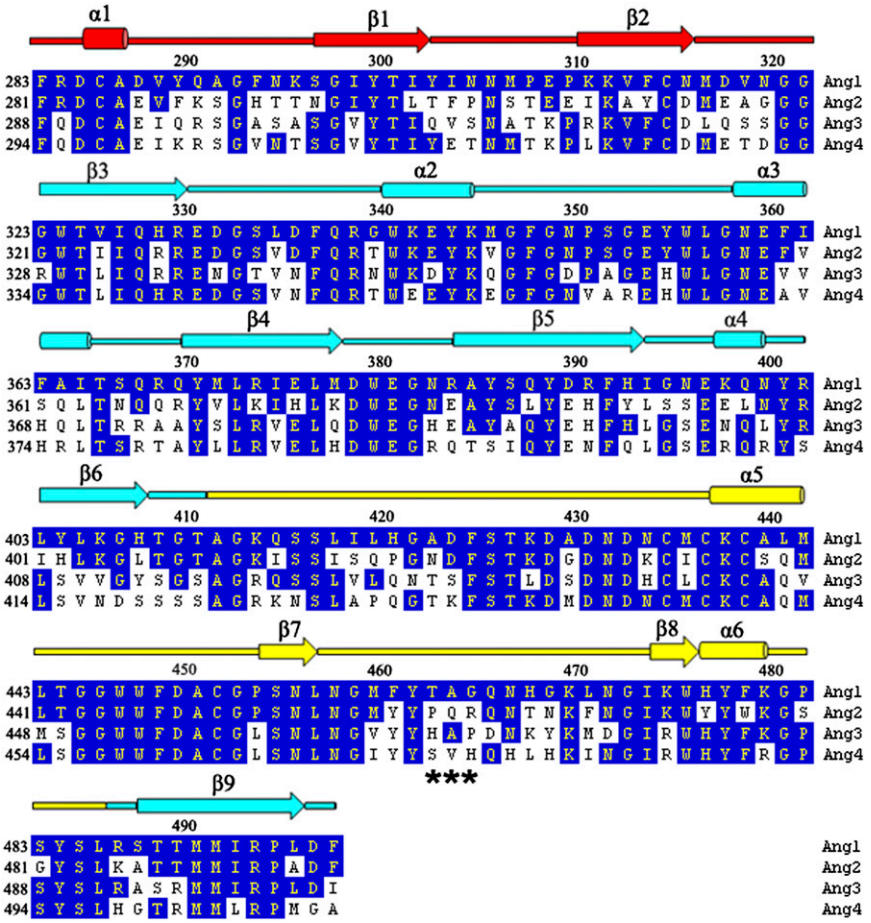

Fig. S1. Structure-based sequence alignment of the four angiopoietin ligands. Regions of conserved sequence to human angiopoietin (Ang)1 are highlighted in blue. The three subdomains (A, B, and P) are displayed in red, cyan, and yellow, respectively, on the secondary structure diagram. Black asterisks mark the β7-β8 loop sequence mutated in the Ang2-TAG chimera.

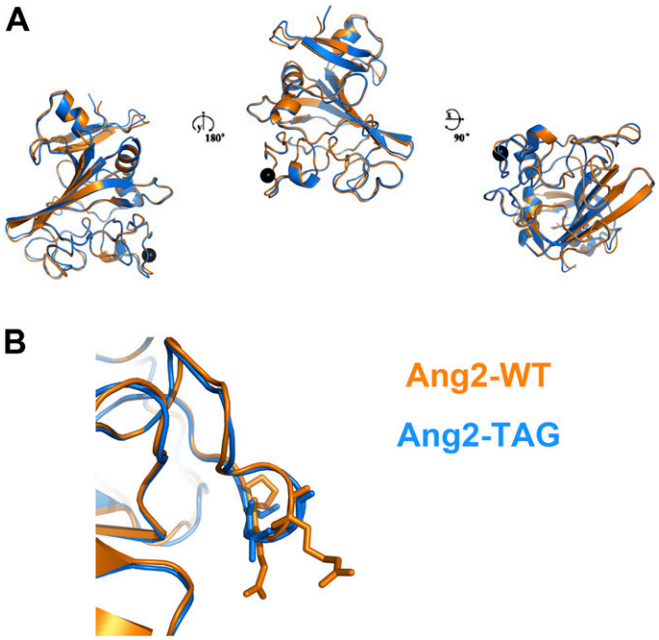

Fig. S2. Structural alignment of the wild-type Ang2 receptor-binding domain (Ang2-RBD) (shown in orange) and the Ang2-RBD TAG chimera (shown in blue). Close-up view of the T-A-G or P-Q-R residues within the Ang2-TAG or Ang2-WT structures.

Table S1. Summary of crystallographic analysis

	Ang1	Ang1/Tie2	Ang2-TAG
Crystal			
Resolution, Å	2.5	4.5	1.9
Wavelength, Å	1.033	1.033	1.54
Completeness, %	99.3	91.8	98.5
Redundancy, fold	4.4	5.2	8.0
I/σI	26.1/3.1	21.4/2.9	14.3
R_{merge}	8.3	11.0	7.5
Space group	P6422	I4122	I222
Cell dimensions, Å	$a = b = 80.97$ $c = 187.22$	$a = b = 189.53$ $c = 334.87$	$a = 46.69 = b = 79.06$ $c = 135.54$
Refinement			
Resolution, Å	30–2.7	30.0–4.5	8.0–1.9
Reflections, working/test	11,907/649	16,829/841	18,675/945
R_{work}/R_{free}	19.5/25.1	30.8/33.3	20.8/23.0
rmsds			
Bonds, Å	0.022	0.018	0.006
Angle, degrees	1.98	1.71	1.41

The dataset was collected from a single crystal. $R_{merge} = \Sigma|I - \langle I\rangle|/\Sigma I$, where I is the observed intensity, and $\langle I\rangle$ is the average intensity obtained from multiple observations of symmetry-related reflections. rmsd in bond lengths and angles are the respective rmsds from ideal values.