Supporting Information

Fan et al. 10.1073/pnas.1717621115

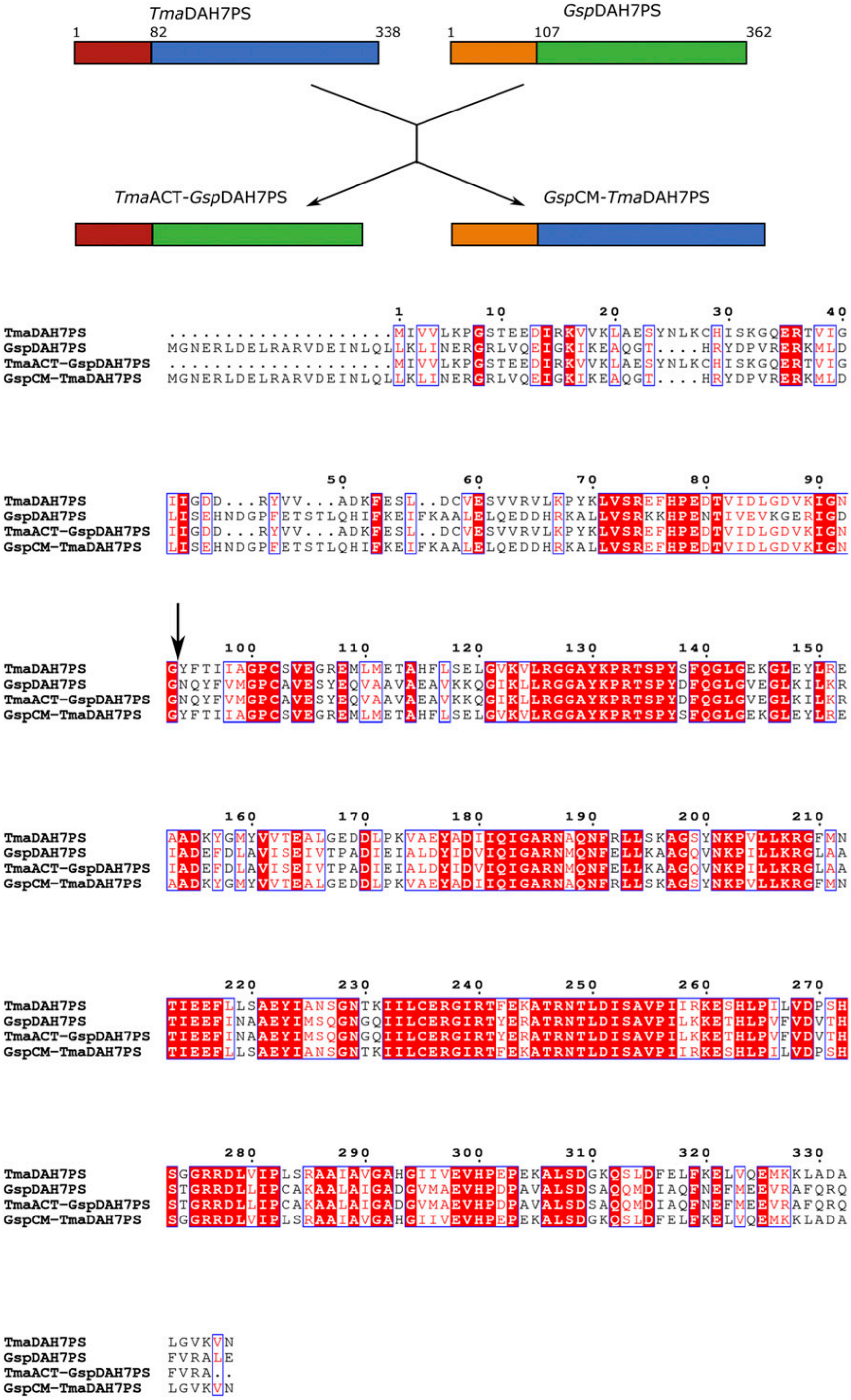

Fig. S1. (*Upper*) Scheme of chimera design. Red represents ACT domain from *Tma*DAH7PS, orange represents CM domain from *Gsp*DAH7PS, blue represents catalytic domain of *Tma*DAH7PS, and green represents catalytic domain of *Gsp*DAH7PS. (*Lower*) Alignment of wild-type parent proteins and two protein chimeras. Black arrow identifies the fusion site.

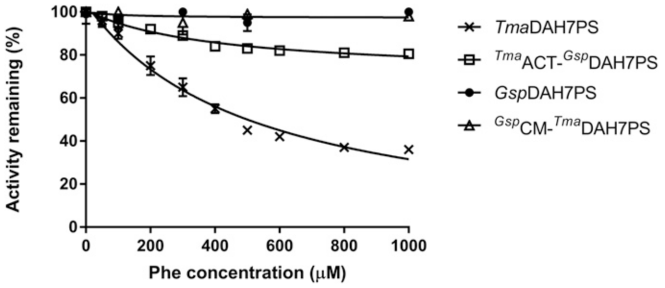

Fig. S2. DAH7PS activity of the parent and chimeric proteins in the presence of 1 mM Phe. Wild-type *Tma*DAH7PS and ^{Tma}ACT-^{Gsp}DAH7PS showed inhibition with Phe.

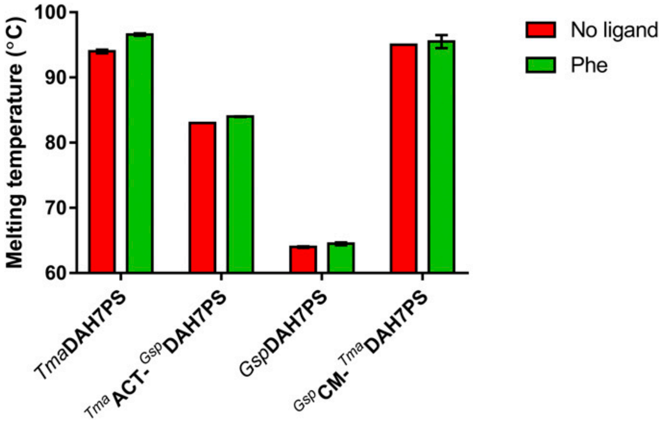

Fig. S3. Thermostability of the four proteins in the presence or absence of 1 mM Phe.

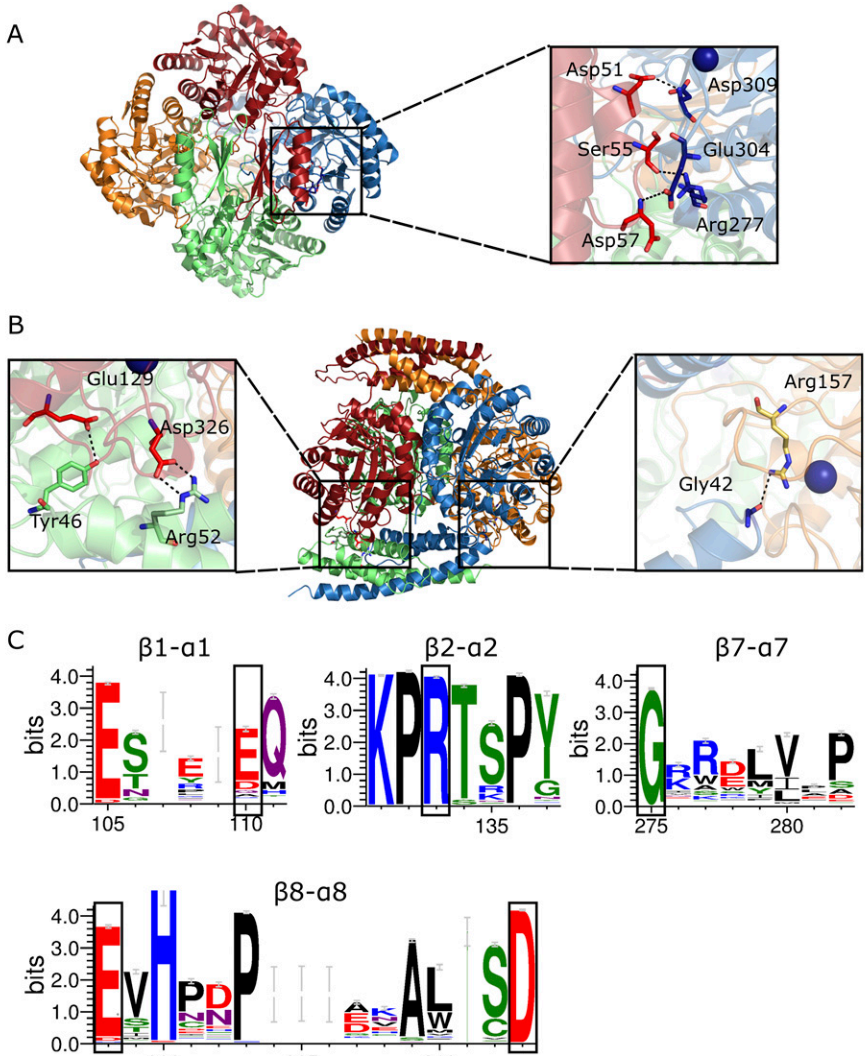

Fig. S4. Analysis of key interactions associated with allostery. Key residues involved in interactions between regulatory and catalytic domains are identified in *Tma*DAH7PS (*A*) and *Gsp*DAH7PS (*B*). (*C*) Partial alignment of type Iβ DAH7PS sequences, showing segments of the catalytic barrel. Black rectangles highlight the location of key barrel residues identified in *A* and *B*. Figure was formatted with Weblogo3.

Table S1. Primers designed to amplify the genes encoding for the chimeras

PCR step	^{Tma}ACT-^{Gsp}DAH7PS	^{Gsp}CM-^{Tma}DAH7PS
PCR amplifying regulatory domain and linker region with overlap	5′GCTTCGAAGGAGATAGAACCATGATTGTCGTTTTGAAACCC 3′	5′GCTTCGAAGGAGATAGAACCATGGGTAATGAACGTCTGGAT 3′
	5′GACGAAATATTGATTGCCGTTTCCTATCTTCACATCT 3′	5′CGCTATGATGGTGAAATACTGATTGCCATCACCAAT 3′
PCR amplifying catalytic domain with overlap	5′GTGAAGATAGGAAACGGCAATCAATATTTCGTCATGGG 3′	5′AATCAGTATTTCACCATCATAGCGGGACCG 3′
	5′GGGGACCACTTTGTACAAGAAAGCTGGGTCTTATGCACGAACAAACTGACG 3′	5′GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAATTCACCTTCACCCCCAG 3′
Generic PCR fusing the above products	5′GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAGGAGATAGAACCATG 3′	5′GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAGGAGATAGAACCATG 3′
	5′GGGGACCACTTTGTACAAGAAAG 3′	5′GGGGACCACTTTGTACAAGAAAG 3′

Table S2. Structural parameters from SAXS profile of each chimera in the absence or presence of Tyr or prephenate

Structural parameter	^{Tma}ACT-^{Gsp}DAH7PS (apo)	^{Tma}ACT-^{Gsp}DAH7PS (tyr)	^{Gsp}CM-^{Tma}DAH7PS(apo)	^{Gsp}CM-^{Tma}DAH7PS (prephenate)
I(0), cm^{-1}*	0.12 ± 0.003	0.116 ± 0.002	0.408 ± 0.002	0.397 ± 0.003
R_g, Å*	33.96 ± 0.08	32.71 ± 0.08	36.89 ± 0.2	34.76 ± 0.2
I(0), cm^{-1}†	0.12 ± 0.001	0.116 ± 0.001	0.408 ± 0.001	0.397 ± 0.001
D_{max}, Å	104.16	101.35	120.71	118.43
R_g, Å†	34.04 ± 0.2	32.75 ± 0.2	36.91 ± 0.2	34.77 ± 0.2
Porod volume estimate, Å^3	226,364	222,091	274,596	258,918
Fit with crystal/model structure, $\chi^{2‡}$	1.08	0.7	0.78	1.33

*From pair distribution function. Data presented as mean ± SD.

†From Guinier plot. Data presented as mean ± SD.

‡From CRYSOL.