

## *Supplementary Data*

### **Modular Assembly of Phosphite Dehydrogenase and Phenylacetone Monooxygenase for Tuning Cofactor Regeneration**

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**Table S1.** Oligonucleotide primer for PTDH and PAMO ORF amplification.

Primer	Primer (direction 5'-3'/ sequence)
PTDH For	CCTGAAGGTCTCGTGGTATGCTGCCGAACTGGTCATCACCCATC
PTDH Rev	CCCGGTCTCTCACCGTCAGCCGCAGGGTTGGCTTTTCG
PAMO for	CCTGAAGGTCTCGTGGTATGGCCGGGCAGACGACTGTC
PAMO rev	CCCGGTCTCTCACCGGTGAGGACGAAACCTTCGTA
PAMO Bsa mut for	CTGCGCTCAGCAACATGCTGGTGTCTATC
PAMO Bsa mut rev	CACGTGCTGTTCGATAGACACCAGCATGTTG

**Table S2.** Synthetic gene constructs.

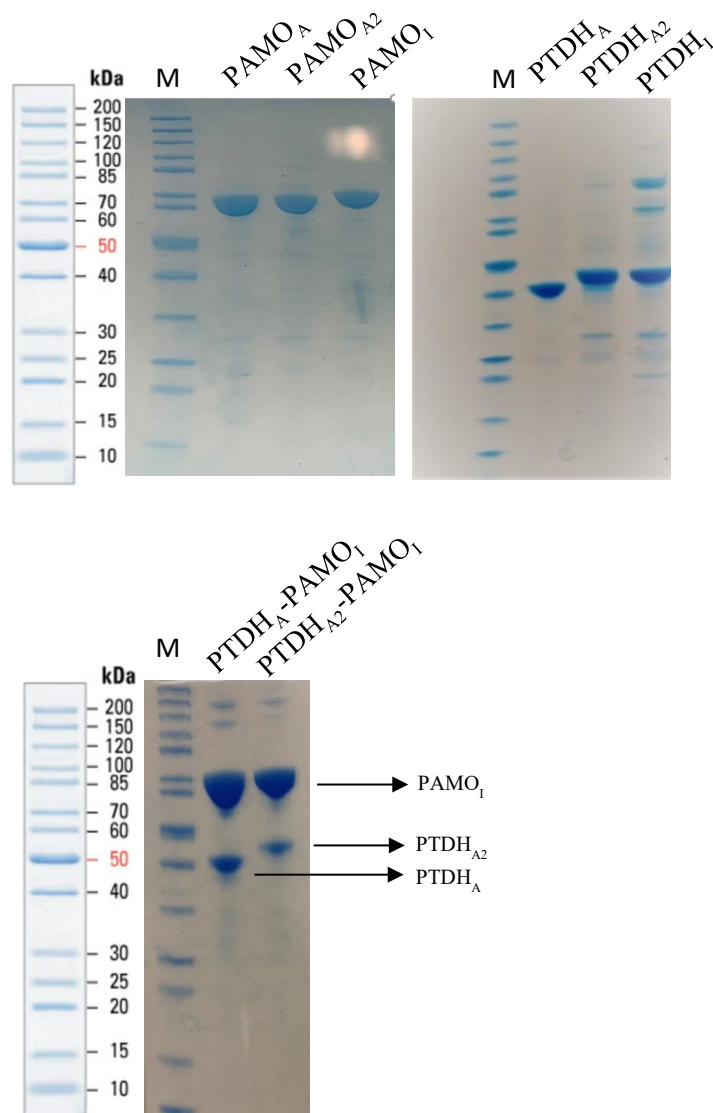
Synthetic genes	Base sequences
RIAD	CCTGAAGGTCTCGGGTGGTGGTGGTAGCGGTGGCGGTGGTTCAG
RIAD-RIAD	GCGGCGGTGGTTGCAGAGACCGCTAAAGTTGCGGTCTCTTTGCG GTCTGGAACAGTATGCAAATCAGCTGGCAGATCAGATTATCAAA GAAGCAACCGAAGGTTGCTAACTTGAGAGACCGGGAATGAAGG TCTCGTTGCGGTAGCCTGCGTGAATGTGAACTGTATGTTTCAGAAA CATAATATTCAGGCCCTGCTGAAAGATAGCATTGTTTCAGCTGTGT ACCGCACGTCCGGAACGTCCGATGGCATTCTGCGCGAATATTTT GAACGTCTGGA AAAAGAAGAAGCCAAATAACTTGAGAGACCGG AC
RIDD	CAAAGGTCTCATTGCGGTCTGGAACAGTATGCAAATCAGCTGGC AGATCAGATTATCAAAGAAGCAACCGAAGGTTGCGGCGGTGGTG GTAGCGGTGGCGGTGGTTCAGGCGGCGGTGGTTGTGGCCTGGAA CAGTACGCGAATCAGCTGGCCGATCAGATCATCAAAGAAGCGAC CGAAGGCTGTAACTTGAGAGACCAATGAAAGACGTTTCGATAT GCTATAGCTATTTAGACTATATGGATATGCTATCGATAGATCGAT CGGATATCGATTTAAATTTCGATTTAAATTATTATGCTATAGGCT ATAG

**Table S3.** Molecular weights of size exclusion chromatography standards.

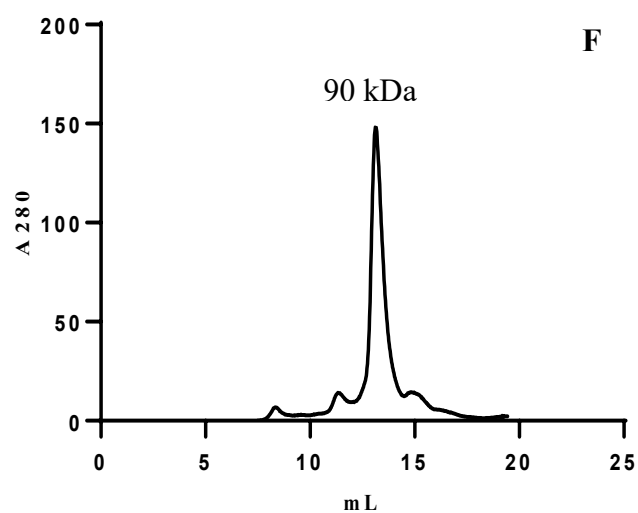
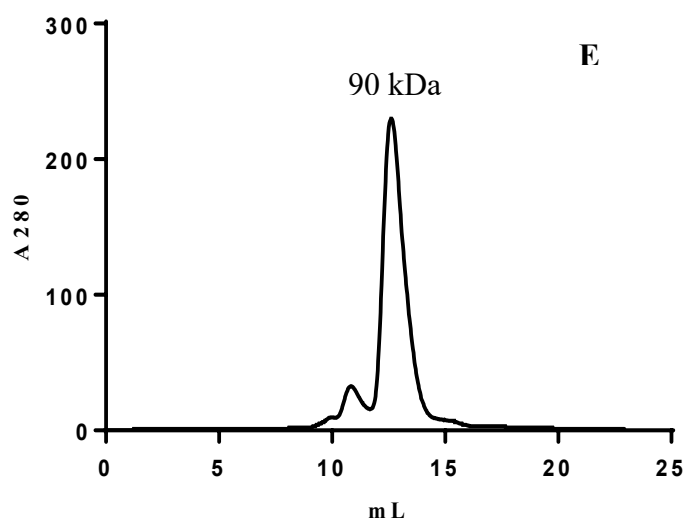
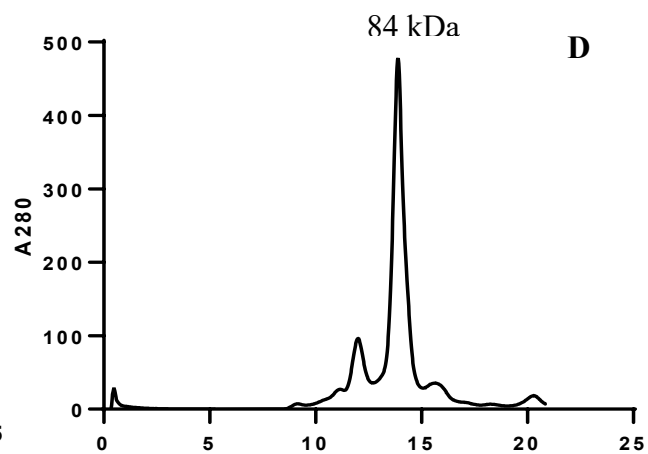
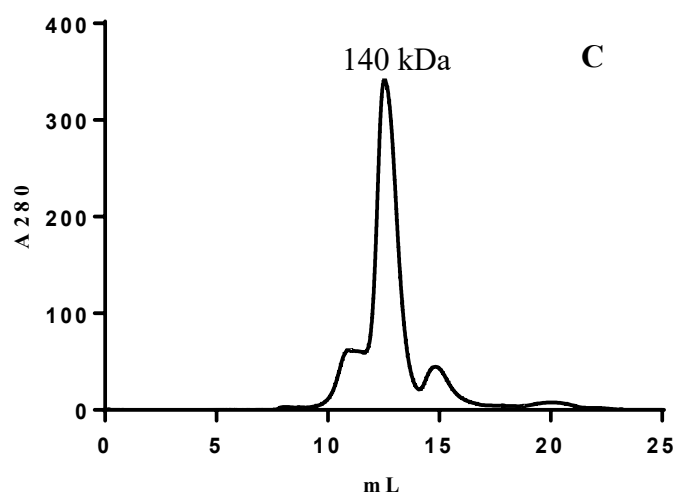
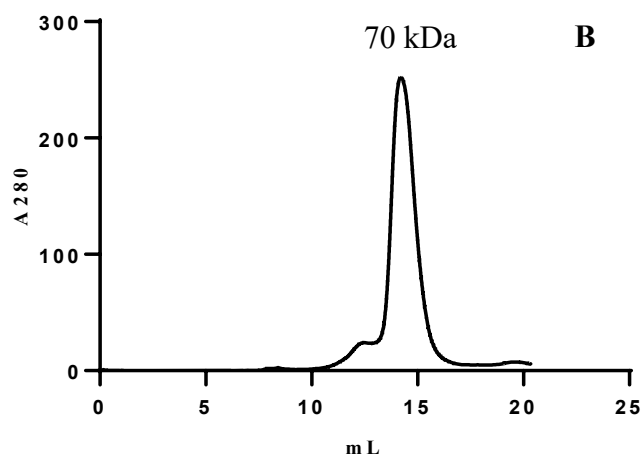
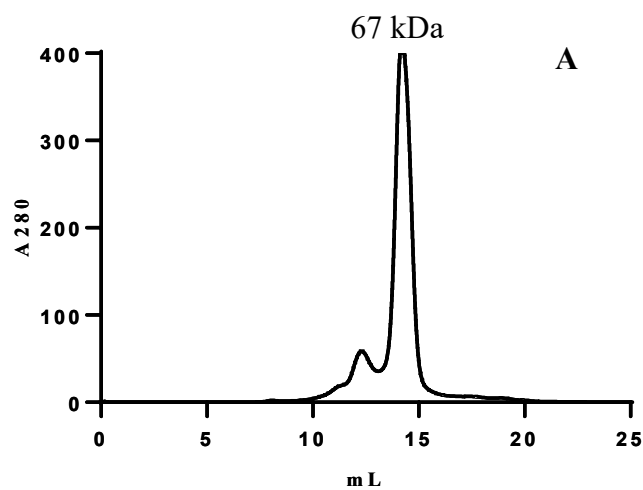
Standard Protein	MW	Log MW	Elution Vol (mL)
Thyroglobulin	670000	5.83	9.48
$\gamma$ -globulin	158000	5.20	12.5
Ovalbumine	44000	4.64	15.0
Myoglobin	17000	4.23	16.82
Vitamin B12	1350	3.13	19.75

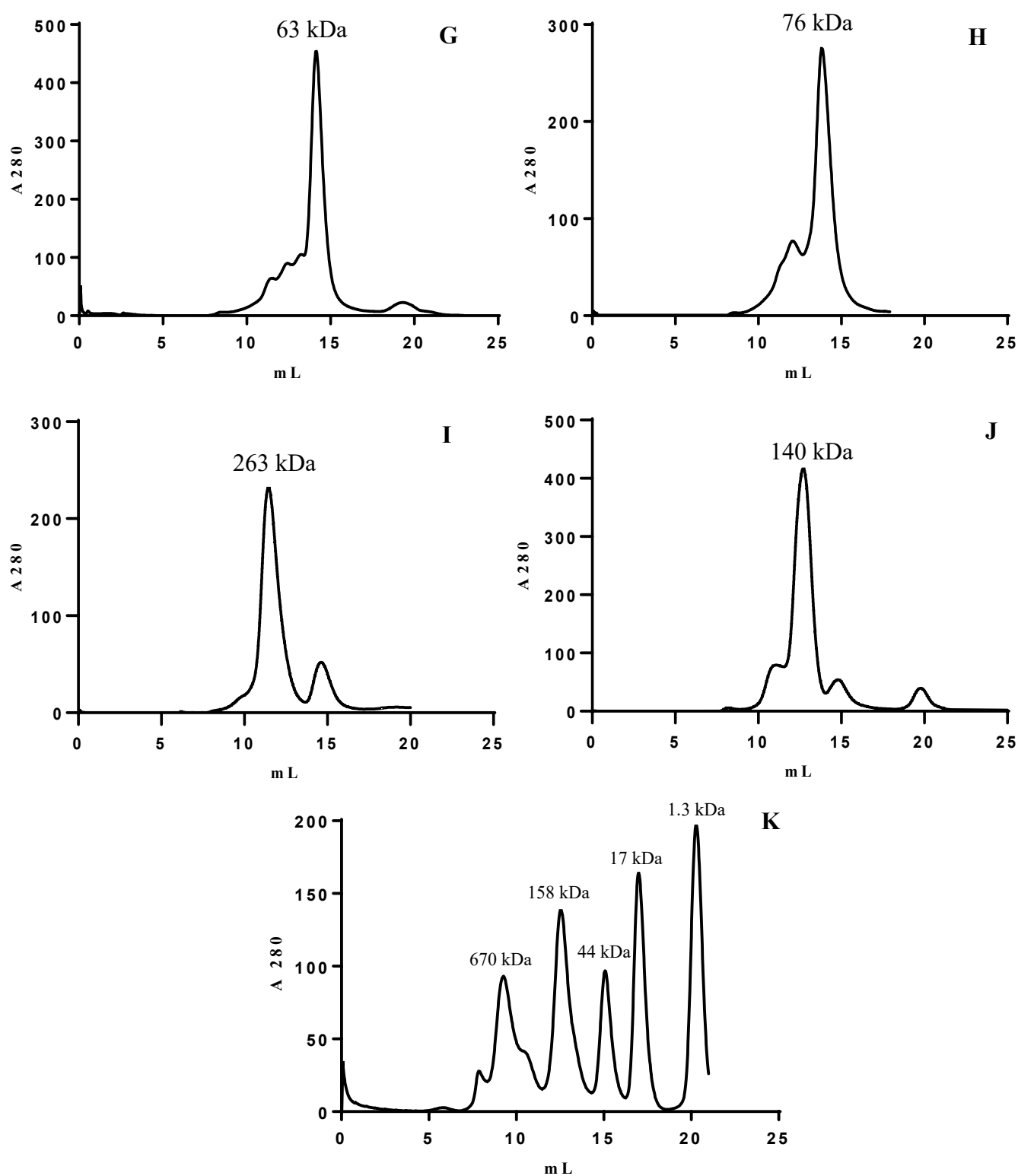
**Table S4.** Conversion of bicyclo[3.2.0]hept-2-en-6-one. Conversion was measured by GC-MS analysis, based on product peak areas.

Enzymes complexes	Time (hours)	Conversion (%)
PTDH <sub>A</sub> -PAMO <sub>I</sub>	5	59±4.2
	24	88±0.2
PTDH <sub>A2</sub> -PAMO <sub>I</sub>	5	60±0.7
	24	94.5±2.6
PAMO <sub>A</sub> -PTDH <sub>I</sub>	5	60±5.6
	24	78.5±0.7
PAMO <sub>A2</sub> -PTDH <sub>I</sub>	5	61.5±0.2
	24	77.1±2.6
PTDH-PAMO	5	68±2.8
	24	94.5±2.1



**Figure S1.** SDS-PAGE analysis. A: analysis of purified tagged PAMO variants; B: analysis of purified tagged PTDH variants; C: complex PTDH<sub>A</sub>-PAMO<sub>I</sub> and PTDH<sub>A2</sub>-PAMO<sub>I</sub>.





**Figure S2.** Size exclusion chromatogram of (A) PAMO<sub>A</sub>, (B) PAMO<sub>A2</sub>, (C) PAMO<sub>I</sub>, (D) PTDH<sub>A</sub>, (E) PTDH<sub>A2</sub>, (F) PTDH<sub>I</sub>, (G) PAMO<sub>A</sub>-PTDH<sub>I</sub>, (H) PAMO<sub>A2</sub>-PTDH<sub>I</sub>, (I) PAMO<sub>A</sub>-PAMO<sub>I</sub>, (J) PAMO<sub>A2</sub>-PAMO<sub>I</sub>, (K) size exclusion protein standards.