Supporting Information

Le Coq and Ghosh 10.1073/pnas.1105613108

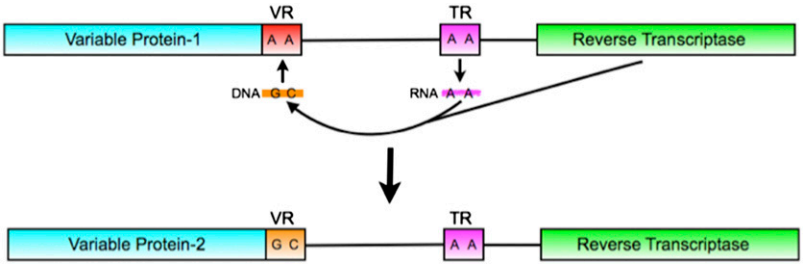

Fig. S1. Diversity generation. Genetic information is transferred from the invariant TR to the protein-encoding the VR at the C terminus of the DGR-variable protein through the action of the DGR reverse transcriptase on TR RNA. Two adenines in the TR are shown to be randomly mutated to other bases (G and C here) and incorporated into the coding locus of the variable protein to give rise to a new variant.

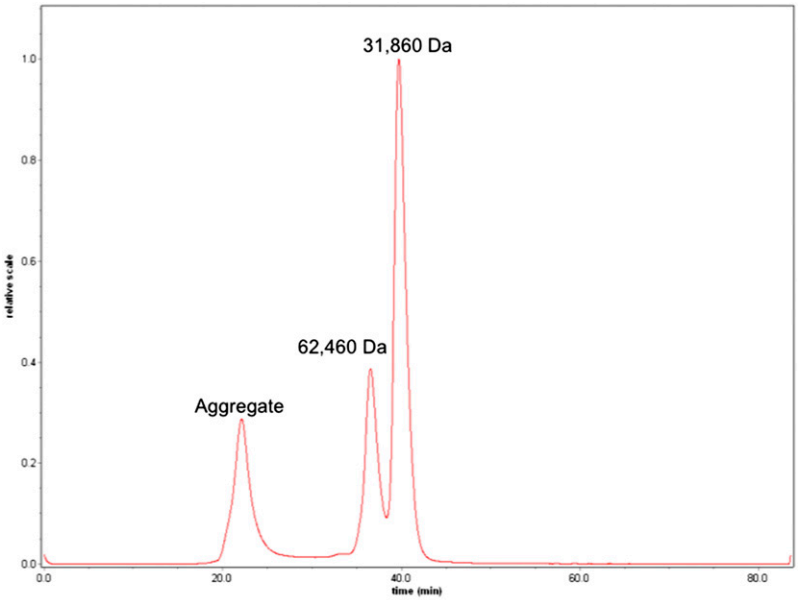

Fig. S2. Size-exclusion profile of TvpA. The molecular masses determined for TvpA by static light scattering of peak fractions are indicated. The calculated molecular mass of TvpA is 32,136 Da.

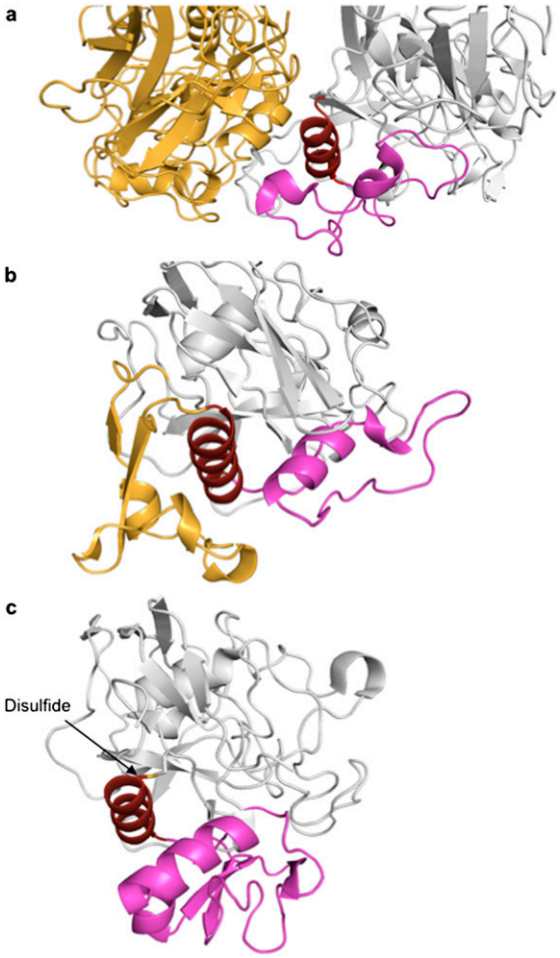

Fig. S3. The role of insert 1′. (*A*) Ribbon representation of one of the protomer–protomer interfaces in trimeric Mtd. The gray protomer has the α1 helix in red and insert 1 in magenta. The second protomer is in gold. (*B*) Ribbon representation of TvpA, with the α1 helix colored red, insert 1 magenta, and insert 1′ gold. The rest of TvpA is colored gray. (*C*) Ribbon representation of *h*FGE. The disulfide bond between C218 and C365 is represented as sticks. The α1 helix is red and insert 1 is magenta. The rest of *h*FGE is colored gray.

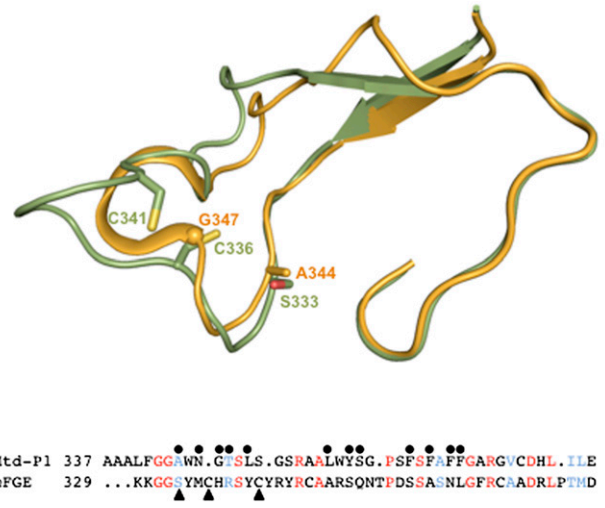

Fig. S4. Relationship of Mtd to FGE. Superposition of the VR of Mtd-P1 (orange) and the catalytic site of *h*FGE (green) in Cα representation. *Bottom*: Sequence alignment of the regions shown above. Mtd-P1 variable residues denoted by spheres and *h*FGE catalytic residues by arrows. Identical residues are in red and chemically similar ones are in blue.

Table S1. Crystallographic statistics

Parameter	Native	Hg derivative
Data collection		
Space group	$P2_12_12_1$	$P2_12_12_1$
Cell dimensions *a, b, c*, Å	41.39, 77.63, 88.92	41.59, 77.24, 87.37
Wavelength, Å	1.033	0.98792
Resolution, Å*	44.46–1.40 (1.46–1.40)	38.63–2.10 (2.21–2.10)
Completeness, %*	99.9 (100)	99.4 (99.9)
R_{merge}, %*	10.7 (31.7)	9.3 (33.8)
I/σI*	3.5 (2.2)	6.3 (2.2)
Redundancy*	7.2 (7.0)	6.6 (6.2)
Refinement		
Resolution, Å	44.46–1.40	
No. of reflections	411,914	
R_{work}/R_{free}, %	14.6/17.3	
No. of atoms		
Protein	2296	
Ligand/ion	36/3	
Water	256	
B factors, $Å^2$		
Protein	13.06	
Ligand/ion	28.02/17.03	
Water	25.28	
rmsd		
Bond lengths, Å	0.0063	
Bond angles, °	1.096	

*Values in parentheses are for the highest resolution shell.