Table S1 Data collection, phasing and refinement

Data Collection	**MORF1$^{79-190}$ NaBr**	**MORF1$^{79-190}$ Native**	**MORF9$^{86-186}$**
Wavelength (Å)	0.916	1.771	0.918
Temperature (K)	100	100	100
Space Group	P1	$P2_1$[a]	$P6_522$
Unit Cell (Å, °)	39.28 44.94 68.20	68.89 69.81 69.32	73.87 73.87 264.94
	98.10 91.98 111.96	90.0 108.95 90.0	90.0 90.0 120.0
Resolution (Å)	50 – 1.5 (1.54 – 1.50)	50 - 1.94 (1.99 - 1.94)	50 – 2.25 (2.38 – 2.25)
Reflections			
Unique	66951 (4771)	44847 (2880)	21313 (3327)
Completeness (%)	97.6 (94.0)	96.7 (83.9)	99.6 (99.0)
Redundancy	6.5 (3.6)	6.1 (4.7)	10.5 (10.8)
I/σ(I)	10.29 (1.50)	11.82 (2.32)	16.99 (1.56)
R_{sym}(I)[b]	0.11 (0.79)	0.11 (0.63)	0.09 (1.42)
CC(1/2)[c]	99.7 (56.3)	99.6 (56.9)	99.9 (77.2)
Phasing			
Resolution (Å)	38 – 1.5		
Br-sites	26		
Phasing Power (acentric)			
isomorphous	-		
anomalous	0.8		
R_{Cullis}(acentric)			
isomorphous	-		
Anomalous	0.88		
Figure of merit (FOM)	0.27		
Refinement			
Resolution (Å)	37.99 - 1.5	34.81 - 1.94	46.01 – 2.25
Reflections			
Number	66950	44844	21308
Completeness (%)	97.8	96.8	99.6
Test Set (%)	5.0	5.0	5.0
R_{work}[d]	0.1573	0.163	0.195
R_{free}[d]	0.1923	0.192	0.238
ESU (Å)[e]	0.15	n.a.	0.29
Contents of A.U.[f]			
Protein (Molecules)	4	4	2
Protein (Residues)	459	460	202
Water Oxygens	474	416	157
Mean B-Factors (Å^2)			
Wilson	12.44	n.a.	50.1
Protein	21.38	32.32	59.7
Water	31.05	34.52	58.4
Ramachandran Plot[g]			
Favored (%)	97.84	97.35	96.97
Outliers (%)	0	0	0
Rmsd[h]			
Bond Lengths (Å)	0.013	0.007	0.009
Bond Angles (°)	1.240	0.830	0.979
Dihedral Angles (°)	19.00	16.57	13.83

[a] pseudo-merohedral twinned, twin law: h, -k, l, twin fraction 0.14

[b] $R_{sym}(I) = \Sigma_{hkl}\Sigma_i |I_i(hkl) - \langle I(hkl)\rangle| / \Sigma_{hkl}\Sigma_i |I_i(hkl)|$; for n independent reflections and i observations of a given reflection; $\langle I(hkl)\rangle$ – average intensity of the i observations

[c] Correlation factor CC(1/2) between random half-datasets for reporting results in XDS CORRECT and XSCALE (51).

[d] $R = \Sigma_{hkl} ||F_{obs}| - |F_{calc}|| / \Sigma_{hkl} |F_{obs}|$; R_{work} – $hkl \notin T$; R_{free} – $hkl \in T$; R_{all} – all reflections;

[e] ESU – estimated overall coordinate error based on maximum likelihood

[f] A.U. – asymmetric unit

[g] Calculated with MolProbity (52) [h] Rmsd – root-mean-square deviation from target geometry

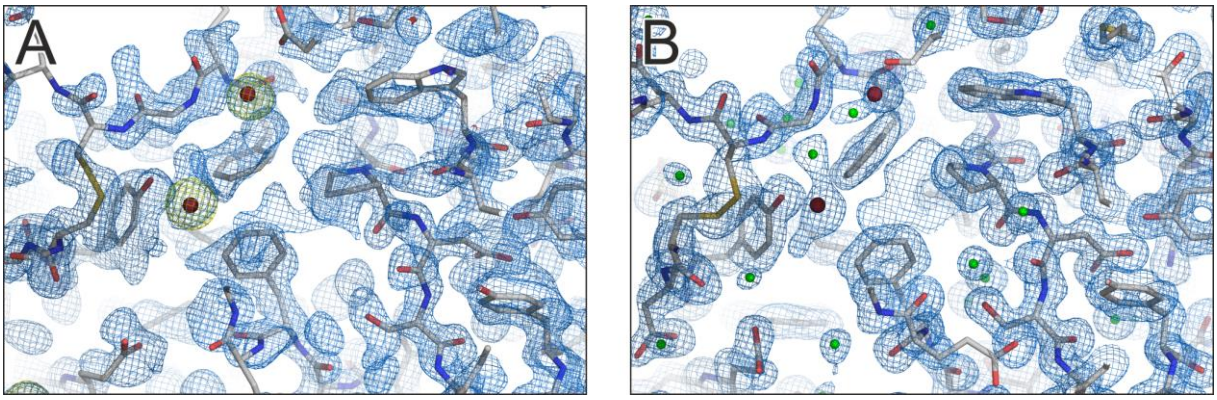

Figure S1 Quality of the experimental and refined electron density maps of MORF$^{79\text{-}190}$. **(A)** Central region of the MORF$^{79\text{-}190}$ tetrameric structure (grey) and surrounding experimental solvent-flattened electron density shown as blue mesh contoured at the 1 σ level. An anomalous density map of the Br-signal calculated with initial phases is shown as yellow mesh, contoured at the 5 σ level (**B)** The final $2F_o$-F_c electron density map covering the same region as in (A) is shown as a blue mesh, contoured at the 1 σ level. Residues are shown as sticks and colored by atom type. Carbon - grey; nitrogen – blue; oxygen – red; sulfur – yellow. Water oxygens are shown as green spheres, bromide ions as fire brick spheres

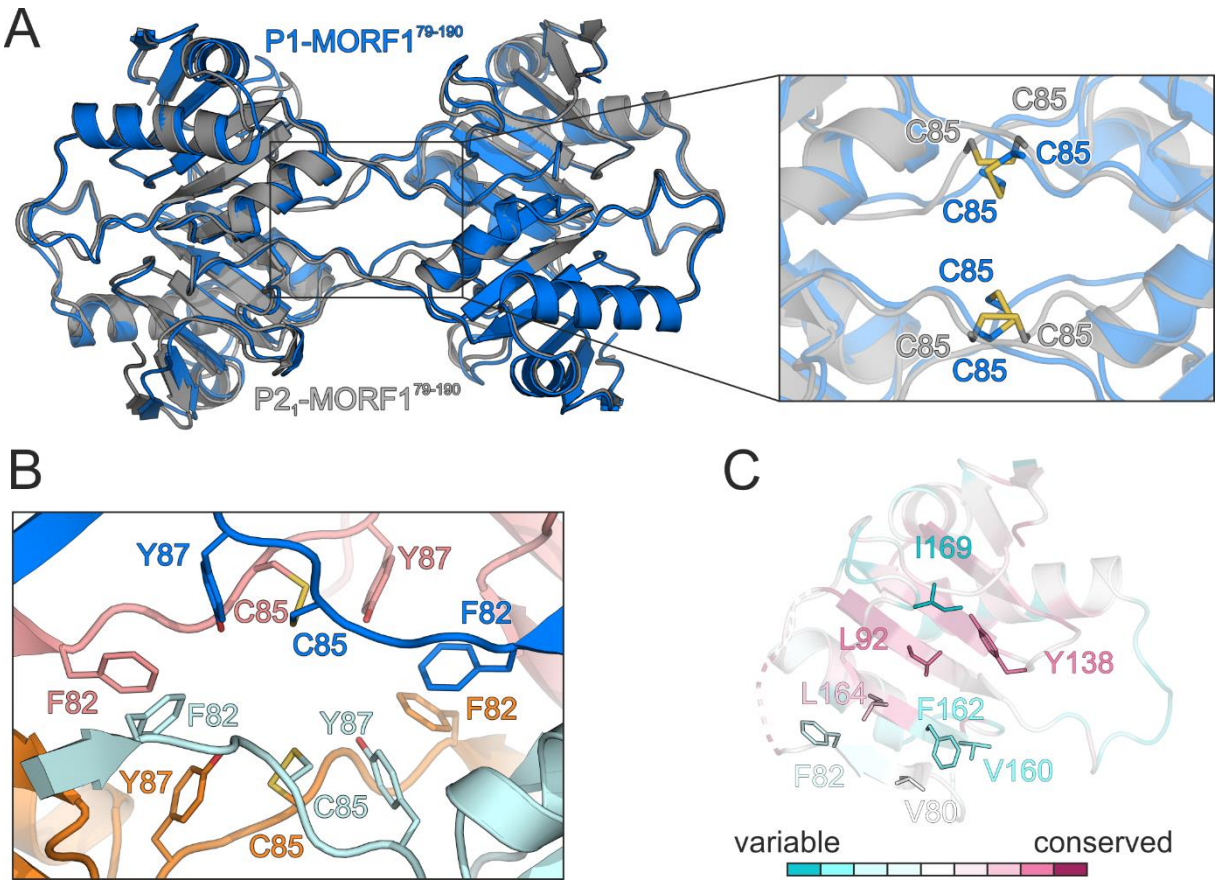

Figure S2 Flexibility of the central tetrameric interface in two crystal lattices and conservation of the hydrophobic MORF$^{79-190}$ dimerization interface. **(A)** P1 (marine) and P2$_1$ (grey) crystal structures of tetrameric MORF$^{79-190}$ superimposed. Inset – Close-up view illustrates the intrinsic flexibility of the central interface. Disulfide bridges are shown as sticks. Carbon - as for the respective molecule; sulfur - yellow, **(B)** F82 and Y87 (shown as sticks) of all four MORF$^{79-190}$ chains form a hydrophobic cage at the central interface surrounding the two disulfide bridges. Carbon - as for the respective molecule; oxygen – red; sulfur – yellow. **(C)** Conservation scores including 124 non-redundant MORF-related sequences obtained by CONSURF (30) plotted on the structure of MORF$^{79-190}$. Residues forming the main hydrophobic dimerization interface are shown as sticks. Dashed lines in the ribbon plots represent modeled residues G84-D86 of MORF1$^{79-190}$.

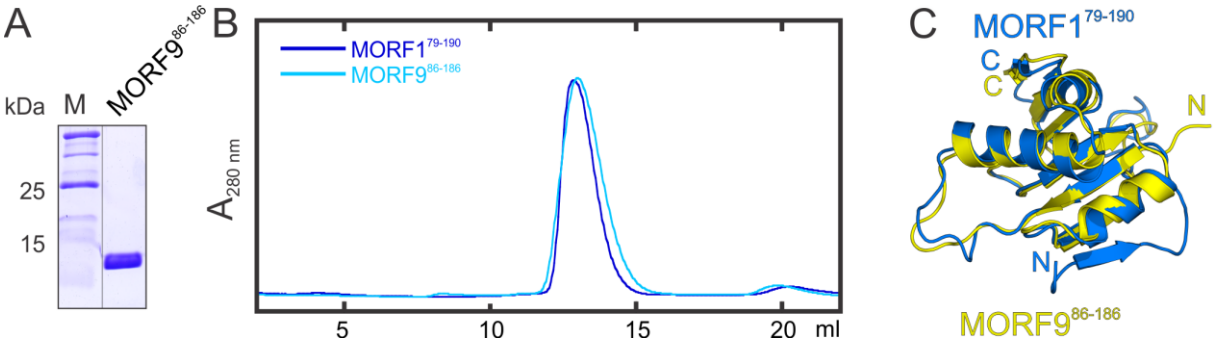

Figure S3 Quality of MORF9$^{86-186}$ preparation and comparison of MORF1$^{79-190}$ and MORF9$^{86-186}$ by gel filtration and structural superimposition**(A)** SDS PAGE analysis of MORF9$^{86-186}$ **(B)** Analytical gel filtration (Superdex 75) to compare the molecular weight of MORF1$^{79-190}$ (blue) and MORF9$^{86-186}$ (cyan). Absorbance was monitored at 280 nm. **(C)** MORF1$^{79-190}$ (marine blue) and MORF9$^{86-186}$ (yellow) monomers superimposed.