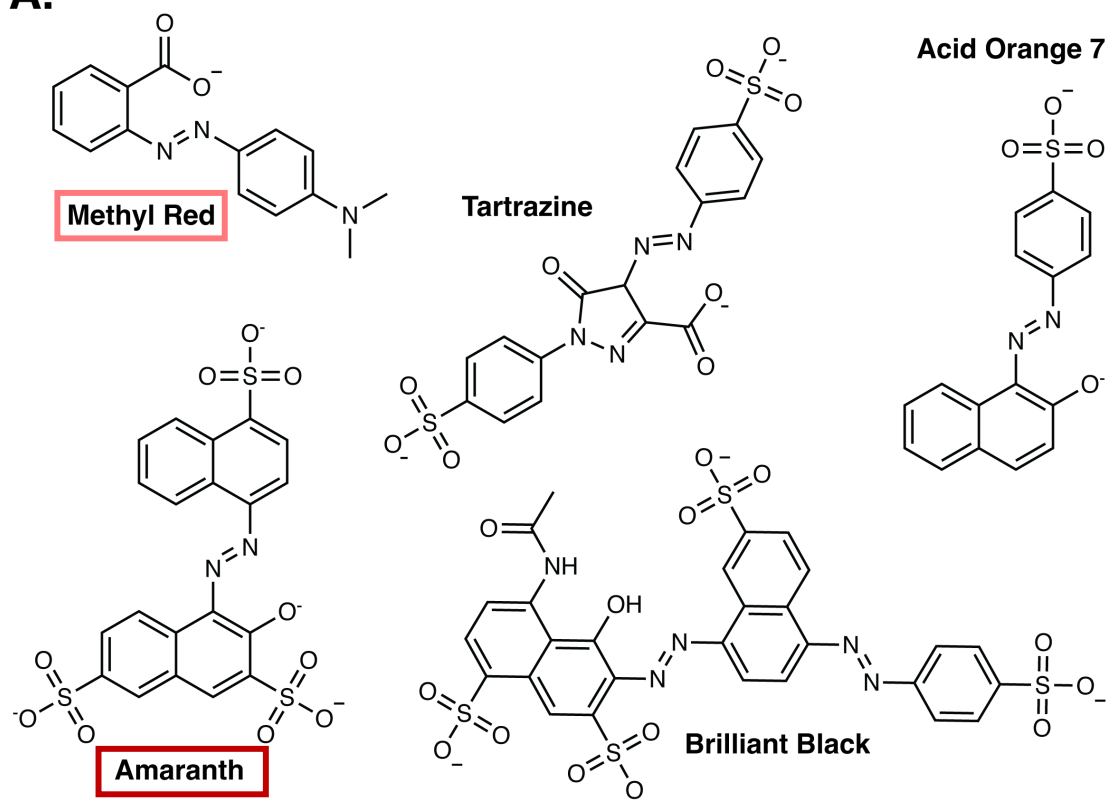
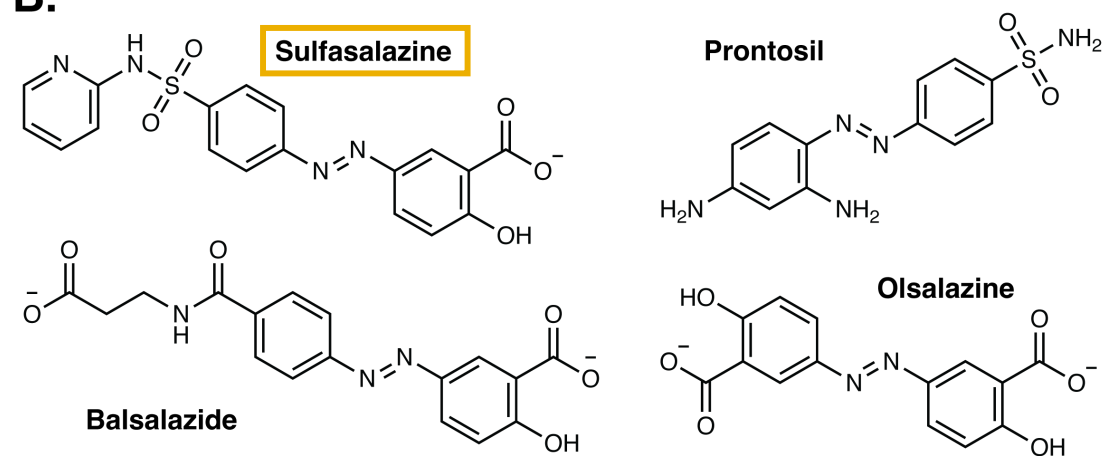


Supplemental Figure 1

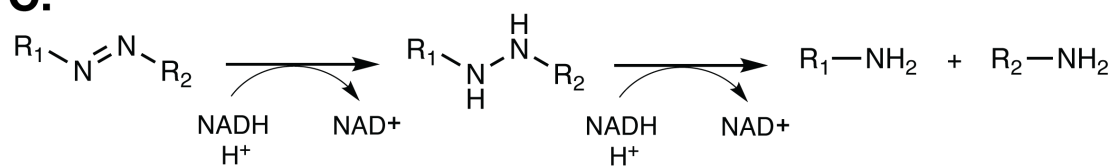
A.



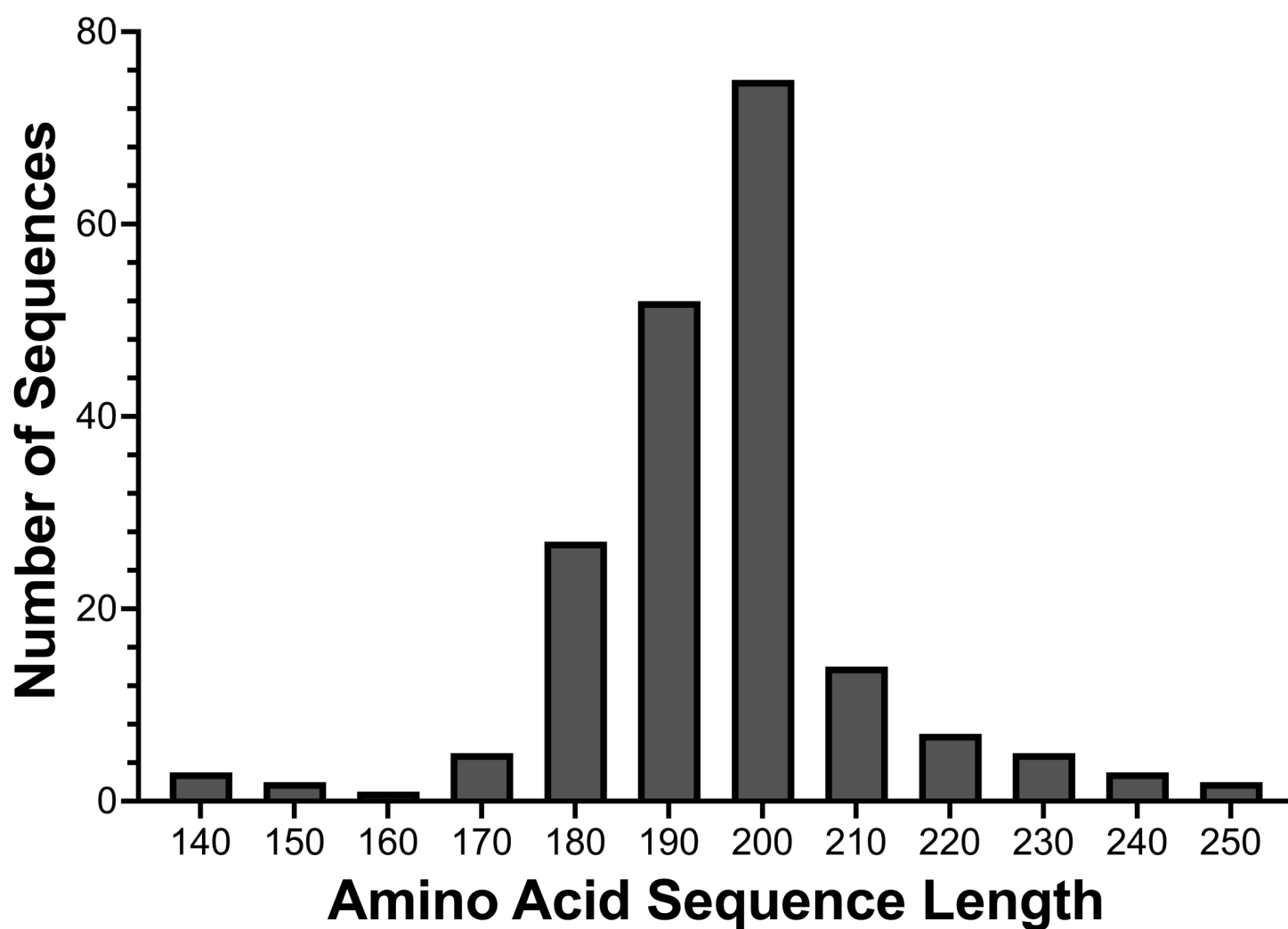
B.



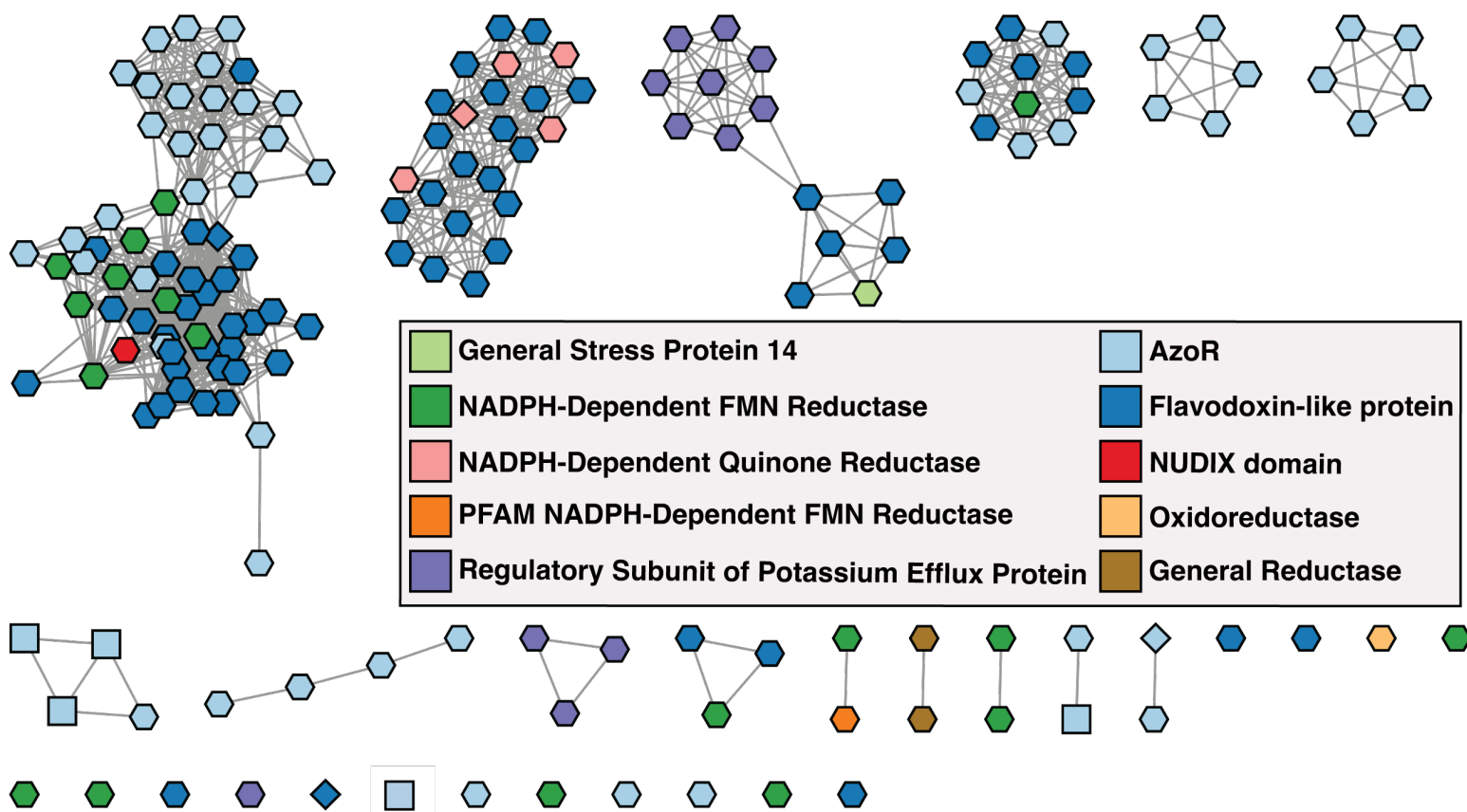
C.



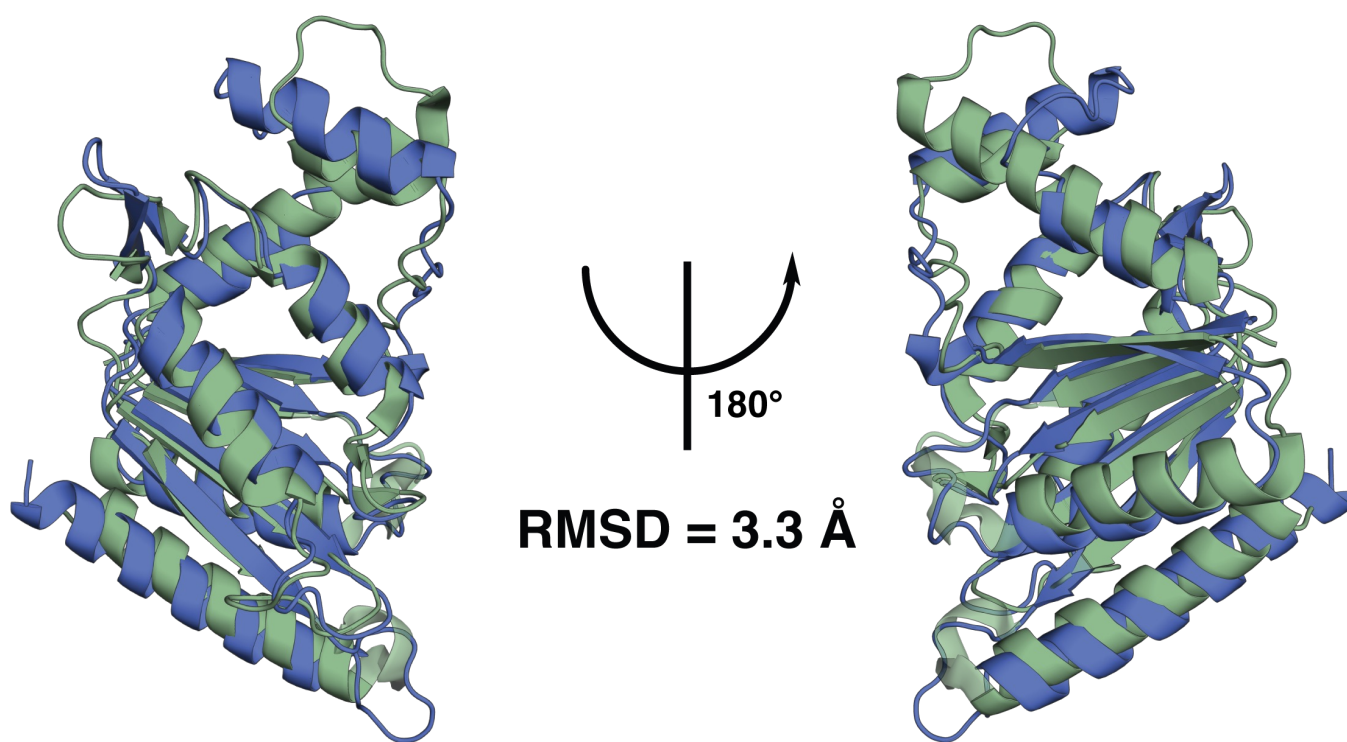
AzoR Sequence Length Distribution Across IGC and IBDMDB



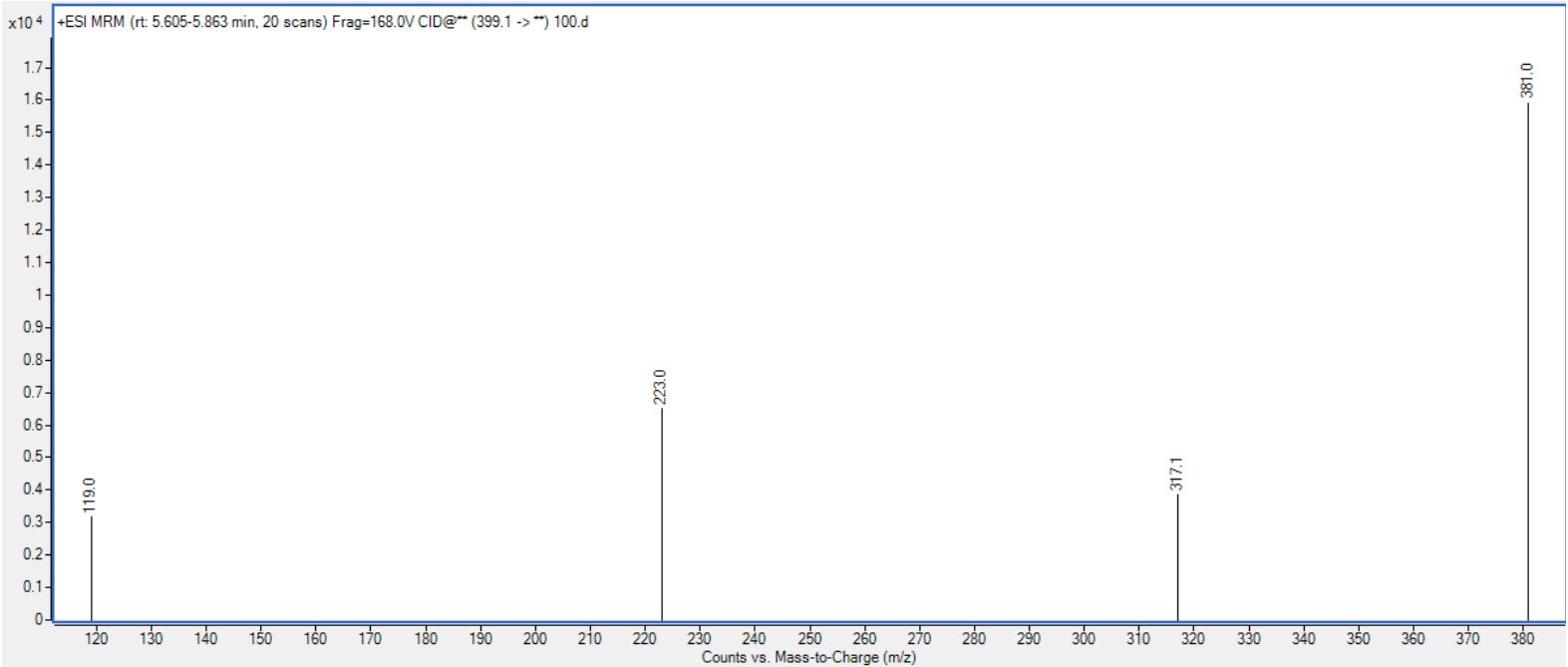
Supplemental Figure 3



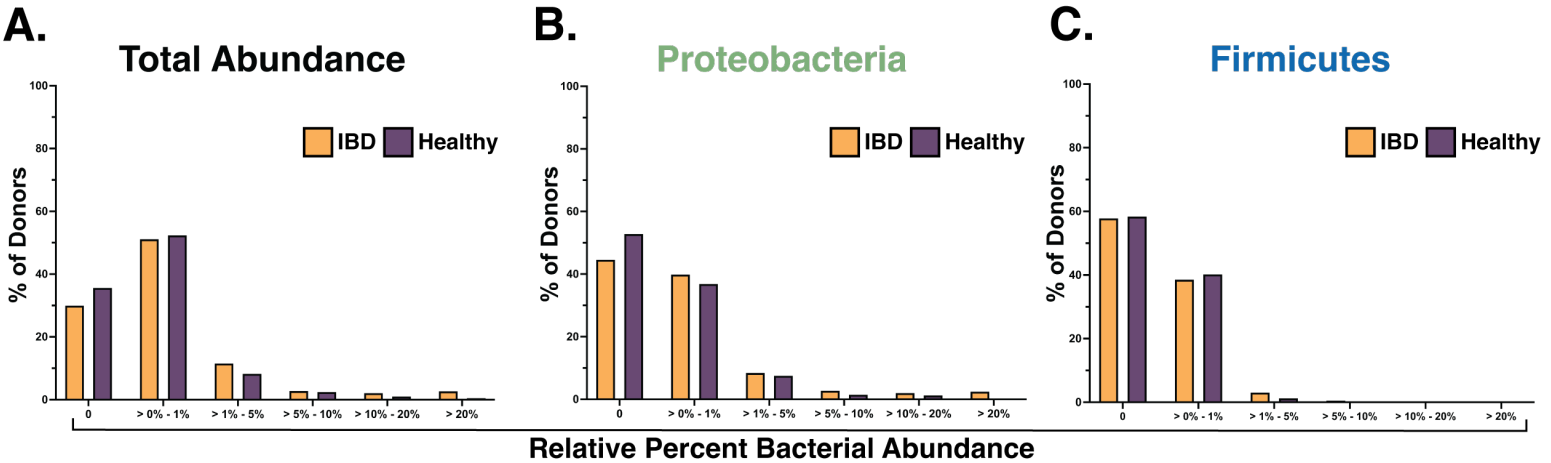
Supplemental Figure 4



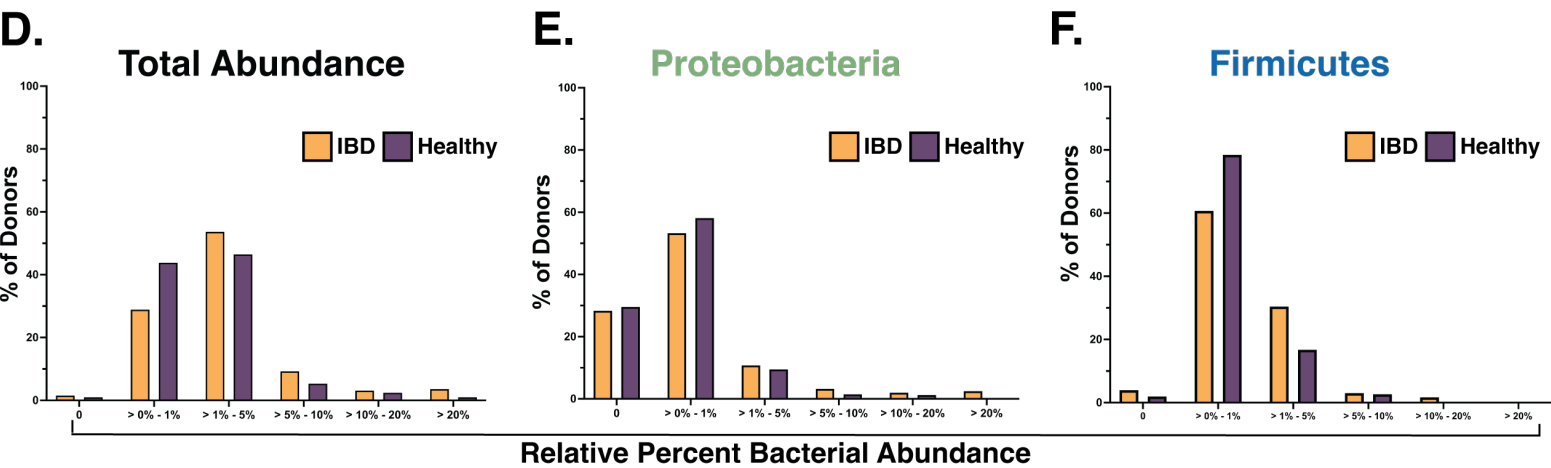
Supplemental Figure 5



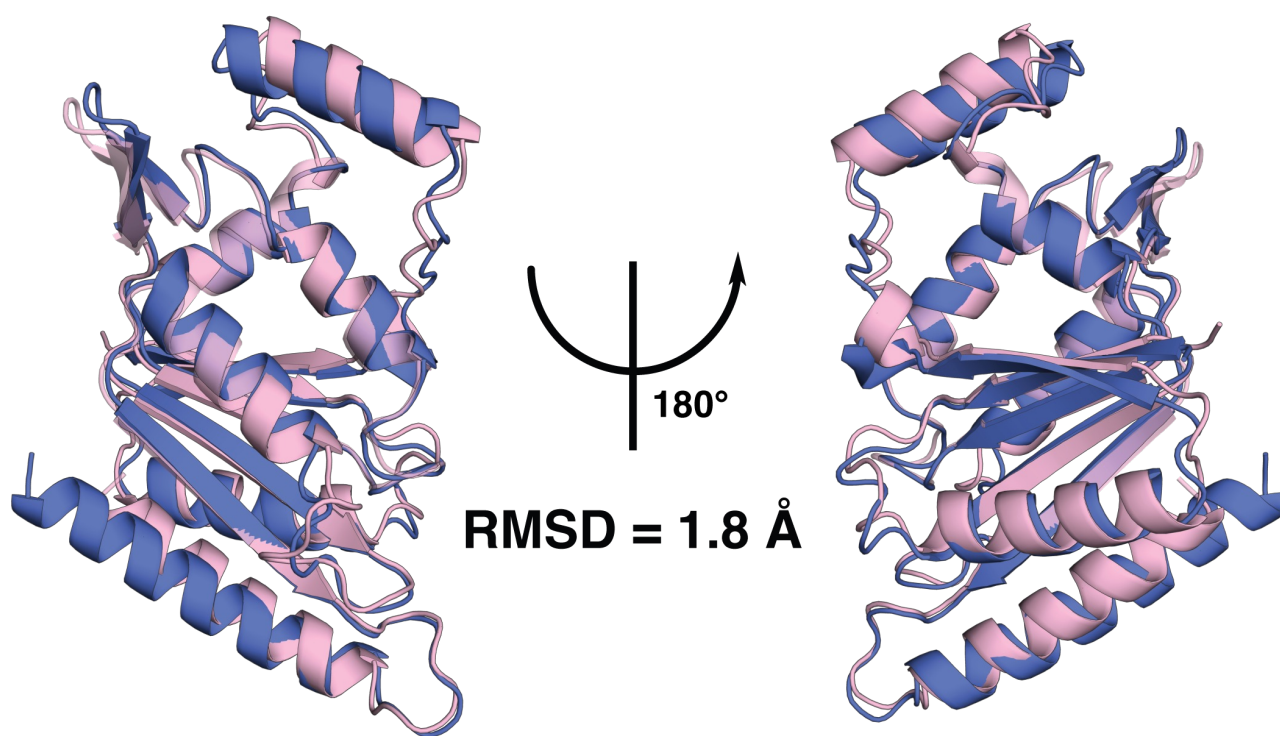
EC Annotation



Integrative Analysis



Supplemental Figure 7



**Supplemental
Table 1**

	<i>Azoreductase from Clostridium sp. Marseille-P7770 bound to flavin mononucleotide</i>
PDB accession code	TBD
Wavelength (Å)	
Resolution range (Å)	42.66 - 1.40 (1.45 - 1.40)
Space group	I 1 21
a, b, c (Å)	55.4, 58.8, 64.8
a, b, g (°)	90, 107, 90
Total reflections	70,684 (6,555)
Unique reflections	38,076 (3,748)
Multiplicity	1.9 (1.7)
Completeness (%)	97.10 (96.03)
Mean I/σ(I)	11.3 (6.0)
Wilson B-factor (Å ²)	13.4
R _{merge} (%)	0.025 (0.072)
R _{meas} (%)	0.035 (0.102)
R _{pim} (%)	0.025 (0.072)
CC _{1/2}	0.998 (0.983)
CC*	1 (0.996)
Refinement Statistics	
Resolution range (Å)	1.45 - 1.40
Reflections used in refinement	38,072 (3,747)
Reflections used for R _{free}	1,999 (197)
R _{cryst}	0.162 (0.167)
R _{free}	0.178 (0.197)
CC _{work}	0.965 (0.936)
CC _{free}	0.946 (0.915)
Number of non-hydrogen atoms	1,778
macromolecules	1,622
ligands	31
solvent	125
Protein residues	207
RMS bonds (Å)	0.009
RMS angles (°)	1.08
Ramachandran favored (%)	98.5
Ramachandran allowed (%)	1
Ramachandran outliers (%)	0.5
Rotamer outliers (%)	0
Clashscore	3.4
Average B-factor (Å ²)	17.7
Macromolecules (Å ²)	17.3
Ligands (Å ²)	10.8
Solvent (Å ²)	24.8