

SUPPLEMENTAL MATERIAL

Table S1. PATHWAYS predicted coupling values (using HARLEM software) (17-19) and optimal electron-transfer paths for various Tyr and Trp candidates in *Mtb* KatG (PDB Code 2CCA)^a:

Donor/Acceptor	Optimal pathway	Pathway distance (Å)	Predicted coupling
Y229/Heme Fe	Y229⇒W107⇒Heme	5.009	1.8896x10 ⁻³
Y353/Heme Fe	Y353⇒MET377→LEU378⇒Heme	11.180	3.7048x10 ⁻⁵
W107/Heme Fe	W107⇒Heme	3.350	2.1812x10 ⁻²
W91/Heme Fe	W91⇒HOH47⇒HOH487⇒Heme	6.882	2.0077x10 ⁻⁴
Y337(predicted doublet)/Heme	Y337→LEU336⇒PHE332⇒HIS270→Heme	14.768	1.1826x10 ⁻⁶
Y413(predicted doublet)/Heme	Y413→TRP412⇒Heme	8.815	4.3806x10 ⁻⁴
Y197(predicted doublet)/Heme	Y197⇒ARG114→TYR113⇒MET255⇒TYR229⇒TRP107⇒Heme	19.421	2.4165x10 ⁻⁸
Y28(predicted doublet)/Heme	Y28→LYS27⇒PRO40→TRP39⇒SER134→TRP135→PRO136→ASP137⇒HOH89⇒Heme	36.249	2.7150x10 ⁻¹⁴
Y210(predicted singlet)/Heme	Y210⇒ASP247→ILE248⇒Heme	12.343	1.1444x10 ⁻⁶
Y339(predicted singlet)/Heme	Y339⇒PRO375→THR376→MET377→LEU378⇒Heme	18.553	1.6502x10 ⁻⁷
Y353/Y229	Y353→GLN352→TRP351⇒HOH247⇒PRO232→ASN231→VAL230→Y229	16.613	1.7736x10 ⁻⁶
W91/Y229	W91⇒SER140→ALA139→ASN138→ASP137→ILE228→Y229	19.549	1.8413x10 ⁻⁷

^a A through-bond coupling is indicated by →; through-space jumps and hydrogen bonds are indicated by ⇒.