

Electronic Supplementary Information (ESI)

**Heterologous production and functional characterization of
Bradyrhizobium japonicum copper-containing nitrite reductase and its
physiological redox partner cytochrome *c*₅₅₀**

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Fig. S1 Size-exclusion chromatography performed on a Superdex 75 column equilibrated with 10 mM Tris-HCl buffer pH 8.0 plus 200 mM NaCl. Calibration curve (Left): Aprotinin (A, 6.5 kDa), Ribonuclease (R, 13.7 kDa), Carbonic Anhydrase (CA, 29 kDa), Ovalbumin (44 kDa) and Conalbumin (75 kDa). M, D and T indicate monomer, dimer, and tetramer, respectively. Right: runs from a diluted (~ 0.25 mg/mL) sample (red) and concentrated (~ 20 mg/mL) sample (black).

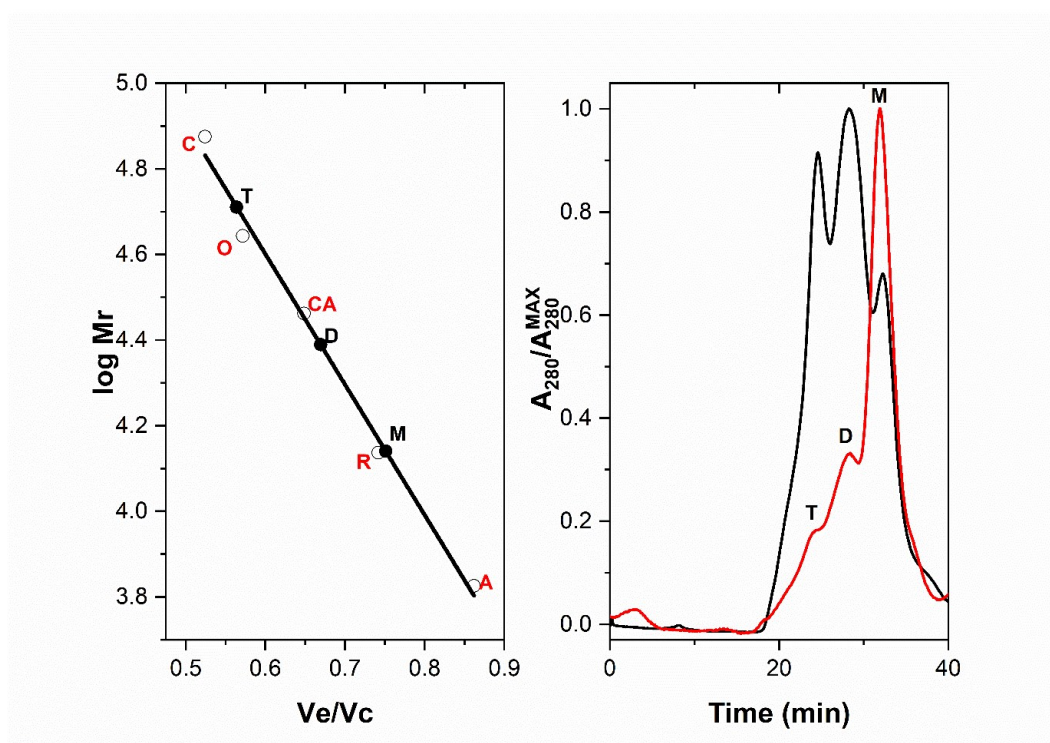
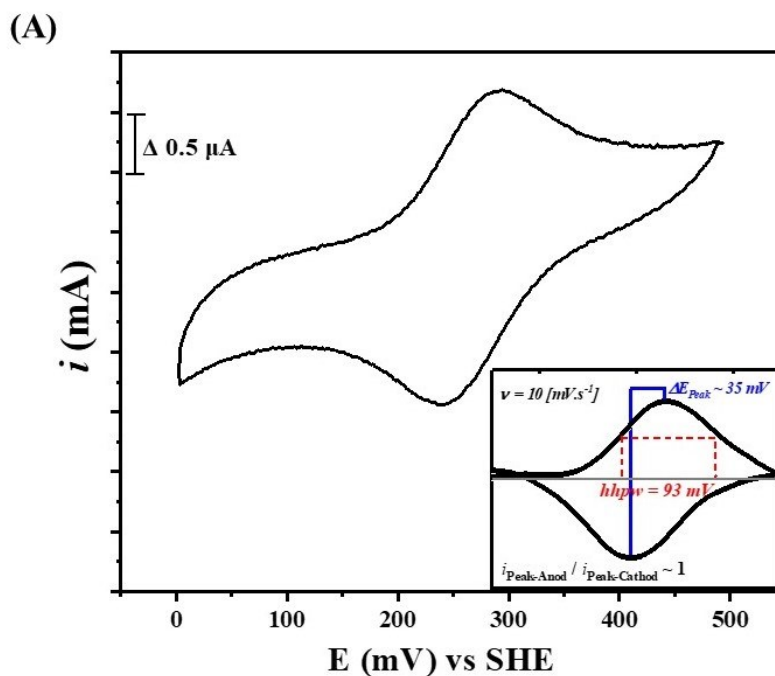
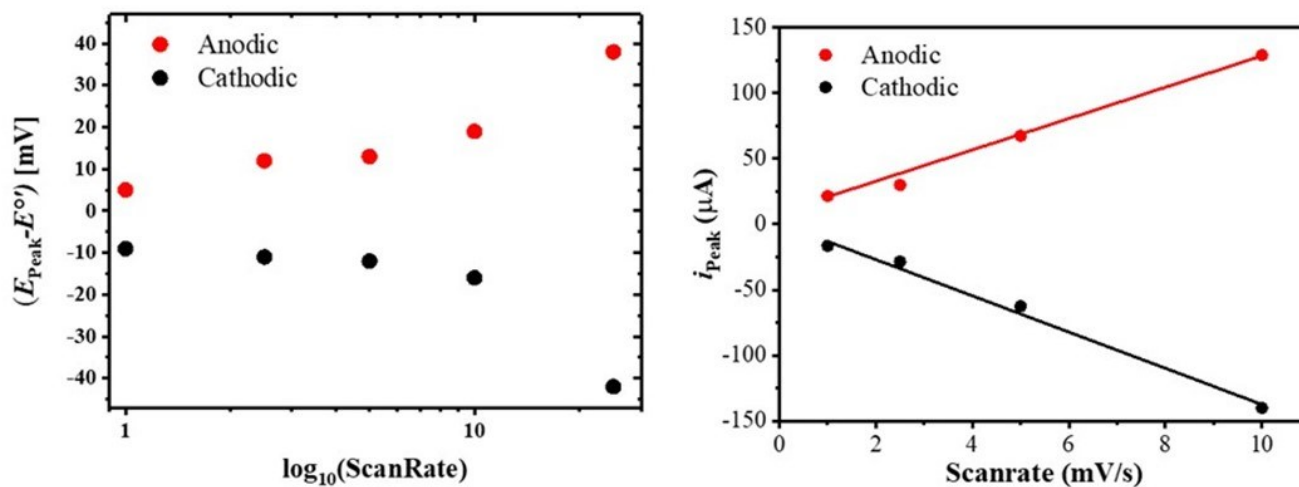


Fig. S2 Panel A. Cyclic voltammograms of *BjCycA* using 1 mM 4,4'-dithiopyridine as promoter of the protein-electrode interaction and 500 mM glycine as protein stabilizer. The inset shows a blank-subtracted voltammogram recorded at $\nu=10 \text{ mV}\cdot\text{s}^{-1}$. Typical voltammogram features indicate that the system behaves as thin-layer at this scan rate, e.g. i_{Peak} ratio ~ 1 , half-height peak width $\sim 90 \text{ mV}$, and ΔE_{Peak} lower than $59/n \text{ mV}$. **Panel B.** Left, Laviron plot showing the variation of the anodic and cathodic peaks potentials (E_{Peak}) as a function of the logarithm of the scan rate. Right, Linear fitting of the variation of CV cathodic and anodic peaks current (i_{Peak}) with the scan rate (right), adding evidence to the thin-layer



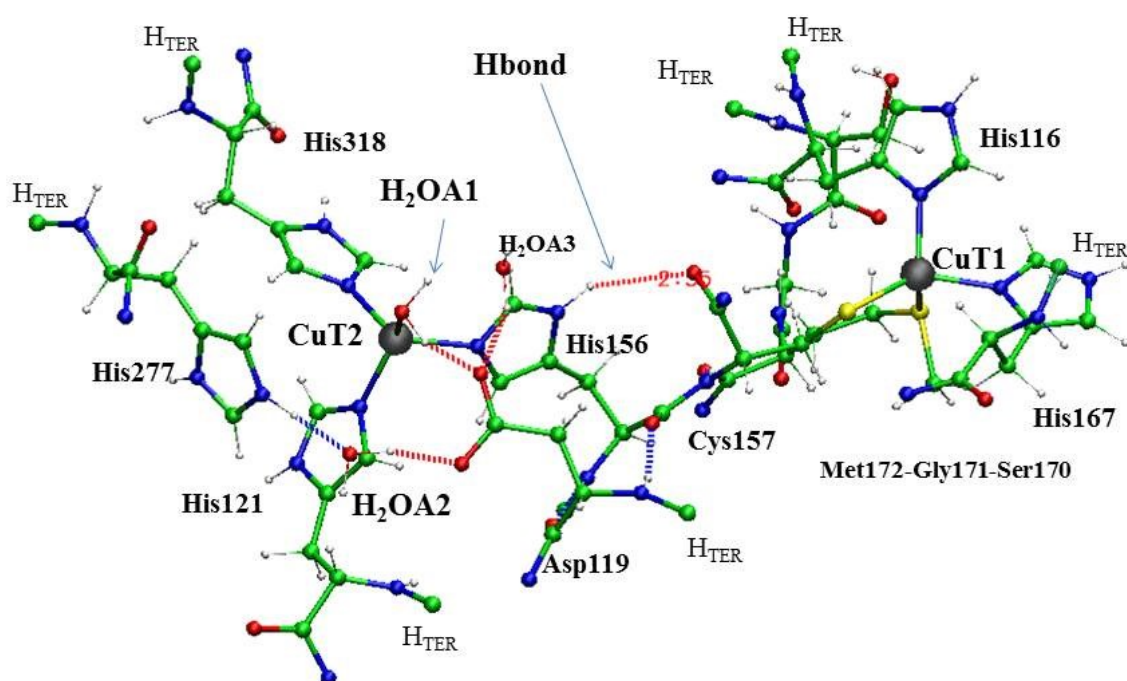
(B)



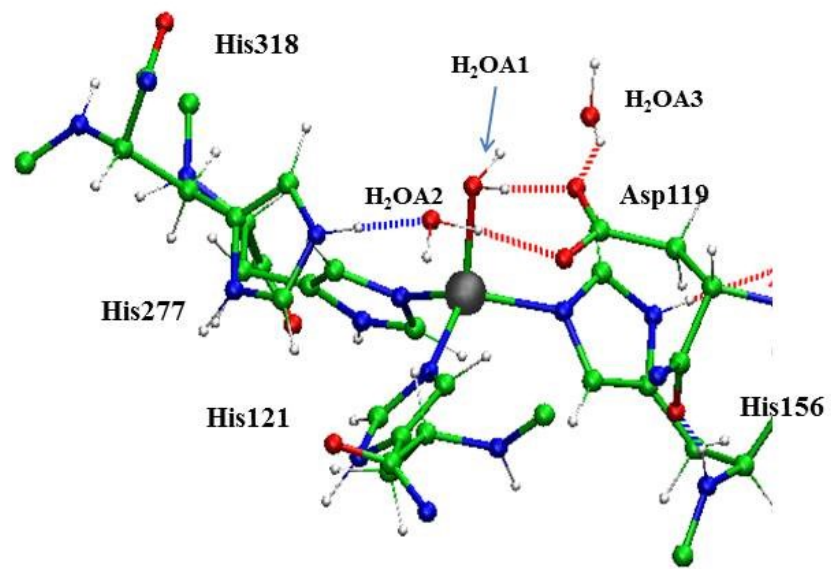
behavior.

Fig. S3 QM part of the QM/MM calculations. Panel A includes residues His328, His121, His156, which are the ligands of the catalytic copper atom T2, His116, His167, Cys157, which are nearest neighbors of copper atom at T1, and the weaker Met 172 ligand, and the second sphere residues Asp119 (Asp_{CAT}), His277 (His_{CAT}), Gly171, and Ser170. The color codes are green for carbon, blue for Nitrogen, red Oxygens, light grey for hydrogen, yellow for sulfur, and grey for Cu. Water hydrogen bond interactions and the hydrogen bond (His156)-N^{δ1}H...O=C-(Cys157) are indicated as red dashed lines. Three water molecules were included based on structural data of other similar copper-nitrite reductases (PDB 1OE1 and 5F7B), H2OA1 bonded to T2 copper, H2OA2 which is bridging His_{CAT} and Asp_{CAT} and H2OA3 bonded to Asp_{CAT}. His_{CAT} and Asp_{CAT} are protonated and deprotonated, respectively. Panels B and C are overviews in different projection of the of the T1 and T2 sites shown in Panel A, respectively. Cartesian coordinates of the atoms are given at the end of the document.

(A)



(B)



(C)

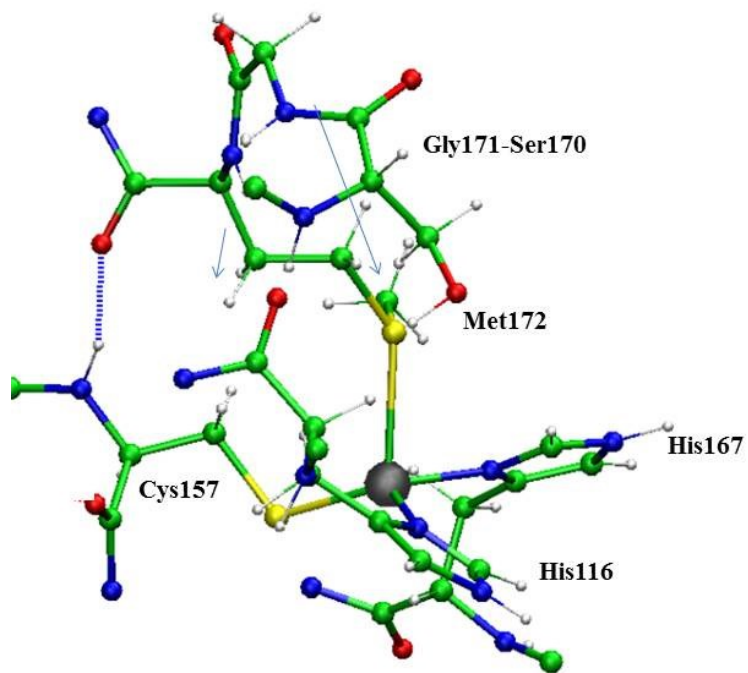


Fig. S4 Computed T1 UV-vis absorption spectra of *Bj*NirK (pink) and *Sm*NirK (green) determined by TDDFT using the HSEh1PBE functional and the basis set 6-31(d,p). The inset shows the model used in the computation.

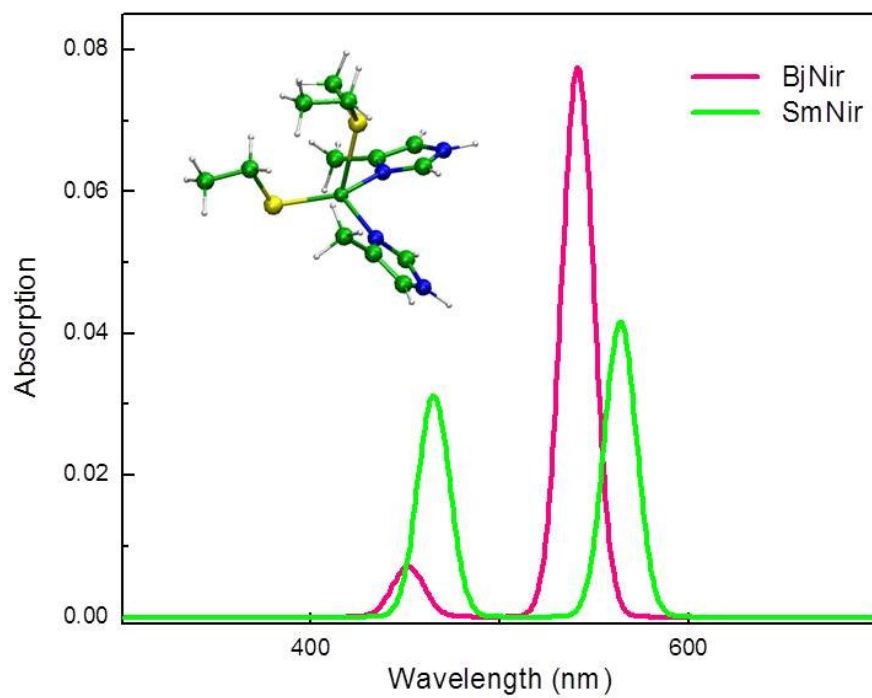


Fig. S5 EPR spectra of *Bj*NirK at pH 10 showing two type 2 copper (II) overlapping spectral components (red and pink). $g_{1,2,3} = 2.190, 2.052, 2.023, A_{1,2,3} = 7$ mT for T1 (blue), $g_{1,2,3} = 2.231, 2.055, 2.040, A_{1,2,3} = 20.6$ mT for the major component (T2_I; red) and $g_{1,2,3} = 2.345, 2.055, 2.055, A_{1,2,3} = 16$ mT for the minor component (T2_{II}; pink); T1:T2_I:T2_{II} ratio of 1:0.8:0.2

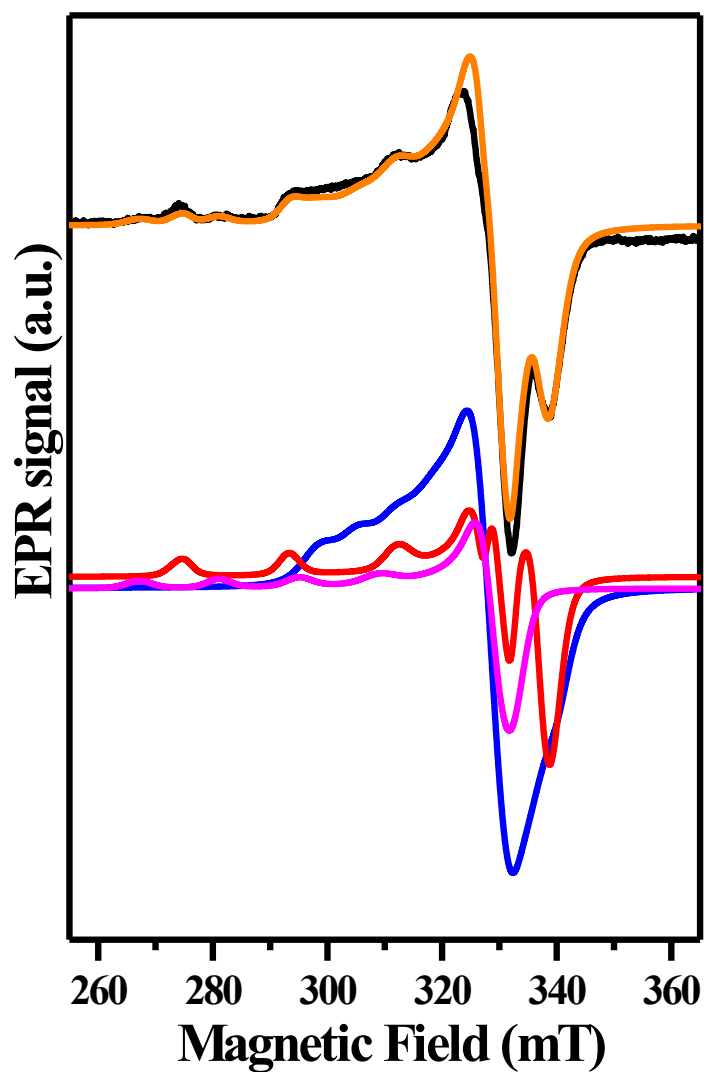
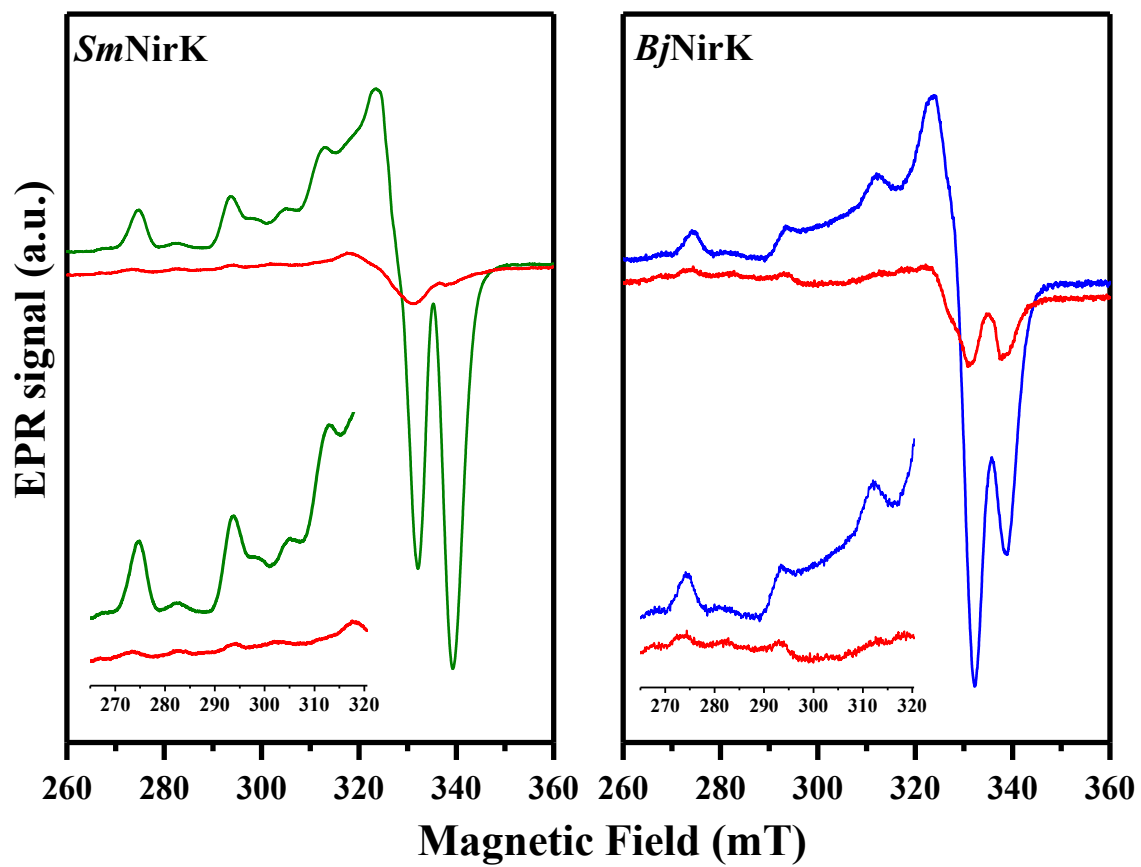


Fig. S6 EPR spectra of as-purified *Bj*NirK (blue) and *Sm*NirK (green) at pH 10 and upon ascorbate reduction (red) under anaerobic conditions.



Cartesian coordinates of the QM part including PDB and residue names and residue numbers.

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H (PDBName=HB1, ResName=HIS, ResNum=277_A)	21.372926	34.413826	36.41224
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C (PDBName=CE1, ResName=HIS, ResNum=277_A)	20.109754	35.420939	32.81599
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H (PDBName=HB1, ResName=CYS, ResNum=157_C)	30.259432	42.259999	25.61636
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H (PDBName=HA, ResName=SER, ResNum=170_C)	35.807342	46.857381	32.86236
C (PDBName=CB, ResName=SER, ResNum=170_C)	35.883715	45.679367	31.09955
H (PDBName=HB1, ResName=SER, ResNum=170_C)	35.179544	45.109138	30.47127
H (PDBName=HB2, ResName=SER, ResNum=170_C)	36.265103	46.517751	30.51674
O (PDBName=OG, ResName=SER, ResNum=170_C)	36.996143	44.896552	31.45969
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C (PDBName=C, ResName=SER, ResNum=170_C)	34.095305	47.260140	31.67676
O (PDBName=O, ResName=SER, ResNum=170_C)	34.481005	48.233106	31.02451
N (PDBName=N, ResName=GLY, ResNum=171_C)	32.790575	46.948709	31.85384
H (PDBName=HN, ResName=GLY, ResNum=171_C)	32.605939	46.213558	32.53681
C (PDBName=CA, ResName=GLY, ResNum=171_C)	31.753428	47.846542	31.41385
H (PDBName=HA1, ResName=GLY, ResNum=171_C)	32.245657	48.739721	31.02407
H (PDBName=HA2, ResName=GLY, ResNum=171_C)	31.104778	48.128540	32.24520
C (PDBName=C, ResName=GLY, ResNum=171_C)	30.865854	47.324163	30.30424
O (PDBName=O, ResName=GLY, ResNum=171_C)	29.987963	48.004660	29.78482
N (PDBName=N, ResName=MET, ResNum=172_C)	31.035450	46.018873	29.92594
H (PDBName=HN, ResName=MET, ResNum=172_C)	31.791248	45.472682	30.33283
C (PDBName=CA, ResName=MET, ResNum=172_C)	30.345798	45.562999	28.73737
H (PDBName=HA, ResName=MET, ResNum=172_C)	30.192840	46.451164	28.10517
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H (PDBName=HB1, ResName=MET, ResNum=172_C)	31.229448	43.599627	28.55499
H (PDBName=HB2, ResName=MET, ResNum=172_C)	30.462135	44.222622	27.09773
C (PDBName=CG, ResName=MET, ResNum=172_C)	32.440199	45.009101	27.45845
H (PDBName=HG1, ResName=MET, ResNum=172_C)	32.363333	46.050531	27.14346
H (PDBName=HG2, ResName=MET, ResNum=172_C)	33.185642	44.959089	28.25437
S (PDBName=SD, ResName=MET, ResNum=172_C)	33.155825	44.119445	26.04375
C (PDBName=CE, ResName=MET, ResNum=172_C)	32.079558	44.659287	24.69130
H (PDBName=HE1, ResName=MET, ResNum=172_C)	32.509564	44.263267	23.76831
H (PDBName=HE2, ResName=MET, ResNum=172_C)	31.059119	44.288105	24.80346
H (PDBName=HE3, ResName=MET, ResNum=172_C)	32.069733	45.749979	24.63458
C (PDBName=C, ResName=MET, ResNum=172_C)	28.973037	45.047984	29.13499

O (PDBName=O, ResName=MET, ResNum=172_C)	28.708939	43.848006	29.05398
Cu (PDBName=CU, ResName=CU, ResNum=371_C)	33.670940	41.571406	25.32516
Cu (PDBName=CU, ResName=CU, ResNum=372_C)	24.143311	37.176540	32.03380
O (PDBName=OH2, ResName=TIP, ResNum=H2OA1)	24.616881	35.363636	31.36837
H (PDBName=H1, ResName=TIP, ResNum= H2OA1)	25.570500	35.151785	31.32262
H (PDBName=H1, ResName=TIP, ResNum= H2OA1)	24.424233	35.445356	30.38111
O (PDBName=OH2, ResName=TIP, ResNum= H2OA2)	21.163819	34.710027	
29.33100			
H (PDBName=H2, ResName=TIP, ResNum= H2OA2)	21.870471	35.256894	28.89342
H (PDBName=H1, ResName=TIP, ResNum= H2OA2)	20.366372	35.120051	28.96894
O (PDBName=OH2, ResName=TIP, ResNum= H2OA3)	26.991407	35.186405	
30.07555			
H (PDBName=H2, ResName=TIP, ResNum= H2OA3)	26.331322	35.459955	29.39188
H (PDBName=H1, ResName=TIP, ResNum= H2OA3)	27.297514	34.319042	29.80244