slope: 258.88, r_val: 0.49

Legend:
- ● Fragment Stability Benchmark.oeb
- ◆ Fragment Stability Benchmark.oeb
- ✖ OpenFF Full TorsionDrive Benchmark 1.oeb
- ◀ OpenFF Gen 2 Torsion Set 3 Pfizer Discrepancy 2.oeb
- ▶ OpenFF Gen 2 Torsion Set 4 eMolecules Discrepancy 2.oeb
- ★ OpenFF Group1 Torsions.oeb
- ◆ OpenFF Rowley Biaryl v1.0.oeb
- ⋈ Pfizer Discrepancy Torsion Dataset 1.oeb
- ● SMIRNOFF Coverage Torsion Set 1.oeb
- ■ Fragment Stability Benchmark.oeb
- ✚ OpenFF Fragmenter Validation 1.0.oeb
- ▷ OpenFF Gen 2 Torsion Set 2 Coverage 2.oeb
- ◤ OpenFF Gen 2 Torsion Set 4 eMolecules Discrepancy.oeb
- ● OpenFF Gen 2 Torsion Set 5 Bayer 2.oeb
- ◆ OpenFF Primary TorsionDrive Benchmark 1.oeb
- ✕ OpenFF-benchmark-ligand-fragments-v1.0.oeb
- ● SMIRNOFF Coverage Torsion Set 1.oeb

X-axis: Wiberg Bond Order

Y-axis: Torsion barrier (kJ/mol)