

Table 9. Geometrical parameters for the optimized $[(\text{CO})_2\text{Re}(\text{C}_5\text{H}_4)\text{C}\equiv\text{C}(\text{C}_5\text{H}_4)\text{Re}[(\text{CO})_2](\text{alkane})$ complexes, calculated at the BP86/ 6-31G*, LANL2DZ level of theory

DFT(BP86)	<i>Interacting</i>				<i>C-H</i>	<i>Average</i>
	<i>Pair of</i>	<i>M-H</i>	<i>M-C</i>	<i>M-H-C</i>	<i>bound</i>	<i>C-H free</i>
	<i>Atoms</i>	<i>Distance</i>	<i>distance</i>	<i>angle</i>	<i>distance</i>	<i>distance</i>
Methane	Re ₁ -C	1.946	2.634	113.303	1.164	1.100
	Re ₂ -C		4.119			
Ethane	Re ₁ -C1	1.973	2.745	120.500	1.154	1.101
	Re ₂ -C2	1.975	2.747	120.412	1.156	1.100
Propane	Re ₁ -C1	1.952	2.716	119.456	1.159	1.102
	Re ₂ -C3	1.995	2.829	125.554	1.156	1.101
Butane	Re ₁ -C1	1.951	2.718	119.872	1.155	1.103
	Re ₂ -C4	1.958	2.731	120.557	1.153	1.102
Pentane	Re ₁ -C1	1.965	2.792	124.766	1.158	1.100
	Re ₂ -C5	1.985	2.870	130.260	1.154	1.099
Cyclopropane	Re ₁ -C1	1.979	2.671	114.669	1.148	1.090
	Re ₂ -C2	1.987	2.710	117.514	1.141	1.090
Cyclobutane	Re ₁ -C1	1.88	2.66	119.44	1.17	1.101
Cyclopentane	Re ₁ -C1	1.939	2.838	130.372	1.167	1.098
	Re ₂ -C2	1.972	2.754	120.861	1.161	1.100
Cyclohexane	Re ₁ -C1	2.01	3.01	141.605	1.162	1.102
	Re ₂ -C2	2.14	2.91	121.013	1.146	1.104

“M-H distance” and “M-C distance” are the distances between the designated Re atom (“M” = Re₁ or Re₂) and the H and C atoms, respectively, of the C-H σ -bond that interacts most strongly with that particular Re atom (i.e. the C-H σ -bond that lies in closest proximity to that Re atom). The designations “C1”, “C2”, etc. indicate the position along the alkane chain / ring of the CH₃ / CH₂ group that is interacting with the designated Re atom. “M-H-C angle” is the angle between the Re atom and the aforementioned C-H bond. “C-H bound distance” is the length of the aforementioned C-H bond. “Average C-H free distance” is the average length of the remaining C-H bonds that are located on the same CH₃ (linear alkanes)/ CH₂ (cyclic alkanes) group as the interacting bond (in the case of cyclic alkanes, “Average C-H free distance” is simply one bond length, not an average of two lengths).