Supporting Informaiton

Quantum Mechanistic insights on Aryl Propargyl Ether Claisen Rearrangement

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Table S1: Relative Gibbs free energy of the aryl propargyl ether Claisen Rearrangement with methyl group on phenyl segment in solvent phase (Unit: kcal/mol) at M06/6-31+G**// B3LYP/6-31+G* level.

	o-CH_3	p- CH_3	m- CH_3-1	m- CH_3-2
Reactant	0.0	0.0	0.0	0.0
TS1	37.0	38.2	37.7	36.7
Int1	2.4	3.6	2.4	2.8
TS2-1	51.5	52.9	51.0	51.9
TS2-2	32.5	34.5	30.8	32.2
Int2	-21.3	-21.4	-21.5	-18.8
TSa3	3.6	4.4	3.5	5.2
Inta3	-22.5	-21.5	-22.7	-19.9
Tsa4	-12.4	-11.1	-12.2	-9.8
Inta4	-17.0	-16.5	-17.4	-14.3
TSa5	-5.3	-4.5	-5.6	-4.0
ProductA	-37.2	-37.2	-36.8	-35.6
Intb2	188.1	188.1	187.0	189.1
TSb3	202.8	203.8	204.2	203.6
Product B complex	183.4	183.6	185.4	184.2
TSc3	48.2	49.3	50.7	50.2
Intc3	-38.1	-38.1	-37.0	-37.4
TSc4	29.1	29.6	29.9	30.0
ProductB	-51.8	-51.2	-50.6	-50.8

Table S2: Relative Gibbs free energy of the aryl propargyl ether Claisen Rearrangement with chloride group on phenyl segment in solvent phase (Unit: kcal/mol)

	o-Cl	p-Cl	m-Cl-1	m-Cl-2
Reactant	0.0	0.0	0.0	0.0
TS1	36.4	38.1	37.7	36.7
Int1	3.4	4.5	2.7	2.6
TS2-1	53.2	53.7	52.2	52.0
TS2-2	33.7	36.0	32.4	33.7
Int2	-21.1	-20.7	-21.3	-20.1
TSa3	3.8	4.9	3.7	4.5
Inta3	-23.1	-21.5	-22.5	-20.7
Tsa4	-11.5	-10.4	-11.6	-10.0
Inta4	-17.8	-16.3	-17.3	-14.2
TSa5	-5.7	-4.8	-5.9	-5.0
ProductA	-37.1	-36.9	-37.0	-36.9
Intb2	180.8	182.8	181.6	182.5
TSb3	198.4	199.7	199.5	198.8
Product B complex	179.6	179.0	180.4	178.4
TSc3	50.1	49.7	50.5	49.4
Intc3	-37.4	-37.3	-37.2	-37.9
TSc4	29.7	29.7	29.9	29.2
ProductB	-51.6	-51.5	-51.1	-51.9

Table S3: Relative Gibbs free energy of the aryl propargyl ether Claisen Rearrangement with methoxyl group on phenyl segment in solvent phase (Unit: kcal/mol)

	o-OCH_3	p- OCH_3	m- OCH_3-1	m- OCH_3-2
Reactant	0.0	0.0	0.0	0.0
TS1	36.1	38.0	35.3	33.6
Int1	2.3	5.3	0.2	-0.9
TS2-1	53.2	54.5	48.9	48.8
TS2-2	34.1	37.8	27.9	25.9
Int2	-20.9	-20.5	-21.1	-20.5
TSa3	3.8	5.2	2.6	2.7
Inta3	-23.8	-21.1	-24.1	-23.0
Tsa4	-12.5	-10.3	-13.2	-12.6
Inta4	-17.9	-16.0	-18.2	-17.9
TSa5	-5.2	-3.7	-6.6	-6.6
ProductA	-36.8	-36.6	-36.8	-36.5
Intb2	186.7	188.7	186.3	186.3
TSb3	202.8	204.0	204.0	203.5
Product B complex	183.2	182.4	186.5	184.8
TSc3	48.7	48.8	52.1	51.1
Intc3	-37.6	-37.3	-36.9	-37.4
TSc4	29.5	29.8	30.5	30.0
ProductB	-52.1	-51.2	-49.7	-50.9

Table S4: Relative Gibbs free energy of the aryl propargyl ether Claisen Rearrangement with methyl group on phenyl and propargyl segment in solvent phase (Unit: kcal/mol)

	o-CH_3	p- CH_3	m- CH_3-1	m- CH_3-2
Reactant	0.0	0.0	0.0	0.0
TS1	35.3	36.7	36.1	35.5
Int1	3.3	5.1	3.3	3.4
TS2-1	52.1	54.4	51.6	52.9
TS2-2	34.6	38.3	34.2	35.1
Int2	-20.6	-19.8	-21.1	-17.9
TSa3	1.2	2.8	1.5	3.4
Inta3	-25.5	-24.0	-25.2	-22.6
Tsa4	-13.0	-11.1	-12.4	-9.8
Inta4	-20.2	-18.4	-20.0	-16.9
TSa5	-9.6	-8.1	-9.7	-8.0
ProductA	-37.8	-37.3	-37.4	-36.0
Intb2	188.4	190.2	188.4	191.6
TSb3	207.2	207.6	208.4	207.8
Product B complex	188.2	190.1	191.1	188.8
TSc3	49.1	51.1	51.7	51.3
Intc3	-38.1	-37.7	-36.5	-36.6
TSc4	28.3	30.3	30.1	30.4
ProductB	-48.3	-46.3	-46.7	-46.7

Table S5: Relative Gibbs free energy of the arnyl propargyl ether Claisen Rearrangement with chloro group on phenyl segment and methyl group on propargyl segment in solvent phase (Unit: kcal/mol)

	o-Cl	p-Cl	m-Cl-1	m-Cl-2
Reactant	0.0	0.0	0.0	0.0
TS1	34.2	36.0	35.8	34.8
Int1	4.2	5.5	4.3	4.1
TS2-1	53.5	54.7	53.1	53.1
TS2-2	35.7	38.4	34.6	36.2
Int2	-20.7	-20.0	-19.9	-19.2
TSa3	0.9	2.7	1.7	2.3
Inta3	-26.1	-23.8	-25.0	-23.1
Tsa4	-12.6	-10.9	-11.7	-9.8
Inta4	-20.4	-18.6	-20.0	-17.4
TSa5	-10.7	-8.9	-10.2	-9.2
ProductA	-38.2	-37.4	-37.3	-37.2
Intb2	182.1	184.9	184.4	184.6
TSb3	201.9	203.8	203.5	202.7
Product B complex	184.6	182.4	186.3	184.3
TSc3	50.6	50.3	51.6	50.3
Intc3	-37.3	-36.3	-36.4	-37.3
TSc4	29.2	30.0	29.9	29.2
ProductB	-47.6	-47.1	-46.6	-47.3

Table S6: Relative Gibbs free energy of the aryl propargyl ether Claisen Rearrangement with methoxy group on phenyl segment and methyl group on propargyl segment in solvent phase (Unit: kcal/mol)

	o-OCH_3	p- OCH_3	m- OCH_3-1	m- OCH_3-2
Reactant	0.0	0.0	0.0	0.0
TS1	34.2	36.0	35.6	33.9
Int1	3.1	6.8	2.2	0.3
TS2-1	53.7	55.6	50.2	49.2
TS2-2	35.1	41.1	28.6	28.6
Int2	-20.4	-19.7	-20.6	-19.6
TSa3	1.5	3.4	0.6	0.9
Inta3	-26.5	-22.8	-26.7	-25.5
Tsa4	-13.1	-10.8	-13.8	-13.1
Inta4	-20.3	-17.9	-21.0	-21.7
TSa5	-9.6	-7.6	-10.9	-10.7
ProductA	-37.5	-37.0	-37.4	-37.1
Intb2	188.6	189.9	187.9	189.0
TSb3	206.0	207.8	208.1	207.8
Product B complex	188.1	188.6	192.0	190.9
TSc3	49.3	49.8	53.1	51.9
Intc3	-37.3	-36.1	-36.2	-37.0
TSc4	29.2	30.3	30.9	30.2
ProductB	-47.9	-46.7	-45.9	-46.6

Table S7: Relative Gibbs free energy of the aryl propargyl ether Claisen Rearrangement with methyl group on phenyl segment and dimethyl groups on propargyl segment in solvent phase (Unit: kcal/mol)

	o-CH_3	p- CH_3	m- CH_3-1	m- CH_3-2
Reactant	0.0	0.0	0.0	0.0
TS1	29.9	31.4	31.9	30.3
Int1	1.0	2.8	1.4	1.6
TS2-1	50.2	52.4	50.6	50.9
TS2-2	32.2	36.6	32.5	31.6
Int2	-23.0	-21.9	-22.2	-20.1
TSa3	-3.8	-1.8	-2.9	-1.2
Inta3	-29.0	-27.3	-27.0	-24.7
Tsa4	-15.3	-13.7	-14.5	-12.5
Inta4	-21.0	-19.1	-21.4	-19.0
TSa5	-12.1	-10.7	-11.6	-10.7
ProductA	-41.3	-40.6	-40.2	-39.6
Intb2	187.7	190.0	187.6	190.9
TSb3	208.7	209.1	209.6	208.9
Product B complex	184.9	189.2	191.7	186.9
TSc3	47.6	49.2	51.0	49.5
Intc3	-39.7	-38.7	-38.5	-39.1
TSc4	26.5	27.5	28.4	27.4
ProductB	-48.3	-46.6	-45.2	-46.3

Table S8: Relative Gibbs free energy of the aryl propargyl ether Claisen Rearrangement with chloride group on phenyl segment and dimethyl groups on propargyl segment in solvent phase (Unit: kcal/mol)

	o-Cl	p-Cl	m-Cl-1	m-Cl-2
Reactant	0.0	0.0	0.0	0.0
TS1	29.0	30.6	30.2	29.4
Int1	2.7	3.5	2.5	1.3
TS2-1	51.9	52.6	51.3	51.2
TS2-2	34.6	37.2	32.6	34.2
Int2	-23.4	-22.1	-22.3	-21.4
TSa3	-3.6	-2.7	-3.5	-2.6
Inta3	-30.3	-27.7	-27.4	-27.0
Tsa4	-14.7	-13.2	-14.5	-12.9
Inta4	-20.6	-19.6	-22.3	-18.3
TSa5	-13.4	-11.8	-12.9	-11.9
ProductA	-40.8	-40.7	-40.8	-40.5
Intb2	181.6	184.7	183.3	184.8
TSb3	201.8	204.2	203.9	202.8
Product B complex	182.7	182.5	187.6	181.4
TSc3	49.4	48.8	49.9	48.6
Intc3	-39.2	-38.6	-38.7	-39.7
TSc4	26.7	26.9	27.4	25.8
ProductB	-46.5	-46.5	-46.1	-46.7

Table S9: Relative Gibbs free energy of the aryl propargyl ether Claisen Rearrangement with methoxyl group on phenyl segment and dimethyl groups on propargyl segment in solvent phase (Unit: kcal/mol)

	o-OCH_3	p- OCH_3	m- OCH_3-1	m- OCH_3-2
Reactant	0.0	0.0	0.0	0.0
TS1	29.3	31.0	31.0	29.2
Int1	1.3	5.1	0.1	-2.0
TS2-1	52.1	54.1	48.1	47.7
TS2-2	33.3	40.6	25.5	25.8
Int2	-22.7	-21.3	-22.4	-21.7
TSa3	-2.9	-1.1	-4.3	-3.7
Inta3	-29.6	-26.5	-29.8	-29.3
Tsa4	-15.7	-12.6	-16.0	-16.0
Inta4	-20.8	-18.3	-21.8	-20.9
TSa5	-12.3	-9.8	-13.4	-12.9
ProductA	-40.6	-39.6	-40.9	-40.5
Intb2	188.3	190.9	186.1	188.2
TSb3	208.0	209.3	208.9	208.2
Product B complex	185.4	186.6	189.9	188.1
TSc3	48.0	48.8	51.5	50.3
Intc3	-39.3	-37.9	-38.4	-39.2
TSc4	27.2	28.0	28.9	27.9
ProductB	-47.0	-45.7	-45.1	-46.3

Table S10: The energy barrier of the first two steps and breaking and forming bond distances for methyl group on aromatic segment with zero, mono and dimethyl group on the aliphatic segment in N, N-diethylaniline at M06/6-31+G**//B3LYP/6-31+G* level.

	Parent	1a-o	1a-p	1a-m1	1a-m2	1b-o	1b-p	1b-m1	1b-m2	1c-o	1c-p	1c-m1	1c-m2
Step1	37.9	37.0	38.2	37.7	36.7	35.3	36.7	36.1	35.5	29.9	31.4	31.9	30.3
Step2	30.6	30.1	30.9	28.4	29.4	31.3	33.2	30.9	31.7	31.2	33.8	31.1	30.0
C3-O4	1.431	1.430	1.430	1.431	1.431	1.439	1.439	1.439	1.439	1.454	1.453	1.454	1.454
C1-C10	3.970	3.968	3.979	3.978	3.983	3.929	3.937	3.933	3.941	3.737	3.745	3.7378	3.744

* ortho- is denoted by o-; para- is denoted by p-; meta-1 is denoted by m1; meta-2 is denoted by m2.; a,b and c represents the zero, mono and dimethyl group on the aliphatic segment, respectively.

Table S11: The energy barrier of the first two steps and breaking and forming bond distances for chloro group on aromatic segment with zero, mono and dimethyl group on the aliphatic segment in N, N-diethylaniline at M06/6-31+G**//B3LYP/6-31+G* level.

	Parent	2a-o	2a-p	2a-m1	2a-m2	2b-o	2b-p	2b-m1	2b-m2	2c-o	2c-p	2c-m1	2c-m2
Step1	37.9	36.4	38.1	37.7	36.7	34.2	36.0	35.8	34.8	29.0	30.6	30.2	29.4
Step2	30.6	30.3	31.5	29.7	31.1	31.5	32.9	30.3	32.1	31.9	33.7	30.1	32.9
C3-O4	1.431	1.434	1.433	1.434	1.434	1.444	1.442	1.443	1.443	1.460	1.457	1.458	1.459
C1-C10	3.969	3.959	3.960	3.966	3.947	3.917	3.917	3.930	3.901	3.730	3.725	3.725	3.708

* ortho- is denoted by o-; para- is denoted by p-; meta-1 is denoted by m1; meta-2 is denoted by m2.; a,b and c represents the zero, mono and dimethyl group on the aliphatic segment, respectively.

Table S12: The energy barrier of the first two steps and breaking and forming bond distances for methoxy group on aromatic segment with zero, mono and dimethyl group on the aliphatic segment in N, N-diethylaniline at M06/6-31+G**//B3LYP/6-31+G* level.

	Parent	3a-o	3a-p	3a-m1	3a-m2	3b-o	3b-p	3b-m1	3b-m2	3c-o	3c-p	3c-m1	3c-m2
Step1	37.9	36.1	38.0	35.3	33.6	34.2	36.0	35.6	33.9	29.3	31.0	31.0	29.2
Step2	30.6	31.8	32.5	27.7	25.9	32.0	34.3	26.4	28.3	32.0	35.5	25.4	27.8
C3-O4	1.431	1.430	1.429	1.431	1.432	1.439	1.437	1.440	1.440	1.454	1.464	1.455	1.455
C1-C10	3.969	3.966	3.968	3.978	3.973	3.920	3.925	3.938	3.925	3.756	3.695	3.743	3.7234

* ortho- is denoted by o-; para- is denoted by p-; meta-1 is denoted by m1; meta-2 is denoted by m2.; a,b and c represents the zero, mono and dimethyl group on the aliphatic segment, respectively.

Table S13: The calculated pK_a of derivative of aryl propargyl ether

$-CH_3$	Parent	1a-o	1a-p	1a-m1	1a-m2	1b-o	1b-p	1b-m1	1b-m2	1c-o	1c-p	1c-m1	1c-m2
D	13.5	13.9	14.3	14.1	14.0	14.3	14.6	14.4	14.3	14.8	14.9	14.9	14.7
PX	14.8	15.2	15.6	15.5	15.3	15.6	16.0	15.7	15.6	16.1	16.2	16.2	16.0

CH_3 on phenyl ring; 1a- R_1,R_2= H; 1b- R_1-H, R_2-Me; 1c- R_1-Me, R_2-Me

-Cl	Parent	1a-o	1a-p	1a-m1	1a-m2	1b-o	1b-p	1b-m1	1b-m2	1c-o	1c-p	1c-m1	1c-m2
D	13.5	11.0	12.1	11.6	11.8	11.6	12.6	12.1	12.2	12.0	13.0	12.5	12.7
PX	14.8	12.3	13.5	13.0	13.1	12.9	13.9	13.4	13.6	13.3	14.4	13.8	14.0

Cl on phenyl ring; 1a- R_1,R_2= H; 1b- R_1-H, R_2-Me; 1c- R_1-Me, R_2-Me

$-OCH_3$	Parent	1a-o	1a-p	1a-m1	1a-m2	1b-o	1b-p	1b-m1	1b-m2	1c-o	1c-p	1c-m1	1c-m2
D	13.5	13.3	13.8	13.3	13.5	14.0	14.2	13.7	13.8	14.4	14.6	13.5	14.4
PX	14.8	14.7	15.2	14.6	14.8	15.3	15.6	15.0	15.1	15.7	15.9	14.8	15.7

-OCH3 on phenyl ring; 1a- R_1,R_2= H; 1b- R_1-H, R_2-Me; 1c- R_1-Me, R_2-Me

The definition of pK_a is

$$pK_a = -logK_a$$

and since

$$\Delta G^*_{soln} = -2.303RTlogK_a$$

$$pK_a = \frac{\Delta G^*_{soln}}{2.303RT}$$

where

$$\Delta G^*_{soln} = \Delta G^*_{gas} + \sum_{i=1}^{N\ products} \Delta G^*_{solv,i} - \sum_{j=1}^{N\ reactants} \Delta G^*_{solv,j}$$

where * denotes a standard state of 1M.

There are different thermodynamic cycles are used in the literature, which determinedΔG_{soln}. The main two thermodynamic cycles are Direct (D) and proton exchange (PX), respectively. The development of high-level composite methods, such as Gaussian-n series, has facilitated the calculation of accurate gas-phase energies. The use of continuum solvent model, such as PCM, can deliver the solvation free energies accurate to within 1 kcal/mol for neutral solutes. However, pK_a calculations invariably involve the ionic species, for which errors incurred by CSM are considerably large, around 4 kcal/mol. The reason for ionic species with large error is the CSM do not take account of direct solute-solvent interaction such as hydrogen bonding. In order to improve the accuracy of solution-phase free energies, the thermodynamic cycles are used. The principle reason for using the thermodynamic cycle is that CSM deliver the accurate solvation energies and the low levels of theory are not sufficiently accurate to reproduce accurate total free energies in solution. By using the thermodynamic cycle, one can make use of high-level ab initio calculations in the gas phase to improve the accuracy of the resulting free energies of reaction.

Direct (D) Method

Figure S1: Direct thermodynamic cycle

$$\begin{tikzcd}
HA_{(g)} \arrow[r, "\Delta G_{(g)}"] & H^{+}_{(g)} \arrow[d, "\Delta G_{solv}(H^{+})"] & + & A^{-}_{(g)} \arrow[d, "\Delta G_{solv}(A^{-})"] \\
HA_{(soln)} \arrow[u, "-\Delta G_{solv}(HA)"] \arrow[r, "\Delta G_{(soln)}"'] & H^{+}_{(soln)} & + & A^{-}_{(soln)}
\end{tikzcd}$$

According to the Fig. 1, the ΔG_{soln} is calculated as:

$$\Delta G_{soln} = \Delta G_{(g)} + \Delta G_{(solv)}(A^{-}) + \Delta G_{(solv)}(H^{+}) - \Delta G_{(solv)}(HA)$$

$$\Delta G_{(g)} = G_{(g)}(A^{-}) + G_{(g)}(H^{+}) - G_{(g)}(HA)$$

The direct thermodynamic cycle is commonly used because it is simple. However, this approach is not enough for accuracy because this direct cycle involves two ionic species and their error of solvation energies are much larger. Therefore, the experimental solvation free energy of the proton is required in the direct cycle. The value of $\Delta G_{(solv)}(H^{+})$ had debated in the literatures for some time, but this value generally accepted is -265.9 kcal/mol.

Proton Exchange (PX) Method

Figure S2: Proton exchange thermodynamic cycle. HRef is the reference acid.

$$\begin{tikzcd}
HA_{(g)} & + & Ref^{-}_{(g)} \arrow[r, "\Delta G_{(g)}"] & HRef_{(g)} \arrow[d, "\Delta G_{solv}(HRef)"] & + \\
HA_{(soln)} \arrow[u, "-\Delta G_{solv}(HA)"'] & + & Ref^{-}_{(soln)} \arrow[u, "-\Delta G_{solv}(Ref^{-})"'] \arrow[r, "\Delta G_{(soln)}"'] & HRef_{(soln)} & +
\end{tikzcd}$$

According to the Figure S2, the ΔG_{soln} is calculated as:

$$pKa = \frac{\Delta G_{soln}}{2.303RT} + pK_a(HRef)$$

$$\Delta G_{soln} = \Delta G_{(g)} + \Delta G_{(solv)}(A^-) + \Delta G_{(solv)}(HRef) - \Delta G_{(solv)}(HA) - \Delta G_{(solv)}(Ref^-)$$

$$\Delta G_{(g)} = G_{(g)}(A^-) + G_{(g)}(HRef) - G_{(g)}(HA) - G_{(g)}(Ref^-)$$

The proton exchange thermodynamic cycle is more reliable because the number of anionic species is conserved on both side of equation thereby allowing for cancellation of some of the errors incurred in CMS calculation. In addition, this approach also allows for further cancellation of errors in the gas phase free energy. However, the success of this method depend on the choice of reference acid, with best results expected if HRef is similar to HA in their structure, since the errors incurred by the CSM are likely to be very similar and therefore should mostly cancel from $\Delta\Delta G_{(solv)}$. As consequence, accurate experimental pK_a of reference acid value is required and this may limit the proton exchange method to calculate the pK_a.