

Supporting Information

Projector-based embedding eliminates density functional dependence for QM/MM calculations of reactions in enzymes and solution

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1.1 Comparison of adiabatic mapping and nudged elastic band methods

As there is often an energy barrier associated with reaction, we need to use some method to drive the reaction of interest. Simple geometric reaction coordinates e.g. bond lengths or a combination of distances, but can have limitations for complicated reactions. The validity of the reaction coordinate used to model the reaction ($r = d(\text{C2-O17}) - d(\text{C4-C14})/\text{\AA}$) was tested using NEB methods.^{1, 2} Geometries from one the pathway with chorismate only in the QM region were taken for a NEB calculation. The reactant complex and product complex (fully optimized in QoMMMa without reaction coordinate restraints) were used as the end points for the NEB calculation, with 5 additional geometries created between these two endpoints using linear interpolation of Cartesian Coordinates. The seven images were subsequently subjected to NEB optimization and NEB forces were only applied to the QM atoms using a spring force constant of $k = 150 \text{ kcal/mol \AA}^2$. To obtain a more detailed representation of the pathway near the transition state, a second stage of NEB optimization was run. At this stage, 10 different images were used using the same spring force constant. The second and fifth image of the first stage were used as the edge points for NEB (and thus fixed). These points were chosen as they enclose a region of the profile where the reaction coordinate changes more sharply in adiabatic mapping. Images 3 and 4 from the first stage were also included, with additional images created between them, using linear interpolation. Three additional images were added between images 2 (now edge point) and 3, two between images 3 and 4 and one between 4 and 5 (edge point), giving a total of ten images in the second stage simulation. As before, the edge images were fixed and all the other images were free to move. After the second-stage NEB was converged,

the structures were subjected to a climbing-image NEB¹ procedure to obtain the fully optimized profile.

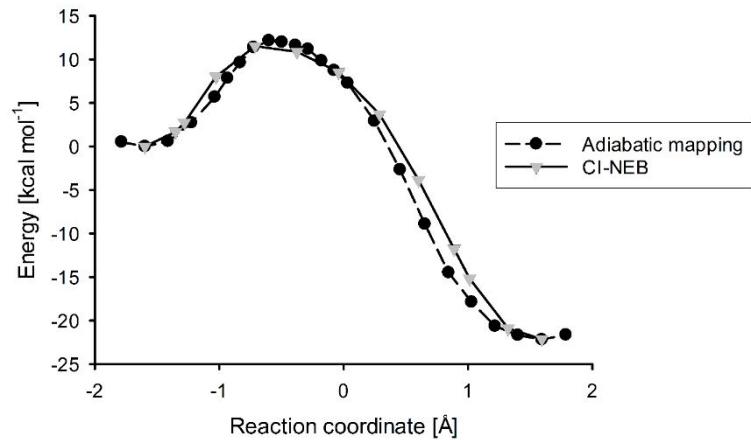


Figure S1. A comparison of potential energy profiles for the conversion of chorismate to prephenate generated using adiabatic mapping and climbing image nudged elastic band (CI-NEB) methods at the B3LYP/6-31G(d)/CHARMM27 level of theory. No reaction coordinate was used in the generation of the CI-NEB profile, the geometric properties were extracted from the images to facilitate comparison. All energies are relative to the reactant ($r = -1.8 \text{ \AA}$).

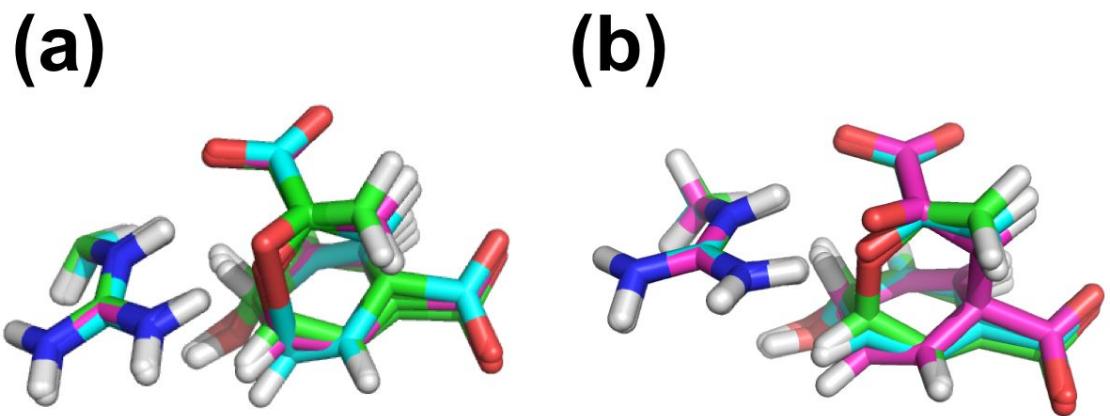


Figure S2. A comparison of the geometry of the arginine sidechain at the reactant (green), TS (cyan) and product (pink) (a) when it is included in QM/MM optimizations at the MM level and (b) when it is included in the QM region in QM/MM calculations at the B3LYP/6-31G(d)/CHARMM27 level of theory. Note that there is very little change in the internal geometry of the arginine sidechain along the path at either level of theory.

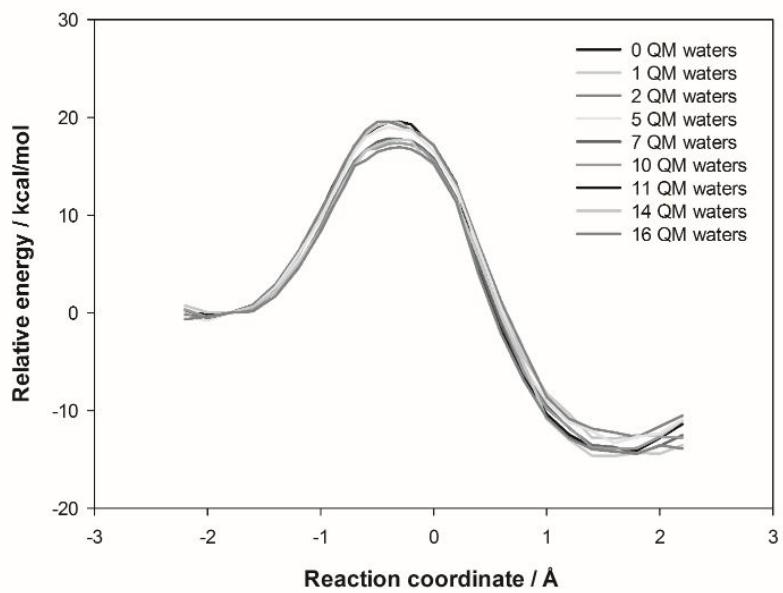


Figure S3. Potential energy profiles for the conversion of chorismate to prephenate in water calculated at the B3LYP/6-31G(d)/CHARMM27 level of theory with chorismate/TS/prephenate and an increasing number of water molecules treated by QM (see Figure 3 for the QM configurations). All energies are relative to the reactant ($r = -1.8 \text{ \AA}$).

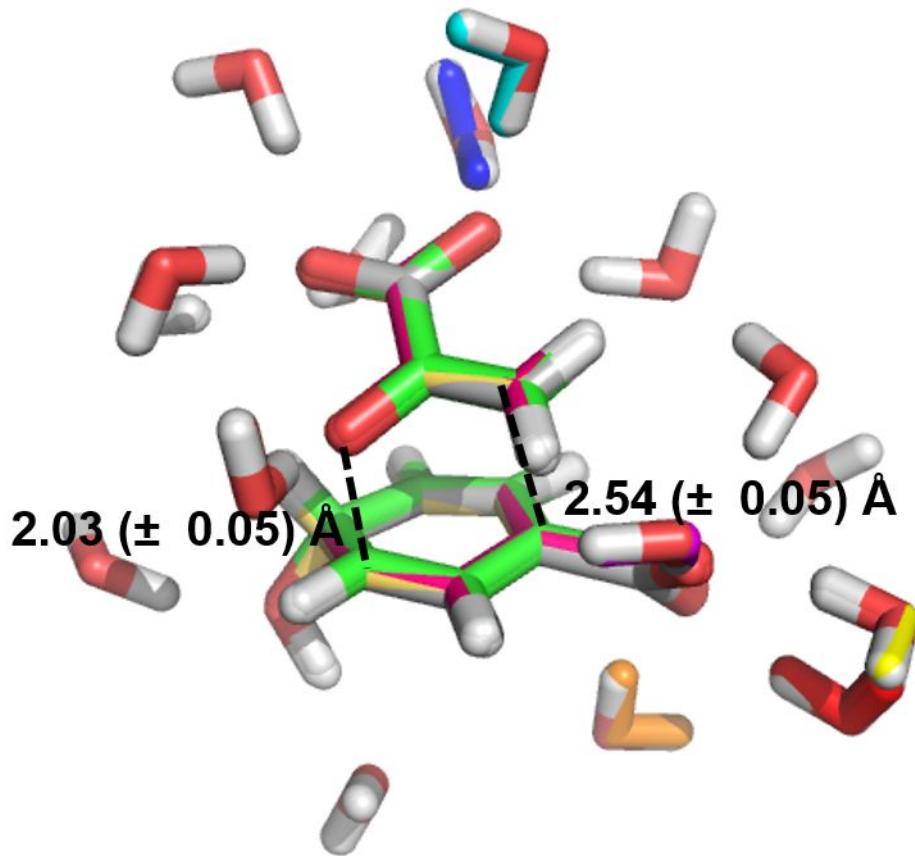


Figure S4. The structure of the approximate TSs for the conversion of chorismate to prephenate in water calculated at the B3LYP/6-31G(d)/CHARMM27 level of theory with chorismate/TS/prephenate and an increasing number of water molecules treated by QM (see Figure 3 for the QM configurations).

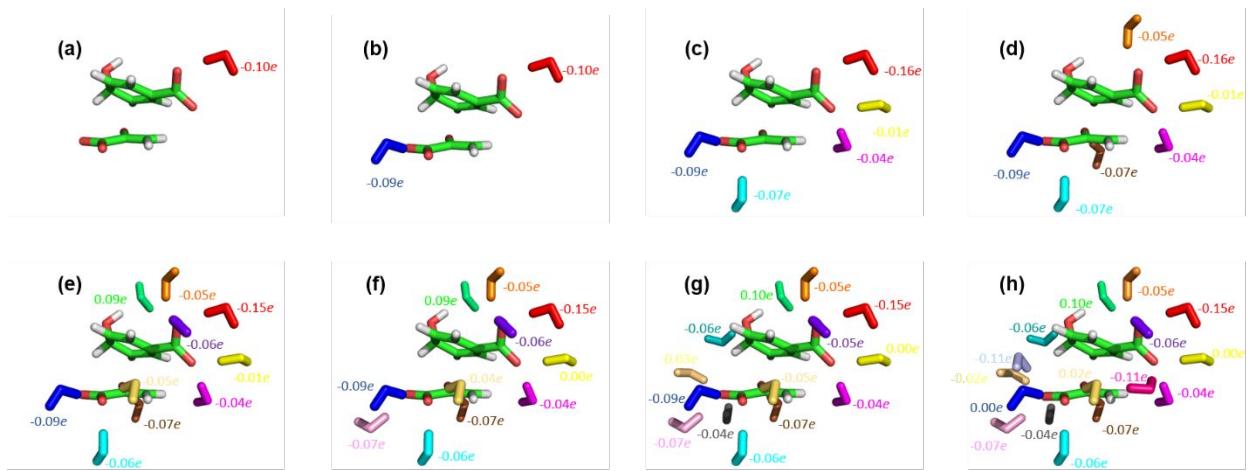


Figure S5. Charge distribution on the water molecules from Mulliken population analysis of the TS in the different water clusters (B3LYP/6-31G(d)/CHARMM27). The overall charge of the system in all models is $-2e$. The water molecules are shown in different colors to aid comparison between different clusters.

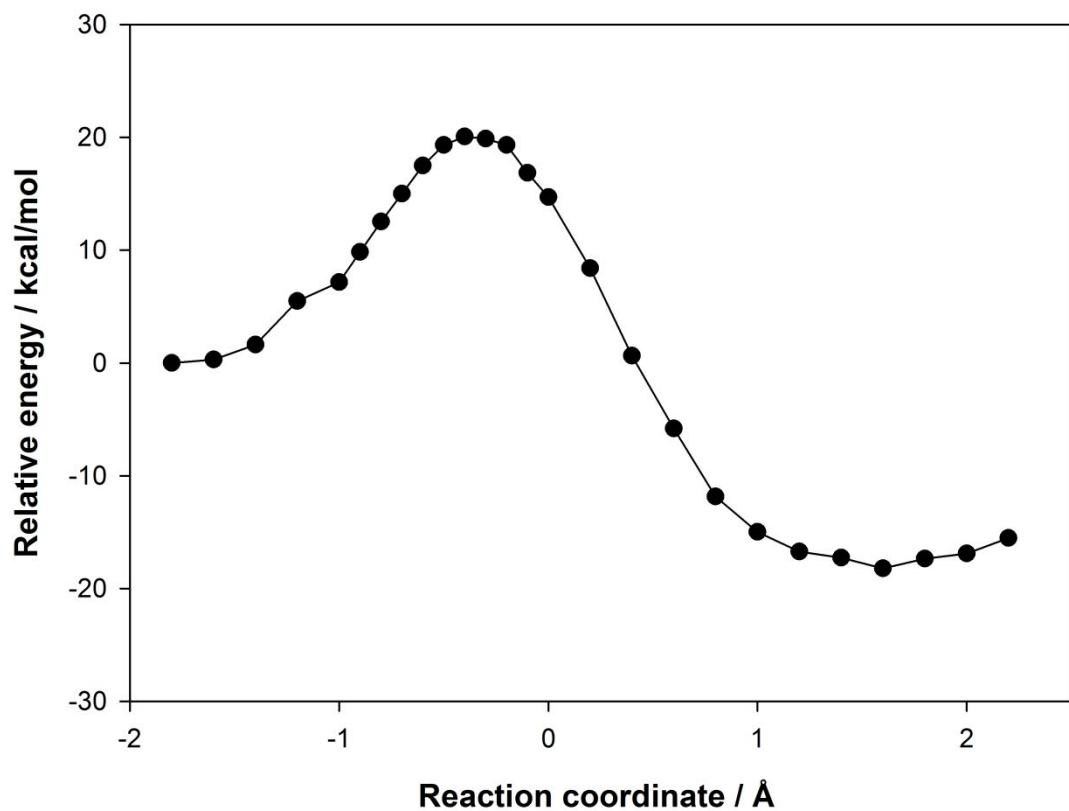


Figure S6. Potential energy profile for the rearrangement of chorismate to prephenate in solution calculated using projector-based embedding of the SCS-MP2 method in B3LYP with 7 of water molecules in sub-system B. A mixed basis set was used for the SCS-MP2 method with oxygen atoms treated by the aug-cc-pVTZ basis and all other atoms by the cc-p-VTZ basis. The geometries are taken from B3LYP/6-31G(d)/CHARMM27 pathway calculations treating chorismate/TS/prephenate and 7 water molecules by QM. All energies are relative to the reactant ($r = -1.8 \text{ \AA}$).

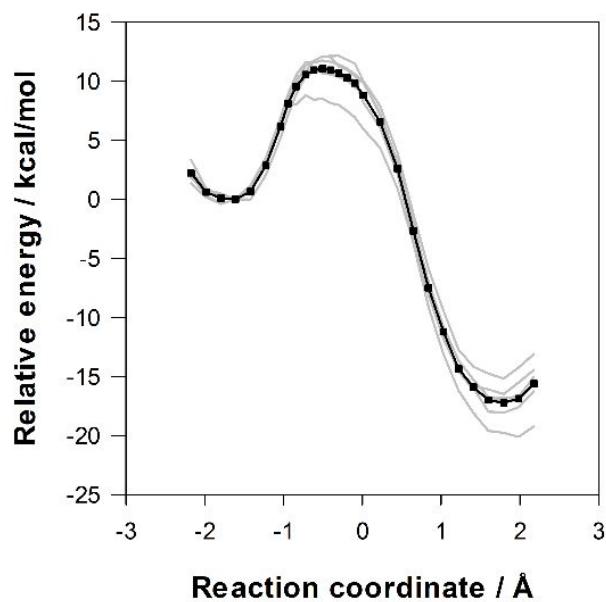


Figure S7. Potential energy profiles for the conversion of chorismate to prephenate generated using adiabatic mapping techniques treating the 24 atoms of chorismate/TS/prephenate by QM in calculations at the B3LYP/6-31G(d)/CHARMM27 level of theory. The individual profiles are shown as grey lines with the average profile shown as black squares. All energies are relative to the reactant ($r = -1.8 \text{ \AA}$).

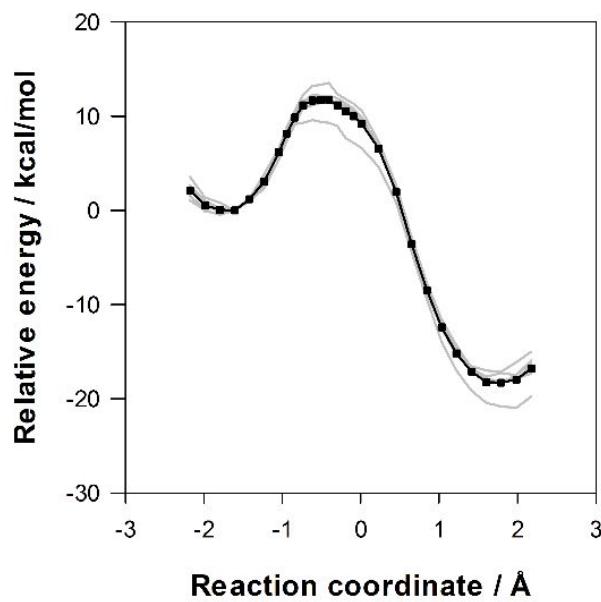


Figure S8. Potential energy profiles for the conversion of chorismate to prephenate generated using adiabatic mapping techniques treating chorismate/TS/prephenate and the sidechain of Arg90 (37 atoms) by QM in calculations at the B3LYP/6-31G(d)/CHARMM27 level of theory. The individual profiles are shown as grey lines with the average profile shown as black squares. All energies are relative to the reactant ($r = -1.8 \text{ \AA}$).

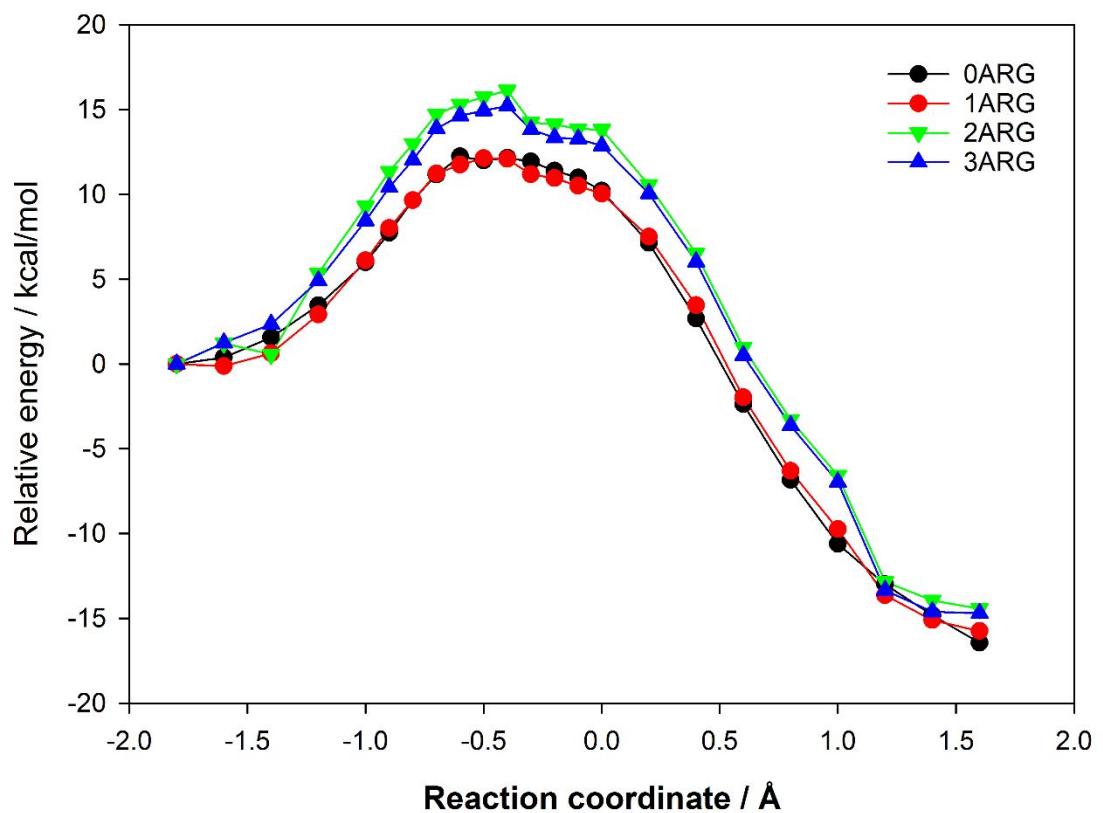


Figure S9. B3LYP/aug-cc-pVDZ//B3LYP/6-31G(d)/CHARMM27 profiles for different QM region sizes (see main text for details). All energies are relative to the reactant ($r = -1.8 \text{ \AA}$).

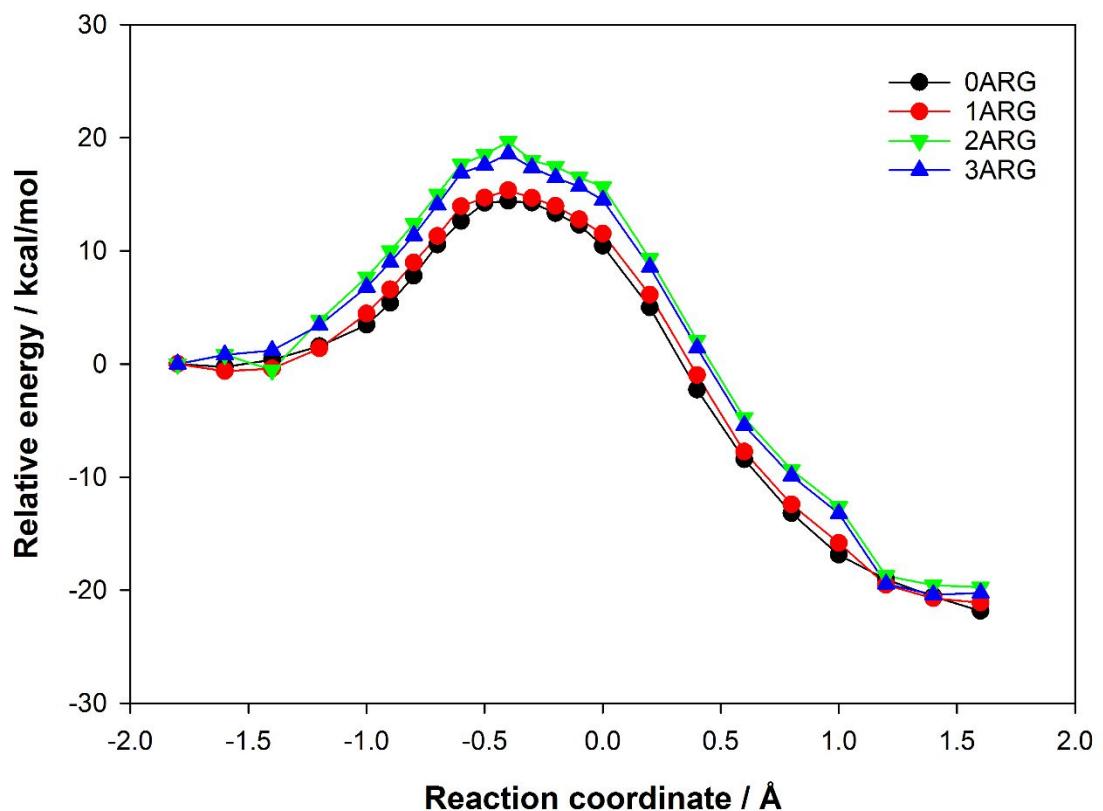


Figure S10. SCS-MP2-in-B3LYP/aug-cc-pVDZ//B3LYP/6-31G(d)/CHARMM27 profiles for different QM region sizes (see main text for details). All energies are relative to the reactant ($r = -1.8 \text{ \AA}$).

Table S1. The CHARMM27 atom types used and partial atomic charges used for chorismate.

Atom	Type	Charge / e
C	CT1	0.693
C1	CT1	0.542
C2	CE1	-0.386
C3	CE1	-0.035
C4	CE1	-0.465
C5	CE1	-0.025
H	HA	-0.139
H1	HA1	0.131
H2	HA1	0.132
H3	HA1	0.087
O	OH1	-0.762
H4	H	0.36
H5	HA	0.006
C6	CC	0.849
O1	OC	-0.817
O2	OC	-0.829
O3	OS	-0.578
C7	CE1	0.267
C8	CC	0.81
C9	CE2	-0.555
H6	HA2	0.147
H7	HA2	0.19
O4	OC	-0.818
O5	OC	-0.805

Table S2. A comparison of partial atomic charges in different sized clusters of chorismate/TS/prephenate and water molecules from Mulliken population analysis³ used in the B3LYP/6-31G(d)/CHARMM27 QM/MM calculations at the reactant (R), transition state (TS) and product (P). All charges are given in atomic units (*e*), see Figure 1 in the main text for atom numbering.

	0 QM water			1 QM water			2 QM waters		
	R	TS	P	R	TS	P	R	TS	P
C1	0.056	-0.100	-0.159	0.056	-0.084	-0.155	0.057	-0.083	-0.156
C2	0.080	0.073	0.077	0.080	0.075	0.073	0.079	0.077	0.073
C3	-0.197	-0.090	-0.095	-0.195	-0.093	-0.092	-0.197	-0.094	-0.091
C4	0.119	0.021	-0.093	0.124	0.026	-0.091	0.124	0.023	-0.093
C5	-0.143	-0.137	-0.140	-0.142	-0.139	-0.138	-0.144	-0.140	-0.138
C6	-0.121	-0.089	-0.091	-0.119	-0.086	-0.091	-0.120	-0.088	-0.092
H7	0.171	0.179	0.159	0.173	0.181	0.160	0.175	0.182	0.160
H8	0.150	0.156	0.146	0.153	0.160	0.149	0.153	0.161	0.151
H9	0.154	0.165	0.156	0.157	0.164	0.157	0.159	0.166	0.158
H10	0.135	0.137	0.124	0.136	0.136	0.126	0.138	0.138	0.128
O11	-0.753	-0.759	-0.778	-0.752	-0.760	-0.777	-0.752	-0.759	-0.776
H12	0.476	0.481	0.484	0.478	0.483	0.484	0.479	0.483	0.484
H13	0.164	0.187	0.166	0.165	0.188	0.168	0.164	0.187	0.167
C14	0.534	0.564	0.611	0.553	0.581	0.630	0.553	0.583	0.630
O15	-0.771	-0.738	-0.741	-0.709	-0.685	-0.681	-0.708	-0.684	-0.679
O16	-0.750	-0.753	-0.775	-0.741	-0.746	-0.770	-0.739	-0.744	-0.769
O17	-0.606	-0.605	-0.523	-0.604	-0.602	-0.521	-0.604	-0.602	-0.517
C18	0.329	0.401	0.428	0.329	0.395	0.428	0.334	0.401	0.436
C19	0.569	0.560	0.556	0.569	0.565	0.559	0.577	0.575	0.571
C20	-0.360	-0.399	-0.340	-0.363	-0.398	-0.342	-0.361	-0.399	-0.343
H21	0.166	0.142	0.146	0.167	0.143	0.147	0.170	0.145	0.148
H22	0.155	0.160	0.168	0.156	0.162	0.171	0.158	0.164	0.174
O23	-0.771	-0.775	-0.750	-0.771	-0.776	-0.752	-0.717	-0.721	-0.701

O24	-0.787	-0.781	-0.736	-0.785	-0.783	-0.737	-0.772	-0.772	-0.731
SUM	-2.000	-2.000	-2.000	-1.886	-1.895	-1.892	-1.793	-1.801	-1.806
O				-0.987	-0.981	-0.987	-0.989	-0.983	-0.985
H				0.448	0.451	0.452	0.449	0.452	0.452
H				0.425	0.425	0.427	0.426	0.426	0.426
O							-0.982	-0.983	-0.981
H							0.430	0.428	0.430
H							0.460	0.461	0.464
SUM				-0.114	-0.105	-0.108	-0.207	-0.199	-0.194

	5 QM waters			7 QM waters			10 QM waters		
	R	TS	P	R	TS	P	R	TS	P
C1	0.054	-0.094	-0.159	0.046	-0.094	-0.156	0.047	-0.095	-0.160
C2	0.079	0.077	0.077	0.083	0.080	0.074	0.086	0.078	0.078
C3	-0.194	-0.093	-0.097	-0.189	-0.092	-0.093	-0.191	-0.097	-0.099
C4	0.124	0.032	-0.091	0.112	0.016	-0.097	0.113	0.028	-0.094
C5	-0.142	-0.137	-0.138	-0.142	-0.139	-0.139	-0.146	-0.140	-0.144
C6	-0.122	-0.094	-0.097	-0.123	-0.094	-0.098	-0.129	-0.104	-0.107
H7	0.177	0.185	0.164	0.180	0.189	0.165	0.177	0.187	0.161
H8	0.159	0.163	0.153	0.164	0.169	0.157	0.162	0.168	0.153
H9	0.162	0.172	0.162	0.162	0.172	0.164	0.163	0.173	0.162
H10	0.141	0.143	0.130	0.143	0.144	0.132	0.147	0.149	0.136
O11	-0.752	-0.757	-0.774	-0.752	-0.759	-0.774	-0.769	-0.775	-0.791
H12	0.479	0.484	0.484	0.482	0.487	0.486	0.441	0.444	0.446
H13	0.166	0.190	0.168	0.170	0.192	0.171	0.164	0.188	0.165
C14	0.539	0.563	0.611	0.547	0.568	0.612	0.545	0.565	0.619
O15	-0.689	-0.664	-0.659	-0.646	-0.624	-0.619	-0.605	-0.584	-0.588
O16	-0.633	-0.636	-0.652	-0.634	-0.635	-0.653	-0.629	-0.630	-0.648
O17	-0.604	-0.609	-0.523	-0.572	-0.555	-0.476	-0.574	-0.567	-0.482

C18	0.336	0.406	0.438	0.337	0.393	0.435	0.334	0.397	0.436
C19	0.581	0.580	0.568	0.583	0.584	0.571	0.579	0.577	0.553
C20	-0.373	-0.406	-0.351	-0.373	-0.407	-0.351	-0.372	-0.413	-0.361
H21	0.172	0.146	0.150	0.173	0.150	0.151	0.176	0.148	0.149
H22	0.152	0.160	0.173	0.158	0.169	0.179	0.158	0.166	0.176
O23	-0.672	-0.677	-0.658	-0.672	-0.677	-0.660	-0.623	-0.628	-0.607
O24	-0.766	-0.765	-0.711	-0.762	-0.762	-0.718	-0.756	-0.756	-0.703
SUM	-1.624	-1.632	-1.634	-1.527	-1.524	-1.537	-1.504	-1.522	-1.552
O	-0.891	-0.886	-0.888	-0.891	-0.885	-0.886	-0.889	-0.885	-0.886
H	0.426	0.426	0.427	0.425	0.425	0.427	0.427	0.427	0.428
H	0.447	0.452	0.452	0.450	0.452	0.452	0.450	0.453	0.452
O	-0.929	-0.934	-0.937	-0.929	-0.934	-0.937	-0.929	-0.935	-0.937
H	0.437	0.438	0.436	0.437	0.437	0.435	0.437	0.438	0.436
H	0.455	0.454	0.452	0.456	0.456	0.454	0.456	0.455	0.453
O	-1.009	-1.005	-1.007	-0.986	-0.994	-0.976	-0.985	-0.997	-0.971
H	0.419	0.423	0.423	0.458	0.460	0.454	0.458	0.460	0.452
H	0.425	0.424	0.423	0.476	0.471	0.473	0.475	0.470	0.473
O	-0.980	-0.980	-0.974	-1.008	-1.005	-1.009	-1.008	-1.001	-1.006
H	0.473	0.474	0.477	0.421	0.423	0.423	0.422	0.425	0.424
H	0.443	0.438	0.435	0.425	0.424	0.424	0.428	0.427	0.427
O	-0.985	-0.986	-0.982	-0.926	-0.919	-0.923	-0.869	-0.865	-0.859
H	0.430	0.430	0.430	0.426	0.421	0.424	0.475	0.478	0.478
H	0.463	0.463	0.467	0.446	0.449	0.449	0.481	0.481	0.473
O				-0.979	-0.978	-0.973	-0.928	-0.924	-0.930
H				0.474	0.474	0.476	0.427	0.422	0.427
H				0.443	0.438	0.435	0.446	0.451	0.452
O				-0.985	-0.984	-0.982	-0.964	-0.957	-0.955
H				0.430	0.429	0.430	0.471	0.472	0.473
H				0.464	0.464	0.467	0.433	0.429	0.427

O							-0.978	-0.977	-0.968
H							0.473	0.474	0.475
H							0.443	0.438	0.433
O							-0.982	-0.985	-0.981
H							0.430	0.430	0.431
H							0.465	0.464	0.467
O							-0.974	-0.973	-0.967
H							0.469	0.472	0.475
H							0.444	0.454	0.456
SUM	-0.376	-0.368	-0.366	-0.473	-0.476	-0.463	-0.496	-0.478	-0.448

	11 QM waters			14 QM waters			16 QM waters		
	R	TS	P	R	TS	P	R	TS	P
C1	0.046	-0.103	-0.158	0.048	-0.105	-0.160	0.048	-0.103	-0.155
C2	0.086	0.078	0.077	0.079	0.073	0.073	0.076	0.069	0.070
C3	-0.191	-0.090	-0.095	-0.193	-0.092	-0.100	-0.194	-0.095	-0.097
C4	0.112	0.019	-0.096	0.111	0.019	-0.093	0.113	0.022	-0.098
C5	-0.148	-0.141	-0.146	-0.147	-0.137	-0.138	-0.144	-0.135	-0.139
C6	-0.129	-0.105	-0.109	-0.130	-0.106	-0.112	-0.136	-0.108	-0.111
H7	0.178	0.187	0.161	0.181	0.190	0.162	0.182	0.190	0.161
H8	0.162	0.168	0.153	0.164	0.170	0.156	0.166	0.173	0.155
H9	0.164	0.175	0.164	0.168	0.178	0.166	0.166	0.175	0.163
H10	0.147	0.150	0.137	0.149	0.150	0.137	0.148	0.148	0.135
O11	-0.770	-0.777	-0.791	-0.725	-0.735	-0.749	-0.724	-0.734	-0.747
H12	0.442	0.444	0.446	0.445	0.447	0.451	0.445	0.447	0.452
H13	0.164	0.188	0.164	0.162	0.184	0.162	0.160	0.183	0.161
C14	0.545	0.570	0.618	0.546	0.571	0.620	0.551	0.574	0.622
O15	-0.605	-0.585	-0.587	-0.604	-0.584	-0.588	-0.602	-0.581	-0.584
O16	-0.629	-0.629	-0.649	-0.628	-0.629	-0.648	-0.598	-0.597	-0.611

O17	-0.575	-0.563	-0.473	-0.574	-0.560	-0.460	-0.575	-0.563	-0.461
C18	0.342	0.409	0.439	0.342	0.410	0.441	0.348	0.417	0.441
C19	0.589	0.578	0.558	0.592	0.576	0.557	0.601	0.586	0.570
C20	-0.371	-0.415	-0.358	-0.369	-0.416	-0.364	-0.374	-0.423	-0.363
H21	0.177	0.148	0.147	0.178	0.149	0.148	0.178	0.152	0.152
H22	0.160	0.168	0.178	0.162	0.170	0.179	0.163	0.171	0.182
O23	-0.626	-0.626	-0.606	-0.627	-0.626	-0.607	-0.628	-0.629	-0.612
O24	-0.717	-0.709	-0.669	-0.649	-0.638	-0.609	-0.623	-0.611	-0.585
SUM	-1.446	-1.463	-1.495	-1.319	-1.340	-1.377	-1.253	-1.271	-1.298
O	-0.888	-0.885	-0.886	-0.958	-0.950	-0.948	-0.958	-0.949	-0.949
H	0.427	0.427	0.428	0.454	0.456	0.457	0.454	0.457	0.456
H	0.450	0.453	0.452	0.435	0.433	0.431	0.436	0.432	0.431
O	-0.929	-0.934	-0.936	-0.888	-0.885	-0.885	-0.892	-0.888	-0.888
H	0.437	0.438	0.436	0.427	0.427	0.427	0.432	0.432	0.433
H	0.456	0.456	0.454	0.451	0.453	0.453	0.450	0.452	0.452
O	-0.986	-0.997	-0.975	-0.927	-0.932	-0.935	-0.924	-0.931	-0.934
H	0.458	0.461	0.455	0.437	0.438	0.436	0.437	0.438	0.435
H	0.476	0.470	0.474	0.456	0.455	0.454	0.456	0.455	0.454
O	-1.009	-1.002	-1.007	-0.952	-0.952	-0.944	-0.955	-0.955	-0.951
H	0.422	0.425	0.424	0.486	0.486	0.483	0.486	0.486	0.483
H	0.428	0.428	0.428	0.425	0.425	0.424	0.426	0.427	0.430
O	-0.869	-0.865	-0.860	-0.990	-1.001	-0.976	-0.982	-0.990	-0.995
H	0.475	0.479	0.478	0.459	0.462	0.452	0.425	0.434	0.437
H	0.481	0.481	0.473	0.475	0.470	0.475	0.437	0.447	0.444
O	-0.928	-0.925	-0.929	-1.008	-1.002	-1.006	-0.990	-1.001	-0.979
H	0.427	0.423	0.426	0.422	0.425	0.424	0.459	0.462	0.455
H	0.446	0.451	0.451	0.428	0.427	0.427	0.475	0.470	0.474
O	-0.964	-0.957	-0.954	-0.867	-0.862	-0.857	-1.008	-1.001	-1.006
H	0.471	0.472	0.473	0.477	0.480	0.481	0.422	0.426	0.425

H	0.433	0.429	0.427	0.482	0.482	0.474	0.429	0.428	0.428
O	-0.973	-0.976	-0.975	-0.928	-0.926	-0.931	-0.866	-0.863	-0.855
H	0.431	0.434	0.434	0.427	0.423	0.427	0.477	0.481	0.478
H	0.476	0.475	0.479	0.447	0.451	0.451	0.482	0.482	0.473
O	-0.978	-0.976	-0.970	-0.963	-0.957	-0.953	-0.928	-0.925	-0.933
H	0.475	0.475	0.476	0.472	0.473	0.472	0.427	0.423	0.428
H	0.443	0.438	0.435	0.433	0.429	0.426	0.447	0.452	0.453
O	-0.983	-0.986	-0.981	-0.957	-0.954	-0.943	-0.966	-0.960	-0.957
H	0.433	0.432	0.433	0.475	0.474	0.476	0.473	0.473	0.473
H	0.466	0.465	0.468	0.455	0.449	0.437	0.432	0.428	0.425
O	-0.972	-0.972	-0.965	-0.973	-0.978	-0.976	-0.953	-0.949	-0.937
H	0.470	0.473	0.476	0.433	0.435	0.435	0.476	0.475	0.477
H	0.444	0.454	0.455	0.477	0.476	0.481	0.454	0.450	0.440
O				-0.976	-0.974	-0.969	-0.922	-0.923	-0.919
H				0.475	0.475	0.476	0.414	0.411	0.404
H				0.442	0.438	0.434	0.402	0.403	0.410
O				-0.982	-0.984	-0.982	-0.975	-0.980	-0.980
H				0.433	0.433	0.433	0.432	0.434	0.435
H				0.467	0.466	0.469	0.479	0.478	0.482
O				-0.974	-0.973	-0.965	-0.974	-0.973	-0.965
H				0.471	0.473	0.475	0.475	0.476	0.474
H				0.444	0.454	0.456	0.441	0.437	0.434
O							-0.914	-0.917	-0.915
H							0.439	0.438	0.439
H							0.473	0.474	0.476
O							-0.913	-0.922	-0.920
H							0.479	0.480	0.481
H							0.448	0.458	0.461

SUM	-0.554	-0.537	-0.505	-0.681	-0.660	-0.623	-0.747	-0.729	-0.702
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Table S3. A comparison of distances involved in hydrogen bonds between Arg90 and chorismate at the reactant (R), transition state (TS) and product (P) with chorismate/TS/prephenate only as the QM region and chorismate/TS/prephenate and Arg90 treated by QM. See Figure 1 in the main text for atom numbering.

		R		TS		P	
		$d(\text{HH11} - \text{O17}) / \text{\AA}$		$d(\text{HH11} - \text{O17}) / \text{\AA}$		$d(\text{HH11} - \text{O17}) / \text{\AA}$	
		Arg90 MM	Arg90 QM	Arg90 MM	Arg90 QM	Arg90 MM	Arg90 QM
1		1.72	1.90	1.69	1.78	1.74	1.90
2		1.74	1.91	1.68	1.78	1.7	1.86
3		1.78	1.89	1.70	1.78	1.75	1.87
4		1.79	1.95	1.75	1.85	1.77	1.96
5		1.77	1.85	1.69	1.74	1.77	1.87
6		1.74	1.91	1.68	1.8	1.75	1.89
AVERAGE		1.76	1.90	1.70	1.79	1.75	1.89
		(0.03)	(0.03)	(0.03)	(0.04)	(0.03)	(0.04)
		R		TS		P	
		$d(\text{HE1} - \text{O24}) / \text{\AA}$		$d(\text{HE1} - \text{O24}) / \text{\AA}$		$d(\text{HE1} - \text{O24}) / \text{\AA}$	
		Arg90 MM	Arg90 QM	Arg90 MM	Arg90 QM	Arg90 MM	Arg90 QM
1		1.87	1.93	1.96	1.99	2.00	2.07
2		1.81	1.84	1.9	1.9	1.85	1.96
3		1.99	1.93	2.11	2.05	2.12	2.07
4		1.95	2.01	2.06	2.08	2.1	2.17
5		1.8	1.83	1.89	1.88	1.86	1.92
6		1.81	1.87	1.86	1.90	1.87	1.98
AVERAGE		1.87	1.90	1.96	1.97	1.97	2.03
		(0.08)	(0.07)	(0.10)	(0.09)	(0.12)	(0.09)

Table S4. A comparison of (average) partial atomic charges of the oxygen atoms of chorismate from Mulliken population analysis³ used in the B3LYP/6-31G(d)/CHARMM27 QM/MM calculations at the reactant (R), transition state (TS) and product (P) with chorismate/TS/prephenate only as the QM region and chorismate/TS/prephenate and Arg90 treated by QM. All charges are given in atomic units (*e*), see Figure 1 in the main text for atom numbering.

ATOM NAME	Mulliken Population B3LYP/6-31G(d)/CHARMM27								
	CHO	R CHO + Arg90	Diff	CHO	TS CHO + Arg90	Diff	CHO	P CHO + Arg90	Diff
O11	-0.73	-0.73	0.00	-0.74	-0.73	0.00	-0.76	-0.73	0.00
O15	-0.73	-0.74	-0.01	-0.72	-0.74	-0.01	-0.74	-0.74	-0.01
O16	-0.67	-0.66	0.00	-0.66	-0.65	0.01	-0.65	-0.65	0.01
O17	-0.64	-0.59	0.05	-0.67	-0.59	0.07	-0.55	-0.59	0.07
O23	-0.77	-0.75	0.01	-0.79	-0.77	0.02	-0.75	-0.77	0.02
O24	-0.72	-0.67	0.05	-0.72	-0.68	0.04	-0.69	-0.68	0.04

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