

Supporting Information

Mechanistic Study of ATP Hydrolysis Reaction in Dynein Motor Protein

Rabindra Nath Manna, Mandira Dutta, and Biman Jana*

School of Chemical Sciences, Indian Association for the Cultivation of Science, Jadavpur,
Kolkata 700032, India

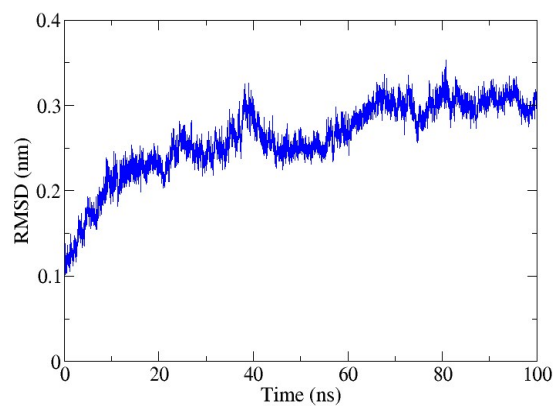


Figure S1. Time evolution of root means square deviation (RMSD) of protein backbone obtained from classical MD simulations.

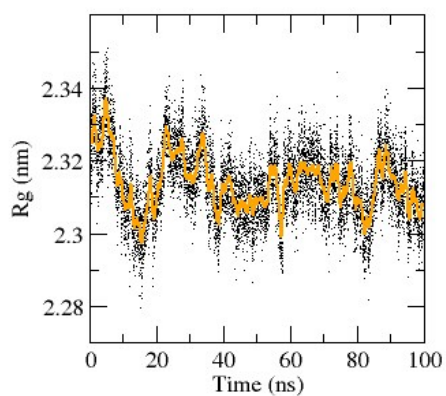
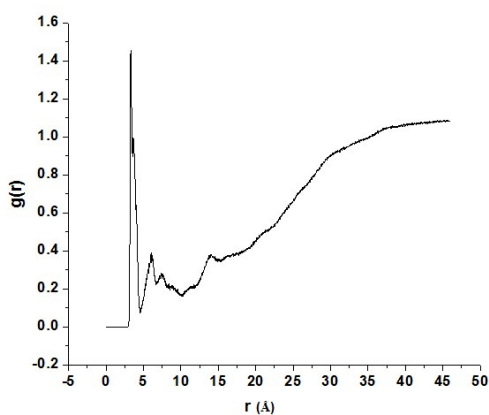
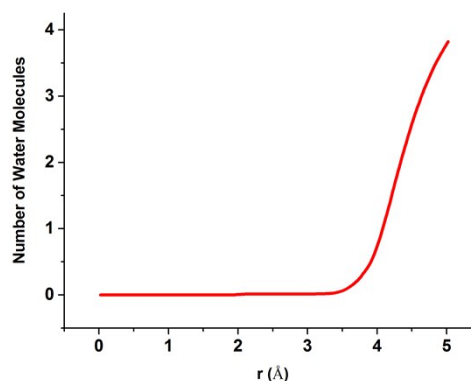


Figure S2: Time evolution of the radius of gyration (R_g) of protein obtained from the classical MD simulations.

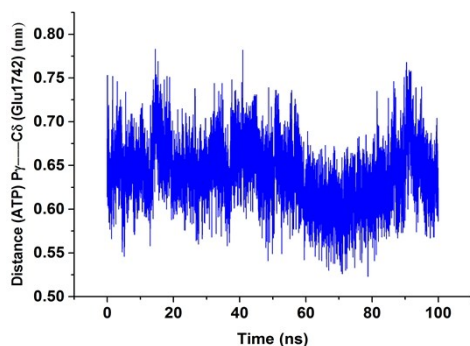


(A)

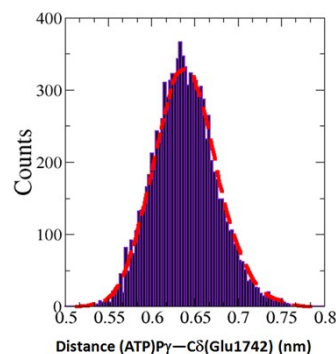


(B)

Figure S3. (A) A plot of radial distribution function $g(r)$ between terminal phosphorous (P_γ) and O_w atom of water molecules obtained from classical MD simulations. (B) A plot of coordination number of water molecules along the distance between Mg^{2+} and O_w atom of water molecules are obtained from 100ns MD simulations.



(A)



(B)

Figure S4. (A) Time evolution of distance between P_γ atom of ATP and C_δ atom of Glu1742 obtained from the classical MD simulations. (B) Histogram plot of interatomic distance between P_γ atom of ATP and C_δ atom of Glu1742.

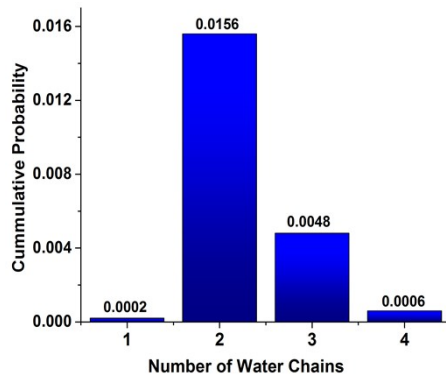
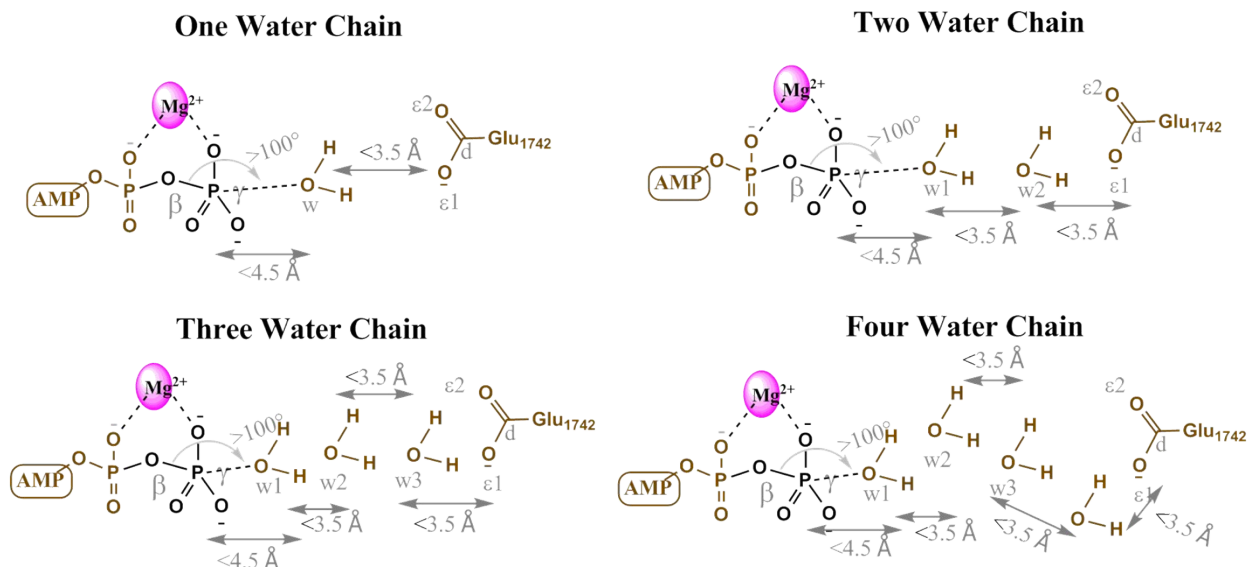


Figure S5. Cumulative probability of water chains with applied conditions is displayed. The applied conditions for the water chains are described in below.

Water chain Criteria:



Scheme S1. Representations of different types of water chains between γ -phosphate of ATP molecule and Glu1742 are proposed.

The existence of a **one water chain** is counted, if (1) the distance between oxygen atom of lytic water and γ -phosphate (P_γ) atom of ATP molecule is less than 4.5 Å. Criteria (2) is an attack angle ($\angle O_w-P_\gamma-O_\beta$) by the lytic water on γ -phosphate moiety should be greater than 100 degrees. Criteria (3) is the distance of the lytic water oxygen to an oxygen atom of carboxylic moiety of the Glu1742 is less than 3.5 Å. (Figure S5)

Furthermore, **two-water chains** are counted, if conditions of (1) and (2) for the one water chain were satisfied. In addition, (3) the distance between an attacking water oxygen atom and second water oxygen atom should be less than 3.5 Å. Next, (4) the oxygen atom of the second water molecule to any oxygen atom of the Glu1742 carboxylate group is less than 3.5 Å.

Similarly, **three water chains** are considered, if conditions of (1), (2) and (3) for the two water chains are fulfilled. Additionally, (4) the distance between a second water oxygen atom and third water oxygen atom was less than 3.5 Å. (5) The distance of the third water oxygen was less than 3.5 Å to an oxygen atom of carboxylic moiety of the Glu1742.

Four water chains are assumed if conditions of (1), (2), (3) and (4) for three water chains were satisfied. Furthermore, (5) the distance between a third water oxygen atom and fourth water oxygen atom was < 3.5 Å. Along with (6) the distance of the fourth water oxygen was <3.5 Å to any oxygen atom of the carboxylic moiety of the Glu1742.

Herein, **Cumulative probability** is defined as a ratio a particular type of water chains and total numbers of possible water chains are present in between γ -phosphate of ATP and Glu1742 along with satisfied applied aforementioned water chain criteria.

Table S1. Average key distances (Å), angle (degree), relative potential energy (in kcal/mol) for all the stationary points of the model A for the ATP hydrolysis reaction in dynein motor obtained at the B3LYP/6-31+G(d,p)/OPLS level of theory.

Model A	ES	TSa	EP
d(O _{β} (ATP) - P _{γ} (ATP))	1.65	1.74	3.35
d(O _{ω1} (H ₂ O) - P _{γ} (ATP))	3.14	2.16	1.60
d(O _{ω1} (H ₂ O) - H ₁ (H ₂ O))	0.99	1.93	3.34
d(H ₁ (H ₂ O) - O _{γ1} (ATP))	2.67	0.98	1.02
d(H ₂ (H ₂ O) - O _{ϵ} (Glu1742))	1.80	1.96	1.79
d(Mg ²⁺ - O _{α2} (ATP))	1.90	1.98	1.98
d(Mg ²⁺ - O _{β2} (ATP))	1.99	1.94	2.04
d(Mg ²⁺ - O _{γ2} (ATP))	1.87	1.90	2.03
d(Mg ²⁺ - O _{β} (ATP))	3.03	3.01	2.04
d(H _n (Asn1792) - O _{γ3} (ATP))	2.29	2.38	2.06
d(H _r (Arg2109) - O _{ω1} (H ₂ O))	1.86	2.08	2.96
< (O _{ω1} (H ₂ O) - P _{γ} (ATP) - O _{β} (ATP))	168.18	165.84	172.03
ΔG	0	39.6	1.4

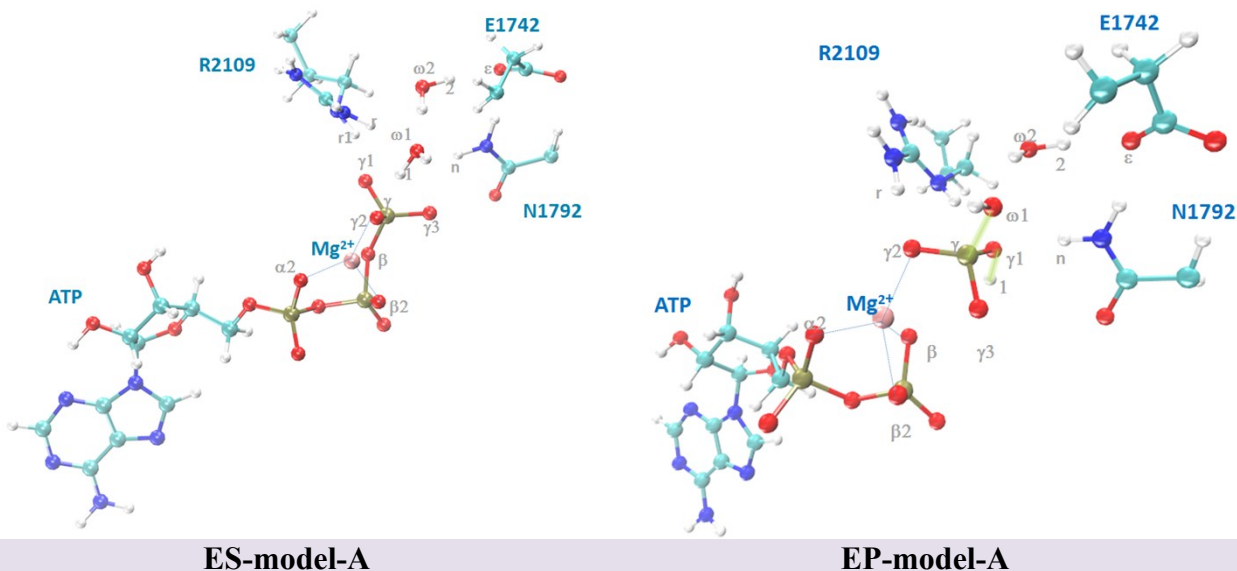


Figure S6. Enzyme-substrate (ES) and enzyme product (EP) structures for the model A are shown. Atom colors: C (cyan), N (blue), O (red), H (white), P (tan) and Mg^{2+} (pink).

Table S2. Average key distances (Å), angle (degree) and relative potential energy (in kcal/mol) for all the stationary points of model B for the ATP hydrolysis reaction in dynein motor obtained at the B3LYP/6-31+G(d,p)/OPLS level of theory.

Model B	ES	TSb	EP
$d(O_{\beta}(ATP) - P_{\gamma}(ATP))$	1.79	2.29	3.25
$d(O_{\omega 1}(H_2O) - P_{\gamma}(ATP))$	2.80	1.76	1.60
$d(O_{\omega 1}(H_2O) - H_1(H_2O))$	0.97	1.24	1.91
$d(O_{\omega 2}(H_2O) - H_1(H_2O))$	1.96	1.16	0.97
$d(O_{\omega 2}(H_2O) - H_2(H_2O))$	0.98	1.11	2.82
$d(H_2(H_2O) - O_{\gamma 2}(ATP))$	1.79	1.30	0.98
$d(H_2(H_2O) - O_{\epsilon}(E1742))$	4.66	4.03	4.76
$d(Mg^{2+} - O_{\alpha 2}(ATP))$	1.91	1.92	1.94
$d(Mg^{2+} - O_{\gamma 2}(ATP))$	1.91	1.95	1.98
$d(Mg^{2+} - O_{\beta 2}(ATP))$	2.03	2.03	2.08
$d(Mg^{2+} - O_{\beta}(ATP))$	2.35	2.07	2.08
$d(H_n(N1792) - O_{\gamma 3}(ATP))$	1.66	1.54	1.64
$< (O_{\omega 1}(H_2O) - P_{\gamma}(ATP) - O_{\beta}(ATP))$	177.79	174.46	168.48
ΔG	0	26.4	-2.5

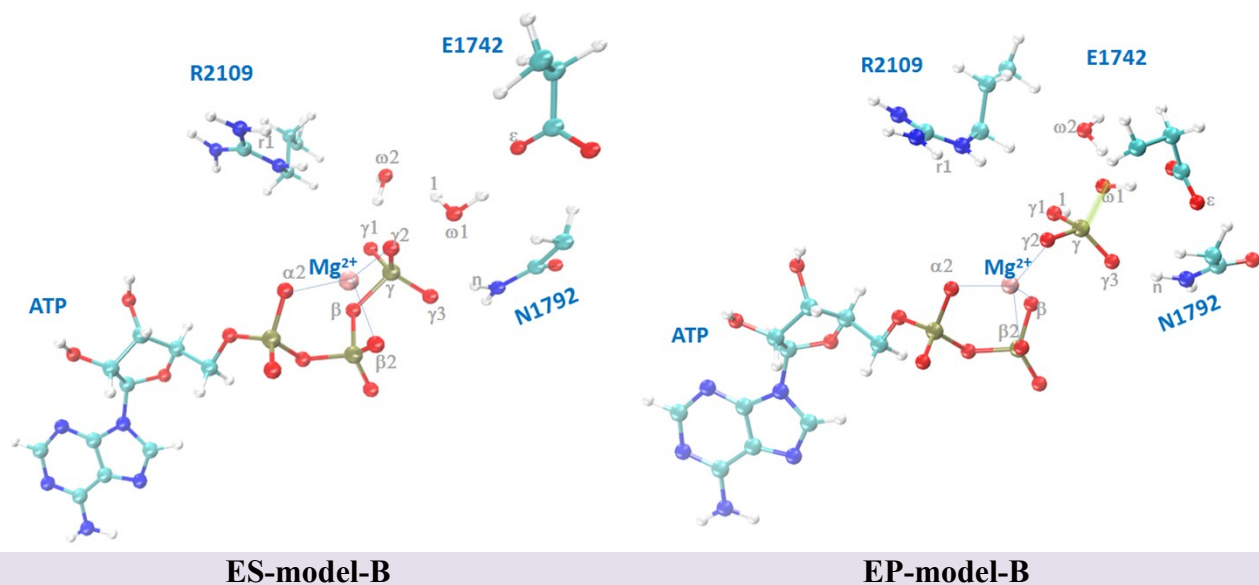


Figure S7. Enzyme-substrate (ES) and enzyme product (EP) structures for the model B are presented. Atom colors: C (cyan), N (blue), O (red), H (white), P (tan) and Mg^{2+} (pink).

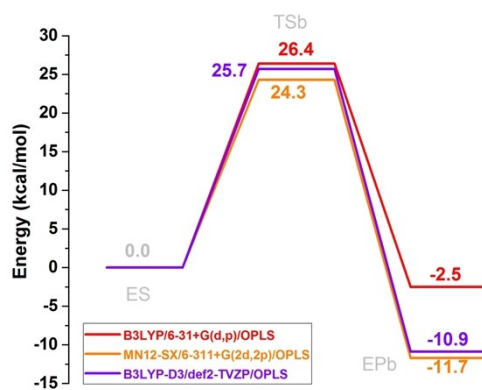
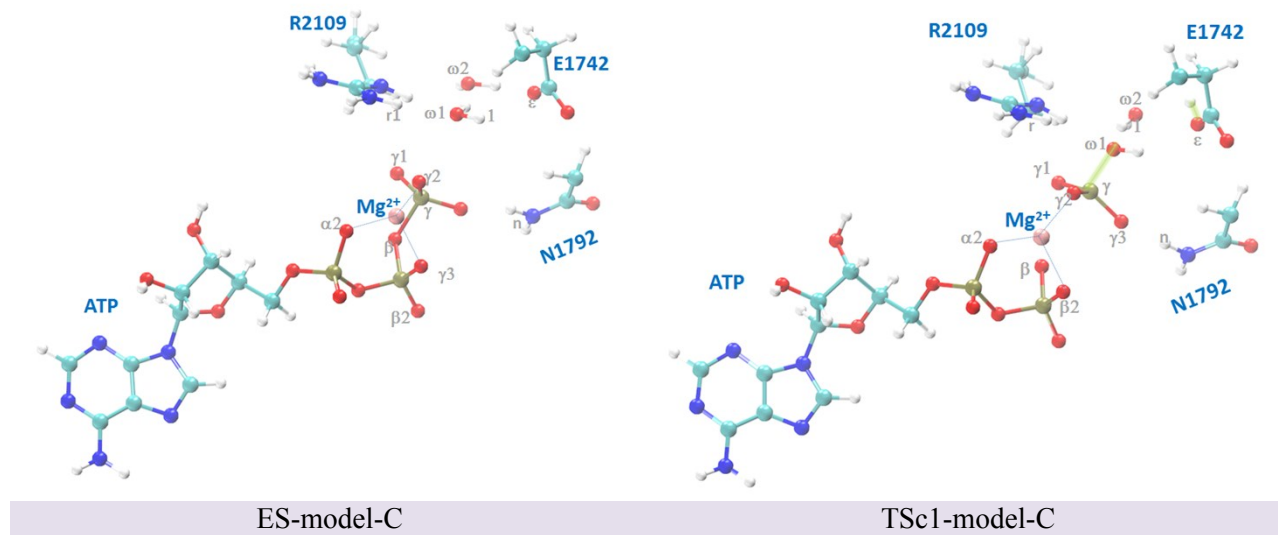


Figure S8. Potential energy profile (in kcal/mol) for the model B obtained at the three different levels of theories.

Table S3. Average key distances (Å), angle (degree) and relative potential energy (in kcal/mol) for all the stationary points of model C for the ATP hydrolysis reaction obtained at the B3LYP/6-31+G(d,p)/OPLS level of theory.

Model C	ES	TSc1	INT	TSc2	EP
d(O _β (ATP) - P _γ (ATP))	1.75	2.23	3.10	3.43	3.61
d(O _{ω1} (H ₂ O) - P _γ (ATP))	3.23	2.26	1.66	1.63	1.59
d(O _{ω1} (H ₂ O) - H ₁ (H ₂ O))	0.98	0.99	1.82	3.91	3.26
d(O _{ω2} (H ₂ O) - H ₁ (H ₂ O))	1.85	1.66	0.99	0.98	0.97
d(O _{ω2} (H ₂ O) - H ₂ (H ₂ O))	0.98	1.01	2.16	1.11	1.01
d(H ₂ (H ₂ O) - O _ε (E1742))	1.87	1.51	0.99	1.34	1.59
d(H ₃ (H ₂ O) - O _{ω2} (H ₂ O))	0.97	0.96	0.98	1.14	1.52
d(H ₃ (H ₂ O) - O _{γ2} (ATP))	5.02	4.80	4.44	1.30	1.02
d(Mg ²⁺ - O _{α2} (ATP))	1.86	1.87	1.90	1.93	1.90
d(Mg ²⁺ - O _{β2} (ATP))	1.99	2.02	2.08	2.06	2.05
d(Mg ²⁺ - O _{γ2} (ATP))	1.86	1.92	1.96	1.94	1.88
d(Mg ²⁺ - O _β (ATP))	2.61	2.13	2.02	2.00	1.98
d(H _n (N1792) - O _{γ3} (ATP))	1.93	1.88	1.85	1.72	1.72
d(H _r (R2109) - O _{ω1} (H ₂ O))	3.09	3.47	3.43	3.93	3.75
< (O _{ω1} (H ₂ O) - P _γ (ATP) - O _β (ATP))	163.02	170.3	175.11	163.7	163.86
ΔG	0	21.1	-14.9	-8.8	-18.6



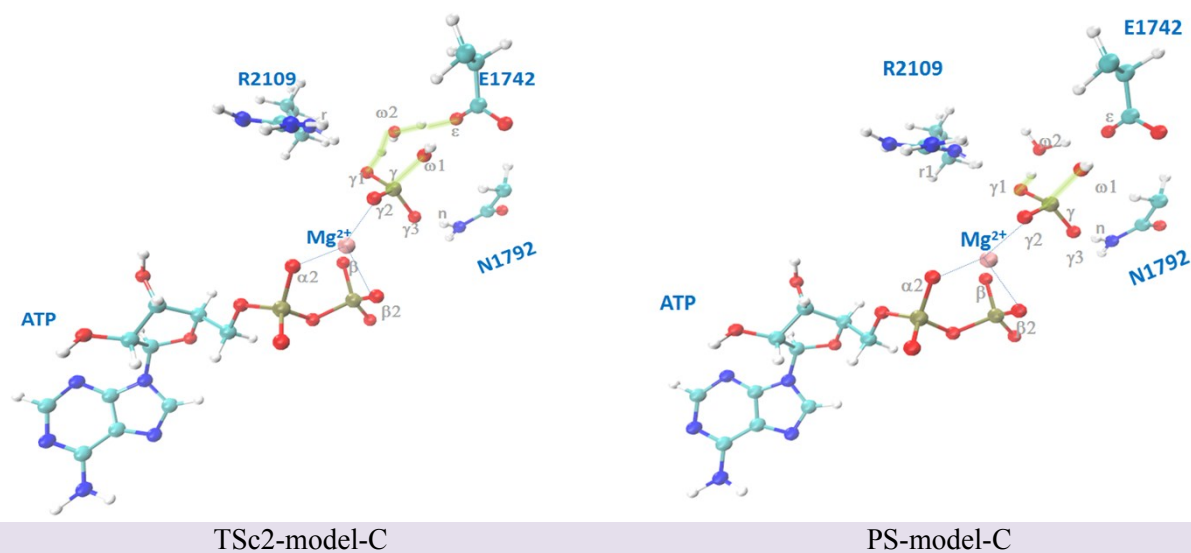


Figure S9. Enzyme-substrate (ES), enzyme-intermediate (INT), transition state (TSC1 and TSC2) and enzyme product (EP) structures for the model C are presented.

Table S4. Average key distances (Å), angle (degree) and relative potential energy (in kcal/mol) for all the stationary points for the large QM region of model C for the ATP hydrolysis reaction obtained at the B3LYP/6-31+G(d,p)/OPLS level of theory.

Model C	ES	TSc1	INT	TSc2	EP
$d(O_{\beta}(ATP) - P_{\gamma}(ATP))$	1.58	2.39	3.05	3.14	3.19
$d(O_{\omega 1}(H_2O) - P_{\gamma}(ATP))$	2.94	1.85	1.62	1.68	1.63
$d(O_{\omega 1}(H_2O) - H_1(H_2O))$	0.98	1.14	1.79	2.27	2.28
$d(O_{\omega 2}(H_2O) - H_1(H_2O))$	1.86	1.28	0.98	0.97	0.97
$d(O_{\omega 2}(H_2O) - H_2(H_2O))$	0.99	1.10	1.75	1.18	1.00
$d(H_2(H_2O) - O_{\epsilon}(E1742))$	1.52	1.32	1.01	1.26	1.98
$d(H_3(H_2O) - O_{\omega 2}(H_2O))$	0.99	0.97	0.99	1.12	1.70
$d(H_3(H_2O) - O_{\gamma 3}(ATP))$	4.84	4.30	1.96	1.33	1.00
$d(Mg^{2+} - O_{\alpha 2}(ATP))$	2.07	2.07	2.07	2.09	2.08
$d(Mg^{2+} - O_{\beta 2}(ATP))$	2.03	1.99	1.98	1.98	1.98
$d(Mg^{2+} - O_{\gamma 2}(ATP))$	1.99	2.07	1.99	1.99	2.01
$d(Mg^{2+} - O_{\beta}(ATP))$	3.29	3.26	3.47	3.52	3.53
$d(Mg^{2+} - Od1(Asp1741))$	2.19	2.22	2.12	2.12	2.13
$d(Mg^{2+} - Od2(Asp1741))$	2.14	2.18	2.20	2.17	2.16
$d(Mg^{2+} - Og1(Thr1696))$	2.48	2.55	4.08	4.02	4.09
$d(H_n(N1792) - O_{\gamma 3}(ATP))$	2.00	1.81	1.83	1.92	1.88
$d(H_r(R2109) - O_{\omega 1}(H_2O))$	3.48	3.05	2.41	2.42	2.67
$< (O_{\omega 1}(H_2O) - P_{\gamma}(ATP) - O_{\beta}(ATP))$	169.61	175.65	173.92	174.26	171.63
ΔG	0	16.2	-13.4	-10.1	-18.0

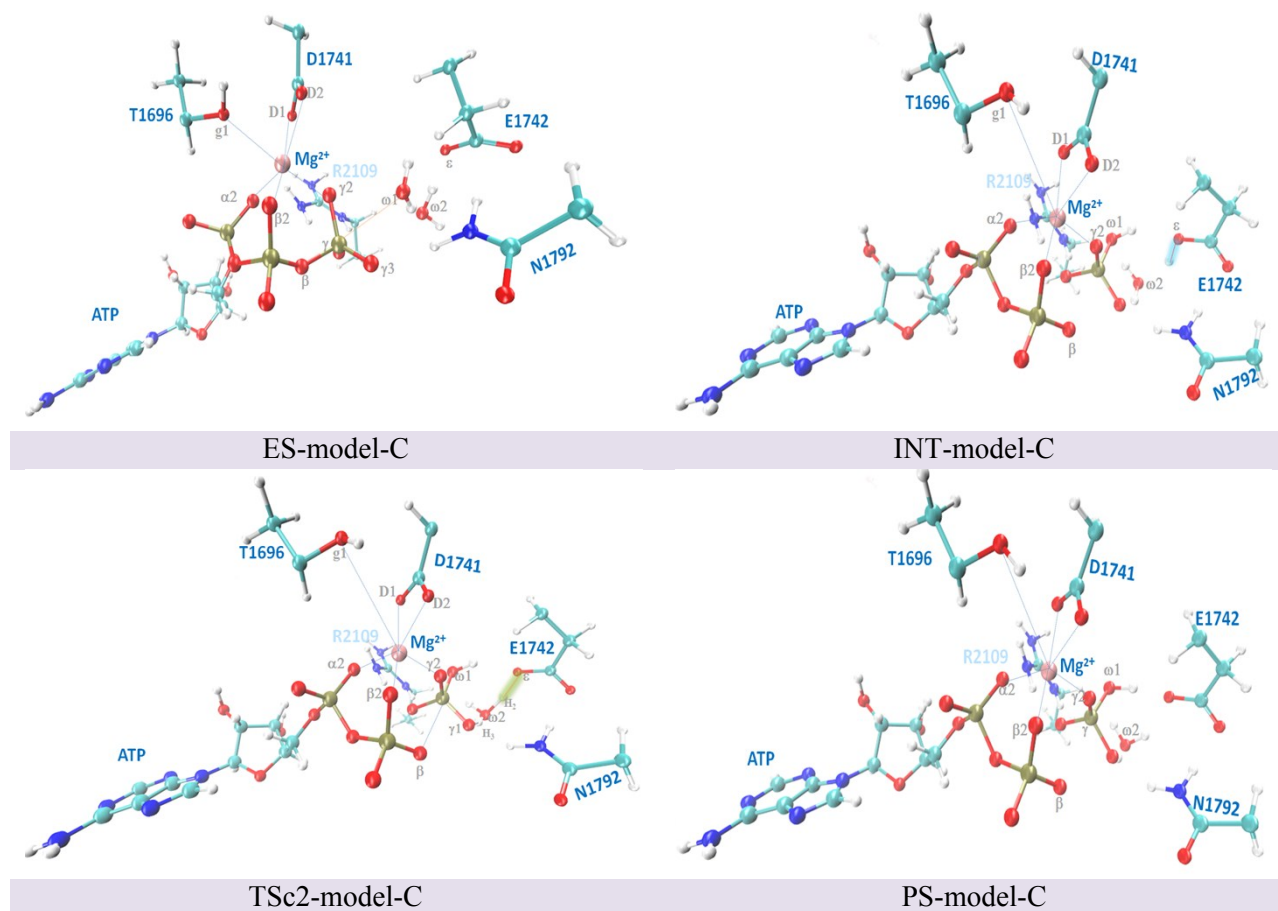


Figure S10. Enzyme-substrate (ES), enzyme-intermediate (INT), transition state (TSC2) and enzyme product (EP) structures for the larger QM region of model C are shown.

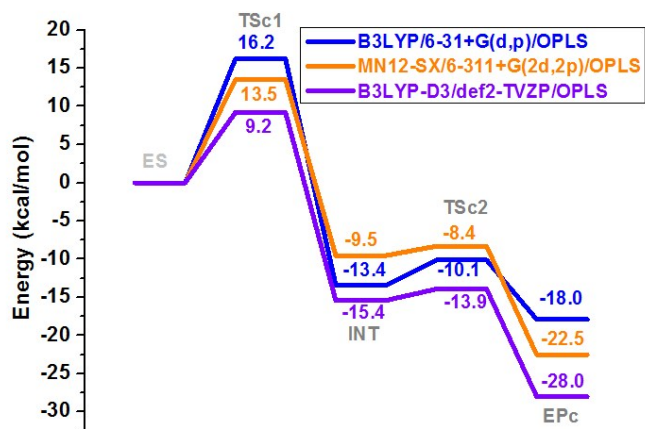


Figure S11. Potential energy profile (in kcal/mol) for model C with large QM region obtained at the three different levels of theories.

pdb|4RH7|Homo
 pdb|3VKG|Dictyostelium
 pdb|4AKI|Saccharomyces
 pdb|3J67|Strongylocentrotus
 pdb|3QMZ|Schistosoma
 pdb|5VH9|Saccharomyces

CCVQMVDSEFYQYTYEQGNASKLVYTPLTDKCYLTLTQAMKMG LGNPPYGPAGTGKTESV
 LVIHMANATFYFGFEYLIGERLVQTPLTDRCYLTLTQALESRMGGNPFGPAGTGKTETV
 VFISQSGYLLQYKFEYIGIPERLIYTPLLLIGFATLTDLSLHQKYGGCFFGPAGTGKTETV
 VFISQSGYLLQYKFEYIGIPERLIYTPLLLIGFATLTDLSLHQKYGGCFFGPAGTGKTETV
 VFISQSGYLLQYKFEYIGIPERLIYTPLLLIGFATLTDLSLHQKYGGCFFGPAGTGKTETV
 VFISQSGYLLQYKFEYIGIPERLIYTPLLLIGFATLTDLSLHQKYGGCFFGPAGTGKTETV

E1742

pdb|4RH7|Homo
 pdb|3VKG|Dictyostelium
 pdb|4AKI|Saccharomyces
 pdb|3J67|Strongylocentrotus
 pdb|3QMZ|Schistosoma
 pdb|5VH9|Saccharomyces

KALGGLLRQVLVFNCDGIDVKSMDGRIFVGLVKCGAWGCFDEFNRLEESVLSAVSMQIQ
 KALGSQLGRFVLVFCDEGFDLQAMSRIFVGLCQCGAWGCFDEFNRLEERILSAVSQIQ
 KAFGQNLGRVVVFNCDDSFQYVLSRLLVGITQIGAWGCFDEFNRLEDEKVL SAVSANIQ
 KAFGQNLGRVVVFNCDDSFQYVLSRLLVGITQIGAWGCFDEFNRLEDEKVL SAVSANIQ
 KAFGQNLGRVVVFNCDDSFQYVLSRLLVGITQIGAWGCFDEFNRLEDEKVL SAVSANIQ
 KAFGQNLGRVVVFNCDDSFQYVLSRLLVGITQIGAWGCFDEFNRLEDEKVL SAVSANIQ

N1792

pdb|4RH7|Homo
 pdb|3VKG|Dictyostelium
 pdb|4AKI|Saccharomyces
 pdb|3J67|Strongylocentrotus
 pdb|3QMZ|Schistosoma
 pdb|5VH9|Saccharomyces

TIQDALKNHRTVCELL-GKEVEVNSNGIFITINPAGKGYGGRQKLPDNLKQLFRPVAMS
 TIQVALKENSKEVELLGGKNISLHQDMGIFVTINP--GYAGRSNLPDNLKKLFRSMAMI
 QIQNGLVQKSHITLL-EEETPLSPHTAVFITLNP--GYNGRSEL PENLKKSFREFSMK
 QIQNGLVQKSHITLL-EEETPLSPHTAVFITLNP--GYNGRSEL PENLKKSFREFSMK
 QIQNGLVQKSHITLL-EEETPLSPHTAVFITLNP--GYNGRSEL PENLKKSFREFSMK
 QIQNGLVQKSHITLL-EEETPLSPHTAVFITLNP--GYNGRSEL PENLKKSFREFSMK

pdb|4RH7|Homo
 pdb|3VKG|Dictyostelium
 pdb|4AKI|Saccharomyces
 pdb|3J67|Strongylocentrotus
 pdb|3QMZ|Schistosoma
 pdb|5VH9|Saccharomyces

HPDNELIAEVILYSEGFDAKVLRSKLVAIFNLSRELLTPQOHYDWGLRALKTVLRGSGN
 KPDREMAIQVMLYSQGFKAIEVLAKIVPLFKLCQEQLSAQSHYDFGLRALKSVLVSAGG
 SPQSGTIAEMILQIMGFEDSKSLASKIVHFLELLSSKSSSMNHYHFLRLTLK-----G
 SPQSGTIAEMILQIMGFEDSKSLASKIVHFLELLSSKSSSMNHYHFLRLTLK-----G
 SPQSGTIAEMILQIMGFEDSKSLASKIVHFLELLSSKSSSMNHYHFLRLTLK-----G
 SPQSGTIAEMILQIMGFEDSKSLASKIVHFLELLSSKSSSMNHYHFLRLTLK-----G

pdb|4RH7|Homo
 pdb|3VKG|Dictyostelium
 pdb|4AKI|Saccharomyces
 pdb|3J67|Strongylocentrotus
 pdb|3QMZ|Schistosoma
 pdb|5VH9|Saccharomyces

LLRQLNKSQGTQANESH-----IVVQALRLNTMSKFTFDCTRFDALIKD
 IKRKCQPPQLPPIIDAESKTADQIYCQYIEGVLLNSINDTMIPKLVAADDIPLIQSLLLD
 VLRNCSPL-ISEFGEKEK-----TVVESLKRVLPSLGDDEL VFKDELSK
 VLRNCSPL-ISEFGEKEK-----TVVESLKRVLPSLGDDEL VFKDELSK
 VLRNCSPL-ISEFGEKEK-----TVVESLKRVLPSLGDDEL VFKDELSK
 VLRNCSPL-VSEFGEKEK-----TVVESLKRVLPSLGDDEL VFKDELSK

pdb|4RH7|Homo
 pdb|3VKG|Dictyostelium
 pdb|4AKI|Saccharomyces
 pdb|3J67|Strongylocentrotus
 pdb|3QMZ|Schistosoma
 pdb|5VH9|Saccharomyces

VFPGIELKEVEYDELSAALKQVFEEANYEIPNQIKKALELYEQLCQRMGVVIVGPSGAG
 VFPGSQLQPIQMDQLKKIKQEIARHLVTQEWVEKILQLHQILNINHGMVMVGPSSGGG
 IFDSAG-TPLNSKAIVQCLKDAGQSGFSMSEEFLLKCMQFYMQKTQQALILVKGAGCG
 IFDSAG-TPLNSKAIVQCLKDAGQSGFSMSEEFLLKCMQFYMQKTQQALILVKGAGCG
 IFDSAG-TPLNSKAIVQCLKDAGQSGFSMSEEFLLKCMQFYMQKTQQALILVKGAGCG
 IFDSAG-TPLNSKAIVQCLKDAGQSGFSMSEEFLLKCMQFYMQKTQQALILVKGAGCG

pdb|4RH7|Homo
 pdb|3VKG|Dictyostelium
 pdb|4AKI|Saccharomyces
 pdb|3J67|Strongylocentrotus
 pdb|3QMZ|Schistosoma
 pdb|5VH9|Saccharomyces

KSTLWRMLRAALCKTGKVVQK-YTMNPKAMPYQLLGHIDMDTREWSGVL TNSARQVVR
 KTTSEVYVLEAIEQVDNIKSEAHVMDPKAITKDQLFGSLDLTTREWTDGLFTATLRRIID
 KTATWKTVIDAMAI FDGHANVVYVIDTKVLTKESLYGSMLKATLEWRDGLFTSILRRVND
 KTATWKTVIDAMAI FDGHANVVYVIDTKVLTKESLYGSMLKATLEWRDGLFTSILRRVND
 KTATWKTVIDAMAI FDGHANVVYVIDTKVLTKESLYGSMLKATLEWRDGLFTSILRRVND
 KTATWKTVIDAMAI FDGHANVVYVIDTKVLTKESLYGSMLKATLEWRDGLFTSILRRVND



Figure S12: Multiple sequence alignment (MSA) analysis of AAA1-AAA2 domain of dynein motor. Dynein motor protein sequences of different organisms (such as *Schistosoma japonicum*, *Homo Sapiens*, *Saccharomyces cerevisiae* S288C, *Dictyostelium Discoideum*, *Saccharomyces cerevisiae*, *Strongylocentrotus purpuratus*) were obtained from the NCBI (www.ncbi.nlm.nih.gov website) protein sequence database. Muscle program was used for MSA analysis.¹ Here, E1742, N1742, and R2109 residues are marked in rectangle boxes.

Table S5: Imaginary frequencies (cm^{-1}) of the transition state structures (TSa, TSb, TSc1, and TSc2) for the ATP hydrolysis in dynein motor at the B3LYP/6-31+G(d,p)/OPLS level of theory.

Transition State	Imaginary Frequencies (cm^{-1})
TSa	-171.59
TSb	-945.70
TSc1	-186.58
TSc2	-505.53
TSc1(Large QM)	-492.01
TSc2(Large QM)	-820.54

Table S6: Calculated potential energy (kJ/mol) of the all the stationary structures for the ATP hydrolysis reaction catalyzed by dynein enzyme at the B3LYP/6-31+G(d,p)/OPLS level of theory.

Model A				
RS		TSa	EP	
-9513503.4899		-9513338.093	-9513497.4579	
Model B				
RS		TSb	EP	
-9513545.0194		-9513434.8755	-9513555.5948	
Model C				
RS	TSc1	INT	TSc2	EP
-9513579.5109	-9513491.4749	-9513641.6527	-9513616.3627	-9513657.2787
Model C (Larger QM)				
-10933886.2507	-10933817.8954	-10933942.6574	-10933928.9953	-10933961.667

Table S7: Calculated potential energy (kJ/mol) of the all the stationary structures for model C of the ATP hydrolysis reaction obtained at the B3LYP/def2-TVZP/OPLS and MN12-SX/6-311+G(2d,2p)/OPLS levels of theories.

	Model C				
	RS	TSc1	INT	TSc2	EP
B3LYP/def2-TVZP/OPLS	-9635055.5851	-9634992.4009	-9635173.144	-9635163.053	-9635167.5899
MN12-SX/6-311+G(2d,2p)/OPLS	-9629045.4427	-9628974.5723	-9629178.7989	-9629142.7554	-9629172.6881
	Model C (larger QM)				
	RS	TSc1	INT	TSc2	EP
B3LYP/def2-TVZP/OPLS	-11093548.891	-11093510.5591	-11093613.8524	-11093607.5362	-11093666.6321
MN12-SX/6-311+G(2d,2p)/OPLS	-11086124.0118	-11086067.4808	-11086163.7524	-11086159.2242	-11086218.4391

Table S8: Calculated potential energy (kJ/mol) of the all the stationary structures for model B of the ATP hydrolysis reaction obtained at the B3LYP/def2-TVZP/OPLS and MN12-SX/6-311+G(2d,2p)/OPLS levels of theories.

	Model B		
	RS	TSb	EP
B3LYP/def2-TVZP/OPLS	-9634924.2076	-9634816.459	-9634969.7868
MN12-SX/6-311+G(2d,2p)/OPLS	-9628925.7218	-9628823.8196	-9628974.6551

Cartesian coordinates of QM region of optimized transition states structures for the ATP hydrolysis reaction catalyzed by dynein motor at the B3LYP/6-31+G(d,p)/OPLS level of theory.

TSa-model-A				TSb-model-A			
C	47.9460655416	42.4402601144	48.7431301174	C	47.7154540401	42.9481596448	48.2264418742
H	48.9297642359	42.7944694147	49.0646110752	H	48.7397527680	43.2748282322	48.4159091828
H	47.8342433236	41.4140067608	49.0891563941	H	47.7012558727	41.8588846998	48.3164848172
C	47.9574219096	42.4647668510	47.2228150815	C	47.2987362355	43.3272892453	46.7968242967
O	47.3472781906	41.5799687926	46.5661598078	O	46.1996268735	42.9051982517	46.3696208430
O	48.6221075555	43.3822358393	46.6224085538	O	48.0735751721	44.0596839557	46.0850459711
C	46.1674454590	44.8669692416	44.2481924282	C	46.5410832842	44.8014312168	42.5513765528
O	45.8346496837	45.8087791795	43.4682169644	O	46.9762243609	44.0151001625	41.6694854226
N	46.6904587703	45.0639197006	45.4330592256	N	46.5586504374	46.0990132899	42.3453491408
H	47.1726187069	44.2974017005	45.9040932446	H	46.3324065624	46.8514790021	43.0283723625
H	46.6953409709	45.9803653324	45.9153083723	H	46.9418094300	46.4200416510	41.4568321555
N	49.7484010612	49.2395267201	47.9716470061	N	49.6623469408	50.5624427585	48.9875770953

H	48.8665821253	49.2039924686	47.4842476261	H	48.8006376104	50.0385532310	48.9120421172
C	49.6568324360	48.9749585814	49.3080946531	C	49.8446926385	51.3399895065	50.0859181856
N	50.6916956773	49.3585889354	50.0499443466	N	50.8065129867	52.2751132020	50.0692516532
H	51.3842594103	49.9600357370	49.6307817018	H	51.0611191053	52.7026531547	49.1909689083
H	50.8166027370	49.1024392668	51.0442760695	H	50.9330676617	52.8323421072	50.9105570160
N	48.5538507922	48.4144802788	49.7686399513	N	49.0874622216	51.1408425782	51.1505898723
H	47.8748405460	48.0306131725	49.1004445361	H	48.3214018443	50.4361576652	51.1167108306
H	48.3123058870	48.2896602210	50.7567688741	H	49.1621077422	51.7392381825	51.9708228235
O	45.3052438604	47.9077774224	45.8471476233	O	46.1137957944	48.1230696170	43.8612436278
P	46.0955411146	48.8594462816	46.6988156764	P	46.9435906534	48.3900574049	45.0970701244
O	47.6798743396	48.9105261052	46.2497068643	O	48.3666609486	49.0151458459	45.1082121415
O	45.9217068290	49.3446018905	48.1310510971	O	46.2372315026	48.5221505865	46.4743190161
O	45.8125677374	50.3432376110	45.8335397008	O	46.1527526720	50.4930900147	44.6420462299
P	44.3043306413	50.9688942304	45.6249177029	P	44.7816495772	51.1592681704	44.2298328616
O	43.8158531234	50.9032577398	44.2109987808	O	44.3570447290	51.2558093261	42.7968970821
O	43.4514800614	50.3373376267	46.7574210524	O	43.7846242768	50.4487492462	45.2591239176
O	44.5208655070	52.5425012236	46.0300806531	O	44.9303643127	52.6875234282	44.8733950495
P	43.9959365057	53.3019221522	47.4231823849	P	44.8356098136	53.0558518584	46.5046405073
O	42.5371304304	53.6276352169	47.3545117370	O	43.4069383728	53.2103051970	46.9150673791
O	44.3960350393	52.3646550288	48.5975305284	O	45.7060208704	51.9976728699	47.2552324910
O	45.0077024285	54.5482087792	47.4532058588	O	45.7645706684	54.3653874868	46.6062230687
C	44.8926849479	55.6766368572	46.5346932790	C	45.4436372836	55.6554090667	46.0639019338
H	44.9256129848	55.3110721439	45.5028452955	H	45.4234615319	55.5856257977	44.9749484499
H	43.9393691957	56.1832434302	46.7002266425	H	44.4685785892	55.9852366379	46.4304203284
C	46.089924294	56.6197474518	46.7515502959	C	46.5300761605	56.6374282008	46.5142231897
H	47.0142702451	56.0456568301	46.6198306541	H	47.5153775776	56.1634418251	46.4105148686
O	46.0195332239	57.6120904217	45.7050421134	O	46.4672338801	57.7704806532	45.6218862189
C	46.1375492867	58.9419350136	46.1995262902	C	46.1993798151	58.9868061787	46.3046663065
H	47.1486041004	59.3387889623	46.0380283706	H	47.0942069776	59.6220615872	46.3145285785
C	46.1873813821	57.3713944912	48.1013595490	C	46.3916533243	57.1772957203	47.9537087529
H	45.4519104849	56.9991595530	48.8224519086	H	45.6996371928	56.5765785562	48.5553639958
O	47.4994663042	57.2616182536	48.6368298881	O	47.6645912055	57.2348968624	48.5850197575
H	47.5910487075	56.4194266577	49.1569949658	H	47.6921841348	56.5576749537	49.2966794498
C	45.8659471034	58.8619453221	47.7366252250	C	45.8225174392	58.612365828	47.7512365828
H	44.8000951299	59.0505209196	47.9180197613	H	44.7314853828	58.5738016800	47.8297540389
O	46.6719701879	59.7149632942	48.5068917888	O	46.3641554999	59.5536200675	48.6468711732
H	46.3402067484	60.6479393196	48.5615354358	H	46.1190704944	59.2906580791	49.5694488574
N	45.2155659292	59.7634316197	45.3855794395	N	45.1963058430	59.7310460430	45.5341271724
C	45.1060706036	61.1496397031	45.2891495252	C	45.1188540736	61.1254423226	45.4961184510
C	44.1657069885	61.3778635008	44.2817850409	C	44.4176666907	61.4263759989	44.3243267555
C	43.8112487589	62.7221990943	44.0223594635	C	44.1800569426	62.8007777402	44.0752919875
N	43.7028738137	60.1919675032	43.7493245036	N	44.0351833830	60.2653449833	46.6651636833
C	44.3480502697	59.2662746129	44.4148061731	C	44.5155223737	59.2909403663	44.4033905135
H	44.2676543225	58.2068278426	44.2398931688	H	44.3942906140	58.2433705782	44.1739991113
N	44.3922952122	63.6987860569	44.7453356969	N	44.5780900338	63.6986046560	45.0002348837
C	45.2806980116	63.3514976001	45.6775345335	C	45.2305652623	63.2648767501	46.0887856510
H	45.7158343006	64.1660982603	46.2538818356	H	45.5258861680	64.0349941423	46.7985548960
N	45.7020403979	62.1159263853	46.0016413423	N	45.5574193429	62.0049112644	46.4083747649
N	42.9056492436	63.0492107715	43.0791202460	N	43.5442626296	63.2851011919	42.9819274628
H	42.3782091522	62.3238948405	42.6231462849	H	43.4327274728	62.7159718554	42.1559754392
H	42.5743399844	63.9976422177	43.0120802852	H	43.5563732976	64.2901548745	42.8677993297
Mg	44.4044250121	50.4237692647	48.4962441632	Mg	45.3467670283	50.2580202361	46.5372817492
O	46.9246677181	47.0445105802	47.5378294113	O	47.6164692451	46.7712681450	45.2891655010
H	46.1834303515	46.5864073016	47.9701403313	H	47.0525213442	46.0198959440	45.5356905622
H	48.0037557362	47.9886234418	46.2516885924	H	48.7940073405	46.7889394619	45.6773755960
O	49.2742780058	46.0629056677	47.5642859373	O	49.8012316057	47.3261252175	45.9109296743
H	48.3309533395	46.3756360472	47.6832948970	H	49.2966626255	48.2611574436	45.6055968372
H	49.1976338091	45.1817677638	47.1543447436	H	50.5460570760	47.1466548759	45.3009646652
H	50.4675570501	48.7739846023	47.4558125362	H	50.3795870207	50.4422094510	48.3012021106
H	46.0593699291	43.9206066118	43.9436970214	H	46.1647357426	44.3453294142	43.3578092366
H	47.2570601124	43.0298067899	49.1646822920	H	47.1415162488	43.3486934614	48.9407023824
TS1-model-C				TS2-model-C			
C	47.8304239355	43.1308968561	48.1323898314	C	47.8465097982	43.1338948633	48.1583822832
H	48.8812707040	43.3385802942	48.3508884248	H	48.8899210188	43.3553853684	48.3961032538
H	47.6883846317	42.0499531037	48.2442256461	H	47.7469083961	42.0448941562	48.2156664286
C	47.4678802388	43.5513438154	46.6962398438	C	47.4997337086	43.5815133894	46.7359406366
O	46.3385682204	43.2105928549	46.2676784538	O	46.3555944792	43.3572245476	46.3010182961
O	48.2762596909	44.2613547688	46.0041617456	O	48.4143203186	44.1403578689	46.0103445050

C	46.4775917270	44.8729015800	42.3561385221	C	46.4616202994	44.8481909970	42.3547645748
O	46.8195457118	44.1262663479	41.4113516385	O	46.8173587040	44.0980800424	41.4107975520
N	46.5146139971	46.1994646438	42.3346230732	N	46.5030075334	46.1687495943	42.3354742847
H	46.4303552182	46.7452887832	43.1934863220	H	46.3805538152	46.7142634230	42.3043102612
H	46.9310447138	46.6817600381	41.5421497216	H	46.9102408263	46.6482136735	41.5370923234
N	49.2784015139	48.9199843471	48.6705516092	N	49.3027931571	48.9434932128	48.6949065595
H	48.6388259515	48.2970816202	48.1843570886	H	48.6284494435	48.5186015906	48.0540164341
C	48.7186241051	49.6421929090	49.6802296849	C	48.7387365268	49.7098104932	49.6764378878
N	49.3754491653	50.6376783301	50.2941079302	N	49.4059114778	50.7134202227	50.2596047110
H	50.3380900014	50.8524243013	50.0825324892	H	50.3523863506	50.9449345728	49.9976531181
H	48.9984300151	51.0542101207	51.1459944370	H	49.0780547999	51.0772526784	51.1678636096
N	47.5000111406	49.3279546923	50.1090765723	N	47.5109393698	49.4364132743	50.0986366575
H	46.8573833803	48.5821433314	49.7852593180	H	46.8786787770	48.6372541132	49.8773261136
H	47.0259330975	49.9308806532	50.7750590778	H	47.0332450844	50.1183447887	50.6797018452
O	46.5231871609	48.0482148484	44.5458849744	O	46.2363239796	47.6420735274	44.6500398324
P	46.8988497922	48.8865673966	45.7527697597	P	46.6703693475	47.7550637501	46.1164281101
O	48.2402394644	49.5401235205	45.9255345468	O	48.1852694225	48.1526331144	46.2496192269
O	45.9638488187	48.8821101772	46.9756931745	O	45.7522057604	48.5844914226	47.0426991288
O	45.9219986697	50.7693029324	45.0783611074	O	45.7517450665	50.8673804317	45.0015622691
P	44.5268072439	51.2402624593	44.4223501490	P	44.3826906716	51.3115771793	44.3753974760
O	44.3805361098	51.2782498360	42.9377207503	O	44.2232971277	51.3495305235	42.8878195201
O	43.5284321107	50.3444560358	45.2685884743	O	43.3795422001	50.4034099655	45.2082770684
O	44.2563293095	52.7432045133	45.0512913070	O	44.0767200927	52.8190539235	44.9951477016
P	43.9243032207	53.1819358207	46.6329316508	P	43.8858902037	53.1436946376	46.6105035747
O	42.4557331235	53.3446858108	46.8570869081	O	42.4408301087	53.3836270611	46.9168086586
O	44.5840179812	52.1146430454	47.5391541775	O	44.5467478438	51.9954179818	47.4193483588
O	44.8323743961	54.4741331654	46.7917955956	O	44.8723450078	54.3972625430	46.7921808730
C	44.8383384955	55.6280367394	45.9164934495	C	44.8383927387	55.5803246952	45.9579739422
H	44.8781776923	55.3044665942	44.8719688602	H	44.8655088002	55.2935717195	44.9027631803
H	43.9291731771	56.2184216488	46.0777594156	H	43.9197771042	56.1448109942	46.1498805903
C	46.1045874938	56.4068869531	46.2812100433	C	46.0846041476	56.4014409100	46.3037631417
H	46.9814255122	55.7772119270	46.0992112704	H	46.9821929656	55.8034160585	46.1162899220
O	46.1754307827	57.5585345146	45.4102004986	O	46.1056614148	57.5495700732	45.4150783062
C	46.1407744425	58.7573995398	46.1687136874	C	46.1114969352	58.7542213605	46.1643557732
H	47.1415471863	59.1707066245	46.3091942924	H	47.1243418755	59.1429276308	46.2929565578
C	46.1296507226	56.9374800931	47.7281865021	C	46.1158428905	56.9541387527	47.7417482084
H	45.5034067770	56.3304951981	48.3870238905	H	45.5003143981	56.3517800373	48.4140798212
O	47.4553386204	57.0160743578	48.2232520125	O	47.4447114606	57.0534103165	48.2316799286
H	47.5733920076	56.3440958882	48.9430063599	H	47.5851819213	56.3593230801	48.9245135421
C	45.5468817878	58.3549602692	47.5345375940	C	45.5213827376	58.3645103265	47.5344849403
H	44.4590956207	58.2905294241	47.4132384088	H	44.4353041742	58.2895707021	47.4108382376
O	45.8714221069	59.2563548810	48.5629726140	O	45.8359434475	59.2779907757	48.5535110633
H	45.0419993880	59.4948156225	49.0418313895	H	45.0070269270	59.5197533365	49.0338395413
N	45.3751980180	59.7487834902	45.4307097616	N	45.3638708077	59.7673400053	45.4333937155
C	45.3294605792	61.1026532290	45.7165741275	C	45.3336798909	61.1207540472	45.7305914172
C	44.3149238237	61.6079558430	44.9010655416	C	44.3247617095	61.6448156684	44.9184931025
C	43.9338194557	62.9491764328	45.1298515862	C	43.9516918642	62.9849809454	45.1660799741
N	43.7626334182	60.6175459072	44.1110547152	N	43.7656530198	60.6682212184	44.1164410037
C	44.4075603659	59.5295967215	44.4609692104	C	44.3983647841	59.5705412265	44.4570440217
H	44.2515901425	58.5468337138	44.0432966235	H	44.2324254793	58.5924403716	44.0320330265
N	44.6157584609	63.6577177154	46.0554424664	N	44.6476529913	63.6814261925	46.0892714185
C	45.6391975948	63.0625843290	46.7031700634	C	45.6684478902	63.0725700340	46.7275673363
H	46.1801650793	63.6962018469	47.4015394957	H	46.2207498770	63.6973978029	47.4246403624
N	46.0581382285	61.7983979747	46.6069651718	N	46.0702834938	61.8039924978	46.6233596377
N	42.8983745806	63.5096653323	44.4732876569	N	42.9108305086	63.5619919014	44.5320777221
H	42.3577072538	62.9440571437	43.8386199275	H	42.3400831689	63.0035711653	43.9171779779
H	42.5131037819	64.3885143530	44.7827358822	H	42.5332203606	64.4345132663	44.8695707520
Mg	44.7905520837	50.3912951159	46.8388766121	Mg	44.8291002417	50.2435797354	46.6691680390
O	47.8040680104	47.0920281710	46.7924989539	O	46.6570286949	46.2544410438	46.7561051482
H	47.2522692631	46.2834593531	46.7700551573	H	46.0173407684	46.1219035350	47.4810020529
H	48.6969517138	46.7794641965	46.4923401938	H	50.3383526387	46.2476460301	45.4414217711
O	50.0899061460	45.9463479685	46.1267697125	O	49.6758059167	46.2336834698	46.1584586639
H	50.7824726548	46.0336130736	45.4564862566	H	49.0206477949	47.1630620504	46.1189526319
H	49.5016876870	45.1360232446	45.9981739183	H	49.1578964839	45.2515256551	46.1372004880
H	50.0644318760	49.1789596521	48.1092245556	H	50.0936685008	49.2438480503	48.1617056946
H	46.1392678066	44.4402874889	43.1918310332	H	46.1164276007	44.4206426640	43.1902551036
H	47.2540186730	43.5916692858	48.8072570342	H	47.2600274689	43.5561524542	48.8495675003
TS1-model-C (larger QM)				TS2-model-C (larger QM)			

C	43.9942108381	38.3654592594	45.0320921843	C	43.5946913439	38.0212737381	44.9880449994
H	44.3026825989	39.3145713556	44.5963210284	H	44.1228278565	38.9858451025	44.9781435934
C	42.4927197557	38.3497938663	45.3299916724	C	42.1139252161	38.2188752447	44.6404752060
H	42.2430244155	39.1620277537	46.0149695574	H	41.6281338302	38.7665444764	45.4532028322
H	41.8870827974	38.4301518797	44.4171222539	H	41.9916486923	38.7612999857	43.6955400714
H	42.2195690386	37.4311048654	45.8413938890	H	41.6215282195	37.2491854371	44.5443791279
O	44.6934584346	38.2925845968	46.2838846106	O	43.5307211119	37.5041374127	46.3250980839
H	44.6810497305	37.3962947088	46.6504331360	H	44.2091408726	36.8267060074	46.5329601608
C	43.4103468840	38.5264377290	49.7889656501	C	43.4328107632	38.3444808742	49.6938459435
H	42.8559494828	39.3446318949	50.2451836567	H	42.8925744805	39.1870206374	50.1277063527
H	42.7664631899	38.0943979966	49.0152097840	H	42.7831922125	37.8714164807	48.9469834780
C	44.6326014081	39.0595679760	49.0485364557	C	44.6374433741	38.8528744915	48.9087751776
O	45.6183460287	38.2770930916	48.8207367567	O	45.6077486580	38.0765416323	48.5986698797
O	44.6670964720	40.2301355713	48.5809941295	O	44.6912754090	40.0636672307	48.5158998324
C	46.8723102937	39.3553354659	53.6197784777	C	47.0769267074	39.1558368232	53.3326316567
H	46.7063164144	39.6722438613	54.6513219453	H	46.2431194095	39.7763511828	53.673297362
H	46.2361080621	39.9688894820	52.9818566771	H	47.3024087007	39.4411597054	52.2980637694
C	48.3561015999	39.5664804633	53.2901745283	C	48.3209161273	39.3150136373	54.1978540683
H	48.5025178260	39.5325432912	52.2063539254	H	49.0647484526	38.5303429807	53.9656118916
H	48.9686317134	38.7763528935	53.7352319669	H	48.0959423518	39.1885126439	55.2677602127
C	48.8110333959	40.8732351133	53.8952167928	C	49.0910558018	40.6118820416	54.0905060586
O	49.6789057855	40.8400207169	54.7761831897	O	50.1329410939	40.7066355490	54.7495857096
O	48.2066124512	41.9258320369	53.4529942935	O	48.6320402306	41.5452821328	53.2897221908
C	52.2686451479	37.8421410655	52.8762235816	C	52.4064192490	37.7652037009	52.8216418797
H	53.1683541459	38.2167155221	53.3774599304	H	53.3898034708	38.0816298036	53.1895118476
H	51.4236410241	38.0754302671	53.5263911670	H	51.6720450064	38.0626798694	53.5741187261
C	52.1950076182	38.5824035356	51.5565252276	C	52.1977329443	38.4980699076	51.5091646123
O	52.9152083308	38.2199875517	50.6179978669	O	52.7639945471	38.1003548077	50.4817303134
N	51.3593758472	39.6241536732	51.4977472521	N	51.4163761920	39.5840218064	51.5790160728
H	50.7667857538	39.8301139025	52.2828097071	H	51.0046886745	39.8511823329	52.4611759567
H	51.1164986416	40.0554347765	50.5977742705	H	51.0904121458	40.1001943818	50.7604127486
C	48.6907402091	46.7594511345	49.3121749275	C	48.7208436926	46.7702545594	49.3049858667
H	49.5828045167	46.2233562172	49.6438446712	H	49.6216450816	46.2299733369	49.6113277599
H	48.7031370076	46.7587331957	48.2206057945	H	48.6847494921	46.7493223327	48.2125554553
C	47.4376933917	46.0487313047	49.8332909965	C	47.4647212262	46.1250752700	49.9029124599
H	46.5544149213	46.6466745749	49.6210840297	H	46.6207508576	46.8100819900	49.8278460195
H	47.4971235246	45.9043667987	50.9150371122	H	47.6163926370	45.9132734300	50.9705389361
N	47.2883649179	44.7585868461	49.1756556413	N	47.1338886260	44.9025727917	49.203017881
H	48.0975197489	44.1363592817	49.1020593021	H	47.8509554921	44.1670997300	49.0930714697
C	46.2242121365	44.3613342462	48.4842461425	C	46.0184243581	44.6540046140	48.5288568390
N	45.0460751196	44.9951237564	48.6294606286	N	44.9392718035	45.4629425624	48.6585670534
H	44.8005676602	45.3079644166	49.5739643614	H	44.7015664465	45.6947928898	49.6330050041
H	44.2588310572	44.6949281197	48.0775547315	H	44.1254035805	45.2694054533	48.0892184782
N	46.3796968631	43.3862347366	47.5820421121	N	46.0264727219	43.6251067030	47.6726294043
H	47.2879491887	42.9249994142	47.5492194181	H	46.8774696494	43.0476471877	47.6314256730
H	45.6050522456	42.8110896790	47.2896379333	H	45.1672416676	43.1555838263	47.4242712481
O	50.3782612765	40.4853292554	49.0062339787	O	49.9140505248	41.4829781724	50.1314358606
P	49.1079931870	41.2847041279	48.9004028523	P	48.5091292505	41.6298651232	49.4838619251
O	49.0114640098	42.7067119568	48.3981382365	O	48.4503606425	42.7125997885	48.3936015221
O	47.7319149870	40.5539847988	48.8453207803	O	47.7793649966	40.3356637906	49.1252157600
O	49.4580444699	40.7636612933	46.5923458951	O	50.0735967071	40.0949744989	47.2301790720
P	49.0359143081	39.5637829917	45.7873822236	P	49.2520101979	39.5079807400	46.0837497005
O	50.1621188300	38.7603293669	45.1378637244	O	50.1134064718	38.7163378907	45.0961256234
O	47.9108172226	38.7241319512	46.4412423471	O	47.9476367417	38.8006078841	46.5321647837
O	48.2867395448	40.1816045615	44.4260765337	O	48.6735581566	40.7863429150	45.1575113014
P	46.8574435111	40.8856369878	44.4502805899	P	47.0949755907	40.9559351015	44.8000474742
O	46.0294789735	40.1882184451	43.4167817210	O	46.5791270586	39.9478467916	43.7977954804
O	46.2912287331	41.0480774012	45.8585763941	O	46.3111576376	41.1467251758	46.1055392554
O	47.2710155511	42.3989050697	43.9565263034	O	47.2306364170	42.4395809461	42.0788564768
C	48.0654376550	42.4518095897	42.7703991411	C	47.9719506867	42.4414288659	42.8496967726
H	49.0572873717	42.0375620044	42.9606101290	H	48.9652612506	42.0051258508	42.9995704254
H	47.5827448858	41.8604627027	41.9889458136	H	47.4299346389	41.8453896099	42.1092304534
C	48.1904410344	43.8969659170	42.2952897878	C	48.1246566749	43.8721896637	42.3293474291
H	48.8908610621	44.4433609204	42.923391980	H	48.8333982243	44.4270582910	42.9450204148
O	48.7600801448	43.8836242746	40.9556214736	O	48.7060310448	43.8046218809	40.9859303275
C	47.7733794961	44.2352373851	40.0143643929	C	47.7389048033	44.1874752577	40.0270357268
H	47.9349600318	45.2546181584	39.6567507309	H	47.9237652933	45.2098611309	39.6774212531
C	46.8470604747	44.6075144247	42.1559036919	C	46.7909554372	44.5971999182	42.1592156856

H	46.1445656738	44.2969487345	42.9243352945	H	46.0745798623	44.3009024128	42.9248519066
O	47.0587585999	46.0194833537	42.2122076431	O	47.0015698912	46.0160727854	42.1958613795
H	46.2104754606	46.4945660176	42.5010638828	H	46.1481432755	46.4955337252	42.4903321598
C	46.4396438505	44.1001730632	40.7620609064	C	46.3948475868	44.0729968235	40.7641450412
H	46.2391234349	43.0318339724	40.8686659128	H	46.1941981016	43.0032642914	40.8813134202
O	45.3534751493	44.7101962898	40.1298792680	O	45.3108331938	44.6818177794	40.1203459300
H	44.5890033455	44.0764099511	40.2385875632	H	44.5414722161	44.0473669002	40.2444816188
N	47.9139617178	43.3857218360	38.8368425119	N	47.8832881452	43.3412475099	38.8410490797
C	47.7361167161	43.7599726627	37.5290355575	C	47.7076808425	43.7205034612	37.5286312036
C	48.0667302886	42.6365393171	36.7770518980	C	48.0449935173	42.5940450360	36.7711362471
C	47.9873444315	42.7602135093	35.3783096229	C	47.9920333131	42.7257661950	35.3682873499
N	48.4379356706	41.5860878284	37.5893849605	N	48.4155260921	41.5413511772	37.5817122071
C	48.3357747713	42.0691207524	38.7983866131	C	48.3099242702	42.0229228070	38.7985091047
H	48.5851303482	41.5426396221	39.7040115857	H	48.5656777388	41.4942882651	39.7039393197
N	47.6275320688	43.9419090219	34.8473440117	N	47.6264941711	43.9098081868	34.8370332840
C	47.3276435045	44.9365744133	35.6721551117	C	47.3121284400	44.9030598169	35.6642465527
H	47.0392719761	45.8654135648	35.1925401659	H	47.0213841493	45.8333244846	35.1826088151
N	47.3414260203	44.9402233391	37.0100731358	N	47.3155594523	44.9037974343	37.0076547941
N	48.2582122297	41.7313386513	34.5609795391	N	48.3056004915	41.7102494178	34.5423853671
H	48.5764774397	40.8602216102	34.9514268645	H	48.5959613065	40.8269802084	34.9271708160
H	48.2445510354	41.8598295492	33.5624489067	H	48.2792236222	41.8439426126	33.5437598041
Mg	46.4883946703	39.7047946489	47.4256083717	Mg	46.5970974016	39.7492445160	47.6325394906
O	49.1583222688	43.6230780188	52.0864828079	O	49.9042625770	43.0989421856	51.9550609311
H	49.9984704551	44.0031708123	52.3784501799	H	50.0229121362	42.3873809201	51.0976098094
H	48.7573457184	42.9793537138	52.8891350588	H	49.4071546452	42.3749166888	52.7492822657
O	48.9772891293	41.6872918418	50.7002293555	O	47.5751969911	42.3141704385	50.6996660429
H	48.2201077735	41.2607681819	51.1455272726	H	47.5894966304	41.7549556907	51.5018856702
H	49.1611515030	42.6792532174	51.2199026601	H	49.1480098063	43.6407498216	51.6654550204
H	48.7202864712	47.7062645958	49.6325985344	H	48.7582156401	47.7207707839	49.6134048098
H	52.3265058334	36.8549231026	52.7277216126	H	52.3871426372	36.7739051375	52.6914283223
H	46.6412932125	38.3898977112	53.4991093023	H	46.7843083403	38.1999345876	53.3076235138
H	43.6160083234	37.7994005028	50.4440383514	H	43.6452443875	37.6538247927	50.3851245649
H	44.2794752149	37.6235829775	44.4252612213	H	44.0515486997	37.3998598291	44.3515498225

¹. R. C. Edgar, MUSCLE: Multiple Sequence Alignment with High Accuracy and High Throughput. *Nucleic Acids Res.* 2004, 32, 1792–1797.