Supplementary File

An epithelial sodium channel (ENaC)-specific aptamer determined through structure-based virtual screening for the development of hypertension early detection system

Dina Ratna Komala¹, Ari Hardianto¹, Shabarni Gaffar¹, Yeni Wahyuni Hartati¹
¹Department of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas Padjadjaran, Indonesia

(Email: dina15004@mail.unpad.ac.id)
Figure S1. Subunits (a) α, (b) β, (c) γ sequences of ENaC protein (PDB ID: 6BQN) retrieved from RCSB Protein Data Bank (PDB). Each subunit has missing residues in the middle of sequence which is indicated by the empty DSSP sign at the secondary structure.
| No | File Name                  | DOPE score     |
|----|---------------------------|----------------|
| 1  | AC.B99900000.pdb          | -14.773.873.438 |
| 2  | AC.B99900001.pdb          | -14.745.553.125 |
| 3  | AC.B99900002.pdb          | **-14.858.033.125** |
| 4  | AC.B99900004.pdb          | -14.795.026.553 |
| 5  | AC.B99900005.pdb          | -14.799.529.688 |
| 6  | AC.B99900006.pdb          | -14.899.976.553 |
| 7  | AC.B99900007.pdb          | -14.786.595.313 |
| 8  | AC.B99900008.pdb          | -14.780.029.688 |
| 9  | AC.B99900009.pdb          | -14.765.890.625 |
| 10 | AC.B99900010.pdb          | -14.818.828.125 |
| 11 | AC.B99900011.pdb          | -14.791.500.000 |
| 12 | AC.B99900012.pdb          | -14.804.873.438 |
| 13 | AC.B99900013.pdb          | -14.850.767.188 |
| 14 | AC.B99900014.pdb          | -14.801.153.125 |
| 15 | AC.B99900015.pdb          | -14.800.145.313 |
| 16 | AC.B99900016.pdb          | -14.797.576.553 |
| 17 | AC.B99900017.pdb          | -14.847.953.125 |
| 18 | AC.B99900018.pdb          | -14.808.014.063 |
| 19 | AC.B99900019.pdb          | -14.829.567.188 |
| 20 | AC.B99900020.pdb          | -14.780.768.750 |
| 21 | AC.B99900021.pdb          | -14.729.807.813 |
| 22 | AC.B99900022.pdb          | -14.716.008.438 |
| 23 | AC.B99900023.pdb          | -14.713.882.813 |
| 24 | AC.B99900024.pdb          | -14.858.175.438 |
| 25 | AC.B99900025.pdb          | -14.752.057.813 |

**Figure S2.** Results of modeling of ENaC protein with subunits A, B and C (PDB ID: 6BQN) using Modeller 9.20 program.
**Figure S3.** Evaluation of ENaC protein model subunits A, B and C using the PROCHECK program (A) before loop optimization, (B) after loop optimization.

**Figure S4.** Three-dimensional structure of ENaC after re-modelling using Modeller 9.20 program.
Table S1. Unfavorable interactions in the iDE-ENaC complex obtained from molecular docking

| No. | iDE Atom Type | Nucleotide | Subunit | ENaC Residue | Atom Type | Interaction                  |
|-----|---------------|------------|---------|--------------|-----------|------------------------------|
| 1   | NE            | C69        | α       | ARG386       | O5'       | Unfavorable Bump             |
| 2   | OD2           | C67        | α       | ASP393       | OP1       | Unfavorable Negative-Negative |
| 3   | O             | G56        | β       | THR280       | N2        | Unfavorable Bump             |
| 4   | O             | G56        | β       | THR280       | H22       | Unfavorable Bump             |
| 5   | O             | G56        | β       | THR280       | H21       | Unfavorable Bump             |
| 6   | HH22          | G57        | β       | ARG324       | H21       | Unfavorable Donor-Donor      |

Table S2. Analysis of iDE-creatinine interactions using Biovia Discovery Studio obtained from molecular docking

| No. | iDE Nucleotide | Atom Type* | Residue | Creatinine Atom Type* | Interaction                  |
|-----|----------------|------------|---------|-----------------------|------------------------------|
| 1   | T43            | OP2        | ARG96   | HH22                  | Hydrogen Bond; Electrostatic |
| 2   | T59            | OP1        | LYS196  | HZ1                   | Hydrogen Bond; Electrostatic |
| 3   | T59            | OP1        | LYS196  | HZ2                   | Hydrogen Bond; Electrostatic |
| 4   | G46            | OP2        | LYS319  | HZ3                   | Hydrogen Bond; Electrostatic |
| 5   | G41            | OP1        | LYS32   | NZ                    | Electrostatic               |
| 6   | T43            | OP2        | ARG96   | NH1                   | Electrostatic               |
| 7   | T17            | OP1        | ARG96   | NH2                   | Electrostatic               |
| 8   | T43            | OP1        | ARG96   | NH2                   | Electrostatic               |
| 9   | A45            | OP1        | LYS319  | NZ                    | Electrostatic               |
| 10  | G15            | OP1        | ARG320  | NH1                   | Electrostatic               |
| 11  | G16            | OP1        | ARG320  | NH1                   | Electrostatic               |
| 12  | G16            | OP2        | ARG320  | NH2                   | Electrostatic               |
| 13  | T43            | OP2        | ARG341  | NH2                   | Electrostatic               |
| 14  | G12            | H21        | ASP195  | OD1                   | Hydrogen Bond               |
| 15  | G12            | H22        | ASP195  | OD1                   | Hydrogen Bond               |
| 16  | C60            | O3'        | THR180  | HG1                   | Hydrogen Bond               |
| 17  | T17            | O4         | SER285  | HG                    | Hydrogen Bond               |
| 18  | G44            | OP2        | THR313  | HG1                   | Hydrogen Bond               |
| 19  | T43            | OP2        | GLN318  | HE22                  | Hydrogen Bond               |
| 20  | T43            | Pi-Orbitals | ALA339 | O                     | Pi-Lone Pair                |
| 21  | C23            | Pi-Orbitals | PHE68  | Pi-Orbitals           | Hydrophobic                 |
| 22  | T43            | Pi-Orbitals | ALA339 | Amide                 | Hydrophobic                 |
| 23  | T17            | Pi-Orbitals | VAL72   | Alkyl                 | Hydrophobic                 |
| 24  | T42            | Pi-Orbitals | ILE69   | Alkyl                 | Hydrophobic                 |
| 25  | T43            | Pi-Orbitals | ALA339 | Alkyl                 | Hydrophobic                 |
| 26  | G56            | Pi-Orbitals | PRO200  | Alkyl                 | Hydrophobic                 |
| 27  | G57            | Pi-Orbitals | VAL198  | Alkyl                 | Hydrophobic                 |
| 28  | C58            | Pi-Orbitals | VAL198  | Alkyl                 | Hydrophobic                 |

*Atom type may refer to orbital systems or moieties for hydrophobic or pi-lone pair interactions.
Table S3. Analysis of iDE-ENaC interactions using Biovia Discovery Studio obtained from molecular docking.

| No | Nucleotide | Atom Type | subunit | Residue | Atom Type | Interaction               |
|----|------------|-----------|---------|---------|-----------|---------------------------|
| 1  | C69        | OP1       | α       | ARG386  | HH21      | Hydrogen Bond; Electrostatic |
| 2  | C69        | OP2       | α       | ARG386  | NH1       | Electrostatic             |
| 3  | C68        | OP1       | α       | ARG386  | NH2       | Electrostatic             |
| 4  | T6         | OP1       | β       | LYS282  | NZ        | Electrostatic             |
| 5  | A7         | OP2       | β       | LYS282  | NZ        | Electrostatic             |
| 6  | C58        | OP1       | β       | LYS282  | NZ        | Electrostatic             |
| 7  | A4         | OP1       | β       | LYS350  | NZ        | Electrostatic             |
| 8  | C69        | OP1       | α       | ARG386  | HE        | Hydrogen Bond             |
| 9  | C69        | OP2       | α       | ASP393  | HN        | Hydrogen Bond             |
| 10 | C68        | OP1       | α       | LYS477  | HN        | Hydrogen Bond             |
| 11 | C67        | O2        | β       | LYS88   | HZ1       | Hydrogen Bond             |
| 12 | C67        | O2        | β       | LYS88   | HZ3       | Hydrogen Bond             |
| 13 | A13        | N3        | β       | ASN378  | HD22      | Hydrogen Bond             |
| 14 | G56        | H1        | β       | MET279  | O         | Hydrogen Bond             |
| 15 | G56        | H22       | β       | MET279  | O         | Hydrogen Bond             |
| 16 | G57        | H21       | β       | MET279  | SD        | Hydrogen Bond             |
| 17 | C69        | HO3’      | β       | LEU83   | O         | Hydrogen Bond             |
| 18 | G57        | Pi-Orbitals | β     | MET279  | SD        | Pi-Sulfur                 |
**Table S4.** Unfavorable interactions in the iDE-creatine complex obtained from molecular docking

| No. | iDE Nucleotide | Atom Type | Creatinine Residue | Atom type | Interaction          |
|-----|----------------|-----------|--------------------|-----------|----------------------|
| 1   | T17            | P         | ILE69              | CD1       | Unfavorable Bump     |
| 2   | T17            | OP2       | ILE69              | CD1       | Unfavorable Bump     |
| 3   | T17            | O4        | VAL72              | CB        | Unfavorable Bump     |
| 4   | T17            | O4        | VAL72              | CG2       | Unfavorable Bump     |
| 5   | T17            | C5        | CYS283             | SG        | Unfavorable Bump     |
| 6   | T17            | C7        | CYS283             | CB        | Unfavorable Bump     |
| 7   | T17            | C7        | CYS283             | SG        | Unfavorable Bump     |
| 8   | G20            | P         | HIS66              | CB        | Unfavorable Bump     |
| 9   | G20            | OP2       | HIS66              | CB        | Unfavorable Bump     |
| 10  | G20            | OP2       | HIS66              | CG        | Unfavorable Bump     |
| 11  | T22            | C7        | PHE68              | CE2       | Unfavorable Bump     |
| 12  | T42            | C7        | PHE68              | C         | Unfavorable Bump     |
| 13  | T42            | C7        | PHE68              | O         | Unfavorable Bump     |
| 14  | T42            | C7        | ILE69              | N         | Unfavorable Bump     |
| 15  | T43            | C5'       | GLN318             | NE2       | Unfavorable Bump     |
| 16  | T43            | C5'       | GLN318             | HE21      | Unfavorable Bump     |
| 17  | T43            | C2'       | ALA339             | CB        | Unfavorable Bump     |
| 18  | T43            | C1'       | ALA339             | CB        | Unfavorable Bump     |
| 19  | T43            | N3        | ASP340             | OD1       | Unfavorable Bump     |
| 20  | T43            | H3        | ASP340             | OD1       | Unfavorable Bump     |
| 21  | A45            | OP1       | LYS319             | CG        | Unfavorable Bump     |
| 22  | A45            | OP1       | LYS319             | CD        | Unfavorable Bump     |
| 23  | A45            | O5'       | LYS319             | CE        | Unfavorable Bump     |
| 24  | A45            | C5'       | LYS319             | CE        | Unfavorable Bump     |
| 25  | A45            | C4'       | LYS319             | CE        | Unfavorable Bump     |
| 26  | G46            | C3'       | GLY321             | CA        | Unfavorable Bump     |
| 27  | G46            | O3'       | GLY321             | N         | Unfavorable Bump     |
| 28  | G46            | O3'       | GLY321             | CA        | Unfavorable Bump     |
| 29  | G46            | O3'       | GLY321             | C         | Unfavorable Bump     |
| 30  | G46            | O3'       | THR322             | N         | Unfavorable Bump     |
| 31  | T47            | P         | ARG320             | C         | Unfavorable Bump     |
| 32  | T47            | OP1       | ARG320             | C         | Unfavorable Bump     |
| 33  | T47            | OP2       | ARG320             | C         | Unfavorable Bump     |
| 34  | T47            | P         | GLY321             | N         | Unfavorable Bump     |
| 35  | T47            | P         | GLY321             | CA        | Unfavorable Bump     |
| 36  | T47            | P         | GLY321             | C         | Unfavorable Bump     |
| 37  | T47            | P         | GLY321             | O         | Unfavorable Bump     |
| 38  | T47            | P         | GLY321             | HN        | Unfavorable Bump     |
| 39  | T47            | OP1       | GLY321             | C         | Unfavorable Bump     |
| 40  | T47            | OP1       | GLY321             | O         | Unfavorable Bump     |
| 41  | T47            | OP2       | GLY321             | N         | Unfavorable Bump     |
|    |     |     |      |          |                  |          |                  |
|----|-----|-----|------|----------|------------------|----------|------------------|
| 43 | T47 | OP2 | GLY321 | CA | Unfavorable Bump |
| 44 | T47 | OP2 | GLY321 | HN | Unfavorable Bump |
| 45 | T47 | O5’ | GLY321 | CA | Unfavorable Bump |
| 46 | T47 | O5’ | GLY321 | C  | Unfavorable Bump |
| 47 | T47 | O5’ | GLY321 | O  | Unfavorable Bump |
| 48 | T47 | C5’ | GLY321 | C  | Unfavorable Bump |
| 49 | T47 | C5’ | GLY321 | O  | Unfavorable Bump |
| 50 | A48 | OP1 | THR322 | O  | Unfavorable Bump |
| 51 | G56 | N2  | PRO200 | CG | Unfavorable Bump |
| 52 | G56 | N2  | PRO200 | CD | Unfavorable Bump |
| 53 | G56 | H21 | PRO200 | CG | Unfavorable Bump |
| 54 | G56 | H21 | PRO200 | CD | Unfavorable Bump |
| 55 | G56 | H22 | PRO200 | CD | Unfavorable Bump |
| 56 | C58 | C4’ | VAL198 | CG1| Unfavorable Bump |
| 57 | C58 | O4’ | VAL198 | CB | Unfavorable Bump |
| 58 | C58 | O4’ | VAL198 | CG1| Unfavorable Bump |
| 59 | C58 | O4’ | VAL198 | CG2| Unfavorable Bump |
| 60 | C60 | C4’ | GLU181 | OE2| Unfavorable Bump |
| 61 | C60 | OP1 | GLU181 | OE2| Unfavorable Negative-Negative |
| 62 | G26 | OP1 | GLU310 | OE1| Unfavorable Negative-Negative |
| 63 | T17 | H3  | VAL72  | HN | Unfavorable Donor-Donor |
| 64 | G46 | H21 | GLY321 | HN | Unfavorable Donor-Donor |
| 65 | G19 | O3’ | GLY65  | O  | Unfavorable Acceptor-Acceptor |
| 66 | G20 | OP1 | GLY65  | O  | Unfavorable Acceptor-Acceptor |
| 67 | T59 | O4’ | ASP195 | OD1| Unfavorable Acceptor-Acceptor |
Table S5. Analysis of iDE-ENaC interactions using Biovia Discovery Studio obtained from the last frame of the 100-ns MD trajectory.

| No | iDE Atom Type | Nucleotide subunit | ENaC Residue | Atom Type | Interaction                  |
|----|---------------|--------------------|--------------|-----------|------------------------------|
| 1  | G21           | OP1                | α            | LYS220    | HZ2 Hydrogen Bond;Electrostatic |
| 2  | G21           | OP1                | α            | LYS220    | HZ3 Hydrogen Bond;Electrostatic |
| 3  | C68           | OP2                | α            | ARG476    | HH12 Hydrogen Bond;Electrostatic |
| 4  | C68           | OP1                | α            | ARG476    | HH22 Hydrogen Bond;Electrostatic |
| 5  | C69           | OP2                | α            | LYS477    | HZ3 Hydrogen Bond;Electrostatic |
| 6  | G57           | OP1                | β            | LYS282    | HZ2 Hydrogen Bond;Electrostatic |
| 7  | G20           | OP2                | β            | ARG259    | NH2 Electrostatic             |
| 8  | T59           | OP1                | β            | ARG324    | NH1 Electrostatic             |
| 9  | C60           | OP1                | β            | ARG324    | NH1 Electrostatic             |
| 10 | A4            | OP1                | β            | LYS350    | NZ Electrostatic              |
| 11 | G57           | N3                 | α            | ASN213    | HD21 Hydrogen Bond            |
| 12 | G55           | O3'                | α            | ASN214    | HD21 Hydrogen Bond            |
| 13 | G20           | O3'                | α            | LYS220    | HZ2 Hydrogen Bond             |
| 14 | G20           | O3'                | α            | LYS220    | HZ3 Hydrogen Bond             |
| 15 | C69           | O2                 | β            | SER82     | HG Hydrogen Bond              |
| 16 | T43           | O2                 | β            | GLN233    | HE22 Hydrogen Bond            |
| 17 | G19           | OP2                | β            | ASN260    | HD22 Hydrogen Bond            |
| 18 | T17           | O2                 | β            | SER263    | HN Hydrogen Bond              |
| 19 | T59           | O3'                | β            | ARG324    | HH12 Hydrogen Bond            |
| 20 | G3            | O3'                | β            | GLN352    | HE21 Hydrogen Bond            |
| 21 | T17           | H3                 | β            | SER263    | OG Hydrogen Bond              |
| 22 | T17           | H3                 | β            | SER263    | O Hydrogen Bond               |
| 23 | G20           | H22                | α            | GLN216    | OE1 Hydrogen Bond             |
| 24 | G56           | H21                | β            | THR280    | O Hydrogen Bond               |
| 25 | G56           | H22                | β            | THR280    | O Hydrogen Bond               |
| 26 | G57           | H22                | β            | MET279    | O Hydrogen Bond               |
| 27 | T43           | Pi-Orbitals        | β            | PRO231    | Alkyl Hydrophobic             |
Table S6. Conservation of Hydrogen bonding in the binding of iDE to ENaC. The hydrogen bonding conservation was extracted from a 100-ns trajectory of molecular dynamics simulation of the complex.

| Subunit | Residue | Atom | Nucleotide | Atom | % Conservation |
|---------|---------|------|------------|------|----------------|
| alpha   | ASN213  | HD21 | G56        | O3'  | 8.2            |
|         |         | HD21 | G57        | OP1  | 5.3            |
|         | ASN214  | ND2  | G19        | H22  | 0.2            |
|         |         | OD1  | G19        | H22  | 0.1            |
|         |         | HD21 | G19        | N2   | 0.1            |
|         |         | HD21 | G55        | N3   | 0.5            |
|         | GLN216  | HE21 | G20        | N3   | 0.6            |
|         |         | HE21 | G20        | O3'  | 1.7            |
|         |         | NE2  | G20        | H22  | 0.2            |
|         |         | OE1  | G20        | H22  | 12.5           |
|         |         | HE21 | G21        | O4'  | 0.1            |
|         |         | HE21 | G21        | OP1  | 0.5            |
|         |         | HE22 | G21        | OP1  | 0.1            |
|         | LYS220  | HZ2  | G20        | O3'  | 0.6            |
|         |         | HZ1  | G20        | O3'  | 0.3            |
|         |         | HZ3  | G20        | O3'  | 0.2            |
|         |         | HZ3  | G21        | OP1  | 6.1            |
|         |         | HZ1  | G21        | OP1  | 6.1            |
|         |         | HZ2  | G21        | OP1  | 4.9            |
|         |         | HZ1  | G21        | OP2  | 0.7            |
|         |         | HZ2  | G21        | OP2  | 0.4            |
|         |         | HZ3  | G21        | OP2  | 0.2            |
|         | ARG386  | HH11 | C69        | O3'  | 0.4            |
|         |         | HH22 | C69        | O3'  | 0.1            |
|         |         | HH12 | C69        | O5'  | 7.1            |
|         |         | HE    | C69        | O5'  | 0.8            |
|         |         | HH22 | C69        | OP1  | 2.1            |
|         |         | HH12 | C69        | OP1  | 20.9           |
|         |         | HH21 | C69        | OP1  | 9.9            |
|         |         | HE    | C69        | OP1  | 5.7            |
|         |         | HH22 | C69        | OP2  | 2.4            |
|         |         | HH21 | C69        | OP2  | 0.4            |
|         | ASP393  | H     | C69        | OP2  | 6.6            |
|         | ARG476  | HH12 | C68        | OP1  | 15.7           |
|         |         | HH22 | C68        | OP1  | 14.7           |
|         |         | HE    | C68        | OP1  | 3.6            |
|         |         | HH11 | C68        | OP1  | 0.7            |
|         |         | HH21 | C68        | OP1  | 0.2            |
|         |         | HH21 | C68        | OP2  | 18.2           |
|         |         | HH22 | C68        | OP2  | 10.9           |
|         |         | HH12 | C68        | OP2  | 7.4            |
|         |         | HH11 | C68        | OP2  | 6.8            |
|         |         | HE    | C68        | OP2  | 6.7            |
|         |         | HH22 | C69        | OP2  | 0.3            |
|         | LYS477  | HZ3  | C68        | OP1  | 7.1            |
|         |         | HZ2  | C68        | OP1  | 6.5            |
|         |         | HZ1  | C68        | OP1  | 6.2            |
|         |         | HZ3  | C69        | OP1  | 10.7           |
|         |         | HZ2  | C69        | OP1  | 10.7           |
|         |         | HZ1  | C69        | OP1  | 10.4           |
|         |         | HZ3  | C69        | OP2  | 7.9            |
|         |         | HZ2  | C69        | OP2  | 5.3            |
|         |         | HZ1  | C69        | OP2  | 4.2            |
| Subunit | Residue | Atom | Nucleotide | Atom | % Conservation |
|---------|---------|------|------------|------|----------------|
| β       | SER82   | HG   | C69        | O2   | 43.8           |
|         |         |      |            |      |                |
|         | LEU83   | H    | C69        | O3'  | 33.7           |
|         | LYS88   | HZ1  | A4         | N3   | 0.5            |
|         |         | HZ3  | A4         | N3   | 0.4            |
|         |         | HZ2  | A4         | O3'  | 0.9            |
|         |         | HZ3  | A4         | O3'  | 0.9            |
|         |         | HZ1  | C67        | O2   | 0.8            |
|         |         | HZ1  | C67        | O2   | 0.4            |
|         |         | HZ2  | C67        | O2   | 0.4            |
|         |         | HZ3  | C69        | OP1  | 0.1            |
|         | GLN233  | HE22 | T43        | O2   | 1.4            |
|         |         | HE21 | T43        | O2   | 0.1            |
|         |         | HE21 | T43        | O4   | 0.4            |
|         |         | HE22 | T43        | O4   | 0.1            |
|         |         | HE22 | T43        | O4'  | 2.3            |
|         |         | HE21 | T43        | O4'  | 1.2            |
|         |         | HE21 | T43        | O5'  | 3.3            |
|         |         | HE21 | T43        | OP1  | 0.2            |
|         |         | HE22 | T43        | OP2  | 4.7            |
|         |         | HE21 | T43        | OP2  | 0.2            |
|         | ARG259  | HH112G20 | OP1  | 14.2 |
|         |         | HH22 | G20        | OP1  | 3.1            |
|         |         | HH21 | G20        | OP1  | 0.7            |
|         |         | HE    | G20        | OP1  | 0.6            |
|         |         | HH11 | G20        | OP1  | 0.3            |
|         |         | HH22 | G20        | OP2  | 19.1           |
|         |         | HH12 | G20        | OP2  | 9.4            |
|         |         | HH21 | G20        | OP2  | 3              |
|         |         | HE    | G20        | OP2  | 0.7            |
|         |         | HH11 | G20        | OP2  | 0.5            |
|         | ASN260  | HD22 | G19        | OP1  | 48.2           |
|         |         | HD22 | G19        | OP2  | 15.9           |
|         | SER263  | H    | T17        | O2   | 56.2           |
|         |         | O     | T17        | H3   | 71.8           |
|         |         | OG    | T17        | H3   | 1.8            |
|         | MET279  | O     | G56        | H21  | 0.1            |
|         |         | O     | G57        | H22  | 52.2           |
|         | THR280  | O     | G56        | H22  | 26             |
|         | LYS282  | HZ3  | T6         | O5'  | 0.2            |
|         |         | HZ2  | T6         | O5'  | 0.1            |
|         |         | HZ2  | T6         | OP1  | 0.4            |
|         |         | HZ3  | T6         | OP1  | 0.4            |
|         |         | HZ3  | T6         | OP2  | 0.2            |
|         |         | HZ2  | A7         | OP1  | 0.2            |
|         |         | HZ3  | A7         | OP1  | 0.1            |
|         |         | HZ1  | A7         | OP2  | 0.5            |
|         |         | HZ3  | A7         | OP2  | 0.3            |
|         |         | HZ2  | A7         | OP2  | 0.1            |
|         |         | HZ2  | G56        | O3'  | 0.3            |
|         |         | HZ1  | G56        | O3'  | 0.1            |
|         |         | HZ1  | G57        | OP1  | 5.6            |
|         |         | HZ2  | G57        | OP1  | 5.2            |
|         |         | HZ3  | G57        | OP1  | 4.3            |
|         |         | HZ2  | G57        | OP2  | 0.4            |
|         |         | HZ1  | G57        | OP2  | 0.3            |
| Subunit | Residue | Atom | Nucleotide | Atom | % Conservation |
|---------|---------|------|------------|------|----------------|
| HZ3     | G57     | OP2  | 0.2        |      |                |
| HZ1     | C58     | OP1  | 6.5        |      |                |
| HZ3     | C58     | OP1  | 4.9        |      |                |
| HZ2     | C58     | OP1  | 4.5        |      |                |
| HZ2     | C58     | OP2  | 1.2        |      |                |
| HZ3     | C58     | OP2  | 0.5        |      |                |
| HZ1     | C58     | OP2  | 0.2        |      |                |
| ARG324  | HH21    | C58  | O3'        | OP2  | 0.7            |
|         | HH11    | C58  | O3'        | OP1  | 0.3            |
|         | HH21    | C58  | OP1        |      | 0.1            |
|         | HH22    | C58  | OP1        |      | 0.1            |
|         | HH22    | T59  | O3'        |      | 0.1            |
|         | HH21    | T59  | O5'        |      | 0.1            |
|         | HH11    | T59  | OP1        |      | 47.2           |
|         | HE      | T59  | OP1        |      | 15.5           |
|         | HH21    | T59  | OP1        |      | 13.5           |
|         | HH21    | T59  | OP2        |      | 12.9           |
|         | HE      | T59  | OP2        |      | 3.1            |
|         | HH11    | T59  | OP2        |      | 0.5            |
|         | HH12    | T59  | OP2        |      | 0.1            |
|         | HH22    | C60  | OP1        |      | 1.7            |
|         | HH12    | C60  | OP1        |      | 1.4            |
|         | HH21    | C60  | OP1        |      | 0.1            |
|         | HH22    | C60  | OP2        |      | 38.7           |
|         | HH12    | C60  | OP2        |      | 37.2           |
| LYS350  | HZ1     | G3   | O3'        |      | 2.4            |
|         | HZ3     | G3   | O3'        |      | 1.5            |
|         | HZ2     | G3   | O3'        |      | 0.9            |
|         | HZ1     | A4   | OP1        |      | 32.5           |
|         | HZ3     | A4   | OP1        |      | 21.5           |
|         | HZ2     | A4   | OP1        |      | 20.4           |
| GLN352  | HE21    | G3   | O3'        |      | 20.6           |
|         | HE22    | G3   | O3'        |      | 0.2            |
|         | HE22    | G3   | OP1        |      | 22.3           |
|         | HE21    | G3   | OP1        |      | 0.2            |
|         | HE22    | A4   | OP1        |      | 4.9            |
|         | HE21    | A4   | OP1        |      | 1.7            |
|         | HE21    | A4   | OP2        |      | 3.6            |
|         | HE22    | A4   | OP2        |      | 0.2            |
| ASN378  | HD21    | A13  | O3'        |      | 2.5            |
|         | HD21    | A13  | O4'        |      | 0.1            |
|         | HD22    | T59  | O3'        |      | 4              |
|         | HD21    | T59  | O3'        |      | 0.2            |
|         | HD21    | T59  | O4'        |      | 0.2            |
|         | HD22    | T59  | OP1        |      | 0.6            |
|         | HD22    | C60  | OP1        |      | 8.5            |
|         | HD21    | C60  | OP1        |      | 3              |
|         | HD21    | C60  | OP2        |      | 0.8            |