



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Aug 1, 2017 – 11:15 AM EDT

PDB ID : 5XMI
EMDB ID: : EMD-6733
Title : Cryo-EM Structure of the ATP-bound VPS4 mutant-E233Q hexamer (masked)
Authors : Sun, S.; Li, L.; Yang, F.; Wang, X.; Fan, F.; Li, X.; Wang, H.; Sui, S.
Deposited on : unknown
Resolution : 3.90 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

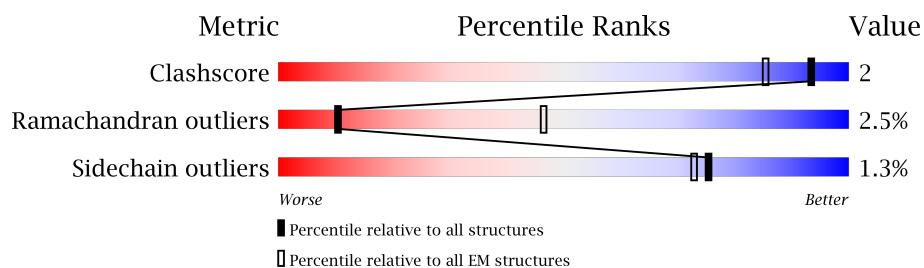
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore | 125131 | 1336 |
| Ramachandran outliers | 121729 | 1120 |
| Sidechain outliers | 121581 | 1026 |

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | A | 437 | |
| 1 | B | 437 | |
| 1 | C | 437 | |
| 1 | D | 437 | |
| 1 | E | 437 | |
| 1 | F | 437 | |

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14969 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Vacuolar protein sorting-associated protein 4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 1 | A | 319 | Total | C | N | O | S | 0 | 0 |
| | | | 2469 | 1552 | 419 | 489 | 9 | | |
| 1 | B | 319 | Total | C | N | O | S | 0 | 0 |
| | | | 2469 | 1552 | 419 | 489 | 9 | | |
| 1 | C | 319 | Total | C | N | O | S | 0 | 0 |
| | | | 2469 | 1552 | 419 | 489 | 9 | | |
| 1 | D | 319 | Total | C | N | O | S | 0 | 0 |
| | | | 2469 | 1552 | 419 | 489 | 9 | | |
| 1 | E | 319 | Total | C | N | O | S | 0 | 0 |
| | | | 2469 | 1552 | 419 | 489 | 9 | | |
| 1 | F | 319 | Total | C | N | O | S | 0 | 0 |
| | | | 2469 | 1552 | 419 | 489 | 9 | | |

There are 6 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| A | 233 | GLN | GLU | engineered mutation | UNP P52917 |
| B | 233 | GLN | GLU | engineered mutation | UNP P52917 |
| C | 233 | GLN | GLU | engineered mutation | UNP P52917 |
| D | 233 | GLN | GLU | engineered mutation | UNP P52917 |
| E | 233 | GLN | GLU | engineered mutation | UNP P52917 |
| F | 233 | GLN | GLU | engineered mutation | UNP P52917 |

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



- | | | |
|------|------|-----|
| A136 | THR | MET |
| V149 | GLU | SER |
| I150 | TYR | THR |
| L151 | LEU | GLY |
| P152 | ASN | ASP |
| V153 | ARG | PHE |
| | ALA | LEU |
| P156 | GLN | LYS |
| H157 | LEU | GLY |
| I169 | LYS | ILE |
| | LYS | GLU |
| D201 | HIS | LEU |
| G208 | LEU | VAL |
| E209 | GLN | GLN |
| S210 | SER | LYS |
| | GLU | ALA |
| V214 | ALA | ASP |
| K225 | ALA | ASP |
| | LYS | THR |
| Q233 | LYS | ALA |
| V234 | SER | THR |
| | PRO | GLN |
| T240 | SER | TYR |
| | ALA | GLU |
| E247 | GLY | ALA |
| | SER | TYR |
| E255 | GLY | THR |
| | SER | ALA |
| M260 | ASN | TYR |
| | GLY | TYR |
| V263 | GLY | ASN |
| | ASN | GLY |
| G274 | LYS | LEU |
| A275 | LYS | ASP |
| T276 | ILE | TYR |
| | SER | LEU |
| | GLN | MET |
| I310 | GLN | MET |
| | GLU | LEU |
| E435 | GLU | ALA |
| G436 | GLY | LEU |
| N437 | GLU | LYS |
| | ASP | TYR |
| | ASN | GLY |
| | GLY | LYS |
| | GLY | ASN |
| | GLU | PRO |
| | ASP | LYS |
| | ASN | SER |
| | LYS | LYS |
| | LYS | ASP |
| | LEU | LEU |
| | ARG | ILE |
| | GLY | ARG |
| | ALA | ALA |
| | I119 | LYS |
| | | THR |

4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| Reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | Depositor |
| Number of particles used | 106918 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 50 | Depositor |
| Minimum defocus (nm) | Not provided | Depositor |
| Maximum defocus (nm) | Not provided | Depositor |
| Magnification | Not provided | Depositor |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-------------|-------------|-------------|
| | | RMSZ | $\# Z > 2$ | RMSZ | $\# Z > 2$ |
| 1 | A | 0.45 | 0/2511 | 0.68 | 0/3395 |
| 1 | B | 0.41 | 0/2511 | 0.57 | 0/3395 |
| 1 | C | 0.41 | 0/2511 | 0.54 | 0/3395 |
| 1 | D | 0.41 | 0/2511 | 0.55 | 0/3395 |
| 1 | E | 0.41 | 0/2511 | 0.57 | 0/3395 |
| 1 | F | 0.41 | 0/2511 | 0.56 | 0/3395 |
| All | All | 0.42 | 0/15066 | 0.58 | 0/20370 |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1 | A | 0 | 3 |
| 1 | B | 0 | 1 |
| 1 | C | 0 | 1 |
| All | All | 0 | 5 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 1 | A | 225 | LYS | Peptide |
| 1 | A | 315 | THR | Peptide |
| 1 | A | 416 | THR | Peptide |
| 1 | B | 225 | LYS | Peptide |

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| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 1 | C | 225 | LYS | Peptide |

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 2469 | 0 | 2477 | 13 | 0 |
| 1 | B | 2469 | 0 | 2477 | 3 | 0 |
| 1 | C | 2469 | 0 | 2477 | 9 | 0 |
| 1 | D | 2469 | 0 | 2477 | 5 | 0 |
| 1 | E | 2469 | 0 | 2477 | 6 | 0 |
| 1 | F | 2469 | 0 | 2477 | 10 | 0 |
| 2 | B | 31 | 0 | 12 | 0 | 0 |
| 2 | C | 31 | 0 | 12 | 0 | 0 |
| 2 | D | 31 | 0 | 12 | 0 | 0 |
| 2 | E | 31 | 0 | 12 | 0 | 0 |
| 2 | F | 31 | 0 | 12 | 0 | 0 |
| All | All | 14969 | 0 | 14922 | 45 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (45) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:A:172:TYR:HB2 | 1:A:279:PRO:HG3 | 1.79 | 0.65 |
| 1:B:417:VAL:HG13 | 1:B:422:LEU:HD22 | 1.82 | 0.61 |
| 1:E:237:LEU:HD12 | 1:E:238:THR:HG23 | 1.83 | 0.60 |
| 1:A:169:ILE:HB | 1:A:273:LEU:HD23 | 1.83 | 0.60 |
| 1:A:315:THR:HG22 | 1:A:316:PRO:HD3 | 1.84 | 0.58 |
| 1:E:257:LEU:HD21 | 1:E:286:ILE:HG12 | 1.86 | 0.56 |
| 1:A:304:ARG:NH1 | 1:A:331:THR:O | 2.44 | 0.51 |
| 1:D:263:VAL:HG23 | 1:D:268:GLN:HB3 | 1.92 | 0.51 |
| 1:A:198:SER:OG | 1:A:233:GLN:NE2 | 2.44 | 0.51 |
| 1:B:337:SER:O | 1:B:341:VAL:HG23 | 2.11 | 0.49 |
| 1:F:234:VAL:HG22 | 1:F:276:THR:HB | 1.94 | 0.49 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:A:151:LEU:HD21 | 1:A:158:LEU:HD22 | 1.94 | 0.49 |
| 1:C:305:THR:HG23 | 1:C:324:TYR:HB3 | 1.95 | 0.48 |
| 1:B:429:THR:O | 1:B:433:GLY:N | 2.46 | 0.48 |
| 1:E:237:LEU:CD1 | 1:E:238:THR:HG23 | 2.43 | 0.47 |
| 1:E:317:CYS:SG | 1:E:318:VAL:HG22 | 2.55 | 0.47 |
| 1:F:136:ALA:HB2 | 1:F:310:ILE:CD1 | 2.46 | 0.46 |
| 1:C:225:LYS:HB3 | 1:C:226:PRO:HD2 | 1.97 | 0.46 |
| 1:C:319:LEU:O | 1:C:320:THR:HG23 | 2.16 | 0.46 |
| 1:F:214:VAL:HG11 | 1:F:255:GLU:HG3 | 1.98 | 0.45 |
| 1:A:225:LYS:HB3 | 1:A:226:PRO:HD2 | 1.99 | 0.45 |
| 1:E:373:LEU:N | 1:E:395:GLU:O | 2.49 | 0.45 |
| 1:A:338:ASP:O | 1:A:342:VAL:HG23 | 2.15 | 0.45 |
| 1:E:225:LYS:HB3 | 1:E:226:PRO:HD2 | 1.99 | 0.45 |
| 1:F:233:GLN:N | 1:F:275:ALA:O | 2.50 | 0.45 |
| 1:F:136:ALA:HB2 | 1:F:310:ILE:HD12 | 1.98 | 0.45 |
| 1:D:202:LEU:HD11 | 1:D:214:VAL:HG22 | 1.98 | 0.45 |
| 1:C:145:LEU:HD23 | 1:C:169:ILE:HG21 | 1.99 | 0.44 |
| 1:F:169:ILE:O | 1:F:274:GLY:N | 2.49 | 0.44 |
| 1:F:260:MET:HA | 1:F:263:VAL:HG12 | 1.99 | 0.44 |
| 1:F:149:VAL:O | 1:F:153:VAL:HG23 | 2.18 | 0.44 |
| 1:A:138:LEU:HD11 | 1:A:296:ILE:HG23 | 2.00 | 0.43 |
| 1:C:221:ALA:HB2 | 1:C:229:ILE:HD11 | 2.00 | 0.43 |
| 1:D:145:LEU:HD22 | 1:D:186:VAL:HG21 | 2.00 | 0.43 |
| 1:C:257:LEU:O | 1:C:289:ARG:NH2 | 2.52 | 0.43 |
| 1:C:349:GLN:HB3 | 1:C:350:PRO:HD3 | 2.00 | 0.43 |
| 1:A:199:SER:O | 1:A:203:VAL:HG23 | 2.19 | 0.42 |
| 1:D:234:VAL:HG23 | 1:D:282:LEU:HD13 | 2.00 | 0.42 |
| 1:C:373:LEU:HD11 | 1:C:391:ILE:HG21 | 2.02 | 0.42 |
| 1:F:151:LEU:HB3 | 1:F:152:PRO:HD3 | 2.02 | 0.42 |
| 1:A:286:ILE:HG23 | 1:A:432:PHE:CE2 | 2.55 | 0.42 |
| 1:D:149:VAL:HG22 | 1:D:271:LEU:CD2 | 2.50 | 0.42 |
| 1:A:351:ILE:HD12 | 1:F:151:LEU:HD23 | 2.02 | 0.41 |
| 1:C:145:LEU:HD23 | 1:C:169:ILE:HD13 | 2.02 | 0.41 |
| 1:A:240:THR:O | 1:A:240:THR:HG23 | 2.20 | 0.41 |

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|----|
| 1 | A | 317/437 (72%) | 276 (87%) | 31 (10%) | 10 (3%) | 5 | 40 |
| 1 | B | 317/437 (72%) | 282 (89%) | 28 (9%) | 7 (2%) | 8 | 47 |
| 1 | C | 317/437 (72%) | 283 (89%) | 27 (8%) | 7 (2%) | 8 | 47 |
| 1 | D | 317/437 (72%) | 277 (87%) | 31 (10%) | 9 (3%) | 6 | 43 |
| 1 | E | 317/437 (72%) | 284 (90%) | 26 (8%) | 7 (2%) | 8 | 47 |
| 1 | F | 317/437 (72%) | 283 (89%) | 27 (8%) | 7 (2%) | 8 | 47 |
| All | All | 1902/2622 (72%) | 1685 (89%) | 170 (9%) | 47 (2%) | 10 | 44 |

All (47) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 226 | PRO |
| 1 | A | 290 | PHE |
| 1 | A | 312 | VAL |
| 1 | A | 314 | ASP |
| 1 | B | 226 | PRO |
| 1 | D | 292 | ARG |
| 1 | E | 226 | PRO |
| 1 | A | 208 | GLY |
| 1 | A | 282 | LEU |
| 1 | A | 291 | GLU |
| 1 | A | 317 | CYS |
| 1 | B | 312 | VAL |
| 1 | C | 226 | PRO |
| 1 | D | 243 | GLU |
| 1 | E | 207 | MET |
| 1 | F | 208 | GLY |
| 1 | F | 247 | GLU |
| 1 | A | 266 | ASP |
| 1 | A | 287 | ARG |
| 1 | B | 357 | ALA |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | C | 138 | LEU |
| 1 | C | 202 | LEU |
| 1 | C | 240 | THR |
| 1 | D | 318 | VAL |
| 1 | E | 291 | GLU |
| 1 | F | 156 | PRO |
| 1 | F | 435 | GLU |
| 1 | B | 242 | GLY |
| 1 | B | 247 | GLU |
| 1 | C | 243 | GLU |
| 1 | D | 138 | LEU |
| 1 | E | 238 | THR |
| 1 | E | 245 | GLU |
| 1 | E | 260 | MET |
| 1 | E | 317 | CYS |
| 1 | F | 157 | HIS |
| 1 | B | 301 | LEU |
| 1 | D | 225 | LYS |
| 1 | D | 240 | THR |
| 1 | D | 266 | ASP |
| 1 | F | 210 | SER |
| 1 | C | 266 | ASP |
| 1 | F | 225 | LYS |
| 1 | B | 318 | VAL |
| 1 | D | 436 | GLY |
| 1 | C | 178 | GLY |
| 1 | D | 433 | GLY |

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|-----|-------|---------------|-----------|----------|-------------|
| 1 | A | 272/367 (74%) | 263 (97%) | 9 (3%) | 43 73 |
| 1 | B | 272/367 (74%) | 270 (99%) | 2 (1%) | 87 94 |
| 1 | C | 272/367 (74%) | 268 (98%) | 4 (2%) | 70 87 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|-------------|----|
| 1 | D | 272/367 (74%) | 271 (100%) | 1 (0%) | 93 | 96 |
| 1 | E | 272/367 (74%) | 269 (99%) | 3 (1%) | 78 | 89 |
| 1 | F | 272/367 (74%) | 270 (99%) | 2 (1%) | 87 | 94 |
| All | All | 1632/2202 (74%) | 1611 (99%) | 21 (1%) | 75 | 88 |

All (21) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 138 | LEU |
| 1 | A | 200 | SER |
| 1 | A | 202 | LEU |
| 1 | A | 233 | GLN |
| 1 | A | 258 | VAL |
| 1 | A | 281 | GLN |
| 1 | A | 282 | LEU |
| 1 | A | 315 | THR |
| 1 | A | 414 | ARG |
| 1 | B | 202 | LEU |
| 1 | B | 323 | ASP |
| 1 | C | 223 | GLU |
| 1 | C | 281 | GLN |
| 1 | C | 318 | VAL |
| 1 | C | 320 | THR |
| 1 | D | 290 | PHE |
| 1 | E | 127 | LYS |
| 1 | E | 318 | VAL |
| 1 | E | 355 | GLN |
| 1 | F | 201 | ASP |
| 1 | F | 240 | THR |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 233 | GLN |
| 1 | A | 268 | GLN |
| 1 | A | 281 | GLN |
| 1 | C | 281 | GLN |
| 1 | C | 437 | ASN |
| 1 | E | 216 | GLN |
| 1 | E | 265 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | F | 277 | ASN |

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|-------------|-------------|------|-------------|
| | | | | | Counts | RMSZ | $\# Z > 2$ | Counts | RMSZ | $\# Z > 2$ |
| 2 | ATP | B | 501 | - | 27,33,33 | 1.05 | 2 (7%) | 25,52,52 | 1.76 | 2 (8%) |
| 2 | ATP | C | 501 | - | 27,33,33 | 1.04 | 2 (7%) | 25,52,52 | 1.84 | 2 (8%) |
| 2 | ATP | D | 501 | - | 27,33,33 | 1.04 | 2 (7%) | 25,52,52 | 1.79 | 2 (8%) |
| 2 | ATP | E | 501 | - | 27,33,33 | 1.04 | 2 (7%) | 25,52,52 | 1.77 | 2 (8%) |
| 2 | ATP | F | 501 | - | 27,33,33 | 1.04 | 2 (7%) | 25,52,52 | 1.85 | 2 (8%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|------------|---------|
| 2 | ATP | B | 501 | - | - | 0/18/38/38 | 0/3/3/3 |
| 2 | ATP | C | 501 | - | - | 0/18/38/38 | 0/3/3/3 |
| 2 | ATP | D | 501 | - | - | 0/18/38/38 | 0/3/3/3 |
| 2 | ATP | E | 501 | - | - | 0/18/38/38 | 0/3/3/3 |
| 2 | ATP | F | 501 | - | - | 0/18/38/38 | 0/3/3/3 |

All (10) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|------|-------------|----------|
| 2 | E | 501 | ATP | C2-N3 | 2.07 | 1.35 | 1.32 |
| 2 | F | 501 | ATP | C2-N3 | 2.09 | 1.35 | 1.32 |
| 2 | C | 501 | ATP | C2-N3 | 2.10 | 1.35 | 1.32 |
| 2 | B | 501 | ATP | C2-N3 | 2.17 | 1.35 | 1.32 |
| 2 | D | 501 | ATP | C2-N3 | 2.18 | 1.35 | 1.32 |
| 2 | B | 501 | ATP | C5-C4 | 3.21 | 1.47 | 1.40 |
| 2 | D | 501 | ATP | C5-C4 | 3.22 | 1.47 | 1.40 |
| 2 | F | 501 | ATP | C5-C4 | 3.23 | 1.47 | 1.40 |
| 2 | C | 501 | ATP | C5-C4 | 3.23 | 1.47 | 1.40 |
| 2 | E | 501 | ATP | C5-C4 | 3.28 | 1.47 | 1.40 |

All (10) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 2 | F | 501 | ATP | N3-C2-N1 | -7.02 | 122.74 | 128.86 |
| 2 | C | 501 | ATP | N3-C2-N1 | -7.02 | 122.74 | 128.86 |
| 2 | D | 501 | ATP | N3-C2-N1 | -6.86 | 122.88 | 128.86 |
| 2 | E | 501 | ATP | N3-C2-N1 | -6.80 | 122.93 | 128.86 |
| 2 | B | 501 | ATP | N3-C2-N1 | -6.80 | 122.94 | 128.86 |
| 2 | C | 501 | ATP | C4-C5-N7 | -3.14 | 106.38 | 109.41 |
| 2 | F | 501 | ATP | C4-C5-N7 | -3.12 | 106.39 | 109.41 |
| 2 | B | 501 | ATP | C4-C5-N7 | -3.05 | 106.46 | 109.41 |
| 2 | D | 501 | ATP | C4-C5-N7 | -2.94 | 106.57 | 109.41 |
| 2 | E | 501 | ATP | C4-C5-N7 | -2.81 | 106.69 | 109.41 |

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.