# wwPDB EM Validation Summary Report ⓘ

May 14, 2024 – 05:53 am BST

| | | |
|---|---|---|
| PDB ID | : | 6Z2X |
| EMDB ID | : | EMD-11051 |
| Title | : | Mec1-Ddc2 (F2244L mutant) in complex with Mg AMP-PNP (State II) |
| Authors | : | Yates, L.A.; Zhang, X. |
| Deposited on | : | 2020-05-18 |
| Resolution | : | 3.20 Å(reported) |
| Based on initial model | : | 6Z2W |

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

---

The following versions of software and data (see references ⓘ) were used in the production of this report:

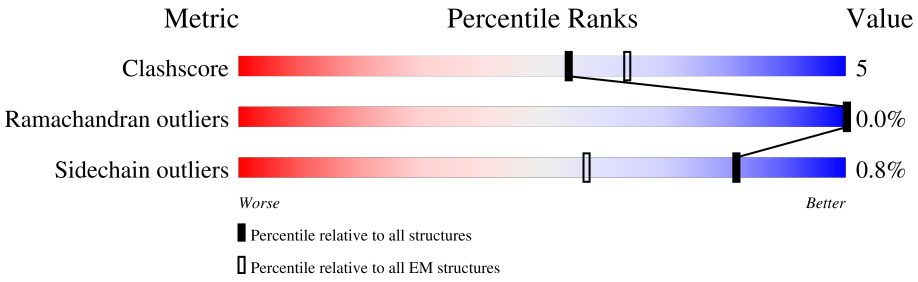
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev92 |
| Mogul | : | 1.8.4, CSD as541be (2020) |
| MolProbity | : | 4.02b-467 |
| buster-report | : | 1.1.7 (2018) |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | FAILED |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.36.2 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 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 | 158937 | 4297 |
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=5%

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | C | 747 | 60% 15% 25% |
| 1 | D | 747 | 59% 15% 25% |
| 2 | E | 2368 | 83% 14% • |
| 2 | F | 2368 | 83% 15% • |

# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 46604 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 DNA damage checkpoint protein LCD1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 1 | D | 558 | Total | C | N | O | S | 1 | 0 |
| | | | 4576 | 2954 | 753 | 846 | 23 | | |
| 1 | C | 558 | Total | C | N | O | S | 1 | 0 |
| | | | 4576 | 2954 | 753 | 846 | 23 | | |

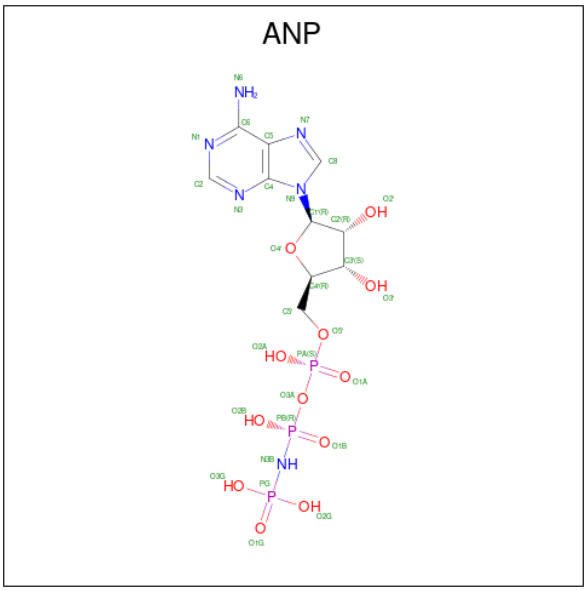
- Molecule 2 is a protein called Serine/threonine-protein kinase MEC1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 2 | E | 2325 | Total | C | N | O | S | 0 | 0 |
| | | | 18692 | 12029 | 3127 | 3459 | 77 | | |
| 2 | F | 2325 | Total | C | N | O | S | 0 | 0 |
| | | | 18692 | 12029 | 3127 | 3459 | 77 | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| E | 2244 | LEU | PHE | engineered mutation | UNP P38111 |
| F | 2244 | LEU | PHE | engineered mutation | UNP P38111 |

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).




| Mol | Chain | Residues | Atoms | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|
| 3 | E | 1 | Total | C | N | O | P | 0 |
| | | | 31 | 10 | 6 | 12 | 3 | |
| 3 | F | 1 | Total | C | N | O | P | 0 |
| | | | 31 | 10 | 6 | 12 | 3 | |

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 4 | E | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 4 | F | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

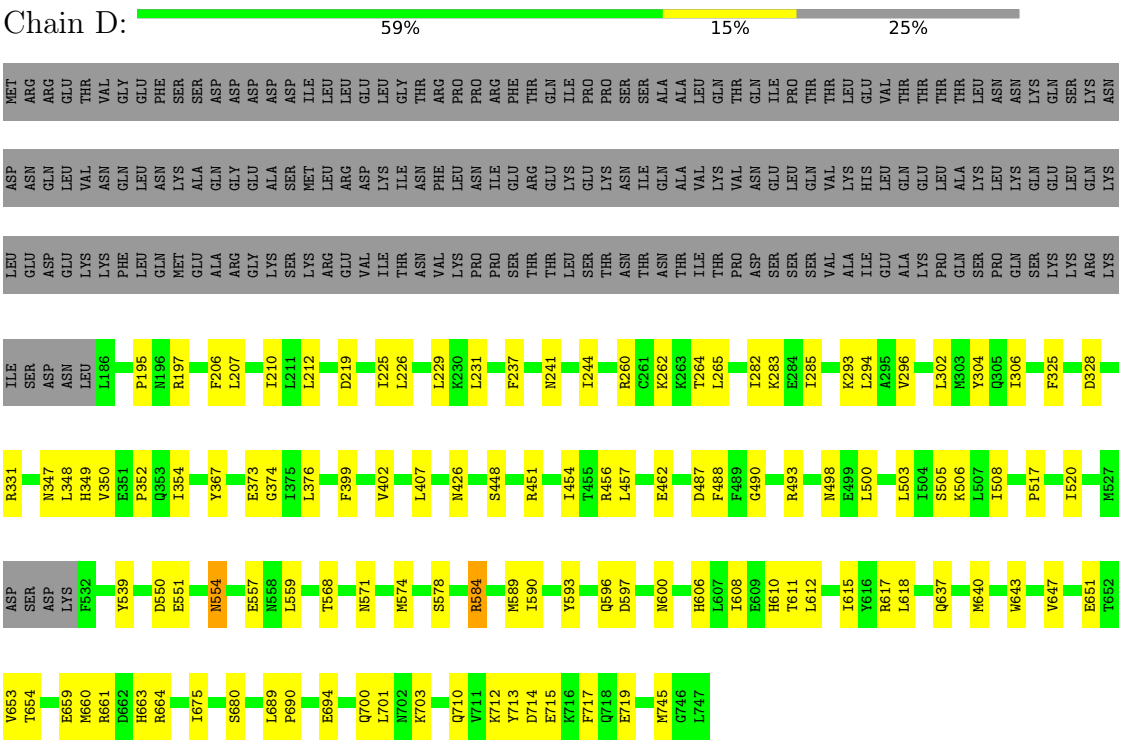
| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 5 | E | 2 | Total | Mg | 0 |
| | | | 2 | 2 | |
| 5 | F | 2 | Total | Mg | 0 |
| | | | 2 | 2 | |

# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

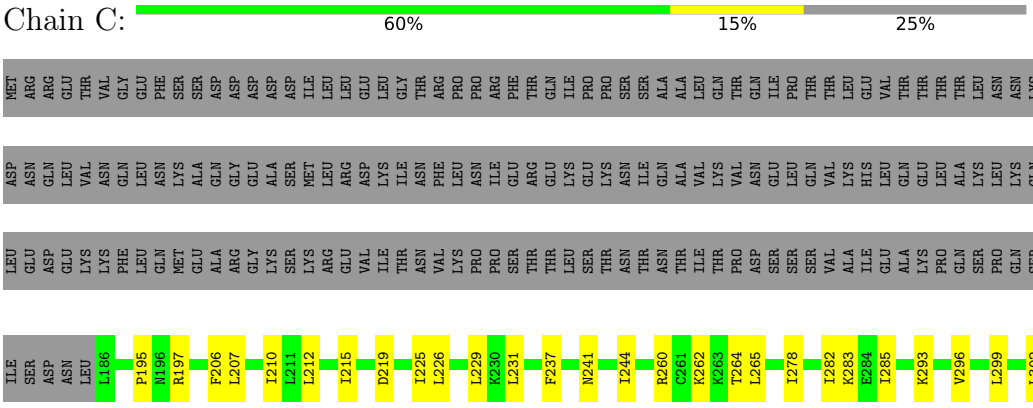
• Molecule 1: DNA damage checkpoint protein LCD1

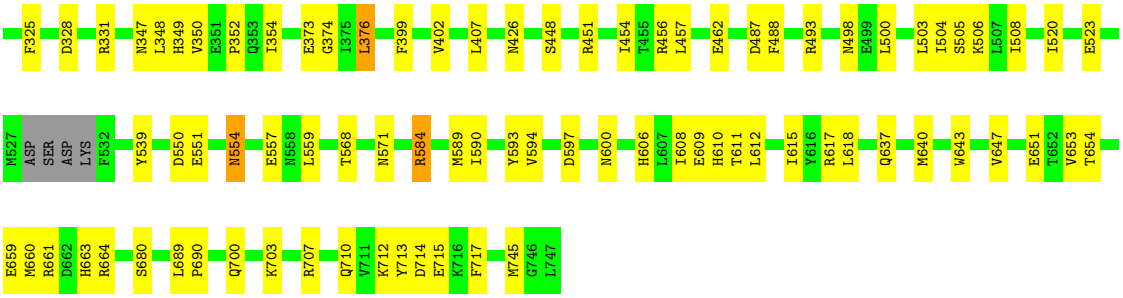
Chain D:




• Molecule 1: DNA damage checkpoint protein LCD1

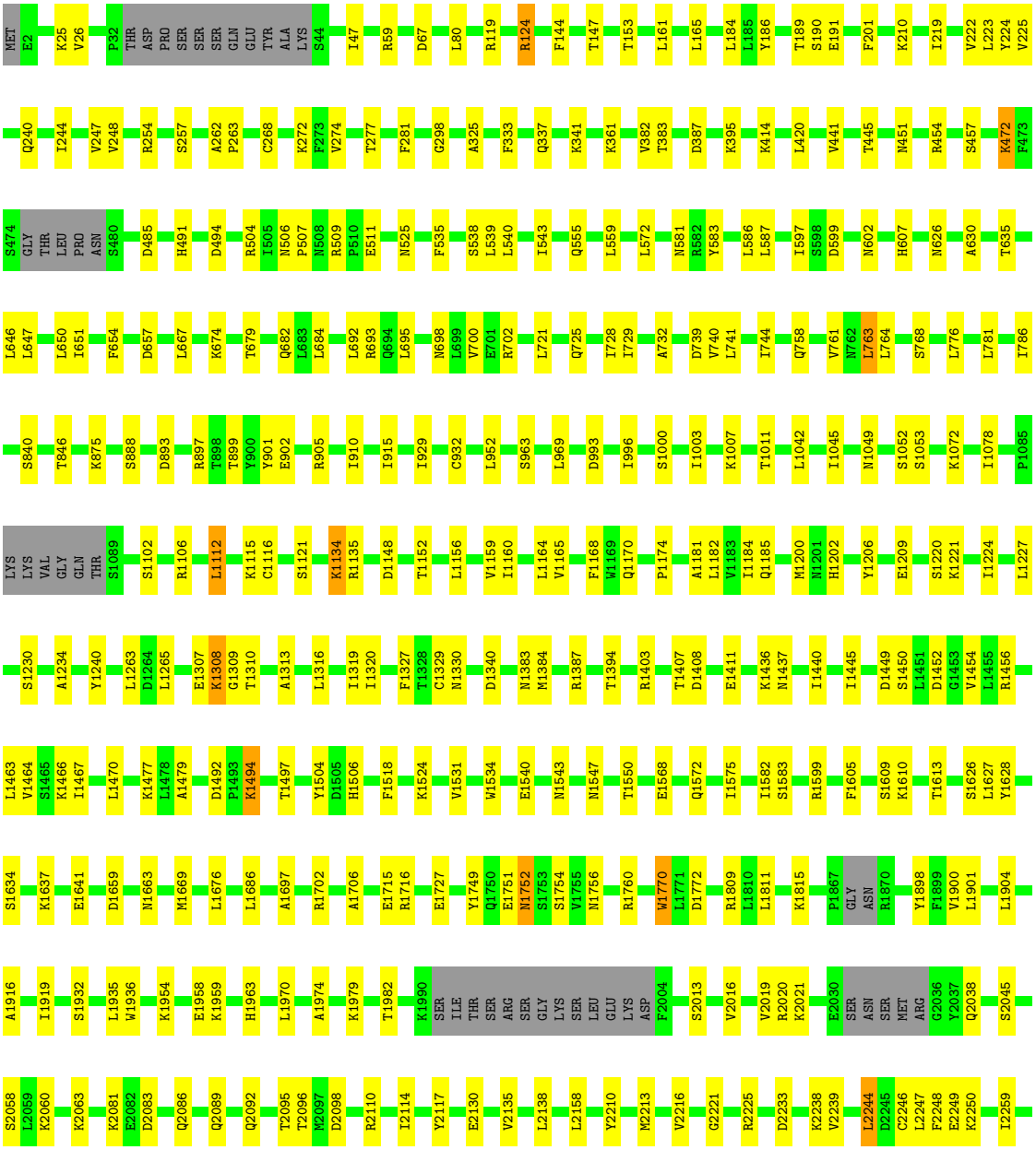
Chain C:





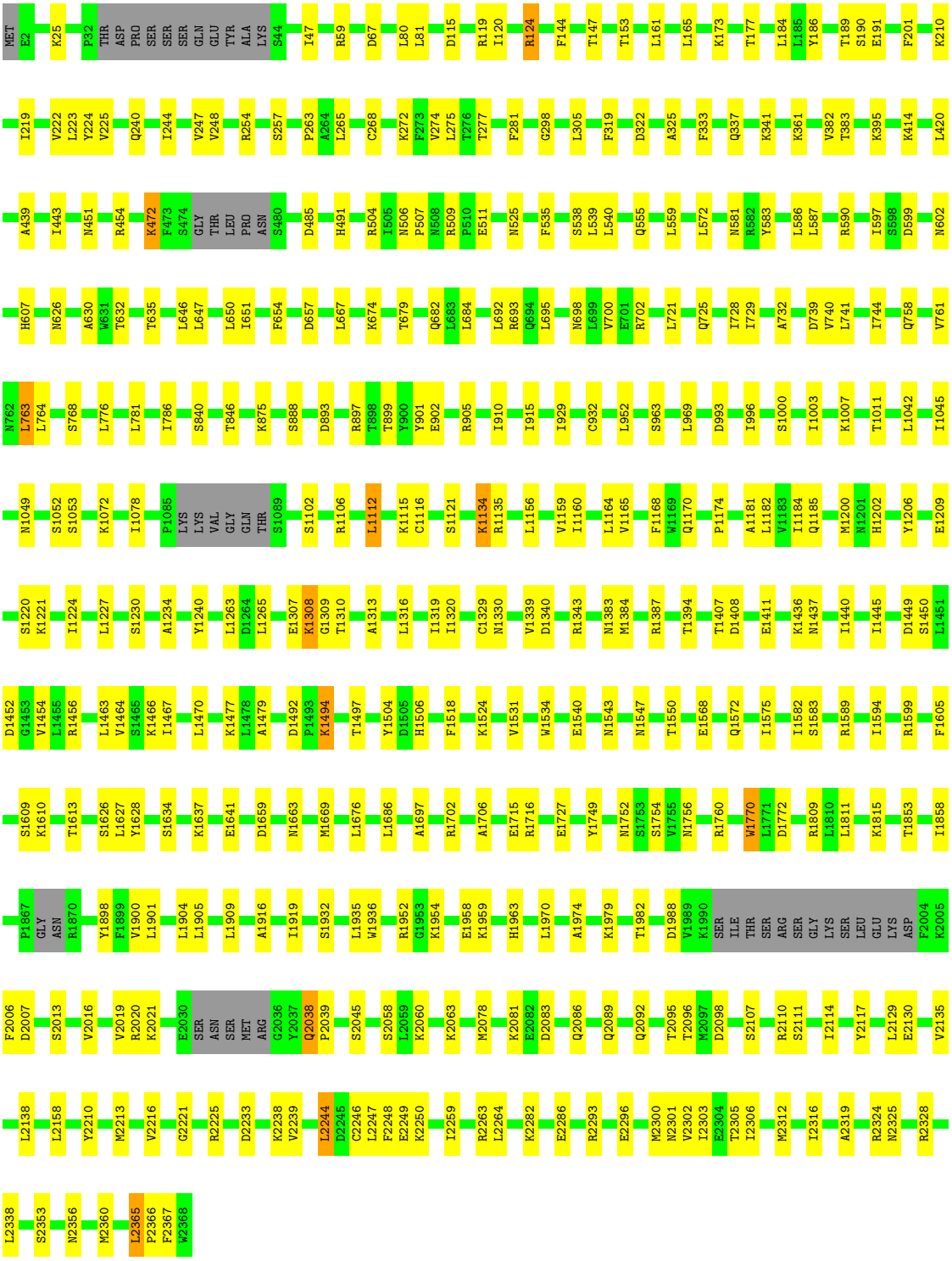

• Molecule 2: Serine/threonine-protein kinase MEC1

Chain E: 83% 14%




• Molecule 2: Serine/threonine-protein kinase MEC1

Chain F:

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C2 | Depositor |
| Number of particles used | 12205 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | TFS KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 51 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | 81000 | Depositor |
| Image detector | GATAN K3 (6k 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: MG, ANP, ZN

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 | $\#\|Z\| > 5$ | RMSZ | $\#\|Z\| > 5$ |
| 1 | C | 0.41 | 0/4664 | 0.66 | 4/6303 (0.1%) |
| 1 | D | 0.41 | 0/4664 | 0.66 | 4/6303 (0.1%) |
| 2 | E | 0.35 | 0/19078 | 0.61 | 8/25836 (0.0%) |
| 2 | F | 0.35 | 0/19078 | 0.61 | 8/25836 (0.0%) |
| All | All | 0.37 | 0/47484 | 0.62 | 24/64278 (0.0%) |

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 |
|---|---|---|---|
| 2 | E | 0 | 7 |
| 2 | F | 0 | 7 |
| All | All | 0 | 14 |

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | F | 1408 | ASP | CB-CG-OD1 | 7.97 | 125.47 | 118.30 |
| 2 | E | 1408 | ASP | CB-CG-OD1 | 7.96 | 125.47 | 118.30 |
| 1 | C | 376 | LEU | CA-CB-CG | -6.62 | 100.07 | 115.30 |
| 1 | D | 376 | LEU | CA-CB-CG | -6.60 | 100.13 | 115.30 |
| 2 | E | 657 | ASP | CB-CG-OD1 | 6.49 | 124.14 | 118.30 |

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 2 | E | 1307 | GLU | Peptide |
| 2 | E | 1308 | LYS | Peptide |
| 2 | E | 1752 | ASN | Peptide |
| 2 | E | 1754 | SER | Peptide |
| 2 | E | 472 | LYS | Peptide |

## 5.2 Too-close contacts (i)

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 | C | 4576 | 0 | 4635 | 64 | 0 |
| 1 | D | 4576 | 0 | 4635 | 67 | 0 |
| 2 | E | 18692 | 0 | 18657 | 193 | 0 |
| 2 | F | 18692 | 0 | 18656 | 204 | 0 |
| 3 | E | 31 | 0 | 13 | 1 | 0 |
| 3 | F | 31 | 0 | 13 | 1 | 0 |
| 4 | E | 1 | 0 | 0 | 0 | 0 |
| 4 | F | 1 | 0 | 0 | 0 | 0 |
| 5 | E | 2 | 0 | 0 | 0 | 0 |
| 5 | F | 2 | 0 | 0 | 0 | 0 |
| All | All | 46604 | 0 | 46609 | 505 | 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 5.

The worst 5 of 505 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) |
|---|---|---|---|
| 2:E:2135:VAL:HG21 | 3:E:2401:ANP:H2 | 1.73 | 0.69 |
| 2:E:1506:HIS:O | 2:E:1702:ARG:NH2 | 2.26 | 0.69 |
| 2:F:2135:VAL:HG21 | 3:F:2401:ANP:H2 | 1.73 | 0.69 |
| 2:F:1506:HIS:O | 2:F:1702:ARG:NH2 | 2.26 | 0.68 |
| 2:F:776:LEU:HD23 | 2:F:840:SER:HB2 | 1.77 | 0.66 |

There are no symmetry-related clashes.

## 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

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 | C | 555/747 (74%) | 511 (92%) | 44 (8%) | 0 | 100 | 100 |
| 1 | D | 555/747 (74%) | 511 (92%) | 44 (8%) | 0 | 100 | 100 |
| 2 | E | 2311/2368 (98%) | 2119 (92%) | 191 (8%) | 1 (0%) | 100 | 100 |
| 2 | F | 2311/2368 (98%) | 2119 (92%) | 191 (8%) | 1 (0%) | 100 | 100 |
| All | All | 5732/6230 (92%) | 5260 (92%) | 470 (8%) | 2 (0%) | 100 | 100 |

All (2) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | E | 1309 | GLY |
| 2 | F | 1309 | GLY |

### 5.3.2 Protein sidechains (i)

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 | C | 517/698 (74%) | 514 (99%) | 3 (1%) | 86 | 94 |
| 1 | D | 517/698 (74%) | 514 (99%) | 3 (1%) | 86 | 94 |
| 2 | E | 2068/2174 (95%) | 2050 (99%) | 18 (1%) | 78 | 91 |
| 2 | F | 2068/2174 (95%) | 2050 (99%) | 18 (1%) | 78 | 91 |
| All | All | 5170/5744 (90%) | 5128 (99%) | 42 (1%) | 82 | 93 |

5 of 42 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | F | 472 | LYS |
| 2 | F | 1384 | MET |
| 2 | F | 525 | ASN |
| 2 | F | 969 | LEU |
| 2 | F | 1477 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | E | 2356 | ASN |
| 2 | F | 986 | ASN |
| 2 | F | 2317 | GLN |
| 2 | F | 682 | GLN |
| 2 | F | 1274 | HIS |

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

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 | $\#\|Z\|>2$ |
| 3 | ANP | E | 2401 | 5 | 29,33,33 | 1.09 | 4 (13%) | 31,52,52 | 1.27 | 3 (9%) |
| 3 | ANP | F | 2401 | 5 | 29,33,33 | 1.09 | 4 (13%) | 31,52,52 | 1.27 | 3 (9%) |

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 |
|---|---|---|---|---|---|---|---|
| 3 | ANP | E | 2401 | 5 | - | 7/14/38/38 | 0/3/3/3 |
| 3 | ANP | F | 2401 | 5 | - | 7/14/38/38 | 0/3/3/3 |

The worst 5 of 8 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 3 | E | 2401 | ANP | PB-O3A | -2.89 | 1.55 | 1.59 |
| 3 | F | 2401 | ANP | PB-O3A | -2.87 | 1.55 | 1.59 |
| 3 | F | 2401 | ANP | PG-O1G | 2.28 | 1.49 | 1.46 |
| 3 | E | 2401 | ANP | PG-O1G | 2.27 | 1.49 | 1.46 |
| 3 | F | 2401 | ANP | PG-N3B | 2.23 | 1.69 | 1.63 |

The worst 5 of 6 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 3 | F | 2401 | ANP | PB-O3A-PA | -4.71 | 116.02 | 132.62 |
| 3 | E | 2401 | ANP | PB-O3A-PA | -4.71 | 116.03 | 132.62 |
| 3 | F | 2401 | ANP | O1G-PG-N3B | -2.28 | 108.41 | 111.77 |
| 3 | E | 2401 | ANP | O1G-PG-N3B | -2.28 | 108.41 | 111.77 |
| 3 | E | 2401 | ANP | C5-C6-N6 | 2.26 | 123.78 | 120.35 |

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

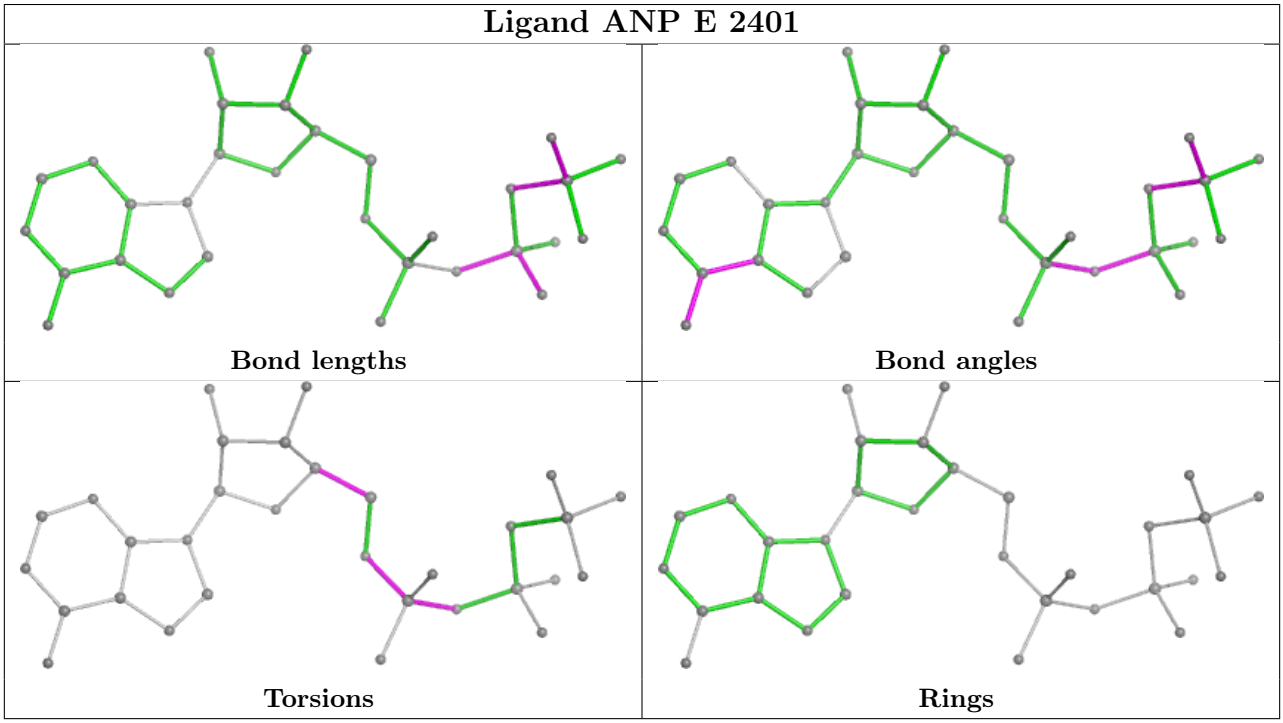
| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 3 | E | 2401 | ANP | C5'-O5'-PA-O1A |
| 3 | E | 2401 | ANP | O4'-C4'-C5'-O5' |
| 3 | E | 2401 | ANP | C3'-C4'-C5'-O5' |
| 3 | F | 2401 | ANP | C5'-O5'-PA-O1A |
| 3 | F | 2401 | ANP | O4'-C4'-C5'-O5' |

There are no ring outliers.

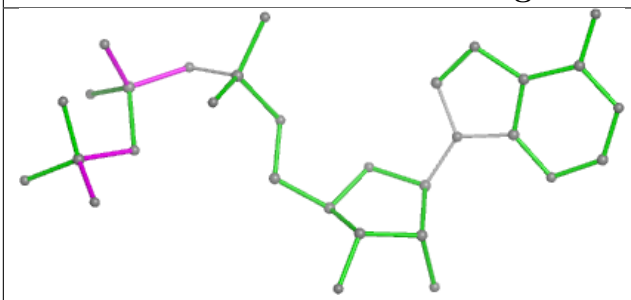
2 monomers are involved in 2 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 3 | E | 2401 | ANP | 1 | 0 |
| 3 | F | 2401 | ANP | 1 | 0 |

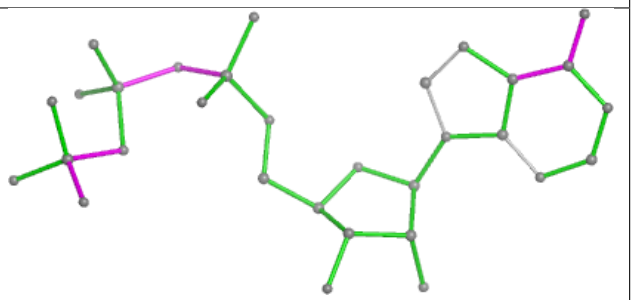
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



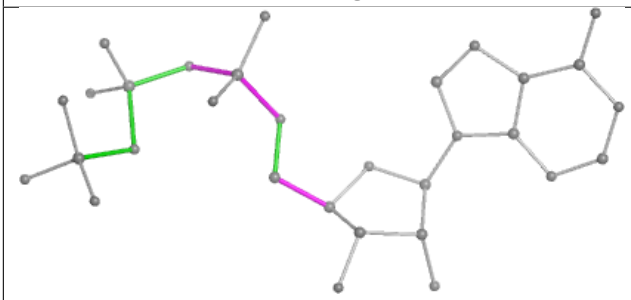
**Ligand ANP F 2401**



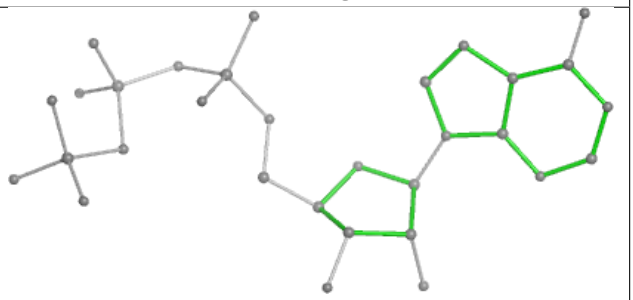
Bond lengths



Bond angles



Torsions



Rings

## 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.

# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11051. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections

This section was not generated.

## 6.2 Central slices

This section was not generated.

## 6.3 Largest variance slices

This section was not generated.

## 6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

## 6.5 Orthogonal surface views

This section was not generated.

## 6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

# 7 Map analysis

This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution

This section was not generated.

## 7.2 Volume estimate versus contour level

This section was not generated.

## 7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

# 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

# 9 Map-model fit

This section was not generated.