

wwPDB NMR Structure Validation Summary Report (i)

Apr 16, 2023 – 07:22 AM EDT

PDB ID : 7R7P BMRB ID : 30929

Title : Immature HIV-1 CACTD-SP1 lattice with Bevirimat (BVM) and Inositol hex-

akisphosphate (IP6)

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Deposited on : 2021-06-25

This is a wwPDB NMR Structure 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/NMRValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

wwPDB-RCI : v 1n 11 5 13 A (Berjanski et al., 2005)

PANAV : Wang et al. (2010)

wwPDB-ShiftChecker : v1.2

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

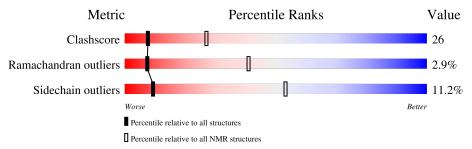
Validation Pipeline (wwPDB-VP) : 2.32.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLID\text{-}STATE\ NMR$

The overall completeness of chemical shifts assignment is 9%.

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 $(\# \mathrm{Entries})$ | $ m NMR~archive \ (\#Entries)$ | | |
|-----------------------|---------------------------------------|--------------------------------|--|--|
| Clashscore | 158937 | 12864 | | |
| Ramachandran outliers | 154571 | 11451 | | |
| Sidechain outliers | 154315 | 11428 | | |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 | G | 102 | 51% | 43% | 6% | | | |
| 1 | Н | 102 | 54% | 44% | • | | | |
| 1 | I | 102 | 55% | 39% | 6% | | | |
| 1 | J | 102 | 52% | 41% | 7% | | | |
| 1 | K | 102 | 59% | 37% | • | | | |
| 1 | L | 102 | 61% | 36% | . | | | |



2 Ensemble composition and analysis (i)

This entry contains 5 models. Model 1 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

| Well-defined (core) protein residues | | | | | | | | |
|--------------------------------------|---------------------------|-------------------|--------------|--|--|--|--|--|
| Well-defined core | Residue range (total) | Backbone RMSD (Å) | Medoid model | | | | | |
| 1 | G:144-G:245, H:144-H:245, | 0.49 | 1 | | | | | |
| | I:144-I:245, J:144-J:245, | | | | | | | |
| | K:144-K:245, L:144-L:245 | | | | | | | |
| | (612) | | | | | | | |

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters and 1 single-model cluster was found.

| Cluster number | Models |
|-----------------------|--------|
| 1 | 3, 5 |
| 2 | 1, 4 |
| Single-model clusters | 2 |



3 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9444 atoms, of which 4728 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Gag polyprotein.

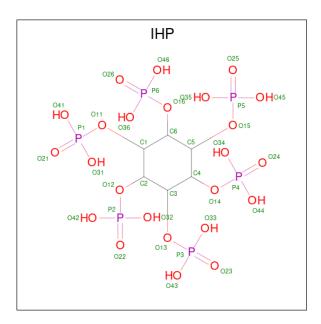
| Mol | Chain | Residues | | | Aton | ns | | | Trace |
|-----|-------|-------------------|-------|-----|------|-----|-----|---|-------|
| 1 | G | 102 | Total | С | Н | N | О | S | 0 |
| 1 | G | 102 | 1551 | 479 | 778 | 136 | 151 | 7 | 0 |
| 1 | Н | 102 | Total | С | Н | N | О | S | 0 |
| 1 | 11 | 102 | 1551 | 479 | 778 | 136 | 151 | 7 | 0 |
| 1 | I | 102 | Total | С | Н | N | О | S | 0 |
| 1 | 1 1 | | 1551 | 479 | 778 | 136 | 151 | 7 | 0 |
| 1 | J | 102 | Total | С | Η | N | О | S | 0 |
| 1 | 9 | 102 | 1551 | 479 | 778 | 136 | 151 | 7 | 0 |
| 1 | K | 102 | Total | С | Н | N | О | S | 0 |
| 1 | | 102 | 1551 | 479 | 778 | 136 | 151 | 7 | |
| 1 | L | 109 | Total | С | Н | N | О | S | 0 |
| | | $L \mid 102 \mid$ | 1551 | 479 | 778 | 136 | 151 | 7 | |

There are 18 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| G | 144 | GLY | - | expression tag | UNP Q72497 |
| G | 145 | GLY | - | expression tag | UNP Q72497 |
| G | 241 | THR | PRO | engineered mutation | UNP Q72497 |
| Н | 144 | GLY | - | expression tag | UNP Q72497 |
| Н | 145 | GLY | - | expression tag | UNP Q72497 |
| Н | 241 | THR | PRO | engineered mutation | UNP Q72497 |
| I | 144 | GLY | - | expression tag | UNP Q72497 |
| I | 145 | GLY | - | expression tag | UNP Q72497 |
| I | 241 | THR | PRO | engineered mutation | UNP Q72497 |
| J | 144 | GLY | - | expression tag | UNP Q72497 |
| J | 145 | GLY | - | expression tag | UNP Q72497 |
| J | 241 | THR | PRO | engineered mutation | UNP Q72497 |
| K | 144 | GLY | - | expression tag | UNP Q72497 |
| K | 145 | GLY | - | expression tag | UNP Q72497 |
| K | 241 | THR | PRO | engineered mutation | UNP Q72497 |
| L | 144 | GLY | | expression tag | UNP Q72497 |
| L | 145 | GLY | - | expression tag | UNP Q72497 |
| L | 241 | THR | PRO | engineered mutation | UNP Q72497 |

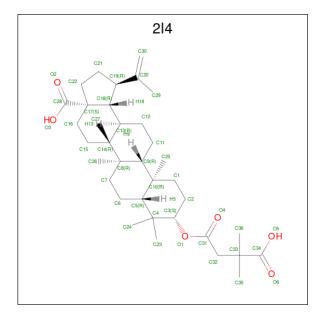
• Molecule 2 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$) (labeled as "Ligand of Interest" by depositor).





| Mol | Chain | Residues | Atoms | | | | |
|-----|-------|----------|-------|---|---|----|---|
| 9 | С | 1 | Total | С | Н | О | Р |
| 2 | G | 1 | 42 | 6 | 6 | 24 | 6 |

• Molecule 3 is 3alpha-[(3-carboxy-3-methylbutanoyl)oxy]-8alpha,9beta,10alpha,13alpha,17al pha,19beta-lup-20(29)-en-28-oic acid (three-letter code: 2I4) (formula: $C_{36}H_{56}O_6$) (labeled as "Ligand of Interest" by depositor).



| Mol | Chain | Residues | Atoms | | | |
|-----|-------|----------|-------|----|----|---|
| 9 | т | 1 | Total | С | Н | О |
| 3 | 1 | 1 | 96 | 36 | 54 | 6 |

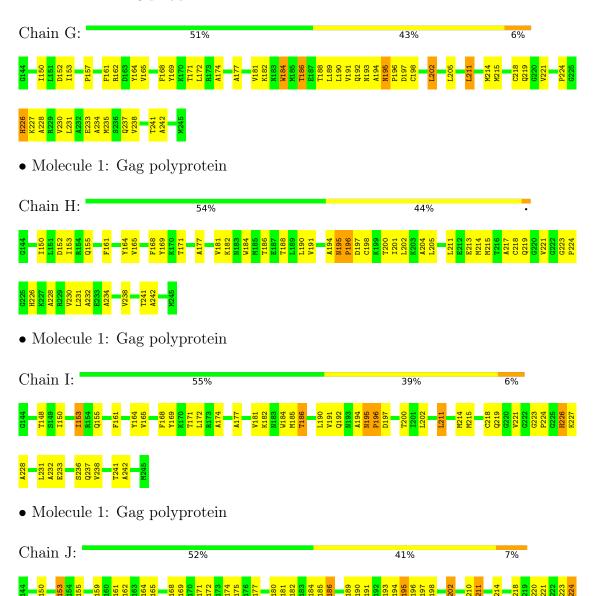


4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

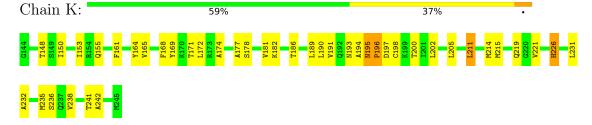
• Molecule 1: Gag polyprotein



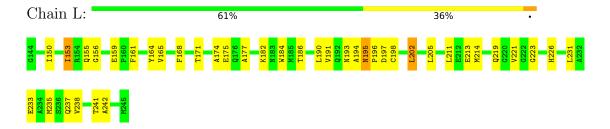




• Molecule 1: Gag polyprotein



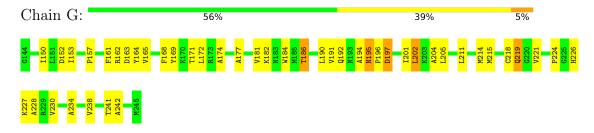
• Molecule 1: Gag polyprotein



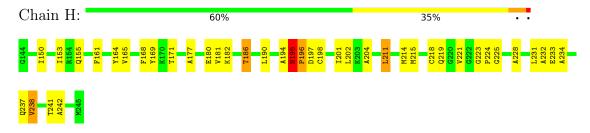
4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 1. Colouring as in section 4.1 above.

• Molecule 1: Gag polyprotein

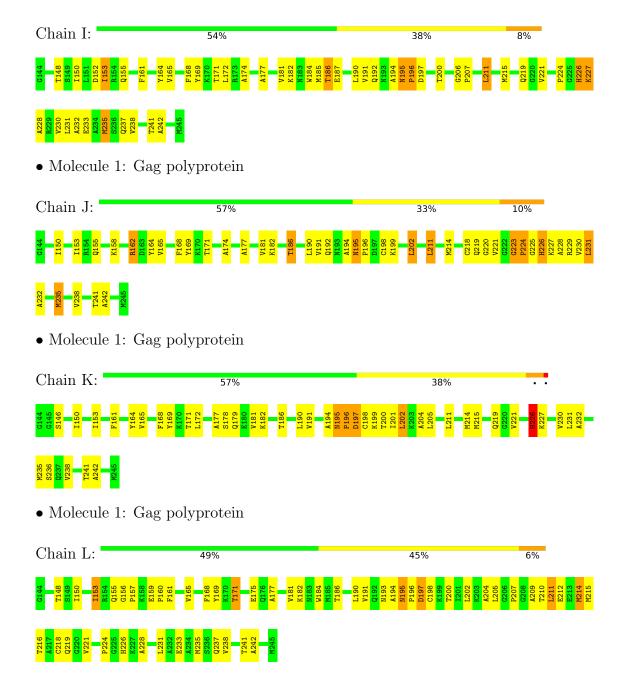


• Molecule 1: Gag polyprotein



• Molecule 1: Gag polyprotein







5 Refinement protocol and experimental data overview (i)



The models were refined using the following method: *simulated annealing*.

Of the 100 calculated structures, 5 were deposited, based on the following criterion: structures with the lowest energy.

The following table shows the software used for structure solution, optimisation and refinement.

| Software name | Classification | Version |
|---------------|-----------------------|---------|
| TALOS-N | structure calculation | |
| X-PLOR NIH | structure calculation | 2.53 |
| X-PLOR NIH | refinement | 2.53 |

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

| Chemical shift file(s) | working_cs.cif |
|--|----------------|
| Number of chemical shift lists | 1 |
| Total number of shifts | 770 |
| Number of shifts mapped to atoms | 770 |
| Number of unparsed shifts | 0 |
| Number of shifts with mapping errors | 0 |
| Number of shifts with mapping warnings | 0 |
| Assignment completeness (well-defined parts) | 9% |

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.



6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: IHP, 2I4

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 (average) 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 | G | 0.91 ± 0.02 | $0\pm0/785~(~0.0\pm~0.0\%)$ | 0.97 ± 0.02 | $0\pm0/1060~(~0.0\pm~0.0\%)$ | |
| 1 | Н | 0.83 ± 0.02 | $0\pm0/785~(~0.0\pm~0.0\%)$ | 0.94 ± 0.01 | $0\pm0/1060~(~0.0\pm~0.0\%)$ | |
| 1 | I | 0.89 ± 0.03 | $0\pm0/785~(~0.0\pm~0.0\%)$ | 0.96 ± 0.03 | $0\pm0/1060~(~0.0\pm~0.0\%)$ | |
| 1 | J | 0.87 ± 0.02 | $0\pm0/785~(~0.0\pm~0.0\%)$ | 0.97 ± 0.01 | $1\pm0/1060$ ($0.1\pm$ 0.0%) | |
| 1 | K | 0.88 ± 0.01 | $0\pm0/785~(~0.0\pm~0.1\%)$ | 0.95 ± 0.01 | $1\pm0/1060$ ($0.1\pm$ 0.0%) | |
| 1 | L | 0.85 ± 0.01 | $0\pm0/785~(~0.0\pm~0.0\%)$ | 0.95 ± 0.01 | $0\pm0/1060~(~0.0\pm~0.0\%)$ | |
| All | All | 0.87 | 1/23550 ($0.0%$) | 0.96 | 10/31800 (0.0%) | |

All unique bond outliers are listed below.

| Mol | Chain | Res | Type | Atoms | 7. | $Observed(\AA)$ | Ideal(Å) | Mod | |
|-------|-------|---------|----------|----------|-------|-----------------|-----------|-------|-------|
| IVIOI | Chain | 1 1 CCS | s Type | 71001115 | | Observed(A) | Ideal(11) | Worst | Total |
| 1 | K | 226 | HIS | C-N | -5.09 | 1.22 | 1.34 | 1 | 1 |

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

| Mal | Iol Chain Dog To | | s Type Atoms | | 7 | Observed(0) | $Ideal(^{o})$ | Models | | | |
|-----|------------------|-----|--------------|----------------------------|-------|---------------------------------|---------------|----------------------|---|-------|-------|
| Mol | Chain | Res | Type | Atoms Z Observed() Ideal() | | $f{Z} \; 	ext{Observed}(^o)$ | | toms Z Observed() 10 | | Worst | Total |
| 1 | K | 226 | HIS | CA-CB-CG | -7.11 | 101.51 | 113.60 | 2 | 4 | | |
| 1 | J | 226 | HIS | CA-CB-CG | -6.56 | 102.45 | 113.60 | 2 | 3 | | |
| 1 | I | 226 | HIS | CA-CB-CG | -5.98 | 103.44 | 113.60 | 2 | 1 | | |
| 1 | L | 226 | HIS | CA-CB-CG | -5.04 | 105.03 | 113.60 | 5 | 1 | | |
| 1 | G | 226 | HIS | CA-CB-CG | -5.03 | 105.05 | 113.60 | 3 | 1 | | |

There are no chirality outliers.

There are no planarity outliers.



6.2 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 each 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 averaged over the ensemble.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes |
|-----|-------|-------|----------|----------|---------|
| 1 | G | 773 | 778 | 775 | 40±1 |
| 1 | Н | 773 | 778 | 775 | 45±5 |
| 1 | I | 773 | 778 | 775 | 39±4 |
| 1 | J | 773 | 778 | 775 | 48±4 |
| 1 | K | 773 | 778 | 775 | 45±2 |
| 1 | L | 773 | 778 | 775 | 36±6 |
| 3 | I | 42 | 54 | 0 | 2±1 |
| All | All | 23580 | 23640 | 23280 | 1200 |

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 26.

5 of 672 unique clashes are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|------------------|------------------|----------|-------------|--------|-------|
| Atom-1 | Atom-2 | Clash(A) | Distance(A) | Worst | Total |
| 1:G:234:ALA:HB1 | 1:H:232:ALA:HB2 | 0.91 | 1.42 | 5 | 3 |
| 1:K:234:ALA:HB1 | 1:L:232:ALA:HB2 | 0.88 | 1.43 | 5 | 1 |
| 1:L:165:VAL:HG12 | 1:L:190:LEU:HD11 | 0.86 | 1.42 | 5 | 1 |
| 1:K:221:VAL:HG22 | 1:K:226:HIS:CE1 | 0.84 | 2.07 | 1 | 4 |
| 1:J:191:VAL:HG22 | 1:J:202:LEU:HD22 | 0.83 | 1.48 | 5 | 1 |

6.3 Torsion angles (i)

6.3.1 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 NMR 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 | G | $100/102\ (98\%)$ | 92±2 (92±2%) | 6±2 (6±2%) | 2±0 (2±0%) | 11 | 52 |
| 1 | Н | $100/102\ (98\%)$ | 91±3 (91±3%) | 7±2 (7±2%) | 3±1 (3±1%) | 8 | 42 |
| 1 | I | $100/102\ (98\%)$ | 86±3 (86±3%) | 11±3 (11±3%) | 3±1 (3±1%) | 7 | 40 |

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| Continued | trom | mmoninonic | maaa |
|----------------|------|------------|-------|
| COHABABACA | | DIEUIUU | DUIUE |
| 0 0 1000100000 | | | |

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles |
|-----|-------|-----------------|--------------|--------------|------------|-------------|
| 1 | J | 100/102 (98%) | 88±1 (88±1%) | 8±1 (8±1%) | 4±0 (4±0%) | 6 34 |
| 1 | K | 100/102 (98%) | 87±2 (87±2%) | 9±2 (9±2%) | 3±1 (3±1%) | 7 38 |
| 1 | L | 100/102 (98%) | 86±2 (86±2%) | 11±2 (11±2%) | 3±1 (3±1%) | 7 40 |
| All | All | 3000/3060 (98%) | 2653 (88%) | 259 (9%) | 88 (3%) | 7 41 |

5 of 34 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

| Mol | Chain | Res | Type | Models (Total) |
|-----|-------|-----|------|----------------|
| 1 | G | 195 | ASN | 5 |
| 1 | G | 196 | PRO | 5 |
| 1 | Н | 195 | ASN | 5 |
| 1 | Н | 196 | PRO | 5 |
| 1 | I | 195 | ASN | 5 |

6.3.2 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 NMR 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 | G | 83/83 (100%) | 74±3 (90±3%) | 9±3 (10±3%) | 10 55 | | |
| 1 | Н | 83/83 (100%) | 75±4 (90±4%) | 8±4 (10±4%) | 11 57 | | |
| 1 | I | 83/83 (100%) | 72±2 (86±3%) | 11±2 (14±3%) | 7 47 | | |
| 1 | J | 83/83 (100%) | 73±1 (88±1%) | 10±1 (12±1%) | 8 51 | | |
| 1 | K | 83/83 (100%) | 75±1 (90±1%) | 8±1 (10±1%) | 11 56 | | |
| 1 | L | 83/83 (100%) | 74±2 (89±3%) | 9±2 (11±3%) | 9 53 | | |
| All | All | 2490/2490 (100%) | 2211 (89%) | 279 (11%) | 9 53 | | |

5 of 137 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

| Mol | Chain | Res | Type | Models (Total) |
|-----|-------|-----|------|----------------|
| 1 | G | 184 | TRP | 5 |
| 1 | G | 211 | LEU | 5 |
| 1 | G | 241 | THR | 5 |

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| Mol | Chain | Res | Type | Models (Total) |
|-----|-------|-----|------|----------------|
| 1 | Н | 241 | THR | 5 |
| 1 | I | 153 | ILE | 5 |

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

| Mal | Tuno | Chain | Ros | Ros | Pog | Tiple | | Bond len | gths |
|-------|------|-------|-----|-------|----------|-----------------|----------------------|----------|-----------------------|
| IVIOI | туре | Chain | nes | LIIIK | Counts | RMSZ | #Z>2 | | |
| 2 | IHP | G | 301 | - | 36,36,36 | 1.61 ± 0.00 | $7\pm0 \ (19\pm0\%)$ | | |
| 3 | 2I4 | I | 301 | - | 46,46,46 | 2.89 ± 0.01 | 16±0 (34±0%) | | |

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.



| Mal | Type | Chain | Dag | Timle | | Bond an | gles |
|------|------|-------|-----|-------|----------|-----------------|-----------------------|
| MIOI | туре | Chain | nes | Lilik | Counts | RMSZ | #Z>2 |
| 2 | IHP | G | 301 | - | 54,60,60 | 1.17 ± 0.00 | 5±0 (10±0%) |
| 3 | 2I4 | I | 301 | - | 77,78,78 | 2.37 ± 0.00 | $28\pm0 \ (36\pm0\%)$ |

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 | 2I4 | I | 301 | - | - | $0\pm0,25,114,114$ | $0\pm0,5,5,5$ |
| 2 | IHP | G | 301 | - | - | $0\pm0,30,54,54$ | $0\pm0,1,1,1$ |

5 of 23 unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

| Mol | Chain | ain Res | Pag Type | Atoms | Z | Observed(Å) | $Ideal(\mathring{A})$ | Models | |
|-------|-------|---------|----------|---------|-------|-------------|-----------------------|--------|-------|
| IVIOI | Chain | nes | Type | Atoms | | Observed(A) | Ideal(A) | Worst | Total |
| 3 | I | 301 | 2I4 | C33-C34 | 11.11 | 1.62 | 1.52 | 2 | 5 |
| 3 | I | 301 | 2I4 | C17-C28 | 6.79 | 1.63 | 1.52 | 5 | 5 |
| 3 | I | 301 | 2I4 | C6-C5 | 6.38 | 1.64 | 1.53 | 5 | 5 |
| 3 | I | 301 | 2I4 | C8-C14 | 6.29 | 1.69 | 1.59 | 5 | 5 |
| 2 | G | 301 | IHP | P2-O12 | 5.24 | 1.69 | 1.59 | 5 | 5 |

5 of 34 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

| Mol | Chain | Res | Type | Atoma | 7 | $\mathbf{Observed}(^o)$ | $\mathrm{Ideal}(^{o})$ | Models | |
|------|-------|-----|------|-------------|------|-------------------------|------------------------|--------|-------|
| WIOI | Chain | nes | Type | Atoms | | | | Worst | Total |
| 3 | I | 301 | 2I4 | C22-C17-C18 | 6.89 | 93.57 | 101.11 | 5 | 5 |
| 3 | I | 301 | 2I4 | C12-C13-C14 | 6.42 | 117.83 | 110.99 | 2 | 5 |
| 3 | I | 301 | 2I4 | C18-C19-C20 | 5.67 | 126.72 | 117.03 | 4 | 5 |
| 3 | I | 301 | 2I4 | C8-C14-C13 | 5.35 | 103.11 | 108.59 | 1 | 5 |
| 3 | I | 301 | 2I4 | C21-C19-C18 | 4.95 | 98.02 | 103.33 | 4 | 5 |

There are no chirality outliers.

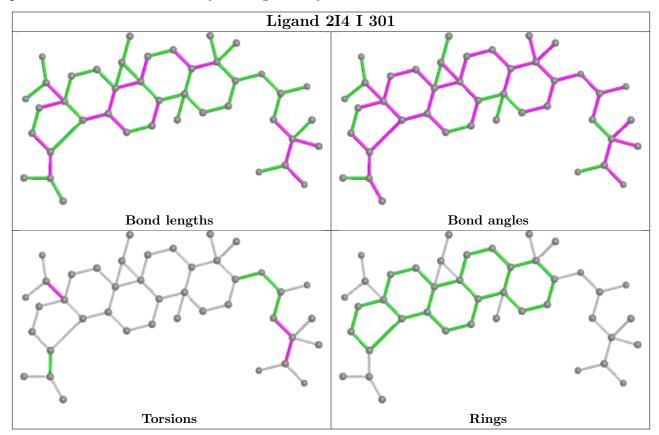
There are no torsion outliers.

There are no ring outliers.

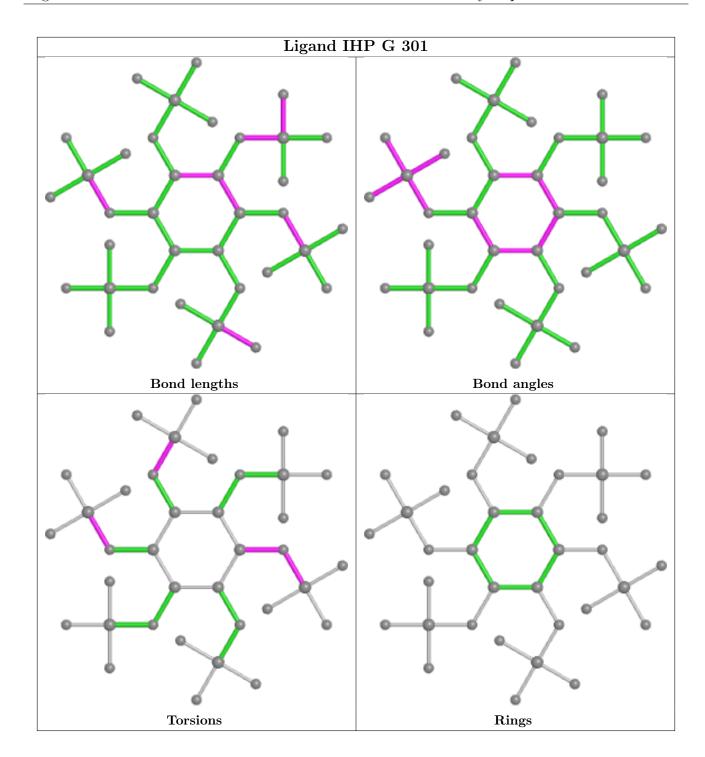
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.







6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 9% for the well-defined parts and 9% for the entire structure.

7.1 Chemical shift list 1

File name: working cs.cif

Chemical shift list name: BVMIP6_chemicalshift_040721.str

7.1.1 Bookkeeping (i)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

| Total number of shifts | 770 |
|---|-----|
| Number of shifts mapped to atoms | 770 |
| Number of unparsed shifts | 0 |
| Number of shifts with mapping errors | 0 |
| Number of shifts with mapping warnings | 0 |
| Number of shift outliers (ShiftChecker) | 0 |

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

| Nucleus | # values | Correction \pm precision, ppm | Suggested action |
|----------------------------|----------|-----------------------------------|-------------------------------------|
| $^{13}\mathrm{C}_{\alpha}$ | 98 | -1.43 ± 0.74 | None needed (imprecise) |
| $^{13}C_{\beta}$ | 88 | 0.27 ± 0.17 | None needed ($< 0.5 \text{ ppm}$) |
| ¹³ C′ | 93 | -1.35 ± 0.46 | Should be applied |
| ^{15}N | 95 | -0.04 ± 0.78 | None needed ($< 0.5 \text{ ppm}$) |

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 9%, i.e. 744 atoms were assigned a chemical shift out of a possible 8047. 0 out of 84 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

| | Total | $^{1}\mathrm{H}$ | $^{13}\mathbf{C}$ | $^{15}{ m N}$ |
|-----------|----------------|------------------|-------------------|---------------|
| Backbone | 398/3042 (13%) | 117/1242 (9%) | 191/1224 (16%) | 90/576 (16%) |
| Sidechain | 316/4662 (7%) | 112/3036 (4%) | 200/1440 (14%) | 4/186 (2%) |

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| | Total | $^{1}\mathbf{H}$ | $^{13}\mathbf{C}$ | $^{15}{ m N}$ |
|----------|---------------|------------------|-------------------|---------------|
| Aromatic | 30/343 (9%) | 9/168~(5%) | 18/162 (11%) | 3/13 (23%) |
| Overall | 744/8047 (9%) | 238/4446 (5%) | 409/2826 (14%) | 97/775 (13%) |

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots (i)

The image below reports random coil index values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain G:

