



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 09:06 PM UTC

PDB ID : 7F1X / pdb\_00007f1x  
Title : X-ray crystal structure of visual arrestin complexed with inositol 1,4,5-triphosphate  
Authors : Jang, K.; Kang, M.; Eger, B.T.; Choe, H.W.; Ernst, O.P.; Kim, Y.J.  
Deposited on : 2021-06-10  
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

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>.

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

|                                |   |                                                                  |
|--------------------------------|---|------------------------------------------------------------------|
| MolProbity                     | : | 4-5-2 with Phenix2.0                                             |
| Mogul                          | : | 2022.3.0, CSD as543be (2022)                                     |
| Xtriage (Phenix)               | : | 2.0                                                              |
| EDS                            | : | 3.0                                                              |
| Buster-report                  | : | wwPDB partial adaption of 1.1.7 (2018)                           |
| Percentile statistics          | : | 20250101.v01 (using entries in the PDB archive January 1st 2025) |
| CCP4                           | : | 9.0.010 (Gargrove)                                               |
| Density-Fitness                | : | 1.0.12                                                           |
| Ideal geometry (proteins)      | : | Engh & Huber (2001)                                              |
| Ideal geometry (DNA, RNA)      | : | Parkinson et al. (1996)                                          |
| Validation Pipeline (wwPDB-VP) | : | 2.49                                                             |

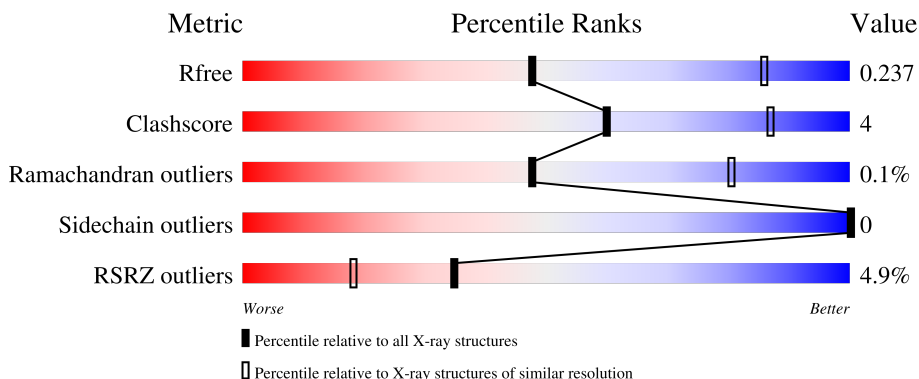
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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<br>(#Entries) | Similar resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-------------------------------------------------------|
| $R_{free}$            | 180053                      | 2672 (3.00-3.00)                                      |
| Clashscore            | 190562                      | 2977 (3.00-3.00)                                      |
| Ramachandran outliers | 187476                      | 2877 (3.00-3.00)                                      |
| Sidechain outliers    | 187428                      | 2880 (3.00-3.00)                                      |
| RSRZ outliers         | 180081                      | 2671 (3.00-3.00)                                      |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain                                                                                 |
|-----|-------|--------|--------------------------------------------------------------------------------------------------|
| 1   | A     | 404    | <div> <div>%</div> <div> <div></div> <div>77%</div> <div>13%</div> <div>10%</div> </div> </div>  |
| 1   | B     | 404    | <div> <div>9%</div> <div> <div></div> <div>79%</div> <div>12%</div> <div>10%</div> </div> </div> |
| 1   | C     | 404    | <div> <div>%</div> <div> <div></div> <div>78%</div> <div>10%</div> <div>11%</div> </div> </div>  |
| 1   | D     | 404    | <div> <div>6%</div> <div> <div></div> <div>81%</div> <div>9%</div> <div>10%</div> </div> </div>  |

## 2 Entry composition [i](#)

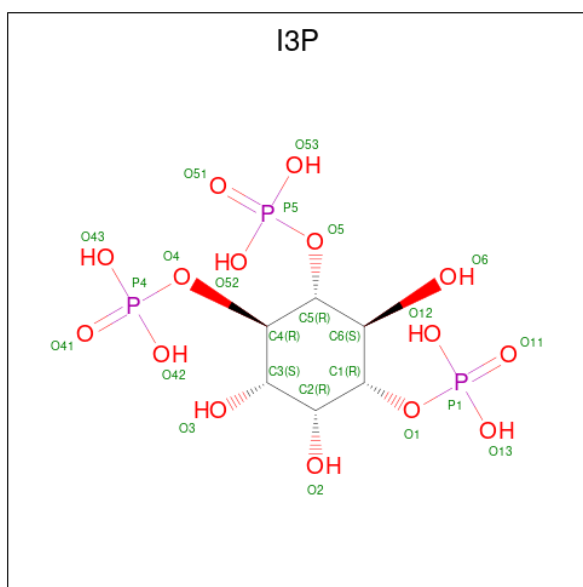
There are 5 unique types of molecules in this entry. The entry contains 11598 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 S-arrestin.

| Mol | Chain | Residues | Atoms |      |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 1   | A     | 364      | Total | C    | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 2876  | 1840 | 487 | 541 | 8 |         |         |       |
| 1   | B     | 365      | Total | C    | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 2880  | 1846 | 485 | 540 | 9 |         |         |       |
| 1   | C     | 359      | Total | C    | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 2838  | 1817 | 481 | 532 | 8 |         |         |       |
| 1   | D     | 365      | Total | C    | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 2881  | 1845 | 486 | 541 | 9 |         |         |       |

- Molecule 2 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (CCD ID: I3P) (formula:  $C_6H_{15}O_{15}P_3$ ) (labeled as "Ligand of Interest" by depositor).



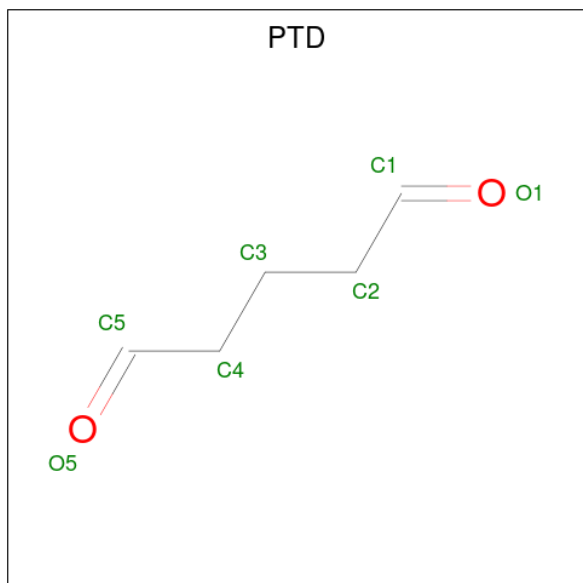
| Mol | Chain | Residues | Atoms |   |    |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|----|---|---------|---------|
| 2   | A     | 1        | Total | C | O  | P | 0       | 0       |
|     |       |          | 24    | 6 | 15 | 3 |         |         |
| 2   | B     | 1        | Total | C | O  | P | 0       | 0       |
|     |       |          | 24    | 6 | 15 | 3 |         |         |

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| Mol | Chain | Residues | Atoms |   |    |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|----|---|---------|---------|
| 2   | C     | 1        | Total | C | O  | P | 0       | 0       |
|     |       |          | 24    | 6 | 15 | 3 |         |         |
| 2   | D     | 1        | Total | C | O  | P | 0       | 0       |
|     |       |          | 24    | 6 | 15 | 3 |         |         |

- Molecule 3 is PENTANEDIAL (CCD ID: PTD) (formula:  $C_5H_8O_2$ ) (labeled as "Ligand of Interest" by depositor).



| Mol | Chain | Residues | Atoms |   |   |  | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|--|---------|---------|
| 3   | A     | 1        | Total | C | O |  | 0       | 0       |
|     |       |          | 7     | 5 | 2 |  |         |         |
| 3   | B     | 1        | Total | C | O |  | 0       | 0       |
|     |       |          | 7     | 5 | 2 |  |         |         |
| 3   | D     | 1        | Total | C | O |  | 0       | 0       |
|     |       |          | 7     | 5 | 2 |  |         |         |

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula:  $C_2H_6O_2$ ) (labeled as "Ligand of Interest" by depositor).



| Mol | Chain | Residues | Atoms |   |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---------|---------|
| 4   | C     | 1        | Total | C | O | 0       | 0       |
|     |       |          | 4     | 2 | 2 |         |         |

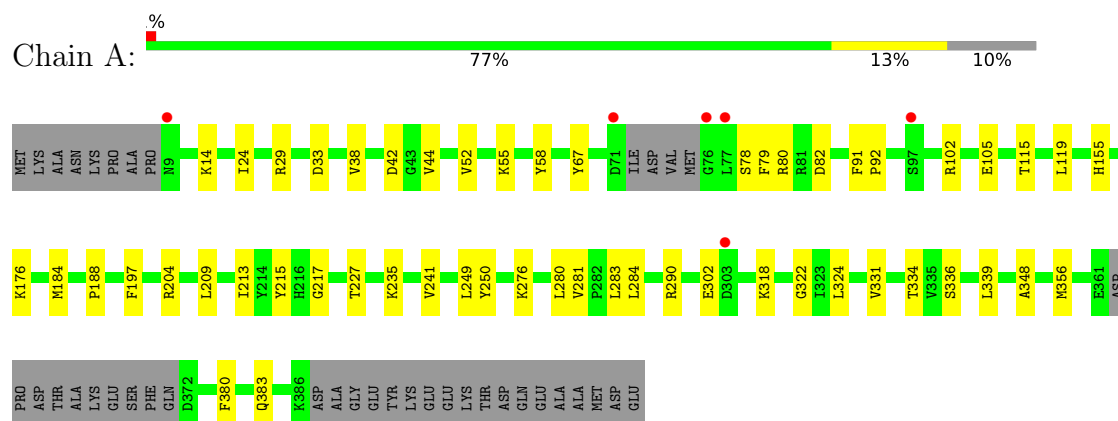
- Molecule 5 is water.

| Mol | Chain | Residues | Atoms |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 5   | A     | 2        | Total | O | 0       | 0       |
|     |       |          | 2     | 2 |         |         |

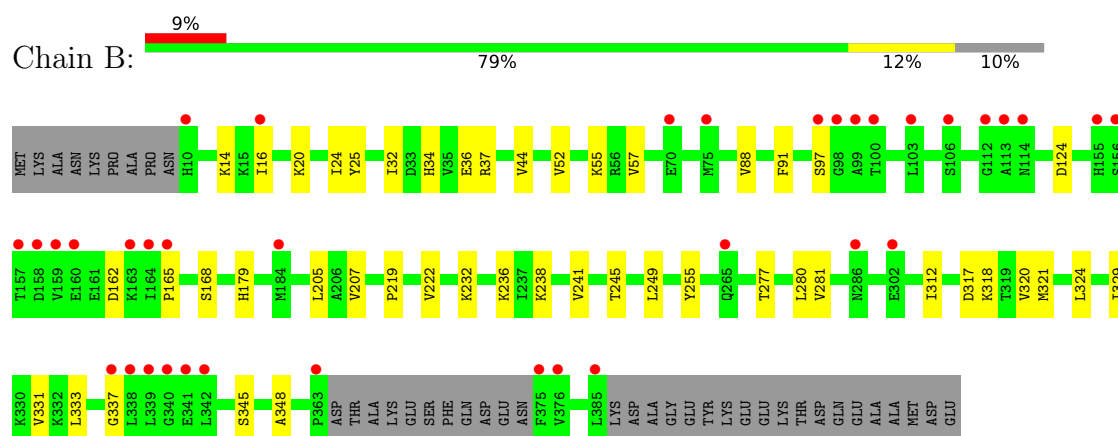
### 3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

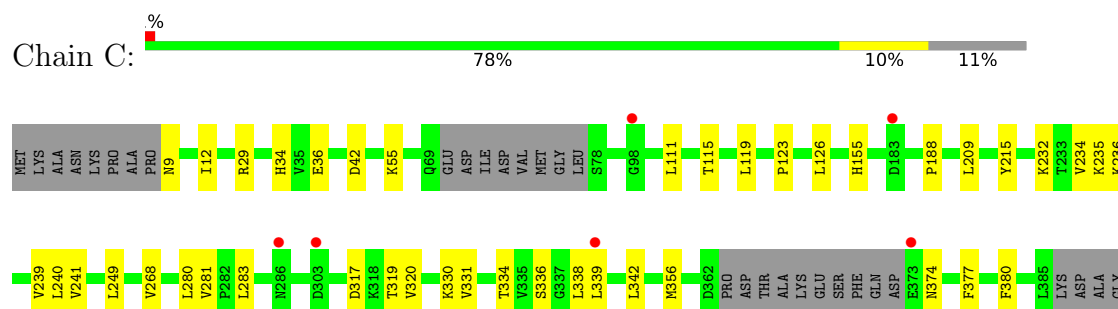
#### • Molecule 1: S-arrestin



#### • Molecule 1: S-arrestin

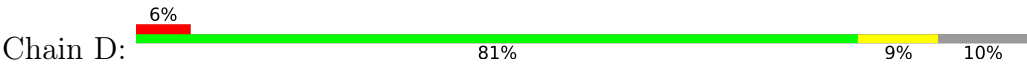


#### • Molecule 1: S-arrestin



GLU  
TYR  
LYS  
GLU  
LYS  
LYS  
THR  
ASP  
GLN  
GLU  
ALA  
ALA  
MET  
ASP  
GLU

● Molecule 1: S-arrestin



MET  
LYS  
ALA  
ASN  
LYS  
PRO  
ALA  
PRO  
ASN  
H10  
K14  
D19  
I24  
Y25  
L26  
D30  
V38  
D42  
V52  
E70  
D71  
I72  
D73  
V74  
H75  
Y84  
V84  
G95  
M114  
L119  
L126  
A151  
H155  
S156  
T157  
D158  
V159  
E160  
E161  
D162  
K163  
I164  
K167

L172  
K176  
P181  
M184  
A190  
E191  
S208  
L209  
Y215  
V241  
T245  
L249  
Y255  
S272  
L280  
N287  
R290  
T299  
L324  
V331  
G337  
L338  
L339  
L342  
T343  
A348  
M356  
D362  
PRO  
ASP  
THR  
ALA  
LYS  
GLU  
SER  
PHE  
GLN  
ASP

GLU  
N374  
R382  
L385  
LYS  
ASP  
ALA  
GLY  
GLU  
TYR  
LYS  
GLU  
GLU  
LYS  
THR  
ASP  
GLN  
GLU  
ALA  
ALA  
MET  
ASP  
GLU

## 4 Data and refinement statistics

| Property                                                                | Value                                                       | Source           |
|-------------------------------------------------------------------------|-------------------------------------------------------------|------------------|
| Space group                                                             | C 2 2 21                                                    | Depositor        |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$                | 167.57Å 187.70Å 190.82Å<br>90.00° 90.00° 90.00°             | Depositor        |
| Resolution (Å)                                                          | 46.92 – 3.00<br>46.92 – 3.00                                | Depositor<br>EDS |
| % Data completeness<br>(in resolution range)                            | 98.8 (46.92-3.00)<br>98.8 (46.92-3.00)                      | Depositor<br>EDS |
| $R_{merge}$                                                             | 0.07                                                        | Depositor        |
| $R_{sym}$                                                               | (Not available)                                             | Depositor        |
| $\langle I/\sigma(I) \rangle$ <sup>1</sup>                              | 4.08 (at 3.01Å)                                             | Xtriage          |
| Refinement program                                                      | PHENIX 1.10_2155                                            | Depositor        |
| R, $R_{free}$                                                           | 0.206 , 0.239<br>0.205 , 0.237                              | Depositor<br>DCC |
| $R_{free}$ test set                                                     | 3011 reflections (4.99%)                                    | wwPDB-VP         |
| Wilson B-factor (Å <sup>2</sup> )                                       | 71.2                                                        | Xtriage          |
| Anisotropy                                                              | 0.185                                                       | Xtriage          |
| Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> ) | 0.34 , 55.7                                                 | EDS              |
| L-test for twinning <sup>2</sup>                                        | $\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$ | Xtriage          |
| Estimated twinning fraction                                             | No twinning to report.                                      | Xtriage          |
| $F_o, F_c$ correlation                                                  | 0.93                                                        | EDS              |
| Total number of atoms                                                   | 11598                                                       | wwPDB-VP         |
| Average B, all atoms (Å <sup>2</sup> )                                  | 73.0                                                        | wwPDB-VP         |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, I3P, PTD

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   | A     | 0.14         | 0/2932      | 0.35        | 0/3971      |
| 1   | B     | 0.14         | 0/2938      | 0.31        | 0/3983      |
| 1   | C     | 0.13         | 0/2894      | 0.34        | 0/3921      |
| 1   | D     | 0.13         | 0/2938      | 0.33        | 0/3982      |
| All | All   | 0.14         | 0/11702     | 0.33        | 0/15857     |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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   | A     | 2876  | 0        | 2943     | 32      | 0            |
| 1   | B     | 2880  | 0        | 2953     | 27      | 0            |
| 1   | C     | 2838  | 0        | 2906     | 24      | 0            |
| 1   | D     | 2881  | 0        | 2952     | 22      | 0            |
| 2   | A     | 24    | 0        | 9        | 0       | 0            |
| 2   | B     | 24    | 0        | 9        | 0       | 0            |
| 2   | C     | 24    | 0        | 9        | 0       | 0            |
| 2   | D     | 24    | 0        | 9        | 0       | 0            |
| 3   | A     | 7     | 0        | 8        | 1       | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 3   | B     | 7     | 0        | 8        | 0       | 0            |
| 3   | D     | 7     | 0        | 8        | 1       | 0            |
| 4   | C     | 4     | 0        | 6        | 0       | 0            |
| 5   | A     | 2     | 0        | 0        | 0       | 0            |
| All | All   | 11598 | 0        | 11820    | 101     | 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 4.

The worst 5 of 101 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:55:LYS:HD3   | 1:A:155:HIS:HB3  | 1.66                     | 0.76              |
| 1:D:42:ASP:HB3   | 1:D:119:LEU:HD12 | 1.72                     | 0.69              |
| 1:B:52:VAL:HG13  | 1:B:55:LYS:HB2   | 1.77                     | 0.66              |
| 1:C:239:VAL:HG22 | 1:C:331:VAL:HG22 | 1.80                     | 0.64              |
| 1:D:342:LEU:HD12 | 1:D:343:THR:HG23 | 1.79                     | 0.63              |

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 X-ray entries followed by that with respect to entries of similar resolution.

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     | 358/404 (89%)   | 344 (96%)  | 14 (4%) | 0        | 100         | 100 |
| 1   | B     | 361/404 (89%)   | 339 (94%)  | 22 (6%) | 0        | 100         | 100 |
| 1   | C     | 353/404 (87%)   | 340 (96%)  | 13 (4%) | 0        | 100         | 100 |
| 1   | D     | 361/404 (89%)   | 347 (96%)  | 13 (4%) | 1 (0%)   | 36          | 70  |
| All | All   | 1433/1616 (89%) | 1370 (96%) | 62 (4%) | 1 (0%)   | 48          | 80  |

All (1) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | D     | 95  | 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 X-ray entries followed by that with respect to entries of similar resolution.

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     | 326/359 (91%)   | 326 (100%)  | 0        | 100         | 100 |
| 1   | B     | 327/359 (91%)   | 327 (100%)  | 0        | 100         | 100 |
| 1   | C     | 322/359 (90%)   | 322 (100%)  | 0        | 100         | 100 |
| 1   | D     | 327/359 (91%)   | 327 (100%)  | 0        | 100         | 100 |
| All | All   | 1302/1436 (91%) | 1302 (100%) | 0        | 100         | 100 |

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | D     | 359 | GLN  |
| 1   | D     | 357 | HIS  |
| 1   | D     | 114 | ASN  |
| 1   | C     | 305 | ASN  |
| 1   | D     | 195 | GLN  |

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry

8 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 |
| 3   | PTD  | B     | 502 | -    | 4,6,6        | 1.29 | 1 (25%)  | 3,5,5       | 0.63 | 0        |
| 3   | PTD  | D     | 502 | -    | 4,6,6        | 1.28 | 1 (25%)  | 3,5,5       | 0.71 | 0        |
| 3   | PTD  | A     | 502 | -    | 4,6,6        | 1.29 | 1 (25%)  | 3,5,5       | 0.57 | 0        |
| 2   | I3P  | A     | 501 | -    | 24,24,24     | 1.44 | 3 (12%)  | 39,39,39    | 0.84 | 0        |
| 4   | EDO  | C     | 502 | -    | 3,3,3        | 0.43 | 0        | 2,2,2       | 0.40 | 0        |
| 2   | I3P  | D     | 501 | -    | 24,24,24     | 1.36 | 3 (12%)  | 39,39,39    | 0.82 | 2 (5%)   |
| 2   | I3P  | B     | 501 | -    | 24,24,24     | 1.40 | 3 (12%)  | 39,39,39    | 0.78 | 0        |
| 2   | I3P  | C     | 501 | -    | 24,24,24     | 1.39 | 3 (12%)  | 39,39,39    | 0.78 | 1 (2%)   |

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   | PTD  | B     | 502 | -    | -       | 0/4/4/4    | -       |
| 3   | PTD  | D     | 502 | -    | -       | 1/4/4/4    | -       |
| 3   | PTD  | A     | 502 | -    | -       | 1/4/4/4    | -       |
| 2   | I3P  | A     | 501 | -    | -       | 2/15/39/39 | 0/1/1/1 |
| 4   | EDO  | C     | 502 | -    | -       | 0/1/1/1    | -       |
| 2   | I3P  | D     | 501 | -    | -       | 3/15/39/39 | 0/1/1/1 |
| 2   | I3P  | B     | 501 | -    | -       | 2/15/39/39 | 0/1/1/1 |
| 2   | I3P  | C     | 501 | -    | -       | 1/15/39/39 | 0/1/1/1 |

The worst 5 of 15 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z    | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|------|-------------|----------|
| 2   | A     | 501 | I3P  | P1-O1 | 3.66 | 1.65        | 1.59     |
| 2   | A     | 501 | I3P  | P5-O5 | 3.58 | 1.65        | 1.59     |

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| Mol | Chain | Res | Type | Atoms | Z    | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|------|-------------|----------|
| 2   | C     | 501 | I3P  | P4-O4 | 3.52 | 1.65        | 1.59     |
| 2   | B     | 501 | I3P  | P5-O5 | 3.50 | 1.65        | 1.59     |
| 2   | D     | 501 | I3P  | P5-O5 | 3.49 | 1.65        | 1.59     |

All (3) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms    | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 2   | C     | 501 | I3P  | P1-O1-C1 | -2.28 | 117.35      | 123.43   |
| 2   | D     | 501 | I3P  | P1-O1-C1 | -2.04 | 117.98      | 123.43   |
| 2   | D     | 501 | I3P  | P4-O4-C4 | -2.00 | 118.09      | 123.43   |

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

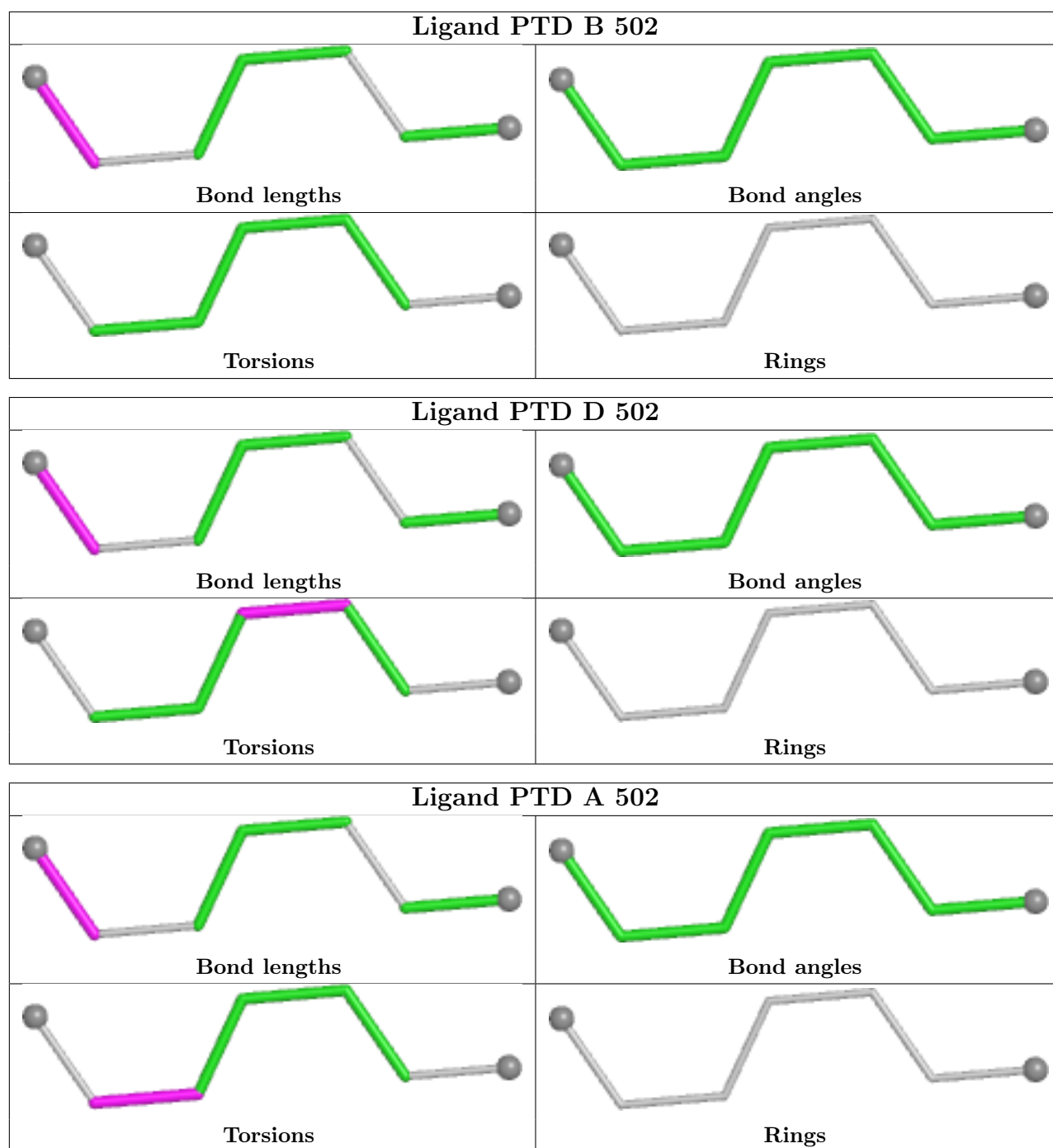
| Mol | Chain | Res | Type | Atoms        |
|-----|-------|-----|------|--------------|
| 3   | A     | 502 | PTD  | C3-C4-C5-O5  |
| 2   | A     | 501 | I3P  | C1-O1-P1-O11 |
| 2   | D     | 501 | I3P  | C4-O4-P4-O41 |
| 3   | D     | 502 | PTD  | C1-C2-C3-C4  |
| 2   | B     | 501 | I3P  | C1-O1-P1-O13 |

There are no ring outliers.

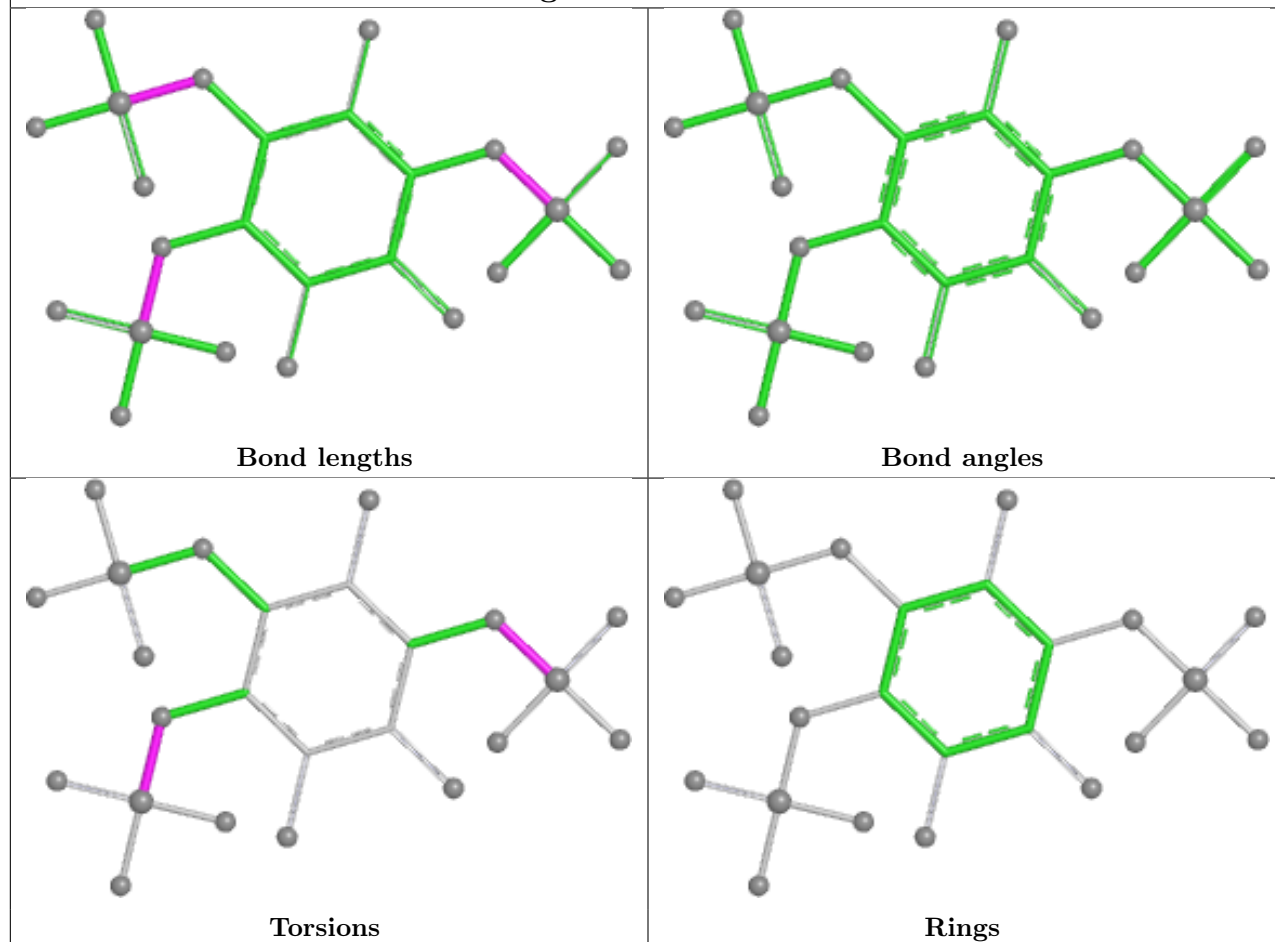
2 monomers are involved in 2 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 3   | D     | 502 | PTD  | 1       | 0            |
| 3   | A     | 502 | PTD  | 1       | 0            |

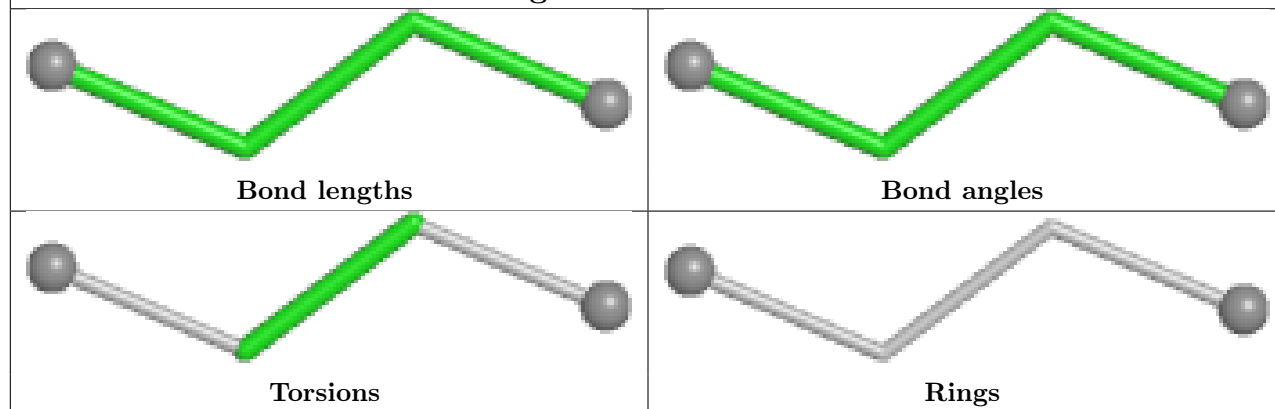
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



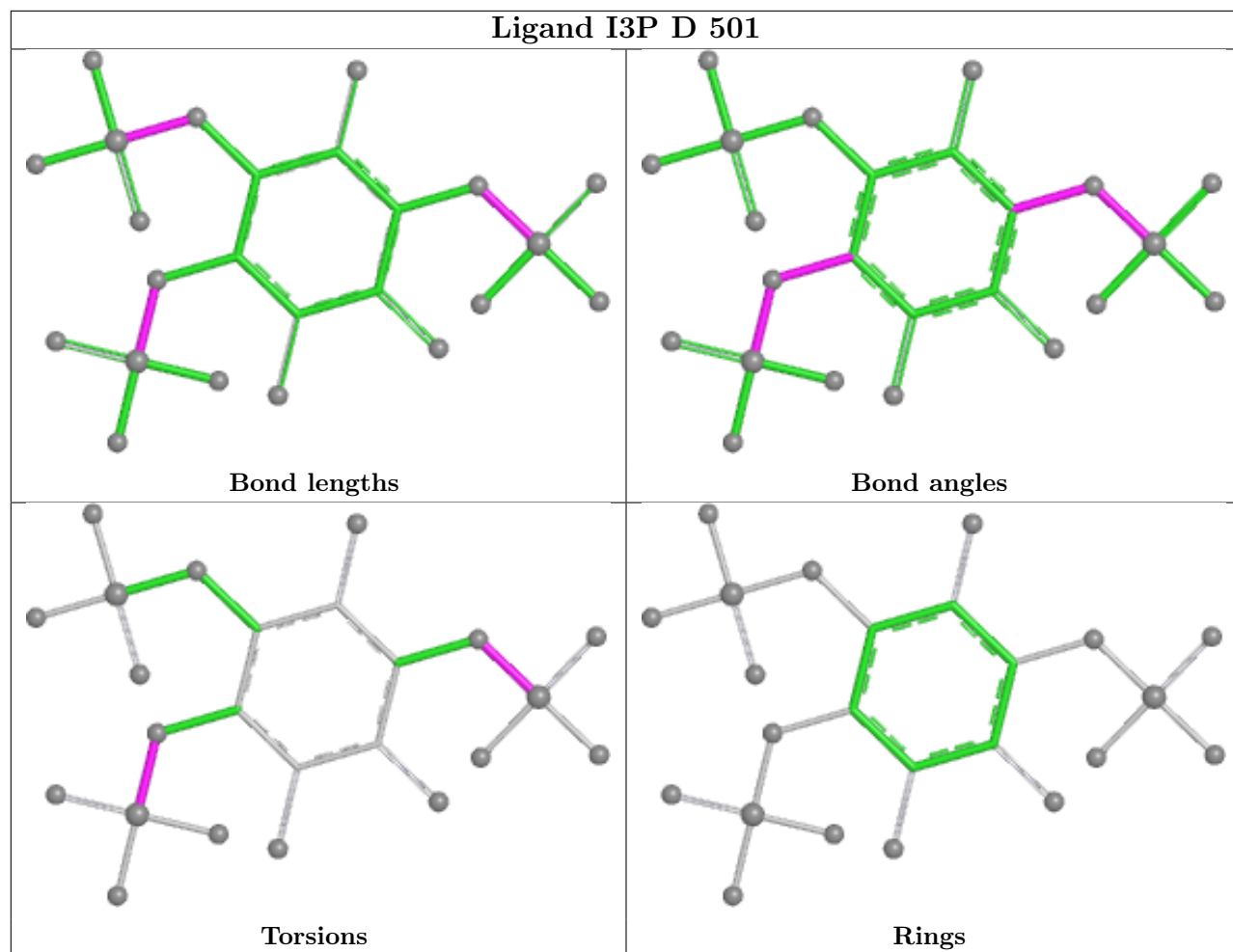
## Ligand I3P A 501



## Ligand EDO C 502

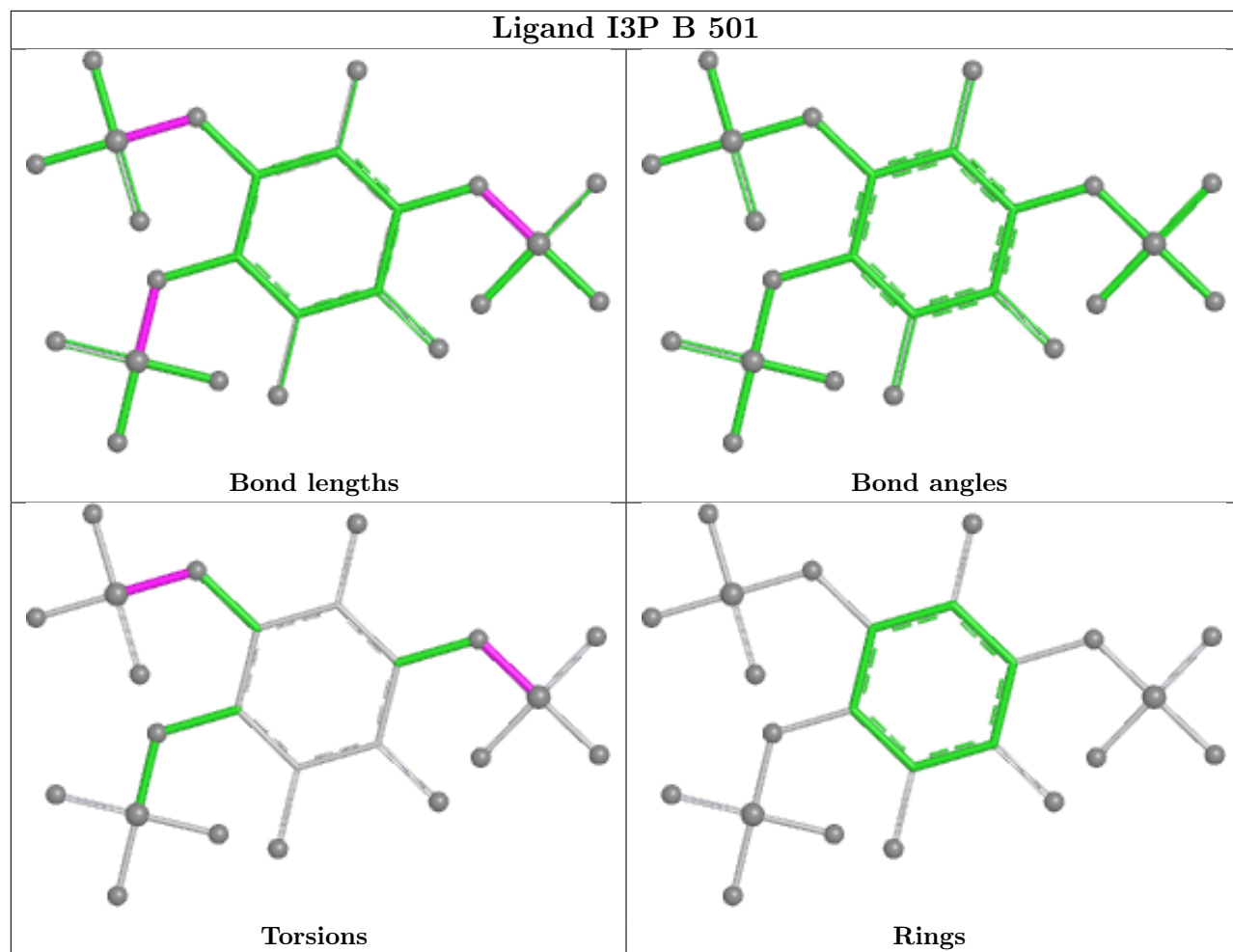


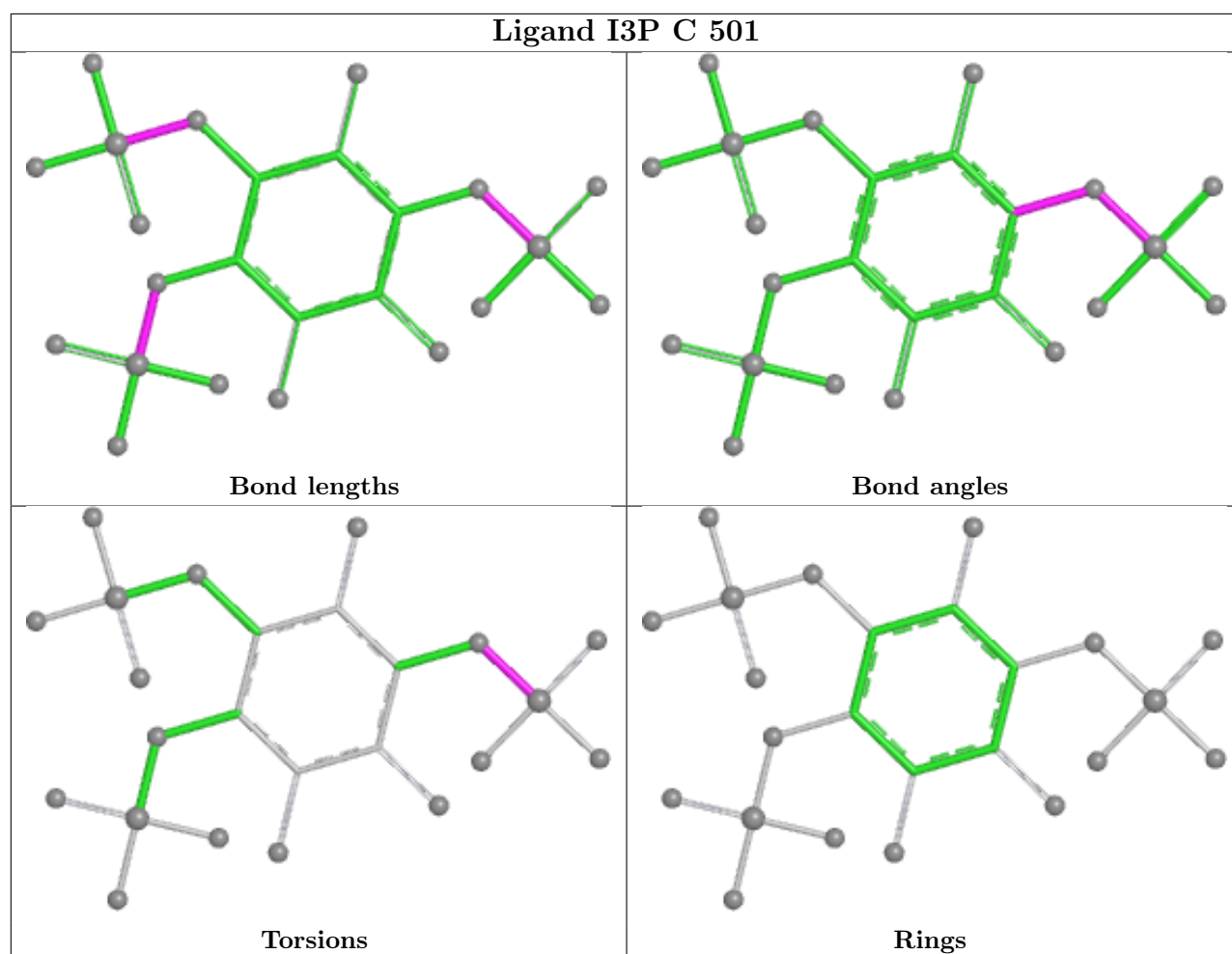
## Ligand I3P D 501





## Ligand I3P B 501





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed        | <RSRZ> | #RSRZ>2       | OWAB(Å <sup>2</sup> ) | Q<0.9 |
|-----|-------|-----------------|--------|---------------|-----------------------|-------|
| 1   | A     | 364/404 (90%)   | -0.07  | 6 (1%) 70 47  | 39, 56, 89, 107       | 0     |
| 1   | B     | 365/404 (90%)   | 0.63   | 36 (9%) 13 7  | 48, 88, 149, 180      | 0     |
| 1   | C     | 359/404 (88%)   | -0.02  | 6 (1%) 69 45  | 42, 59, 93, 110       | 0     |
| 1   | D     | 365/404 (90%)   | 0.23   | 23 (6%) 26 13 | 39, 67, 118, 137      | 0     |
| All | All   | 1453/1616 (89%) | 0.19   | 71 (4%) 35 18 | 39, 65, 132, 180      | 0     |

The worst 5 of 71 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1   | B     | 385 | LEU  | 7.0  |
| 1   | B     | 157 | THR  | 6.1  |
| 1   | C     | 339 | LEU  | 4.3  |
| 1   | D     | 159 | VAL  | 4.0  |
| 1   | D     | 72  | ILE  | 3.9  |

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

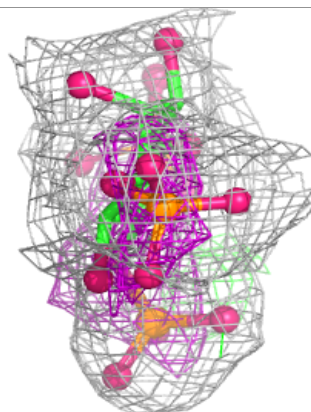
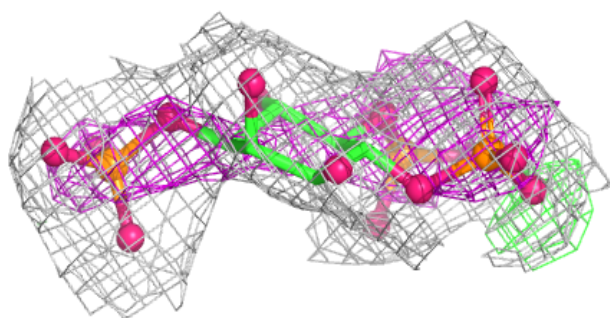
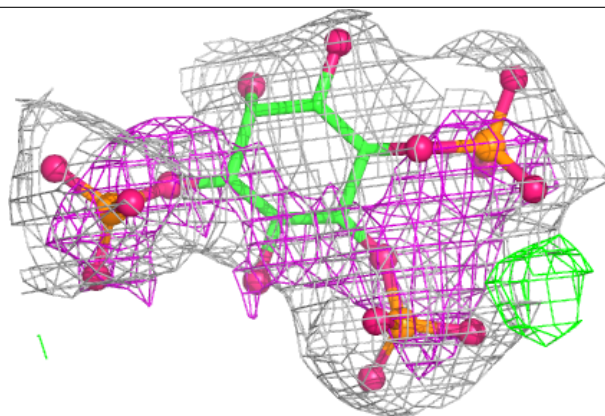
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR  | B-factors( $\text{\AA}^2$ ) | Q<0.9 |
|-----|------|-------|-----|-------|------|------|-----------------------------|-------|
| 2   | I3P  | A     | 501 | 24/24 | 0.79 | 0.14 | 81,92,105,114               | 0     |
| 2   | I3P  | B     | 501 | 24/24 | 0.79 | 0.14 | 111,127,136,141             | 0     |
| 2   | I3P  | C     | 501 | 24/24 | 0.85 | 0.13 | 78,99,106,117               | 0     |
| 2   | I3P  | D     | 501 | 24/24 | 0.86 | 0.13 | 74,103,128,140              | 0     |
| 3   | PTD  | B     | 502 | 7/7   | 0.89 | 0.12 | 61,73,84,86                 | 0     |
| 3   | PTD  | A     | 502 | 7/7   | 0.94 | 0.08 | 38,41,48,49                 | 0     |
| 3   | PTD  | D     | 502 | 7/7   | 0.94 | 0.09 | 47,49,65,74                 | 0     |
| 4   | EDO  | C     | 502 | 4/4   | 0.95 | 0.09 | 37,38,42,43                 | 0     |

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

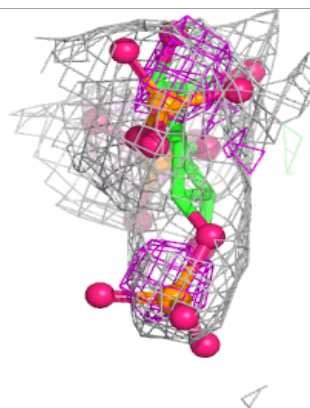
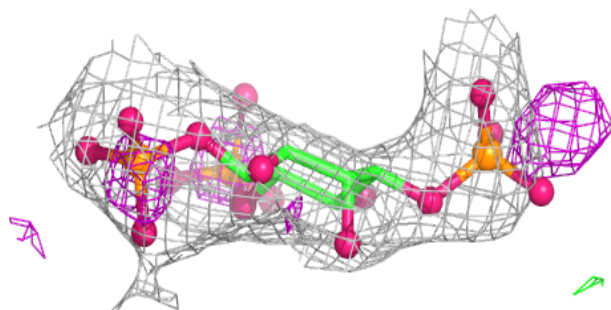
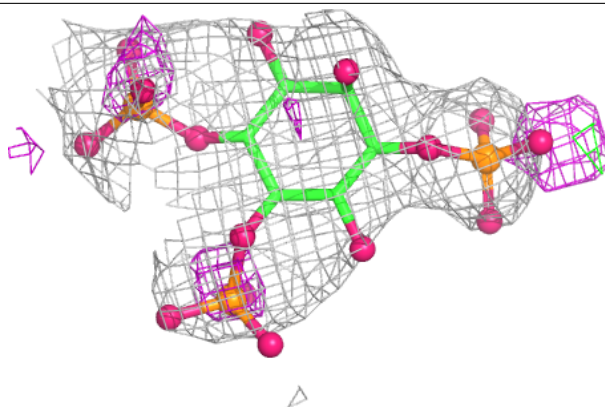
**Electron density around I3P A 501:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



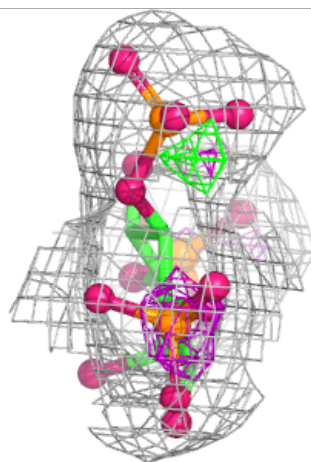
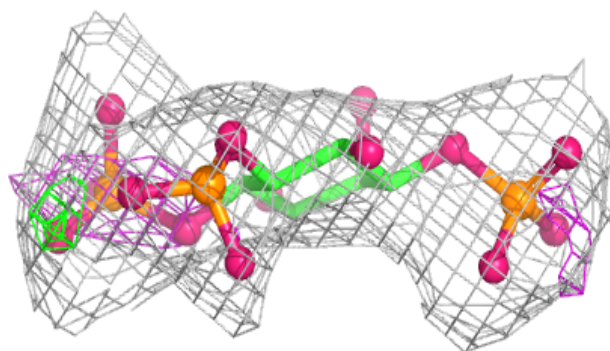
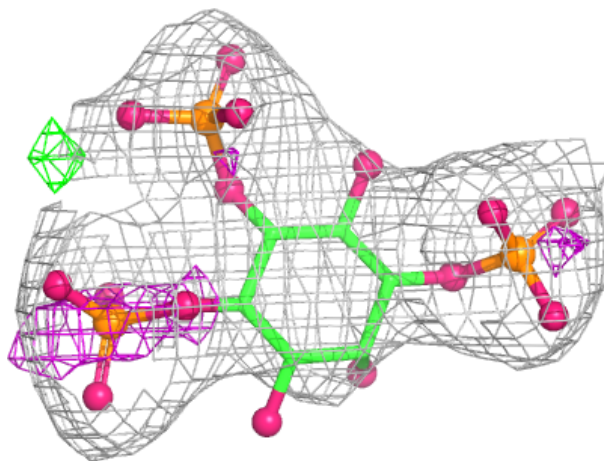
**Electron density around I3P B 501:**

$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



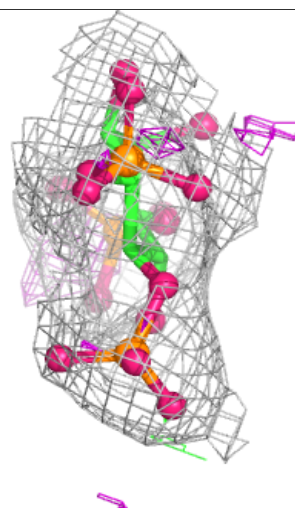
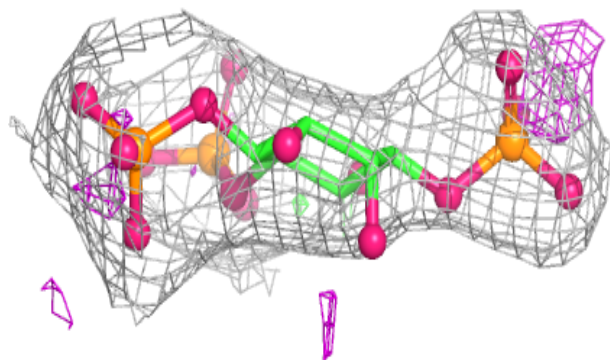
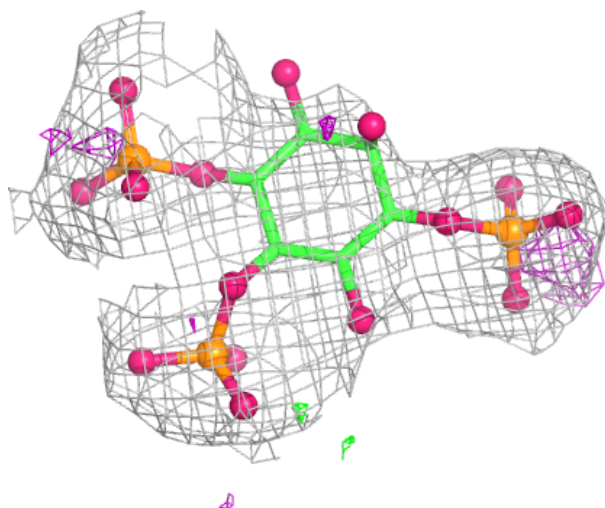
**Electron density around I3P C 501:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around I3P D 501:**

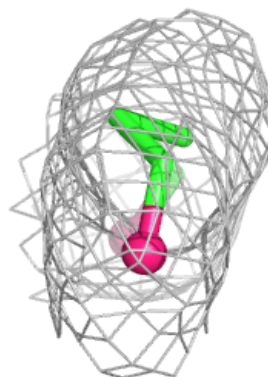
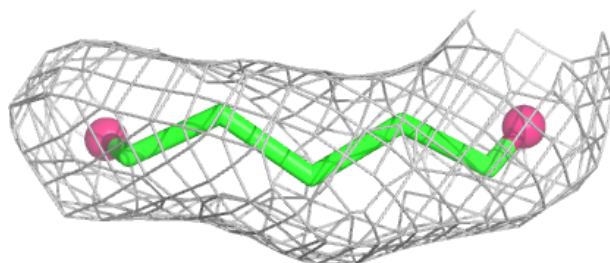
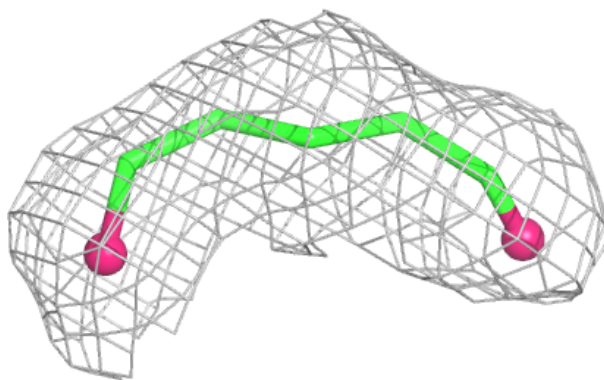
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



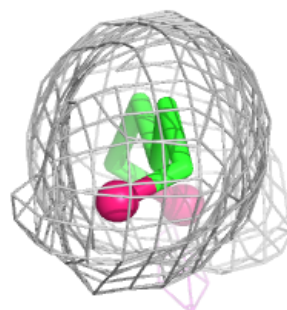
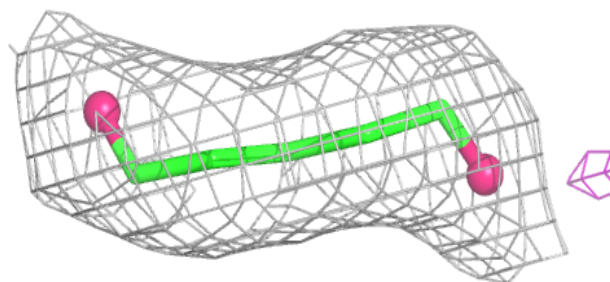
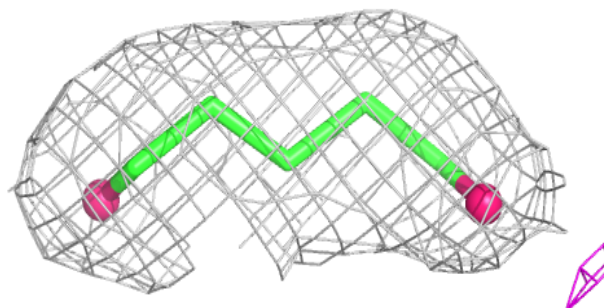


**Electron density around PTD B 502:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around PTD A 502:**

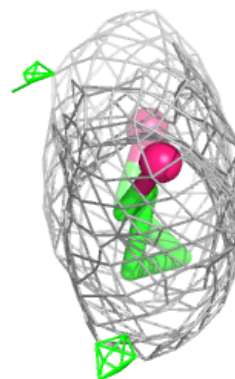
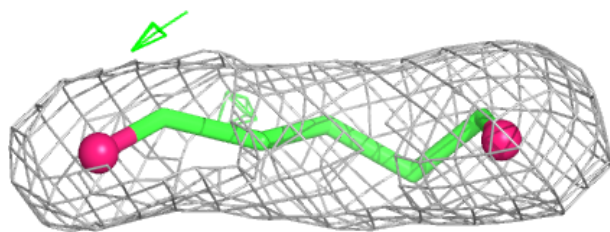
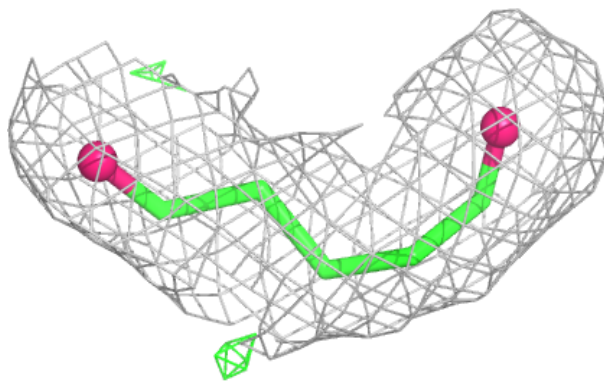
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





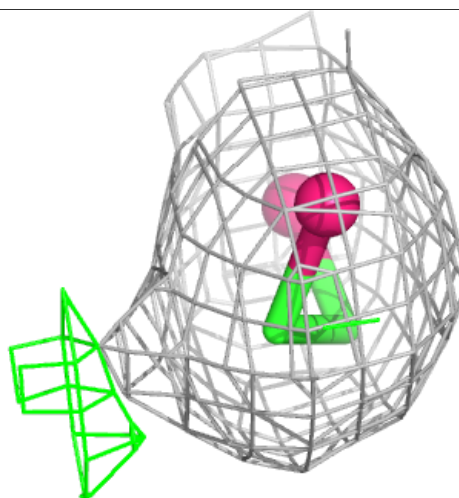
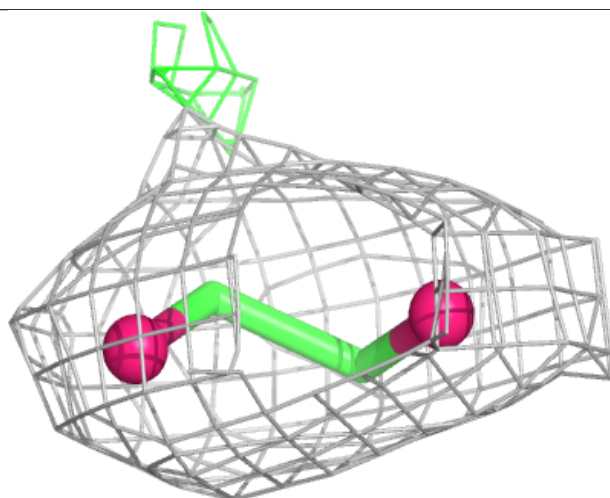
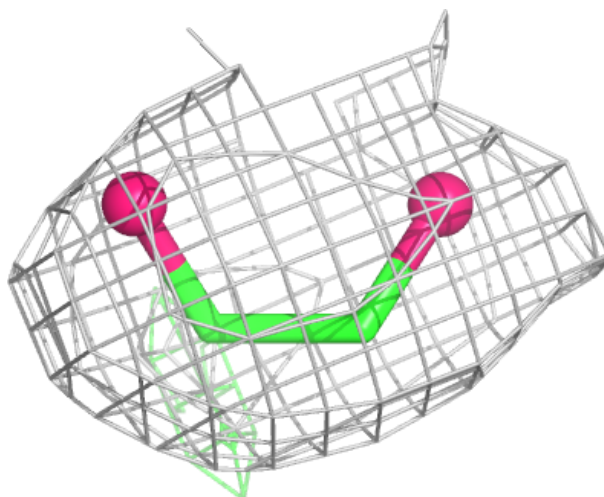
**Electron density around PTD D 502:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around EDO C 502:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.