# wwPDB X-ray Structure Validation Summary Report (i)

Sep 20, 2023 – 10:01 AM EDT

| | | |
|---|---|---|
| PDB ID | : | 5J33 |
| Title | : | Isopropylmalate dehydrogenase in complex with NAD+ |
| Authors | : | Jez, J.M.; Lee, S.G. |
| Deposited on | : | 2016-03-30 |
| Resolution | : | 3.49 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
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.

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

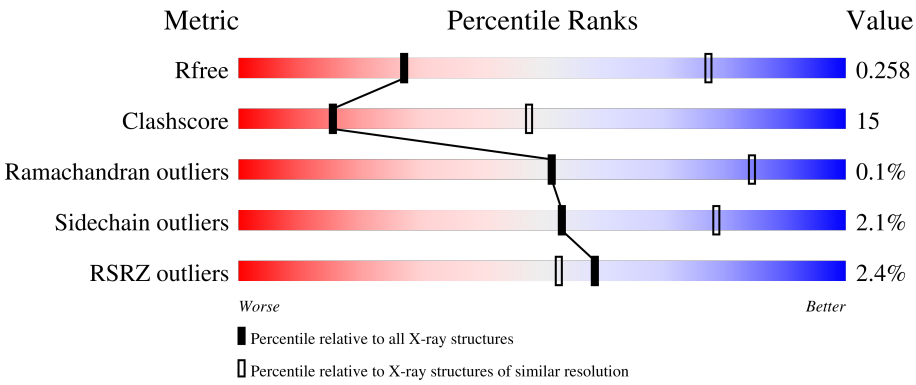
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.35.1 |
| buster-report | : | 1.1.7 (2018) |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.35.1 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.49 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) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| $R_{free}$ | 130704 | 1659 (3.60-3.40) |
| Clashscore | 141614 | 1036 (3.58-3.42) |
| Ramachandran outliers | 138981 | 1005 (3.58-3.42) |
| Sidechain outliers | 138945 | 1006 (3.58-3.42) |
| RSRZ outliers | 127900 | 1559 (3.60-3.40) |

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 >=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% 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 | 405 | 2% 62% 26% • 11% |
| 1 | B | 405 | 2% 62% 26% • 11% |
| 1 | C | 405 | % 63% 25% • 11% |
| 1 | D | 405 | 2% 59% 28% • 12% |
| 1 | E | 405 | 60% 28% • 11% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | F | 405 | 61% 27% 11% |
| 1 | G | 405 | 4% 65% 22% 11% |
| 1 | H | 405 | 5% 58% 28% 12% |

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|---|---|---|---|---|---|---|---|
| 3 | SO4 | G | 502 | - | - | X | - |

# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 22043 atoms, of which 0 are hydrogens and 0 are deuteriums.

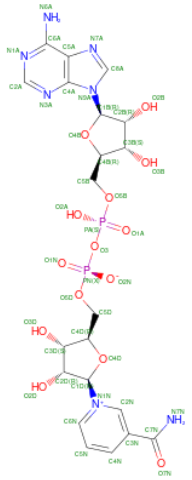
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 3-isopropylmalate dehydrogenase 2, chloroplastic.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 1 | A | 360 | 2718 | 1712 | 468 | 528 | 10 | 0 | 0 | 0 |
| 1 | B | 359 | 2709 | 1707 | 466 | 526 | 10 | 0 | 0 | 0 |
| 1 | C | 359 | 2709 | 1707 | 466 | 526 | 10 | 0 | 0 | 0 |
| 1 | D | 358 | 2700 | 1701 | 464 | 525 | 10 | 0 | 0 | 0 |
| 1 | E | 359 | 2709 | 1707 | 466 | 526 | 10 | 0 | 0 | 0 |
| 1 | F | 359 | 2709 | 1707 | 466 | 526 | 10 | 0 | 0 | 0 |
| 1 | G | 359 | 2709 | 1707 | 466 | 526 | 10 | 0 | 0 | 0 |
| 1 | H | 355 | 2671 | 1683 | 458 | 520 | 10 | 0 | 0 | 0 |

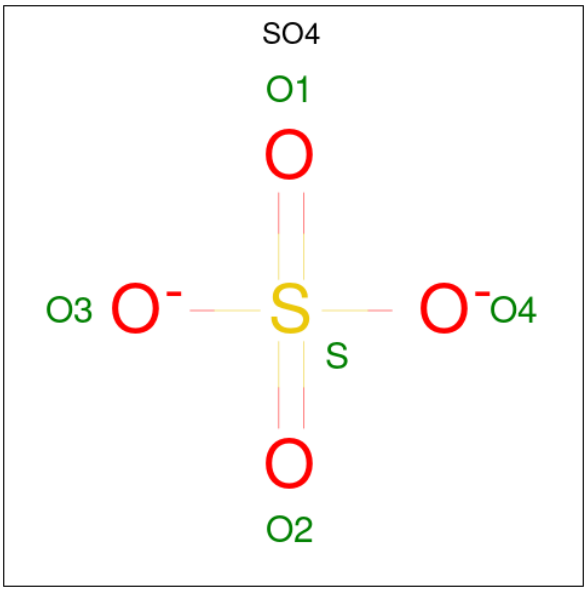
- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).

NAD



| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 2 | A | 1 | 44 | 21 | 7 | 14 | 2 | 0 | 0 |
| | | | Total | C | N | O | P | | |
| 2 | A | 1 | 44 | 21 | 7 | 14 | 2 | 0 | 0 |
| | | | Total | C | N | O | P | | |
| 2 | C | 1 | 44 | 21 | 7 | 14 | 2 | 0 | 0 |
| | | | Total | C | N | O | P | | |
| 2 | D | 1 | 44 | 21 | 7 | 14 | 2 | 0 | 0 |
| | | | Total | C | N | O | P | | |
| 2 | D | 1 | 44 | 21 | 7 | 14 | 2 | 0 | 0 |
| | | | Total | C | N | O | P | | |
| 2 | E | 1 | 44 | 21 | 7 | 14 | 2 | 0 | 0 |
| | | | Total | C | N | O | P | | |
| 2 | G | 1 | 44 | 21 | 7 | 14 | 2 | 0 | 0 |
| | | | Total | C | N | O | P | | |
| 2 | H | 1 | 44 | 21 | 7 | 14 | 2 | 0 | 0 |

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: $O_4S$).




| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 3 | A | 1 | Total O S<br>5 4 1 | 0 | 0 |
| 3 | A | 1 | Total O S<br>5 4 1 | 0 | 0 |
| 3 | C | 1 | Total O S<br>5 4 1 | 0 | 0 |
| 3 | C | 1 | Total O S<br>5 4 1 | 0 | 0 |
| 3 | D | 1 | Total O S<br>5 4 1 | 0 | 0 |
| 3 | D | 1 | Total O S<br>5 4 1 | 0 | 0 |
| 3 | E | 1 | Total O S<br>5 4 1 | 0 | 0 |
| 3 | G | 1 | Total O S<br>5 4 1 | 0 | 0 |
| 3 | H | 1 | Total O S<br>5 4 1 | 0 | 0 |
| 3 | H | 1 | Total O S<br>5 4 1 | 0 | 0 |

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 4 | A | 2 | Total Mg<br>2 2 | 0 | 0 |
| 4 | C | 2 | Total Mg<br>2 2 | 0 | 0 |

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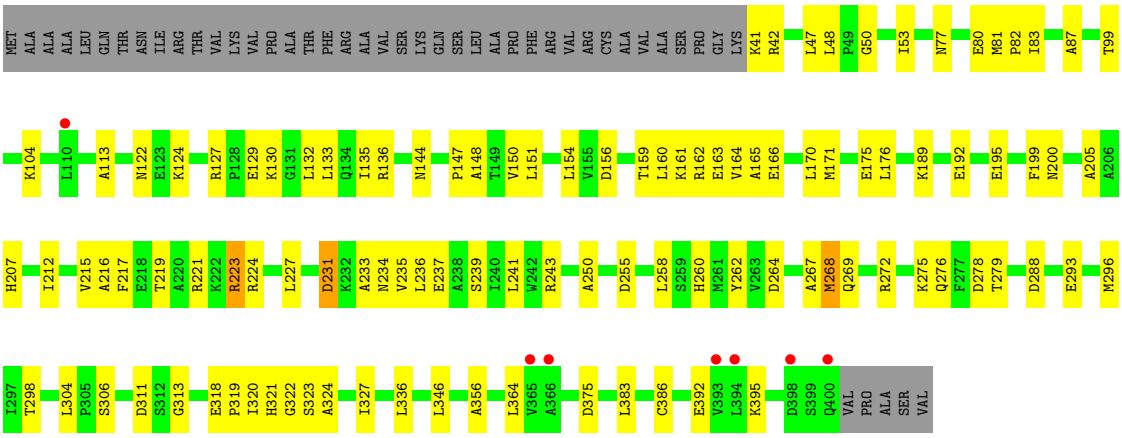
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | Mg | | |
| 4 | D | 2 | 2 | 2 | 0 | 0 |
| | | | Total | Mg | | |
| 4 | E | 1 | 1 | 1 | 0 | 0 |

# 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.

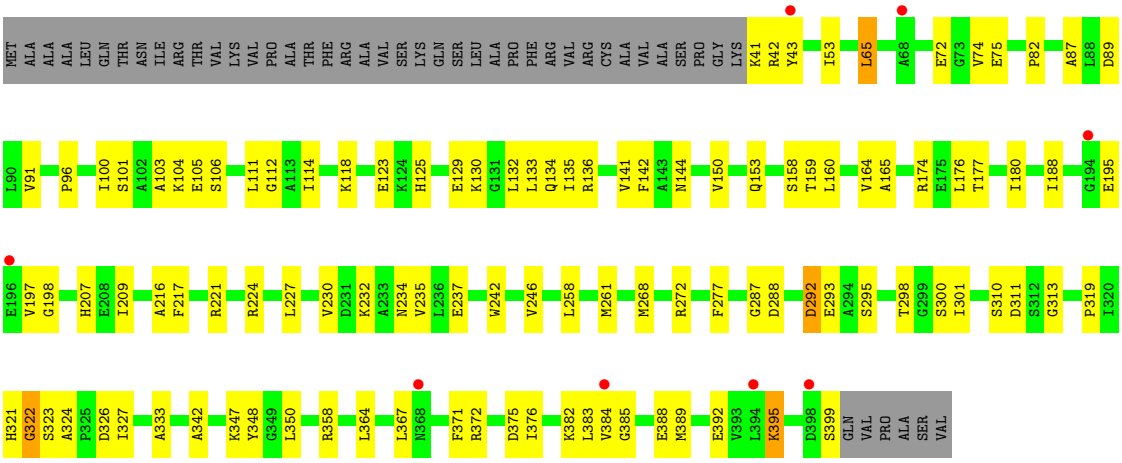
• Molecule 1: 3-isopropylmalate dehydrogenase 2, chloroplastic

Chain A:



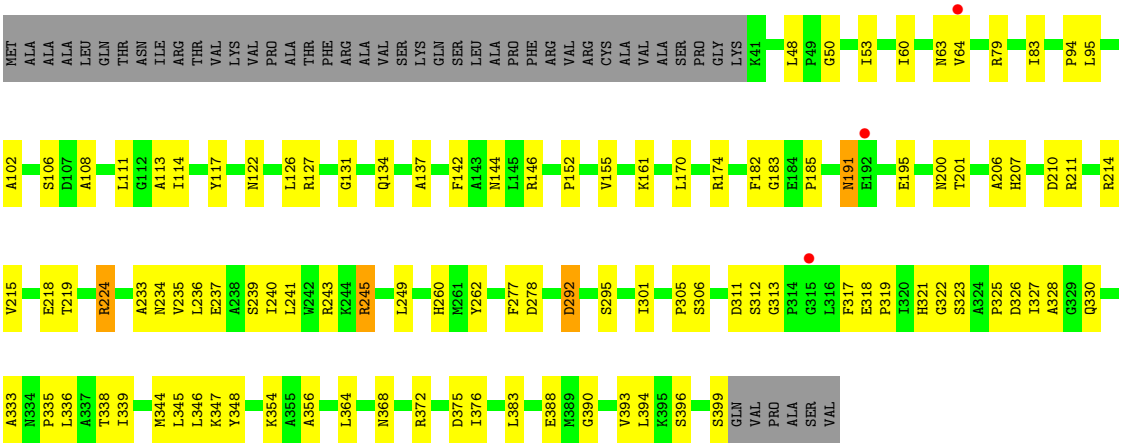

• Molecule 1: 3-isopropylmalate dehydrogenase 2, chloroplastic

Chain B:



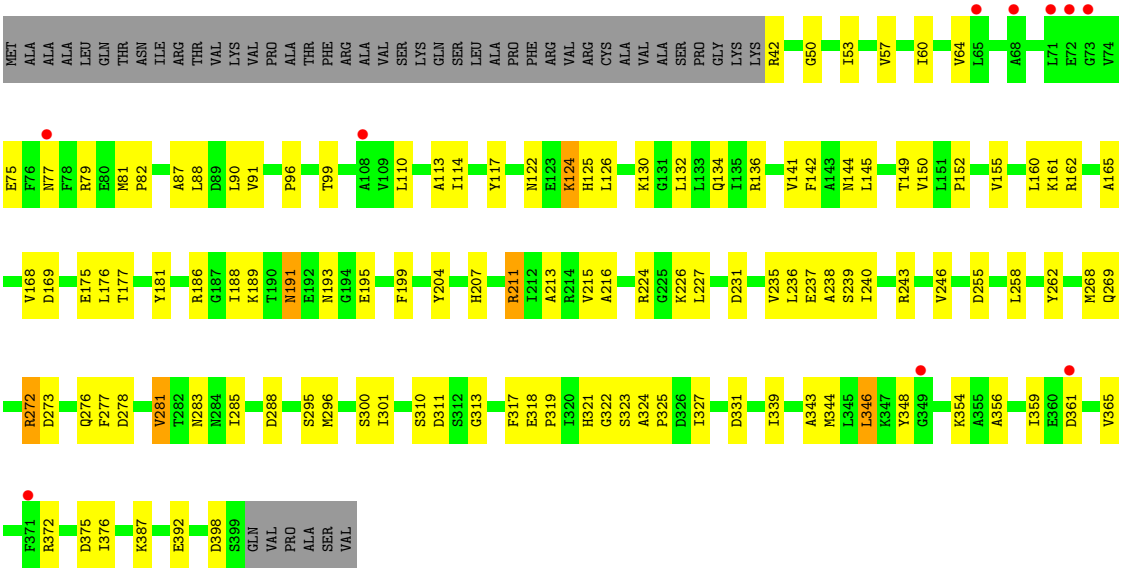

• Molecule 1: 3-isopropylmalate dehydrogenase 2, chloroplastic

Chain C:



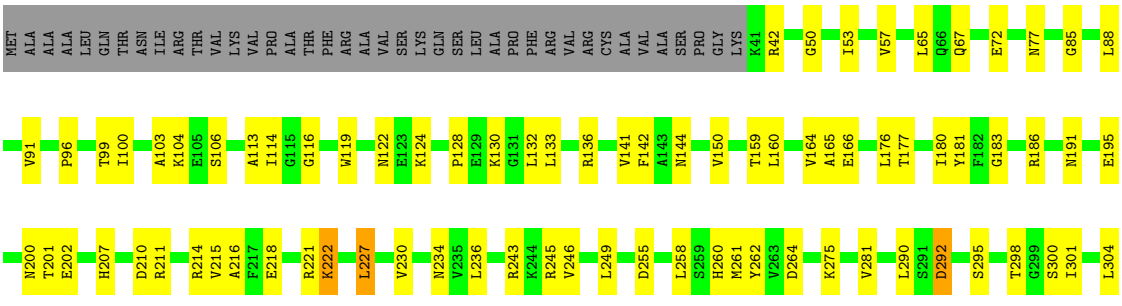

• Molecule 1: 3-isopropylmalate dehydrogenase 2, chloroplastic

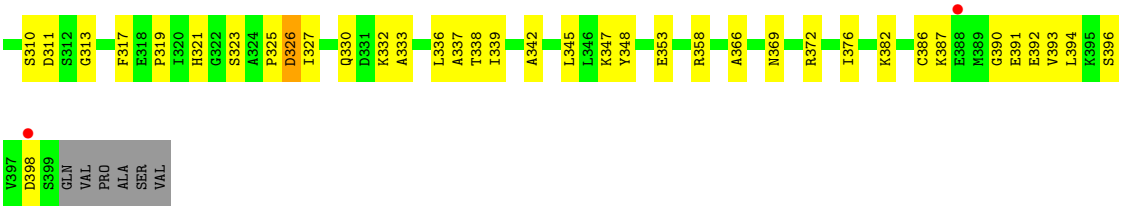
Chain D:




• Molecule 1: 3-isopropylmalate dehydrogenase 2, chloroplastic

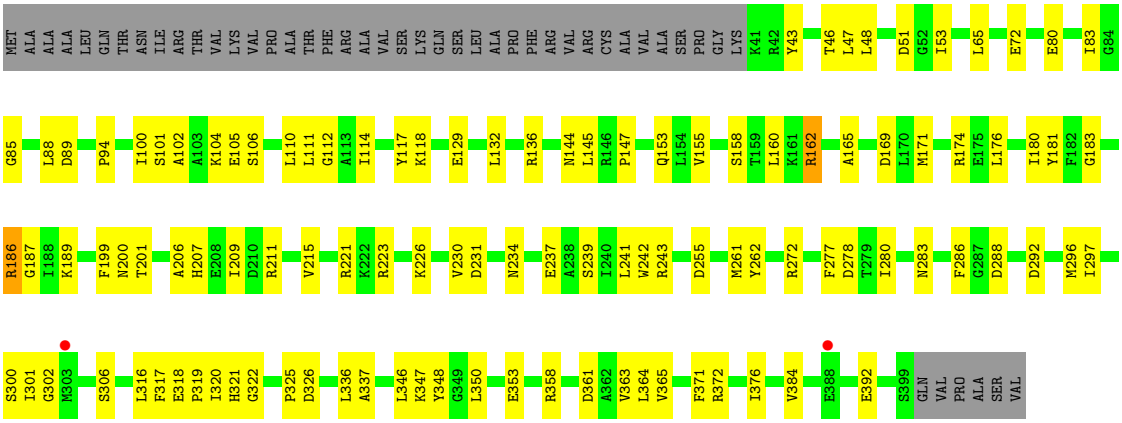
Chain E:





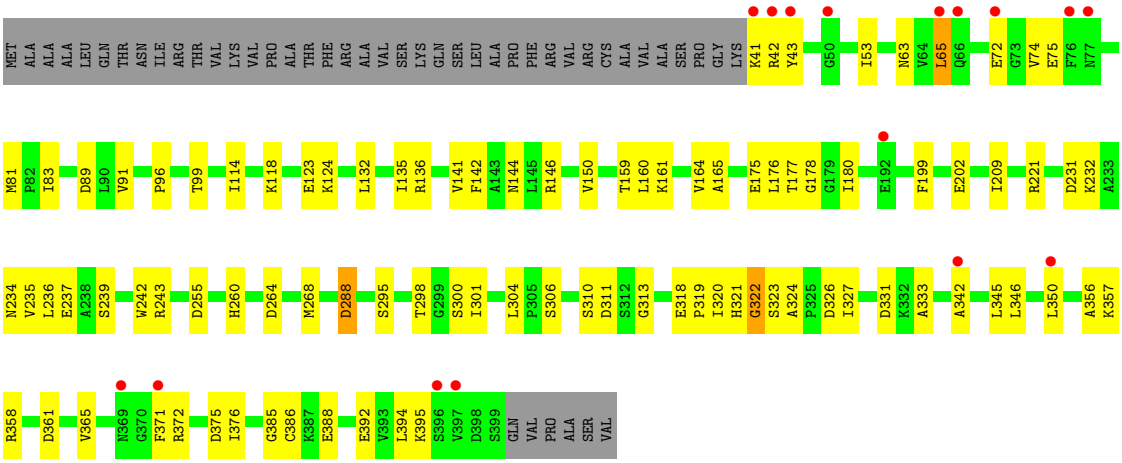

• Molecule 1: 3-isopropylmalate dehydrogenase 2, chloroplastic

Chain F:



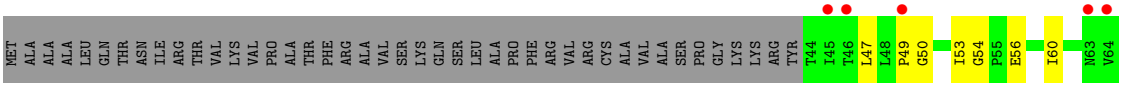

• Molecule 1: 3-isopropylmalate dehydrogenase 2, chloroplastic

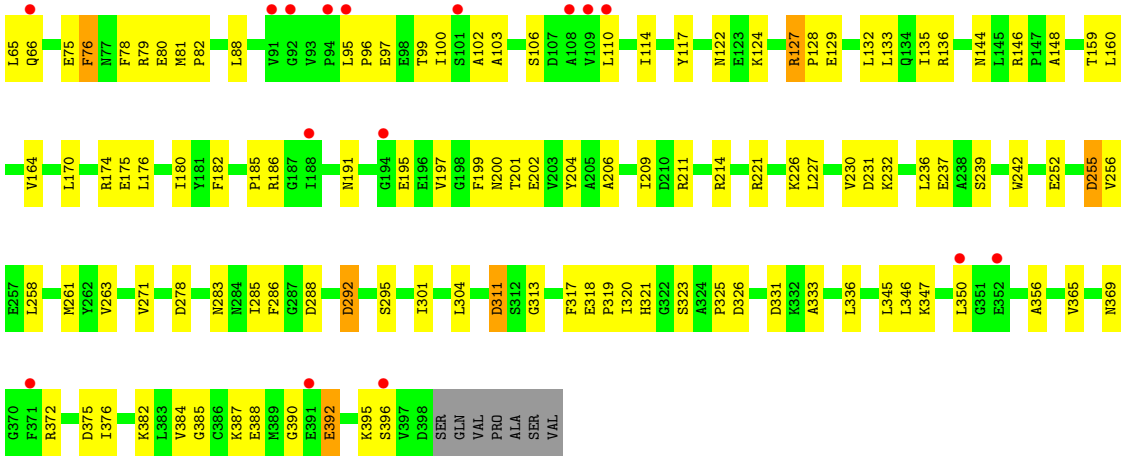
Chain G:




• Molecule 1: 3-isopropylmalate dehydrogenase 2, chloroplastic

Chain H:




L65 Q66 E75 F76 N77 F78 R79 E80 M81 P82 L88 V91 G92 V93 P94 L95 P96 E97 E98 T99 I100 S101 A102 A103 S106 D107 A108 V109 L110 I114 Y117 N122 E123 K124 R127 P128 E129 L132 L133 Q134 I135 R136 N144 L145 R146 P147 A148 T159 L160
V164 L170 R174 E175 L176 I180 Y181 F182 P185 R186 G187 I188 N191 G194 E195 E196 V197 G198 F199 N200 T201 E202 V203 Y204 A205 A206 I209 D210 R211 R214 R221 K226 L227 V230 D231 K232 L236 E237 A238 S239 W242 E252 D255 V256
E257 L258 M261 Y262 V263 V271 D278 N283 N284 I285 F286 G287 D288 D292 S295 I301 L304 D311 S312 G313 F317 E318 P319 I320 H321 G322 S323 A324 P325 D326 D331 K332 A333 L336 L345 L346 K347 L350 G351 E352 A356 V365 N369
G370 F371 R372 D375 I376 K382 L383 V384 G385 G386 K387 E388 M389 G390 E391 E392 K395 S396 V397 D398 SER GLN VAL PRO ALA SER VAL

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 21 21 21 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 77.20Å 132.87Å 349.43Å<br>90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 46.73 – 3.49<br>49.84 – 3.49 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 97.8 (46.73-3.49)<br>88.7 (49.84-3.49) | Depositor<br>EDS |
| $R_{merge}$ | (Not available) | Depositor |
| $R_{sym}$ | 0.24 | Depositor |
| $< I/\sigma(I) >$ [1] | 2.61 (at 3.48Å) | Xtriage |
| Refinement program | PHENIX (1.10.1_2155: ???) | Depositor |
| R, $R_{free}$ | 0.189 , 0.261<br>0.190 , 0.258 | Depositor<br>DCC |
| $R_{free}$ test set | 2330 reflections (5.08%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 57.2 | Xtriage |
| Anisotropy | 0.481 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.33 , 36.1 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.46$, $< L^2 > = 0.29$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o$,$F_c$ correlation | 0.91 | EDS |
| Total number of atoms | 22043 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 58.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.36% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: NAD, SO4, MG

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 | 0.61 | 1/2759 (0.0%) | 0.72 | 1/3733 (0.0%) |
| 1 | B | 0.58 | 0/2750 | 0.72 | 1/3721 (0.0%) |
| 1 | C | 0.58 | 0/2750 | 0.72 | 1/3721 (0.0%) |
| 1 | D | 0.57 | 2/2741 (0.1%) | 0.72 | 1/3710 (0.0%) |
| 1 | E | 0.59 | 1/2750 (0.0%) | 0.71 | 0/3721 |
| 1 | F | 0.59 | 1/2750 (0.0%) | 0.70 | 0/3721 |
| 1 | G | 0.57 | 0/2750 | 0.71 | 2/3721 (0.1%) |
| 1 | H | 0.51 | 0/2711 | 0.67 | 0/3670 |
| All | All | 0.58 | 5/21961 (0.0%) | 0.71 | 6/29718 (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 |
|---|---|---|---|
| 1 | H | 0 | 1 |

All (5) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | F | 392 | GLU | CB-CG | 8.63 | 1.68 | 1.52 |
| 1 | D | 392 | GLU | CB-CG | 6.23 | 1.64 | 1.52 |
| 1 | E | 392 | GLU | CB-CG | 5.67 | 1.62 | 1.52 |
| 1 | D | 281 | VAL | CB-CG2 | -5.54 | 1.41 | 1.52 |
| 1 | A | 386 | CYS | CB-SG | -5.36 | 1.73 | 1.81 |

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

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | C | 245 | ARG | NE-CZ-NH2 | -6.78 | 116.91 | 120.30 |
| 1 | A | 231 | ASP | CB-CG-OD1 | 5.95 | 123.65 | 118.30 |
| 1 | G | 288 | ASP | CB-CG-OD1 | 5.39 | 123.15 | 118.30 |
| 1 | B | 322 | GLY | N-CA-C | -5.31 | 99.82 | 113.10 |
| 1 | D | 346 | LEU | CB-CG-CD1 | -5.03 | 102.44 | 111.00 |

There are no chirality outliers.

All (1) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | H | 392 | GLU | 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 | A | 2718 | 0 | 2754 | 86 | 0 |
| 1 | B | 2709 | 0 | 2746 | 89 | 0 |
| 1 | C | 2709 | 0 | 2746 | 88 | 0 |
| 1 | D | 2700 | 0 | 2733 | 98 | 0 |
| 1 | E | 2709 | 0 | 2746 | 86 | 0 |
| 1 | F | 2709 | 0 | 2746 | 89 | 0 |
| 1 | G | 2709 | 0 | 2746 | 65 | 0 |
| 1 | H | 2671 | 0 | 2702 | 98 | 0 |
| 2 | A | 88 | 0 | 49 | 7 | 0 |
| 2 | C | 44 | 0 | 26 | 3 | 0 |
| 2 | D | 88 | 0 | 50 | 7 | 0 |
| 2 | E | 44 | 0 | 25 | 3 | 0 |
| 2 | G | 44 | 0 | 26 | 6 | 0 |
| 2 | H | 44 | 0 | 25 | 3 | 0 |
| 3 | A | 10 | 0 | 0 | 0 | 0 |
| 3 | C | 10 | 0 | 0 | 0 | 0 |
| 3 | D | 10 | 0 | 0 | 0 | 0 |
| 3 | E | 5 | 0 | 0 | 0 | 0 |
| 3 | G | 5 | 0 | 0 | 7 | 0 |
| 3 | H | 10 | 0 | 0 | 0 | 0 |
| 4 | A | 2 | 0 | 0 | 0 | 0 |
| 4 | C | 2 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 4 | D | 2 | 0 | 0 | 0 | 0 |
| 4 | E | 1 | 0 | 0 | 0 | 0 |
| All | All | 22043 | 0 | 22120 | 652 | 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 15.

The worst 5 of 652 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:H:186:ARG:NH2 | 1:H:199:PHE:O | 1.93 | 0.99 |
| 1:G:288:ASP:OD1 | 3:G:502:SO4:O4 | 1.78 | 0.99 |
| 2:A:501:NAD:H51A | 2:A:501:NAD:H8A | 1.47 | 0.96 |
| 1:H:186:ARG:NH2 | 1:H:199:PHE:C | 2.19 | 0.96 |
| 1:B:72:GLU:OE2 | 1:B:358:ARG:NH2 | 2.02 | 0.93 |

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 | 358/405 (88%) | 343 (96%) | 15 (4%) | 0 | 100 | 100 |
| 1 | B | 357/405 (88%) | 337 (94%) | 20 (6%) | 0 | 100 | 100 |
| 1 | C | 357/405 (88%) | 342 (96%) | 13 (4%) | 2 (1%) | 25 | 64 |
| 1 | D | 356/405 (88%) | 340 (96%) | 16 (4%) | 0 | 100 | 100 |
| 1 | E | 357/405 (88%) | 340 (95%) | 17 (5%) | 0 | 100 | 100 |
| 1 | F | 357/405 (88%) | 342 (96%) | 15 (4%) | 0 | 100 | 100 |
| 1 | G | 357/405 (88%) | 342 (96%) | 15 (4%) | 0 | 100 | 100 |
| 1 | H | 353/405 (87%) | 332 (94%) | 21 (6%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles |
|---|---|---|---|---|---|---|
| All | All | 2852/3240 (88%) | 2718 (95%) | 132 (5%) | 2 (0%) | 51 84 |

All (2) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | C | 191 | ASN |
| 1 | C | 312 | SER |

### 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 | 288/323 (89%) | 279 (97%) | 9 (3%) | 40 70 |
| 1 | B | 287/323 (89%) | 283 (99%) | 4 (1%) | 67 85 |
| 1 | C | 287/323 (89%) | 281 (98%) | 6 (2%) | 53 79 |
| 1 | D | 286/323 (88%) | 279 (98%) | 7 (2%) | 49 76 |
| 1 | E | 287/323 (89%) | 281 (98%) | 6 (2%) | 53 79 |
| 1 | F | 287/323 (89%) | 284 (99%) | 3 (1%) | 76 88 |
| 1 | G | 287/323 (89%) | 284 (99%) | 3 (1%) | 76 88 |
| 1 | H | 283/323 (88%) | 273 (96%) | 10 (4%) | 36 67 |
| All | All | 2292/2584 (89%) | 2244 (98%) | 48 (2%) | 53 79 |

5 of 48 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | E | 292 | ASP |
| 1 | G | 65 | LEU |
| 1 | E | 326 | ASP |
| 1 | F | 162 | ARG |
| 1 | G | 395 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | E | 200 | ASN |
| 1 | F | 321 | HIS |
| 1 | H | 283 | ASN |
| 1 | G | 144 | ASN |
| 1 | D | 283 | ASN |

### 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 25 ligands modelled in this entry, 7 are monoatomic - leaving 18 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 | $\#\|Z\| > 2$ |
| 2 | NAD | C | 501 | - | 42,48,48 | 2.18 | 10 (23%) | 50,73,73 | 1.88 | 14 (28%) |
| 2 | NAD | G | 501 | - | 42,48,48 | 2.25 | 10 (23%) | 50,73,73 | 1.87 | 13 (26%) |
| 3 | SO4 | A | 502 | 2 | 4,4,4 | 0.29 | 0 | 6,6,6 | 0.58 | 0 |
| 3 | SO4 | A | 505 | 4,2 | 4,4,4 | 0.47 | 0 | 6,6,6 | 0.42 | 0 |
| 3 | SO4 | E | 502 | 4,2 | 4,4,4 | 0.27 | 0 | 6,6,6 | 0.59 | 0 |
| 3 | SO4 | H | 502 | - | 4,4,4 | 0.47 | 0 | 6,6,6 | 0.93 | 0 |
| 3 | SO4 | H | 503 | 2 | 4,4,4 | 0.51 | 0 | 6,6,6 | 0.38 | 0 |
| 3 | SO4 | D | 502 | 4,2 | 4,4,4 | 0.51 | 0 | 6,6,6 | 0.53 | 0 |
| 3 | SO4 | C | 502 | 4 | 4,4,4 | 0.15 | 0 | 6,6,6 | 0.48 | 0 |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 2 | NAD | A | 501 | 3 | 42,48,48 | 2.16 | 12 (28%) | 50,73,73 | 2.59 | 20 (40%) |
| 3 | SO4 | C | 503 | - | 4,4,4 | 0.45 | 0 | 6,6,6 | 1.25 | 1 (16%) |
| 2 | NAD | D | 503 | 3 | 42,48,48 | 2.29 | 10 (23%) | 50,73,73 | 1.30 | 9 (18%) |
| 2 | NAD | A | 504 | 3 | 42,48,48 | 2.25 | 11 (26%) | 50,73,73 | 1.56 | 10 (20%) |
| 2 | NAD | E | 501 | 3 | 42,48,48 | 2.24 | 11 (26%) | 50,73,73 | 1.84 | 13 (26%) |
| 2 | NAD | H | 501 | 3 | 42,48,48 | 2.35 | 12 (28%) | 50,73,73 | 2.18 | 17 (34%) |
| 2 | NAD | D | 501 | 3 | 42,48,48 | 2.30 | 11 (26%) | 50,73,73 | 2.50 | 20 (40%) |
| 3 | SO4 | G | 502 | - | 4,4,4 | 0.99 | 0 | 6,6,6 | 1.66 | 1 (16%) |
| 3 | SO4 | D | 504 | 4,2 | 4,4,4 | 0.13 | 0 | 6,6,6 | 0.30 | 0 |

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 | NAD | C | 501 | - | - | 14/26/62/62 | 0/5/5/5 |
| 2 | NAD | G | 501 | - | - | 9/26/62/62 | 0/5/5/5 |
| 2 | NAD | A | 501 | 3 | - | 14/26/62/62 | 0/5/5/5 |
| 2 | NAD | D | 503 | 3 | - | 11/26/62/62 | 0/5/5/5 |
| 2 | NAD | A | 504 | 3 | - | 9/26/62/62 | 0/5/5/5 |
| 2 | NAD | E | 501 | 3 | - | 13/26/62/62 | 0/5/5/5 |
| 2 | NAD | H | 501 | 3 | - | 10/26/62/62 | 0/5/5/5 |
| 2 | NAD | D | 501 | 3 | - | 7/26/62/62 | 0/5/5/5 |

The worst 5 of 87 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 2 | A | 504 | NAD | C7N-N7N | 7.95 | 1.48 | 1.33 |
| 2 | H | 501 | NAD | C2B-C1B | -7.87 | 1.41 | 1.53 |
| 2 | D | 503 | NAD | C7N-N7N | 7.74 | 1.47 | 1.33 |
| 2 | D | 501 | NAD | C2B-C1B | -7.60 | 1.42 | 1.53 |
| 2 | G | 501 | NAD | C2B-C1B | -7.17 | 1.42 | 1.53 |

The worst 5 of 118 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | A | 501 | NAD | C3N-C7N-N7N | 8.73 | 128.23 | 117.75 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | H | 501 | NAD | C5N-C4N-C3N | -7.59 | 111.36 | 120.34 |
| 2 | D | 501 | NAD | C5N-C4N-C3N | -7.32 | 111.68 | 120.34 |
| 2 | D | 501 | NAD | C3N-C7N-N7N | 6.69 | 125.78 | 117.75 |
| 2 | A | 501 | NAD | C5N-C4N-C3N | -6.34 | 112.84 | 120.34 |

There are no chirality outliers.

5 of 87 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 2 | A | 501 | NAD | C5B-O5B-PA-O1A |
| 2 | A | 501 | NAD | O4D-C1D-N1N-C2N |
| 2 | A | 501 | NAD | O4D-C1D-N1N-C6N |
| 2 | A | 501 | NAD | C2D-C1D-N1N-C2N |
| 2 | A | 504 | NAD | C5D-O5D-PN-O1N |

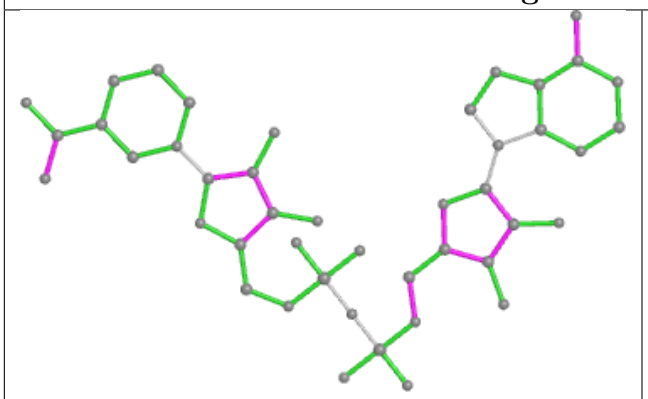
There are no ring outliers.

9 monomers are involved in 32 short contacts:

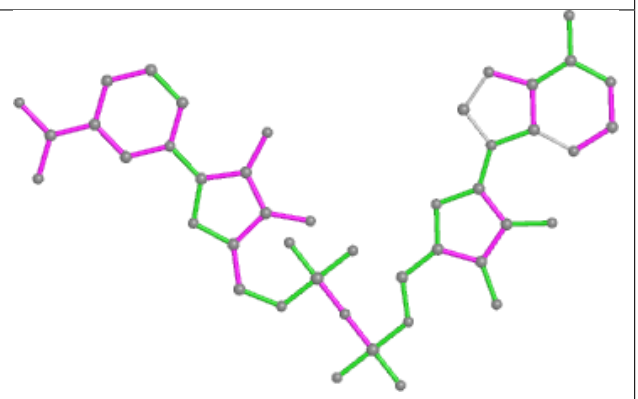
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 2 | C | 501 | NAD | 3 | 0 |
| 2 | G | 501 | NAD | 6 | 0 |
| 2 | A | 501 | NAD | 5 | 0 |
| 2 | D | 503 | NAD | 4 | 0 |
| 2 | A | 504 | NAD | 2 | 0 |
| 2 | E | 501 | NAD | 3 | 0 |
| 2 | H | 501 | NAD | 3 | 0 |
| 2 | D | 501 | NAD | 3 | 0 |
| 3 | G | 502 | SO4 | 7 | 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.

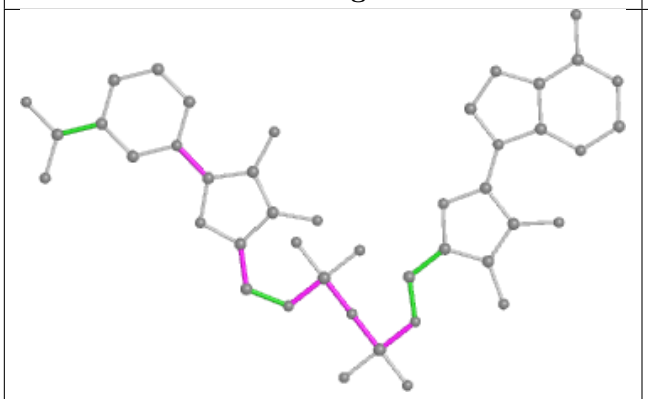
**Ligand NAD C 501**



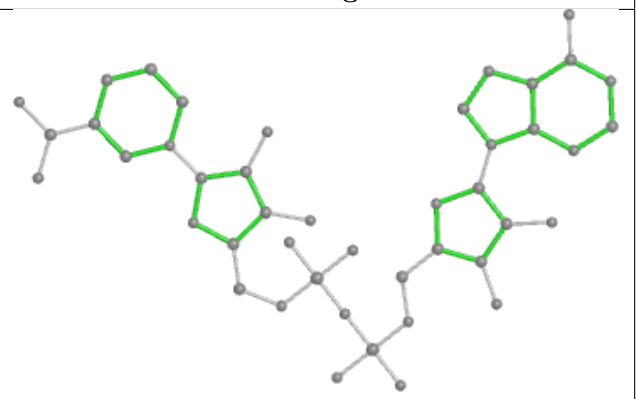
**Bond lengths**



**Bond angles**

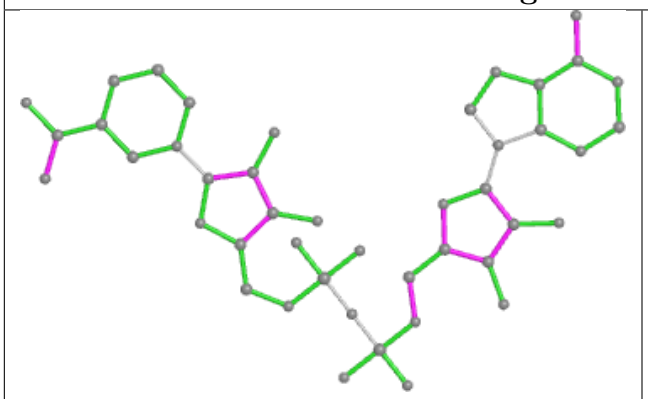


**Torsions**

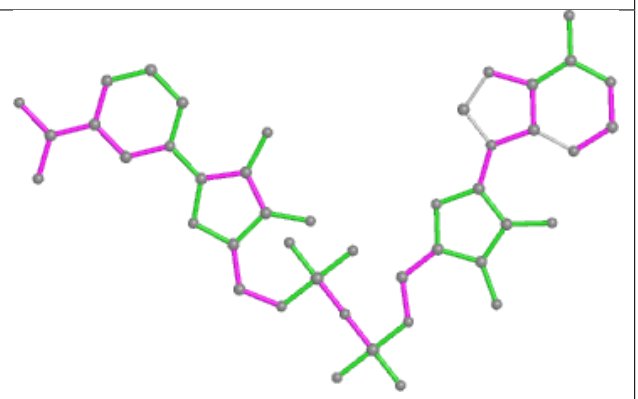


**Rings**

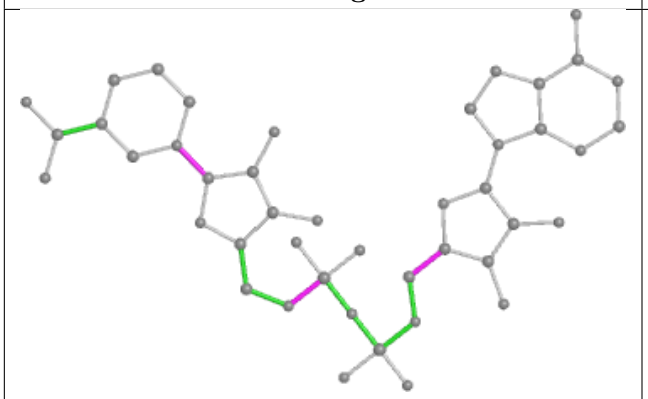
**Ligand NAD G 501**



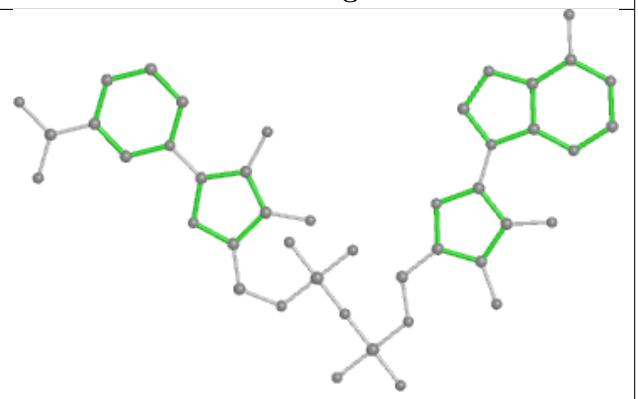
**Bond lengths**



**Bond angles**

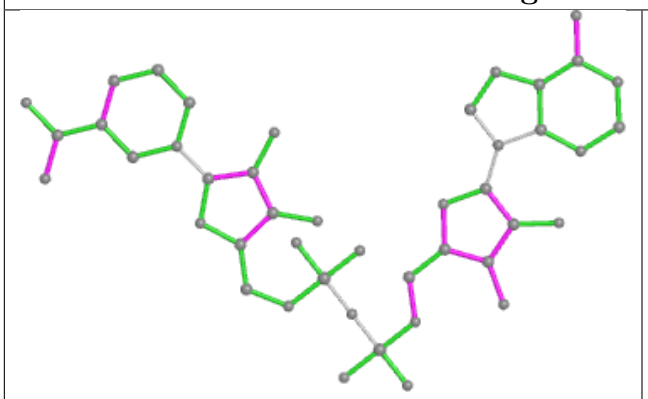


**Torsions**

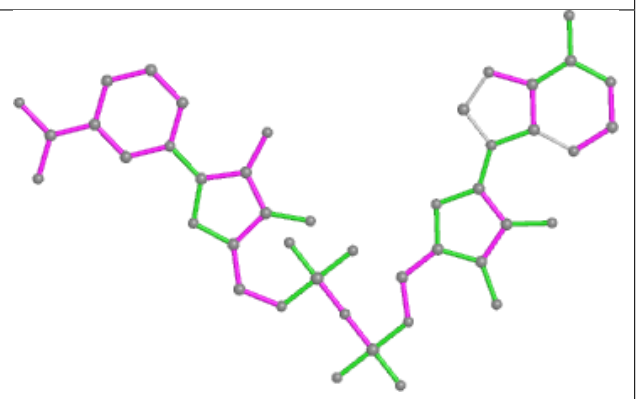


**Rings**

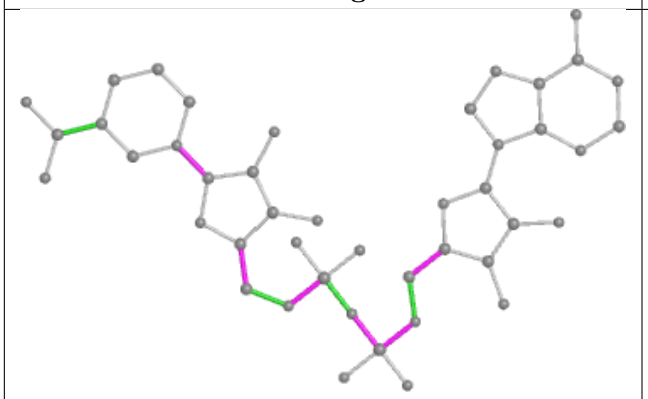
**Ligand NAD A 501**



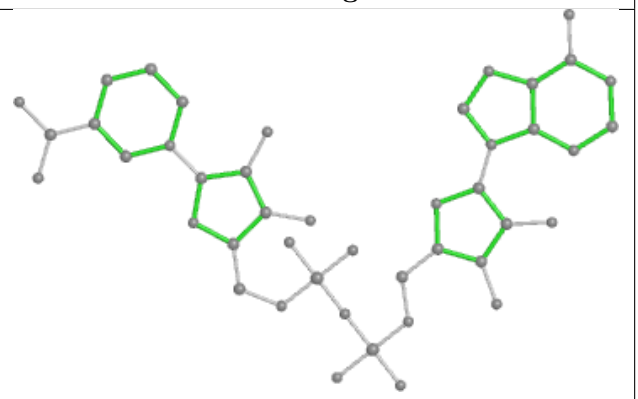
**Bond lengths**



**Bond angles**

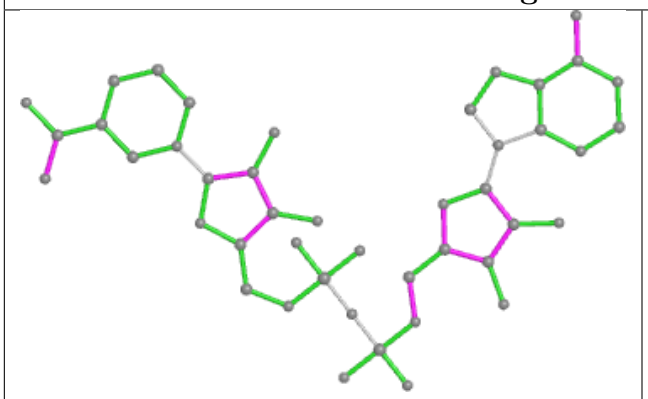


**Torsions**

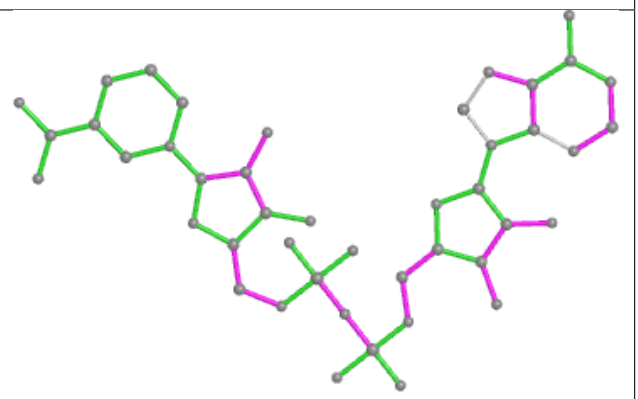


**Rings**

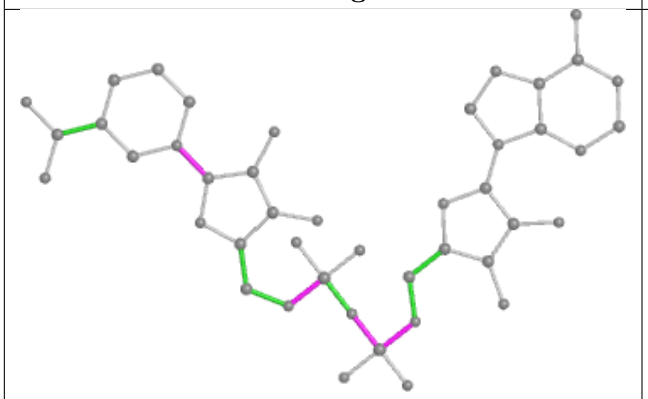
**Ligand NAD D 503**



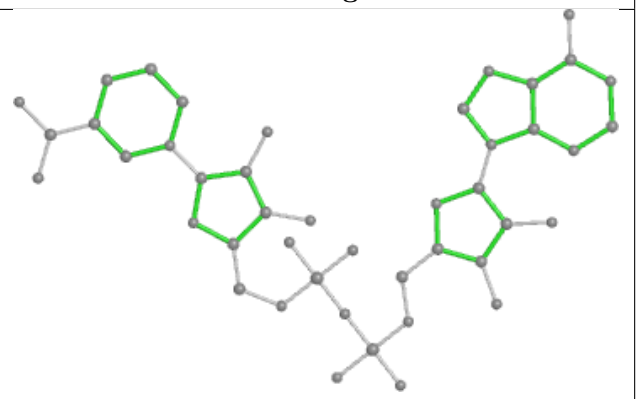
**Bond lengths**



**Bond angles**

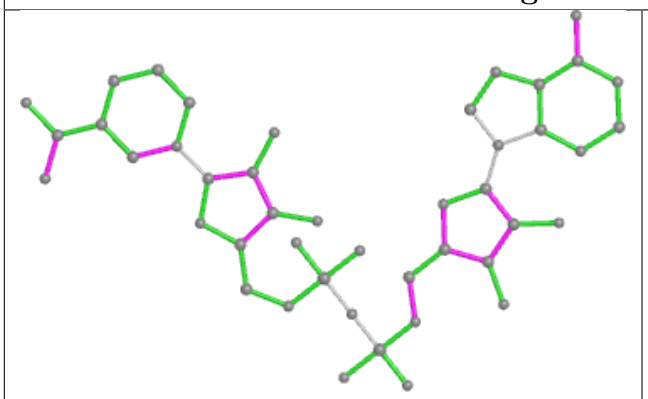


**Torsions**

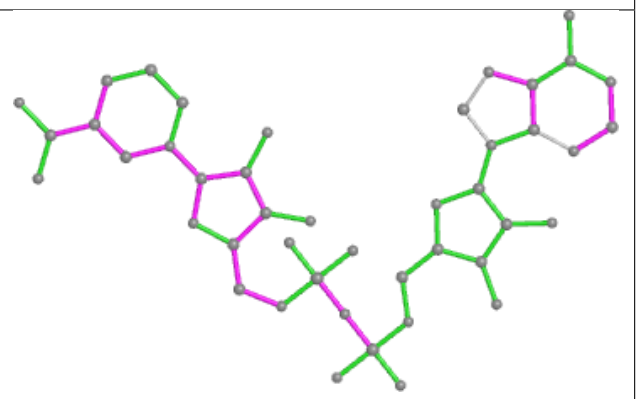


**Rings**

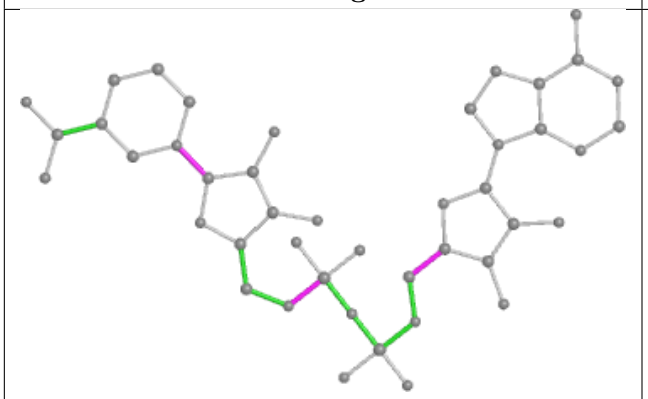
**Ligand NAD A 504**



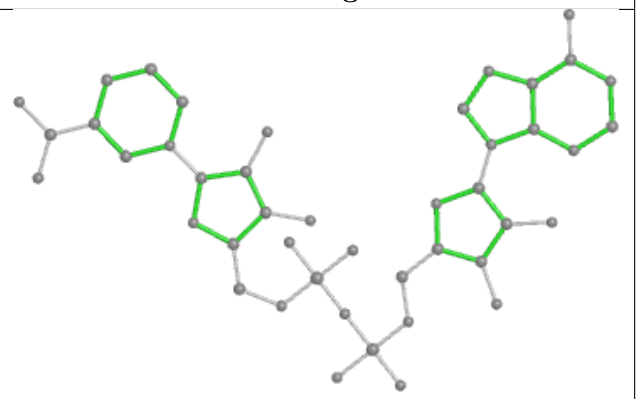
**Bond lengths**



**Bond angles**

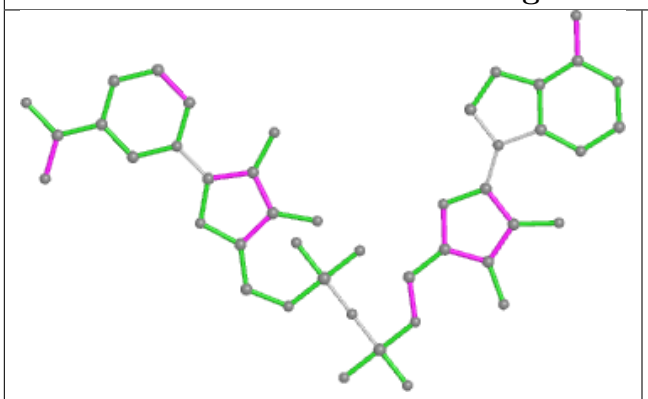


**Torsions**

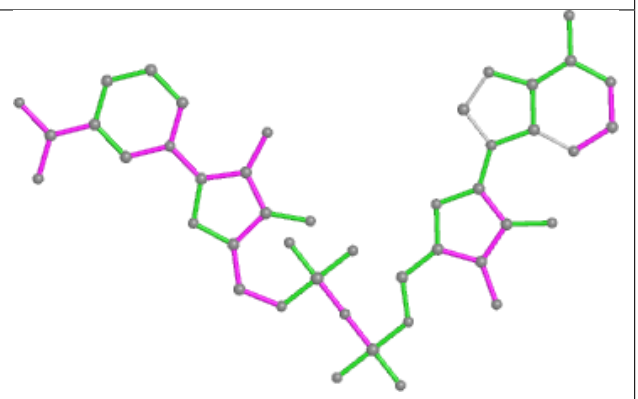


**Rings**

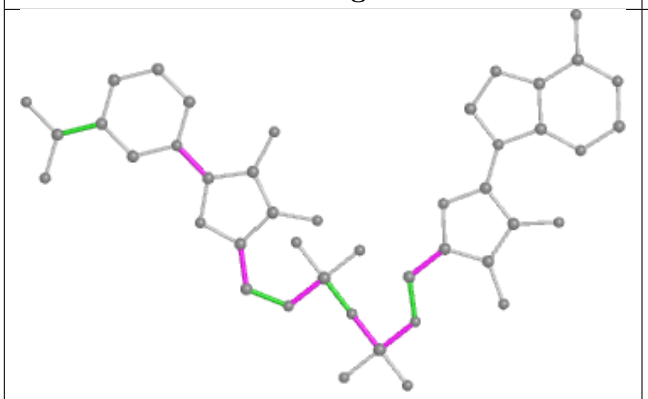
**Ligand NAD E 501**



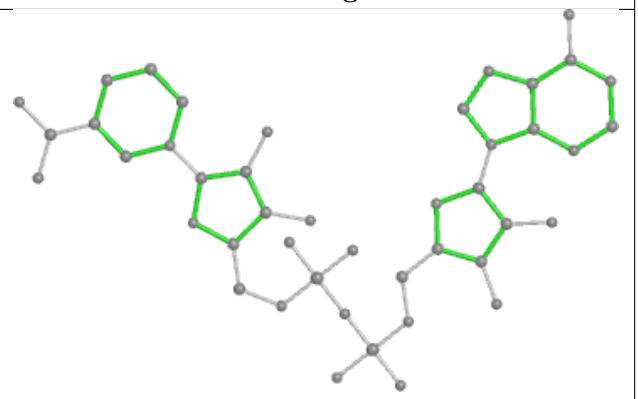
**Bond lengths**



**Bond angles**

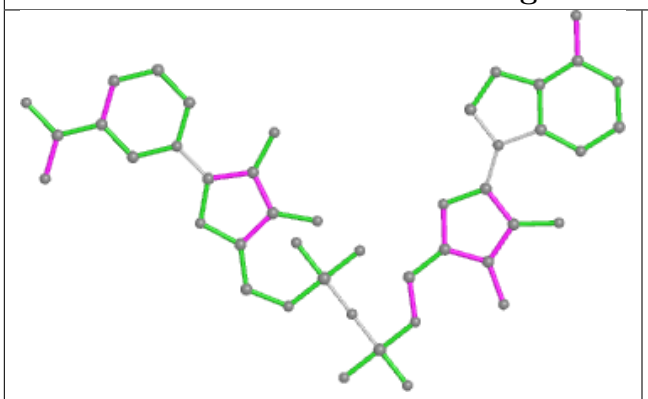


**Torsions**

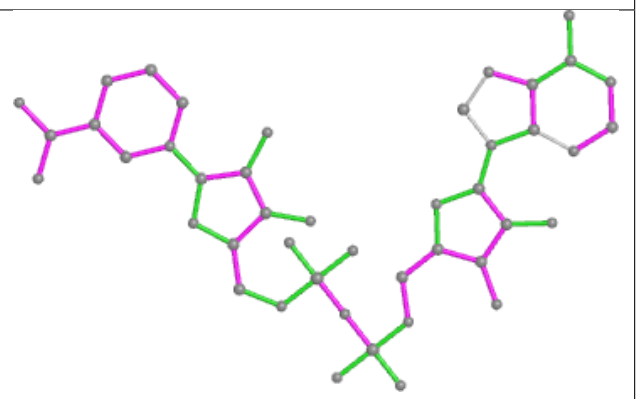


**Rings**

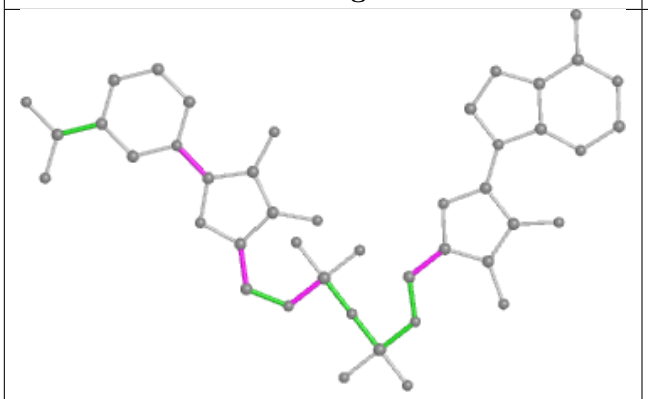
**Ligand NAD H 501**



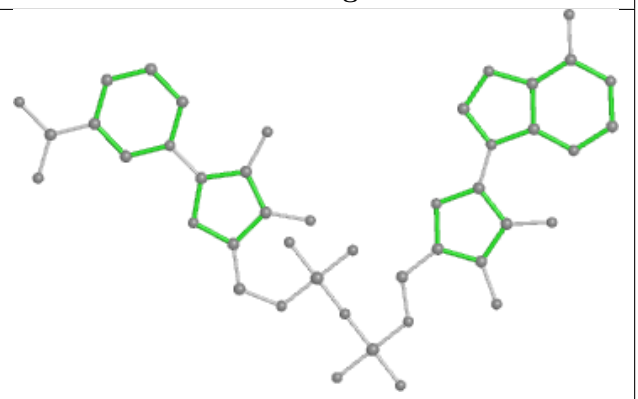
**Bond lengths**



**Bond angles**

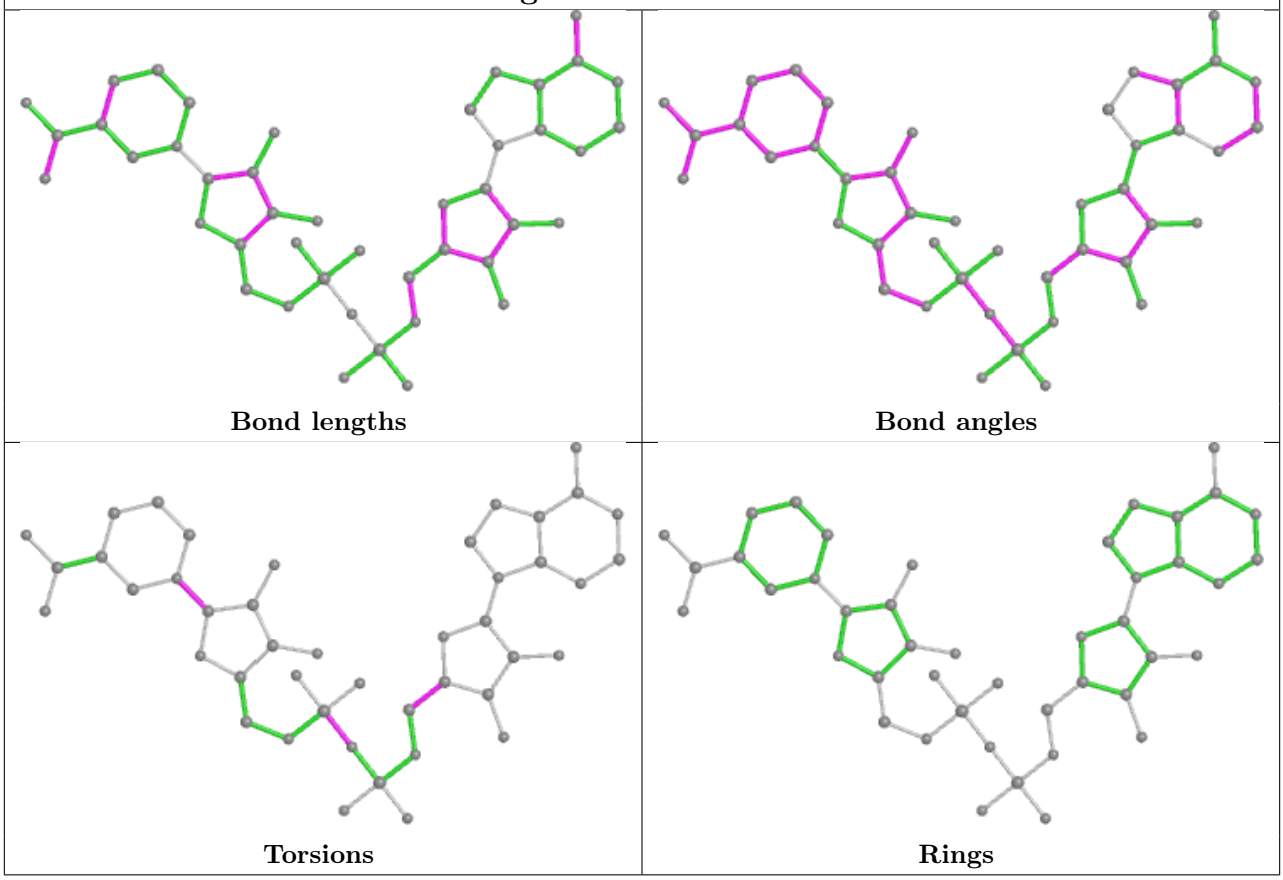


**Torsions**



**Rings**

**Ligand NAD D 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, $95^{th}$ 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$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 1 | A | 360/405 (88%) | 0.20 | 7 (1%) | 66 | 61 | 32, 52, 78, 123 | 0 |
| 1 | B | 359/405 (88%) | 0.09 | 8 (2%) | 62 | 56 | 36, 50, 76, 120 | 0 |
| 1 | C | 359/405 (88%) | 0.22 | 3 (0%) | 86 | 81 | 34, 57, 88, 135 | 0 |
| 1 | D | 358/405 (88%) | 0.25 | 10 (2%) | 53 | 47 | 36, 54, 81, 107 | 0 |
| 1 | E | 359/405 (88%) | 0.15 | 2 (0%) | 89 | 86 | 33, 50, 74, 106 | 0 |
| 1 | F | 359/405 (88%) | 0.13 | 2 (0%) | 89 | 86 | 37, 52, 78, 143 | 0 |
| 1 | G | 359/405 (88%) | 0.33 | 16 (4%) | 33 | 29 | 39, 59, 94, 132 | 0 |
| 1 | H | 355/405 (87%) | 0.35 | 21 (5%) | 22 | 20 | 35, 67, 110, 140 | 0 |
| All | All | 2868/3240 (88%) | 0.22 | 69 (2%) | 59 | 53 | 32, 54, 89, 143 | 0 |

The worst 5 of 69 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | G | 397 | VAL | 4.2 |
| 1 | H | 92 | GLY | 3.3 |
| 1 | C | 192 | GLU | 3.1 |
| 1 | G | 192 | GLU | 3.0 |
| 1 | G | 66 | GLN | 3.0 |

## 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 monosaccharides in this entry.

## 6.4 Ligands (i)

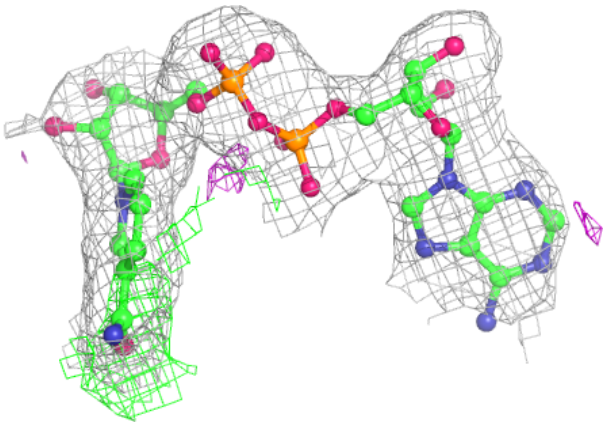
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, $95^{th}$ percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

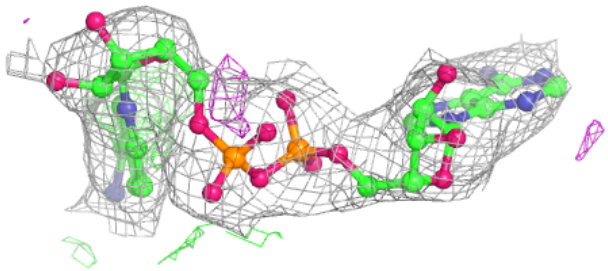
| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 3 | SO4 | H | 503 | 5/5 | 0.70 | 0.29 | 93,109,115,116 | 0 |
| 4 | MG | A | 503 | 1/1 | 0.78 | 0.14 | 37,37,37,37 | 0 |
| 3 | SO4 | D | 502 | 5/5 | 0.81 | 0.32 | 81,85,89,96 | 0 |
| 4 | MG | E | 503 | 1/1 | 0.84 | 0.20 | 71,71,71,71 | 0 |
| 4 | MG | D | 505 | 1/1 | 0.86 | 0.18 | 79,79,79,79 | 0 |
| 3 | SO4 | D | 504 | 5/5 | 0.86 | 0.26 | 74,76,80,92 | 0 |
| 3 | SO4 | C | 503 | 5/5 | 0.87 | 0.22 | 35,37,55,57 | 0 |
| 4 | MG | C | 504 | 1/1 | 0.88 | 0.14 | 63,63,63,63 | 0 |
| 3 | SO4 | G | 502 | 5/5 | 0.89 | 0.30 | 85,94,102,115 | 0 |
| 3 | SO4 | E | 502 | 5/5 | 0.89 | 0.20 | 58,59,69,96 | 0 |
| 4 | MG | A | 506 | 1/1 | 0.90 | 0.27 | 32,32,32,32 | 0 |
| 4 | MG | D | 506 | 1/1 | 0.92 | 0.08 | 47,47,47,47 | 0 |
| 3 | SO4 | A | 502 | 5/5 | 0.92 | 0.26 | 58,63,72,103 | 0 |
| 3 | SO4 | H | 502 | 5/5 | 0.93 | 0.18 | 35,36,46,47 | 0 |
| 2 | NAD | G | 501 | 44/44 | 0.93 | 0.23 | 34,55,104,143 | 0 |
| 2 | NAD | A | 501 | 44/44 | 0.94 | 0.23 | 41,47,124,155 | 0 |
| 2 | NAD | A | 504 | 44/44 | 0.94 | 0.21 | 26,39,87,135 | 0 |
| 4 | MG | C | 505 | 1/1 | 0.94 | 0.15 | 32,32,32,32 | 0 |
| 2 | NAD | H | 501 | 44/44 | 0.95 | 0.18 | 37,41,74,113 | 0 |
| 2 | NAD | D | 501 | 44/44 | 0.95 | 0.21 | 34,47,97,110 | 0 |
| 2 | NAD | D | 503 | 44/44 | 0.95 | 0.22 | 40,52,80,95 | 0 |
| 2 | NAD | C | 501 | 44/44 | 0.95 | 0.23 | 45,51,65,70 | 0 |
| 2 | NAD | E | 501 | 44/44 | 0.96 | 0.21 | 35,48,88,99 | 0 |
| 3 | SO4 | C | 502 | 5/5 | 0.96 | 0.15 | 45,47,48,52 | 0 |
| 3 | SO4 | A | 505 | 5/5 | 0.97 | 0.19 | 40,43,50,74 | 0 |

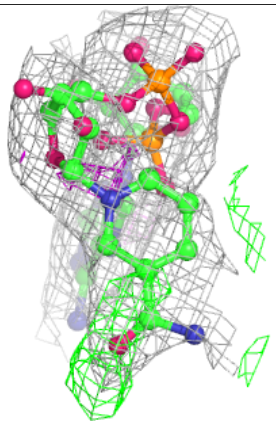
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around NAD G 501:**

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

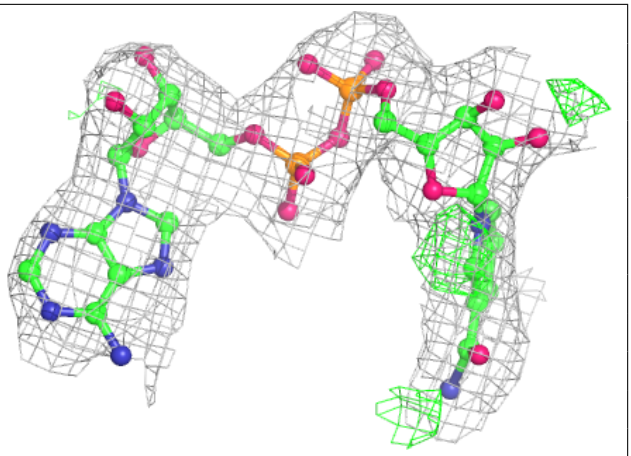


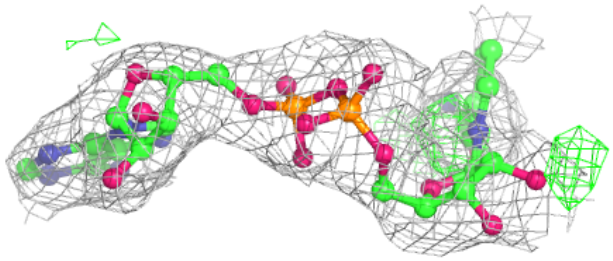


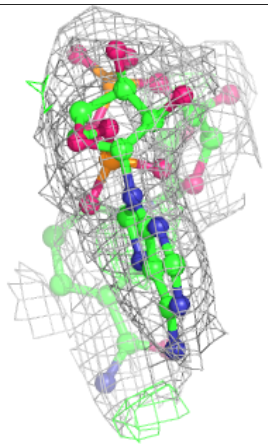


**Electron density around NAD A 501:**

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

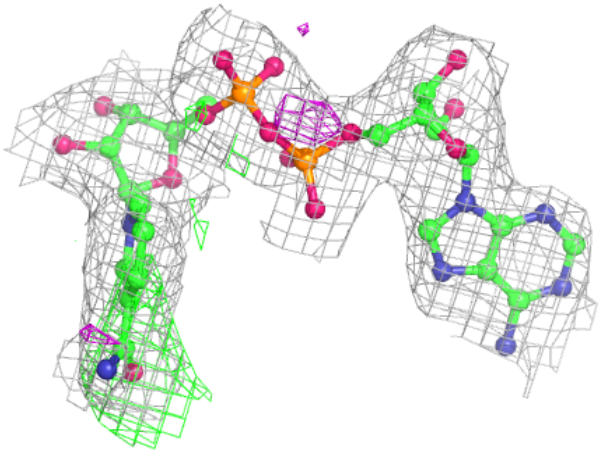


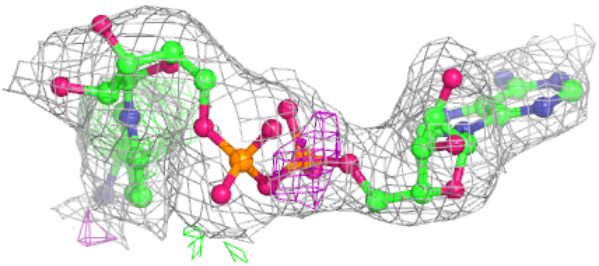


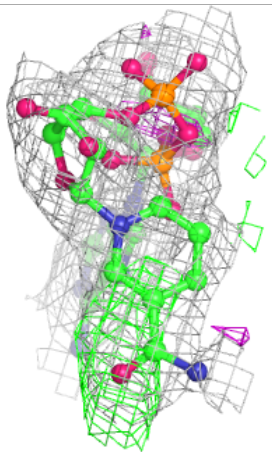


**Electron density around NAD A 504:**

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

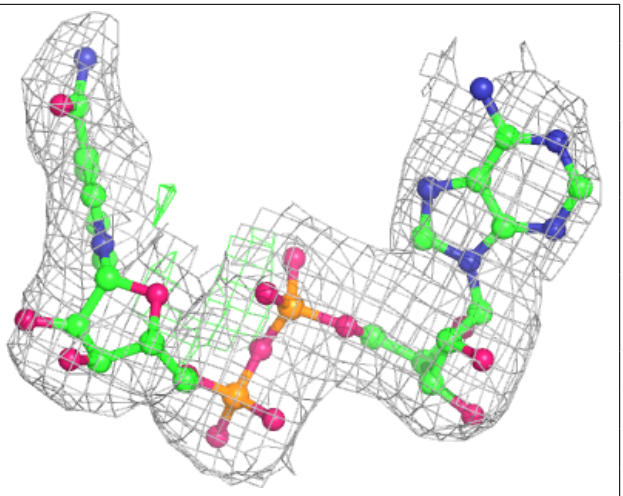


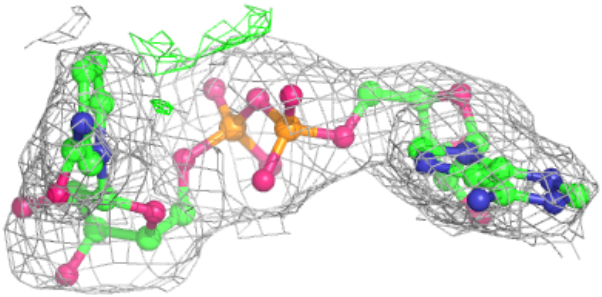


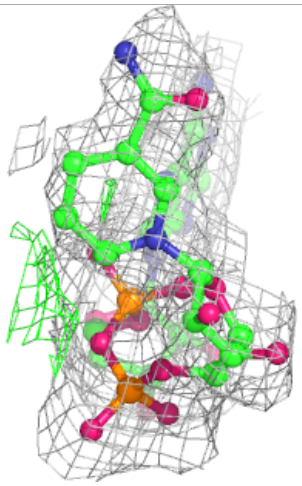


**Electron density around NAD H 501:**

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

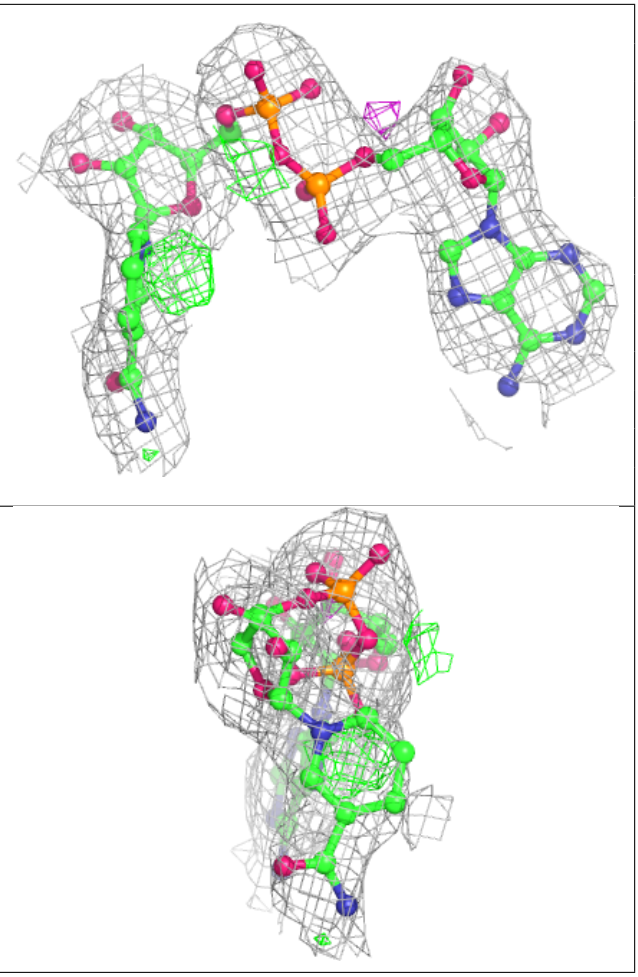






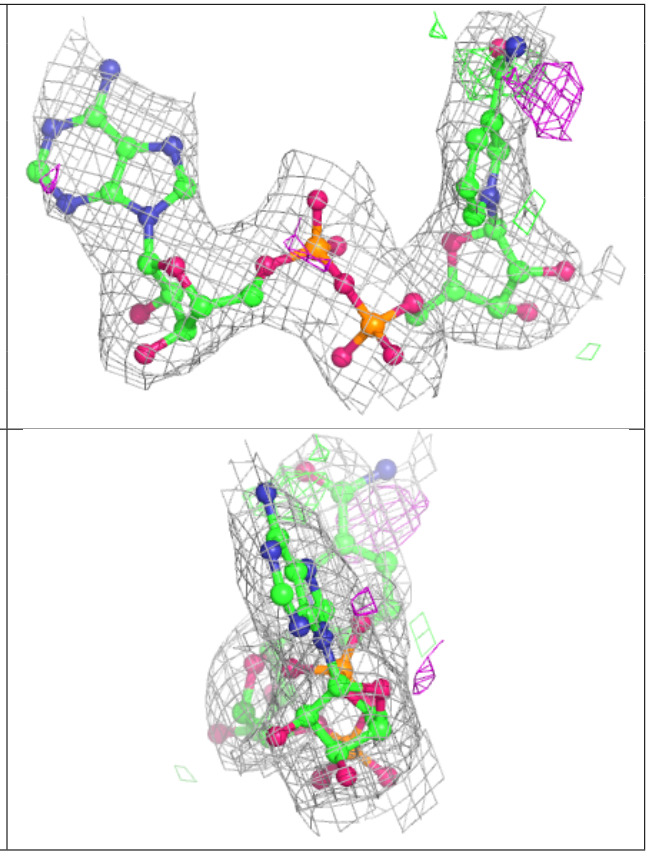
**Electron density around NAD D 501:**

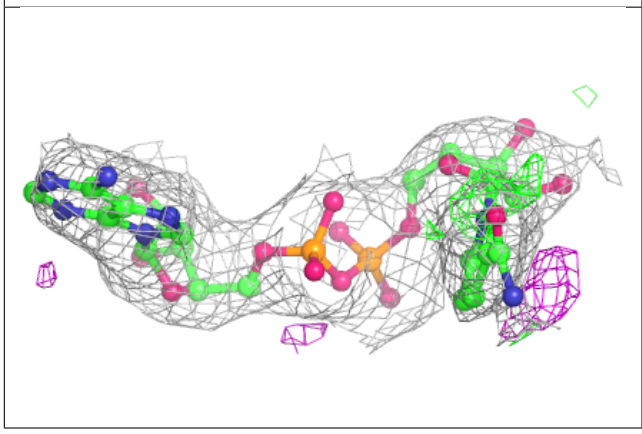
$2mF_o$-$DF_c$ (at 0.7 rmsd) in gray
$mF_o$-$DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



**Electron density around NAD D 503:**

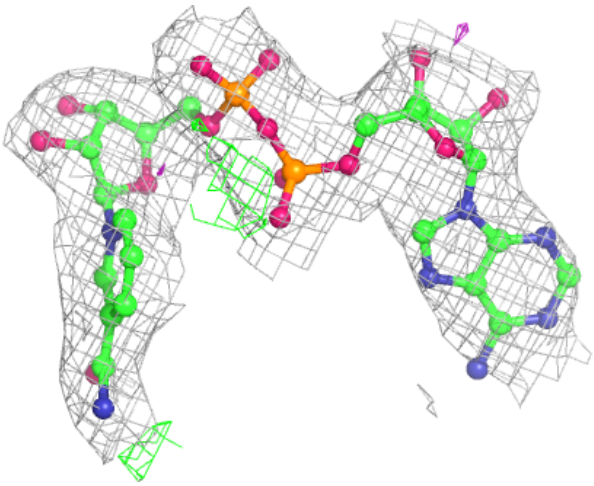
$2mF_o$-$DF_c$ (at 0.7 rmsd) in gray
$mF_o$-$DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

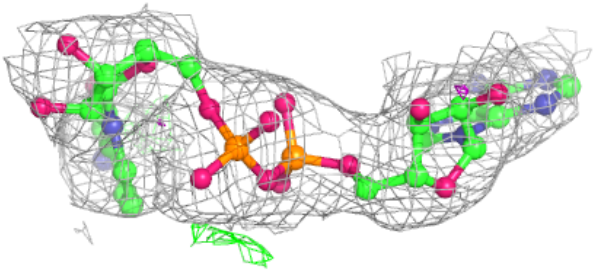


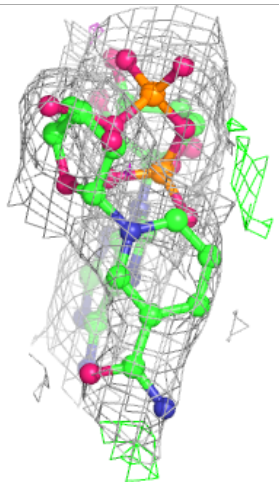


**Electron density around NAD C 501:**

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

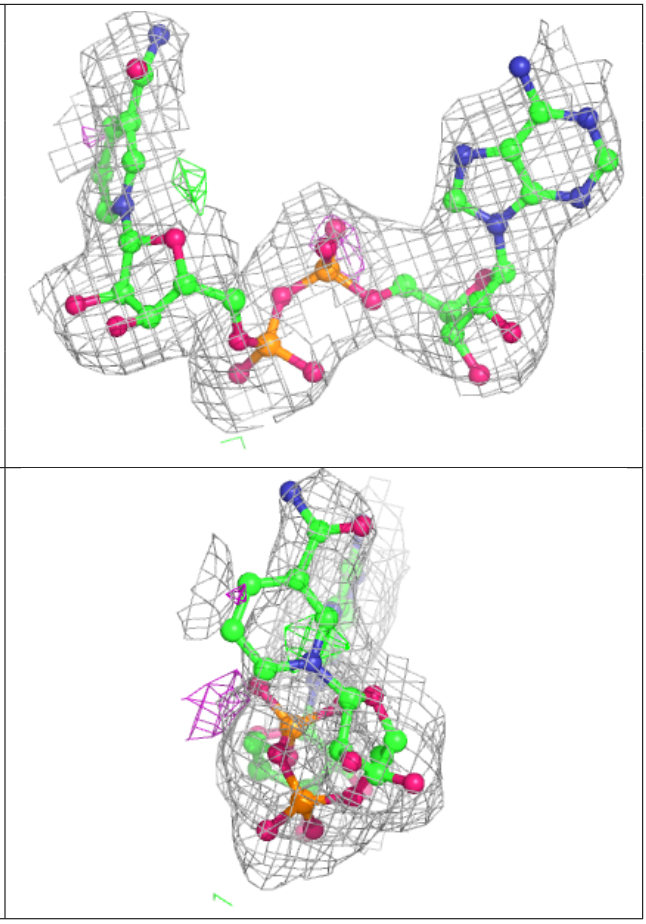






**Electron density around NAD E 501:**

$2mF_o$-$DF_c$ (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.