# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2023 – 07:22 AM EDT

| | | |
|---|---|---|
| PDB ID | : | 1IG9 |
| Title | : | Structure of the Replicating Complex of a Pol Alpha Family DNA Polymerase |
| Authors | : | Franklin, M.C.; Wang, J.; Steitz, T.A. |
| Deposited on | : | 2001-04-17 |
| Resolution | : | 2.60 Å(reported) |

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

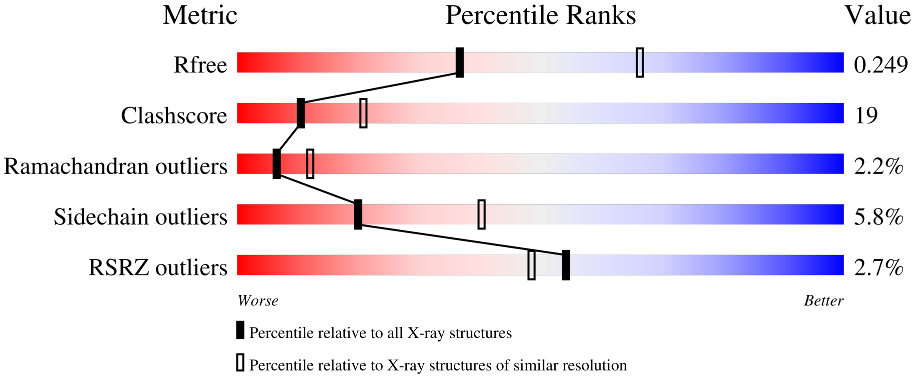
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.35 |
| buster-report | : | 1.1.7 (2018) |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 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 Overall quality at a glance

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

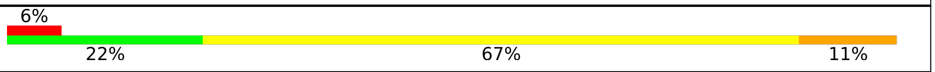
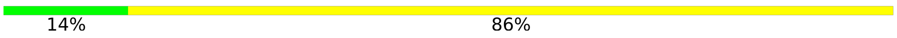
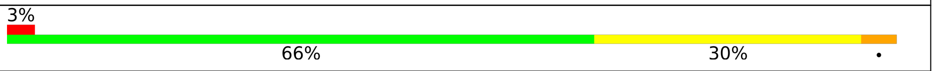
The reported resolution of this entry is 2.60 Å.

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 | 3163 (2.60-2.60) |
| Clashscore | 141614 | 3518 (2.60-2.60) |
| Ramachandran outliers | 138981 | 3455 (2.60-2.60) |
| Sidechain outliers | 138945 | 3455 (2.60-2.60) |
| RSRZ outliers | 127900 | 3104 (2.60-2.60) |

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 | T | 18 |  |
| 2 | P | 14 |  |
| 3 | A | 903 |  |

# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8394 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 DNA chain called 5'-D(*AP*CP*AP*GP*GP*TP*AP*AP*GP*CP*AP*GP*TP*CP*CP*GP*CP*G)-3'.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | | |
| 1 | T | 18 | 369 | 175 | 74 | 103 | 17 | 0 | 0 | 0 |

- Molecule 2 is a DNA chain called 5'-D(*GP*CP*GP*GP*AP*CP*TP*GP*CP*TP*TP*AP*CP*(DOC))-3'.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | | |
| 2 | P | 14 | 281 | 135 | 51 | 82 | 13 | 0 | 0 | 0 |

- Molecule 3 is a protein called DNA POLYMERASE.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 3 | A | 901 | 7355 | 4724 | 1224 | 1374 | 33 | 0 | 0 | 0 |

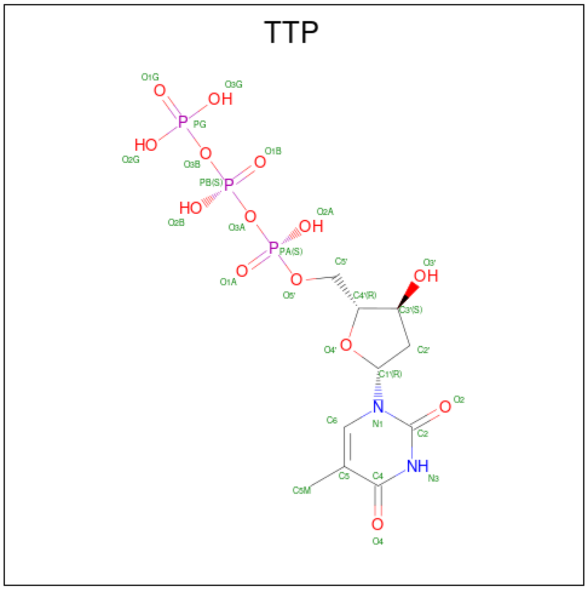
There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 222 | ALA | ASP | engineered mutation | UNP Q38087 |
| A | 327 | ALA | ASP | engineered mutation | UNP Q38087 |

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | Ca | | |
| 4 | A | 4 | 4 | 4 | 0 | 0 |

- Molecule 5 is THYMIDINE-5'-TRIPHOSPHATE (three-letter code: TTP) (formula: $C_{10}H_{17}N_2O_{14}P_3$).



| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 5 | A | 1 | 29 | 10 | 2 | 14 | 3 | 0 | 0 |

- Molecule 6 is water.

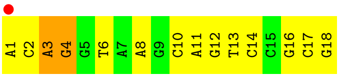
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | O | | |
| 6 | T | 31 | 31 | 31 | 0 | 0 |
| 6 | P | 19 | 19 | 19 | 0 | 0 |
| 6 | A | 306 | 306 | 306 | 0 | 0 |

# 3 Residue-property plots ⓘ

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.

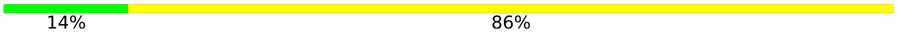
- Molecule 1: 5’-D(*AP*CP*AP*GP*GP*TP*AP*AP*GP*CP*AP*GP*TP*CP*CP*GP*CP*G )-3’

Chain T:



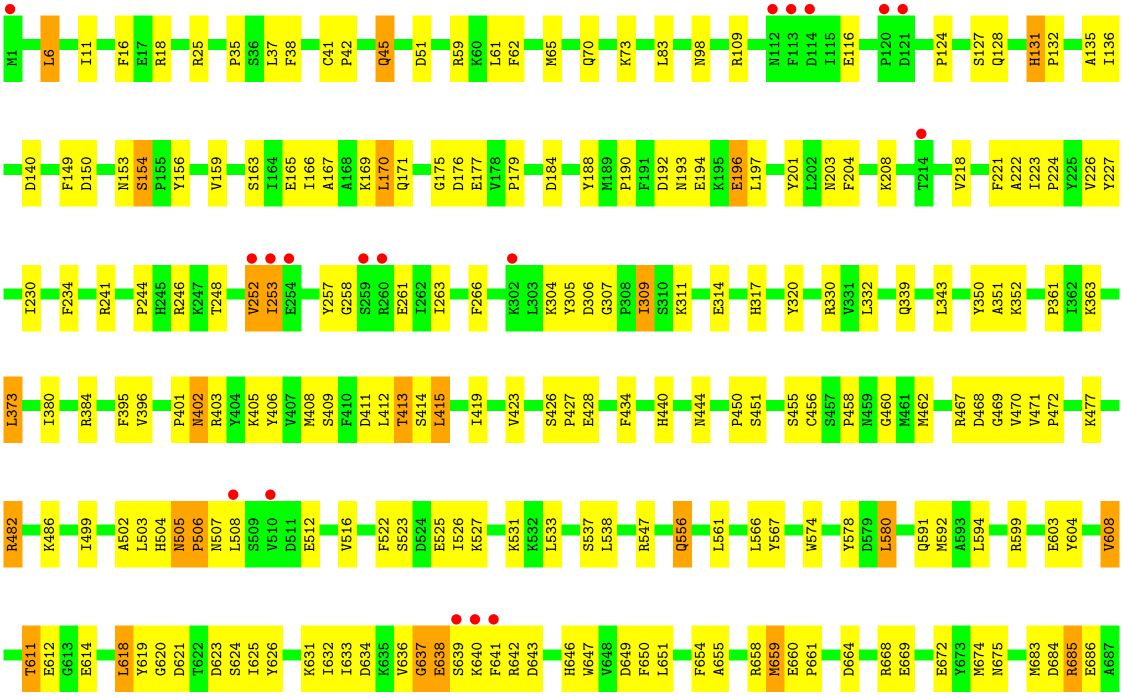
- Molecule 2: 5’-D(*GP*CP*GP*GP*AP*CP*TP*GP*CP*TP*TP*AP*CP*(DOC))-3’

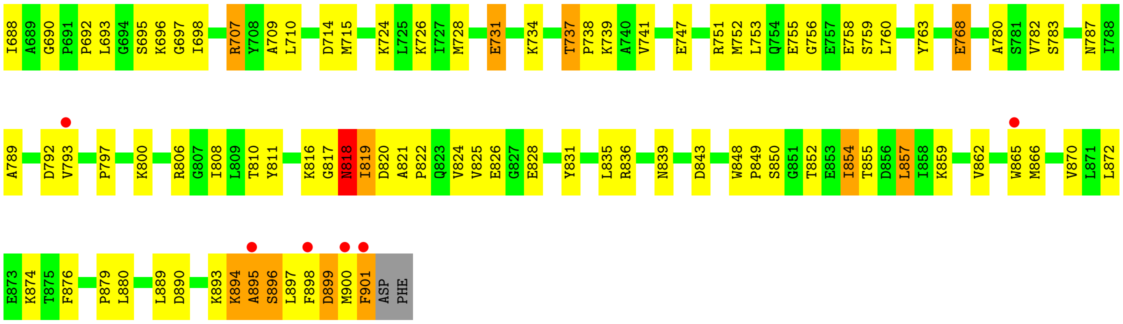
Chain P:



- Molecule 3: DNA POLYMERASE

Chain A:




I688
A689
G690
P691
P692
L693
G694
S695
K696
G697
I698
R707
Y708
A709
L710
D714
M715
K724
L725
K726
I727
M728
E731
K734
T737
P738
K739
A740
V741
E747
R751
M752
L753
Q754
E755
G756
E757
E758
S759
L760
Y763
E768
A780
S781
V782
S783
N787
I788
A789
D792
V793
P797
K800
R806
G807
I808
L809
T810
Y811
K816
G817
N818
I819
D820
A821
P822
Q823
V824
V825
E826
G827
E828
Y831
L835
R836
N839
D843
W848
P849
S850
G851
T852
E853
I854
T855
D856
L857
I858
K859
V862
W865
M866
V870
L871
L872
E873
K874
T875
F876
P879
L880
L889
D890
K893
K894
A895
S896
L897
F898
D899
M900
F901
ASP
PHE

# 4 Data and refinement statistics ⓘ

| Property | Value | Source |
|---|---|---|
| Space group | P 21 21 21 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 80.79Å 118.60Å 128.00Å<br>90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 29.75 – 2.60<br>29.75 – 2.60 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 96.7 (29.75-2.60)<br>96.8 (29.75-2.60) | Depositor<br>EDS |
| $R_{merge}$ | 0.09 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 3.17 (at 2.61Å) | Xtriage |
| Refinement program | CNS 1.0 | Depositor |
| R, $R_{free}$ | 0.197 , 0.258<br>0.190 , 0.249 | Depositor<br>DCC |
| $R_{free}$ test set | 3733 reflections (9.71%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 57.4 | Xtriage |
| Anisotropy | 0.171 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.33 , 63.8 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.49$, $< L^2 > = 0.32$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o$,$F_c$ correlation | 0.95 | EDS |
| Total number of atoms | 8394 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 61.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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

## 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TTP, DOC, CA

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 | T | 0.47 | 0/415 | 0.78 | 0/639 |
| 2 | P | 0.40 | 0/294 | 0.68 | 0/452 |
| 3 | A | 0.36 | 0/7535 | 0.58 | 0/10182 |
| All | All | 0.37 | 0/8244 | 0.60 | 0/11273 |

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 | T | 0 | 2 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | T | 3 | DA | Sidechain |
| 1 | T | 4 | DG | Sidechain |

## 5.2 Too-close contacts

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | T | 369 | 0 | 202 | 22 | 0 |
| 2 | P | 281 | 0 | 159 | 13 | 0 |
| 3 | A | 7355 | 0 | 7254 | 265 | 0 |
| 4 | A | 4 | 0 | 0 | 0 | 0 |
| 5 | A | 29 | 0 | 13 | 2 | 0 |
| 6 | A | 306 | 0 | 0 | 17 | 0 |
| 6 | P | 19 | 0 | 0 | 0 | 0 |
| 6 | T | 31 | 0 | 0 | 2 | 0 |
| All | All | 8394 | 0 | 7628 | 290 | 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 19.

All (290) 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) |
|---|---|---|---|
| 3:A:415:LEU:HD22 | 3:A:623:ASP:HB3 | 1.37 | 1.04 |
| 2:P:114:DC:H2” | 2:P:115:DOC:H5’ | 1.36 | 1.03 |
| 3:A:402:ASN:ND2 | 3:A:403:ARG:H | 1.57 | 1.01 |
| 3:A:402:ASN:HD22 | 3:A:403:ARG:N | 1.59 | 1.00 |
| 2:P:105:DG:H4’ | 2:P:106:DA:OP1 | 1.64 | 0.96 |
| 3:A:402:ASN:HD22 | 3:A:403:ARG:H | 0.92 | 0.91 |
| 3:A:614:GLU:HG2 | 3:A:631:LYS:HE3 | 1.53 | 0.91 |
| 3:A:373:LEU:CD1 | 3:A:470:VAL:HG11 | 2.03 | 0.88 |
| 3:A:642:ARG:HB2 | 3:A:642:ARG:HH11 | 1.38 | 0.86 |
| 2:P:113:DA:C5’ | 3:A:734:LYS:HG2 | 2.07 | 0.84 |
| 3:A:894:LYS:HE3 | 3:A:894:LYS:HA | 1.57 | 0.84 |
| 3:A:822:PRO:HD2 | 3:A:855:THR:CG2 | 2.10 | 0.81 |
| 3:A:258:GLY:HA3 | 6:A:1251:HOH:O | 1.81 | 0.80 |
| 3:A:408:MET:HE1 | 3:A:651:LEU:HB3 | 1.62 | 0.80 |
| 1:T:16:DG:H2” | 1:T:17:DC:C5’ | 2.13 | 0.79 |
| 3:A:405:LYS:HZ2 | 3:A:406:TYR:HE1 | 1.32 | 0.77 |
| 2:P:113:DA:H5” | 3:A:734:LYS:HG2 | 1.66 | 0.77 |
| 3:A:193:ASN:HD21 | 3:A:196:GLU:CD | 1.88 | 0.76 |
| 3:A:373:LEU:HD11 | 3:A:470:VAL:HG11 | 1.68 | 0.75 |
| 3:A:822:PRO:HD2 | 3:A:855:THR:HG22 | 1.68 | 0.75 |
| 3:A:170:LEU:HD22 | 3:A:170:LEU:H | 1.52 | 0.74 |
| 1:T:10:DC:H6 | 1:T:10:DC:H5’ | 1.54 | 0.72 |
| 2:P:114:DC:C2’ | 2:P:115:DOC:H5’ | 2.18 | 0.72 |
| 1:T:16:DG:H2” | 1:T:17:DC:H5” | 1.72 | 0.71 |
| 3:A:618:LEU:HD13 | 3:A:618:LEU:H | 1.56 | 0.71 |
| 3:A:642:ARG:HB2 | 3:A:642:ARG:NH1 | 2.05 | 0.71 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 3:A:685:ARG:HH22 | 3:A:714:ASP:HB3 | 1.56 | 0.71 |
| 3:A:373:LEU:HD23 | 3:A:380:ILE:HG22 | 1.75 | 0.69 |
| 3:A:223:ILE:HB | 3:A:224:PRO:HD3 | 1.75 | 0.69 |
| 3:A:373:LEU:HD13 | 3:A:470:VAL:HG11 | 1.73 | 0.69 |
| 2:P:103:DC:H2" | 2:P:104:DG:C8 | 2.28 | 0.69 |
| 1:T:10:DC:H2" | 1:T:11:DA:O5' | 1.92 | 0.69 |
| 3:A:188:TYR:CE2 | 3:A:190:PRO:HG3 | 2.28 | 0.68 |
| 3:A:825:VAL:HB | 3:A:828:GLU:HG3 | 1.74 | 0.68 |
| 3:A:505:ASN:CG | 3:A:505:ASN:O | 2.31 | 0.68 |
| 3:A:252:VAL:HG23 | 3:A:253:ILE:H | 1.59 | 0.67 |
| 3:A:241:ARG:HA | 3:A:246:ARG:NH1 | 2.09 | 0.67 |
| 3:A:428:GLU:OE2 | 3:A:470:VAL:HG22 | 1.94 | 0.67 |
| 3:A:508:LEU:HD22 | 3:A:508:LEU:H | 1.60 | 0.67 |
| 3:A:408:MET:CE | 3:A:651:LEU:HB3 | 2.25 | 0.66 |
| 3:A:632:ILE:HD13 | 3:A:654:PHE:HE1 | 1.60 | 0.66 |
| 3:A:599:ARG:O | 3:A:603:GLU:HG3 | 1.95 | 0.66 |
| 3:A:685:ARG:HH22 | 3:A:714:ASP:CB | 2.10 | 0.65 |
| 3:A:41:CYS:HB2 | 3:A:42:PRO:HD2 | 1.79 | 0.65 |
| 3:A:149:PHE:HB3 | 3:A:197:LEU:HD21 | 1.78 | 0.65 |
| 3:A:222:ALA:O | 3:A:226:VAL:HG12 | 1.97 | 0.65 |
| 3:A:128:GLN:HE21 | 3:A:128:GLN:HA | 1.61 | 0.64 |
| 3:A:738:PRO:HB3 | 3:A:780:ALA:O | 1.96 | 0.64 |
| 2:P:114:DC:H2" | 2:P:115:DOC:C5' | 2.23 | 0.63 |
| 3:A:471:VAL:HB | 3:A:472:PRO:HD3 | 1.79 | 0.63 |
| 3:A:647:TRP:HA | 3:A:650:PHE:HB3 | 1.79 | 0.63 |
| 1:T:16:DG:H2" | 1:T:17:DC:H5' | 1.80 | 0.63 |
| 3:A:412:LEU:HD12 | 3:A:412:LEU:N | 2.14 | 0.62 |
| 3:A:618:LEU:HD13 | 3:A:626:TYR:O | 2.00 | 0.62 |
| 3:A:471:VAL:HG13 | 3:A:566:LEU:HD21 | 1.80 | 0.62 |
| 3:A:808:ILE:HD13 | 3:A:824:VAL:HG11 | 1.81 | 0.61 |
| 1:T:1:DA:H2" | 1:T:2:DC:O5' | 1.99 | 0.61 |
| 3:A:685:ARG:NH2 | 3:A:714:ASP:HB3 | 2.14 | 0.61 |
| 3:A:395:PHE:HB2 | 3:A:591:GLN:HG2 | 1.83 | 0.60 |
| 3:A:642:ARG:H | 3:A:646:HIS:CD2 | 2.19 | 0.60 |
| 6:T:32:HOH:O | 3:A:874:LYS:HD2 | 2.02 | 0.60 |
| 2:P:113:DA:H5' | 3:A:734:LYS:HG2 | 1.83 | 0.60 |
| 3:A:304:LYS:NZ | 3:A:304:LYS:HB3 | 2.17 | 0.60 |
| 3:A:862:VAL:O | 3:A:866:MET:HG3 | 2.01 | 0.60 |
| 1:T:3:DA:OP2 | 3:A:361:PRO:HD2 | 2.02 | 0.60 |
| 3:A:751:ARG:HD3 | 3:A:759:SER:OG | 2.02 | 0.59 |
| 1:T:10:DC:H5' | 1:T:10:DC:C6 | 2.36 | 0.59 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 3:A:128:GLN:HA | 3:A:128:GLN:NE2 | 2.17 | 0.59 |
| 3:A:405:LYS:NZ | 3:A:405:LYS:HB3 | 2.17 | 0.59 |
| 3:A:793:VAL:HG12 | 3:A:793:VAL:O | 2.03 | 0.59 |
| 3:A:505:ASN:ND2 | 3:A:531:LYS:O | 2.36 | 0.58 |
| 3:A:894:LYS:HA | 3:A:894:LYS:CE | 2.32 | 0.58 |
| 3:A:309:ILE:HD13 | 3:A:309:ILE:O | 2.03 | 0.58 |
| 3:A:599:ARG:HG2 | 3:A:599:ARG:HH11 | 1.69 | 0.58 |
| 3:A:604:TYR:OH | 3:A:658:ARG:HB3 | 2.04 | 0.58 |
| 3:A:707:ARG:HH11 | 3:A:707:ARG:HB3 | 1.69 | 0.58 |
| 3:A:165:GLU:CD | 3:A:165:GLU:H | 2.07 | 0.58 |
| 3:A:855:THR:HB | 3:A:857:LEU:CD2 | 2.33 | 0.58 |
| 3:A:685:ARG:HD2 | 6:A:1123:HOH:O | 2.03 | 0.57 |
| 3:A:724:LYS:HB2 | 3:A:724:LYS:NZ | 2.20 | 0.57 |
| 3:A:817:GLY:O | 3:A:819:ILE:N | 2.38 | 0.57 |
| 3:A:896:SER:C | 3:A:898:PHE:H | 2.08 | 0.57 |
| 1:T:16:DG:C2’ | 1:T:17:DC:H5” | 2.35 | 0.56 |
| 3:A:428:GLU:OE1 | 3:A:428:GLU:N | 2.34 | 0.56 |
| 3:A:11:ILE:HD12 | 3:A:16:PHE:CD2 | 2.40 | 0.55 |
| 3:A:632:ILE:HD13 | 3:A:654:PHE:CE1 | 2.41 | 0.55 |
| 3:A:692:PRO:HB2 | 3:A:695:SER:OG | 2.06 | 0.55 |
| 3:A:731:GLU:O | 3:A:737:THR:HG21 | 2.05 | 0.55 |
| 3:A:611:THR:HG23 | 3:A:612:GLU:N | 2.22 | 0.55 |
| 3:A:456:CYS:O | 3:A:674:MET:HG3 | 2.06 | 0.55 |
| 3:A:854:ILE:HD12 | 3:A:862:VAL:HG11 | 1.88 | 0.55 |
| 3:A:163:SER:HB3 | 3:A:166:ILE:HD12 | 1.89 | 0.55 |
| 3:A:631:LYS:HA | 3:A:634:ASP:HB2 | 1.89 | 0.55 |
| 1:T:8:DA:H4’ | 3:A:707:ARG:HD2 | 1.89 | 0.55 |
| 3:A:664:ASP:HB3 | 6:A:1023:HOH:O | 2.07 | 0.54 |
| 3:A:395:PHE:HD2 | 3:A:594:LEU:HD12 | 1.73 | 0.54 |
| 3:A:159:VAL:HG21 | 3:A:317:HIS:CD2 | 2.43 | 0.54 |
| 3:A:604:TYR:O | 3:A:608:VAL:HG23 | 2.07 | 0.54 |
| 3:A:642:ARG:HH11 | 3:A:642:ARG:CB | 2.17 | 0.54 |
| 1:T:17:DC:H2” | 1:T:18:DG:O5’ | 2.08 | 0.54 |
| 3:A:806:ARG:O | 3:A:810:THR:HG23 | 2.08 | 0.54 |
| 2:P:106:DA:H2” | 2:P:107:DC:O5’ | 2.06 | 0.53 |
| 3:A:768:GLU:HG2 | 3:A:872:LEU:HD21 | 1.90 | 0.53 |
| 3:A:696:LYS:HB3 | 3:A:756:GLY:HA3 | 1.90 | 0.53 |
| 1:T:3:DA:H2” | 1:T:4:DG:H5’ | 1.90 | 0.53 |
| 1:T:12:DG:H2” | 1:T:13:DT:H5’ | 1.90 | 0.53 |
| 1:T:11:DA:OP1 | 3:A:874:LYS:HE3 | 2.09 | 0.53 |
| 3:A:655:ALA:HA | 3:A:659:MET:HB2 | 1.91 | 0.53 |

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| **Atom-1** | **Atom-2** | **Interatomic distance (Å)** | **Clash overlap (Å)** |
|---|---|---|---|
| 3:A:825:VAL:HB | 3:A:828:GLU:CG | 2.39 | 0.53 |
| 3:A:686:GLU:HG3 | 3:A:715:MET:CE | 2.38 | 0.53 |
| 3:A:451:SER:HB3 | 3:A:456:CYS:SG | 2.48 | 0.52 |
| 3:A:633:ILE:HD11 | 3:A:651:LEU:HD21 | 1.91 | 0.52 |
| 3:A:306:ASP:OD2 | 3:A:307:GLY:N | 2.43 | 0.52 |
| 3:A:505:ASN:N | 3:A:506:PRO:CD | 2.73 | 0.52 |
| 3:A:821:ALA:HB1 | 3:A:855:THR:HG21 | 1.92 | 0.52 |
| 3:A:697:GLY:HA3 | 3:A:753:LEU:O | 2.09 | 0.52 |
| 3:A:620:GLY:HA2 | 3:A:624:SER:O | 2.10 | 0.52 |
| 3:A:664:ASP:O | 3:A:668:ARG:HG3 | 2.09 | 0.52 |
| 3:A:817:GLY:O | 3:A:819:ILE:HG13 | 2.10 | 0.52 |
| 3:A:167:ALA:HA | 3:A:176:ASP:HB2 | 1.92 | 0.52 |
| 3:A:637:GLY:O | 3:A:639:SER:N | 2.43 | 0.52 |
| 1:T:11:DA:H2” | 1:T:12:DG:C8 | 2.45 | 0.52 |
| 3:A:504:HIS:C | 3:A:506:PRO:HD2 | 2.30 | 0.51 |
| 3:A:658:ARG:O | 3:A:661:PRO:HD2 | 2.11 | 0.51 |
| 2:P:105:DG:C4’ | 2:P:106:DA:OP1 | 2.50 | 0.51 |
| 3:A:224:PRO:HG3 | 6:A:1072:HOH:O | 2.10 | 0.51 |
| 3:A:482:ARG:NH2 | 5:A:1005:TTP:O2G | 2.44 | 0.51 |
| 3:A:525:GLU:CD | 3:A:525:GLU:H | 2.14 | 0.51 |
| 3:A:203:ASN:ND2 | 3:A:241:ARG:HH12 | 2.09 | 0.50 |
| 3:A:384:ARG:HD3 | 6:A:1253:HOH:O | 2.11 | 0.50 |
| 3:A:818:ASN:HD22 | 3:A:818:ASN:H | 1.59 | 0.50 |
| 3:A:197:LEU:C | 3:A:197:LEU:HD13 | 2.32 | 0.50 |
| 3:A:797:PRO:HD3 | 6:A:1146:HOH:O | 2.12 | 0.50 |
| 3:A:170:LEU:HD22 | 3:A:170:LEU:N | 2.24 | 0.50 |
| 3:A:618:LEU:HD22 | 3:A:619:TYR:N | 2.27 | 0.50 |
| 3:A:685:ARG:HH22 | 3:A:714:ASP:CG | 2.15 | 0.50 |
| 3:A:351:ALA:O | 3:A:352:LYS:HB2 | 2.12 | 0.50 |
| 3:A:83:LEU:HD12 | 3:A:83:LEU:H | 1.77 | 0.49 |
| 3:A:660:GLU:HB2 | 3:A:661:PRO:HD3 | 1.93 | 0.49 |
| 3:A:726:LYS:HG2 | 6:A:1164:HOH:O | 2.12 | 0.49 |
| 1:T:2:DC:H5’ | 3:A:574:TRP:CD1 | 2.47 | 0.49 |
| 3:A:153:ASN:HB2 | 3:A:192:ASP:O | 2.12 | 0.49 |
| 3:A:758:GLU:HB2 | 6:A:1137:HOH:O | 2.12 | 0.49 |
| 3:A:855:THR:HB | 3:A:857:LEU:HD21 | 1.94 | 0.49 |
| 3:A:611:THR:HG21 | 3:A:614:GLU:CB | 2.42 | 0.49 |
| 3:A:350:TYR:OH | 3:A:477:LYS:HE3 | 2.12 | 0.48 |
| 3:A:898:PHE:O | 3:A:901:PHE:HB2 | 2.14 | 0.48 |
| 3:A:636:VAL:O | 3:A:637:GLY:O | 2.31 | 0.48 |
| 3:A:686:GLU:HG3 | 3:A:715:MET:HE3 | 1.96 | 0.48 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 3:A:643:ASP:C | 3:A:693:LEU:HD12 | 2.33 | 0.48 |
| 3:A:533:LEU:HD12 | 3:A:537:SER:CB | 2.44 | 0.48 |
| 3:A:824:VAL:HG22 | 3:A:849:PRO:HD3 | 1.96 | 0.48 |
| 3:A:642:ARG:H | 3:A:646:HIS:HD2 | 1.59 | 0.48 |
| 3:A:440:HIS:O | 3:A:444:ASN:ND2 | 2.47 | 0.48 |
| 3:A:707:ARG:NH2 | 3:A:731:GLU:OE2 | 2.46 | 0.48 |
| 3:A:857:LEU:HD23 | 3:A:857:LEU:H | 1.79 | 0.48 |
| 3:A:797:PRO:HG3 | 3:A:806:ARG:NH1 | 2.29 | 0.47 |
| 3:A:244:PRO:HD2 | 3:A:266:PHE:O | 2.14 | 0.47 |
| 3:A:561:LEU:HD23 | 6:A:1172:HOH:O | 2.13 | 0.47 |
| 3:A:894:LYS:HE3 | 3:A:894:LYS:CA | 2.39 | 0.47 |
| 3:A:859:LYS:O | 3:A:862:VAL:HG13 | 2.15 | 0.47 |
| 3:A:684:ASP:HB3 | 6:A:1261:HOH:O | 2.15 | 0.47 |
| 3:A:486:LYS:HB2 | 3:A:556:GLN:HG3 | 1.97 | 0.47 |
| 3:A:685:ARG:HG2 | 3:A:686:GLU:N | 2.29 | 0.46 |
| 3:A:132:PRO:HB3 | 3:A:194:GLU:OE2 | 2.15 | 0.46 |
| 3:A:599:ARG:HG2 | 3:A:599:ARG:NH1 | 2.31 | 0.46 |
| 3:A:697:GLY:HA2 | 3:A:755:GLU:O | 2.16 | 0.46 |
| 3:A:405:LYS:O | 3:A:690:GLY:HA2 | 2.16 | 0.46 |
| 3:A:499:ILE:O | 3:A:503:LEU:HG | 2.16 | 0.46 |
| 3:A:808:ILE:O | 3:A:811:TYR:HB3 | 2.16 | 0.46 |
| 2:P:109:DG:O4' | 3:A:800:LYS:HE2 | 2.15 | 0.46 |
| 3:A:625:ILE:HG12 | 3:A:683:MET:HE2 | 1.98 | 0.46 |
| 3:A:839:ASN:HA | 3:A:865:TRP:CD2 | 2.51 | 0.46 |
| 3:A:131:HIS:ND1 | 3:A:131:HIS:N | 2.64 | 0.45 |
| 3:A:128:GLN:NE2 | 3:A:128:GLN:CA | 2.79 | 0.45 |
| 3:A:406:TYR:CD1 | 3:A:406:TYR:N | 2.84 | 0.45 |
| 3:A:413:THR:O | 3:A:414:SER:C | 2.55 | 0.45 |
| 3:A:578:TYR:CE2 | 3:A:580:LEU:HD13 | 2.51 | 0.45 |
| 3:A:415:LEU:O | 3:A:419:ILE:HG13 | 2.16 | 0.45 |
| 1:T:2:DC:H2" | 1:T:3:DA:OP1 | 2.15 | 0.45 |
| 2:P:110:DC:H2" | 2:P:111:DT:C5' | 2.47 | 0.45 |
| 3:A:163:SER:CB | 3:A:166:ILE:HD12 | 2.45 | 0.45 |
| 3:A:502:ALA:C | 3:A:504:HIS:H | 2.20 | 0.45 |
| 3:A:876:PHE:O | 3:A:879:PRO:HG2 | 2.17 | 0.45 |
| 1:T:3:DA:P | 3:A:361:PRO:HD2 | 2.57 | 0.45 |
| 3:A:793:VAL:HG12 | 6:A:1111:HOH:O | 2.17 | 0.45 |
| 3:A:870:VAL:CG1 | 3:A:874:LYS:HD3 | 2.47 | 0.45 |
| 1:T:11:DA:H2" | 1:T:12:DG:H8 | 1.80 | 0.45 |
| 3:A:409:SER:OG | 3:A:686:GLU:HB3 | 2.17 | 0.45 |
| 3:A:402:ASN:ND2 | 3:A:403:ARG:N | 2.34 | 0.45 |

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| **Atom-1** | **Atom-2** | **Interatomic distance (Å)** | **Clash overlap (Å)** |
|---|---|---|---|
| 3:A:848:TRP:CE2 | 3:A:854:ILE:HG12 | 2.51 | 0.45 |
| 3:A:136:ILE:HB | 3:A:149:PHE:HB2 | 1.99 | 0.44 |
| 3:A:116:GLU:HB2 | 3:A:135:ALA:HB3 | 1.99 | 0.44 |
| 3:A:363:LYS:HE3 | 6:A:1110:HOH:O | 2.17 | 0.44 |
| 3:A:523:SER:O | 3:A:527:LYS:HG3 | 2.18 | 0.44 |
| 3:A:612:GLU:HA | 3:A:612:GLU:OE1 | 2.17 | 0.44 |
| 3:A:751:ARG:NH1 | 3:A:763:TYR:HB2 | 2.32 | 0.44 |
| 3:A:787:ASN:N | 3:A:826:GLU:OE2 | 2.50 | 0.44 |
| 3:A:889:LEU:HD23 | 3:A:890:ASP:H | 1.82 | 0.44 |
| 3:A:127:SER:HA | 3:A:261:GLU:OE2 | 2.17 | 0.44 |
| 3:A:578:TYR:CZ | 3:A:580:LEU:HD13 | 2.53 | 0.44 |
| 3:A:61:LEU:HD13 | 3:A:62:PHE:N | 2.33 | 0.44 |
| 3:A:241:ARG:HG2 | 3:A:246:ARG:NH1 | 2.33 | 0.44 |
| 3:A:401:PRO:O | 3:A:402:ASN:HB2 | 2.18 | 0.44 |
| 3:A:599:ARG:HA | 6:A:1248:HOH:O | 2.17 | 0.44 |
| 3:A:547:ARG:NH2 | 6:A:1205:HOH:O | 2.50 | 0.44 |
| 3:A:639:SER:C | 3:A:641:PHE:H | 2.21 | 0.44 |
| 3:A:816:LYS:HD3 | 3:A:816:LYS:C | 2.37 | 0.44 |
| 3:A:304:LYS:HZ3 | 3:A:305:TYR:H | 1.66 | 0.43 |
| 3:A:263:ILE:HD12 | 3:A:263:ILE:N | 2.33 | 0.43 |
| 3:A:405:LYS:NZ | 3:A:406:TYR:HE1 | 2.09 | 0.43 |
| 1:T:12:DG:H1’ | 1:T:13:DT:H5” | 2.00 | 0.43 |
| 3:A:415:LEU:HD22 | 3:A:623:ASP:CB | 2.27 | 0.43 |
| 3:A:25:ARG:HD2 | 6:A:1113:HOH:O | 2.16 | 0.43 |
| 3:A:512:GLU:O | 3:A:512:GLU:HG3 | 2.19 | 0.43 |
| 2:P:108:DT:H1’ | 3:A:800:LYS:NZ | 2.33 | 0.43 |
| 3:A:633:ILE:O | 3:A:637:GLY:N | 2.51 | 0.43 |
| 3:A:70:GLN:NE2 | 3:A:73:LYS:HE2 | 2.34 | 0.43 |
| 3:A:169:LYS:HB2 | 3:A:175:GLY:HA3 | 2.00 | 0.43 |
| 3:A:426:SER:HB2 | 3:A:472:PRO:HD3 | 2.01 | 0.43 |
| 3:A:482:ARG:HH22 | 5:A:1005:TTP:PG | 2.42 | 0.43 |
| 3:A:171:GLN:HG2 | 3:A:177:GLU:OE2 | 2.19 | 0.43 |
| 3:A:402:ASN:ND2 | 3:A:403:ARG:HG2 | 2.33 | 0.43 |
| 3:A:412:LEU:HD22 | 3:A:415:LEU:HD13 | 2.01 | 0.43 |
| 3:A:458:PRO:HG3 | 3:A:592:MET:SD | 2.59 | 0.43 |
| 3:A:516:VAL:HG21 | 3:A:522:PHE:CE1 | 2.53 | 0.43 |
| 3:A:37:LEU:C | 3:A:38:PHE:CD1 | 2.92 | 0.43 |
| 3:A:836:ARG:HE | 3:A:836:ARG:HB2 | 1.59 | 0.43 |
| 3:A:154:SER:C | 3:A:156:TYR:H | 2.23 | 0.42 |
| 3:A:455:SER:HA | 3:A:675:ASN:O | 2.19 | 0.42 |
| 3:A:395:PHE:CB | 3:A:591:GLN:HG2 | 2.48 | 0.42 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 3:A:35:PRO:HG3 | 3:A:65:MET:HA | 2.01 | 0.42 |
| 3:A:889:LEU:HD23 | 3:A:890:ASP:N | 2.34 | 0.42 |
| 3:A:70:GLN:HE22 | 3:A:73:LYS:CE | 2.32 | 0.42 |
| 3:A:412:LEU:HG | 3:A:683:MET:HB2 | 2.01 | 0.42 |
| 3:A:747:GLU:HA | 3:A:747:GLU:OE2 | 2.20 | 0.42 |
| 3:A:789:ALA:O | 3:A:792:ASP:HB2 | 2.20 | 0.42 |
| 3:A:150:ASP:OD2 | 3:A:317:HIS:CE1 | 2.73 | 0.42 |
| 3:A:468:ASP:CG | 3:A:469:GLY:H | 2.23 | 0.42 |
| 3:A:611:THR:HG21 | 3:A:614:GLU:HB3 | 2.00 | 0.42 |
| 3:A:738:PRO:HG2 | 3:A:741:VAL:CG2 | 2.49 | 0.42 |
| 3:A:203:ASN:HD22 | 3:A:241:ARG:HH12 | 1.67 | 0.42 |
| 3:A:505:ASN:O | 3:A:506:PRO:C | 2.58 | 0.42 |
| 3:A:831:TYR:CD2 | 3:A:850:SER:HA | 2.55 | 0.42 |
| 3:A:899:ASP:O | 3:A:901:PHE:N | 2.53 | 0.42 |
| 3:A:6:LEU:HB2 | 3:A:18:ARG:O | 2.19 | 0.42 |
| 3:A:38:PHE:CD1 | 3:A:38:PHE:N | 2.88 | 0.42 |
| 3:A:38:PHE:CE2 | 3:A:59:ARG:HB2 | 2.54 | 0.42 |
| 3:A:163:SER:OG | 3:A:165:GLU:HG2 | 2.20 | 0.42 |
| 3:A:201:TYR:O | 3:A:204:PHE:HB3 | 2.20 | 0.42 |
| 3:A:405:LYS:NZ | 3:A:406:TYR:CE1 | 2.84 | 0.42 |
| 3:A:547:ARG:HA | 3:A:547:ARG:HD3 | 1.87 | 0.42 |
| 3:A:895:ALA:O | 3:A:897:LEU:N | 2.52 | 0.42 |
| 3:A:460:GLY:HA3 | 6:A:1141:HOH:O | 2.18 | 0.42 |
| 3:A:373:LEU:HD12 | 3:A:373:LEU:HA | 1.78 | 0.42 |
| 3:A:434:PHE:CE2 | 3:A:450:PRO:HB3 | 2.55 | 0.42 |
| 3:A:611:THR:CG2 | 3:A:614:GLU:HB3 | 2.50 | 0.41 |
| 1:T:13:DT:H2" | 1:T:14:DC:C6 | 2.55 | 0.41 |
| 3:A:116:GLU:HB3 | 3:A:320:TYR:OH | 2.20 | 0.41 |
| 3:A:252:VAL:HG23 | 3:A:253:ILE:N | 2.32 | 0.41 |
| 3:A:782:VAL:HG12 | 3:A:783:SER:N | 2.35 | 0.41 |
| 3:A:226:VAL:O | 3:A:230:ILE:HG13 | 2.20 | 0.41 |
| 3:A:423:VAL:O | 3:A:423:VAL:HG12 | 2.19 | 0.41 |
| 3:A:503:LEU:HD23 | 3:A:538:LEU:HD13 | 2.03 | 0.41 |
| 3:A:870:VAL:HG13 | 3:A:874:LYS:HD3 | 2.01 | 0.41 |
| 3:A:234:PHE:CD1 | 3:A:234:PHE:N | 2.88 | 0.41 |
| 3:A:311:LYS:O | 3:A:314:GLU:HG2 | 2.21 | 0.41 |
| 3:A:396:VAL:HG22 | 3:A:621:ASP:OD1 | 2.20 | 0.41 |
| 3:A:508:LEU:HD22 | 3:A:508:LEU:N | 2.31 | 0.41 |
| 3:A:408:MET:HE2 | 3:A:688:ILE:HG12 | 2.03 | 0.41 |
| 3:A:455:SER:O | 3:A:462:MET:HA | 2.21 | 0.41 |
| 3:A:619:TYR:CG | 3:A:620:GLY:N | 2.89 | 0.41 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 3:A:227:TYR:CE1 | 3:A:248:THR:HG21 | 2.56 | 0.41 |
| 3:A:412:LEU:N | 3:A:412:LEU:CD1 | 2.82 | 0.41 |
| 3:A:647:TRP:O | 3:A:650:PHE:HB3 | 2.20 | 0.41 |
| 3:A:51:ASP:HB2 | 6:A:1183:HOH:O | 2.20 | 0.41 |
| 3:A:221:PHE:O | 3:A:224:PRO:HD2 | 2.21 | 0.41 |
| 1:T:6:DT:H73 | 6:T:36:HOH:O | 2.21 | 0.40 |
| 3:A:668:ARG:NH1 | 3:A:668:ARG:HG2 | 2.36 | 0.40 |
| 3:A:669:GLU:O | 3:A:672:GLU:HB3 | 2.21 | 0.40 |
| 3:A:426:SER:OG | 3:A:427:PRO:HD2 | 2.20 | 0.40 |
| 3:A:751:ARG:CZ | 3:A:763:TYR:HB2 | 2.51 | 0.40 |
| 3:A:698:ILE:HG12 | 3:A:752:MET:O | 2.20 | 0.40 |
| 3:A:709:ALA:O | 3:A:710:LEU:HD23 | 2.21 | 0.40 |
| 3:A:850:SER:O | 3:A:852:THR:HG23 | 2.21 | 0.40 |
| 3:A:150:ASP:OD2 | 3:A:317:HIS:HE1 | 2.04 | 0.40 |
| 3:A:505:ASN:O | 3:A:507:ASN:N | 2.54 | 0.40 |
| 3:A:109:ARG:HD3 | 3:A:140:ASP:OD2 | 2.22 | 0.40 |
| 3:A:523:SER:H | 3:A:526:ILE:HD12 | 1.86 | 0.40 |
| 3:A:686:GLU:HG3 | 3:A:715:MET:HE1 | 2.02 | 0.40 |

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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 |
|---|---|---|---|---|---|---|
| 3 | A | 899/903 (100%) | 815 (91%) | 64 (7%) | 20 (2%) | 6 12 |

All (20) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | A | 818 | ASN |
| 3 | A | 893 | LYS |
| 3 | A | 899 | ASP |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | A | 252 | VAL |
| 3 | A | 415 | LEU |
| 3 | A | 467 | ARG |
| 3 | A | 637 | GLY |
| 3 | A | 820 | ASP |
| 3 | A | 895 | ALA |
| 3 | A | 896 | SER |
| 3 | A | 900 | MET |
| 3 | A | 640 | LYS |
| 3 | A | 506 | PRO |
| 3 | A | 638 | GLU |
| 3 | A | 819 | ILE |
| 3 | A | 45 | GLN |
| 3 | A | 253 | ILE |
| 3 | A | 124 | PRO |
| 3 | A | 179 | PRO |
| 3 | A | 608 | VAL |

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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 |
|---|---|---|---|---|---|
| 3 | A | 798/800 (100%) | 752 (94%) | 46 (6%) | 20 40 |

All (46) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | A | 6 | LEU |
| 3 | A | 45 | GLN |
| 3 | A | 98 | ASN |
| 3 | A | 131 | HIS |
| 3 | A | 154 | SER |
| 3 | A | 170 | LEU |
| 3 | A | 184 | ASP |
| 3 | A | 196 | GLU |
| 3 | A | 208 | LYS |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | A | 218 | VAL |
| 3 | A | 257 | TYR |
| 3 | A | 309 | ILE |
| 3 | A | 330 | ARG |
| 3 | A | 332 | LEU |
| 3 | A | 339 | GLN |
| 3 | A | 343 | LEU |
| 3 | A | 373 | LEU |
| 3 | A | 402 | ASN |
| 3 | A | 411 | ASP |
| 3 | A | 413 | THR |
| 3 | A | 482 | ARG |
| 3 | A | 505 | ASN |
| 3 | A | 556 | GLN |
| 3 | A | 567 | TYR |
| 3 | A | 580 | LEU |
| 3 | A | 611 | THR |
| 3 | A | 618 | LEU |
| 3 | A | 638 | GLU |
| 3 | A | 649 | ASP |
| 3 | A | 659 | MET |
| 3 | A | 685 | ARG |
| 3 | A | 707 | ARG |
| 3 | A | 728 | MET |
| 3 | A | 731 | GLU |
| 3 | A | 737 | THR |
| 3 | A | 739 | LYS |
| 3 | A | 760 | LEU |
| 3 | A | 768 | GLU |
| 3 | A | 818 | ASN |
| 3 | A | 835 | LEU |
| 3 | A | 843 | ASP |
| 3 | A | 854 | ILE |
| 3 | A | 857 | LEU |
| 3 | A | 880 | LEU |
| 3 | A | 894 | LYS |
| 3 | A | 901 | PHE |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | A | 40 | HIS |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | A | 70 | GLN |
| 3 | A | 112 | ASN |
| 3 | A | 128 | GLN |
| 3 | A | 158 | ASN |
| 3 | A | 171 | GLN |
| 3 | A | 193 | ASN |
| 3 | A | 203 | ASN |
| 3 | A | 317 | HIS |
| 3 | A | 333 | GLN |
| 3 | A | 402 | ASN |
| 3 | A | 424 | ASN |
| 3 | A | 539 | ASN |
| 3 | A | 546 | GLN |
| 3 | A | 556 | GLN |
| 3 | A | 564 | ASN |
| 3 | A | 646 | HIS |
| 3 | A | 773 | GLN |
| 3 | A | 786 | ASN |
| 3 | A | 787 | ASN |
| 3 | A | 818 | ASN |
| 3 | A | 823 | GLN |

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 2 | DOC | P | 115 | 1,2 | 16,19,20 | 0.48 | 0 | 20,26,29 | 0.45 | 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 | DOC | P | 115 | 1,2 | - | 2/7/18/19 | 0/2/2/2 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 2 | P | 115 | DOC | C3'-C4'-C5'-O5' |
| 2 | P | 115 | DOC | O4'-C4'-C5'-O5' |

There are no ring outliers.

1 monomer is involved in 3 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 2 | P | 115 | DOC | 3 | 0 |

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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 | $\#\|Z\| > 2$ |
| 5 | TTP | A | 1005 | 4 | 26,30,30 | 1.46 | 5 (19%) | 39,47,47 | 1.03 | 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 |
|---|---|---|---|---|---|---|---|
| 5 | TTP | A | 1005 | 4 | - | 6/22/34/34 | 0/2/2/2 |

All (5) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 5 | A | 1005 | TTP | PG-O1G | -3.50 | 1.39 | 1.50 |
| 5 | A | 1005 | TTP | PA-O2A | -2.57 | 1.43 | 1.55 |
| 5 | A | 1005 | TTP | PB-O1B | -2.35 | 1.42 | 1.50 |
| 5 | A | 1005 | TTP | PB-O2B | -2.28 | 1.44 | 1.55 |
| 5 | A | 1005 | TTP | O4-C4 | -2.23 | 1.19 | 1.23 |

All (1) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 5 | A | 1005 | TTP | C6-C5-C4 | -2.47 | 115.96 | 118.03 |

There are no chirality outliers.

All (6) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 5 | A | 1005 | TTP | C5'-O5'-PA-O2A |
| 5 | A | 1005 | TTP | PB-O3B-PG-O2G |
| 5 | A | 1005 | TTP | PB-O3A-PA-O5' |
| 5 | A | 1005 | TTP | C5'-O5'-PA-O3A |
| 5 | A | 1005 | TTP | PA-O3A-PB-O2B |
| 5 | A | 1005 | TTP | C5'-O5'-PA-O1A |

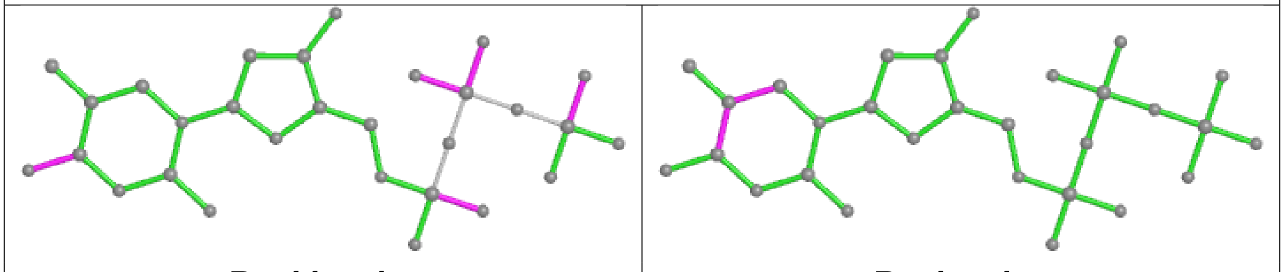
There are no ring outliers.

1 monomer is involved in 2 short contacts:

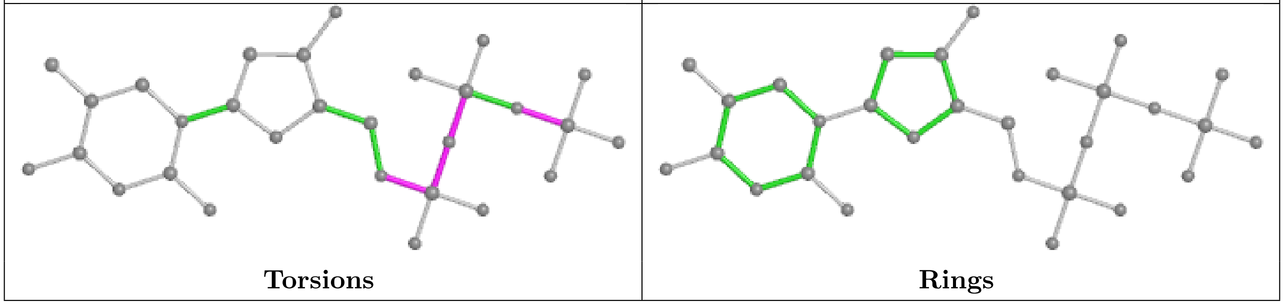
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 5 | A | 1005 | TTP | 2 | 0 |

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 TTP A 1005**



**Bond lengths** **Bond angles**



**Torsions** **Rings**

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

# 6 Fit of model and data ⓘ

## 6.1 Protein, DNA and RNA chains ⓘ

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, 95th 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($\AA^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 1 | T | 18/18 (100%) | -0.23 | 1 (5%) | 24 | 19 | 34, 53, 94, 135 | 0 |
| 2 | P | 13/14 (92%) | -0.32 | 0 | 100 | 100 | 43, 60, 84, 85 | 0 |
| 3 | A | 901/903 (99%) | -0.03 | 24 (2%) | 54 | 48 | 28, 58, 101, 138 | 0 |
| All | All | 932/935 (99%) | -0.04 | 25 (2%) | 54 | 48 | 28, 58, 101, 138 | 0 |

All (25) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 3 | A | 640 | LYS | 4.9 |
| 1 | T | 1 | DA | 4.2 |
| 3 | A | 901 | PHE | 3.4 |
| 3 | A | 900 | MET | 3.3 |
| 3 | A | 508 | LEU | 3.3 |
| 3 | A | 895 | ALA | 3.1 |
| 3 | A | 112 | ASN | 2.9 |
| 3 | A | 121 | ASP | 2.9 |
| 3 | A | 639 | SER | 2.7 |
| 3 | A | 1 | MET | 2.6 |
| 3 | A | 259 | SER | 2.6 |
| 3 | A | 214 | THR | 2.5 |
| 3 | A | 252 | VAL | 2.5 |
| 3 | A | 254 | GLU | 2.4 |
| 3 | A | 114 | ASP | 2.3 |
| 3 | A | 302 | LYS | 2.3 |
| 3 | A | 113 | PHE | 2.3 |
| 3 | A | 793 | VAL | 2.3 |
| 3 | A | 253 | ILE | 2.3 |
| 3 | A | 120 | PRO | 2.2 |
| 3 | A | 510 | VAL | 2.2 |
| 3 | A | 865 | TRP | 2.2 |
| 3 | A | 260 | ARG | 2.1 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 3 | A | 641 | PHE | 2.1 |
| 3 | A | 898 | PHE | 2.0 |

## 6.2 Non-standard residues in protein, DNA, RNA chains (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 |
|---|---|---|---|---|---|---|---|---|
| 2 | DOC | P | 115 | 18/19 | 0.96 | 0.19 | 40,46,56,61 | 0 |

## 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

## 6.4 Ligands (i)

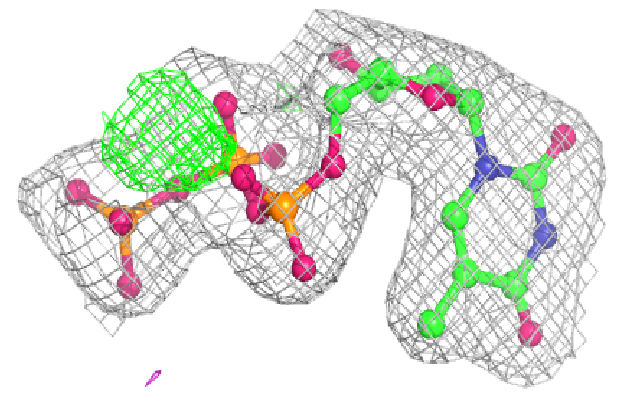
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, $95^{th}$ percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

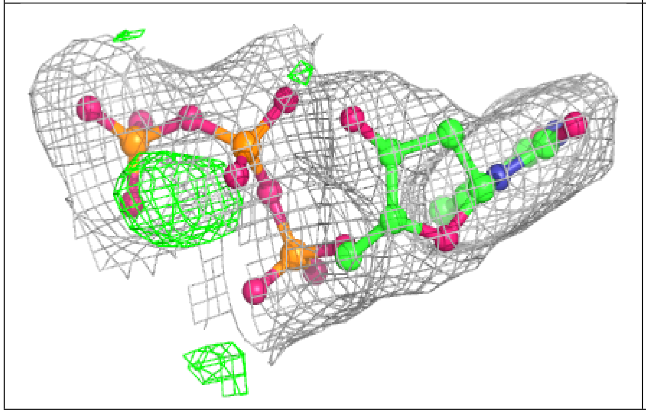
| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 4 | CA | A | 1003 | 1/1 | 0.69 | 0.19 | 105,105,105,105 | 0 |
| 4 | CA | A | 1002 | 1/1 | 0.94 | 0.43 | 79,79,79,79 | 0 |
| 4 | CA | A | 1004 | 1/1 | 0.94 | 0.26 | 99,99,99,99 | 0 |
| 4 | CA | A | 1001 | 1/1 | 0.96 | 0.25 | 44,44,44,44 | 0 |
| 5 | TTP | A | 1005 | 29/29 | 0.97 | 0.22 | 15,40,52,55 | 0 |

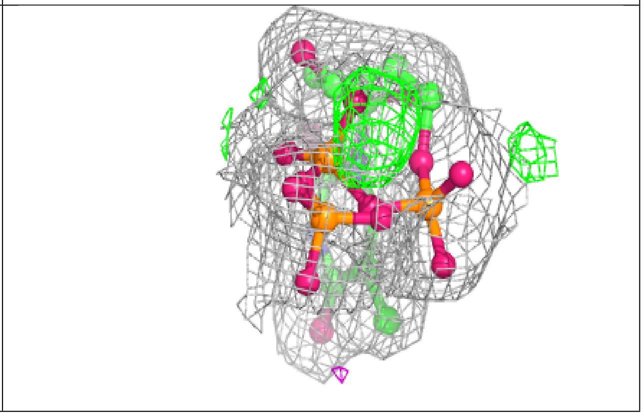
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around TTP A 1005:**

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







## 6.5 Other polymers ⓘ

There are no such residues in this entry.