

Full wwPDB X-ray Structure Validation Report (i)

Nov 1, 2023 – 02:54 PM JST

PDB ID : 5J61

Title : D-aminoacyl-tRNA deacylase (DTD) from Plasmodium falciparum in complex

with glycyl-3'-aminoadenosine at 2.10 Angstrom resolution

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Deposited on : 2016-04-04

Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity: 4.02b-467

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

Xtriage (Phenix) : 1.13

EDS : 2.36

buster-report : 1.1.7 (2018)

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

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

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

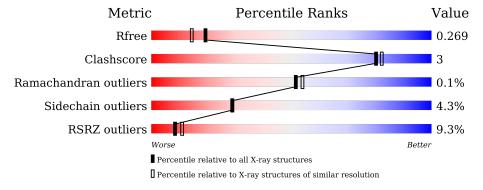
Validation Pipeline (wwPDB-VP) : 2.36

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 2.10 Å.

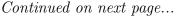
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive	Similar resolution
Wiedile	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	164	7% 83%	8% • 8%
1	В	164	9%	6% • 7%
1	С	164	13%	9% • 7%
1	D	164	6% 82%	11% 7%
1	Е	164	82%	10% • 7%
1	F	164	9%	• • 7%





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Mol	Chain	Length	Quality of chain		
1	G	164	80% 10%)	7%
1	Н	164	8% 81% 9%)	9%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10399 atoms, of which 0 are hydrogens and 0 are deuteriums.

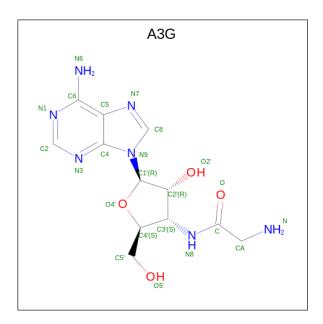
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called D-tyrosyl-tRNA(Tyr) deacylase.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	A	151	Total	С	N	О	S	0	0	0
1	A	191	1248	806	212	226	4	0	0	0
1	В	152	Total	С	N	О	S	0	0	0
1	Б	102	1256	810	214	228	4	0	0	0
1	С	153	Total	С	N	О	S	0	0	0
1		100	1265	815	215	231	4	U	U	U
1	D	152	Total	С	N	О	S	0	0	0
1	D	102	1257	811	213	229	4	0	U	U
1	E	152	Total	С	N	О	S	0	0	0
1	ш	102	1257	809	214	230	4	0	0	U
1	F	152	Total	С	N	О	S	0	0	0
1	I.	102	1257	811	213	229	4	0	U	U
1	G	152	Total	С	N	Ο	S	0	0	0
1	G	102	1256	809	213	230	4		0	U
1	Н	150	Total	С	N	Ο	S	0	0	0
1	11	100	1240	800	211	225	4	U	U	U

• Molecule 2 is 3'-deoxy-3'-(glycylamino)adenosine (three-letter code: A3G) (formula: $C_{12}H_{17}N_7O_4$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total 23	C 12	N 7	O 4	0	0	
2	В	1	Total	С	N	O	0	0	
	Ъ	1	23	12	7	4	0	0	
2	С	1	Total 23	C 12	N 7	O 4	0	0	
2	D	1	Total	С	N	О	0	0	
	D	1	23	12	7	4	0		
2	Е	1	Total	C	N	O	0	0	
			23	12	7	4			
$\frac{1}{2}$	F	1	Total	С	Ν	O	0	0	
			23	12	7	4		-	
$\frac{1}{2}$	G	1	Total	С	N	Ο	0	0	
	G G	1	23	12	7	4	O	Ü	
2	Н	1	Total	С	N	О	0	0	
	11	1	23	12	7	4	U	U	

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	29	Total O 29 29	0	0
3	В	27	Total O 27 27	0	0
3	С	21	Total O 21 21	0	0
3	D	11	Total O 11 11	0	0



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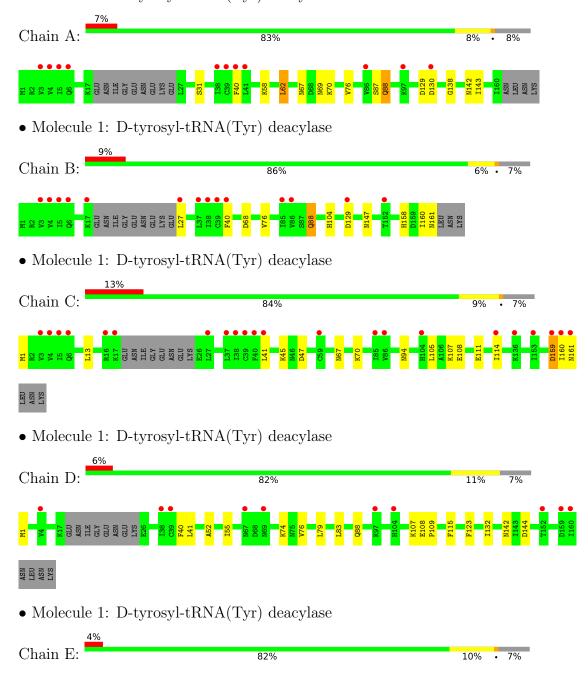
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	22	Total O 22 22	0	0
3	F	30	Total O 30 30	0	0
3	G	21	Total O 21 21	0	0
3	Н	18	Total O 18 18	0	0



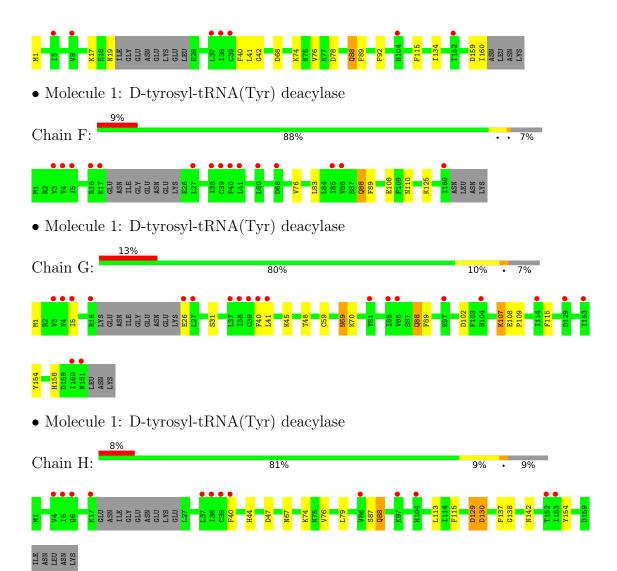
3 Residue-property plots (i)

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: D-tyrosyl-tRNA(Tyr) deacylase









4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	57.16Å 86.44Å 138.16Å	Donogitor
a, b, c, α , β , γ	90.00° 96.39° 90.00°	Depositor
Resolution (Å)	25.00 - 2.10	Depositor
rtesolution (A)	24.79 - 2.09	EDS
% Data completeness	96.2 (25.00-2.10)	Depositor
(in resolution range)	95.7 (24.79-2.09)	EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.32 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
P. P.	0.220 , 0.270	Depositor
R, R_{free}	0.224 , 0.269	DCC
R_{free} test set	3702 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	52.1	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.31 , 39.7	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	0.96	EDS
Total number of atoms	10399	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.57% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



 $^{^1 {\}rm Intensities}$ estimated from amplitudes.

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: A3G

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		
IVIOI	Chain	RMSZ	# Z >5	RMSZ	# Z > 5	
1	A	0.42	0/1271	0.62	0/1712	
1	В	0.39	0/1279	0.61	0/1723	
1	С	0.39	0/1288	0.60	0/1735	
1	D	0.38	0/1280	0.63	0/1724	
1	Е	0.41	0/1280	0.65	0/1724	
1	F	0.41	0/1280	0.60	0/1724	
1	G	0.38	0/1279	0.58	0/1724	
1	Н	0.39	0/1263	0.62	0/1701	
All	All	0.40	0/10220	0.61	0/13767	

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	1248	0	1274	5	0
1	В	1256	0	1280	7	0
1	С	1265	0	1286	6	0
1	D	1257	0	1280	9	0
1	Е	1257	0	1275	6	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1257	0	1280	5	0
1	G	1256	0	1273	9	0
1	Н	1240	0	1263	11	0
2	A	23	0	17	2	0
2	В	23	0	17	0	0
2	С	23	0	17	0	0
2	D	23	0	17	1	0
2	Ε	23	0	17	0	0
2	F	23	0	17	1	0
2	G	23	0	17	1	0
2	Н	23	0	17	2	0
3	A	29	0	0	0	0
3	В	27	0	0	1	0
3	С	21	0	0	0	0
3	D	11	0	0	0	0
3	${ m E}$	22	0	0	0	0
3	F	30	0	0	0	0
3	G	21	0	0	0	0
3	Н	18	0	0	0	0
All	All	10399	0	10347	56	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 3.

All (56) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:D:1:MET:HE3	1:D:55:ILE:HG13	1.75	0.69
1:D:123:PHE:HB3	1:D:132:ILE:HD13	1.78	0.65
1:D:123:PHE:HB3	1:D:132:ILE:CD1	2.31	0.61
1:D:1:MET:HE3	1:D:55:ILE:CG1	2.32	0.59
1:G:69:ASN:HB3	1:G:70:LYS:HG3	1.85	0.59
1:B:104:HIS:HB3	1:F:125:LYS:HE3	1.84	0.59
1:D:76:VAL:HG11	1:D:83:LEU:HD11	1.83	0.59
1:H:74:LYS:HE2	1:H:79:LEU:HD21	1.83	0.59
1:F:88:GLN:HE21	1:F:88:GLN:HA	1.69	0.57
1:F:108:GLU:OE2	1:F:110:ASN:ND2	2.39	0.56
1:H:67:ASN:HA	1:H:74:LYS:HD2	1.89	0.55
1:C:45:LYS:HE3	1:C:105:LEU:HA	1.89	0.54
1:G:40:PHE:HB3	1:G:88:GLN:HG3	1.90	0.54
1:C:111:GLU:O	1:C:114:ILE:HG12	2.09	0.53



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Continued from prev	was page	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:40:PHE:HB3	1:A:88:GLN:HG3	1.91	0.53
2:D:501:A3G:C8	2:D:501:A3G:H5'	2.41	0.55
1:B:129:ASP:N	1:B:129:ASP:OD1	2.43	0.51
1:H:87:SER:HB2	2:H:501:A3G:N3	2.26	0.51
1:A:138:GLY:HA2	2:A:501:A3G:H4'	1.93	0.49
1:H:88:GLN:HE21	1:H:88:GLN:HA	1.76	0.49
1:A:58:LYS:O	1:A:62:LEU:HB2	2.12	0.49
1:B:88:GLN:HE21	1:B:88:GLN:HA	1.78	0.48
1:A:87:SER:HB2	2:A:501:A3G:N3	2.29	0.48
1:E:74:LYS:HE3	1:E:78:ASP:HB3	1.94	0.48
1:H:129:ASP:O	1:H:130:ASP:CB	2.61	0.47
1:E:19:ASN:OD1	1:E:19:ASN:C	2.52	0.47
1:G:5:ILE:HD11	1:G:59:CYS:SG	2.55	0.47
1:F:89:PHE:CD1	2:F:501:A3G:H3'	2.49	0.47
1:B:40:PHE:HB3	1:B:88:GLN:HG3	1.98	0.46
1:C:1:MET:HB3	1:C:47:ASP:OD2	2.15	0.45
1:A:143:ILE:HB	1:B:147:ASN:HB2	1.99	0.45
1:C:160:ILE:HG22	1:C:161:ASN:N	2.31	0.45
1:G:88:GLN:HE21	1:G:88:GLN:HA	1.83	0.43
1:G:1:MET:HE3	1:G:41:LEU:HD11	1.99	0.44
1:G:89:PHE:CD1	2:G:501:A3G:H3'	2.53	0.44
1:C:159:ASP:OD1	1:C:159:ASP:N	2.50	0.44
1:H:40:PHE:HB3	1:H:88:GLN:HG3	2.00	0.44
1:B:160:ILE:HG22	1:B:161:ASN:H	1.83	0.43
1:H:129:ASP:O	1:H:130:ASP:HB3	2.18	0.43
1:G:108:GLU:HG2	1:G:109:PRO:HD2	2.00	0.43
1:E:159:ASP:C	1:E:160:ILE:HD12	2.40	0.42
1:H:44:HIS:N	1:H:47:ASP:OD2	2.40	0.42
1:E:40:PHE:HD2	1:E:88:GLN:HG3	1.85	0.42
1:G:45:LYS:O	1:G:107:LYS:NZ	2.52	0.42
1:D:1:MET:CE	1:D:52:ALA:HA	2.49	0.42
1:H:113:LEU:HD13	1:H:137:PHE:CG	2.55	0.42
1:D:40:PHE:HB3	1:D:88:GLN:HG3	2.01	0.41
1:D:74:LYS:HD2	1:D:79:LEU:HD21	2.03	0.41
1:C:13:LEU:C	1:C:13:LEU:HD23	2.40	0.41
1:E:1:MET:SD	1:E:41:LEU:HD11	2.61	0.41
1:E:42:GLY:C	1:E:92:PHE:HE2	2.24	0.41
1:H:138:GLY:HA2	2:H:501:A3G:H4'	2.03	0.41
1:F:76:VAL:HG11	1:F:83:LEU:HD11	2.04	0.40
1:D:108:GLU:HA	1:D:109:PRO:HD3	1.95	0.40
1:G:154:TYR:CE2	1:H:154:TYR:CE2	3.10	0.40
1.0.101.1110.012	1.11.101.1110.002	0.10	0.40



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Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:27:LEU:N	3:B:601:HOH:O	2.55	0.40

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	Perce	\mathbf{ntiles}
1	A	147/164 (90%)	143 (97%)	4 (3%)	0	100	100
1	В	148/164 (90%)	143 (97%)	5 (3%)	0	100	100
1	С	149/164 (91%)	139 (93%)	10 (7%)	0	100	100
1	D	148/164 (90%)	139 (94%)	9 (6%)	0	100	100
1	E	148/164 (90%)	141 (95%)	7 (5%)	0	100	100
1	F	148/164 (90%)	141 (95%)	7 (5%)	0	100	100
1	G	148/164 (90%)	143 (97%)	5 (3%)	0	100	100
1	Н	146/164 (89%)	137 (94%)	8 (6%)	1 (1%)	22	18
All	All	1182/1312 (90%)	1126 (95%)	55 (5%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Н	130	ASP

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	P	erce	ntiles
1	A	139/151 (92%)	129 (93%)	10 (7%)		14	11
1	В	140/151 (93%)	136 (97%)	4 (3%)		42	46
1	C	141/151 (93%)	134 (95%)	7 (5%)		24	23
1	D	140/151 (93%)	135 (96%)	5 (4%)		35	36
1	E	140/151 (93%)	133 (95%)	7 (5%)		24	23
1	F	140/151 (93%)	139 (99%)	1 (1%)		84	88
1	G	140/151 (93%)	131 (94%)	9 (6%)		17	14
1	Н	138/151 (91%)	133 (96%)	5 (4%)		35	36
All	All	1118/1208 (92%)	1070 (96%)	48 (4%)		29	29

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	SER
1	A	62	LEU
1	A	67	ASN
1	A A A	69	ASN
1	A	70	LYS
1	A A A A A	76	VAL
1	A	88	GLN
1	A	129	ASP
1	A	130	ASP
1	A	142	ASN
1	В	68	ASP
1	В	76	VAL
1	В	88	GLN
1	В	158	HIS
1	С	41	LEU
1	С	67	ASN
1	С	70	LYS
1	С	94	ASN
1	С	107	LYS
1	С	108	GLU
1	С	159	ASP
1	C C C C C D D	41	LEU
1		107	LYS
1	D	115	PHE
1	D	142	ASN



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Mol	Chain	Res	Type
1	D	144	ASP
1	Е	17	LYS
1	Е	68	ASP
1	Е	76	VAL
1	Е	88	GLN
1	Е	89	PHE
1	Е	115	PHE
1	Е	134	ILE
1	F	88	GLN
1	G	26	GLU
1	G	31	SER
1	G	48	THR
1	G	69	ASN
1	G	88	GLN
1	G	102	ASP
1	G	107	LYS
1	G	115	PHE
1	G	158	HIS
1	Н	76	VAL
1	Н	88	GLN
1	Н	115	PHE
1	Н	129	ASP
1	Н	142	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	С	126	GLN
1	D	139	ASN
1	D	142	ASN
1	Е	158	HIS
1	Н	128	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)

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	Во	ond leng	ths	В	ond ang	les
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A3G	D	501	-	21,25,25	1.92	3 (14%)	15,36,36	1.54	1 (6%)
2	A3G	A	501	-	21,25,25	1.79	2 (9%)	15,36,36	1.44	1 (6%)
2	A3G	G	501	-	21,25,25	1.93	2 (9%)	15,36,36	1.42	2 (13%)
2	A3G	F	501	-	21,25,25	1.75	2 (9%)	15,36,36	1.55	1 (6%)
2	A3G	Н	501	-	21,25,25	1.84	2 (9%)	15,36,36	1.52	2 (13%)
2	A3G	С	501	-	21,25,25	1.88	2 (9%)	15,36,36	1.41	1 (6%)
2	A3G	Е	501	-	21,25,25	1.93	2 (9%)	15,36,36	1.60	1 (6%)
2	A3G	В	501	-	21,25,25	2.01	2 (9%)	15,36,36	1.58	3 (20%)

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	A3G	D	501	-	-	2/8/28/28	0/3/3/3
2	A3G	A	501	-	-	4/8/28/28	0/3/3/3
2	A3G	G	501	-	-	5/8/28/28	0/3/3/3
2	A3G	F	501	-	-	3/8/28/28	0/3/3/3
2	A3G	Н	501	-	-	4/8/28/28	0/3/3/3
2	A3G	С	501	-	-	3/8/28/28	0/3/3/3
2	A3G	Е	501	-	-	4/8/28/28	0/3/3/3
2	A3G	В	501	-	-	4/8/28/28	0/3/3/3



All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$Ideal(\AA)$
2	С	501	A3G	O-C	7.01	1.37	1.23
2	В	501	A3G	O-C	7.00	1.37	1.23
2	Н	501	A3G	O-C	6.75	1.37	1.23
2	Е	501	A3G	O-C	6.61	1.36	1.23
2	D	501	A3G	O-C	6.53	1.36	1.23
2	G	501	A3G	O-C	6.43	1.36	1.23
2	F	501	A3G	O-C	6.42	1.36	1.23
2	A	501	A3G	O-C	6.32	1.36	1.23
2	В	501	A3G	O4'-C1'	5.12	1.48	1.41
2	G	501	A3G	O4'-C1'	5.05	1.48	1.41
2	Е	501	A3G	O4'-C1'	4.85	1.47	1.41
2	A	501	A3G	O4'-C1'	4.37	1.47	1.41
2	D	501	A3G	O4'-C1'	4.35	1.47	1.41
2	С	501	A3G	O4'-C1'	3.90	1.46	1.41
2	F	501	A3G	O4'-C1'	3.87	1.46	1.41
2	Н	501	A3G	O4'-C1'	3.65	1.46	1.41
2	D	501	A3G	C5-N7	-2.12	1.32	1.39

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	Е	501	A3G	N3-C2-N1	-5.02	120.84	128.68
2	A	501	A3G	N3-C2-N1	-4.64	121.43	128.68
2	F	501	A3G	N3-C2-N1	-4.53	121.59	128.68
2	G	501	A3G	N3-C2-N1	-4.37	121.85	128.68
2	Н	501	A3G	N3-C2-N1	-4.30	121.95	128.68
2	D	501	A3G	N3-C2-N1	-4.27	122.00	128.68
2	С	501	A3G	N3-C2-N1	-4.24	122.05	128.68
2	В	501	A3G	N3-C2-N1	-4.07	122.31	128.68
2	В	501	A3G	O4'-C4'-C5'	-2.68	103.43	109.21
2	Н	501	A3G	O4'-C4'-C5'	2.22	114.02	109.21
2	В	501	A3G	O-C-N8	2.19	126.66	122.95
2	G	501	A3G	C4-C5-N7	-2.02	107.29	109.40

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	A3G	N8-C-CA-N
2	В	501	A3G	O-C-CA-N
2	В	501	A3G	N8-C-CA-N



Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	С	501	A3G	N8-C-CA-N
2	D	501	A3G	N8-C-CA-N
2	Е	501	A3G	N8-C-CA-N
2	F	501	A3G	N8-C-CA-N
2	G	501	A3G	C3'-C4'-C5'-O5'
2	Н	501	A3G	N8-C-CA-N
2	Н	501	A3G	C3'-C4'-C5'-O5'
2	G	501	A3G	O4'-C4'-C5'-O5'
2	Н	501	A3G	O4'-C4'-C5'-O5'
2	A	501	A3G	O-C-CA-N
2	С	501	A3G	O-C-CA-N
2	D	501	A3G	O-C-CA-N
2	Е	501	A3G	O-C-CA-N
2	F	501	A3G	O-C-CA-N
2	G	501	A3G	O-C-CA-N
2	Н	501	A3G	O-C-CA-N
2	G	501	A3G	N8-C-CA-N
2	A	501	A3G	O4'-C4'-C5'-O5'
2	В	501	A3G	O4'-C4'-C5'-O5'
2	A	501	A3G	C3'-C4'-C5'-O5'
2	Е	501	A3G	C3'-C4'-C5'-O5'
2	F	501	A3G	C3'-C4'-C5'-O5'
2	Е	501	A3G	O4'-C4'-C5'-O5'
2	С	501	A3G	C4'-C3'-N8-C
2	G	501	A3G	C4'-C3'-N8-C
2	В	501	A3G	C3'-C4'-C5'-O5'

There are no ring outliers.

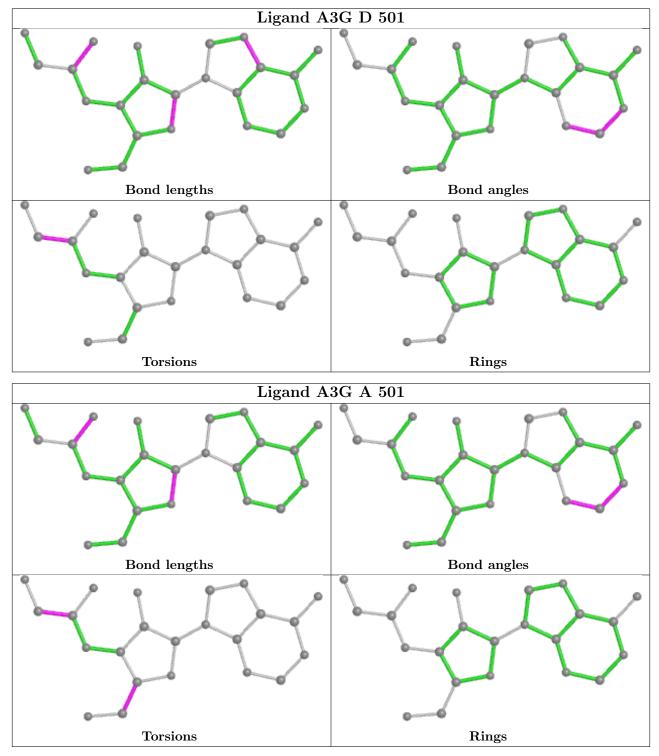
5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	501	A3G	1	0
2	A	501	A3G	2	0
2	G	501	A3G	1	0
2	F	501	A3G	1	0
2	Н	501	A3G	2	0

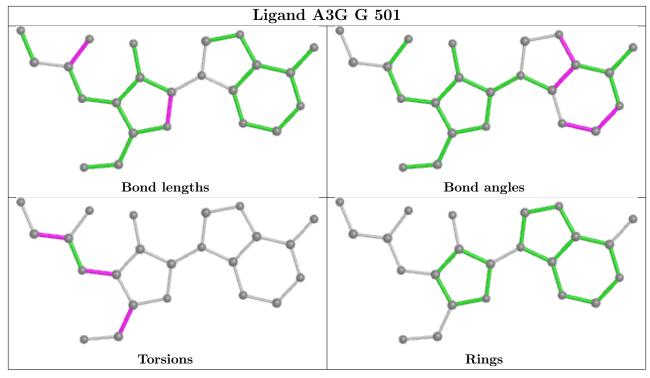
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

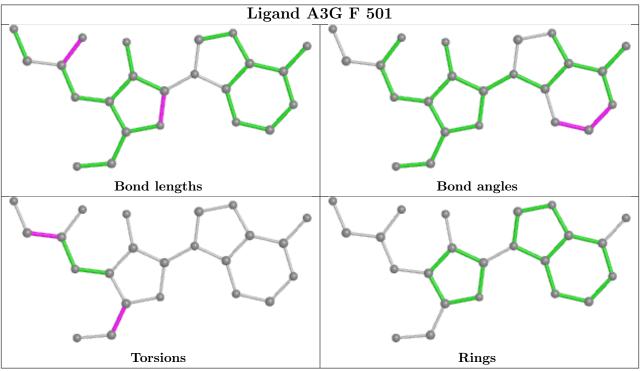


Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD 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.

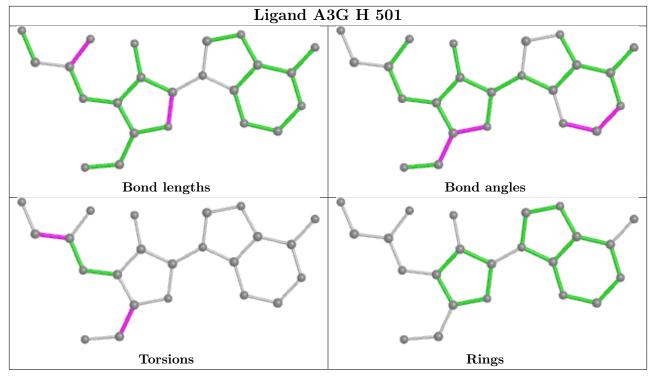


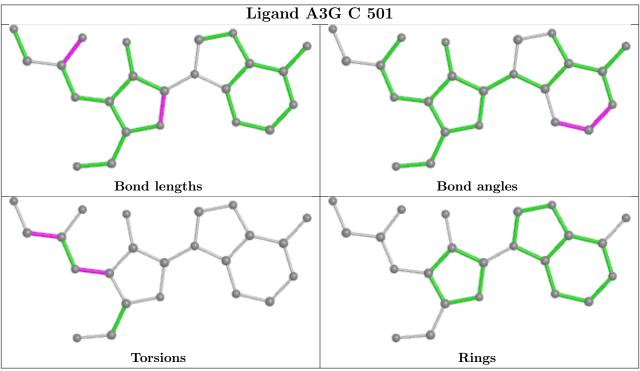




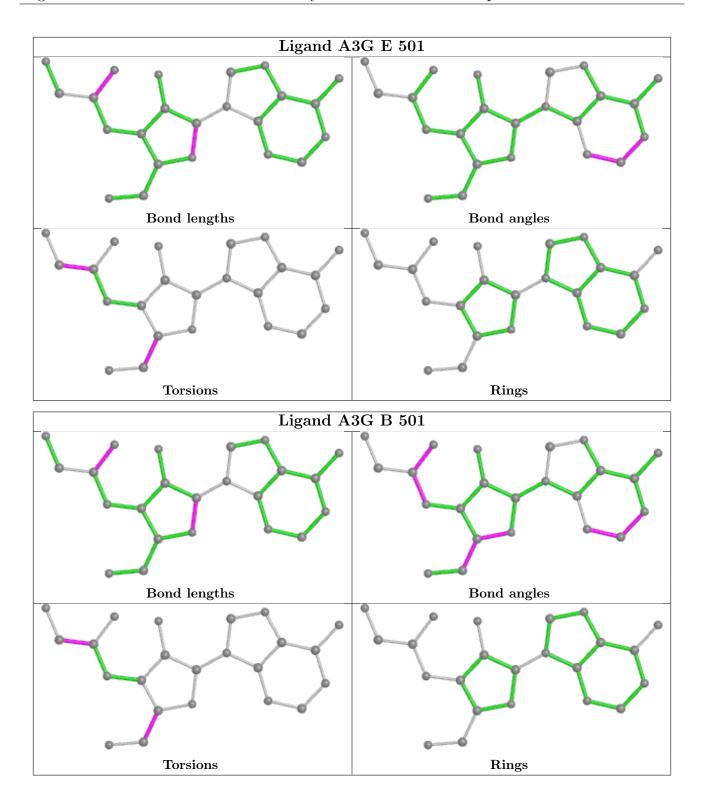












5.7 Other polymers (i)

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>	$\#\mathrm{RSRZ}{>}2$	$OWAB(m \AA^2)$	Q < 0.9
1	A	151/164 (92%)	0.42	11 (7%) 15 19	42, 54, 73, 91	0
1	В	152/164~(92%)	0.38	14 (9%) 9 11	40, 55, 74, 96	0
1	С	153/164 (93%)	0.91	22 (14%) 2 3	40, 63, 92, 111	0
1	D	152/164 (92%)	0.43	10 (6%) 18 23	45, 60, 91, 122	0
1	E	152/164 (92%)	0.27	7 (4%) 32 38	37, 54, 76, 88	0
1	F	152/164 (92%)	0.38	15 (9%) 7 9	36, 53, 76, 101	0
1	G	152/164 (92%)	0.76	21 (13%) 2 4	40, 60, 81, 102	0
1	Н	150/164 (91%)	0.45	13 (8%) 10 13	41, 57, 81, 91	0
All	All	1214/1312 (92%)	0.50	113 (9%) 8 11	36, 56, 82, 122	0

All (113) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	160	ILE	6.3
1	С	160	ILE	6.3
1	G	39	CYS	5.1
1	G	16	ARG	4.8
1	С	39	CYS	4.6
1	G	40	PHE	4.6
1	С	5	ILE	4.5
1	Н	4	VAL	4.5
1	F	17	LYS	4.4
1	С	27	LEU	4.4
1	G	5	ILE	4.3
1	С	86	VAL	4.2
1	С	16	ARG	4.2
1	F	16	ARG	4.1
1	G	3	VAL	4.1
1	G	160	ILE	4.0



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Mol	Chain	$ hootnote{Res}$	Type	RSRZ
1	В	38	ILE	4.0
1	G	27	LEU	4.0
1	В	17	LYS	3.9
1	С	3	VAL	3.9
1	G	41	LEU	3.8
1	D	97	LYS	3.8
1	G	38	ILE	3.8
1	В	5	ILE	3.8
1	A	39	CYS	3.7
1	D	67	ASN	3.7
1	В	4	VAL	3.6
1	G	4	VAL	3.5
1	В	37	LEU	3.5
1	С	85	ILE	3.5
1	A	5	ILE	3.4
1	В	39	CYS	3.4
1	A	38	ILE	3.3
1	A	4	VAL	3.3
1	A	97	LYS	3.2
1	С	41	LEU	3.2
1	С	104	HIS	3.2
1	Е	104	HIS	3.2
1	В	40	PHE	3.1
1	A	41	LEU	3.1
1	Е	38	ILE	3.1
1	A	3	VAL	3.0
1	Н	5	ILE	3.0
1	Е	8	VAL	3.0
1	В	27	LEU	3.0
1	C	4	VAL	2.9
1	A	40	PHE	2.9
1	В	129	ASP	2.9
1	D	4	VAL	2.9
1	С	153	ILE	2.8
1	С	40	PHE	2.8
1	G	86	VAL	2.8
1	С	37	LEU	2.8
1	Н	38	ILE	2.7
1	С	59	CYS	2.7
1	F	60	LEU	2.7
1	F	39	CYS	2.7
1	G	85	ILE	2.7



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Mol	Chain	Res	Type	RSRZ
1	Н	86	VAL	2.7
1	С	38	ILE	2.7
1	D	38	ILE	2.6
1	A	86	VAL	2.6
1	Н	40	PHE	2.6
1	F	41	LEU	2.6
1	В	3	VAL	2.6
1	G	97	LYS	2.6
1	F	38	ILE	2.6
1	Е	152	THR	2.6
1	D	152	THR	2.6
1	D	39	CYS	2.5
1	В	152	THR	2.5
1	Н	39	CYS	2.5
1	F	5	ILE	2.5
1	В	85	ILE	2.5
1	С	114	ILE	2.5
1	В	6	GLN	2.4
1	G	153	ILE	2.4
1	F	40	PHE	2.4
1	С	17	LYS	2.3
1	G	114	ILE	2.3
1	G	161	ASN	2.3
1	С	159	ASP	2.3
1	Н	37	LEU	2.3
1	G	129	ASP	2.3
1	Н	152	THR	2.3
1	С	136	LYS	2.3
1	Н	17	LYS	2.3
1	Н	153	ILE	2.3
1	G	37	LEU	2.2
1	F	68	ASP	2.2
1	F	27	LEU	2.2
1	G	26	GLU	2.2
1	Н	6	GLN	2.2
1	A	130	ASP	2.2
1	A	6	GLN	2.2
1	F	3	VAL	2.2
1	G	104	HIS	2.2
1	С	161	ASN	2.2
1	Е	39	CYS	2.2
1	D	104	HIS	2.2



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Mol	Chain	Res	Type	RSRZ
1	F	160	ILE	2.1
1	F	86	VAL	2.1
1	D	159	ASP	2.1
1	G	81	TYR	2.1
1	Е	37	LEU	2.1
1	F	4	VAL	2.1
1	D	69	ASN	2.1
1	Е	5	ILE	2.1
1	F	85	ILE	2.0
1	Н	97	LYS	2.0
1	Н	104	HIS	2.0
1	В	86	VAL	2.0
1	С	6	GLN	2.0

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)

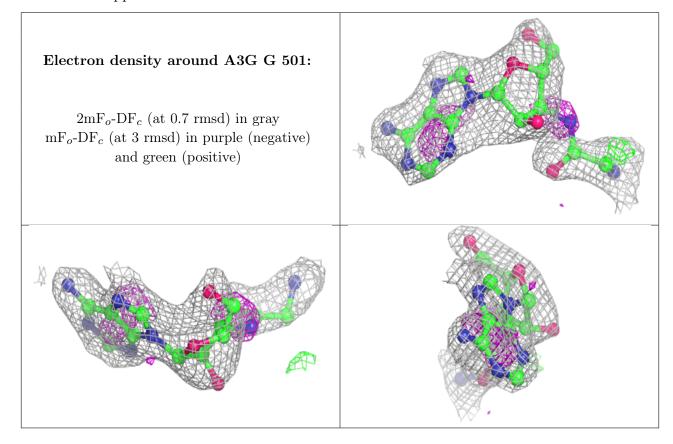
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	A3G	G	501	23/23	0.78	0.24	64,79,84,86	0
2	A3G	F	501	23/23	0.89	0.19	65,78,88,90	0
2	A3G	Н	501	23/23	0.89	0.16	65,69,78,79	0
2	A3G	С	501	23/23	0.91	0.15	55,77,88,98	0
2	A3G	Е	501	23/23	0.92	0.14	67,77,91,92	0
2	A3G	В	501	23/23	0.93	0.12	51,57,66,72	0
2	A3G	A	501	23/23	0.93	0.14	50,65,74,75	0
2	A3G	D	501	23/23	0.95	0.10	48,52,62,67	0

The following is a graphical depiction of the model fit to experimental electron density of all



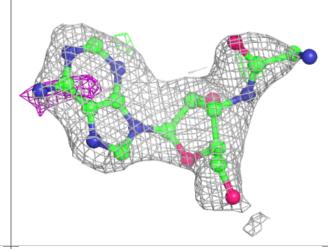
instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

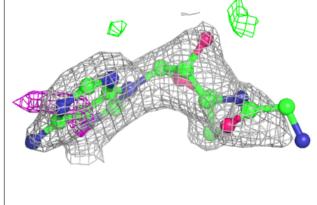


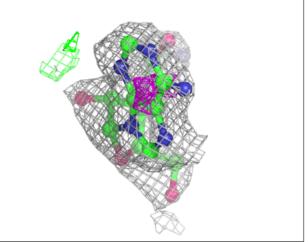


Electron density around A3G F 501:

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



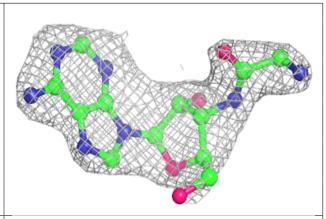


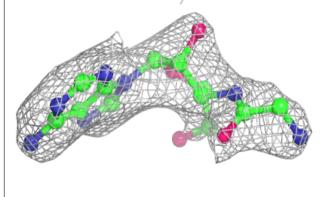


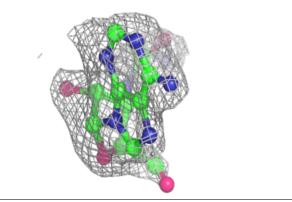


Electron density around A3G H 501:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

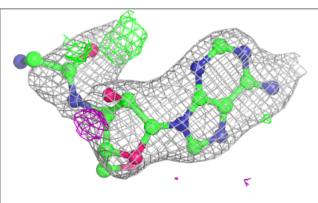


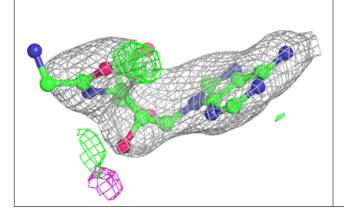


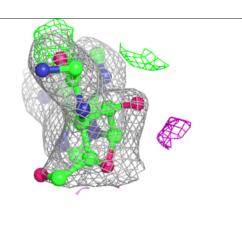


Electron density around A3G C 501:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

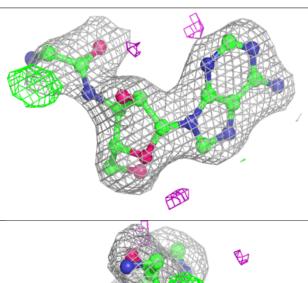


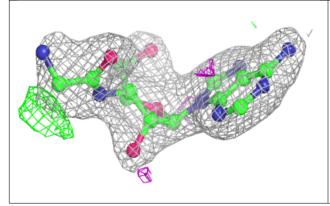


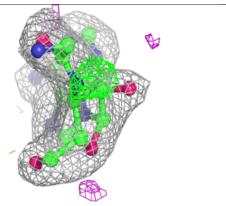




 $2 {\rm mF}_o\text{-}{\rm DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)



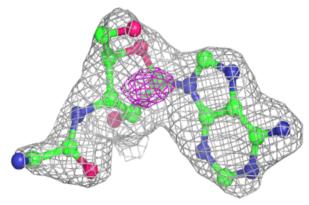


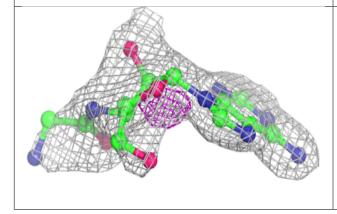


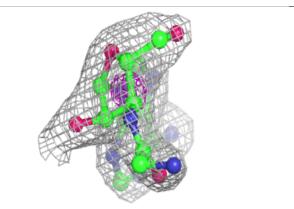


Electron density around A3G A 501:

 $2 {\rm mF}_o\text{-}{\rm DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

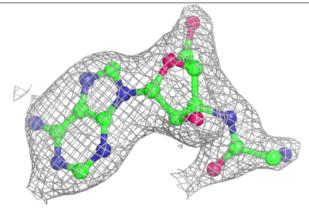


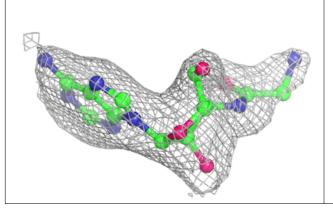


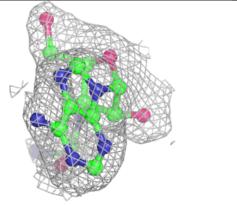


Electron density around A3G D 501:

 $2 {
m mF}_o {
m -DF}_c$ (at 0.7 rmsd) in gray ${
m mF}_o {
m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)









6.5 Other polymers (i)

There are no such residues in this entry.

