



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 15, 2026 – 12:24 AM UTC

PDB ID : 7HK5 / pdb_00007hk5
Title : Crystal Structure of N-methylhydantoinase in complex with 1-methylimidazole-2,4-dione
Authors : Stihle, M.; Benz, J.; Asztalos, P.; Rudolph, M.G.
Deposited on : 2024-10-10
Resolution : 2.07 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

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

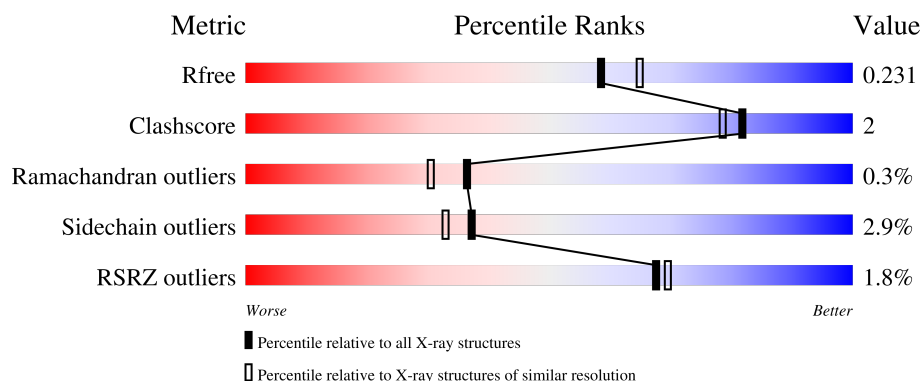
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

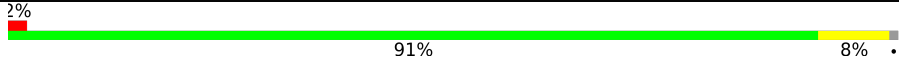
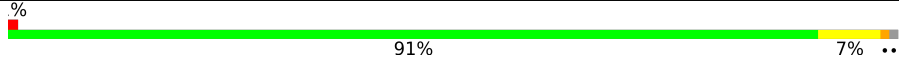
The reported resolution of this entry is 2.07 Å.

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}	180053	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1288	
1	B	1288	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 21201 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.

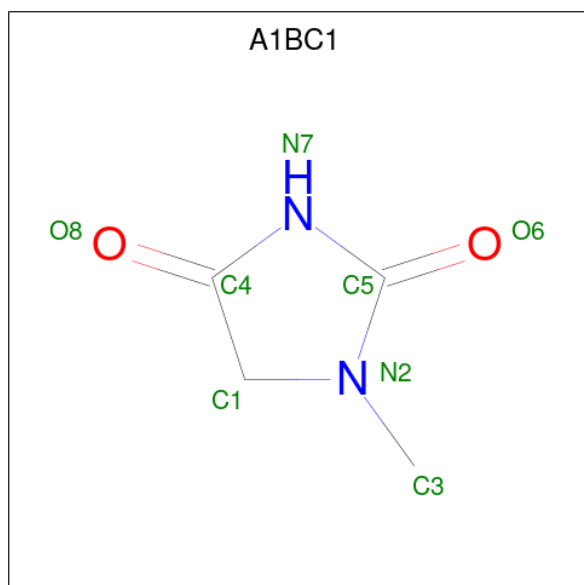
- Molecule 1 is a protein called N-methylhydantoinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1274	Total	C	N	O	S	0	3	0
			9772	6136	1692	1904	40			
1	B	1278	Total	C	N	O	S	0	1	0
			9787	6144	1695	1908	40			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

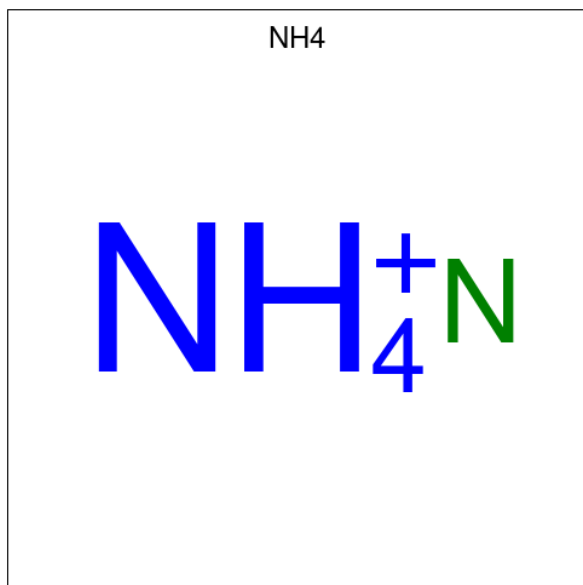
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		

- Molecule 3 is 1-methylimidazolidine-2,4-dione (CCD ID: A1BC1) (formula: C₄H₆N₂O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	2	2		
3	B	1	Total	C	N	O	0	0
			8	4	2	2		

- Molecule 4 is AMMONIUM ION (CCD ID: NH4) (formula: H_4N).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	N	0	0
			1	1		
4	B	1	Total	N	0	0
			1	1		

- Molecule 5 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (CCD ID: BTB) (formula: $\text{C}_8\text{H}_{19}\text{NO}_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

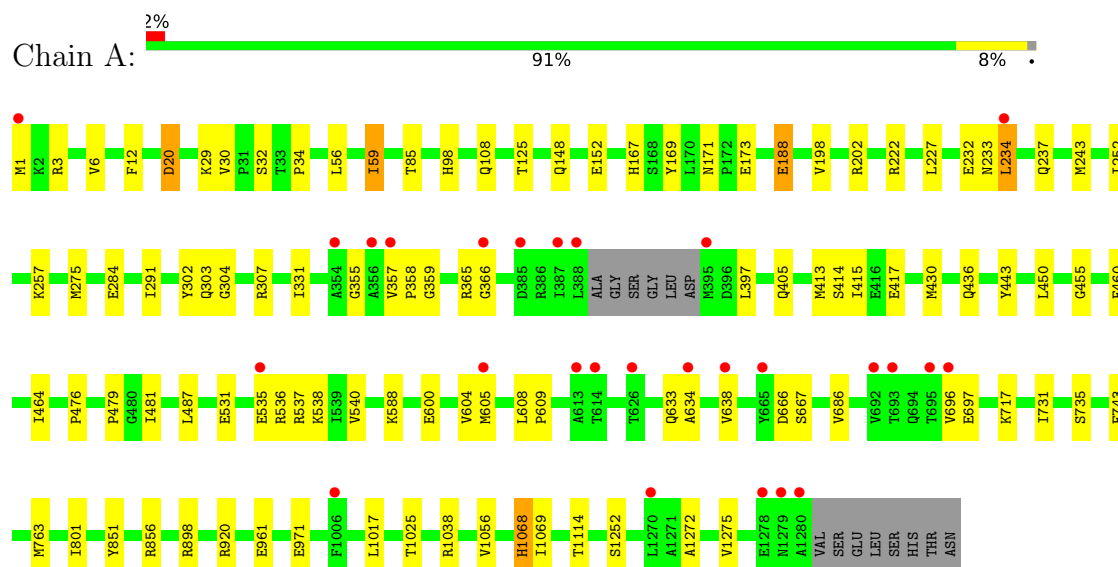
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	803	Total	O	0	0
			803	803		
6	B	805	Total	O	0	0
			805	805		

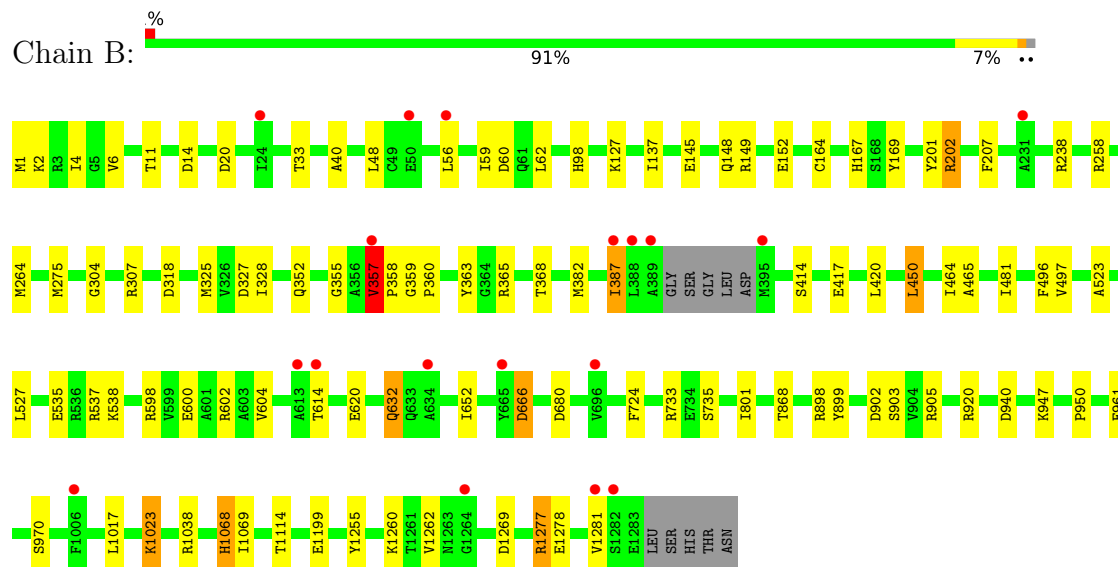
3 Residue-property plots [i](#)

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: N-methylhydantoinase



• Molecule 1: N-methylhydantoinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	219.38Å 219.38Å 135.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.60 – 2.07 49.60 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.60-2.07) 94.6 (49.60-2.07)	Depositor EDS
R_{merge}	0.28	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.96 (at 2.07Å)	Xtriage
Refinement program	PHENIX dev_2363	Depositor
R, R_{free}	0.182 , 0.225 0.188 , 0.231	Depositor DCC
R_{free} test set	9826 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	30.6	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 42.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	21201	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CA, NH4, BTB, A1BC1

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	0.45	1/9974 (0.0%)	0.60	0/13540
1	B	0.43	0/9983	0.58	0/13553
All	All	0.44	1/19957 (0.0%)	0.59	0/27093

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	VAL	C-N	5.02	1.45	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	A	9772	0	9582	46	0
1	B	9787	0	9593	50	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	8	0	0	0	0
3	B	8	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	14	0	19	1	0
6	A	803	0	0	3	0
6	B	805	0	0	4	0
All	All	21201	0	19194	97	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 2.

All (97) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:GLN:HG2	1:A:415:ILE:HD12	1.56	0.86
1:A:275:MET:HE3	1:A:304:GLY:HA2	1.67	0.77
1:B:56:LEU:HD12	1:B:59:ILE:HD12	1.71	0.72
1:B:902:ASP:OD1	1:B:905:ARG:NH2	2.27	0.68
1:B:666:ASP:N	1:B:666:ASP:OD1	2.27	0.67
1:A:307:ARG:NH2	1:A:443:TYR:OH	2.30	0.65
1:B:264:MET:HE2	1:B:325:MET:HE1	1.83	0.60
1:A:232:GLU:C	1:A:234:LEU:H	2.09	0.60
1:B:357:VAL:HB	1:B:358:PRO:CD	2.31	0.60
1:A:666:ASP:OD1	1:A:666:ASP:N	2.35	0.58
1:A:56:LEU:HD12	1:A:59:ILE:HD13	1.87	0.57
1:A:167:HIS:HA	1:A:169:TYR:CE1	2.40	0.56
1:A:358:PRO:HB3	1:A:366:GLY:O	2.06	0.56
1:A:1:MET:O	1:A:20:ASP:HB2	2.04	0.56
1:A:536:ARG:HD2	1:A:605:MET:SD	2.47	0.55
1:B:357:VAL:HB	1:B:358:PRO:HD3	1.87	0.55
1:A:222:ARG:NH1	6:A:2103:HOH:O	2.31	0.55
1:B:148:GLN:O	1:B:152:GLU:HG3	2.07	0.55
1:B:1068:HIS:CG	1:B:1069:ILE:N	2.75	0.55
1:A:717:LYS:NZ	6:A:2110:HOH:O	2.39	0.54
1:B:4:ILE:HD13	1:B:48:LEU:HD23	1.89	0.54
1:B:258[A]:ARG:HH11	1:B:258[A]:ARG:HG2	1.73	0.54
1:A:414:SER:OG	1:A:417:GLU:HG2	2.07	0.54
1:A:331:ILE:HD11	1:A:430:MET:HG2	1.88	0.53
1:A:355:GLY:O	1:A:359:GLY:HA2	2.08	0.53
1:B:4:ILE:HB	1:B:62:LEU:HD13	1.91	0.52
1:B:1255:TYR:O	1:B:1277:ARG:HD3	2.10	0.52
1:B:620:GLU:H	1:B:620:GLU:CD	2.18	0.51
1:A:302:TYR:CE2	1:A:303:GLN:HG2	2.45	0.51
1:A:608:LEU:HD12	1:A:609:PRO:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:355:GLY:O	1:B:359:GLY:HA2	2.11	0.50
1:A:32:SER:O	1:A:34:PRO:HD3	2.12	0.50
1:B:600:GLU:OE2	1:B:602:ARG:NH1	2.45	0.50
1:A:971:GLU:HA	1:A:1025:THR:HA	1.94	0.50
1:B:1:MET:HB2	1:B:60:ASP:OD2	2.12	0.50
1:A:171:ASN:OD1	1:A:173:GLU:HG3	2.12	0.49
1:B:735:SER:HA	1:B:1114:THR:HB	1.94	0.49
1:A:1068:HIS:CG	1:A:1069:ILE:N	2.79	0.49
1:B:14:ASP:HB3	1:B:481:ILE:CD1	2.43	0.48
1:A:1272:ALA:HA	1:A:1275:VAL:HG12	1.95	0.48
1:A:56:LEU:HA	1:A:59:ILE:HD12	1.94	0.48
1:A:291:ILE:O	1:A:455:GLY:HA3	2.14	0.48
1:B:387:ILE:H	1:B:387:ILE:HG13	1.46	0.48
1:B:537:ARG:O	1:B:538:LYS:HD2	2.13	0.48
1:A:243:MET:HE2	1:A:487:LEU:HD23	1.96	0.47
5:B:2003:BTB:H42	5:B:2003:BTB:H72	1.63	0.47
1:B:420:LEU:HD13	1:B:632:GLN:HB2	1.96	0.47
1:B:527:LEU:HD13	1:B:537:ARG:HG2	1.95	0.47
1:A:920:ARG:HH12	1:A:961:GLU:HG2	1.80	0.47
1:A:357:VAL:HB	1:A:358:PRO:CD	2.44	0.47
1:B:11:THR:N	6:B:2127:HOH:O	2.46	0.47
1:B:167:HIS:HA	1:B:169:TYR:CE1	2.50	0.46
1:B:307:ARG:HD2	1:B:327:ASP:OD2	2.16	0.46
1:B:898:ARG:HD3	1:B:899:TYR:CE2	2.50	0.46
1:A:152:GLU:O	6:A:2101:HOH:O	2.21	0.46
1:A:634:ALA:N	1:A:697:GLU:OE2	2.49	0.46
1:B:614:THR:HG22	6:B:2161:HOH:O	2.16	0.46
1:A:537:ARG:O	1:A:538:LYS:HD3	2.17	0.45
1:B:600:GLU:OE2	1:B:602:ARG:NH2	2.49	0.45
1:B:497:VAL:HG12	1:B:598:ARG:HG2	1.97	0.45
1:A:12:PHE:CD2	1:A:29:LYS:HE3	2.51	0.45
1:A:540:VAL:CG1	1:A:600:GLU:HB2	2.47	0.45
1:A:633:GLN:HB3	1:A:638:VAL:HG21	1.97	0.45
1:A:731:ILE:O	1:A:735:SER:HB2	2.17	0.45
1:B:947:LYS:NZ	6:B:2131:HOH:O	2.49	0.45
1:B:1:MET:HG3	1:B:60:ASP:HB2	1.99	0.45
1:A:188:GLU:CD	1:A:188:GLU:H	2.26	0.44
1:B:145:GLU:O	1:B:149:ARG:HG2	2.17	0.44
1:A:735:SER:HA	1:A:1114:THR:HB	1.99	0.44
1:B:733:ARG:HD3	6:B:2467:HOH:O	2.18	0.44
1:B:33:THR:HG23	1:B:40:ALA:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:PRO:HD2	1:B:363:TYR:CE2	2.54	0.43
1:A:696:VAL:HG11	1:A:898:ARG:HE	1.84	0.43
1:B:352:GLN:H	1:B:352:GLN:CD	2.27	0.43
1:A:743:PHE:CZ	1:A:763:MET:HB3	2.53	0.42
1:B:496:PHE:CE1	1:B:523:ALA:HA	2.54	0.42
1:A:851:TYR:CE2	1:A:856:ARG:HB2	2.55	0.42
1:B:450:LEU:HD12	1:B:465:ALA:HB2	2.02	0.42
1:A:85:THR:O	1:A:125:THR:HA	2.19	0.42
1:B:60:ASP:O	1:B:238:ARG:HD2	2.20	0.42
1:B:201:TYR:O	1:B:202:ARG:HB2	2.19	0.42
1:B:950:PRO:HD2	1:B:970:SER:HB2	2.02	0.42
1:A:257:LYS:HE3	1:A:257:LYS:HB2	1.68	0.41
1:A:460:PHE:HB3	1:A:464:ILE:HD12	2.02	0.41
1:A:413:MET:HB3	1:A:417:GLU:HG3	2.03	0.41
1:B:652:ILE:H	1:B:652:ILE:HG12	1.72	0.41
1:B:450:LEU:HD11	1:B:464:ILE:HG22	2.02	0.41
1:B:920:ARG:HH12	1:B:961:GLU:HG2	1.85	0.41
1:B:1023:LYS:HD2	1:B:1023:LYS:HA	1.73	0.41
1:A:148:GLN:O	1:A:152:GLU:HG3	2.21	0.41
1:A:476:PRO:O	1:A:479:PRO:HD3	2.21	0.41
1:B:275:MET:HE3	1:B:304:GLY:HA2	2.03	0.41
1:B:1:MET:N	1:B:20:ASP:HB2	2.36	0.40
1:B:164:CYS:HB3	1:B:207:PHE:CD1	2.56	0.40
1:B:1260:LYS:HE3	1:B:1269:ASP:OD2	2.20	0.40
1:A:232:GLU:C	1:A:234:LEU:N	2.76	0.40
1:B:382:MET:HB3	1:B:382:MET:HE2	1.74	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	Percentiles	
1	A	1273/1288 (99%)	1230 (97%)	40 (3%)	3 (0%)	43	38
1	B	1275/1288 (99%)	1235 (97%)	36 (3%)	4 (0%)	36	30
All	All	2548/2576 (99%)	2465 (97%)	76 (3%)	7 (0%)	36	30

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	108	GLN
1	A	202	ARG
1	B	202	ARG
1	B	365	ARG
1	A	233	ASN
1	B	940	ASP
1	B	357	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	
1	A	1030/1039 (99%)	1001 (97%)	29 (3%)	38	34
1	B	1031/1039 (99%)	1000 (97%)	31 (3%)	36	32
All	All	2061/2078 (99%)	2001 (97%)	60 (3%)	37	33

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	6	VAL
1	A	20	ASP
1	A	30	VAL
1	A	59	ILE
1	A	98	HIS
1	A	188	GLU
1	A	227	LEU
1	A	234	LEU

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Mol	Chain	Res	Type
1	A	237	GLN
1	A	252	ILE
1	A	284	GLU
1	A	365	ARG
1	A	397	LEU
1	A	436	GLN
1	A	450	LEU
1	A	481	ILE
1	A	531	GLU
1	A	535	GLU
1	A	588	LYS
1	A	604	VAL
1	A	667	SER
1	A	686	VAL
1	A	801	ILE
1	A	1017	LEU
1	A	1038	ARG
1	A	1056	VAL
1	A	1068	HIS
1	A	1252	SER
1	B	2	LYS
1	B	6	VAL
1	B	98	HIS
1	B	127	LYS
1	B	137	ILE
1	B	318	ASP
1	B	328	ILE
1	B	357	VAL
1	B	368	THR
1	B	387	ILE
1	B	414	SER
1	B	417	GLU
1	B	450	LEU
1	B	535	GLU
1	B	604	VAL
1	B	632	GLN
1	B	666	ASP
1	B	680	ASP
1	B	724	PHE
1	B	801	ILE
1	B	868	THR
1	B	903	SER

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Mol	Chain	Res	Type
1	B	1017	LEU
1	B	1023	LYS
1	B	1038	ARG
1	B	1068	HIS
1	B	1199	GLU
1	B	1262	VAL
1	B	1277	ARG
1	B	1278	GLU
1	B	1281	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	280	GLN
1	A	500	ASN
1	A	857	GLN
1	B	280	GLN
1	B	478	HIS
1	B	857	GLN
1	B	1028	ASN
1	B	1030	ASN
1	B	1117	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 2 are monoatomic and 2 are modelled with single atom - leaving 3 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$
3	A1BC1	B	2001	2	8,8,8	1.69	2 (25%)	10,11,11	1.55	1 (10%)
5	BTB	B	2003	-	13,13,13	2.00	5 (38%)	7,16,16	0.69	0
3	A1BC1	A	2001	2	8,8,8	1.96	2 (25%)	10,11,11	1.60	1 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	A1BC1	B	2001	2	-	-	0/1/1/1
5	BTB	B	2003	-	-	1/21/21/21	-
3	A1BC1	A	2001	2	-	-	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2001	A1BC1	C4-N7	4.33	1.44	1.37
5	B	2003	BTB	C7-N	4.01	1.53	1.48
5	B	2003	BTB	C5-N	3.19	1.52	1.48
5	B	2003	BTB	C2-N	2.84	1.54	1.48
5	B	2003	BTB	C1-C2	2.76	1.56	1.53
3	B	2001	A1BC1	C4-N7	2.58	1.41	1.37
3	B	2001	A1BC1	C5-N7	2.31	1.42	1.38
5	B	2003	BTB	C3-C2	2.19	1.55	1.53
3	A	2001	A1BC1	C5-N7	2.08	1.42	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2001	A1BC1	C4-N7-C5	-4.60	108.44	112.47
3	B	2001	A1BC1	C4-N7-C5	-3.30	109.58	112.47

There are no chirality outliers.

All (1) torsion outliers are listed below:

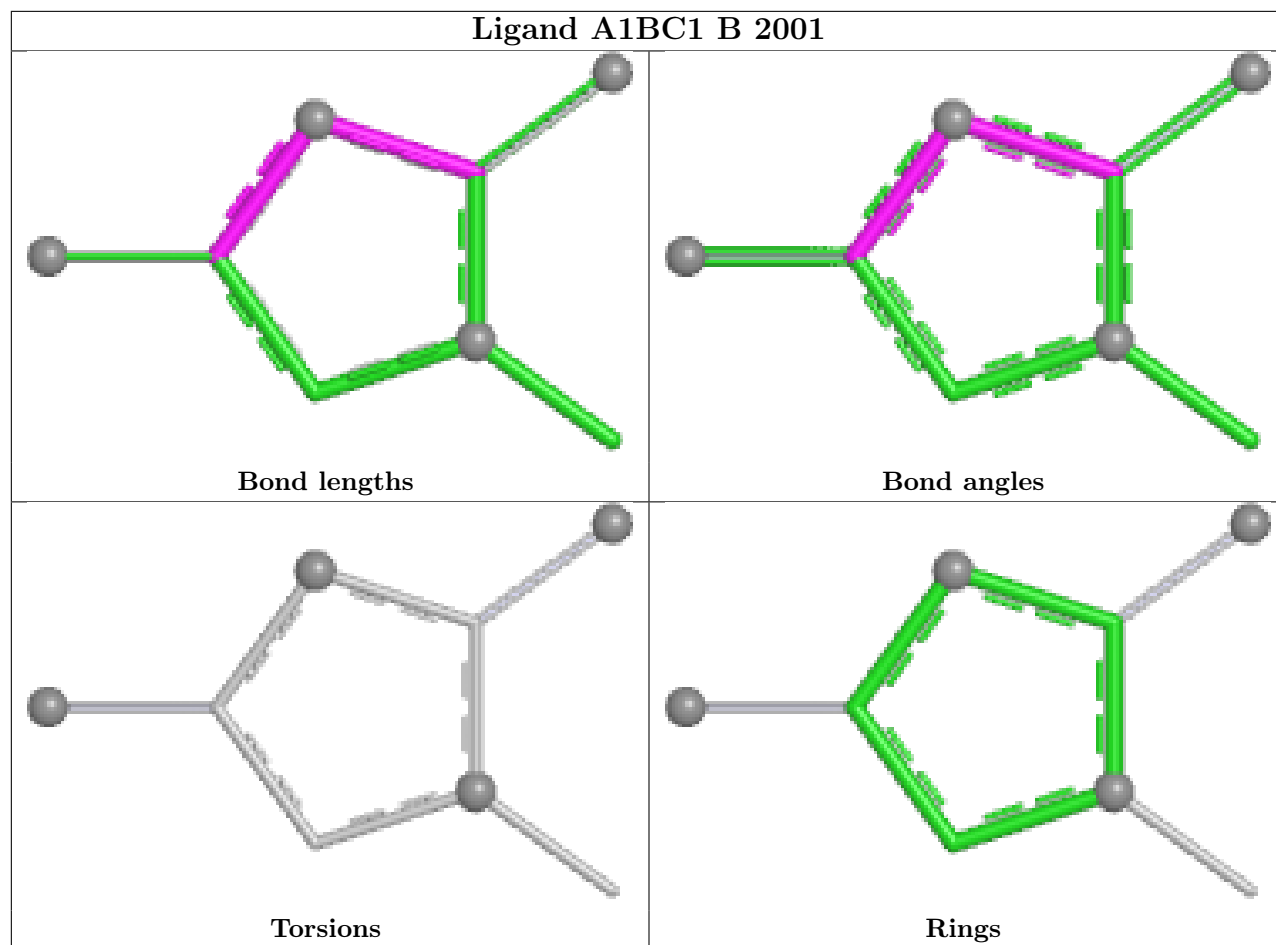
Mol	Chain	Res	Type	Atoms
5	B	2003	BTB	N-C7-C8-O8

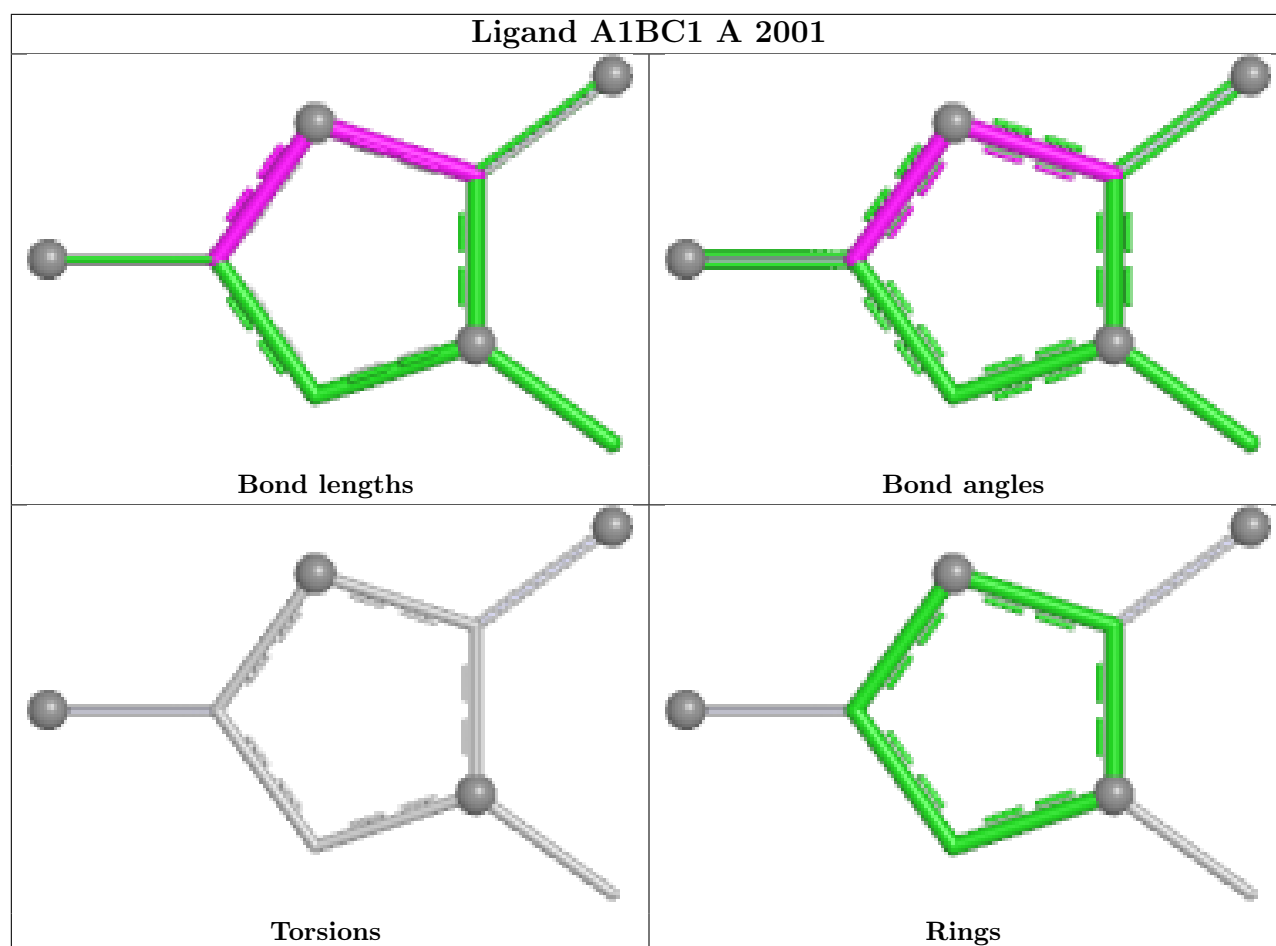
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	2003	BTB	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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

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(Å ²)	Q<0.9
1	A	1274/1288 (98%)	0.10	27 (2%) 63 66	17, 37, 65, 102	3 (0%)
1	B	1278/1288 (99%)	0.10	18 (1%) 73 75	23, 37, 67, 106	1 (0%)
All	All	2552/2576 (99%)	0.10	45 (1%) 67 69	17, 37, 66, 106	4 (0%)

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	388	LEU	4.9
1	A	388	LEU	4.7
1	A	692	VAL	4.6
1	A	387	ILE	4.1
1	B	389	ALA	3.8
1	A	1	MET	3.2
1	A	357	VAL	3.1
1	A	395	MET	3.1
1	B	696	VAL	3.0
1	B	634	ALA	3.0
1	B	395	MET	2.9
1	B	1281	VAL	2.9
1	A	695	THR	2.9
1	B	665	TYR	2.8
1	A	696	VAL	2.8
1	B	614	THR	2.8
1	A	605	MET	2.7
1	B	1006	PHE	2.7
1	A	626	THR	2.7
1	A	1280	ALA	2.7
1	A	634	ALA	2.6
1	A	638	VAL	2.6
1	A	1006	PHE	2.5
1	A	665	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	50	GLU	2.5
1	A	693	THR	2.4
1	B	24	ILE	2.4
1	B	56	LEU	2.3
1	B	357	VAL	2.3
1	A	614	THR	2.3
1	B	387	ILE	2.3
1	A	1270	LEU	2.3
1	A	356	ALA	2.3
1	A	385	ASP	2.3
1	A	613	ALA	2.3
1	A	535	GLU	2.2
1	A	1278	GLU	2.2
1	B	1282	SER	2.2
1	A	366	GLY	2.2
1	B	1264	GLY	2.1
1	A	1279	ASN	2.1
1	B	613	ALA	2.1
1	A	354	ALA	2.0
1	B	231	ALA	2.0
1	A	234	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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, 95th 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(\AA^2)	Q<0.9
4	NH4	B	2002	1/1	0.83	0.12	39,39,39,39	0
5	BTB	B	2003	14/14	0.92	0.09	36,42,47,53	0

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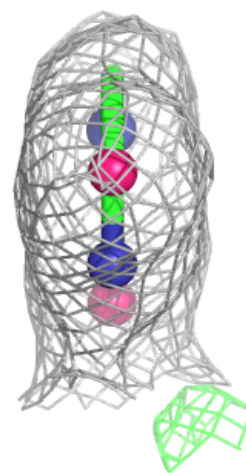
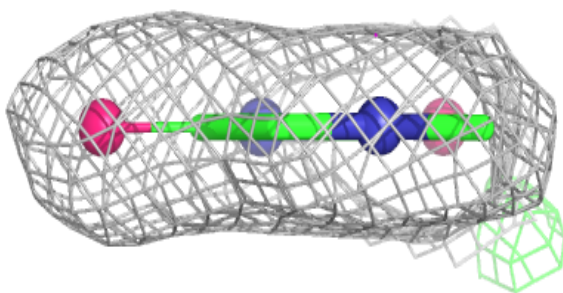
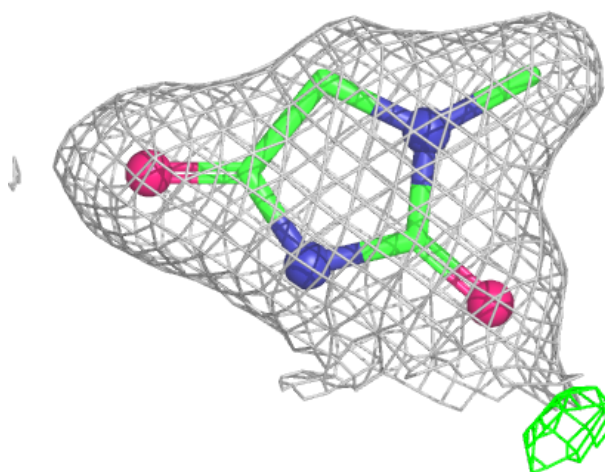
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NH4	A	2002	1/1	0.94	0.08	36,36,36,36	0
3	A1BC1	B	2001	8/8	0.98	0.05	23,26,28,28	0
3	A1BC1	A	2001	8/8	0.98	0.05	22,25,27,27	0
2	CA	B	2000	1/1	0.99	0.05	26,26,26,26	0
2	CA	A	2000	1/1	0.99	0.02	25,25,25,25	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.

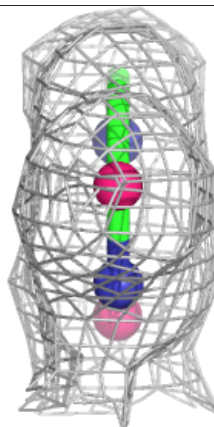
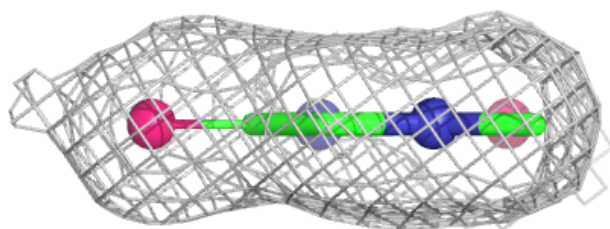
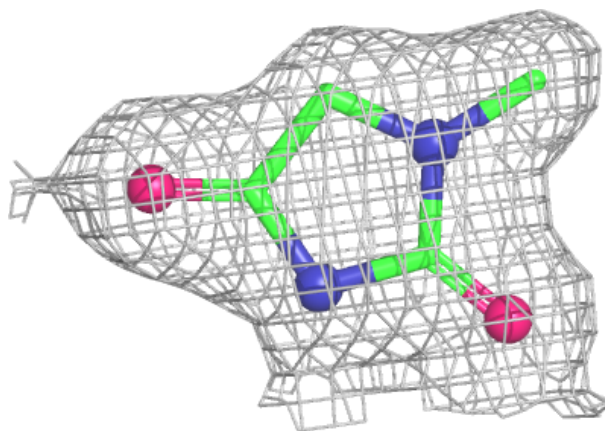
Electron density around A1BC1 B 2001:

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 A1BC1 A 2001:

$2mF_o - DF_c$ (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.