wwPDB X-ray Structure Validation Summary Report (i)

Dec 2, 2023 – 06:25 pm GMT

PDB ID	:	1OI9
Title	:	Structure of human Thr160-phospho CDK2/cyclin A complexed with a 6-cyc lohexylmethyloxy-2-anilino-purine inhibitor
Authors	:	Pratt, D.J.; Endicott, J.A.; Noble, M.E.M.
Deposited on	:	2003-06-10
Resolution	:	2.10 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

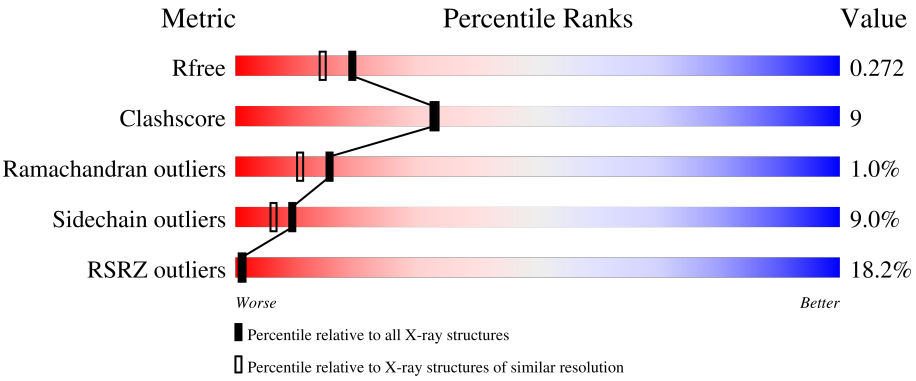
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 (#Entries)	Similar resolution (#Entries, resolution range(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	302	5% 72% 22%
1	C	302	30% 66% 25% 7%
2	B	260	7% 83% 13%
2	D	260	29% 74% 21%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9318 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.

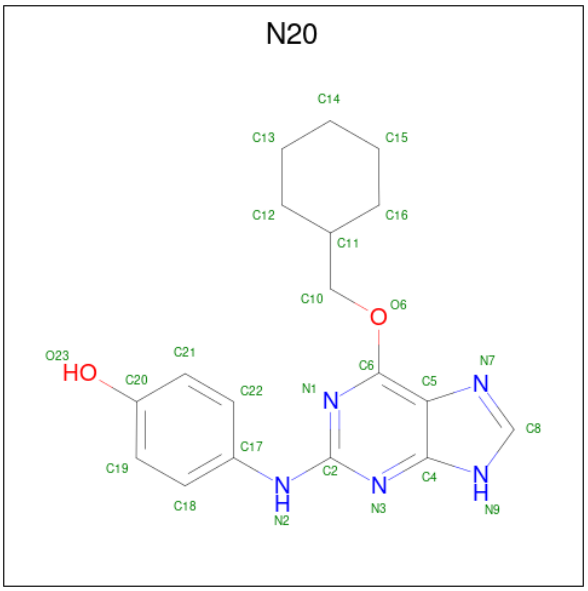
- Molecule 1 is a protein called CELL DIVISION PROTEIN KINASE 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	P	S	0	3	0
			2388	1549	404	426	1	8			
1	C	297	Total	C	N	O	P	S	0	1	0
			2392	1552	405	426	1	8			

- Molecule 2 is a protein called CYCLIN A2.

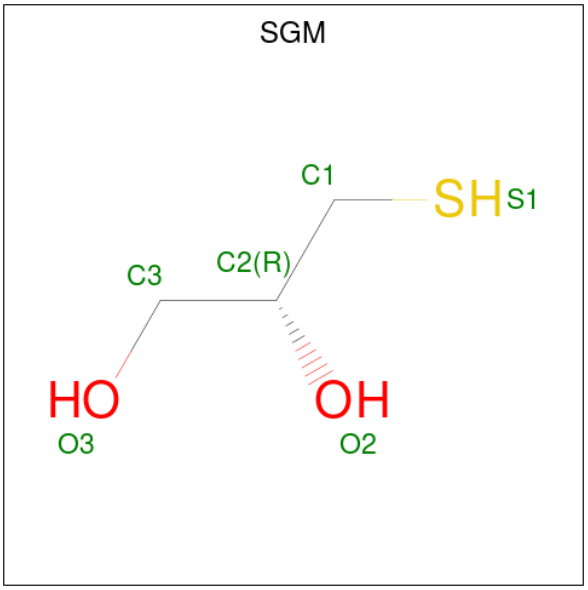
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	258	Total	C	N	O	S	0	2	0
			2089	1354	339	383	13			
2	D	253	Total	C	N	O	S	0	0	0
			2045	1326	333	375	11			

- Molecule 3 is 6-CYCLOHEXYLMETHYLOXY-2-(4'-HYDROXYANILINO)PURINE (three-letter code: N20) (formula: $C_{18}H_{21}N_5O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 25 18 5 2	0	0
3	C	1	Total C N O 25 18 5 2	0	0

- Molecule 4 is MONOTHIOGLYCEROL (three-letter code: SGM) (formula: $C_3H_8O_2S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O S 6 3 2 1	0	0
4	D	1	Total C O S 6 3 2 1	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Mg 1 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	144	Total O 144 144	0	0
6	B	132	Total O 132 132	0	0

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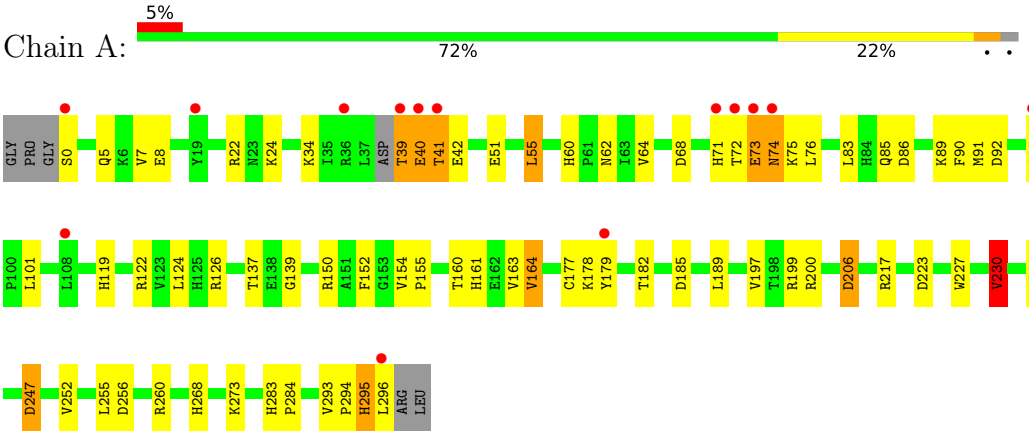
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	41	Total O 41 41	0	0
6	D	24	Total O 24 24	0	0

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.

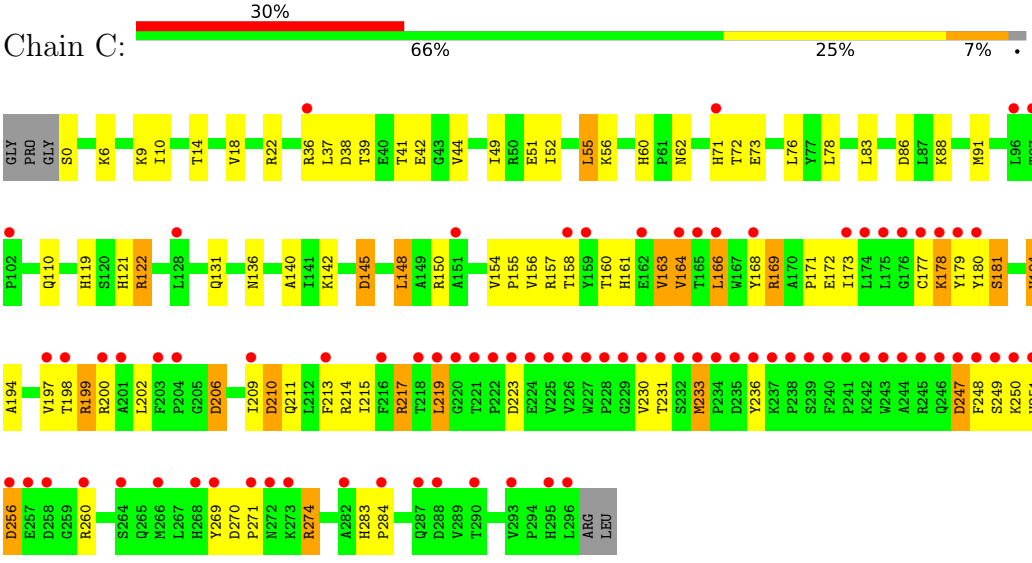
• Molecule 1: CELL DIVISION PROTEIN KINASE 2

Chain A:



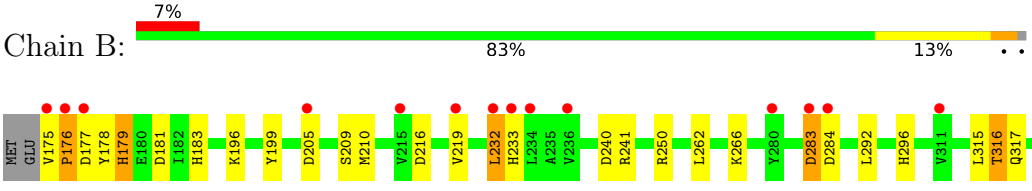
• Molecule 1: CELL DIVISION PROTEIN KINASE 2

Chain C:



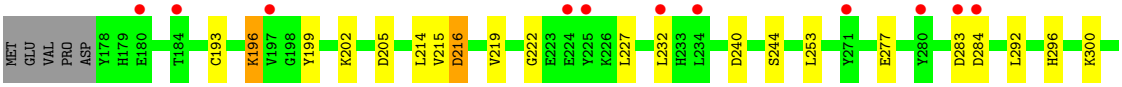
• Molecule 2: CYCLIN A2

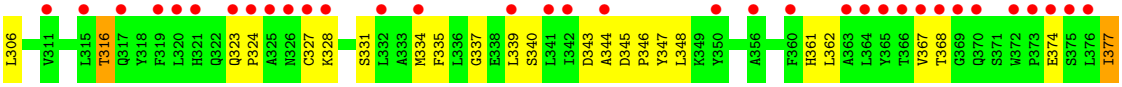
Chain B:

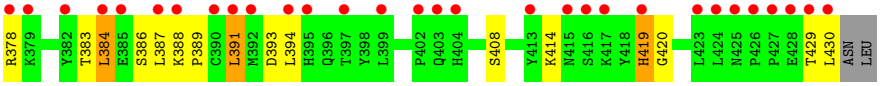


• Molecule 2: CYCLIN A2

Chain D:







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	74.12Å 134.73Å 148.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.10 35.95 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.7 (100.00-2.10) 98.6 (35.95-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.60 (at 2.10Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.233 , 0.276 0.232 , 0.272	Depositor DCC
R_{free} test set	4305 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	29.0	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 53.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	9318	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: N20, TPO, SGM, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.64	0/2451	0.84	10/3324 (0.3%)
1	C	0.50	0/2446	0.75	7/3319 (0.2%)
2	B	0.64	0/2147	0.77	10/2915 (0.3%)
2	D	0.48	0/2094	0.72	6/2842 (0.2%)
All	All	0.57	0/9138	0.77	33/12400 (0.3%)

There are no bond length outliers.

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	230	VAL	CB-CA-C	-6.99	98.12	111.40
1	C	210	ASP	CB-CG-OD2	6.78	124.40	118.30
1	A	247	ASP	CB-CG-OD2	6.76	124.38	118.30
1	A	86	ASP	CB-CG-OD2	6.47	124.12	118.30
1	C	86	ASP	CB-CG-OD2	6.37	124.03	118.30

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	2388	0	2428	45	1
1	C	2392	0	2432	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2089	0	2112	31	1
2	D	2045	0	2070	35	0
3	A	25	0	20	3	0
3	C	25	0	20	2	0
4	B	6	0	7	0	0
4	D	6	0	8	1	0
5	B	1	0	0	0	0
6	A	144	0	0	6	0
6	B	132	0	0	8	0
6	C	41	0	0	4	0
6	D	24	0	0	0	0
All	All	9318	0	9097	158	1

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 9.

The worst 5 of 158 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)
2:B:210:MET:HE3	2:B:250:ARG:HB2	1.45	0.95
2:B:210:MET:CE	2:B:250:ARG:HB2	2.07	0.84
1:A:60:HIS:HD2	1:A:62:ASN:H	1.26	0.84
1:A:227:TRP:O	1:A:230:VAL:HG22	1.84	0.77
1:C:39:THR:HG21	6:C:2023:HOH:O	1.85	0.77

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:ARG:NH2	2:B:374:GLU:OE2[4_456]	2.07	0.13

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	294/302 (97%)	283 (96%)	9 (3%)	2 (1%)	22 18
1	C	295/302 (98%)	270 (92%)	19 (6%)	6 (2%)	7 3
2	B	258/260 (99%)	254 (98%)	3 (1%)	1 (0%)	34 32
2	D	251/260 (96%)	236 (94%)	13 (5%)	2 (1%)	19 15
All	All	1098/1124 (98%)	1043 (95%)	44 (4%)	11 (1%)	15 11

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	176	PRO
1	C	164	VAL
1	C	166	LEU
1	C	178	LYS
1	A	40	GLU

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	263/264 (100%)	239 (91%)	24 (9%)	9 6
1	C	262/264 (99%)	230 (88%)	32 (12%)	5 2
2	B	234/234 (100%)	220 (94%)	14 (6%)	19 16
2	D	227/234 (97%)	209 (92%)	18 (8%)	12 9
All	All	986/996 (99%)	898 (91%)	88 (9%)	9 6

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	197	VAL
2	D	232	LEU
1	C	206	ASP
1	C	247	ASP

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Mol	Chain	Res	Type
2	D	300	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	161	HIS
2	D	361	HIS
2	B	233	HIS
2	B	296	HIS
2	B	317	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	TPO	C	160	1	8,10,11	1.22	1 (12%)	10,14,16	0.78	0
1	TPO	A	160	1	8,10,11	1.39	1 (12%)	10,14,16	0.92	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
1	TPO	C	160	1	-	0/9/11/13	-
1	TPO	A	160	1	-	0/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	160	TPO	P-O1P	3.30	1.61	1.50
1	C	160	TPO	P-O1P	2.54	1.58	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	N20	C	1298	-	25,28,28	0.87	1 (4%)	29,38,38	1.78	5 (17%)
3	N20	A	1298	-	25,28,28	1.15	4 (16%)	29,38,38	1.59	6 (20%)
4	SGM	D	1193	-	5,5,5	0.31	0	5,5,5	0.60	0
4	SGM	B	1193	-	5,5,5	0.67	0	5,5,5	0.47	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
3	N20	C	1298	-	-	0/9/17/17	0/4/4/4
3	N20	A	1298	-	-	0/9/17/17	0/4/4/4
4	SGM	D	1193	-	-	3/4/4/4	-
4	SGM	B	1193	-	-	1/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1298	N20	O6-C6	2.74	1.37	1.35
3	A	1298	N20	C4-N9	2.71	1.39	1.34
3	A	1298	N20	C17-N2	-2.17	1.35	1.40
3	A	1298	N20	C6-N1	2.14	1.35	1.31
3	C	1298	N20	C6-N1	2.08	1.35	1.31

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	1298	N20	C10-O6-C6	4.57	121.87	117.50
3	A	1298	N20	C2-N1-C6	4.48	123.08	115.18
3	C	1298	N20	C2-N1-C6	4.31	122.79	115.18
3	C	1298	N20	C2-N3-C4	4.18	120.03	115.28
3	A	1298	N20	C2-N3-C4	3.63	119.40	115.28

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1193	SGM	O2-C2-C3-O3
4	D	1193	SGM	C1-C2-C3-O3
4	B	1193	SGM	S1-C1-C2-O2
4	D	1193	SGM	S1-C1-C2-O2

There are no ring outliers.

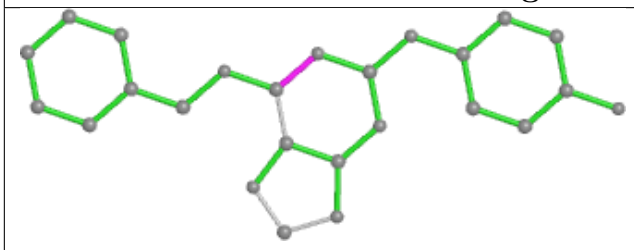
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1298	N20	2	0
3	A	1298	N20	3	0
4	D	1193	SGM	1	0

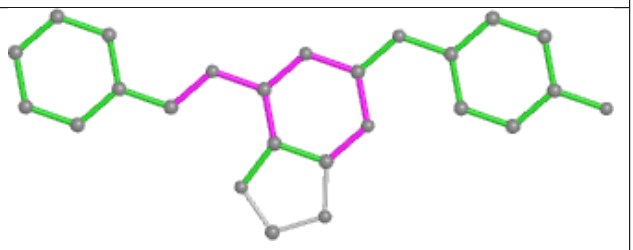
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

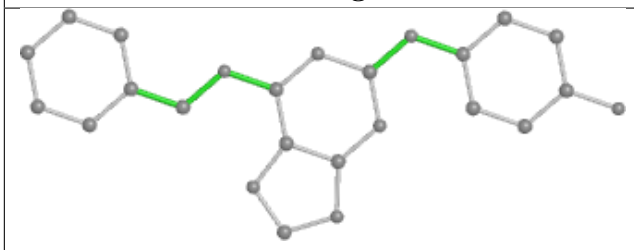
Ligand N20 C 1298



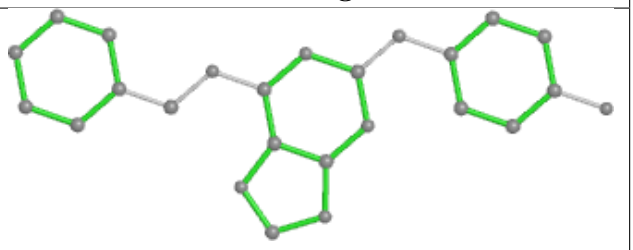
Bond lengths



Bond angles

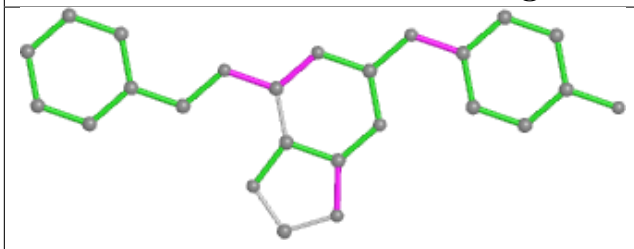


Torsions

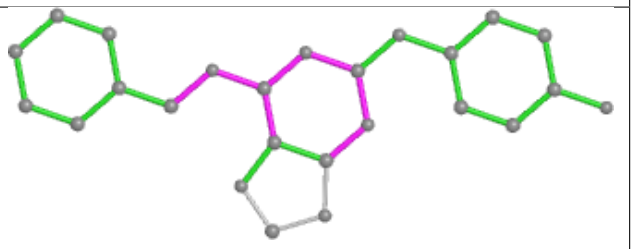


Rings

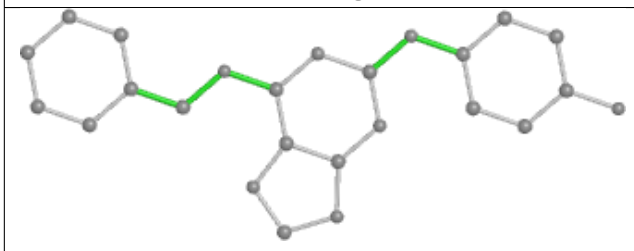
Ligand N20 A 1298



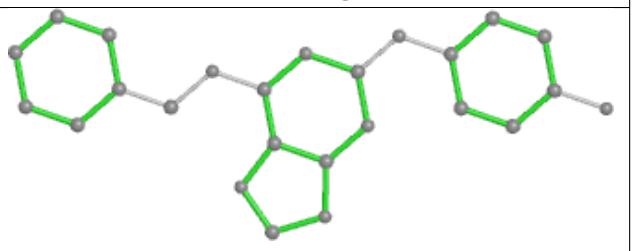
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	295/302 (97%)	0.42	16 (5%) 25 31	12, 21, 45, 62	0
1	C	296/302 (98%)	1.61	91 (30%) 0 0	23, 46, 75, 79	0
2	B	258/260 (99%)	0.43	19 (7%) 14 18	11, 23, 41, 53	0
2	D	253/260 (97%)	1.55	75 (29%) 0 0	21, 49, 70, 76	0
All	All	1102/1124 (98%)	1.00	201 (18%) 1 1	11, 33, 69, 79	0

The worst 5 of 201 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	234	PRO	8.9
1	C	173	ILE	7.4
2	B	175	VAL	7.3
1	C	243	TRP	7.1
1	C	253	PRO	7.1

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

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
1	TPO	C	160	11/12	0.92	0.15	39,48,51,52	0
1	TPO	A	160	11/12	0.99	0.11	14,18,19,20	0

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

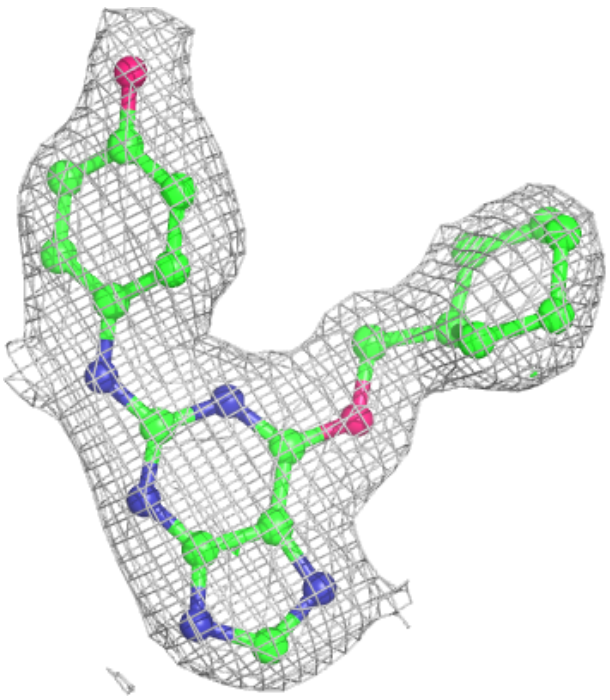
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

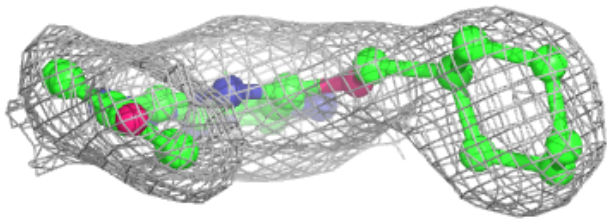
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	SGM	D	1193	6/6	0.85	0.17	51,54,55,55	0
4	SGM	B	1193	6/6	0.91	0.17	34,38,41,47	0
3	N20	C	1298	25/25	0.94	0.14	29,35,38,42	0
3	N20	A	1298	25/25	0.96	0.12	24,26,29,30	0
5	MG	B	1433	1/1	0.99	0.09	35,35,35,35	0

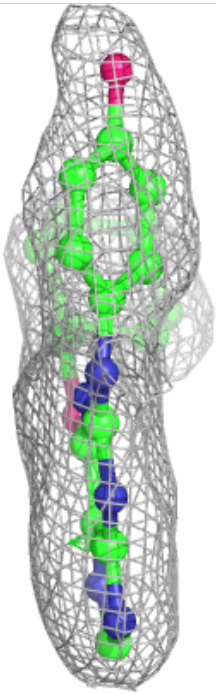
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around N20 C 1298:

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

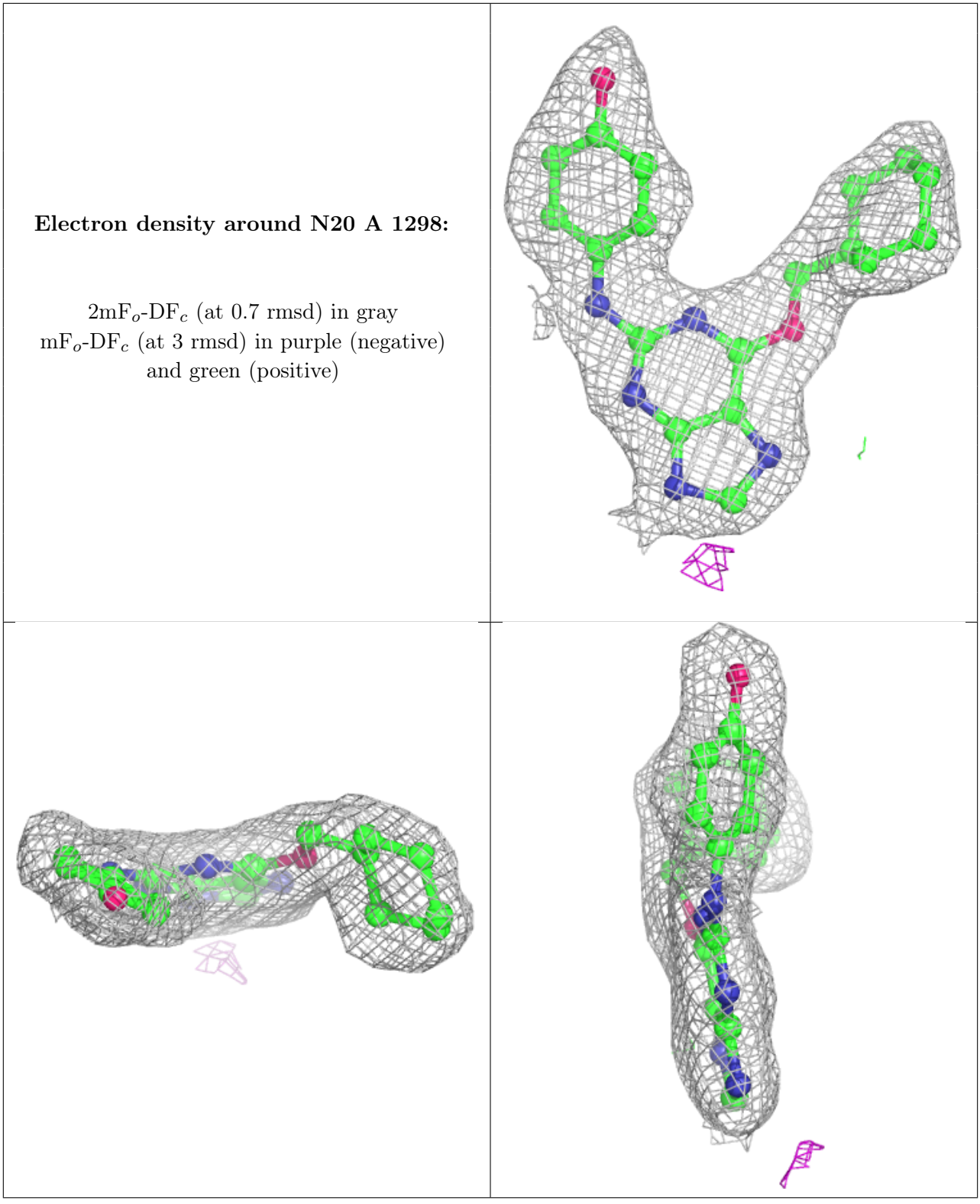






Electron density around N20 A 1298:

$2mF_o$-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.