



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 01:55 PM UTC

PDB ID : 9NLG / pdb_00009nlg
Title : CBASS Pseudomonas syringae Cap5 tetramer with 3'2'-c-GAMP cyclic dinucleotide ligand (His56Ala mutant without Mg²⁺ ions)
Authors : Rechkoblit, O.; Aggarwal, A.K.
Deposited on : 2025-03-03
Resolution : 1.64 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

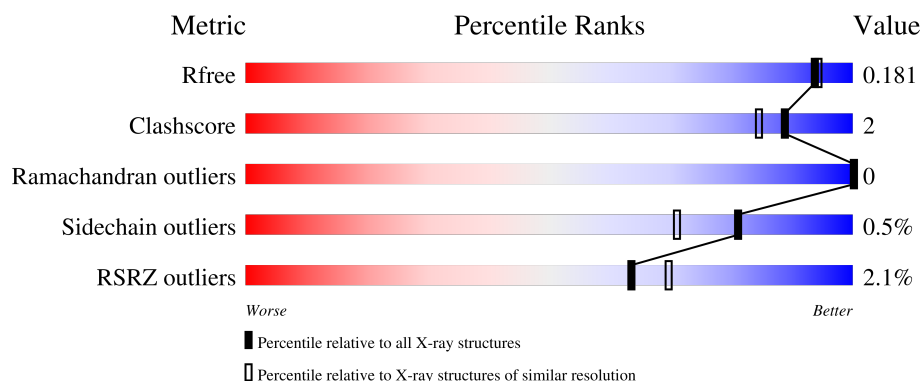
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.64 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	1141 (1.64-1.64)
Clashscore	190562	1171 (1.64-1.64)
Ramachandran outliers	187476	1151 (1.64-1.64)
Sidechain outliers	187428	1150 (1.64-1.64)
RSRZ outliers	180081	1141 (1.64-1.64)

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	388	3% 92% • 5%
1	B	388	% 87% 5% 7%
1	C	388	2% 91% • 5%
1	D	388	2% 87% 5% 8%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24293 atoms, of which 11257 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 HNH endonuclease.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	369	Total	C	H	N	O	S	0	1	0
			5685	1806	2816	514	539	10			
1	B	361	Total	C	H	N	O	S	0	3	0
			5588	1777	2775	498	528	10			
1	C	369	Total	C	H	N	O	S	0	2	0
			5704	1811	2825	515	543	10			
1	D	357	Total	C	H	N	O	S	0	2	0
			5532	1761	2747	494	520	10			

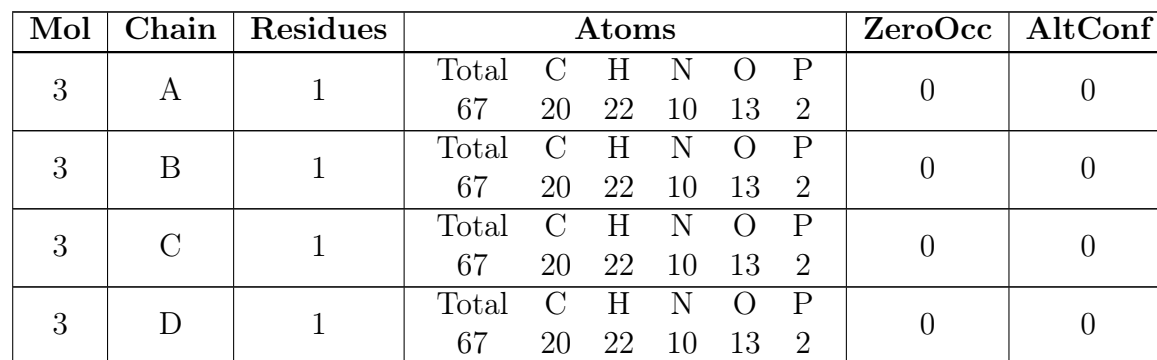
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	56	ALA	HIS	engineered mutation	UNP A0A2P0QGK5
B	56	ALA	HIS	engineered mutation	UNP A0A2P0QGK5
C	56	ALA	HIS	engineered mutation	UNP A0A2P0QGK5
D	56	ALA	HIS	engineered mutation	UNP A0A2P0QGK5

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		

- Molecule 3 is 3'2'-cGAMP (CCD ID: 4UR) (formula: C₂₀H₂₄N₁₀O₁₃P₂) (labeled as "Ligand of Interest" by depositor).



- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	0	0
			12	3	6	3		

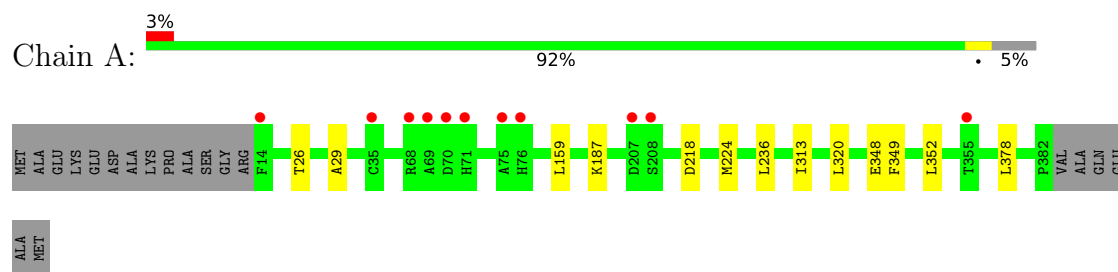
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	388	Total	O	0	0
			388	388		
5	B	391	Total	O	0	0
			391	391		
5	C	376	Total	O	0	0
			376	376		
5	D	345	Total	O	0	0
			345	345		

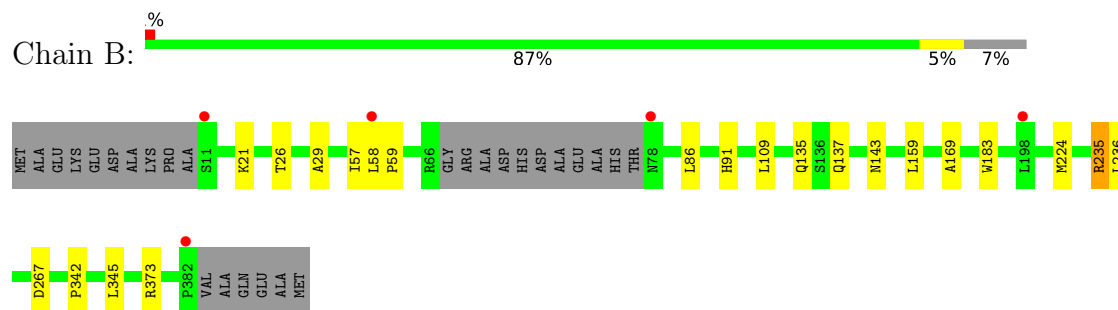
3 Residue-property plots [i](#)

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.

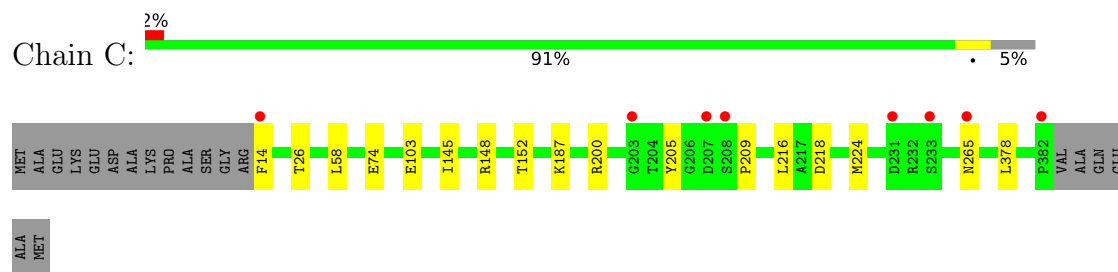
- Molecule 1: HNH endonuclease



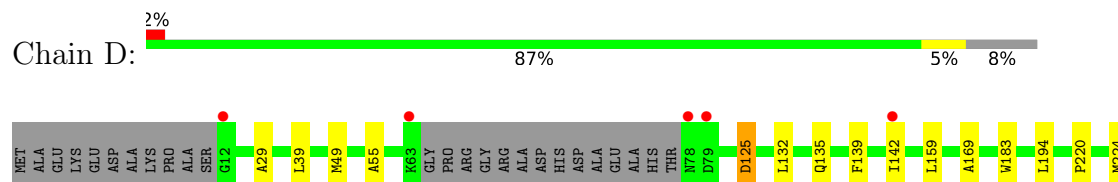
- Molecule 1: HNH endonuclease

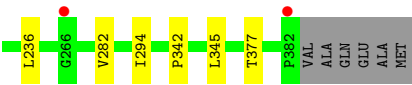


- Molecule 1: HNH endonuclease



- Molecule 1: HNH endonuclease





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	70.56Å 77.83Å 80.99Å 63.40° 80.84° 79.17°	Depositor
Resolution (Å)	45.87 – 1.64 45.87 – 1.64	Depositor EDS
% Data completeness (in resolution range)	94.6 (45.87-1.64) 94.6 (45.87-1.64)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 1.64Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.156 , 0.181 0.156 , 0.181	Depositor DCC
R_{free} test set	8587 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 38.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	24293	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: GOL, 4UR, ZN

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	0.24	0/2938	0.43	0/4003
1	B	0.22	0/2879	0.44	0/3922
1	C	0.21	0/2948	0.41	0/4016
1	D	0.21	0/2850	0.41	0/3882
All	All	0.22	0/11615	0.42	0/15823

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	B	0	2
1	C	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	235	ARG	Sidechain
1	B	373	ARG	Sidechain
1	C	200	ARG	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	A	2869	2816	2813	8	0
1	B	2813	2775	2768	15	0
1	C	2879	2825	2821	9	0
1	D	2785	2747	2745	14	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	45	22	24	0	0
3	B	45	22	24	0	0
3	C	45	22	24	0	0
3	D	45	22	24	0	0
4	B	6	6	8	0	0
5	A	388	0	0	0	0
5	B	391	0	0	1	0
5	C	376	0	0	0	0
5	D	345	0	0	1	0
All	All	13036	11257	11251	43	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 (43) 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:B:159:LEU:HD11	1:B:236[A]:LEU:HD12	1.40	1.00
1:D:159:LEU:HD11	1:D:236[A]:LEU:HD12	1.63	0.80
1:B:58:LEU:HD21	1:B:86:LEU:HD12	1.66	0.78
1:D:282:VAL:HG13	1:D:294:ILE:HD13	1.75	0.67
1:D:282:VAL:HG13	1:D:294:ILE:CD1	2.28	0.64
1:C:224:MET:HE3	1:C:378:LEU:HD13	1.79	0.64
1:A:320:LEU:HD23	1:A:352:LEU:HD12	1.83	0.61
1:D:139:PHE:CD1	1:D:142:ILE:HD11	2.42	0.55
1:B:58:LEU:HD12	1:B:59:PRO:O	2.08	0.54
1:B:159:LEU:HD11	1:B:236[B]:LEU:HD22	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:39:LEU:O	1:D:49:MET:HE1	2.08	0.53
1:B:58:LEU:HD23	1:B:91:HIS:ND1	2.24	0.52
1:A:320:LEU:HD21	1:A:349:PHE:CD2	2.45	0.52
1:B:58:LEU:HD21	1:B:86:LEU:CD1	2.39	0.51
1:B:109:LEU:C	1:B:109:LEU:HD23	2.36	0.51
1:A:224:MET:HE3	1:A:378:LEU:HD13	1.93	0.49
1:B:342:PRO:HD2	1:B:345:LEU:HD22	1.94	0.49
1:A:313:ILE:CG2	1:A:348:GLU:HG3	2.42	0.49
1:D:220:PRO:HG2	1:D:377:THR:HG21	1.93	0.49
1:D:132:LEU:HD22	1:D:194:LEU:HD21	1.95	0.49
1:A:159:LEU:HD11	1:A:236:LEU:HD13	1.94	0.48
1:C:148:ARG:O	1:C:152:THR:HG23	2.13	0.48
1:D:125:ASP:OD1	1:D:125:ASP:C	2.56	0.47
1:B:183:TRP:CE3	1:B:224:MET:HG3	2.49	0.47
1:D:39:LEU:HD13	1:D:55:ALA:HB2	1.95	0.47
1:B:21:LYS:HG2	1:B:57:ILE:HD12	1.96	0.47
1:D:183:TRP:CE3	1:D:224:MET:HG3	2.49	0.47
1:C:26:THR:O	1:D:29:ALA:HA	2.15	0.47
1:A:26:THR:O	1:B:29:ALA:HA	2.15	0.47
1:D:135:GLN:O	1:D:169:ALA:HA	2.15	0.46
1:A:187:LYS:HG2	1:A:224:MET:HE1	1.98	0.45
1:C:145:ILE:HD11	1:C:216:LEU:HB2	2.00	0.44
1:B:235:ARG:HD2	1:B:235:ARG:C	2.44	0.43
1:D:159:LEU:HD11	1:D:236[B]:LEU:HD22	2.00	0.43
1:C:14:PHE:CE1	1:C:74:GLU:HG2	2.53	0.42
1:C:187:LYS:HG2	1:C:224:MET:HE1	2.02	0.42
1:B:137:GLN:OE1	5:B:501:HOH:O	2.21	0.42
1:C:152:THR:HG21	5:D:522:HOH:O	2.19	0.42
1:C:58:LEU:HD21	1:C:103:GLU:CD	2.44	0.42
1:B:135:GLN:O	1:B:169:ALA:HA	2.20	0.41
1:C:205:TYR:HB3	1:C:209:PRO:HB3	2.03	0.41
1:A:29:ALA:HA	1:B:26:THR:O	2.21	0.41
1:D:342:PRO:HD2	1:D:345[A]:LEU:HD12	2.03	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	
1	A	368/388 (95%)	358 (97%)	10 (3%)	0	100	100
1	B	360/388 (93%)	351 (98%)	9 (2%)	0	100	100
1	C	369/388 (95%)	360 (98%)	9 (2%)	0	100	100
1	D	355/388 (92%)	345 (97%)	10 (3%)	0	100	100
All	All	1452/1552 (94%)	1414 (97%)	38 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	303/316 (96%)	302 (100%)	1 (0%)	86	79
1	B	299/316 (95%)	297 (99%)	2 (1%)	76	62
1	C	305/316 (96%)	303 (99%)	2 (1%)	76	62
1	D	295/316 (93%)	294 (100%)	1 (0%)	86	79
All	All	1202/1264 (95%)	1196 (100%)	6 (0%)	81	71

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	218	ASP
1	B	143	ASN

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Mol	Chain	Res	Type
1	B	267	ASP
1	C	218	ASP
1	C	265	ASN
1	D	125	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	HIS
1	A	137	GLN
1	A	196	GLN
1	A	227	GLN
1	A	314	HIS
1	A	358	GLN
1	B	241	HIS
1	B	376	GLN
1	D	82	ASN
1	D	143	ASN
1	D	241	HIS
1	D	244	HIS

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 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	4UR	C	402	-	51,51,51	0.39	0	76,80,80	0.60	0
3	4UR	B	402	-	51,51,51	0.39	0	76,80,80	0.62	0
3	4UR	A	402	-	51,51,51	0.39	0	76,80,80	0.55	0
4	GOL	B	403	-	5,5,5	0.92	0	5,5,5	1.03	0
3	4UR	D	402	-	51,51,51	0.38	0	76,80,80	0.55	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	4UR	C	402	-	-	3/30/62/62	0/6/7/7
3	4UR	B	402	-	-	3/30/62/62	0/6/7/7
3	4UR	A	402	-	-	3/30/62/62	0/6/7/7
4	GOL	B	403	-	-	2/4/4/4	-
3	4UR	D	402	-	-	3/30/62/62	0/6/7/7

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	4UR	C28-O27-P24-O26
3	C	402	4UR	C28-O27-P24-O26
3	D	402	4UR	C28-O27-P24-O26
4	B	403	GOL	O1-C1-C2-C3
4	B	403	GOL	O1-C1-C2-O2
3	A	402	4UR	C28-O27-P24-O25
3	B	402	4UR	C28-O27-P24-O26
3	C	402	4UR	C11-C12-O13-P14
3	A	402	4UR	C11-C12-O13-P14
3	B	402	4UR	C11-C12-O13-P14

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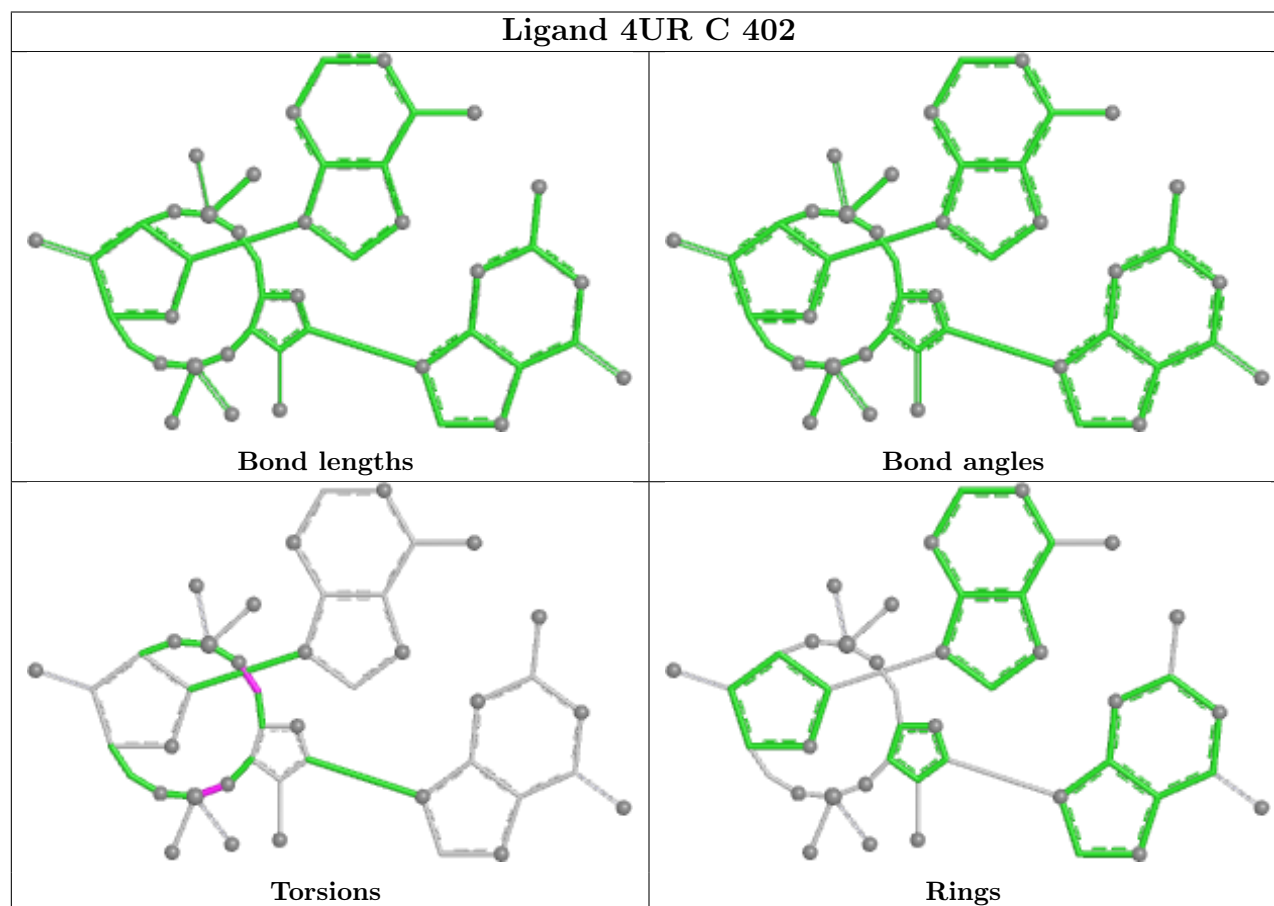
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Mol	Chain	Res	Type	Atoms
3	D	402	4UR	C11-C12-O13-P14
3	B	402	4UR	C28-O27-P24-O25
3	C	402	4UR	C28-O27-P24-O25
3	D	402	4UR	C28-O27-P24-O25

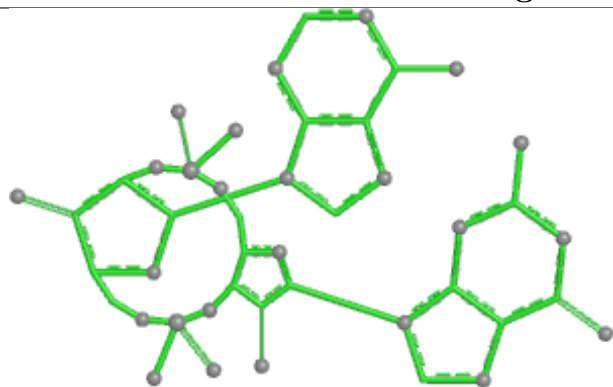
There are no ring outliers.

No monomer is involved in short contacts.

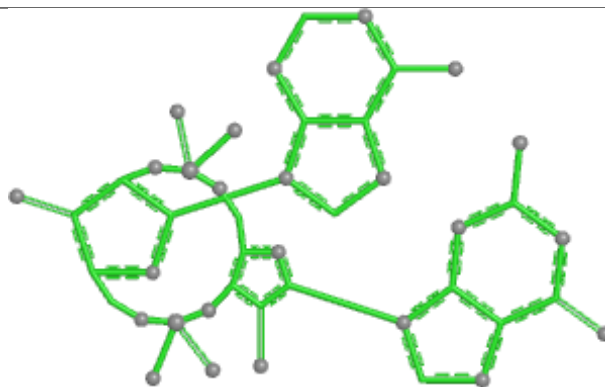
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



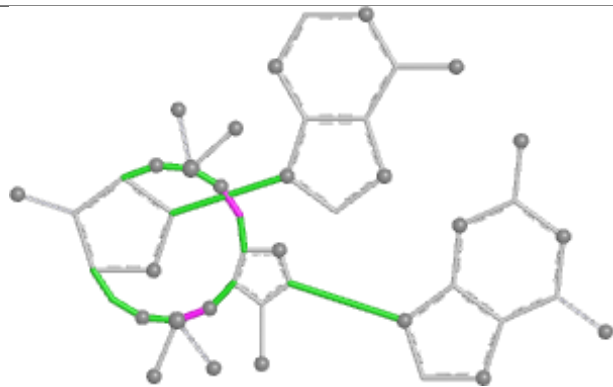
Ligand 4UR B 402



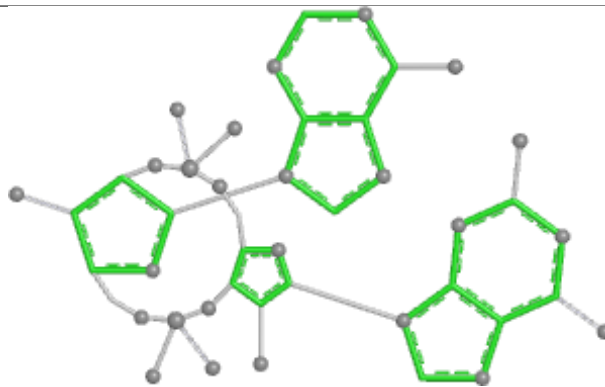
Bond lengths



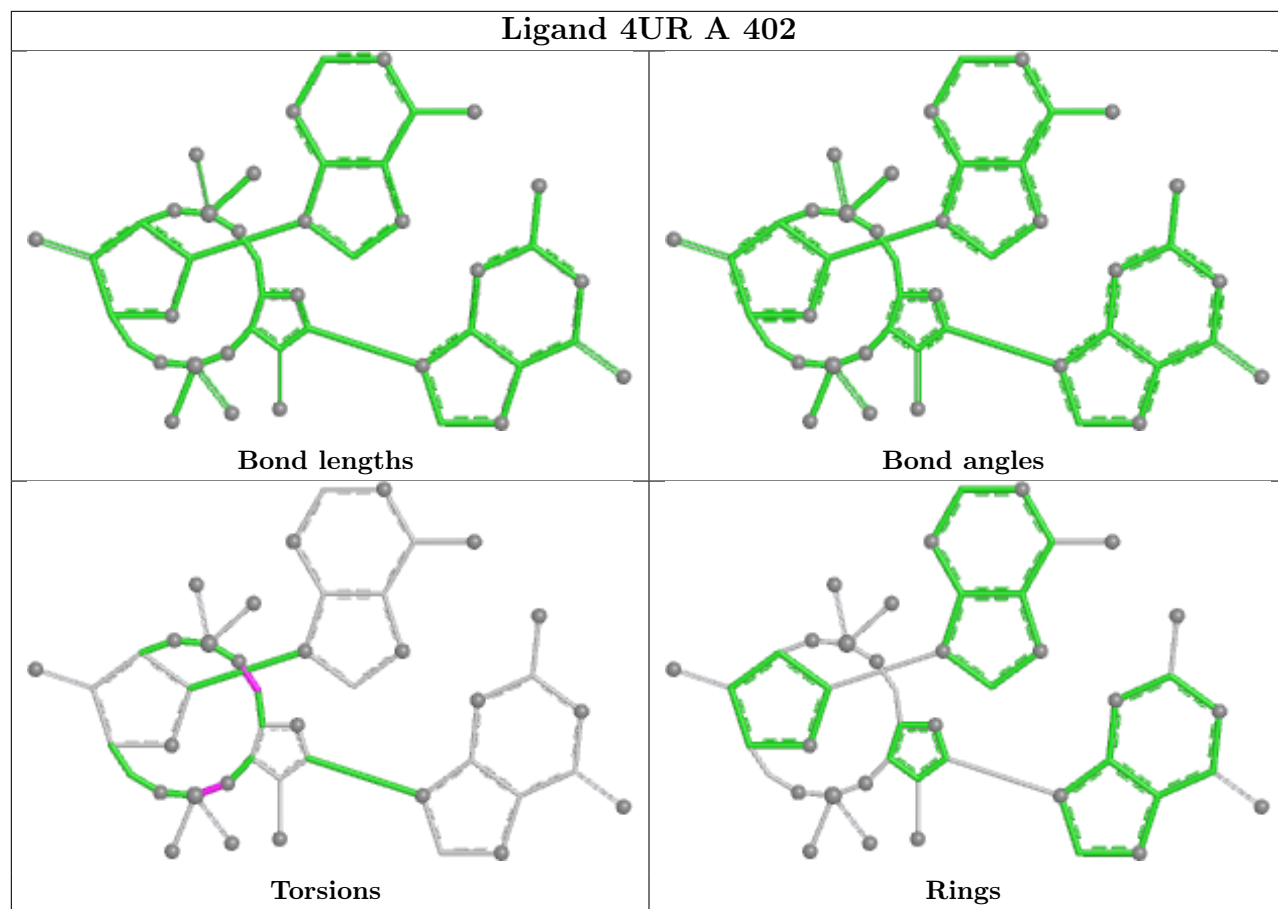
Bond angles

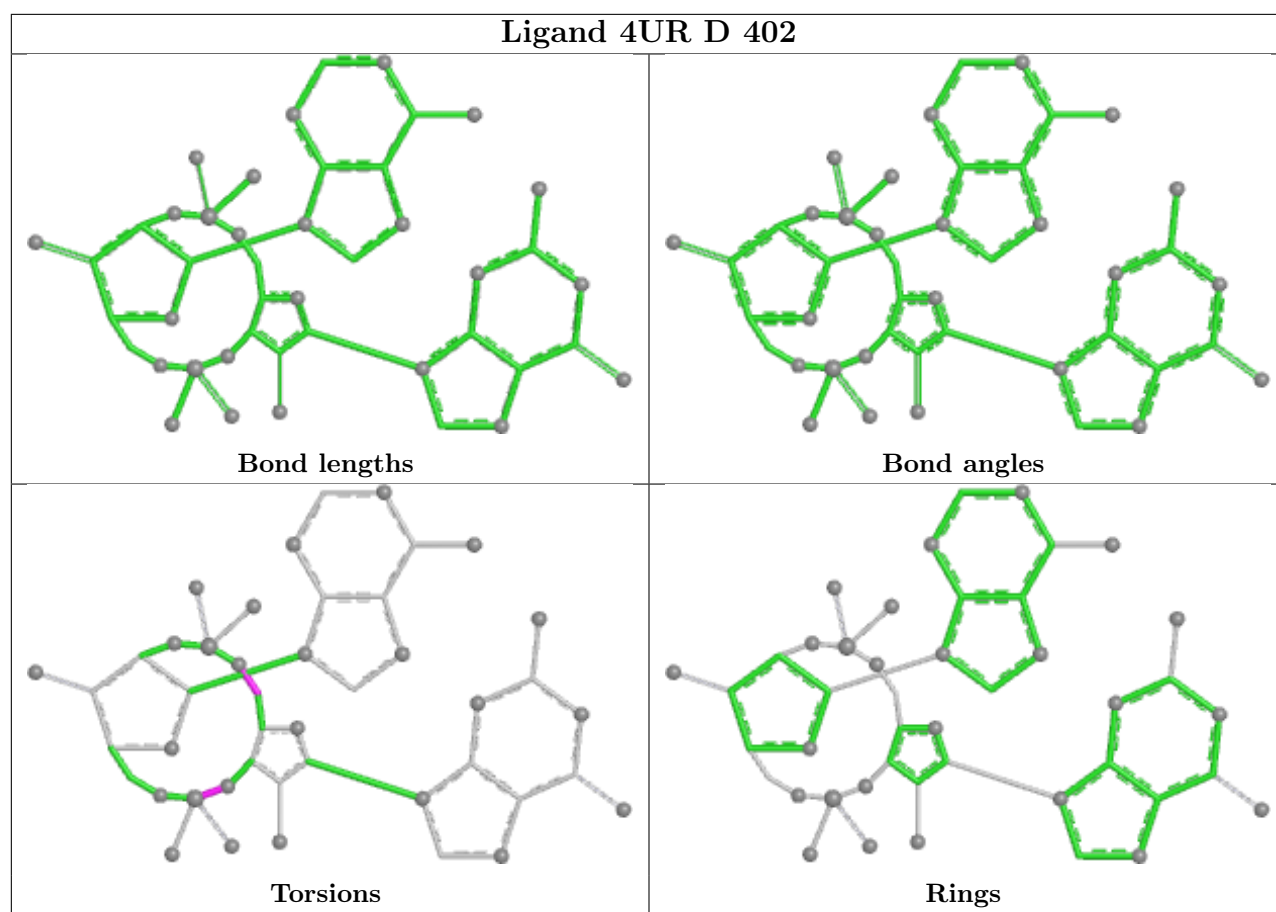


Torsions



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, 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	369/388 (95%)	-0.29	11 (2%) 52 57	11, 21, 54, 78	1 (0%)
1	B	361/388 (93%)	-0.38	5 (1%) 73 79	10, 21, 45, 67	3 (0%)
1	C	369/388 (95%)	-0.31	8 (2%) 62 68	11, 22, 49, 73	2 (0%)
1	D	357/388 (92%)	-0.11	7 (1%) 65 71	8, 24, 50, 67	2 (0%)
All	All	1456/1552 (93%)	-0.27	31 (2%) 63 70	8, 22, 50, 78	8 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	35	CYS	5.9
1	D	382	PRO	4.7
1	D	78	ASN	4.0
1	B	78	ASN	4.0
1	A	14	PHE	3.6
1	B	58	LEU	3.4
1	D	142	ILE	3.3
1	C	14	PHE	3.2
1	A	71	HIS	2.9
1	A	207	ASP	2.8
1	A	75	ALA	2.8
1	A	208	SER	2.8
1	A	68	ARG	2.7
1	A	70	ASP	2.7
1	D	79	ASP	2.6
1	C	382	PRO	2.6
1	D	266	GLY	2.5
1	A	69	ALA	2.5
1	B	382	PRO	2.5
1	B	198	LEU	2.4
1	C	207	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	203	GLY	2.3
1	C	231	ASP	2.3
1	C	233	SER	2.3
1	A	76	HIS	2.2
1	D	63	LYS	2.2
1	D	12	GLY	2.1
1	C	265	ASN	2.1
1	B	11	SER	2.1
1	A	355	THR	2.0
1	C	208	SER	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

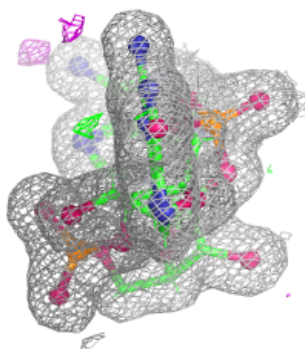
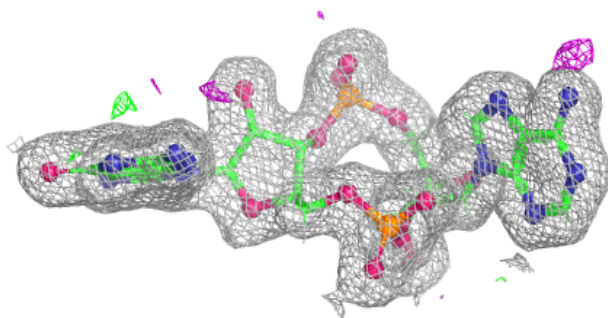
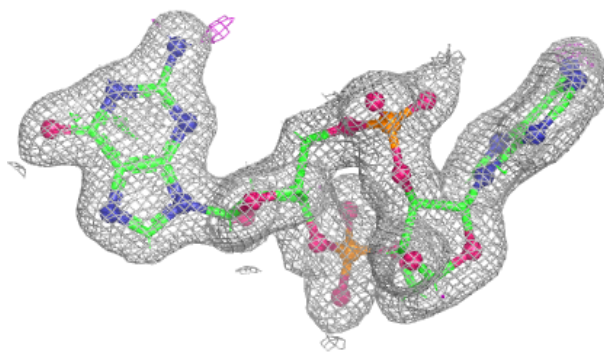
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	B	403	6/6	0.89	0.10	29,38,43,44	0
3	4UR	D	402	45/45	0.98	0.04	13,19,25,25	0
3	4UR	A	402	45/45	0.99	0.03	9,11,14,15	0
3	4UR	B	402	45/45	0.99	0.04	9,15,20,23	0
3	4UR	C	402	45/45	0.99	0.03	9,12,16,17	0
2	ZN	B	401	1/1	0.99	0.02	22,22,22,22	0
2	ZN	D	401	1/1	0.99	0.03	26,26,26,26	0
2	ZN	A	401	1/1	1.00	0.01	14,14,14,14	0
2	ZN	C	401	1/1	1.00	0.01	15,15,15,15	0

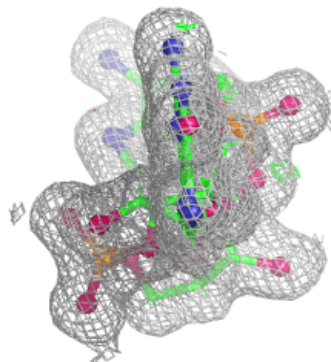
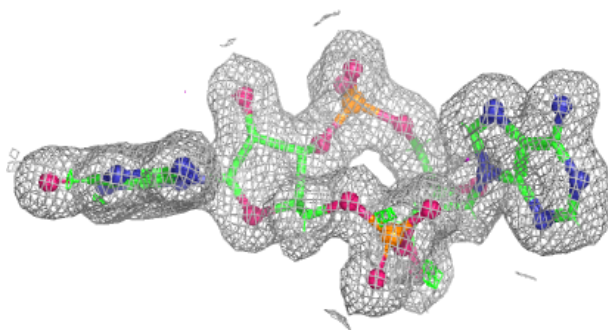
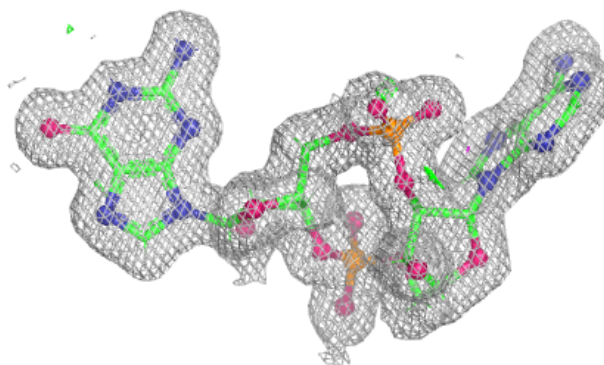
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 4UR D 402:

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

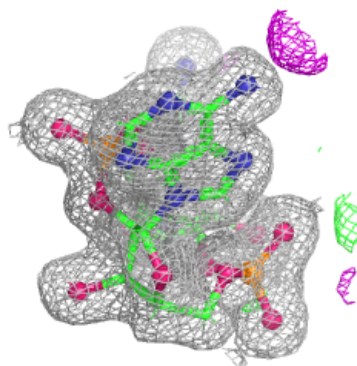
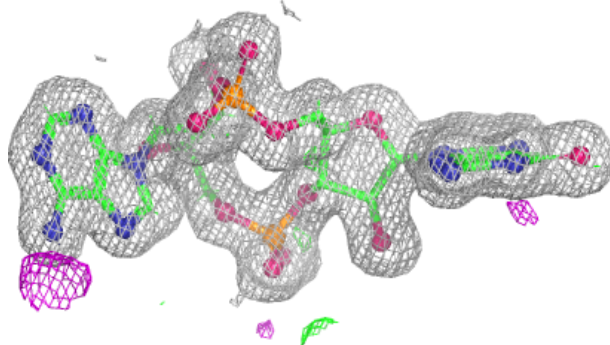
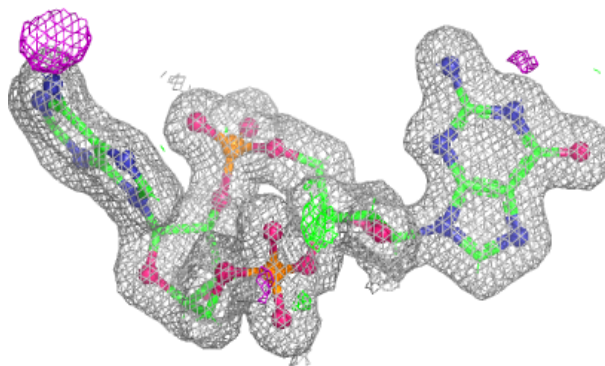
**Electron density around 4UR A 402:**

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

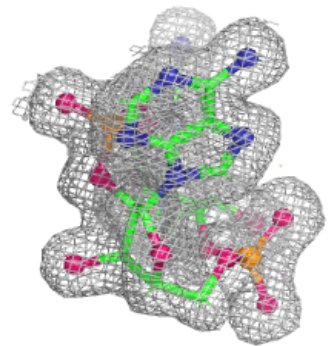
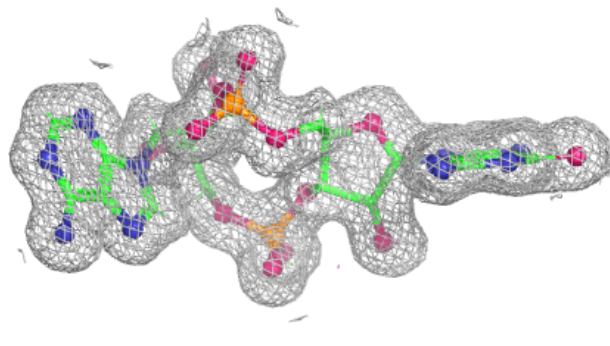
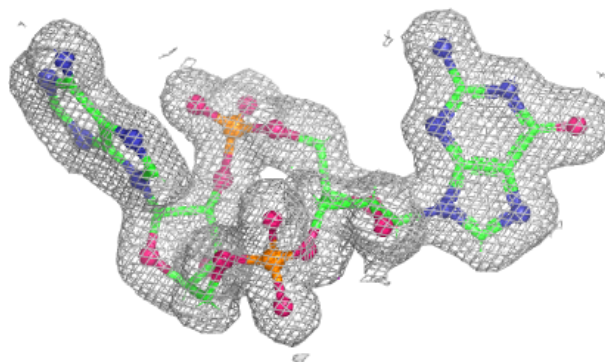


Electron density around 4UR B 402:

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

**Electron density around 4UR C 402:**

$2mF_o-DF_c$ (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.