



# wwPDB X-ray Structure Validation Summary Report

Mar 8, 2026 – 05:04 PM UTC

PDB ID : 6TKA / pdb\_00006tka  
Title : Crystal structure of human O-GlcNAc transferase bound to substrate 7 and a peptide from HCF-1 pro-repeat 2 (11-26)  
Authors : Meek, R.W.; Davies, G.J.  
Deposited on : 2019-11-28  
Resolution : 1.91 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](mailto: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>.

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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)  
Xtrriage (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

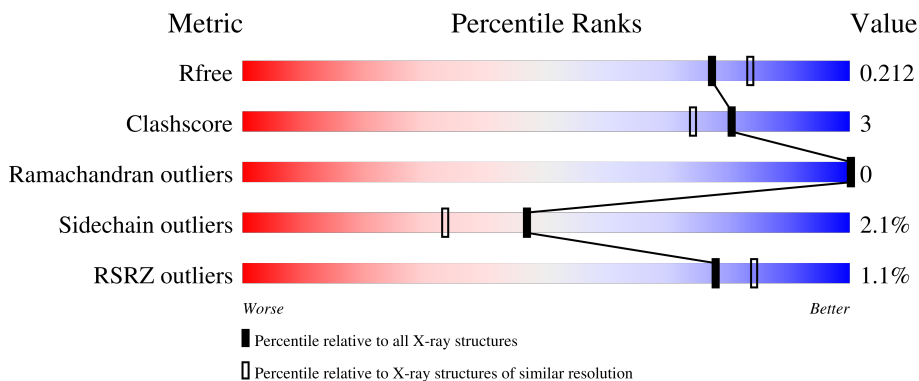
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.91 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	1188 (1.92-1.92)
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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  $\geq 3$ , 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	AAA	727	 0% (upper bar), 87% (green), 8% (yellow), 5% (grey)
2	BBB	16	 6% (upper bar), 62% (green), 19% (yellow), 19% (grey)

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11553 atoms, of which 5664 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 UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	AAA	694	11052	3507	5529	963	1016	37	315	8	0

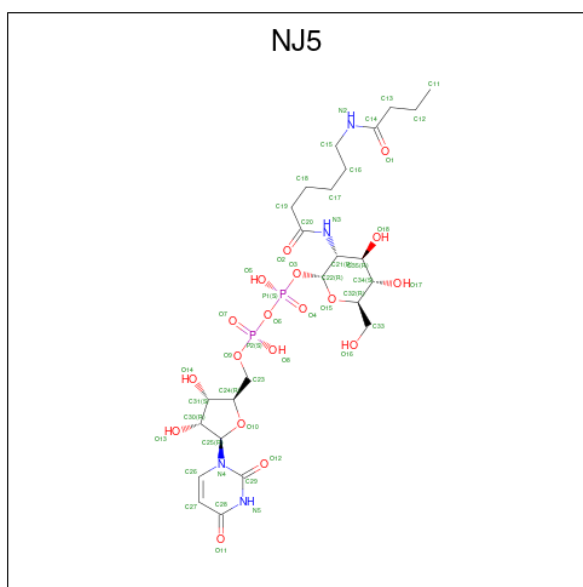
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	310	GLY	-	expression tag	UNP O15294
AAA	311	PRO	-	expression tag	UNP O15294
AAA	312	ALA	-	expression tag	UNP O15294

- Molecule 2 is a protein called HCF-1 pro-repeat 2 (11-26).

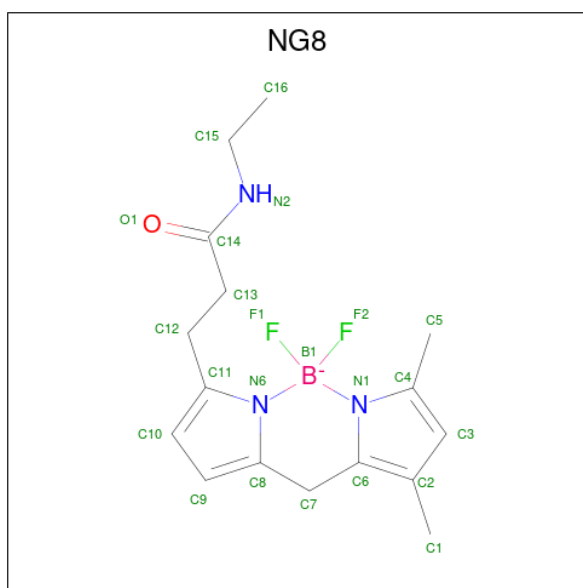
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	BBB	13	165	48	79	14	24	10	0	0

- Molecule 3 is  $[(2 \{R\}, 3 \{S\}, 4 \{R\}, 5 \{R\})-5-[2,4\text{-bis(oxidanylidene)pyrimidin-1-yl}]-3,4\text{-bis(oxidanyl)oxolan-2-yl}]$  methoxy-oxidanyl-phosphoryl  $[(2 \{R\}, 3 \{R\}, 4 \{R\}, 5 \{S\}, 6 \{R\})-3-[6\text{-}(butanoylamino)hexanoylamino]-6\text{-}(hydroxymethyl)-4,5\text{-bis(oxidanyl)oxan-2-yl}]$  hydrogen phosphate (CCD ID: NJ5) (formula:  $C_{25}H_{42}N_4O_{18}P_2$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			P
3	AAA	1	86	25	37	4	18	2	5	0

- Molecule 4 is 3-[2,2-bis(fluoranyl)-10,12-dimethyl-1,3-diaza-2<sup>4</sup>]-boratricyclo[7.3.0.0<sup>3,7</sup>]dodeca-4,6,9,11-tetraen-4-yl]- {N}-ethyl-propanamide (CCD ID: NG8) (formula: C<sub>16</sub>H<sub>21</sub>BF<sub>2</sub>N<sub>3</sub>O).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	B	C	F	H	N		
4	AAA	1	42	1	16	2	19	3	1	0

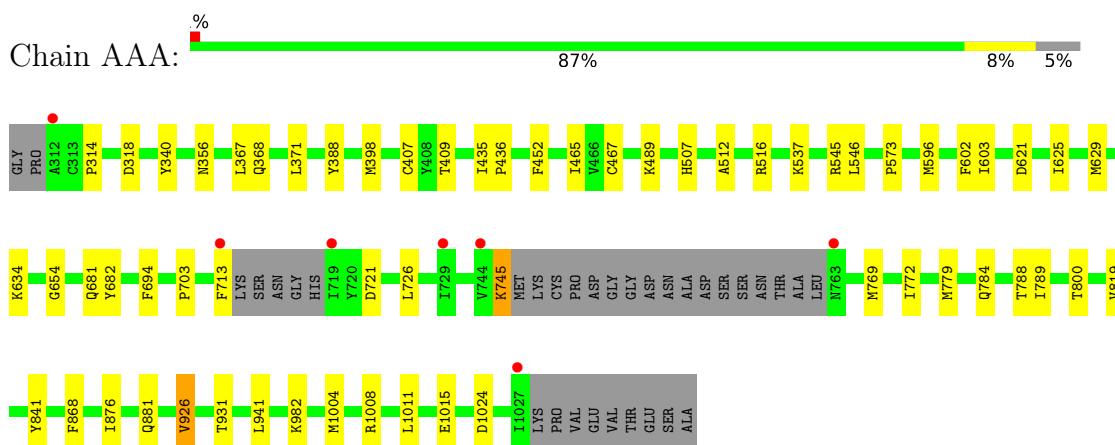
- Molecule 5 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	AAA	199	Total 199	O 199	0	0
5	BBB	9	Total 9	O 9	0	0

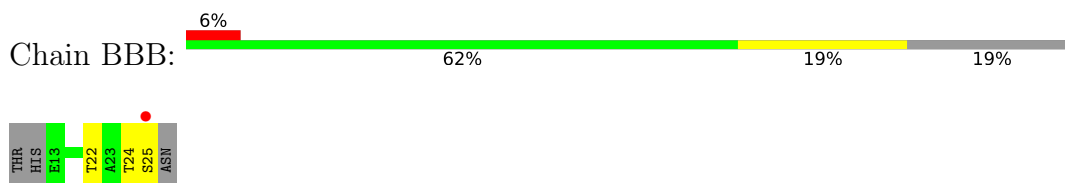
### 3 Residue-property plots [i](#)

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: UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit



- Molecule 2: HCF-1 pro-repeat 2 (11-26)



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.86Å 100.86Å 132.63Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	72.95 – 1.91 72.95 – 1.91	Depositor EDS
% Data completeness (in resolution range)	100.0 (72.95-1.91) 100.0 (72.95-1.91)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.76 (at 1.91Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.184 , 0.233 (Not available) , 0.212	Depositor DCC
$R_{free}$ test set	3089 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.0	Xtrriage
Anisotropy	0.069	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.43 , 52.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	11553	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NG8, NJ5

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	AAA	1.06	1/5668 (0.0%)	1.38	4/7690 (0.1%)
2	BBB	1.01	0/85	1.57	0/117
All	All	1.06	1/5753 (0.0%)	1.38	4/7807 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	703	PRO	C-O	-5.25	1.17	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	409	THR	CB-CA-C	6.97	122.37	110.79
1	AAA	621	ASP	CA-CB-CG	5.09	117.69	112.60
1	AAA	682	TYR	CA-C-O	-5.06	114.89	120.36
1	AAA	721	ASP	CA-CB-CG	5.05	117.66	112.60

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	AAA	5523	5529	5505	28	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	BBB	86	79	78	1	0
3	AAA	49	37	0	0	0
4	AAA	23	19	0	0	0
5	AAA	199	0	0	1	0
5	BBB	9	0	0	1	0
All	All	5889	5664	5583	29	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 3.

The worst 5 of 29 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:AAA:1004:MET:SD	1:AAA:1008:ARG:NH1	2.50	0.84
2:BBB:25:SER:O	5:BBB:101:HOH:O	2.17	0.59
1:AAA:629:MET:O	1:AAA:654:GLY:HA3	2.08	0.53
1:AAA:1011:LEU:O	1:AAA:1015:GLU:HG2	2.09	0.53
1:AAA:745:LYS:H	1:AAA:745:LYS:CD	2.22	0.52

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:AAA:788:THR:HG1	1:AAA:788:THR:HG22[6_554]	1.28	0.32

## 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	AAA	696/727 (96%)	679 (98%)	17 (2%)	0	100	100
2	BBB	11/16 (69%)	11 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	707/743 (95%)	690 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	AAA	603/621 (97%)	592 (98%)	11 (2%)	51	39
2	BBB	10/13 (77%)	8 (80%)	2 (20%)	1	0
All	All	613/634 (97%)	600 (98%)	13 (2%)	47	33

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	881	GLN
1	AAA	926	VAL
2	BBB	24	THR
1	AAA	1024	ASP
2	BBB	22	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

2 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	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NG8	AAA	1102	-	24,25,25	1.30	2 (8%)	31,38,38	1.28	2 (6%)
3	NJ5	AAA	1101	-	50,51,51	0.62	1 (2%)	70,73,73	0.94	3 (4%)

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
4	NG8	AAA	1102	-	-	2/8/24/24	0/3/3/3
3	NJ5	AAA	1101	-	-	9/38/75/75	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	AAA	1102	NG8	C8-N6	3.93	1.40	1.36
4	AAA	1102	NG8	C6-C2	2.66	1.39	1.36
3	AAA	1101	NJ5	P2-O6	-2.30	1.57	1.59

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	AAA	1102	NG8	C12-C11-N6	4.06	125.47	122.62
3	AAA	1101	NJ5	O5-P1-O6	-3.46	97.93	107.27
3	AAA	1101	NJ5	O15-C22-C21	-2.61	105.66	110.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	AAA	1102	NG8	C12-C11-C10	-2.56	125.90	130.13
3	AAA	1101	NJ5	O8-P2-O7	2.17	122.55	112.44

There are no chirality outliers.

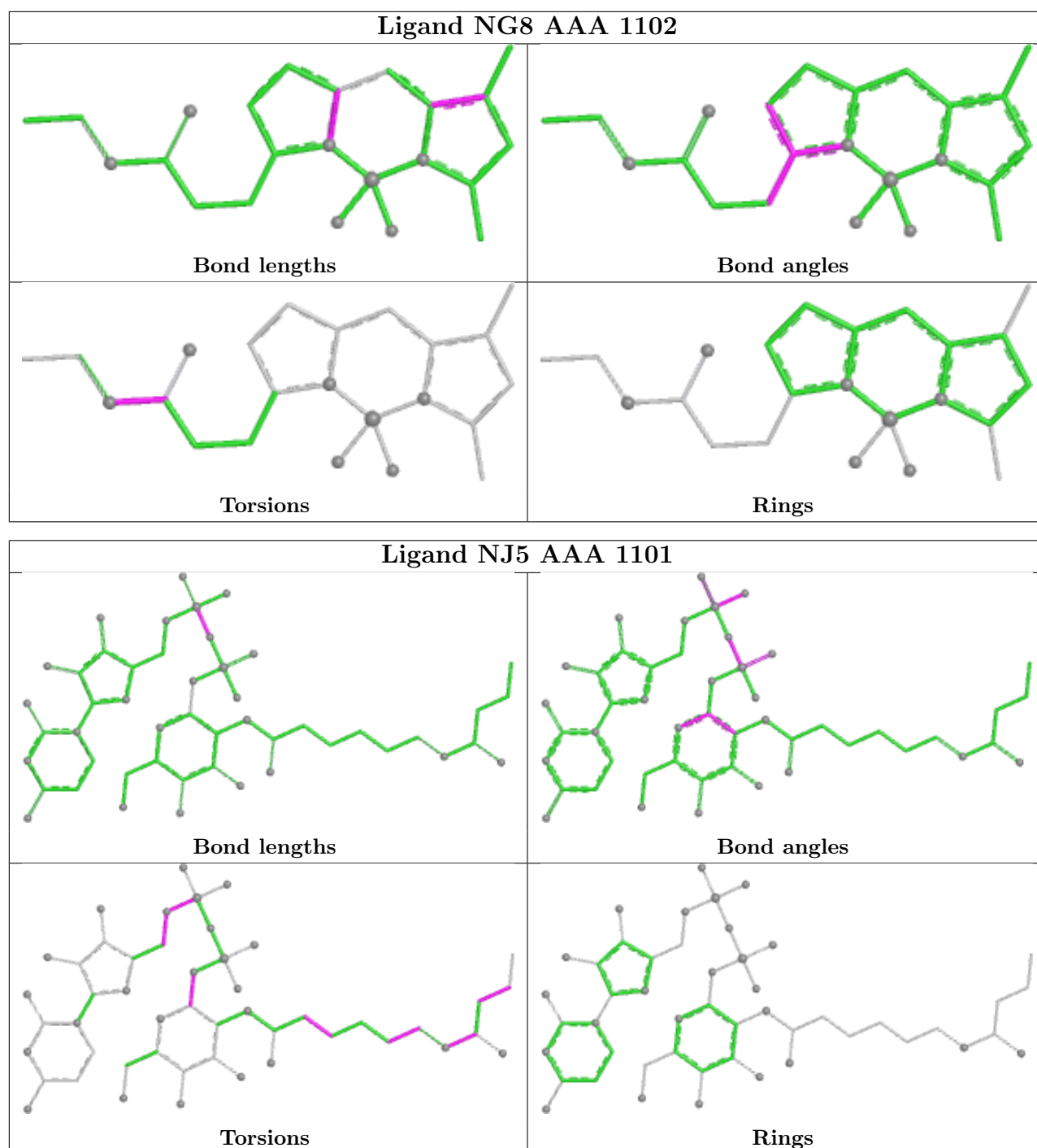
5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	AAA	1101	NJ5	O15-C22-O3-P1
3	AAA	1101	NJ5	C23-O9-P2-O6
3	AAA	1101	NJ5	C24-C23-O9-P2
3	AAA	1101	NJ5	O1-C14-N2-C15
3	AAA	1101	NJ5	C13-C14-N2-C15

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.



## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	AAA	694/727 (95%)	-0.04	7 (1%) 79 85	17, 38, 60, 89	8 (1%)
2	BBB	13/16 (81%)	0.42	1 (7%) 19 23	28, 34, 66, 80	0
All	All	707/743 (95%)	-0.03	8 (1%) 78 84	17, 38, 60, 89	8 (1%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	713	PHE	5.6
1	AAA	312	ALA	5.4
1	AAA	1027	ILE	3.7
1	AAA	744	VAL	3.1
1	AAA	719	ILE	2.8

### 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](#)

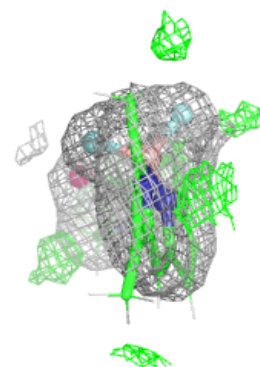
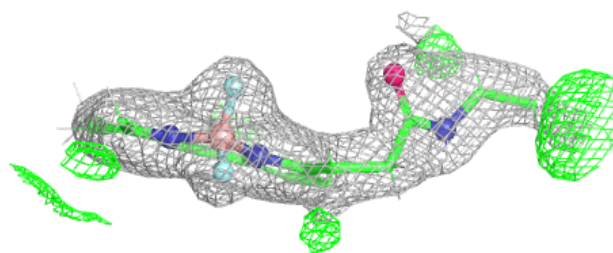
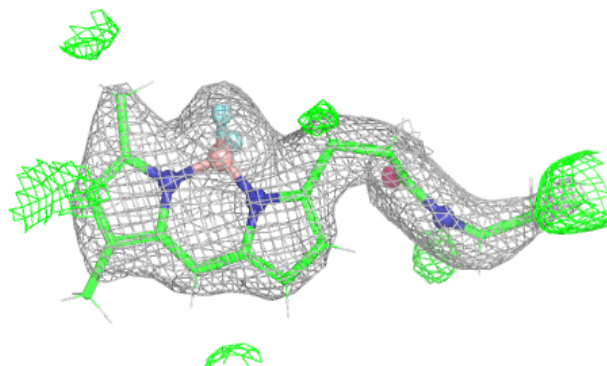
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

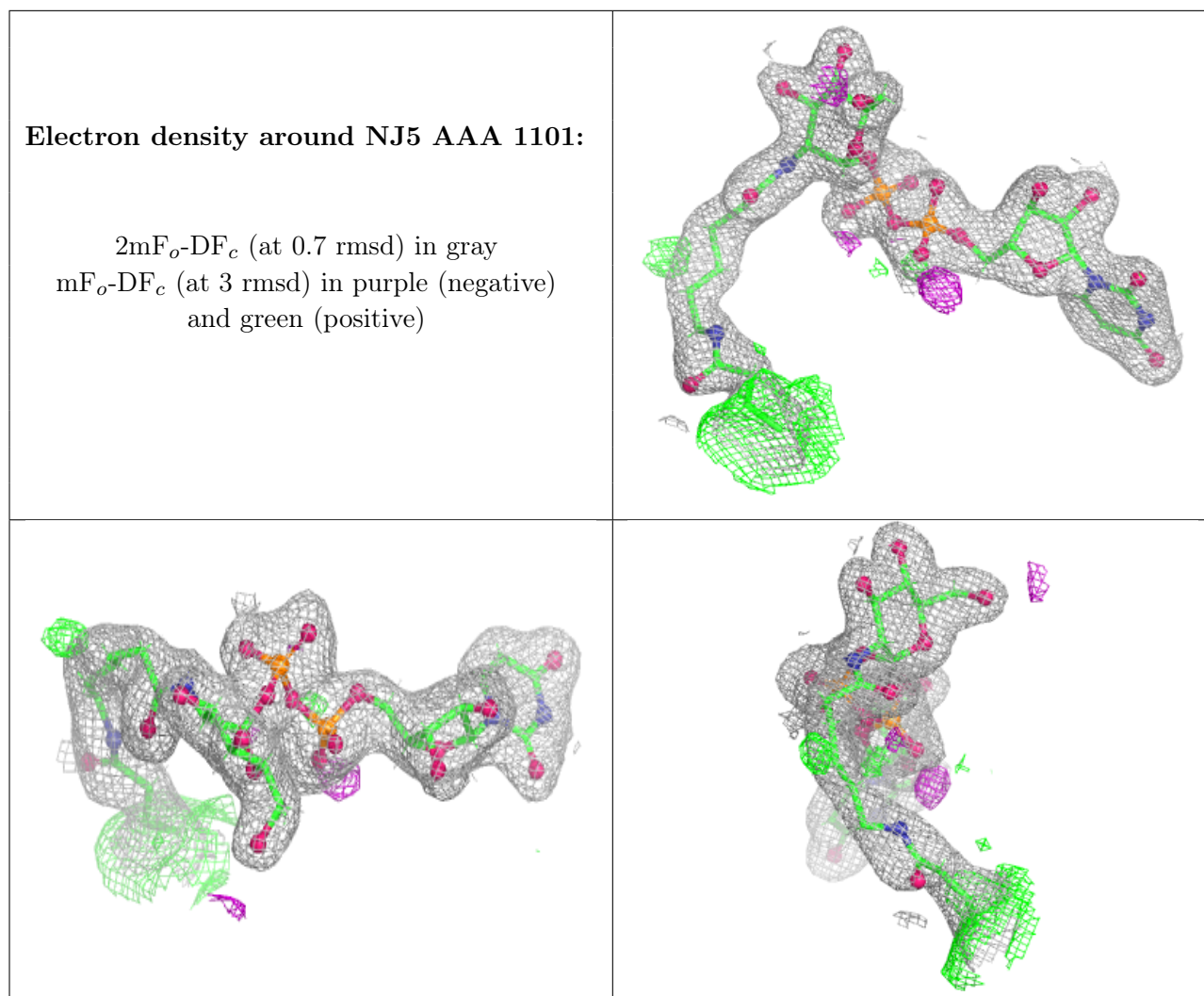
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NG8	AAA	1102	23/23	0.84	0.15	43,59,64,68	1
3	NJ5	AAA	1101	49/49	0.91	0.09	0,38,58,70	5

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 NG8 AAA 1102:**

$2mF_o-DF_c$  (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.