



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:45 PM UTC

PDB ID : 3PV7 / pdb_00003pv7
Title : Crystal structure of NKp30 ligand B7-H6
Authors : Li, Y.
Deposited on : 2010-12-06
Resolution : 2.00 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
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

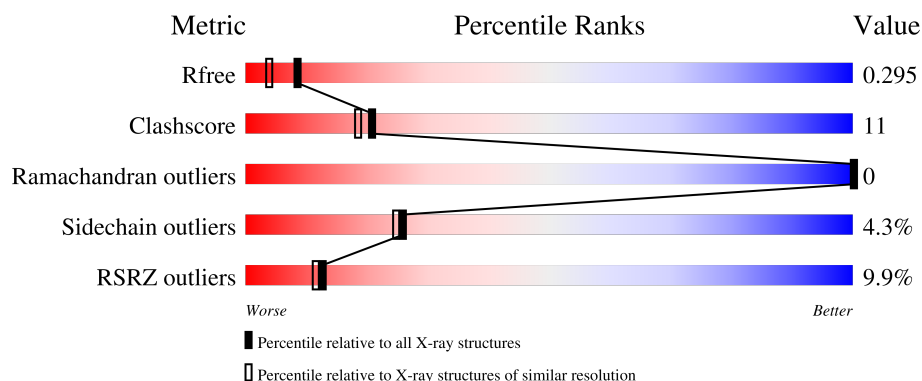
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

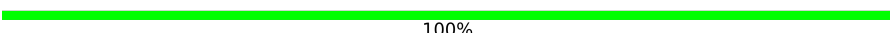
The reported resolution of this entry is 2.00 Å.

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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	248	
2	B	2	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1765 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 Ig-like domain-containing protein DKFZp686O24166/DKFZp686I21167.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	0	0
			1662	1066	273	313	10			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	ALA	-	expression tag	UNP Q68D85
A	263	ALA	-	expression tag	UNP Q68D85
A	264	ALA	-	expression tag	UNP Q68D85
A	265	ALA	-	expression tag	UNP Q68D85
A	266	HIS	-	expression tag	UNP Q68D85
A	267	HIS	-	expression tag	UNP Q68D85
A	268	HIS	-	expression tag	UNP Q68D85
A	269	HIS	-	expression tag	UNP Q68D85
A	270	HIS	-	expression tag	UNP Q68D85
A	271	HIS	-	expression tag	UNP Q68D85

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	33	Total	O	0	0
			33	33		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.30Å 70.60Å 53.20Å 90.00° 100.40° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 50.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-2.00) 99.7 (50.00-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.246 , 0.286 0.258 , 0.295	Depositor DCC
R_{free} test set	1066 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	39.3	Xtriage
Anisotropy	0.314	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 28.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1765	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.58% 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: NAG

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	0.83	1/1701 (0.1%)	1.10	7/2311 (0.3%)

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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	30	MET	SD-CE	5.85	1.94	1.79

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	95	VAL	N-CA-C	-7.83	96.18	107.77
1	A	199	THR	N-CA-C	-5.93	100.33	109.76
1	A	144	ALA	N-CA-C	-5.71	100.40	109.59
1	A	118	GLY	CA-C-N	-5.60	115.27	123.00
1	A	118	GLY	C-N-CA	-5.60	115.27	123.00
1	A	94	ILE	N-CA-C	5.41	115.49	108.35
1	A	166	SER	N-CA-C	5.37	117.23	109.07

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	169	TYR	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	1662	0	1625	38	0
2	B	28	0	25	0	0
3	A	42	0	39	0	0
4	A	33	0	0	0	0
All	All	1765	0	1689	38	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 11.

All (38) 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:31:MET:SD	1:A:36:GLN:HG2	1.90	1.10
1:A:160:LYS:HD2	1:A:212:CYS:HB3	1.59	0.84
1:A:54:GLN:HG3	1:A:55:PRO:HD2	1.63	0.81
1:A:50:ILE:CD1	1:A:124:VAL:HG21	2.13	0.79
1:A:227:GLN:NE2	1:A:240:ARG:HH11	1.83	0.75
1:A:99:ARG:HH22	1:A:108:ARG:HG3	1.54	0.72
1:A:50:ILE:HD11	1:A:124:VAL:HG21	1.73	0.70
1:A:41:ASN:ND2	1:A:113:GLN:HE22	1.94	0.65
1:A:195:ILE:HG13	1:A:212:CYS:HB2	1.79	0.64
1:A:160:LYS:CD	1:A:212:CYS:HB3	2.28	0.62
1:A:50:ILE:HD12	1:A:124:VAL:HG21	1.80	0.61
1:A:36:GLN:HG3	1:A:135:VAL:HG21	1.84	0.60
1:A:59:THR:O	1:A:59:THR:HG22	2.02	0.59
1:A:41:ASN:HD21	1:A:113:GLN:HE22	1.51	0.57
1:A:31:MET:HE3	1:A:47:PHE:CD1	2.41	0.56
1:A:81:PHE:C	1:A:81:PHE:CD1	2.85	0.54
1:A:227:GLN:HE22	1:A:240:ARG:HH11	1.53	0.54
1:A:71:THR:HG23	1:A:72:PHE:CE2	2.44	0.53
1:A:215:LEU:O	1:A:216:ASN:CB	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:PRO:HB3	1:A:168:PHE:HB3	1.91	0.53
1:A:59:THR:O	1:A:59:THR:CG2	2.57	0.52
1:A:90:ARG:HD3	1:A:116:GLU:OE2	2.10	0.52
1:A:31:MET:HE3	1:A:47:PHE:HD1	1.75	0.51
1:A:160:LYS:HD2	1:A:212:CYS:CB	2.37	0.48
1:A:161:TYR:CE1	1:A:215:LEU:HD12	2.49	0.48
1:A:125:VAL:HG23	1:A:125:VAL:O	2.13	0.47
1:A:117:ALA:HB2	1:A:139:VAL:HG23	1.97	0.46
1:A:148:LEU:HB2	1:A:162:MET:HB2	1.98	0.46
1:A:38:THR:HA	1:A:39:PRO:HD3	1.87	0.44
1:A:99:ARG:NH2	1:A:108:ARG:HG3	2.27	0.43
1:A:147:LEU:C	1:A:148:LEU:HD12	2.43	0.42
1:A:58:ILE:HA	1:A:61:MET:HE2	2.01	0.42
1:A:94:ILE:HG13	1:A:95:VAL:N	2.34	0.42
1:A:68:LYS:HG3	1:A:119:GLU:HG2	2.01	0.41
1:A:51:PHE:CD1	1:A:51:PHE:C	2.99	0.41
1:A:72:PHE:CD2	1:A:72:PHE:N	2.89	0.41
1:A:127:THR:HA	1:A:128:PRO:HA	1.88	0.41
1:A:59:THR:O	1:A:83:GLY:HA3	2.21	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	206/248 (83%)	201 (98%)	5 (2%)	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	185/218 (85%)	177 (96%)	8 (4%)	26	25

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	GLU
1	A	90	ARG
1	A	100	LEU
1	A	128	PRO
1	A	150	ASP
1	A	195	ILE
1	A	196	THR
1	A	235	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	54	GLN
1	A	180	GLN
1	A	227	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

2 monosaccharides 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	$\# Z > 2$
2	NAG	B	1	2,1	14,14,15	0.67	0	17,19,21	0.62	0
2	NAG	B	2	2	14,14,15	0.65	0	17,19,21	0.76	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
2	NAG	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

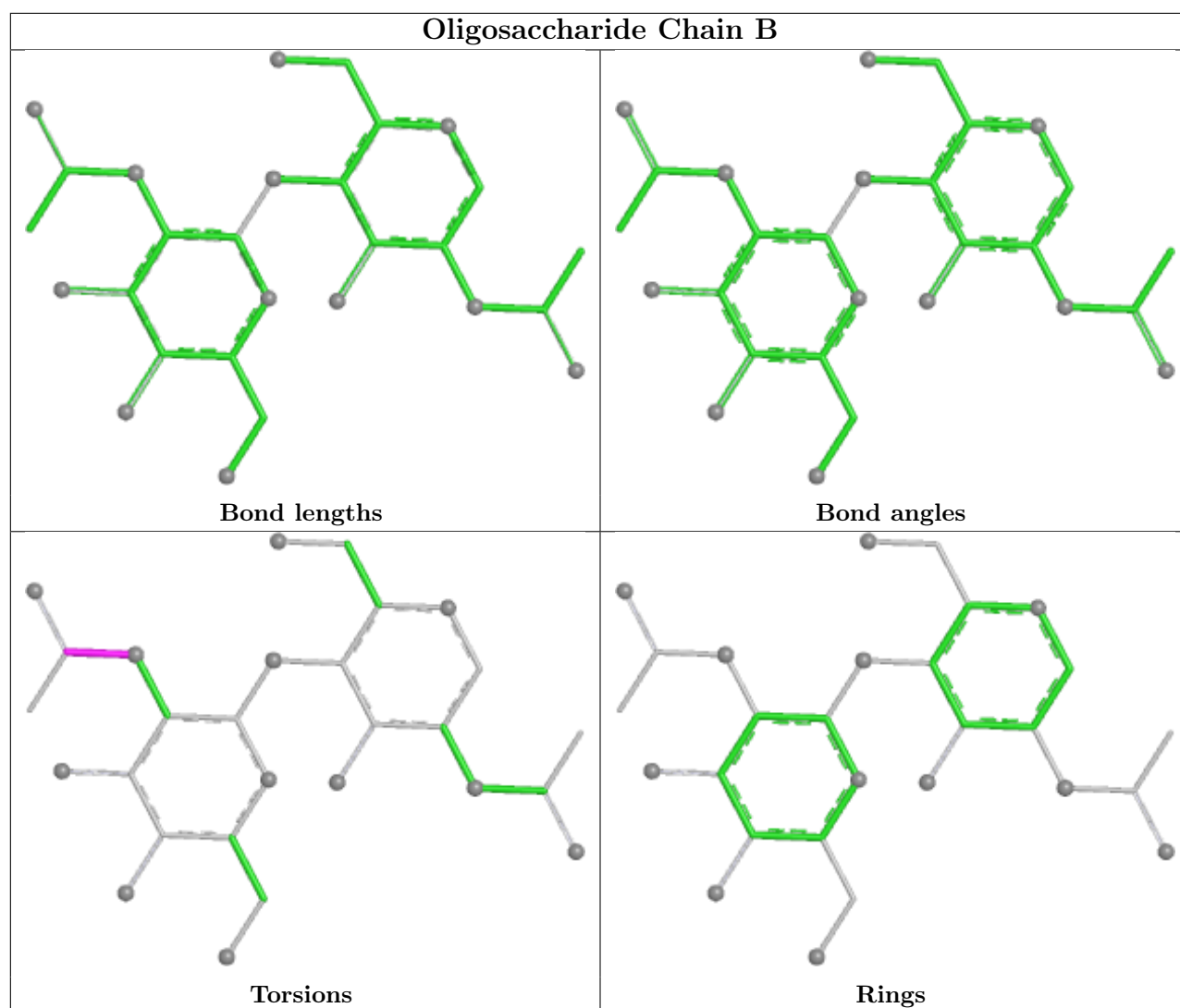
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2

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 oligosaccharide.



5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
3	NAG	A	820	1	14,14,15	0.53	0	17,19,21	0.79	1 (5%)
3	NAG	A	830	1	14,14,15	0.49	0	17,19,21	0.81	0
3	NAG	A	840	1	14,14,15	0.84	1 (7%)	17,19,21	0.67	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	NAG	A	820	1	-	4/6/23/26	0/1/1/1
3	NAG	A	830	1	-	2/6/23/26	0/1/1/1
3	NAG	A	840	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	840	NAG	C1-C2	2.66	1.56	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	820	NAG	C2-N2-C7	-2.26	119.87	122.90

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	820	NAG	C8-C7-N2-C2
3	A	820	NAG	O7-C7-N2-C2
3	A	830	NAG	C8-C7-N2-C2
3	A	830	NAG	O7-C7-N2-C2
3	A	820	NAG	O5-C5-C6-O6
3	A	820	NAG	C4-C5-C6-O6
3	A	840	NAG	O5-C5-C6-O6
3	A	840	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 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	212/248 (85%)	0.81	21 (9%) 13 11	28, 40, 56, 71	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	159	ASP	4.5
1	A	98	TRP	4.5
1	A	216	ASN	4.2
1	A	188	ILE	3.7
1	A	72	PHE	3.4
1	A	82	PHE	3.4
1	A	83	GLY	3.4
1	A	215	LEU	3.3
1	A	236	HIS	3.2
1	A	195	ILE	3.2
1	A	219	GLN	3.2
1	A	24	ALA	3.0
1	A	71	THR	2.8
1	A	245	LEU	2.6
1	A	51	PHE	2.5
1	A	190	ILE	2.5
1	A	196	THR	2.3
1	A	84	ASP	2.3
1	A	203	MET	2.2
1	A	70	LEU	2.2
1	A	115	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

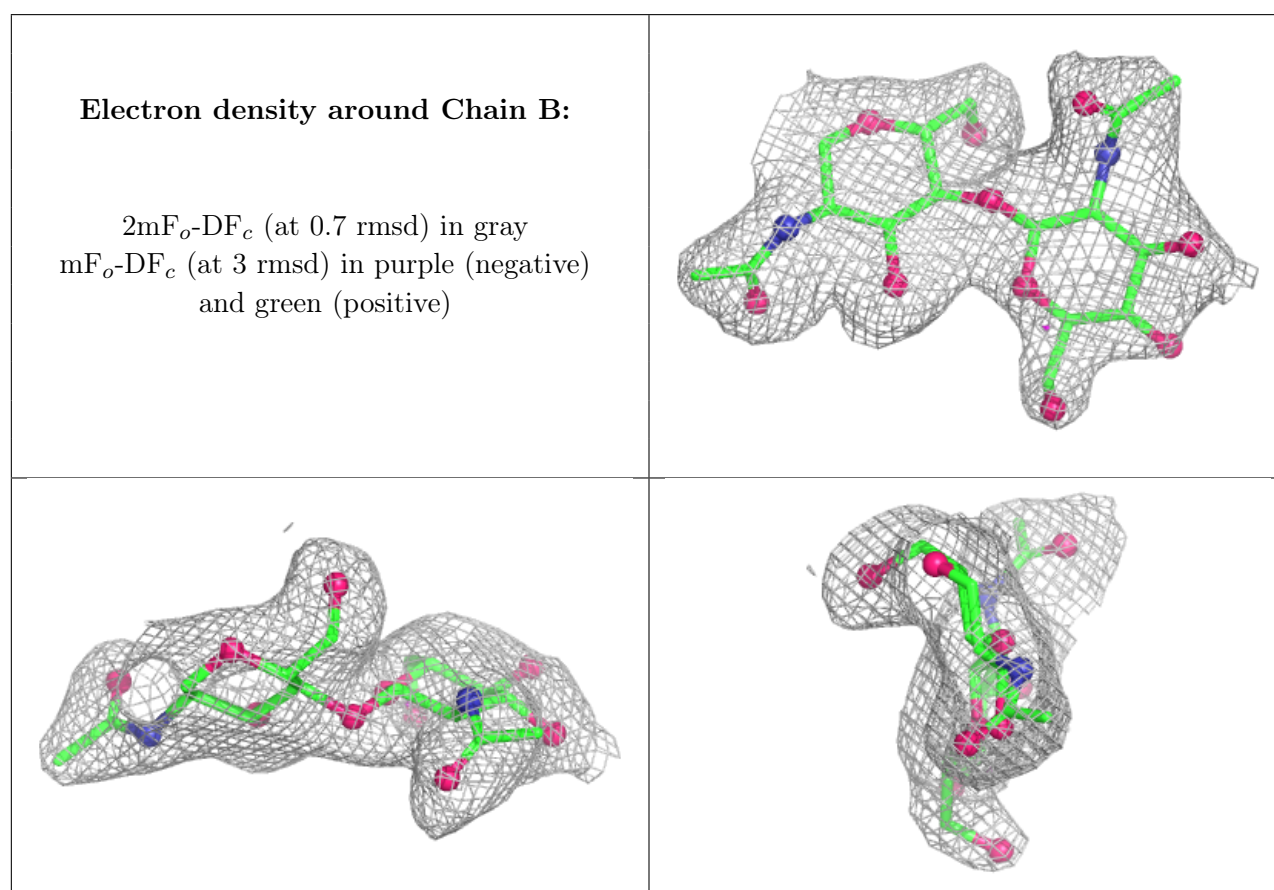
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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
2	NAG	B	2	14/15	0.79	0.14	58,63,64,65	0
2	NAG	B	1	14/15	0.95	0.09	39,41,45,52	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



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($\text{\AA}^2$)	Q<0.9
3	NAG	A	820	14/15	0.65	0.15	64,69,70,70	0
3	NAG	A	830	14/15	0.73	0.14	52,55,56,57	0
3	NAG	A	840	14/15	0.89	0.11	44,47,49,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.