W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report ⓘ

Oct 26, 2021 – 03:05 pm BST

PDB ID	:	7APZ
Title	:	CLIP peptide bound to chicken MHC class II molecule (BL-2) from B2 haplotype with a decamer mode of binding
Authors	:	Halabi, S.; Kaufman, J.
Deposited on	:	2020-10-20
Resolution	:	1.97 Å(reported)

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

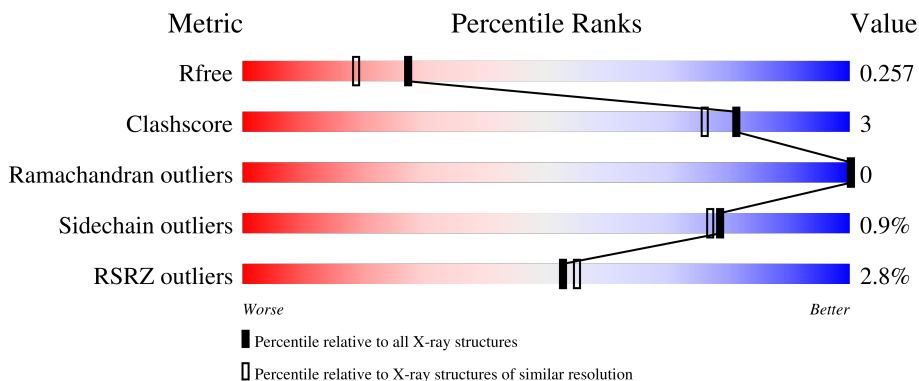|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 1.97 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	Percentile Ranks	Value
Rfree		0.257
Clashscore		3
Ramachandran outliers		0
Sidechain outliers		0.9%
RSRZ outliers		2.8%

Worse ——— *Better*

▌ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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	184	% 96% .
2	B	225	4% 84% 7% 8%

2 Entry composition ⓘ

There are 9 unique types of molecules in this entry. The entry contains 3352 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 MHC class II alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	184	Total	C	N	O	S	0	0	0
			1496	962	255	273	6			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ASP	-	expression tag	UNP Q4U5Z6
A	3	ARG	-	expression tag	UNP Q4U5Z6
A	4	ARG	-	expression tag	UNP Q4U5Z6

- Molecule 2 is a protein called MHC class II beta chain 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	206	Total	C	N	O	S	0	0	0
			1643	1034	284	312	13			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-26	LYS	-	expression tag	UNP B5BSA0
B	-25	MET	-	expression tag	UNP B5BSA0
B	-24	SER	-	expression tag	UNP B5BSA0
B	-23	MET	-	expression tag	UNP B5BSA0
B	-22	SER	-	expression tag	UNP B5BSA0
B	-21	THR	-	expression tag	UNP B5BSA0
B	-20	MET	-	expression tag	UNP B5BSA0
B	-19	ASN	-	expression tag	UNP B5BSA0
B	-18	MET	-	expression tag	UNP B5BSA0
B	-17	PRO	-	expression tag	UNP B5BSA0
B	-16	MET	-	expression tag	UNP B5BSA0
B	-15	ALA	-	expression tag	UNP B5BSA0
B	-14	MET	-	expression tag	UNP B5BSA0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	LYS	-	expression tag	UNP B5BSA0
B	-12	VAL	-	expression tag	UNP B5BSA0
B	-11	GLY	-	expression tag	UNP B5BSA0
B	-11A	GLY	-	expression tag	UNP B5BSA0
B	-11B	GLY	-	expression tag	UNP B5BSA0
B	-11C	GLY	-	expression tag	UNP B5BSA0
B	-11D	SER	-	expression tag	UNP B5BSA0
B	-11E	GLY	-	expression tag	UNP B5BSA0
B	-11F	GLY	-	expression tag	UNP B5BSA0
B	-9	GLY	-	expression tag	UNP B5BSA0
B	-8	GLY	-	expression tag	UNP B5BSA0
B	-7	SER	-	expression tag	UNP B5BSA0
B	-1	GLY	-	expression tag	UNP B5BSA0
B	0	GLY	-	expression tag	UNP B5BSA0
B	1	GLY	-	expression tag	UNP B5BSA0
B	2	GLY	-	expression tag	UNP B5BSA0
B	3	SER	-	expression tag	UNP B5BSA0

- Molecule 3 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).
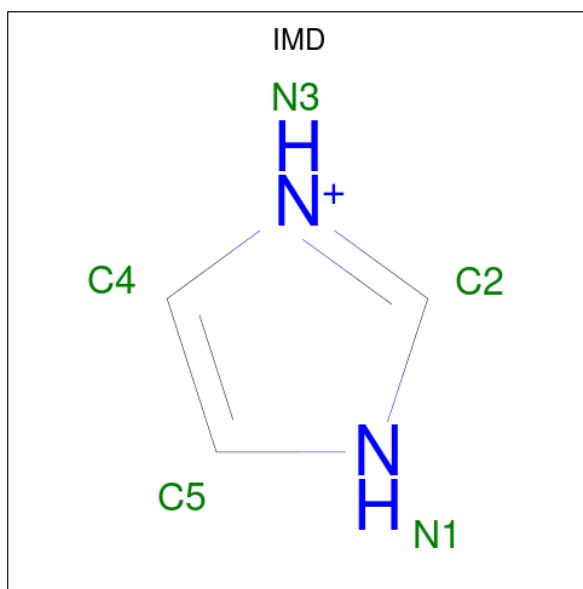
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 5	C 3	N 2	0	0
3	B	1	Total 5	C 3	N 2	0	0

- Molecule 4 is ACETYL GROUP (three-letter code: ACE) (formula: C_2H_4O).

ACE

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

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	5	Total 5	Zn 5	0	0
5	B	5	Total 5	Zn 5	0	0

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 7	C 4	O 3	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).
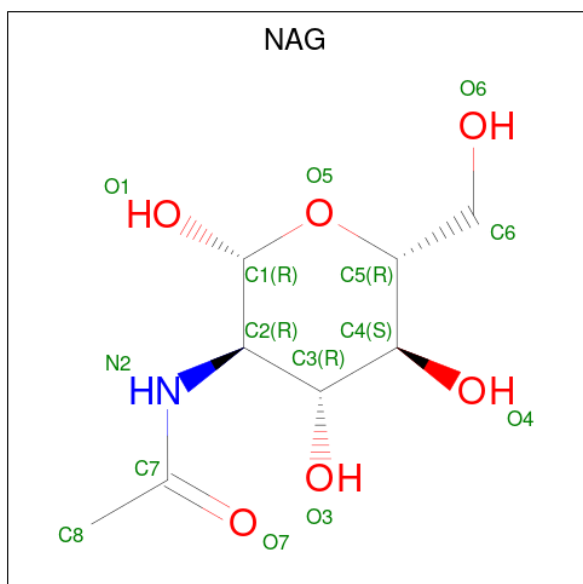
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total 14	C 8	N 1	O 5	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total 15	C 8	N 1	O 6	0	0

• Molecule 8 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total 1	Ni 1	0	0

• Molecule 9 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	69	Total 69	O 69	0	0
9	B	57	Total 57	O 57	0	0

3 Residue-property plots ⓘ

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: MHC class II alpha chain
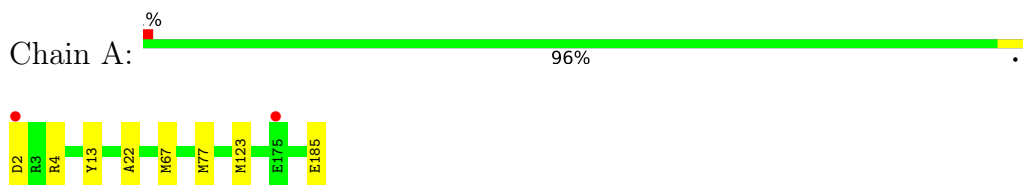
Chain A:

• Molecule 2: MHC class II beta chain 2

Chain B:
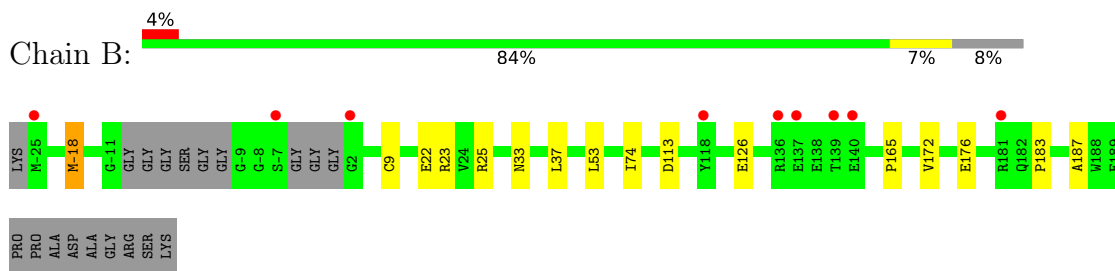
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	82.80Å　82.80Å　263.07Å 90.00°　90.00°　120.00°	Depositor
Resolution (Å)	69.28　–　1.97 69.19　–　1.97	Depositor EDS
% Data completeness (in resolution range)	98.8 (69.28-1.97) 98.8 (69.19-1.97)	Depositor EDS
R_{merge}	0.53	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.55 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.210　,　0.255 0.220　,　0.257	Depositor DCC
R_{free} test set	1913 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	26.9	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< |L| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3352	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: IMD, NI, ZN, NAG, PEG, ACE

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	0.69	0/1544	0.88	1/2101 (0.0%)
2	B	0.69	0/1680	0.87	1/2275 (0.0%)
All	All	0.69	0/3224	0.87	2/4376 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	4	ARG	NE-CZ-NH1	5.70	123.15	120.30
2	B	33	ASN	CB-CA-C	5.14	120.67	110.40

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	1496	0	1397	4	0
2	B	1643	0	1568	13	0
3	A	5	0	5	1	0
3	B	5	0	5	1	0
4	A	15	0	15	1	0
4	B	15	0	15	1	0
5	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	5	0	0	0	0
6	A	7	0	10	0	0
7	B	29	0	28	1	0
8	B	1	0	0	0	0
9	A	69	0	0	1	0
9	B	57	0	0	1	0
All	All	3352	0	3043	16	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 3.

All (16) 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:22:ALA:HB1	4:A:203:ACE:H3	1.80	0.62
3:A:201:IMD:C4	9:A:324:HOH:O	2.52	0.58
1:A:13:TYR:CE1	1:A:67:MET:HA	2.46	0.51
2:B:37:LEU:HD22	2:B:53:LEU:HB3	1.93	0.49
2:B:22:GLU:HB2	7:B:212:NAG:H62	1.94	0.49
2:B:25:ARG:HD2	9:B:342:HOH:O	2.14	0.46
2:B:113:ASP:OD2	3:B:205:IMD:C2	2.65	0.44
2:B:176:GLU:HG2	2:B:183:PRO:HG3	1.99	0.43
2:B:-18:MET:HE3	2:B:74:ILE:HD12	2.00	0.43
2:B:113:ASP:OD2	2:B:165:PRO:HG2	2.18	0.43
2:B:-18:MET:CE	2:B:74:ILE:HD12	2.50	0.42
2:B:23:ARG:HD2	4:B:203:ACE:H1	2.02	0.42
1:A:77:MET:CE	2:B:9:CYS:HB2	2.49	0.41
2:B:37:LEU:HD21	2:B:53:LEU:HD23	2.03	0.41
1:A:2:ASP:OD2	2:B:126:GLU:HG2	2.20	0.41
2:B:172:VAL:HG22	2:B:187:ALA:HB2	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	182/184 (99%)	178 (98%)	4 (2%)	0	100	100
2	B	200/225 (89%)	194 (97%)	6 (3%)	0	100	100
All	All	382/409 (93%)	372 (97%)	10 (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	154/155 (99%)	152 (99%)	2 (1%)	69	64
2	B	179/188 (95%)	178 (99%)	1 (1%)	86	85
All	All	333/343 (97%)	330 (99%)	3 (1%)	78	77

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	123	MET
1	A	185	GLU
2	B	-18	MET

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

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 (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 26 ligands modelled in this entry, 11 are monoatomic - leaving 15 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	$\#|Z| > 2$
4	ACE	A	203	-	1,2,2	0.52	0	1,1,1	0.24	0
4	ACE	A	202	-	1,2,2	0.19	0	1,1,1	0.32	0
4	ACE	A	208	-	1,2,2	0.20	0	1,1,1	0.33	0
3	IMD	B	205	-	3,5,5	0.29	0	4,5,5	0.66	0
3	IMD	A	201	-	3,5,5	0.36	0	4,5,5	0.69	0
4	ACE	A	209	-	1,2,2	0.50	0	1,1,1	0.35	0
7	NAG	B	208	2	14,14,15	0.83	0	17,19,21	2.37	7 (41%)
6	PEG	A	211	-	6,6,6	0.21	0	5,5,5	0.09	0
4	ACE	B	201	-	1,2,2	0.30	0	1,1,1	0.35	0
4	ACE	B	202	-	1,2,2	0.43	0	1,1,1	0.11	0
4	ACE	B	204	-	1,2,2	0.47	0	1,1,1	0.31	0
4	ACE	A	207	-	1,2,2	0.48	0	1,1,1	0.32	0
4	ACE	B	206	-	1,2,2	0.28	0	1,1,1	0.30	0
7	NAG	B	212	-	15,15,15	0.83	0	21,21,21	1.60	4 (19%)
4	ACE	B	203	-	1,2,2	0.37	0	1,1,1	0.27	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
7	NAG	B	208	2	-	0/6/23/26	0/1/1/1
3	IMD	B	205	-	-	-	0/1/1/1
3	IMD	A	201	-	-	-	0/1/1/1
6	PEG	A	211	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	B	212	-	-	2/6/26/26	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	B	208	NAG	C1-O5-C5	5.93	120.23	112.19
7	B	212	NAG	C4-C3-C2	4.77	117.33	110.34
7	B	208	NAG	O5-C5-C6	3.86	113.26	107.20
7	B	208	NAG	C4-C3-C2	-3.03	106.58	111.02
7	B	208	NAG	C3-C4-C5	-2.82	105.22	110.24
7	B	212	NAG	C1-C2-C3	2.50	113.96	110.54
7	B	208	NAG	O3-C3-C2	2.48	114.60	109.47
7	B	208	NAG	C2-N2-C7	2.32	126.21	122.90
7	B	212	NAG	O3-C3-C4	-2.25	105.16	110.35
7	B	208	NAG	O7-C7-N2	2.21	126.02	121.95
7	B	212	NAG	O1-C1-C2	2.14	113.66	109.22

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	212	NAG	O5-C5-C6-O6
7	B	212	NAG	C4-C5-C6-O6
6	A	211	PEG	O1-C1-C2-O2
6	A	211	PEG	O2-C3-C4-O4

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	203	ACE	1	0
3	B	205	IMD	1	0
3	A	201	IMD	1	0
7	B	212	NAG	1	0
4	B	203	ACE	1	0

5.7 Other polymers ⓘ

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(Å²)	Q<0.9
1	A	184/184 (100%)	0.10	2 (1%)	80	82	20, 28, 47, 86	0
2	B	206/225 (91%)	0.41	9 (4%)	34	36	22, 34, 59, 87	0
All	All	390/409 (95%)	0.26	11 (2%)	53	55	20, 31, 55, 87	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	181	ARG	5.0
2	B	139	THR	4.4
1	A	2	ASP	4.1
2	B	2	GLY	3.8
2	B	136	ARG	3.5
2	B	140	GLU	3.5
1	A	175	GLU	2.7
2	B	118	TYR	2.6
2	B	-7	SER	2.5
2	B	-25	MET	2.2
2	B	137	GLU	2.1

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 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, 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
7	NAG	B	212	15/15	0.60	0.25	89,100,105,105	0
4	ACE	A	208	3/3	0.61	0.26	57,57,61,66	0
4	ACE	B	202	3/3	0.62	0.20	41,41,47,48	0
4	ACE	A	202	3/3	0.62	0.20	49,49,54,57	0
4	ACE	B	201	3/3	0.64	0.36	54,54,55,56	0
4	ACE	B	204	3/3	0.65	0.19	45,45,45,50	0
4	ACE	A	207	3/3	0.66	0.34	45,45,50,52	0
4	ACE	B	206	3/3	0.75	0.16	49,49,55,57	0
4	ACE	A	203	3/3	0.75	0.33	44,44,45,47	0
7	NAG	B	208	14/15	0.78	0.12	58,66,70,72	0
3	IMD	B	205	5/5	0.79	0.19	76,79,79,80	0
5	ZN	B	213	1/1	0.79	0.30	121,121,121,121	0
6	PEG	A	211	7/7	0.83	0.20	66,72,75,76	0
4	ACE	A	209	3/3	0.84	0.37	49,49,57,57	0
5	ZN	B	210	1/1	0.85	0.07	90,90,90,90	0
4	ACE	B	203	3/3	0.86	0.20	44,44,50,51	0
3	IMD	A	201	5/5	0.91	0.14	52,53,59,62	0
5	ZN	A	212	1/1	0.92	0.08	98,98,98,98	0
5	ZN	B	214	1/1	0.94	0.07	79,79,79,79	0
5	ZN	A	206	1/1	0.95	0.06	87,87,87,87	0
8	NI	B	211	1/1	0.96	0.08	52,52,52,52	0
5	ZN	A	210	1/1	0.98	0.10	68,68,68,68	1
5	ZN	A	204	1/1	0.99	0.08	30,30,30,30	0
5	ZN	B	207	1/1	0.99	0.05	44,44,44,44	0
5	ZN	A	205	1/1	0.99	0.03	48,48,48,48	0
5	ZN	B	209	1/1	1.00	0.12	29,29,29,29	0

6.5 Other polymers (i)

There are no such residues in this entry.