



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:25 PM UTC

PDB ID : 6XCP / pdb_00006xcp
Title : Immune receptor complex
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Deposited on : 2020-06-08
Resolution : 3.30 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

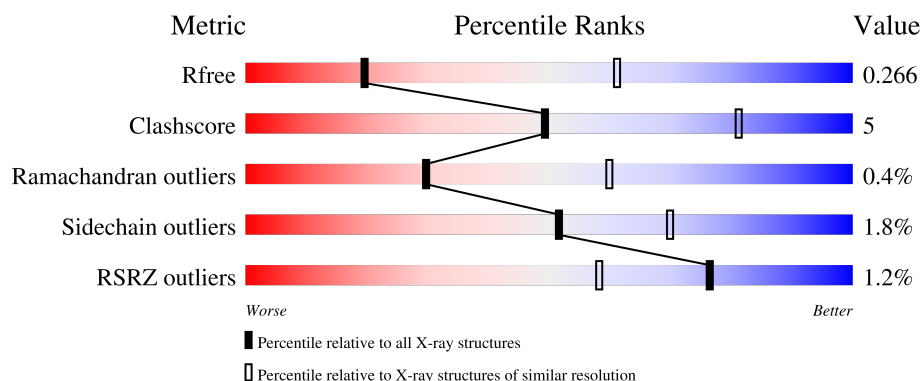
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	193	83% 11% 6%
2	C	230	68% 19% 13%
3	D	203	3% 78% 14% 7%
4	E	240	85% 14%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6351 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 HLA-DQ-alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	182	Total	C	N	O	S	0	0	0
			1429	922	233	271	3			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	CYS	ILE	engineered mutation	UNP Q30069
A	182	SER	-	expression tag	UNP Q30069
A	183	THR	-	expression tag	UNP Q30069
A	184	GLY	-	expression tag	UNP Q30069
A	185	GLY	-	expression tag	UNP Q30069
A	186	ASP	-	expression tag	UNP Q30069
A	187	ASP	-	expression tag	UNP Q30069
A	188	ASP	-	expression tag	UNP Q30069
A	189	ASP	-	expression tag	UNP Q30069
A	190	LYS	-	expression tag	UNP Q30069

- Molecule 2 is a protein called Hybrid insulin peptide, MHC class II HLA-DQ8-beta chain fusion.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	200	Total	C	N	O	S	0	0	0
			1579	996	275	300	8			

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	13	GLY	-	linker	PDB ?
C	14	SER	-	linker	PDB ?
C	15	GLY	-	linker	PDB ?
C	16	GLY	-	linker	PDB ?
C	17	SER	-	linker	PDB ?

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Chain	Residue	Modelled	Actual	Comment	Reference
C	18	ILE	-	linker	PDB ?
C	19	GLU	-	linker	PDB ?
C	20	GLY	-	linker	PDB ?
C	21	ARG	-	linker	PDB ?
C	22	GLY	-	linker	PDB ?
C	23	GLY	-	linker	PDB ?
C	24	SER	-	linker	PDB ?
C	25	GLY	-	linker	PDB ?
C	26	ALA	-	linker	PDB ?
C	27	SER	-	linker	PDB ?
C	220	THR	-	expression tag	UNP O19707
C	221	GLY	-	expression tag	UNP O19707
C	222	GLY	-	expression tag	UNP O19707
C	223	ASP	-	expression tag	UNP O19707
C	224	ASP	-	expression tag	UNP O19707
C	225	ASP	-	expression tag	UNP O19707
C	226	ASP	-	expression tag	UNP O19707
C	227	LYS	-	expression tag	UNP O19707

- Molecule 3 is a protein called T-CELL-RECEPTOR, A2.13-alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	188	Total	C	N	O	S	0	1	0
			1397	866	235	285	11			

- Molecule 4 is a protein called T-CELL-RECEPTOR, A2.13-beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	239	Total	C	N	O	S	0	0	0
			1872	1182	332	352	6			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	O	P	0	0
			5	4	1		

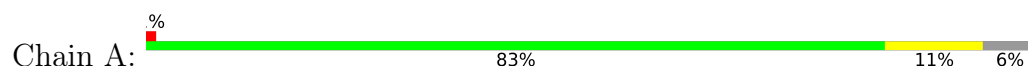
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	5	Total	O	0	0
			5	5		
8	C	7	Total	O	0	0
			7	7		
8	D	9	Total	O	0	0
			9	9		
8	E	14	Total	O	0	0
			14	14		

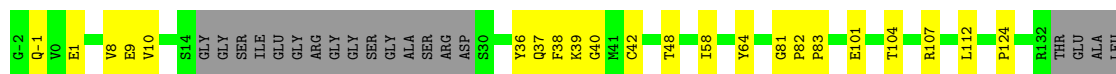
3 Residue-property plots

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.

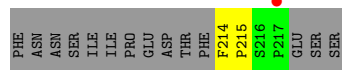
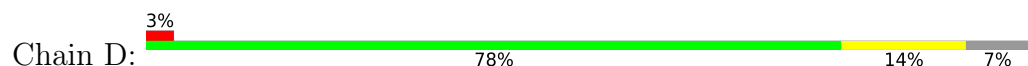
- Molecule 1: MHC class II HLA-DQ-alpha chain



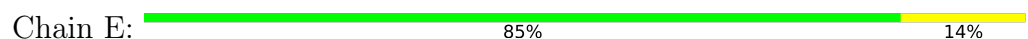
- Molecule 2: Hybrid insulin peptide, MHC class II HLA-DQ8-beta chain fusion



- Molecule 3: T-CELL-RECEPTOR, A2.13-alpha chain



- Molecule 4: T-CELL-RECEPTOR, A2.13-beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.98Å 116.79Å 124.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.73 – 3.30 43.73 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (43.73-3.30) 99.9 (43.73-3.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 3.32Å)	Xtriage
Refinement program	PHENIX 1.15_3459	Depositor
R, R_{free}	0.234 , 0.268 0.237 , 0.266	Depositor DCC
R_{free} test set	754 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	79.4	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6351	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PO4, 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	0.08	0/1472	0.23	0/2015
2	C	0.13	0/1615	0.32	0/2205
3	D	0.08	0/1428	0.29	0/1953
4	E	0.08	0/1923	0.26	0/2620
All	All	0.10	0/6438	0.28	0/8793

There are no bond length outliers.

There are no bond angle outliers.

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	A	1429	0	1333	13	0
2	C	1579	0	1489	25	0
3	D	1397	0	1246	15	0
4	E	1872	0	1760	20	0
5	A	14	0	13	0	0
5	C	14	0	13	1	0
6	C	6	0	8	0	0
7	D	5	0	0	0	0
8	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	C	7	0	0	0	0
8	D	9	0	0	0	0
8	E	14	0	0	0	0
All	All	6351	0	5862	66	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 5.

All (66) 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:C:161:ASN:HD21	2:C:196:ASP:HA	1.55	0.72
2:C:190:MET:HE3	2:C:192:PRO:HG3	1.75	0.66
2:C:37:GLN:HB2	2:C:58:ILE:HB	1.82	0.62
3:D:14:ALA:HB3	3:D:17:ARG:HD3	1.82	0.61
5:C:302:NAG:H83	5:C:302:NAG:H3	1.83	0.61
1:A:17:GLY:O	1:A:19:SER:N	2.33	0.60
4:E:48:GLN:HB3	4:E:51:GLN:HE21	1.67	0.60
1:A:143:HIS:HA	2:C:39:LYS:HZ1	1.68	0.59
2:C:143:VAL:HG22	2:C:187:MET:HG2	1.84	0.58
2:C:124:PRO:HB3	2:C:149:PHE:HB3	1.86	0.57
2:C:9:GLU:HG3	2:C:10:VAL:H	1.69	0.57
1:A:11:ASN:HB2	2:C:38:PHE:HB3	1.89	0.54
4:E:210:PHE:O	4:E:216:ASN:ND2	2.38	0.52
4:E:180:VAL:HG12	4:E:204:LEU:HD13	1.90	0.52
2:C:144:CYS:HB2	2:C:158:TRP:CZ2	2.46	0.51
4:E:40:SER:HB2	4:E:105:ALA:HB3	1.92	0.51
1:A:70:LEU:HD13	2:C:36:TYR:HB2	1.92	0.51
3:D:164:LYS:HD3	4:E:187:LEU:HD21	1.93	0.50
4:E:109:GLU:OE2	4:E:110:ARG:HD2	2.10	0.50
4:E:39:VAL:HG11	4:E:87:SER:HB3	1.93	0.50
1:A:110:ASP:OD1	1:A:111:ASN:N	2.44	0.50
4:E:111:GLU:N	4:E:111:GLU:OE2	2.45	0.49
2:C:147:THR:HG22	2:C:183:GLN:HG3	1.94	0.49
4:E:5:THR:HB	4:E:24:SER:HB3	1.96	0.48
2:C:81:GLY:N	2:C:82:PRO:HD2	2.28	0.48
2:C:64:TYR:HD1	2:C:81:GLY:HA3	1.79	0.48
2:C:1:GLU:OE2	2:C:112:LEU:HD22	2.14	0.48
4:E:6:GLN:NE2	4:E:102:TYR:O	2.44	0.48
4:E:137:VAL:HG23	4:E:247:ALA:HB3	1.96	0.47
2:C:179:ASP:OD1	2:C:181:THR:OG1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:99:SER:HB3	4:E:123:VAL:H	1.80	0.47
3:D:22:PRO:HA	3:D:88:THR:HG22	1.97	0.47
2:C:207:LEU:HD13	2:C:211:ILE:HG13	1.96	0.47
2:C:101:GLU:HA	2:C:104:THR:HB	1.97	0.46
4:E:140:PRO:HD3	4:E:153:LEU:HG	1.98	0.46
3:D:155:ASP:OD1	3:D:156:SER:N	2.48	0.46
3:D:43:ARG:HB3	3:D:53:ILE:HD11	1.98	0.45
4:E:140:PRO:HG3	4:E:151:ALA:HB1	1.98	0.45
1:A:63:ILE:HA	1:A:66:LEU:HD13	1.98	0.45
3:D:201:ASN:N	3:D:201:ASN:OD1	2.51	0.44
4:E:89:MET:HE1	4:E:102:TYR:CD2	2.53	0.44
4:E:217:HIS:HB2	4:E:250:TRP:CZ3	2.52	0.44
2:C:82:PRO:HG2	2:C:83:PRO:HD3	2.00	0.44
1:A:95:SER:O	1:A:103:ASN:ND2	2.50	0.44
2:C:193:GLN:HB2	2:C:196:ASP:OD2	2.18	0.44
3:D:140:ASP:HB3	3:D:143:SER:O	2.18	0.44
3:D:185:SER:OG	4:E:205:ARG:NH2	2.50	0.43
1:A:8:SER:HB2	1:A:25:GLU:HB2	2.00	0.43
2:C:150:TYR:CG	2:C:151:PRO:HA	2.54	0.43
3:D:76:ALA:HB2	3:D:91:LEU:HD23	2.01	0.43
3:D:214:PHE:HA	3:D:215:PRO:HD3	1.87	0.42
1:A:9(A):GLY:HA3	2:C:40:GLY:H	1.84	0.42
1:A:109:VAL:HB	1:A:112:ILE:HD11	2.01	0.42
3:D:127:HIS:O	3:D:127:HIS:ND1	2.53	0.42
2:C:190:MET:HE1	2:C:215:TRP:CZ3	2.55	0.41
3:D:38:TYR:CD1	3:D:57:LEU:HB2	2.55	0.41
4:E:11:LEU:HD12	4:E:11:LEU:HA	1.97	0.41
4:E:55:GLU:OE2	4:E:66:ARG:NH2	2.43	0.41
4:E:105:ALA:HB1	4:E:113:GLN:HB3	2.02	0.41
3:D:54:ILE:HD12	3:D:68:ASN:H	1.85	0.41
1:A:179:GLU:HA	1:A:180:PRO:HD2	1.89	0.41
1:A:58:PHE:HD2	3:D:110:ALA:HB1	1.86	0.40
2:C:152:ALA:HB2	2:C:182:PHE:CE2	2.56	0.40
3:D:155:ASP:HB3	3:D:158:THR:OG1	2.21	0.40
2:C:48:THR:O	2:C:48:THR:OG1	2.37	0.40
1:A:143:HIS:CG	2:C:58:ILE:HD13	2.57	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	180/193 (93%)	167 (93%)	12 (7%)	1 (1%)	21	52
2	C	194/230 (84%)	180 (93%)	14 (7%)	0	100	100
3	D	185/203 (91%)	168 (91%)	16 (9%)	1 (0%)	24	55
4	E	237/240 (99%)	224 (94%)	12 (5%)	1 (0%)	30	60
All	All	796/866 (92%)	739 (93%)	54 (7%)	3 (0%)	30	60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	PRO
4	E	109	GLU
3	D	92	PRO

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	156/176 (89%)	155 (99%)	1 (1%)	78	81
2	C	170/200 (85%)	165 (97%)	5 (3%)	37	62
3	D	149/182 (82%)	145 (97%)	4 (3%)	39	63
4	E	200/211 (95%)	198 (99%)	2 (1%)	68	76
All	All	675/769 (88%)	663 (98%)	12 (2%)	51	70

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	CYS
2	C	-1	GLN
2	C	8	VAL
2	C	42	CYS
2	C	107	ARG
2	C	162	ASP
3	D	27	THR
3	D	80	ILE
3	D	83	ASP
3	D	173	LYS
4	E	45	THR
4	E	109	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	ASN
2	C	-1	GLN
3	D	109	ASN
4	E	18	GLN
4	E	51	GLN
4	E	84	ASN
4	E	113	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](#)

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](#)

4 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	$\# Z > 2$
5	NAG	C	302	2	14,14,15	0.49	0	17,19,21	1.31	2 (11%)
5	NAG	A	201	1	14,14,15	0.52	0	17,19,21	0.50	0
6	GOL	C	301	-	5,5,5	0.94	0	5,5,5	1.07	0
7	PO4	D	301	-	4,4,4	0.96	0	6,6,6	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
5	NAG	C	302	2	-	6/6/23/26	0/1/1/1
5	NAG	A	201	1	-	2/6/23/26	0/1/1/1
6	GOL	C	301	-	-	0/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	302	NAG	C2-N2-C7	4.55	129.00	122.90
5	C	302	NAG	C1-C2-N2	2.09	113.73	110.43

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	302	NAG	O5-C5-C6-O6
5	A	201	NAG	C4-C5-C6-O6
5	C	302	NAG	C8-C7-N2-C2
5	C	302	NAG	O7-C7-N2-C2
5	A	201	NAG	O5-C5-C6-O6
5	C	302	NAG	C4-C5-C6-O6
5	C	302	NAG	C3-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
5	C	302	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	302	NAG	1	0

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, 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	182/193 (94%)	0.26	2 (1%) 78 60	48, 80, 125, 200	0
2	C	200/230 (86%)	0.15	1 (0%) 87 76	51, 70, 115, 134	0
3	D	188/203 (92%)	0.39	7 (3%) 45 31	39, 76, 135, 159	1 (0%)
4	E	239/240 (99%)	0.07	0 100 100	48, 71, 105, 153	0
All	All	809/866 (93%)	0.21	10 (1%) 76 58	39, 73, 123, 200	1 (0%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	158	ASP	3.8
3	D	160	VAL	3.8
3	D	10	SER	3.2
3	D	154	PHE	3.0
2	C	192	PRO	2.5
1	A	175	LEU	2.4
3	D	199	CYS	2.3
3	D	68	ASN	2.2
3	D	217	PRO	2.1
3	D	200	ALA	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
5	NAG	C	302	14/15	0.28	0.20	137,144,149,152	0
5	NAG	A	201	14/15	0.73	0.13	108,112,115,116	0
7	PO4	D	301	5/5	0.78	0.23	113,114,115,115	0
6	GOL	C	301	6/6	0.79	0.16	55,67,68,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.