



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:35 AM UTC

PDB ID : 6V15 / pdb_00006v15
Title : immune receptor complex
Authors : Lim, J.J.; Rossjohn, J.
Deposited on : 2019-11-19
Resolution : 2.80 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

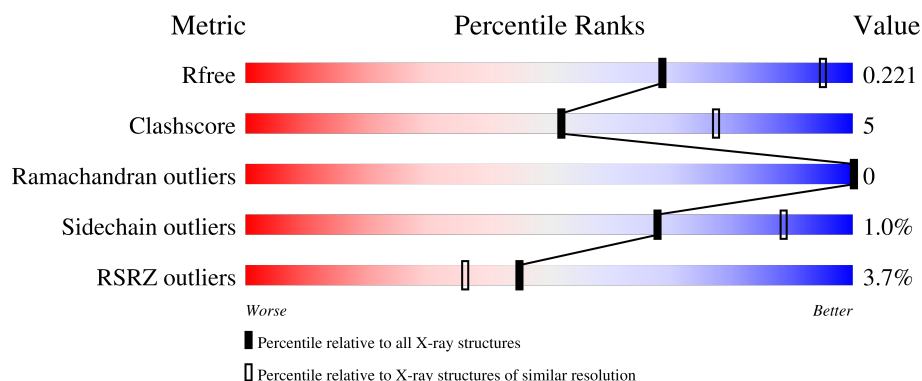
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6567 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 HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	0	0	0
			1426	928	231	262	5			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ILE	-	expression tag	UNP P01903
A	2	LYS	-	expression tag	UNP P01903
A	3	GLU	-	expression tag	UNP P01903
A	4	GLU	-	expression tag	UNP P01903
A	182	THR	-	expression tag	UNP P01903
A	183	SER	-	expression tag	UNP P01903
A	184	GLY	-	expression tag	UNP P01903
A	185	ASP	-	expression tag	UNP P01903
A	186	ASP	-	expression tag	UNP P01903
A	187	ASP	-	expression tag	UNP P01903
A	188	ASP	-	expression tag	UNP P01903
A	189	LYS	-	expression tag	UNP P01903

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-4 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	180	Total	C	N	O	S	0	0	0
			1444	917	250	272	5			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	191	THR	-	expression tag	UNP P13760
B	192	GLY	-	expression tag	UNP P13760
B	193	GLY	-	expression tag	UNP P13760
B	194	ASP	-	expression tag	UNP P13760

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Chain	Residue	Modelled	Actual	Comment	Reference
B	195	ASP	-	expression tag	UNP P13760
B	196	ASP	-	expression tag	UNP P13760
B	197	ASP	-	expression tag	UNP P13760
B	198	LYS	-	expression tag	UNP P13760

- Molecule 3 is a protein called Fibrinogen beta 72,74cit69-81.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	0	0	0
			90	55	18	17			

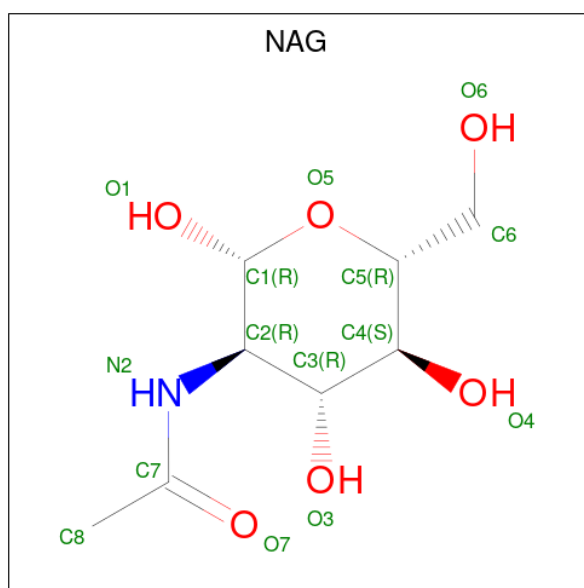
- Molecule 4 is a protein called G08 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	203	Total	C	N	O	S	0	0	0
			1569	983	256	323	7			

- Molecule 5 is a protein called G08 TCR beta chain.

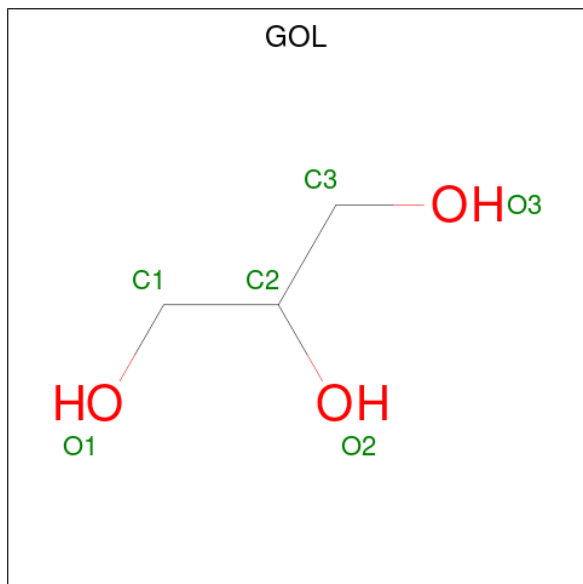
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	241	Total	C	N	O	S	0	0	0
			1927	1223	335	362	7			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	7	Total	O	0	0
			7	7		
8	B	6	Total	O	0	0
			6	6		
8	C	2	Total	O	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	D	9	Total	O	0	0
			9	9		
8	E	21	Total	O	0	0
			21	21		

SEQUENCE-PLOTS INFOmissingINFO

3 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	150.00Å 56.55Å 136.20Å 90.00° 92.20° 90.00°	Depositor
Resolution (Å)	49.09 – 2.80 49.09 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.09-2.80) 99.9 (49.09-2.80)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.197 , 0.233 (Not available) , 0.221	Depositor DCC
R_{free} test set	1408 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	52.1	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6567	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% 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.

4 Model quality

4.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CIR, 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	0.10	0/1471	0.30	0/2012
2	B	0.21	0/1484	0.44	1/2023 (0.0%)
3	C	0.06	0/67	0.16	0/86
4	D	0.10	0/1606	0.34	0/2187
5	E	0.19	0/1980	0.37	0/2698
All	All	0.16	0/6608	0.36	1/9006 (0.0%)

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
3	C	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	33	HIS	N-CA-C	-5.93	98.06	108.08

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	71	TYR	Mainchain

4.2 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	1426	0	1344	14	0
2	B	1444	0	1315	17	0
3	C	90	0	80	0	0
4	D	1569	0	1477	15	0
5	E	1927	0	1842	19	0
6	A	28	0	26	1	0
6	B	14	0	13	0	0
7	A	6	0	8	1	0
7	B	12	0	16	1	0
7	D	6	0	8	1	0
8	A	7	0	0	0	0
8	B	6	0	0	0	0
8	C	2	0	0	0	0
8	D	9	0	0	0	0
8	E	21	0	0	0	0
All	All	6567	0	6129	64	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 (64) 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)
5:E:132:VAL:O	5:E:239:ARG:NH2	2.24	0.70
2:B:74:ALA:HA	2:B:77:THR:HG22	1.74	0.69
2:B:44:VAL:HG11	2:B:48:ARG:HD2	1.75	0.67
2:B:10:GLN:HB2	2:B:31:PHE:HB2	1.78	0.66
4:D:176:LEU:HB3	5:E:183:CYS:HB2	1.78	0.65
1:A:118:ASN:HB2	1:A:166:GLU:HB2	1.80	0.64
1:A:122:LEU:HB2	1:A:162:ASP:HB2	1.79	0.63
2:B:145:THR:HG22	2:B:158:LEU:H	1.62	0.63
2:B:132:PHE:HA	2:B:137:GLU:HA	1.80	0.63
4:D:27:THR:HG21	4:D:31:PRO:HG3	1.82	0.61
1:A:28:GLY:HA2	7:A:203:GOL:H12	1.83	0.59
1:A:97:VAL:HG11	1:A:178:TRP:HZ2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:134:PRO:HD3	5:E:242:PRO:HB3	1.88	0.55
1:A:26:PHE:HB2	1:A:31:ILE:HD11	1.87	0.54
1:A:78:ASN:OD1	6:A:202:NAG:N2	2.41	0.53
4:D:111:THR:HG23	4:D:113:LYS:HG2	1.90	0.52
5:E:47:LYS:H	5:E:47:LYS:HD2	1.73	0.52
1:A:87:PRO:HB3	1:A:112:PHE:HB3	1.91	0.51
1:A:97:VAL:HG11	1:A:178:TRP:CZ2	2.46	0.50
1:A:138:LEU:HB2	1:A:146:ARG:HG3	1.93	0.49
4:D:165:ASP:HB3	4:D:168:VAL:HB	1.94	0.49
2:B:129:VAL:HG13	2:B:175:VAL:HG12	1.93	0.49
4:D:126:PRO:HG3	4:D:175:VAL:HG11	1.95	0.49
4:D:56:VAL:HG21	4:D:83:TYR:HB2	1.95	0.49
2:B:175:VAL:HG22	2:B:184:LEU:HB3	1.95	0.48
4:D:39:LEU:HD13	4:D:87:PHE:HB2	1.94	0.48
5:E:75:ARG:NH1	5:E:98:ASP:OD2	2.42	0.48
4:D:29:GLN:N	4:D:29:GLN:OE1	2.47	0.48
4:D:82:THR:HB	7:D:301:GOL:H2	1.96	0.48
2:B:117:CYS:HB2	2:B:131:TRP:CZ2	2.49	0.47
4:D:40:PHE:HB2	4:D:105:ALA:HB3	1.96	0.47
5:E:101:VAL:HG22	5:E:122:ARG:HD3	1.95	0.47
5:E:54:PHE:HZ	5:E:76:PHE:HB2	1.80	0.47
5:E:54:PHE:CZ	5:E:70:THR:HG21	2.50	0.47
1:A:94:ASN:HB3	1:A:106:ILE:HD11	1.95	0.47
1:A:100:ARG:HA	1:A:154:LEU:HD21	1.97	0.47
4:D:41:TRP:CE2	4:D:89:LEU:HB2	2.50	0.47
5:E:66:ILE:HG22	5:E:67:VAL:HG23	1.96	0.47
5:E:55:SER:HB3	5:E:67:VAL:HB	1.97	0.46
2:B:27:LEU:HD22	2:B:39:ARG:HD2	1.99	0.45
5:E:154:THR:HB	5:E:207:ARG:HG3	1.99	0.45
2:B:34:GLN:H	2:B:34:GLN:HG3	1.45	0.44
5:E:142:PRO:HD2	5:E:213:TRP:CZ2	2.52	0.44
1:A:32:PHE:HB3	1:A:43:TRP:CE3	2.53	0.44
5:E:14:GLN:HB2	5:E:129:LEU:HG	1.98	0.44
5:E:190:LYS:HE3	5:E:193:PRO:HA	2.00	0.43
5:E:214:GLN:HA	5:E:254:ARG:O	2.18	0.43
2:B:97:PRO:HB3	2:B:122:PHE:HB3	1.99	0.43
5:E:29:HIS:HB3	5:E:107:SER:O	2.18	0.43
4:D:175:VAL:HG22	4:D:186:ASN:OD1	2.19	0.42
2:B:7:PHE:HA	2:B:33:HIS:HE1	1.83	0.42
2:B:26:PHE:HB3	2:B:42:SER:HB2	2.02	0.42
2:B:18:PHE:HB2	2:B:23:ARG:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:29:GLN:O	4:D:31:PRO:HD3	2.19	0.41
2:B:39:ARG:HH12	7:B:203:GOL:H31	1.85	0.41
4:D:215:PRO:O	4:D:217:PRO:HD3	2.20	0.41
2:B:25:ARG:NH2	2:B:41:ASP:OD2	2.48	0.41
5:E:71:VAL:HG12	5:E:75:ARG:HG3	2.02	0.41
1:A:80:THR:HA	1:A:81:PRO:HD3	1.93	0.41
2:B:69:GLU:OE1	2:B:69:GLU:N	2.47	0.41
4:D:138:LEU:HB2	4:D:148:VAL:HG22	2.03	0.41
5:E:154:THR:HA	5:E:207:ARG:HA	2.02	0.41
1:A:23:MET:HE2	1:A:23:MET:HB2	1.97	0.40
5:E:54:PHE:CE2	5:E:70:THR:HG21	2.57	0.40

There are no symmetry-related clashes.

4.3 Torsion angles [i](#)

4.3.1 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	175/84 (208%)	171 (98%)	4 (2%)	0	100	100
2	B	-	171 (97%)	5 (3%)	0	100	100
3	C	9/1 (900%)	9 (100%)	0	0	100	100
4	D	201/206 (98%)	190 (94%)	11 (6%)	0	100	100
5	E	239/241 (99%)	237 (99%)	2 (1%)	0	100	100
All	All	800/532 (150%)	778 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

4.3.2 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	A	155/71 (218%)	154 (99%)	1 (1%)	78	92
2	B	-	147 (97%)	4 (3%)	40	75
3	C	4/1 (400%)	4 (100%)	0	100	100
4	D	180/185 (97%)	179 (99%)	1 (1%)	78	92
5	E	212/215 (99%)	211 (100%)	1 (0%)	81	93
All	All	702/472 (149%)	695 (99%)	7 (1%)	68	88

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	147	LYS
2	B	34	GLN
2	B	35	GLU
2	B	170	VAL
2	B	175	VAL
4	D	148	VAL
5	E	75	ARG

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

Mol	Chain	Res	Type
2	B	34	GLN
2	B	70	GLN
4	D	205	ASN
5	E	22	ASN
5	E	29	HIS
5	E	113	ASN
5	E	179	HIS

4.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

7 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	$\# Z > 2$
7	GOL	A	203	-	5,5,5	0.94	0	5,5,5	1.08	0
7	GOL	B	202	-	5,5,5	0.93	0	5,5,5	1.08	0
7	GOL	B	203	-	5,5,5	0.96	0	5,5,5	1.06	0
7	GOL	D	301	-	5,5,5	0.09	0	5,5,5	0.32	0
6	NAG	A	201	1	14,14,15	0.26	0	17,19,21	0.50	0
6	NAG	B	201	2	14,14,15	0.26	0	17,19,21	0.44	0
6	NAG	A	202	1	14,14,15	0.58	0	17,19,21	0.63	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	GOL	A	203	-	-	0/4/4/4	-
7	GOL	B	202	-	-	0/4/4/4	-
7	GOL	B	203	-	-	1/4/4/4	-
7	GOL	D	301	-	-	0/4/4/4	-
6	NAG	A	201	1	-	2/6/23/26	0/1/1/1
6	NAG	B	201	2	-	2/6/23/26	0/1/1/1
6	NAG	A	202	1	-	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 (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	201	NAG	O5-C5-C6-O6
6	A	201	NAG	C4-C5-C6-O6
6	A	201	NAG	O5-C5-C6-O6
6	B	201	NAG	C4-C5-C6-O6
6	A	202	NAG	C3-C2-N2-C7
6	A	202	NAG	C1-C2-N2-C7
7	B	203	GOL	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	203	GOL	1	0
7	B	203	GOL	1	0
7	D	301	GOL	1	0
6	A	202	NAG	1	0

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data [i](#)

5.1 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	81/84 (96%)	-0.02	0	100	100	42, 53, 74, 84	0
3	C	1/1 (100%)	1.46	0	100	100	67, 67, 67, 67	0
4	D	203/206 (98%)	0.05	7 (3%)	48	39	32, 48, 77, 106	0
5	E	241/241 (100%)	-0.12	4 (1%)	69	60	27, 42, 80, 96	0
All	All	526/532 (98%)	-0.03	11 (2%)	45	54	27, 47, 78, 106	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	142	LYS	3.4
5	E	71	VAL	3.1
4	D	143	SER	3.0
5	E	72	PRO	2.9
4	D	140	ASP	2.9
4	D	217	PRO	2.8
4	D	141	SER	2.7
5	E	74	ARG	2.5
4	D	9	GLY	2.1
5	E	238	ASP	2.1
4	D	146	LYS	2.0

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

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

5.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.4 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
6	NAG	B	201	14/15	0.48	0.19	84,97,105,111	0
6	NAG	A	202	14/15	0.50	0.16	84,98,119,131	0
7	GOL	B	203	6/6	0.56	0.19	70,89,93,94	0
7	GOL	B	202	6/6	0.84	0.14	61,72,78,88	0
7	GOL	A	203	6/6	0.84	0.25	72,81,85,90	0
6	NAG	A	201	14/15	0.86	0.12	80,89,104,106	0
7	GOL	D	301	6/6	0.93	0.12	78,80,88,103	0

5.5 Other polymers [i](#)

There are no such residues in this entry.