



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 09:20 AM UTC

PDB ID : 7N2N / pdb_00007n2n
Title : TCR-antigen complex AS4.2-PRPF3-HLA*B27
Authors : Yang, X.; Jude, K.M.; Garcia, K.C.
Deposited on : 2021-05-29
Resolution : 2.60 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

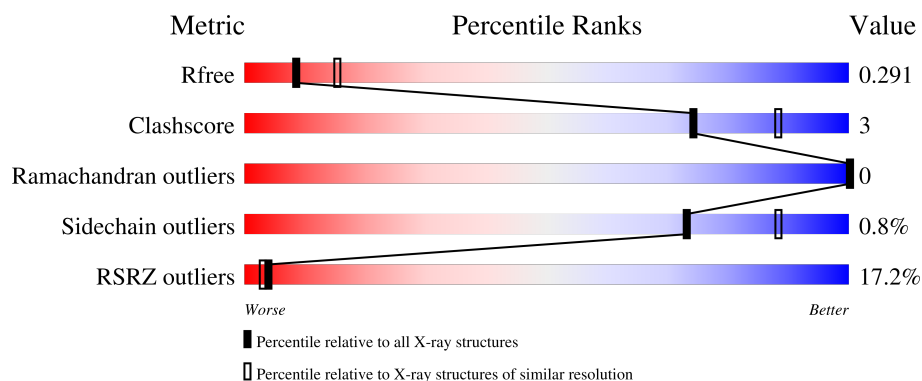
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	C	9	 100%
2	A	278	 14% 91% 8%
3	B	100	 8% 89% 11%
4	D	210	 32% 85% 8% 7%
5	F	242	 11% 90% 10%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6700 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 Pre-mRNA Processing Factor 3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	C	9	Total	C	N	O	0	0	0
			69	45	13	11			

- Molecule 2 is a protein called Human leukocyte antigen (HLA) B27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	275	Total	C	N	O	S	0	1	0
			2241	1392	406	437	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	SER	CYS	conflict	UNP A3F718

- Molecule 3 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769

- Molecule 4 is a protein called T cell receptor alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	196	Total	C	N	O	S	0	0	0
			1500	930	252	311	7			

- Molecule 5 is a protein called T cell receptor beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	241	Total	C	N	O	S	0	0	0
			1916	1212	332	367	5			

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



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

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	D	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		
7	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	F	1	Total	O	S	0	0
			5	4	1		

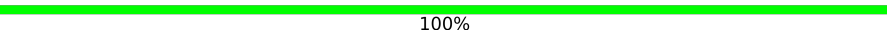
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	C	3	Total 3	O 3	0	0
9	A	26	Total 26	O 26	0	0
9	B	12	Total 12	O 12	0	0
9	D	11	Total 11	O 11	0	0
9	F	14	Total 14	O 14	0	0

3 Residue-property plots [i](#)

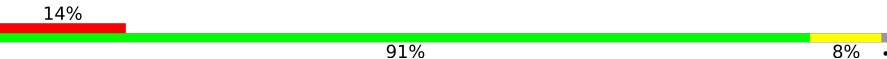
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

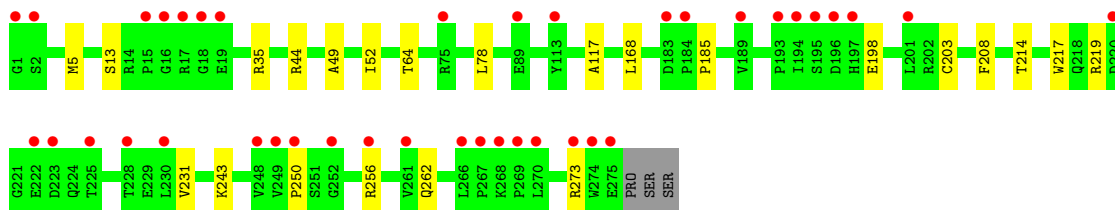
- Molecule 1: Pre-mRNA Processing Factor 3

Chain C:  100%

There are no outlier residues recorded for this chain.

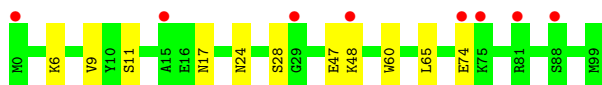
- Molecule 2: Human leukocyte antigen (HLA) B27

Chain A:  14% 91% 8%



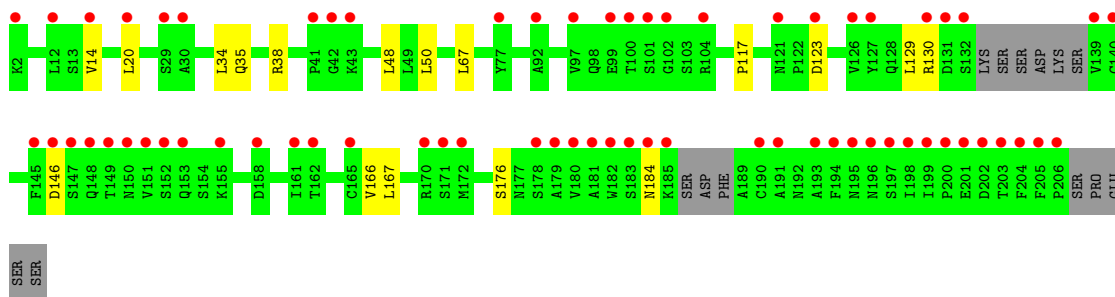
- Molecule 3: Beta-2-microglobulin

Chain B:  8% 89% 11%

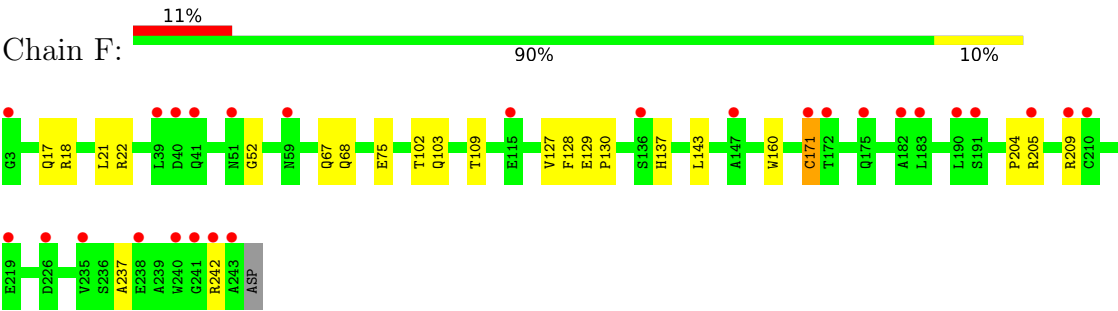


- Molecule 4: T cell receptor alpha chain

Chain D:  32% 85% 8% 7%



- Molecule 5: T cell receptor beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.11Å 53.15Å 106.82Å 90.00° 98.48° 90.00°	Depositor
Resolution (Å)	47.48 – 2.60 47.48 – 2.60	Depositor EDS
% Data completeness (in resolution range)	95.9 (47.48-2.60) 95.9 (47.48-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122+SVN	Depositor
R, R_{free}	0.248 , 0.291 0.248 , 0.291	Depositor DCC
R_{free} test set	1278 reflections (2.11%)	wwPDB-VP
Wilson B-factor (Å ²)	39.2	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.6	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	0.88	EDS
Total number of atoms	6700	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.36% 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, SO4, 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	C	0.16	0/69	0.26	0/91
2	A	0.09	0/2303	0.24	0/3131
3	B	0.10	0/860	0.26	0/1162
4	D	0.09	0/1525	0.27	0/2072
5	F	0.10	0/1967	0.24	0/2680
All	All	0.10	0/6724	0.25	0/9136

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	C	69	0	85	0	0
2	A	2241	0	2100	12	0
3	B	837	0	803	7	0
4	D	1500	0	1436	12	0
5	F	1916	0	1824	15	0
6	B	12	0	16	1	0
6	D	6	0	8	0	0
6	F	6	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	28	0	26	0	0
7	F	14	0	13	1	0
8	F	5	0	0	0	0
9	A	26	0	0	0	0
9	B	12	0	0	1	0
9	C	3	0	0	0	0
9	D	11	0	0	0	0
9	F	14	0	0	0	0
All	All	6700	0	6319	40	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 (40) 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:A:5:MET:HB2	2:A:168:LEU:HD13	1.73	0.70
5:F:204:PRO:HG2	5:F:205:ARG:HH12	1.61	0.65
2:A:13:SER:HB3	2:A:78:LEU:HD13	1.79	0.63
4:D:117:PRO:HG3	4:D:166:VAL:HG11	1.80	0.62
2:A:214:THR:HB	2:A:262:GLN:HB2	1.80	0.62
4:D:14:VAL:HG21	4:D:20:LEU:HD21	1.84	0.58
2:A:44:ARG:HD2	2:A:64:THR:HG21	1.86	0.58
5:F:67:GLN:NE2	7:F:301:NAG:O7	2.39	0.55
3:B:17:ASN:HD21	3:B:74:GLU:HG2	1.73	0.53
5:F:21:LEU:HD22	5:F:109:THR:HG21	1.92	0.52
2:A:185:PRO:HB3	2:A:208:PHE:HB3	1.93	0.51
2:A:219:ARG:CZ	2:A:256:ARG:HH12	2.24	0.51
4:D:35:GLN:HG2	4:D:50:LEU:HG	1.94	0.50
5:F:52:GLY:HA2	5:F:68:GLN:HB3	1.94	0.49
4:D:184:ASN:OD1	4:D:184:ASN:N	2.45	0.48
4:D:50:LEU:HD12	5:F:102:THR:HB	1.95	0.48
5:F:160:TRP:HB2	5:F:209:ARG:HB3	1.95	0.48
3:B:6:LYS:HG2	3:B:28:SER:O	2.14	0.47
5:F:103:GLN:HG3	6:F:302:GOL:H31	1.95	0.47
4:D:167:LEU:HB3	5:F:171:CYS:HB3	1.97	0.47
2:A:219:ARG:NH2	2:A:256:ARG:HH12	2.13	0.47
3:B:24:ASN:HB3	3:B:65:LEU:HD11	1.96	0.46
4:D:129:LEU:HB3	5:F:128:PHE:HB3	1.97	0.46
2:A:231:VAL:O	2:A:243:LYS:NZ	2.36	0.45
5:F:17:GLN:HG3	5:F:18:ARG:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:130:ARG:HB3	5:F:129:GLU:HB2	1.99	0.44
5:F:130:PRO:HD3	5:F:143:LEU:HG	1.98	0.44
4:D:34:LEU:HD13	4:D:67:LEU:HD13	1.99	0.43
4:D:38:ARG:HB3	4:D:48:LEU:HD11	1.99	0.43
2:A:203:CYS:HB2	2:A:217:TRP:CZ2	2.54	0.43
4:D:146:ASP:OD1	4:D:146:ASP:N	2.52	0.42
3:B:47:GLU:HG2	3:B:48:LYS:H	1.84	0.42
5:F:22:ARG:HG2	5:F:75:GLU:HG2	2.02	0.42
3:B:6:LYS:HG3	9:B:203:HOH:O	2.18	0.42
2:A:49:ALA:O	2:A:52:ILE:HG22	2.20	0.42
4:D:123:ASP:OD2	5:F:137:HIS:NE2	2.52	0.42
2:A:198:GLU:HA	2:A:250:PRO:HA	2.02	0.42
5:F:127:VAL:HG13	5:F:237:ALA:HB3	2.02	0.41
2:A:117:ALA:HB2	3:B:60:TRP:CE2	2.56	0.41
3:B:11:SER:O	6:B:101:GOL:O1	2.33	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	C	7/9 (78%)	7 (100%)	0	0	100	100
2	A	274/278 (99%)	265 (97%)	9 (3%)	0	100	100
3	B	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
4	D	190/210 (90%)	184 (97%)	6 (3%)	0	100	100
5	F	239/242 (99%)	228 (95%)	11 (5%)	0	100	100
All	All	808/839 (96%)	780 (96%)	28 (4%)	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	C	7/7 (100%)	7 (100%)	0	100	100
2	A	234/237 (99%)	232 (99%)	2 (1%)	70	87
3	B	95/95 (100%)	94 (99%)	1 (1%)	65	84
4	D	173/187 (92%)	172 (99%)	1 (1%)	78	91
5	F	209/211 (99%)	207 (99%)	2 (1%)	68	86
All	All	718/737 (97%)	712 (99%)	6 (1%)	73	88

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	35	ARG
2	A	273	ARG
3	B	9	VAL
4	D	176	SER
5	F	171	CYS
5	F	242	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	97	ASN
2	A	192	HIS
4	D	3	GLN
4	D	121	ASN
4	D	153	GLN

5.3.3 RNA ⓘ

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](#)

8 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	$\# Z > 2$
6	GOL	F	302	-	5,5,5	1.03	0	5,5,5	0.96	0
7	NAG	D	301	4	14,14,15	0.27	0	17,19,21	0.41	0
6	GOL	D	303	-	5,5,5	0.96	0	5,5,5	1.23	1 (20%)
6	GOL	B	101	-	5,5,5	0.96	0	5,5,5	1.06	0
7	NAG	D	302	4	14,14,15	0.25	0	17,19,21	0.55	0
8	SO4	F	303	-	4,4,4	0.24	0	6,6,6	0.08	0
6	GOL	B	102	-	5,5,5	0.97	0	5,5,5	1.12	0
7	NAG	F	301	5	14,14,15	0.29	0	17,19,21	0.55	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
6	GOL	F	302	-	-	3/4/4/4	-
7	NAG	D	301	4	-	2/6/23/26	0/1/1/1
6	GOL	D	303	-	-	2/4/4/4	-
6	GOL	B	101	-	-	0/4/4/4	-
7	NAG	D	302	4	-	3/6/23/26	0/1/1/1
6	GOL	B	102	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	F	301	5	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	303	GOL	C3-C2-C1	-2.27	103.48	111.80

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	303	GOL	O1-C1-C2-O2
6	D	303	GOL	O1-C1-C2-C3
6	F	302	GOL	C1-C2-C3-O3
7	D	301	NAG	O5-C5-C6-O6
7	D	301	NAG	C4-C5-C6-O6
7	F	301	NAG	O5-C5-C6-O6
7	F	301	NAG	C4-C5-C6-O6
6	F	302	GOL	O2-C2-C3-O3
7	D	302	NAG	O5-C5-C6-O6
7	D	302	NAG	C1-C2-N2-C7
7	F	301	NAG	C1-C2-N2-C7
7	F	301	NAG	C3-C2-N2-C7
7	D	302	NAG	C3-C2-N2-C7
6	F	302	GOL	O1-C1-C2-C3

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	302	GOL	1	0
6	B	101	GOL	1	0
7	F	301	NAG	1	0

5.7 Other polymers [i](#)

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 ⓘ

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(Å ²)	Q<0.9
1	C	9/9 (100%)	0.20	0 100 100	23, 25, 31, 33	0
2	A	275/278 (98%)	0.93	39 (14%) 6 5	19, 39, 89, 107	1 (0%)
3	B	100/100 (100%)	0.80	8 (8%) 18 14	24, 39, 65, 104	0
4	D	196/210 (93%)	1.59	67 (34%) 1 1	27, 53, 98, 123	0
5	F	241/242 (99%)	1.01	27 (11%) 10 8	23, 45, 73, 100	0
All	All	821/839 (97%)	1.09	141 (17%) 4 3	19, 44, 89, 123	1 (0%)

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	F	3	GLY	7.2
4	D	179	ALA	6.0
4	D	194	PHE	4.9
4	D	132	SER	4.7
4	D	206	PRO	4.7
2	A	18	GLY	4.4
4	D	101	SER	4.3
4	D	146	ASP	4.2
4	D	200	PRO	4.0
4	D	202	ASP	3.9
5	F	219	GLU	3.8
2	A	248	VAL	3.7
3	B	0	MET	3.6
2	A	250	PRO	3.6
4	D	43	LYS	3.6
2	A	113	TYR	3.6
4	D	41	PRO	3.6
4	D	102	GLY	3.4
5	F	182	ALA	3.4
2	A	252	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
5	F	242	ARG	3.3
2	A	249	VAL	3.2
4	D	162	THR	3.2
4	D	42	GLY	3.2
2	A	184	PRO	3.2
4	D	199	ILE	3.2
2	A	267	PRO	3.1
4	D	151	VAL	3.1
2	A	196	ASP	3.1
4	D	100	THR	3.1
2	A	223	ASP	3.0
2	A	1	GLY	3.0
4	D	161	ILE	3.0
5	F	243	ALA	3.0
4	D	140	CYS	3.0
4	D	197	SER	3.0
4	D	77	TYR	3.0
4	D	130	ARG	3.0
4	D	99	GLU	3.0
3	B	75	LYS	3.0
2	A	183	ASP	2.9
4	D	149	THR	2.9
4	D	181	ALA	2.9
2	A	193	PRO	2.9
3	B	88	SER	2.9
4	D	191	ALA	2.9
2	A	75	ARG	2.8
4	D	153	GLN	2.8
4	D	152	SER	2.8
5	F	41	GLN	2.8
4	D	29	SER	2.8
4	D	195	ASN	2.8
4	D	196	ASN	2.8
2	A	225	THR	2.8
4	D	147	SER	2.8
4	D	14	VAL	2.8
4	D	172	MET	2.8
5	F	238	GLU	2.8
5	F	191	SER	2.7
2	A	16	GLY	2.7
4	D	180	VAL	2.7
5	F	171	CYS	2.7

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Mol	Chain	Res	Type	RSRZ
5	F	59	ASN	2.7
2	A	195	SER	2.7
2	A	222	GLU	2.7
5	F	136	SER	2.7
4	D	204	PHE	2.7
4	D	198	ILE	2.6
2	A	230	LEU	2.6
4	D	150	ASN	2.6
4	D	171	SER	2.6
5	F	241	GLY	2.6
2	A	197	HIS	2.6
4	D	165	CYS	2.6
5	F	115	GLU	2.6
2	A	89	GLU	2.5
4	D	97	VAL	2.5
4	D	205	PHE	2.5
4	D	203	THR	2.5
5	F	51	ASN	2.5
4	D	182	TRP	2.5
5	F	190	LEU	2.5
3	B	74	GLU	2.5
2	A	2	SER	2.5
4	D	123	ASP	2.5
4	D	145	PHE	2.5
5	F	240	TRP	2.5
2	A	17	ARG	2.4
2	A	256	ARG	2.4
5	F	39	LEU	2.4
2	A	270	LEU	2.4
4	D	170	ARG	2.4
4	D	193	ALA	2.4
2	A	201	LEU	2.4
4	D	184	ASN	2.4
4	D	131	ASP	2.4
4	D	2	LYS	2.4
4	D	155	LYS	2.4
3	B	48	LYS	2.3
4	D	148	GLN	2.3
2	A	19	GLU	2.3
4	D	190	CYS	2.3
4	D	126	VAL	2.3
4	D	92	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
5	F	226	ASP	2.3
3	B	29	GLY	2.3
2	A	220	ASP	2.2
5	F	183	LEU	2.2
5	F	210	CYS	2.2
4	D	127	TYR	2.2
4	D	158	ASP	2.2
4	D	183	SER	2.2
5	F	209	ARG	2.2
5	F	175	GLN	2.2
4	D	139	VAL	2.2
5	F	172	THR	2.2
2	A	266	LEU	2.2
4	D	12	LEU	2.2
4	D	20	LEU	2.2
5	F	235	VAL	2.2
3	B	15	ALA	2.1
4	D	201	GLU	2.1
3	B	81	ARG	2.1
5	F	205	ARG	2.1
2	A	269	PRO	2.1
2	A	268	LYS	2.1
4	D	121	ASN	2.1
2	A	194	ILE	2.1
5	F	40	ASP	2.1
4	D	30	ALA	2.1
2	A	274	TRP	2.1
2	A	275	GLU	2.1
4	D	185	LYS	2.1
2	A	273	ARG	2.1
2	A	228	THR	2.1
2	A	189	VAL	2.1
4	D	178	SER	2.0
5	F	147	ALA	2.0
2	A	261	VAL	2.0
2	A	15	PRO	2.0
4	D	104	ARG	2.0

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 [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($\text{\AA}^2$)	Q<0.9
7	NAG	D	302	14/15	0.59	0.17	62,82,93,99	0
6	GOL	B	102	6/6	0.68	0.17	41,52,55,56	0
7	NAG	F	301	14/15	0.68	0.19	39,59,66,67	0
6	GOL	D	303	6/6	0.74	0.19	56,61,74,79	0
7	NAG	D	301	14/15	0.77	0.16	48,55,60,62	0
6	GOL	F	302	6/6	0.79	0.22	23,33,50,51	0
8	SO4	F	303	5/5	0.82	0.24	70,70,76,89	0
6	GOL	B	101	6/6	0.89	0.16	29,38,47,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.