



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 14, 2023 – 05:57 PM EDT

PDB ID : 7N2R  
Title : AS4.3-PRPF3-HLA\*B27  
Authors : Yang, X.; Jude, K.M.; Garcia, K.C.  
Deposited on : 2021-05-29  
Resolution : 2.28 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](mailto: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>.

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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)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

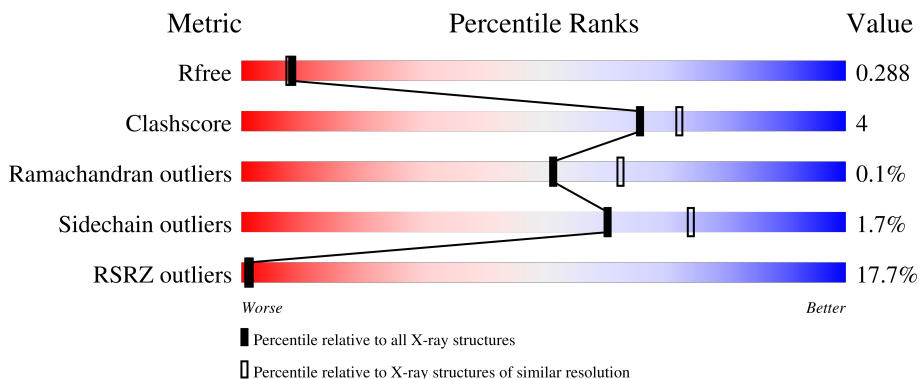
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.28 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))
$R_{free}$	130704	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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  $\geq 3$ , 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	D	204	
2	F	242	
3	A	278	
4	B	100	
5	C	9	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
6	NAG	D	304	-	-	-	X
7	ASP	F	301	-	-	-	X

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6612 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 AS4.3 T cell receptor alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	D	195	1512	944	251	310	7	0	2	0

- Molecule 2 is a protein called AS4.3 T cell receptor beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	F	241	1914	1209	332	367	6	0	0	0

- Molecule 3 is a protein called Human leukocyte antigen (HLA) B27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	259	2119	1324	386	403	6	0	1	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 4 is a protein called Beta-2-microglobulin.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 5 is a protein called Pre-mRNA Processing Factor 3.

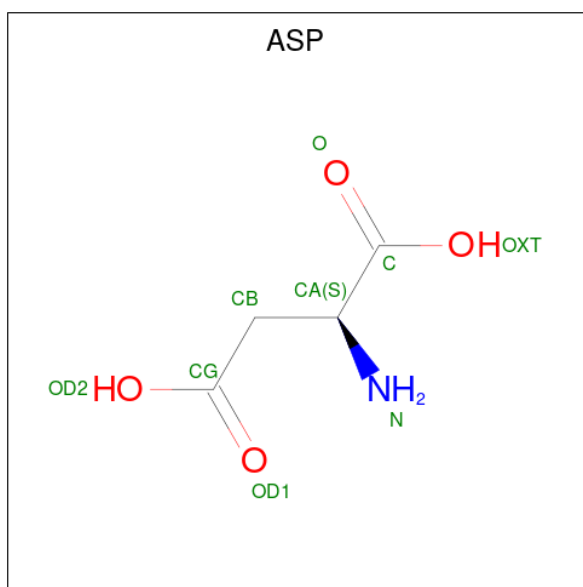
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	C	9	69	45	13	11	0	0	0

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



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

- Molecule 7 is ASPARTIC ACID (three-letter code: ASP) (formula:  $C_4H_7NO_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
7	F	1	9	4	1	4	0	0

- Molecule 8 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



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

- Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

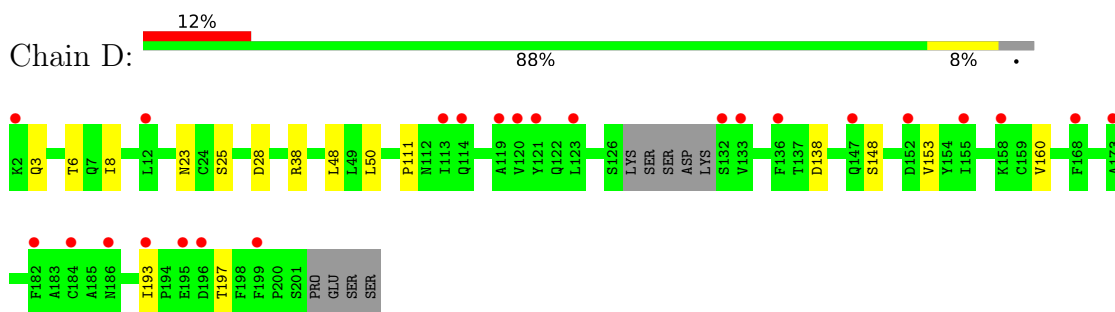
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	D	17	Total	O	0	0
			17	17		
10	F	17	Total	O	0	0
			17	17		
10	A	26	Total	O	0	0
			26	26		
10	B	3	Total	O	0	0
			3	3		

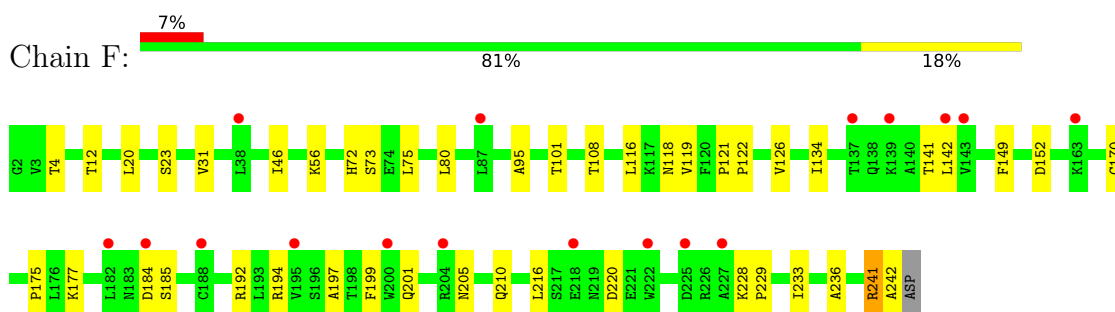
### 3 Residue-property plots [i](#)

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.

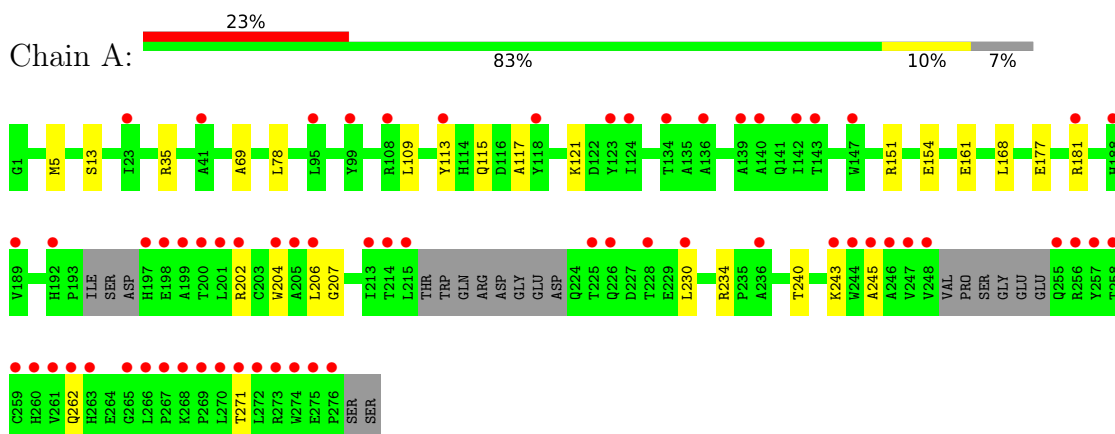
- Molecule 1: AS4.3 T cell receptor alpha chain



- Molecule 2: AS4.3 T cell receptor beta chain

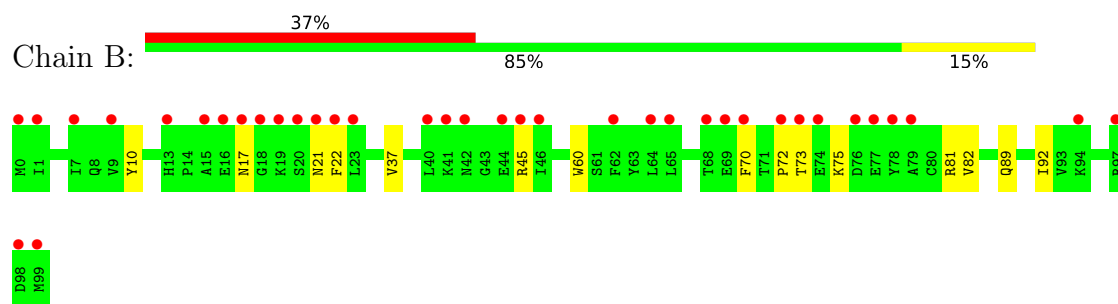


- Molecule 3: Human leukocyte antigen (HLA) B27

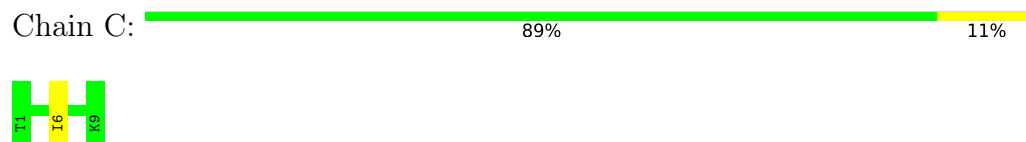


- Molecule 4: Beta-2-microglobulin





- Molecule 5: Pre-mRNA Processing Factor 3



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.68Å 94.42Å 178.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.26 – 2.28 40.26 – 2.28	Depositor EDS
% Data completeness (in resolution range)	99.2 (40.26-2.28) 99.2 (40.26-2.28)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.08 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.19_4080	Depositor
R, $R_{free}$	0.248 , 0.288 0.246 , 0.288	Depositor DCC
$R_{free}$ test set	1991 reflections (4.68%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.3	Xtrriage
Anisotropy	0.484	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 53.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6612	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	86.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: EDO, 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	D	0.29	0/1544	0.50	0/2095
2	F	0.28	0/1965	0.50	0/2679
3	A	0.26	0/2178	0.53	0/2958
4	B	0.25	0/860	0.48	0/1162
5	C	0.32	0/69	0.67	0/91
All	All	0.27	0/6616	0.51	0/8985

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	D	1512	0	1436	9	0
2	F	1914	0	1818	24	0
3	A	2119	0	1997	15	0
4	B	837	0	803	8	0
5	C	69	0	85	1	0
6	D	56	0	52	0	0
6	F	14	0	13	0	0
7	F	9	0	3	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	5	0	0	0	0
8	F	10	0	0	0	0
9	A	4	0	6	0	0
10	A	26	0	0	0	0
10	B	3	0	0	0	0
10	D	17	0	0	0	0
10	F	17	0	0	0	0
All	All	6612	0	6213	51	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 4.

All (51) 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:F:46:ILE:HG13	2:F:56:LYS:HG2	1.73	0.71
1:D:3:GLN:HG2	1:D:28:ASP:HB3	1.78	0.64
1:D:148:SER:HB2	1:D:153:VAL:HG23	1.78	0.63
4:B:81:ARG:HG3	4:B:92:ILE:HG12	1.82	0.61
3:A:177:GLU:O	3:A:181:ARG:NH1	2.34	0.60
2:F:199:PHE:O	2:F:205:ASN:ND2	2.31	0.59
2:F:152:ASP:HB2	2:F:175:PRO:HG2	1.84	0.59
4:B:73:THR:HG22	4:B:75:LYS:H	1.67	0.58
3:A:230:LEU:HD11	3:A:243:LYS:HE3	1.86	0.57
2:F:4:THR:OG1	2:F:23:SER:OG	2.23	0.56
2:F:20:LEU:HD22	2:F:108:THR:HG21	1.87	0.56
3:A:5:MET:HB2	3:A:168:LEU:HD13	1.89	0.55
2:F:121:PRO:HD3	2:F:229:PRO:HB3	1.90	0.54
2:F:116:LEU:HD13	2:F:216:LEU:HD22	1.89	0.54
1:D:193:ILE:HD11	1:D:197:THR:HG21	1.89	0.54
3:A:69:ALA:HB1	5:C:6:ILE:HD11	1.90	0.53
3:A:230:LEU:HD13	3:A:245:ALA:HB2	1.90	0.52
2:F:119:VAL:HG21	2:F:216:LEU:HD21	1.92	0.52
2:F:201:GLN:HB3	7:F:301:ASP:HA	1.92	0.52
1:D:8:ILE:HG13	1:D:23:ASN:HB2	1.93	0.51
4:B:17:ASN:HA	4:B:72:PRO:HG2	1.94	0.50
1:D:111:PRO:HG3	1:D:160:VAL:HG11	1.93	0.49
2:F:241:ARG:HH21	2:F:242:ALA:HB2	1.77	0.49
2:F:126:VAL:HB	2:F:142:LEU:HD21	1.93	0.48
4:B:21:ASN:OD1	4:B:22:PHE:N	2.46	0.48
3:A:115:GLN:HG3	4:B:60:TRP:CH2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:177:LYS:HD2	2:F:185:SER:HB3	1.95	0.48
2:F:134:ILE:HG23	2:F:197:ALA:HB1	1.96	0.48
3:A:13:SER:HB3	3:A:78:LEU:HD13	1.96	0.48
2:F:122:PRO:HB3	2:F:149:PHE:HB3	1.95	0.47
2:F:12:THR:HG21	2:F:80:LEU:HD13	1.97	0.47
3:A:207:GLY:HA2	3:A:240:THR:HB	1.96	0.47
3:A:109:LEU:HD22	3:A:161:GLU:HA	1.97	0.46
2:F:220:ASP:O	2:F:228:LYS:NZ	2.42	0.45
2:F:126:VAL:HG13	2:F:236:ALA:HB3	1.97	0.45
1:D:6:THR:OG1	1:D:25[A]:SER:OG	2.34	0.45
3:A:117:ALA:HB2	4:B:60:TRP:CE2	2.52	0.45
1:D:138:ASP:OD1	2:F:194:ARG:NH1	2.40	0.45
1:D:38:ARG:HB3	1:D:48:LEU:HD11	1.98	0.45
2:F:210:GLN:HG3	2:F:233:ILE:HG23	1.99	0.44
2:F:141:THR:HA	2:F:194:ARG:HA	1.98	0.44
4:B:37:VAL:HG22	4:B:82:VAL:HG22	2.01	0.43
2:F:31:VAL:HG21	2:F:73:SER:HB2	2.01	0.43
3:A:234:ARG:HD2	4:B:10:TYR:CE1	2.54	0.42
3:A:151:ARG:HB3	3:A:154:GLU:HG3	2.01	0.42
2:F:20:LEU:HB2	2:F:75:LEU:HB3	2.02	0.41
1:D:50:LEU:HD12	2:F:101:THR:HB	2.02	0.41
2:F:118:ASN:ND2	2:F:184:ASP:HB2	2.35	0.41
3:A:204:TRP:CE3	3:A:206:LEU:HD21	2.56	0.40
3:A:202:ARG:HD2	3:A:204:TRP:HE1	1.87	0.40
3:A:204:TRP:HE3	3:A:206:LEU:HD21	1.85	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	D	193/204 (95%)	188 (97%)	5 (3%)	0	<a href="#">100</a> <a href="#">100</a>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	239/242 (99%)	228 (95%)	10 (4%)	1 (0%)	34	40
3	A	252/278 (91%)	241 (96%)	11 (4%)	0	100	100
4	B	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
5	C	7/9 (78%)	7 (100%)	0	0	100	100
All	All	789/833 (95%)	754 (96%)	34 (4%)	1 (0%)	51	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	95	ALA

### 5.3.2 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	D	174/182 (96%)	174 (100%)	0	100	100
2	F	209/212 (99%)	205 (98%)	4 (2%)	57	71
3	A	220/237 (93%)	215 (98%)	5 (2%)	50	65
4	B	95/95 (100%)	92 (97%)	3 (3%)	39	52
5	C	7/7 (100%)	7 (100%)	0	100	100
All	All	705/733 (96%)	693 (98%)	12 (2%)	60	74

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

Mol	Chain	Res	Type
2	F	72	HIS
2	F	170	CYS
2	F	192	ARG
2	F	241	ARG
3	A	35	ARG
3	A	113	TYR
3	A	121	LYS

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Mol	Chain	Res	Type
3	A	262	GLN
3	A	271	THR
4	B	45	ARG
4	B	70	PHE
4	B	89	GLN

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

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

10 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	$\# Z  > 2$
8	SO4	F	303	-	4,4,4	0.14	0	6,6,6	0.05	0
6	NAG	D	301	1	14,14,15	0.37	0	17,19,21	0.43	0
6	NAG	D	302	1	14,14,15	0.21	0	17,19,21	0.43	0
7	ASP	F	301	-	6,8,8	1.20	1 (16%)	8,10,10	1.43	2 (25%)
8	SO4	A	302	-	4,4,4	0.14	0	6,6,6	0.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
9	EDO	A	301	-	3,3,3	0.50	0	2,2,2	0.18	0
6	NAG	D	304	1	14,14,15	0.33	0	17,19,21	0.52	0
8	SO4	F	304	-	4,4,4	0.14	0	6,6,6	0.05	0
6	NAG	D	303	1	14,14,15	0.38	0	17,19,21	0.47	0
6	NAG	F	302	2	14,14,15	0.27	0	17,19,21	0.38	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	NAG	D	301	1	-	0/6/23/26	0/1/1/1
6	NAG	D	302	1	-	1/6/23/26	0/1/1/1
7	ASP	F	301	-	-	2/8/8/8	-
9	EDO	A	301	-	-	0/1/1/1	-
6	NAG	D	304	1	-	2/6/23/26	0/1/1/1
6	NAG	D	303	1	-	0/6/23/26	0/1/1/1
6	NAG	F	302	2	-	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)
7	F	301	ASP	OXT-C	-2.13	1.23	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	301	ASP	OXT-C-O	-2.69	117.98	124.09
7	F	301	ASP	OXT-C-CA	2.29	121.18	113.38

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	F	301	ASP	C-CA-CB-CG
6	F	302	NAG	C4-C5-C6-O6
6	F	302	NAG	O5-C5-C6-O6
6	D	304	NAG	C4-C5-C6-O6
6	D	304	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
7	F	301	ASP	N-CA-CB-CG
6	D	302	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	F	301	ASP	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

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	D	195/204 (95%)	0.87	24 (12%) 4 5	49, 72, 119, 158	0
2	F	241/242 (99%)	0.69	17 (7%) 16 19	46, 80, 124, 165	0
3	A	259/278 (93%)	1.52	64 (24%) 0 0	43, 78, 150, 179	0
4	B	100/100 (100%)	2.05	37 (37%) 0 0	58, 102, 155, 176	0
5	C	9/9 (100%)	0.64	0 100 100	49, 50, 62, 64	0
All	All	804/833 (96%)	1.17	142 (17%) 1 1	43, 80, 143, 179	0

All (142) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	B	15	ALA	17.1
3	A	215	LEU	11.7
3	A	261	VAL	11.2
4	B	73	THR	8.7
3	A	273	ARG	7.3
4	B	79	ALA	7.3
3	A	270	LEU	7.3
4	B	99	MET	7.0
3	A	205	ALA	6.6
3	A	276	PRO	6.5
4	B	18	GLY	6.3
3	A	272	LEU	6.3
4	B	45	ARG	6.2
4	B	78	TYR	6.2
3	A	201	LEU	5.7
3	A	266	LEU	5.6
3	A	226	GLN	5.5
3	A	260	HIS	5.3
3	A	192	HIS	5.2
1	D	193	ILE	5.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	F	225	ASP	5.0
1	D	132	SER	4.9
4	B	44	GLU	4.8
3	A	200	THR	4.7
2	F	142	LEU	4.7
1	D	114	GLN	4.7
3	A	248	VAL	4.6
3	A	263	HIS	4.6
3	A	206	LEU	4.6
3	A	257	TYR	4.5
3	A	225	THR	4.5
3	A	230	LEU	4.4
4	B	42	ASN	4.4
4	B	20	SER	4.4
4	B	70	PHE	4.3
4	B	19	LYS	4.2
3	A	269	PRO	4.2
3	A	247	VAL	4.1
3	A	202	ARG	4.1
4	B	72	PRO	4.1
4	B	97	ARG	4.1
1	D	123	LEU	4.1
3	A	214	THR	4.0
4	B	68	THR	4.0
3	A	271	THR	3.9
1	D	121	TYR	3.8
1	D	136	PHE	3.7
3	A	199	ALA	3.7
3	A	258	THR	3.7
3	A	259	CYS	3.7
4	B	77	GLU	3.6
3	A	189	VAL	3.6
4	B	94	LYS	3.6
4	B	74	GLU	3.6
4	B	22	PHE	3.6
4	B	17	ASN	3.6
3	A	198	GLU	3.5
3	A	188	HIS	3.4
2	F	204	ARG	3.4
3	A	243	LYS	3.3
3	A	244	TRP	3.2
3	A	267	PRO	3.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	F	218	GLU	3.2
3	A	213	ILE	3.1
4	B	16	GLU	3.1
3	A	197	HIS	3.1
3	A	274	TRP	3.0
1	D	195	GLU	3.0
3	A	41	ALA	3.0
3	A	108	ARG	3.0
3	A	181	ARG	3.0
4	B	46	ILE	2.9
3	A	143	THR	2.9
3	A	139	ALA	2.9
2	F	137	THR	2.9
2	F	227	ALA	2.9
4	B	7	ILE	2.8
4	B	41	LYS	2.8
3	A	262	GLN	2.8
3	A	134	THR	2.8
2	F	200	TRP	2.8
3	A	236	ALA	2.8
3	A	268	LYS	2.8
4	B	23	LEU	2.8
4	B	69	GLU	2.8
1	D	155	ILE	2.8
1	D	120	VAL	2.7
3	A	136	ALA	2.7
4	B	9	VAL	2.7
3	A	95	LEU	2.7
3	A	275	GLU	2.7
3	A	255	GLN	2.7
1	D	119	ALA	2.7
1	D	182	PHE	2.7
1	D	2	LYS	2.6
2	F	184	ASP	2.6
2	F	195	VAL	2.5
3	A	256	ARG	2.5
2	F	182	LEU	2.5
2	F	87	LEU	2.5
1	D	147[A]	GLN	2.5
4	B	21	ASN	2.5
2	F	163	LYS	2.5
3	A	123	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
3	A	140	ALA	2.4
3	A	245	ALA	2.4
2	F	38	LEU	2.4
3	A	246	ALA	2.4
4	B	1	ILE	2.3
1	D	173	ALA	2.3
3	A	113	TYR	2.3
1	D	186	ASN	2.3
1	D	152	ASP	2.3
2	F	143	VAL	2.3
4	B	76	ASP	2.3
3	A	118	TYR	2.2
4	B	13	HIS	2.2
1	D	113	ILE	2.2
4	B	64	LEU	2.2
4	B	65	LEU	2.2
4	B	40	LEU	2.2
1	D	168	PHE	2.1
4	B	62	PHE	2.1
3	A	124	ILE	2.1
1	D	12	LEU	2.1
1	D	184	CYS	2.1
2	F	222	TRP	2.1
3	A	147	TRP	2.1
3	A	99	TYR	2.1
3	A	228	THR	2.1
1	D	196	ASP	2.1
3	A	204	TRP	2.1
2	F	188	CYS	2.1
1	D	199	PHE	2.1
3	A	142	ILE	2.1
1	D	158	LYS	2.1
3	A	265	GLY	2.0
1	D	133	VAL	2.0
4	B	98	ASP	2.0
3	A	23	ILE	2.0
4	B	0	MET	2.0
2	F	139	LYS	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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
7	ASP	F	301	9/9	0.38	0.55	162,167,168,170	0
6	NAG	D	304	14/15	0.71	0.44	116,121,127,128	0
6	NAG	D	301	14/15	0.77	0.25	85,98,108,110	0
8	SO4	A	302	5/5	0.79	0.19	135,141,149,174	0
8	SO4	F	303	5/5	0.85	0.35	106,108,129,142	0
8	SO4	F	304	5/5	0.85	0.18	108,113,130,131	0
6	NAG	D	303	14/15	0.85	0.22	84,91,95,99	0
6	NAG	D	302	14/15	0.86	0.16	89,104,110,111	0
9	EDO	A	301	4/4	0.88	0.19	61,64,66,68	0
6	NAG	F	302	14/15	0.89	0.18	72,77,81,82	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.