



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 26, 2023 – 01:36 PM EDT

PDB ID : 6CQN  
Title : Crystal structure of F5 TCR -DR11-RQ13 peptide complex  
Authors : Farenc, C.; Gras, S.; Rossjohn, J.  
Deposited on : 2018-03-15  
Resolution : 2.50 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 : 2.35.1  
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) : 2.35.1

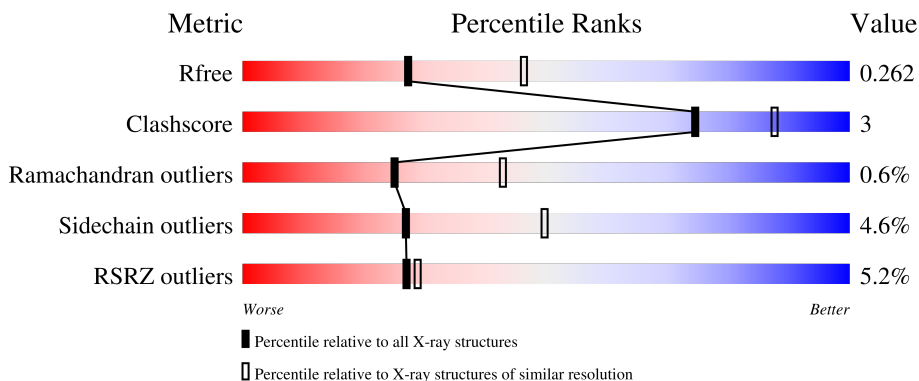
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	A	182	
2	B	190	
3	C	13	
4	D	205	
5	E	245	

## 2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 6871 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
			Total	C	N	O	S			
1	A	178	1464	949	238	272	5	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	182	THR	ALA	conflict	UNP P01903

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-11 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	190	1566	988	274	299	5	0	0	0

- Molecule 3 is a protein called Peptide from Capsid protein p24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	13	113	70	22	21	0	0	0

- Molecule 4 is a protein called F5 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	200	1580	992	263	317	8	0	2	0

- Molecule 5 is a protein called F5 beta chain.

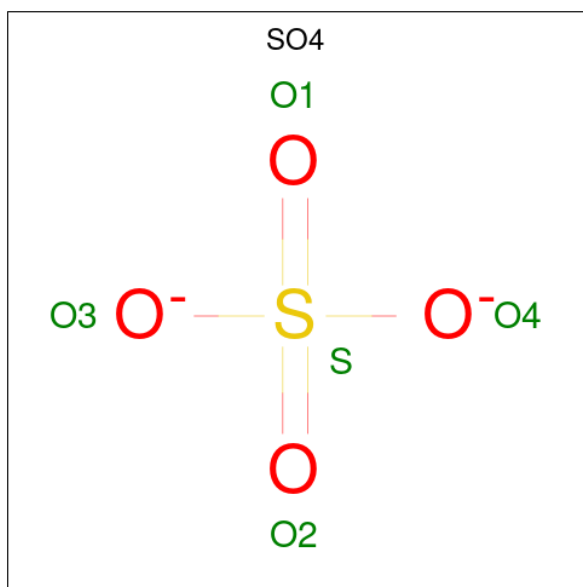
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	244	1965	1246	333	378	8	0	0	0

- 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	A	1	14	8	1	5	0	0
6	A	1	14	8	1	5	0	0

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total O S 5 4 1	0	0
7	B	1	Total O S 5 4 1	0	0
7	B	1	Total O S 5 4 1	0	0
7	E	1	Total O S 5 4 1	0	0

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Cl 1 1	0	0
8	D	1	Total Cl 1 1	0	0

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	C	1	Total Mg 1 1	0	0


- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	41	Total O 41 41	0	0
10	B	25	Total O 25 25	0	0
10	C	2	Total O 2 2	0	0
10	D	23	Total O 23 23	0	0
10	E	41	Total O 41 41	0	0

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

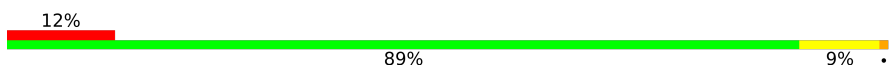
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

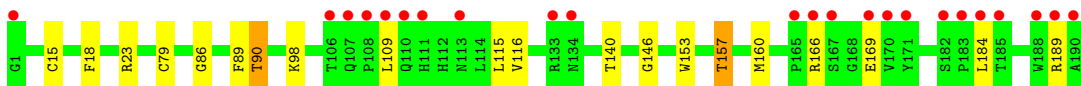
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain

Chain A: 



- Molecule 2: HLA class II histocompatibility antigen, DRB1-11 beta chain

Chain B: 




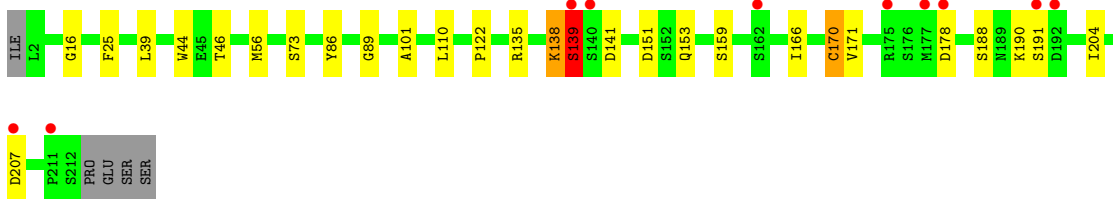
- Molecule 3: Peptide from Capsid protein p24

Chain C: 

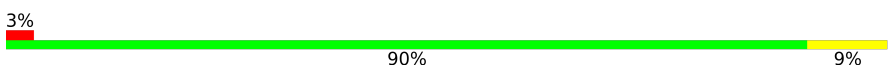
There are no outlier residues recorded for this chain.

- Molecule 4: F5 alpha chain

Chain D: 



- Molecule 5: F5 beta chain

Chain E: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.32Å 205.79Å 70.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.48 – 2.50 41.50 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (42.48-2.50) 100.0 (41.50-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.98 (at 2.51Å)	Xtrriage
Refinement program	BUSTER 2.10.0	Depositor
R, $R_{free}$	0.196 , 0.251 0.207 , 0.262	Depositor DCC
$R_{free}$ test set	2003 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.5	Xtrriage
Anisotropy	0.176	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 43.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6871	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: CL, SO4, NAG, MG

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	0.46	0/1509	0.70	0/2058
2	B	0.44	0/1611	0.70	0/2189
3	C	0.49	0/114	0.68	0/149
4	D	0.47	0/1620	0.69	0/2194
5	E	0.44	0/2019	0.68	0/2744
All	All	0.45	0/6873	0.69	0/9334

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	1464	0	1401	8	0
2	B	1566	0	1455	9	0
3	C	113	0	111	0	0
4	D	1580	0	1506	12	0
5	E	1965	0	1866	10	0
6	A	28	0	26	0	0
7	A	5	0	0	0	0
7	B	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	E	5	0	0	0	0
8	A	1	0	0	0	0
8	D	1	0	0	0	0
9	C	1	0	0	0	0
10	A	41	0	0	0	0
10	B	25	0	0	0	0
10	C	2	0	0	0	0
10	D	23	0	0	0	0
10	E	41	0	0	0	0
All	All	6871	0	6365	36	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 (36) 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:B:15:CYS:HG	2:B:79:CYS:HG	1.06	0.92
5:E:13:THR:HG21	5:E:19:VAL:CG1	2.29	0.62
1:A:91:VAL:HG23	1:A:176:LYS:HB3	1.83	0.61
5:E:13:THR:HG21	5:E:19:VAL:HG11	1.85	0.58
1:A:138:LEU:HB2	1:A:146:ARG:HB2	1.87	0.56
2:B:116:VAL:HG22	2:B:160:MET:HG2	1.90	0.53
4:D:159:SER:HA	4:D:166:ILE:HD12	1.90	0.52
4:D:138:LYS:HA	4:D:139:SER:CB	2.39	0.52
1:A:118:ASN:HB2	1:A:166:GLU:HB2	1.90	0.52
4:D:101:ALA:HB1	4:D:110:LEU:HB3	1.90	0.52
4:D:73:SER:HB2	4:D:86:TYR:HB2	1.90	0.51
1:A:87:PRO:HB3	1:A:112:PHE:HB3	1.93	0.50
2:B:86:GLY:HA2	2:B:89:PHE:CE2	2.48	0.49
4:D:170:CYS:HB3	5:E:187:CYS:SG	2.52	0.49
5:E:133:LEU:HB3	5:E:233:LEU:HD11	1.95	0.48
4:D:151:ASP:OD2	4:D:153:GLN:HB2	2.13	0.48
4:D:122:PRO:HG3	4:D:171:VAL:HG21	1.95	0.48
5:E:13:THR:HG21	5:E:19:VAL:HG12	1.95	0.48
1:A:107:CYS:HB2	1:A:121:TRP:CH2	2.50	0.47
5:E:21:LEU:HD12	5:E:89:LEU:HD23	1.96	0.47
2:B:18:PHE:HB2	2:B:23:ARG:HB3	1.96	0.46
5:E:196:GLN:HB3	5:E:199:LEU:HD13	1.97	0.46
4:D:25:PHE:CD2	4:D:39:LEU:HD13	2.51	0.46
2:B:166:ARG:HB2	2:B:169:GLU:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:146:GLY:O	2:B:157:THR:HG23	2.16	0.45
1:A:91:VAL:CG2	1:A:176:LYS:HB3	2.45	0.44
1:A:122:LEU:HB2	1:A:162:ASP:HB2	2.00	0.44
4:D:138:LYS:HD3	4:D:139:SER:HB2	2.00	0.44
4:D:44:TRP:CZ2	5:E:103:PHE:HZ	2.36	0.43
5:E:10:His:CD2	5:E:170:His:HB3	2.55	0.42
4:D:190:LYS:HB3	4:D:191:SER:HB2	2.01	0.42
2:B:86:GLY:O	2:B:90:THR:HB	2.20	0.41
1:A:29:ASP:HB3	2:B:153:TRP:CE2	2.55	0.41
4:D:16:GLY:O	4:D:89:GLY:HA2	2.20	0.41
5:E:72:PHE:CD1	5:E:76:PHE:HB2	2.56	0.41
2:B:166:ARG:H	2:B:169:GLU:HG3	1.87	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	A	176/182 (97%)	173 (98%)	3 (2%)	0	100	100
2	B	188/190 (99%)	177 (94%)	11 (6%)	0	100	100
3	C	11/13 (85%)	11 (100%)	0	0	100	100
4	D	200/205 (98%)	187 (94%)	10 (5%)	3 (2%)	10	18
5	E	242/245 (99%)	232 (96%)	8 (3%)	2 (1%)	19	35
All	All	817/835 (98%)	780 (96%)	32 (4%)	5 (1%)	25	43

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	46	THR
5	E	73	ASP

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Mol	Chain	Res	Type
5	E	170	HIS
4	D	138	LYS
4	D	139	SER

### 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	A	163/167 (98%)	156 (96%)	7 (4%)	29	53
2	B	170/173 (98%)	162 (95%)	8 (5%)	26	49
3	C	11/11 (100%)	11 (100%)	0	100	100
4	D	179/182 (98%)	170 (95%)	9 (5%)	24	46
5	E	217/218 (100%)	207 (95%)	10 (5%)	27	50
All	All	740/751 (98%)	706 (95%)	34 (5%)	27	50

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	SER
1	A	38	LYS
1	A	46	GLU
1	A	71	GLU
1	A	122	LEU
1	A	132	VAL
1	A	154	LEU
2	B	90	THR
2	B	98	LYS
2	B	109	LEU
2	B	115	LEU
2	B	140	THR
2	B	157	THR
2	B	184	LEU
2	B	189	ARG
4	D	56	MET

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Mol	Chain	Res	Type
4	D	135	ARG
4	D	139	SER
4	D	141	ASP
4	D	170	CYS
4	D	178	ASP
4	D	188	SER
4	D	204	ILE
4	D	207	ASP
5	E	23	CYS
5	E	74	ASP
5	E	77	SER
5	E	80	ARG
5	E	97	GLU
5	E	169	ASP
5	E	170	HIS
5	E	209	ARG
5	E	238	GLU
5	E	260	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	34	GLN
2	B	149	HIS
2	B	177	HIS
5	E	14	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 monosaccharides in this entry.

## 5.6 Ligand geometry

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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
7	SO4	B	202	-	4,4,4	0.11	0	6,6,6	0.17	0
7	SO4	E	301	-	4,4,4	0.15	0	6,6,6	0.06	0
7	SO4	A	203	-	4,4,4	0.17	0	6,6,6	0.05	0
6	NAG	A	201	1	14,14,15	1.93	3 (21%)	17,19,21	1.90	5 (29%)
6	NAG	A	202	1	14,14,15	1.91	5 (35%)	17,19,21	2.07	6 (35%)
7	SO4	B	201	-	4,4,4	0.12	0	6,6,6	0.08	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	A	202	1	-	3/6/23/26	0/1/1/1
6	NAG	A	201	1	-	2/6/23/26	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	201	NAG	O5-C1	4.30	1.50	1.43
6	A	202	NAG	O5-C1	4.24	1.50	1.43
6	A	201	NAG	C7-N2	3.29	1.45	1.34
6	A	202	NAG	C7-N2	2.90	1.44	1.34
6	A	202	NAG	C3-C2	-2.39	1.47	1.52
6	A	202	NAG	C1-C2	-2.31	1.48	1.52
6	A	201	NAG	C3-C2	-2.12	1.48	1.52
6	A	202	NAG	C4-C3	-2.05	1.47	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	201	NAG	O5-C5-C6	4.41	114.12	107.20
6	A	202	NAG	C1-C2-N2	-4.07	103.54	110.49
6	A	201	NAG	C3-C4-C5	3.89	117.18	110.24
6	A	202	NAG	C8-C7-N2	3.68	122.32	116.10
6	A	202	NAG	C1-O5-C5	3.42	116.82	112.19
6	A	201	NAG	O5-C5-C4	2.49	116.89	110.83
6	A	202	NAG	O5-C1-C2	2.40	115.07	111.29
6	A	202	NAG	O7-C7-N2	-2.32	117.68	121.95
6	A	201	NAG	C2-N2-C7	2.31	126.19	122.90
6	A	202	NAG	C3-C4-C5	2.20	114.17	110.24
6	A	201	NAG	O6-C6-C5	2.19	118.81	111.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	202	NAG	C8-C7-N2-C2
6	A	202	NAG	O7-C7-N2-C2
6	A	201	NAG	C1-C2-N2-C7
6	A	201	NAG	C4-C5-C6-O6
6	A	202	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

## 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	A	178/182 (97%)	-0.06	2 (1%) 80 82	21, 39, 65, 80	0
2	B	190/190 (100%)	0.43	23 (12%) 4 4	27, 46, 91, 109	0
3	C	13/13 (100%)	-0.18	0 100 100	24, 31, 46, 75	0
4	D	200/205 (97%)	0.17	10 (5%) 28 30	21, 50, 101, 114	1 (0%)
5	E	244/245 (99%)	0.05	8 (3%) 46 50	21, 47, 78, 118	4 (1%)
All	All	825/835 (98%)	0.14	43 (5%) 27 29	21, 45, 93, 118	5 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	260	ASP	6.7
2	B	109	LEU	6.4
4	D	139	SER	4.5
2	B	189	ARG	4.4
2	B	166	ARG	3.9
2	B	111	HIS	3.7
2	B	190	ALA	3.6
5	E	235	GLU	3.6
2	B	165	PRO	3.5
2	B	167	SER	3.5
2	B	110	GLN	3.4
5	E	199	LEU	3.3
2	B	188	TRP	3.3
4	D	191	SER	3.3
5	E	256	TRP	3.3
2	B	184	LEU	3.2
2	B	170	VAL	3.2
2	B	106	THR	3.2
4	D	178	ASP	3.1
5	E	259	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	1	GLY	2.9
2	B	134	ASN	2.8
4	D	177	MET	2.8
4	D	192	ASP	2.8
5	E	257	GLY	2.7
5	E	221	ARG	2.7
5	E	258	ARG	2.5
2	B	108	PRO	2.5
2	B	133	ARG	2.3
2	B	182	SER	2.3
4	D	175	ARG	2.3
2	B	171	TYR	2.3
4	D	211	PRO	2.2
4	D	207	ASP	2.2
2	B	169	GLU	2.2
2	B	107	GLN	2.2
4	D	140	SER	2.1
4	D	162	SER	2.1
2	B	113	ASN	2.1
1	A	45	LEU	2.0
1	A	171	ASP	2.0
2	B	183	PRO	2.0
2	B	185	THR	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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	SO4	E	301	5/5	0.66	0.20	161,161,161,161	0
7	SO4	A	203	5/5	0.74	0.21	153,154,154,154	0
7	SO4	B	201	5/5	0.76	0.23	144,144,144,144	0
7	SO4	B	202	5/5	0.79	0.19	117,117,118,118	0
6	NAG	A	201	14/15	0.85	0.25	86,91,92,92	0
6	NAG	A	202	14/15	0.87	0.19	57,63,72,73	0
8	CL	A	204	1/1	0.94	0.09	69,69,69,69	0
8	CL	D	301	1/1	0.96	0.21	67,67,67,67	0
9	MG	C	201	1/1	0.99	0.12	22,22,22,22	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.