



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:27 PM UTC

PDB ID : 2CDM / pdb_00002cdm
Title : The structure of TrwC complexed with a 27-mer DNA comprising the recognition hairpin and the cleavage site
Authors : Boer, R.; Russi, S.; Guasch, A.; Lucas, M.; Blanco, A.G.; Perez-Luque, R.; Coll, M.; de la Cruz, F.
Deposited on : 2006-01-25
Resolution : 2.70 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

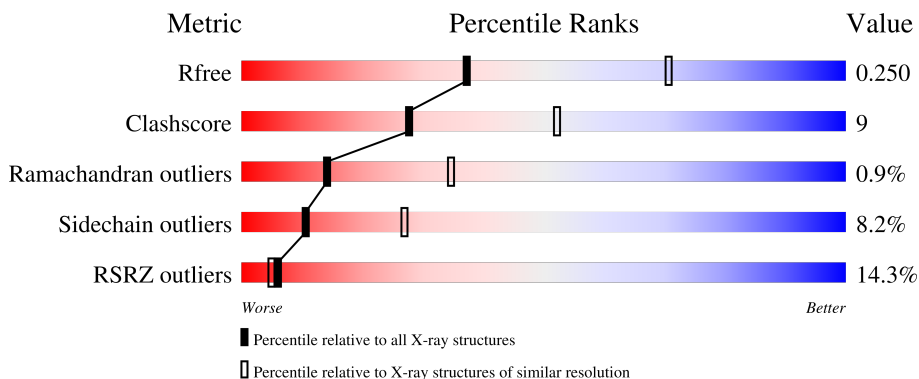
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	293	
1	C	293	
2	B	27	
2	D	27	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5644 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 TRWC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	280	2213	1367	422	420	4	0	0	0
1	C	280	2213	1367	422	420	4	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	PHE	TYR	engineered mutation	UNP Q47673
C	18	PHE	TYR	engineered mutation	UNP Q47673

- Molecule 2 is a DNA chain called 5'-D(*GP*CP*GP*CP*AP*CP*CP*GP*AP*AP *AP*G P*GP*TP*GP*CP*GP*TP*AP*TP*TP*GP*TP*CP*TP*AP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	25	496	235	92	145	24	0	0	1
2	D	24	475	225	87	140	23	0	0	1

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

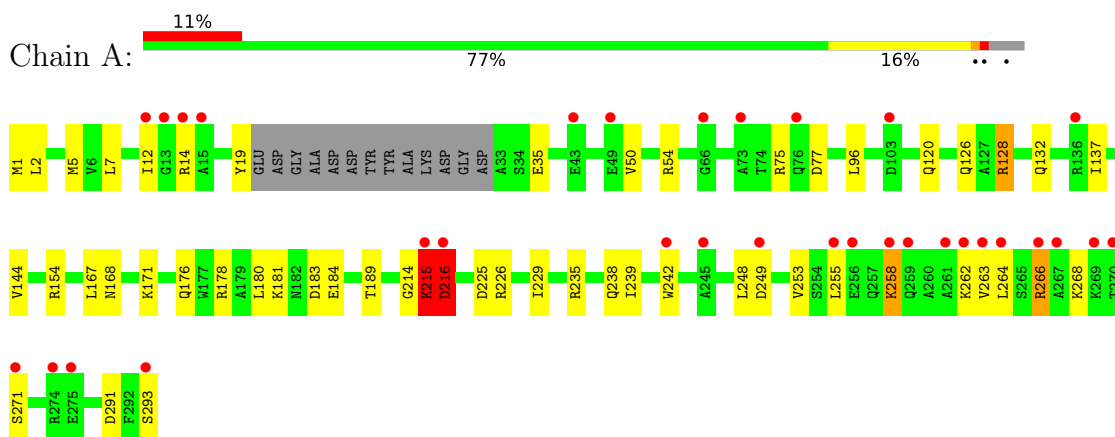
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	120	Total	O	0	0
			120	120		
4	B	14	Total	O	0	0
			14	14		
4	C	97	Total	O	0	0
			97	97		
4	D	6	Total	O	0	0
			6	6		

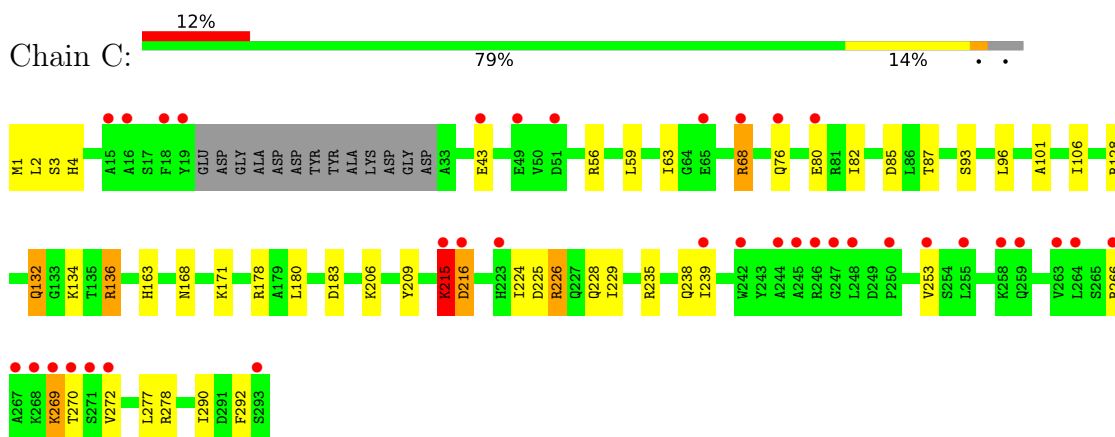
3 Residue-property plots [i](#)

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.

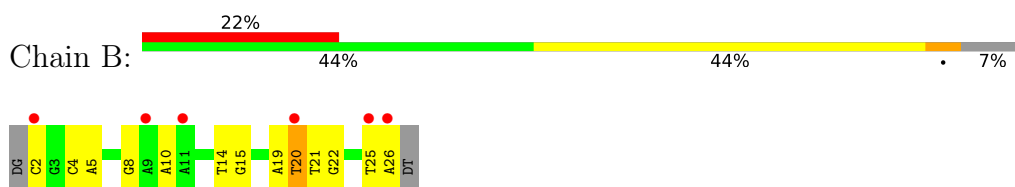
- Molecule 1: TRWC




- Molecule 1: TRWC

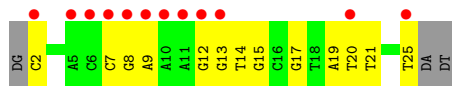


- Molecule 2: 5'-D(*GP*CP*GP*CP*AP*CP*CP*GP*AP*AP *AP*GP*GP*TP*GP*CP*GP*TP*AP*TP*TP*GP*TP*CP*TP*AP*T)-3'



- Molecule 2: 5'-D(*GP*CP*GP*CP*AP*CP*CP*GP*AP*AP *AP*GP*GP*TP*GP*CP*GP*TP*AP*TP*TP*GP*TP*CP*TP*AP*T)-3'

Chain D: 



4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	148.38Å 148.38Å 79.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 2.70 25.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (25.00-2.70) 99.6 (25.00-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 2.72Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.205 , 0.247 0.209 , 0.250	Depositor DCC
R_{free} test set	1377 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	43.1	Xtrriage
Anisotropy	0.010	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.038 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5644	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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: SO4

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	0.61	0/2240	0.84	0/2998
1	C	0.57	0/2240	0.84	1/2998 (0.0%)
2	B	0.49	1/556 (0.2%)	1.13	3/858 (0.3%)
2	D	0.50	1/532 (0.2%)	0.96	0/821
All	All	0.57	2/5568 (0.0%)	0.89	4/7675 (0.1%)

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
1	C	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	DC	O3'-P	-8.34	1.48	1.61
2	B	2	DC	O3'-P	-7.66	1.49	1.61

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	20	DT	O3'-P-O5'	-11.59	86.62	104.00
2	B	20	DT	OP2-P-O3'	-7.45	85.64	108.00
1	C	216	ASP	N-CA-C	-6.80	96.32	110.80
2	B	20	DT	OP1-P-O3'	-6.64	88.09	108.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	215	LYS	Peptide

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	2213	0	2220	37	0
1	C	2213	0	2220	31	0
2	B	496	0	271	23	0
2	D	475	0	260	17	0
3	A	5	0	0	0	0
3	C	5	0	0	0	0
4	A	120	0	0	2	0
4	B	14	0	0	0	0
4	C	97	0	0	3	0
4	D	6	0	0	2	0
All	All	5644	0	4971	93	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 9.

All (93) 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:25:DT:H73	2:B:26:DA:N7	1.89	0.87
1:A:120:GLN:HG2	4:A:2052:HOH:O	1.73	0.87
1:A:14:ARG:HD3	2:B:26:DA:O3'	1.75	0.86
1:A:235:ARG:HH11	1:A:238:GLN:HE21	1.24	0.84
1:A:75:ARG:HB3	1:A:77:ASP:OD1	1.82	0.79
1:A:215:LYS:HA	1:A:215:LYS:NZ	2.02	0.75
1:C:68:ARG:HD3	1:C:68:ARG:H	1.51	0.74
2:D:25:DT:OP1	4:D:2006:HOH:O	2.07	0.70
2:B:19:DA:C4	2:B:20:DT:C7	2.75	0.69
2:D:14:DT:H2'	2:D:15:DG:C8	2.27	0.69
1:A:14:ARG:HH11	2:B:26:DA:H3'	1.57	0.68
1:A:14:ARG:NH1	2:B:26:DA:H3'	2.10	0.66
2:B:19:DA:C4	2:B:20:DT:H71	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:HIS:HE1	2:D:25:DT:H2''	1.61	0.64
1:C:235:ARG:O	1:C:239:ILE:HG12	1.96	0.64
1:C:269:LYS:HG3	1:C:270:THR:H	1.65	0.62
1:C:136:ARG:HH21	1:C:136:ARG:HG3	1.63	0.62
1:A:214:GLY:O	1:A:215:LYS:C	2.43	0.61
1:A:176:GLN:HG3	1:A:178:ARG:NH2	2.17	0.60
1:A:1:MSE:HG2	2:B:22:DG:C2	2.36	0.60
1:A:291:ASP:C	1:A:293:SER:H	2.09	0.59
1:A:215:LYS:HA	1:A:215:LYS:HZ1	1.66	0.59
2:B:25:DT:C6	2:B:25:DT:C5'	2.86	0.59
2:B:25:DT:C6	2:B:25:DT:H5''	2.38	0.58
2:B:10:DA:H2'	2:B:10:DA:N3	2.17	0.58
2:B:19:DA:C4	2:B:20:DT:H73	2.38	0.58
2:D:25:DT:P	4:D:2006:HOH:O	2.60	0.58
1:C:136:ARG:HH21	1:C:136:ARG:CG	2.16	0.58
1:C:178:ARG:HE	2:D:13:DG:H5''	1.68	0.57
1:A:1:MSE:HE1	2:B:21:DT:C2	2.40	0.56
1:A:168:ASN:ND2	1:A:180:LEU:H	2.02	0.56
2:D:19:DA:C4	2:D:20:DT:H73	2.41	0.56
2:D:19:DA:C4	2:D:20:DT:C7	2.89	0.55
1:A:235:ARG:HH11	1:A:238:GLN:NE2	2.00	0.55
1:C:215:LYS:O	1:C:215:LYS:HG2	2.06	0.55
1:A:235:ARG:O	1:A:239:ILE:HG12	2.07	0.54
1:A:215:LYS:O	1:A:216:ASP:HB2	2.09	0.53
1:C:235:ARG:HH11	1:C:238:GLN:HE21	1.56	0.53
1:A:235:ARG:NH1	1:A:238:GLN:HE21	2.02	0.52
2:B:19:DA:C2	2:B:20:DT:H73	2.45	0.52
1:C:59:LEU:HD22	1:C:82:ILE:HD12	1.92	0.51
1:C:272:VAL:HG21	1:C:277:LEU:HD22	1.91	0.51
1:C:76:GLN:H	2:D:7:DC:H5'	1.76	0.51
2:B:19:DA:N3	2:B:20:DT:H73	2.26	0.51
1:A:215:LYS:HA	1:A:215:LYS:HZ2	1.75	0.51
1:C:168:ASN:ND2	1:C:180:LEU:H	2.07	0.51
2:B:8:DG:H21	2:B:10:DA:H2	1.57	0.50
1:A:176:GLN:HE21	1:A:178:ARG:HH22	1.59	0.50
1:C:101:ALA:HB2	1:C:292:PHE:CG	2.47	0.49
1:A:225:ASP:O	1:A:229:ILE:HG12	2.11	0.49
2:B:4:DC:H2''	2:B:5:DA:C8	2.48	0.49
2:B:25:DT:H71	2:B:26:DA:H62	1.76	0.49
2:B:25:DT:H71	2:B:26:DA:N6	2.26	0.49
1:C:136:ARG:HG3	1:C:136:ARG:NH2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MSE:HE1	2:D:21:DT:C2	2.48	0.49
1:C:168:ASN:ND2	4:C:2054:HOH:O	2.46	0.48
1:A:258:LYS:HG2	1:A:262:LYS:HE3	1.94	0.48
2:D:19:DA:N3	2:D:20:DT:H73	2.27	0.48
1:A:226:ARG:HB2	4:A:2099:HOH:O	2.14	0.47
1:A:144:VAL:HG12	1:A:167:LEU:HD12	1.96	0.47
2:D:8:DG:H2''	2:D:9:DA:C8	2.50	0.47
1:A:154:ARG:HH22	1:A:266:ARG:HH21	1.63	0.47
2:B:25:DT:H73	2:B:26:DA:C5	2.49	0.47
1:C:76:GLN:N	2:D:7:DC:OP1	2.48	0.46
1:A:19:TYR:CE2	1:A:50:VAL:O	2.69	0.46
1:C:93:SER:HB2	1:C:224:ILE:HD12	1.98	0.46
1:C:228:GLN:HB3	1:C:290:ILE:HD11	1.98	0.45
1:C:93:SER:HB3	1:C:229:ILE:HD11	1.99	0.45
1:C:132:GLN:C	1:C:134:LYS:H	2.24	0.45
1:C:235:ARG:NH1	1:C:238:GLN:HE21	2.15	0.44
1:A:235:ARG:NH2	1:A:266:ARG:HD2	2.32	0.44
1:C:56:ARG:HD2	4:C:2024:HOH:O	2.18	0.44
1:A:54:ARG:HA	1:A:54:ARG:HD2	1.86	0.44
1:C:225:ASP:OD1	1:C:228:GLN:HG3	2.18	0.44
1:A:128:ARG:NH2	2:B:15:DG:O6	2.44	0.43
1:A:126:GLN:OE1	1:A:184:GLU:HG2	2.18	0.43
1:C:4:HIS:HA	1:C:85:ASP:O	2.19	0.43
1:C:226:ARG:HD2	4:C:2077:HOH:O	2.19	0.42
2:B:19:DA:N9	2:B:20:DT:H71	2.34	0.42
1:C:128:ARG:NH2	2:D:15:DG:O6	2.39	0.42
1:A:154:ARG:HH22	1:A:266:ARG:NH2	2.17	0.41
2:B:14:DT:H2'	2:B:15:DG:C8	2.55	0.41
1:C:87:THR:HG21	2:D:25:DT:H1'	2.02	0.41
1:C:106:ILE:HD11	1:C:209:TYR:CE1	2.54	0.41
2:D:12:DG:H2''	2:D:13:DG:O5'	2.21	0.41
1:A:137:ILE:HD13	1:A:181:LYS:HE2	2.03	0.41
1:A:235:ARG:HD2	1:A:238:GLN:NE2	2.36	0.41
1:A:242:TRP:CZ2	1:A:264:LEU:HD13	2.56	0.41
1:A:255:LEU:HD21	2:B:20:DT:H72	2.02	0.40
1:A:215:LYS:O	1:A:216:ASP:CB	2.69	0.40
1:C:183:ASP:OD2	2:D:17:DG:N2	2.49	0.40
2:D:19:DA:C4	2:D:20:DT:H71	2.55	0.40
1:A:168:ASN:HD22	1:A:180:LEU:H	1.69	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	276/293 (94%)	262 (95%)	11 (4%)	3 (1%)	11	29
1	C	276/293 (94%)	258 (94%)	16 (6%)	2 (1%)	18	41
All	All	552/586 (94%)	520 (94%)	27 (5%)	5 (1%)	14	35

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	ASP
1	A	271	SER
1	A	215	LYS
1	C	215	LYS
1	C	216	ASP

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	225/230 (98%)	205 (91%)	20 (9%)	9	23
1	C	225/230 (98%)	208 (92%)	17 (8%)	12	30
All	All	450/460 (98%)	413 (92%)	37 (8%)	10	27

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU

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Mol	Chain	Res	Type
1	A	5	MSE
1	A	7	LEU
1	A	12	ILE
1	A	35	GLU
1	A	96	LEU
1	A	128	ARG
1	A	132	GLN
1	A	171	LYS
1	A	183	ASP
1	A	189	THR
1	A	215	LYS
1	A	216	ASP
1	A	248	LEU
1	A	249	ASP
1	A	253	VAL
1	A	258	LYS
1	A	263	VAL
1	A	266	ARG
1	A	268	LYS
1	C	2	LEU
1	C	3	SER
1	C	43	GLU
1	C	63	ILE
1	C	68	ARG
1	C	80	GLU
1	C	96	LEU
1	C	132	GLN
1	C	136	ARG
1	C	171	LYS
1	C	206	LYS
1	C	215	LYS
1	C	226	ARG
1	C	253	VAL
1	C	266	ARG
1	C	269	LYS
1	C	278	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	62	ASN

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Mol	Chain	Res	Type
1	A	132	GLN
1	A	168	ASN
1	A	176	GLN
1	A	197	ASN
1	A	202	HIS
1	A	218	ASN
1	A	238	GLN
1	C	62	ASN
1	C	126	GLN
1	C	132	GLN
1	C	163	HIS
1	C	168	ASN
1	C	197	ASN
1	C	218	ASN
1	C	238	GLN
1	C	257	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](#)

2 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
3	SO4	C	1294	-	4,4,4	0.23	0	6,6,6	0.25	0
3	SO4	A	1294	-	4,4,4	0.24	0	6,6,6	0.28	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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, 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	276/293 (94%)	0.35	32 (11%) 9 8	15, 33, 85, 92	28 (10%)
1	C	276/293 (94%)	0.62	36 (13%) 7 6	20, 42, 90, 102	9 (3%)
2	B	25/27 (92%)	0.75	6 (24%) 2 1	28, 55, 88, 93	0
2	D	24/27 (88%)	1.46	12 (50%) 0 0	29, 68, 105, 107	0
All	All	601/640 (93%)	0.54	86 (14%) 6 5	15, 38, 89, 107	37 (6%)

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	256	GLU	7.9
1	C	76	GLN	7.6
1	A	216	ASP	5.9
1	A	275	GLU	5.9
1	C	68	ARG	5.7
1	C	258	LYS	5.5
1	A	43	GLU	5.2
1	A	15	ALA	5.1
1	C	259	GLN	5.1
1	C	43	GLU	4.9
1	A	76	GLN	4.8
1	C	266	ARG	4.7
1	A	136	ARG	4.6
1	A	293	SER	4.4
1	C	293	SER	4.3
2	D	25	DT	4.3
1	A	264	LEU	4.0
1	A	242	TRP	3.9
2	B	11	DA	3.9
1	C	19	TYR	3.8
1	C	270	THR	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	266	ARG	3.7
1	C	255	LEU	3.7
1	C	15	ALA	3.7
2	D	20	DT	3.5
1	C	267	ALA	3.5
1	C	264	LEU	3.4
1	C	244	ALA	3.4
1	C	216	ASP	3.4
2	B	2	DC	3.3
1	C	253	VAL	3.2
1	A	255	LEU	3.1
1	A	270	THR	3.1
1	C	242	TRP	3.0
1	A	249	ASP	3.0
1	A	215	LYS	2.9
1	C	269	LYS	2.9
1	A	261	ALA	2.9
1	A	259	GLN	2.9
1	C	246	ARG	2.9
1	C	215	LYS	2.9
2	B	26	DA	2.7
1	C	250	PRO	2.7
1	A	66	GLY	2.7
1	A	258	LYS	2.7
2	D	9	DA	2.7
1	C	263	VAL	2.7
1	C	248	LEU	2.7
2	D	11	DA	2.7
2	D	5	DA	2.6
1	A	271	SER	2.6
1	A	269	LYS	2.6
1	A	49	GLU	2.6
1	A	263	VAL	2.6
2	D	6	DC	2.5
1	A	245	ALA	2.5
2	B	25	DT	2.5
1	C	247	GLY	2.5
1	C	51	ASP	2.5
1	C	271	SER	2.4
2	D	2	DC	2.4
2	B	20	DT	2.4
1	A	267	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	16	ALA	2.3
1	C	245	ALA	2.3
1	A	262	LYS	2.3
2	B	9	DA	2.2
1	C	268	LYS	2.2
1	A	14	ARG	2.2
1	C	272	VAL	2.2
1	C	223	HIS	2.2
1	C	239	ILE	2.2
1	A	12	ILE	2.2
1	C	65	GLU	2.1
1	A	73	ALA	2.1
1	A	274	ARG	2.1
2	D	12	DG	2.1
1	C	80	GLU	2.1
2	D	13	DG	2.1
1	A	13	GLY	2.1
1	A	103	ASP	2.0
1	C	18	PHE	2.1
2	D	7	DC	2.0
1	C	49	GLU	2.0
2	D	8	DG	2.0
2	D	10	DA	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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
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3	SO4	A	1294	5/5	0.96	0.09	51,52,53,54	0
3	SO4	C	1294	5/5	0.97	0.07	48,49,49,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.