



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:20 PM UTC

PDB ID : 7H4E / pdb_00007h4e
Title : Group deposition for crystallographic fragment screening of Cocksackievirus A16 (G-10) 2A protease – Crystal structure of Cocksackievirus A16 (G-10) 2A protease in complex with Z17497990 (A71EV2A-x0739)
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Deposited on : 2024-04-04
Resolution : 1.58 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)

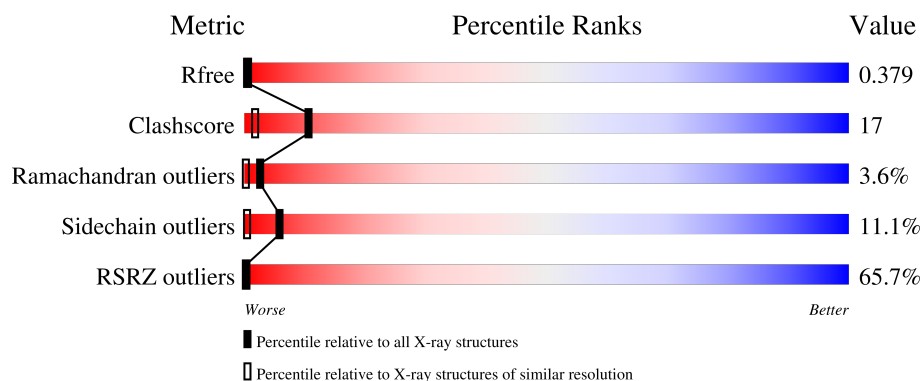
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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	150	

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:

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	S07	A	201	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 1362 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.

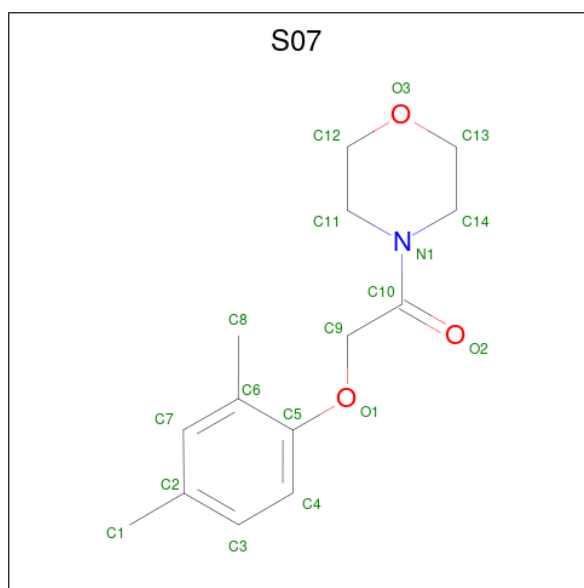
- Molecule 1 is a protein called Protease 2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	140	1103	686	196	214	7	0	3	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLN	-	expression tag	UNP Q65900
A	2	GLU	-	expression tag	UNP Q65900
A	3	GLN	-	expression tag	UNP Q65900
A	4	THR	-	expression tag	UNP Q65900
A	5	GLY	-	expression tag	UNP Q65900
A	6	GLY	-	expression tag	UNP Q65900

- Molecule 2 is 2-(2,4-dimethylphenoxy)-1-morpholin-4-yl-ethanone (CCD ID: S07) (formula: $C_{14}H_{19}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			18	14	1	3		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



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

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

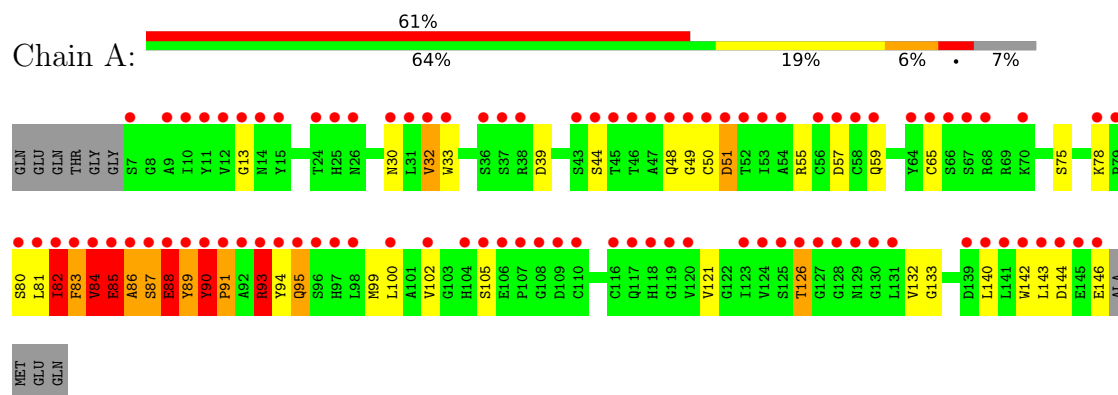
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	219	Total	O	0	0
			219	219		

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: Protease 2A



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	85.94Å 56.43Å 32.24Å 90.00° 94.71° 90.00°	Depositor
Resolution (Å)	42.86 – 1.58 42.86 – 1.58	Depositor EDS
% Data completeness (in resolution range)	98.7 (42.86-1.58) 98.8 (42.86-1.58)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 1.58Å)	Xtriage
Refinement program	REFMAC 5.8.0267, REFMAC5	Depositor
R, R_{free}	0.270 , 0.346 0.320 , 0.379	Depositor DCC
R_{free} test set	1081 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 82.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	1362	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.84% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, DMS, S07, 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	1.29	5/1129 (0.4%)	1.66	25/1535 (1.6%)

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	A	1	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	83	PHE	N-CA	9.00	1.56	1.46
1	A	84	VAL	N-CA	7.50	1.55	1.46
1	A	102	VAL	C-O	5.76	1.29	1.24
1	A	82	ILE	C-N	5.25	1.40	1.33
1	A	65	CYS	C-O	5.02	1.29	1.23

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	91	PRO	CB-CA-C	-9.93	95.18	111.56
1	A	89	TYR	N-CA-C	-8.93	91.77	110.80
1	A	83	PHE	N-CA-C	8.74	120.17	108.38
1	A	90	TYR	N-CA-CB	8.21	126.03	109.28
1	A	89	TYR	CA-C-N	-8.21	106.75	121.69
1	A	89	TYR	C-N-CA	-8.21	106.75	121.69
1	A	88	GLU	CB-CA-C	7.39	125.12	110.42
1	A	82	ILE	O-C-N	-7.26	113.50	122.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	TYR	N-CA-CB	6.76	121.91	110.49
1	A	88	GLU	N-CA-CB	-6.56	99.41	110.49
1	A	93	ARG	CA-C-O	-6.28	114.56	121.28
1	A	85	GLU	N-CA-C	6.25	120.74	108.18
1	A	83	PHE	CA-CB-CG	5.99	119.79	113.80
1	A	91	PRO	N-CA-C	-5.92	100.28	112.47
1	A	51	ASP	CA-C-N	5.84	131.97	122.81
1	A	51	ASP	C-N-CA	5.84	131.97	122.81
1	A	84	VAL	N-CA-C	5.68	121.15	109.34
1	A	32	VAL	N-CA-C	-5.52	106.81	111.56
1	A	51	ASP	CA-C-O	-5.51	114.75	121.36
1	A	85	GLU	CB-CA-C	-5.49	102.69	111.86
1	A	95	GLN	CB-CA-C	5.19	120.75	110.42
1	A	91	PRO	CA-C-N	-5.18	111.64	121.54
1	A	91	PRO	C-N-CA	-5.18	111.64	121.54
1	A	85	GLU	CB-CG-CD	-5.18	103.79	112.60
1	A	90	TYR	O-C-N	5.01	125.38	121.47

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	95	GLN	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	82	ILE	Mainchain

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	1103	0	1034	36	0
2	A	18	0	0	0	0
3	A	1	0	0	0	0
4	A	16	0	24	1	0
5	A	5	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	219	0	0	26	2
All	All	1362	0	1058	37	3

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 17.

All (37) 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)
1:A:88:GLU:HA	6:A:312:HOH:O	1.05	1.20
1:A:39:ASP:HB2	1:A:93:ARG:HH22	1.46	0.80
1:A:32:VAL:O	6:A:301:HOH:O	2.02	0.78
1:A:86:ALA:HB2	6:A:495:HOH:O	1.84	0.76
1:A:84:VAL:HG13	6:A:475:HOH:O	1.86	0.75
1:A:49:GLY:O	6:A:302:HOH:O	2.04	0.73
1:A:78:LYS:O	6:A:303:HOH:O	2.06	0.73
1:A:82:ILE:HG21	1:A:100:LEU:HD11	1.73	0.70
1:A:55:ARG:O	6:A:304:HOH:O	2.10	0.68
1:A:51:ASP:OD2	6:A:305:HOH:O	2.14	0.65
1:A:85:GLU:HG3	6:A:406:HOH:O	1.97	0.63
1:A:39:ASP:HB2	1:A:93:ARG:NH2	2.14	0.62
1:A:33:TRP:HA	6:A:301:HOH:O	2.04	0.56
1:A:93:ARG:HD2	6:A:315:HOH:O	2.04	0.56
1:A:30:ASN:HB3	1:A:44:SER:OG	2.07	0.55
1:A:50:CYS:HA	6:A:302:HOH:O	2.06	0.55
1:A:13:GLY:O	1:A:48:GLN:HA	2.07	0.54
1:A:78:LYS:HB2	6:A:366:HOH:O	2.07	0.54
1:A:144:ASP:OD2	6:A:306:HOH:O	2.18	0.54
1:A:90:TYR:N	6:A:323:HOH:O	2.39	0.54
1:A:78:LYS:HA	6:A:403:HOH:O	2.07	0.53
1:A:142:TRP:NE1	6:A:313:HOH:O	2.32	0.53
1:A:88:GLU:HB2	6:A:311:HOH:O	2.08	0.52
1:A:140:LEU:HB2	1:A:143:LEU:HD12	1.91	0.52
1:A:126:THR:O	1:A:133:GLY:N	2.33	0.51
1:A:93:ARG:NH1	6:A:315:HOH:O	2.35	0.51
4:A:203:DMS:H11	6:A:368:HOH:O	2.11	0.51
1:A:126:THR:HG22	6:A:343:HOH:O	2.14	0.48
1:A:84:VAL:HG13	6:A:364:HOH:O	2.13	0.48
1:A:105:SER:HB2	1:A:132:VAL:HB	1.95	0.47
1:A:99:MET:HE1	1:A:121:VAL:HG12	1.96	0.47
1:A:59:GLN:O	1:A:75:SER:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57[A]:ASP:HA	6:A:336:HOH:O	2.19	0.43
1:A:82:ILE:O	1:A:94:TYR:C	2.62	0.42
1:A:49:GLY:C	6:A:302:HOH:O	2.58	0.41
1:A:55:ARG:NE	6:A:306:HOH:O	2.54	0.40
1:A:48:GLN:NE2	6:A:338:HOH:O	2.53	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:374:HOH:O	6:A:420:HOH:O[1_556]	1.88	0.32
5:A:207:SO4:O3	5:A:207:SO4:O3[2_556]	1.99	0.21
6:A:451:HOH:O	6:A:472:HOH:O[1_554]	2.08	0.12

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	A	141/150 (94%)	127 (90%)	9 (6%)	5 (4%)	3 0

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	95	GLN
1	A	87	SER
1	A	88	GLU
1	A	91	PRO
1	A	86	ALA

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	A	120/124 (97%)	106 (88%)	14 (12%)	5 0

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80[A]	SER
1	A	80[B]	SER
1	A	81	LEU
1	A	82	ILE
1	A	83	PHE
1	A	84	VAL
1	A	85	GLU
1	A	87	SER
1	A	88	GLU
1	A	89	TYR
1	A	90	TYR
1	A	93	ARG
1	A	126	THR
1	A	146	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 7 ligands modelled in this entry, 1 is 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
4	DMS	A	205	-	3,3,3	0.22	0	3,3,3	0.04	0
2	S07	A	201	-	19,19,19	0.69	1 (5%)	25,25,25	1.16	3 (12%)
4	DMS	A	203	-	3,3,3	0.22	0	3,3,3	0.17	0
4	DMS	A	204	-	3,3,3	0.27	0	3,3,3	0.12	0
4	DMS	A	206	-	3,3,3	0.28	0	3,3,3	0.07	0
5	SO4	A	207	-	4,4,4	0.35	0	6,6,6	0.07	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
2	S07	A	201	-	-	8/9/17/17	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	201	S07	O1-C9	-2.27	1.37	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	S07	O1-C9-C10	-3.79	99.42	109.83
2	A	201	S07	C14-N1-C10	-2.94	113.14	122.83
2	A	201	S07	C11-N1-C10	2.43	130.84	122.83

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	S07	C9-C10-N1-C11
2	A	201	S07	C9-C10-N1-C14
2	A	201	S07	O2-C10-N1-C14
2	A	201	S07	O2-C10-C9-O1
2	A	201	S07	C6-C5-O1-C9
2	A	201	S07	C4-C5-O1-C9
2	A	201	S07	C10-C9-O1-C5
2	A	201	S07	O2-C10-N1-C11

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	203	DMS	1	0
5	A	207	SO4	0	1

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	140/150 (93%)	4.84	92 (65%) 0 0	4, 21, 47, 96	35 (25%)

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	84	VAL	21.0
1	A	83	PHE	19.3
1	A	91	PRO	19.1
1	A	86	ALA	18.6
1	A	92	ALA	17.8
1	A	81	LEU	17.6
1	A	89	TYR	17.5
1	A	90	TYR	17.5
1	A	123	ILE	15.1
1	A	87	SER	14.8
1	A	124	VAL	14.6
1	A	94	TYR	14.0
1	A	88	GLU	13.0
1	A	93	ARG	12.8
1	A	110	CYS	11.1
1	A	36[A]	SER	11.0
1	A	80[A]	SER	10.8
1	A	96	SER	10.8
1	A	130	GLY	10.7
1	A	104	HIS	10.3
1	A	98	LEU	10.0
1	A	108	GLY	9.9
1	A	95	GLN	9.9
1	A	97	HIS	9.3
1	A	47	ALA	8.8
1	A	85	GLU	8.8
1	A	129	ASN	8.3

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Mol	Chain	Res	Type	RSRZ
1	A	49	GLY	8.3
1	A	82	ILE	8.1
1	A	48	GLN	8.0
1	A	105	SER	7.6
1	A	15	TYR	7.4
1	A	125	SER	7.2
1	A	128	GLY	6.8
1	A	141	LEU	6.7
1	A	12	VAL	6.4
1	A	109	ASP	6.2
1	A	57[A]	ASP	6.0
1	A	126	THR	5.9
1	A	13	GLY	5.9
1	A	107	PRO	5.8
1	A	45	THR	5.7
1	A	46	THR	5.7
1	A	142	TRP	5.7
1	A	146	GLU	5.2
1	A	14	ASN	5.1
1	A	106	GLU	4.7
1	A	140	LEU	4.6
1	A	50	CYS	4.5
1	A	37	SER	4.4
1	A	53	ILE	4.4
1	A	145	GLU	4.4
1	A	11	TYR	4.3
1	A	56	CYS	4.3
1	A	79	PRO	4.2
1	A	100	LEU	4.1
1	A	58	CYS	4.0
1	A	52	THR	4.0
1	A	143	LEU	3.8
1	A	44	SER	3.7
1	A	119	GLY	3.7
1	A	102	VAL	3.7
1	A	30	ASN	3.5
1	A	144	ASP	3.5
1	A	31	LEU	3.4
1	A	139	ASP	3.2
1	A	67	SER	3.2
1	A	33	TRP	3.2
1	A	32	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	25	HIS	3.0
1	A	54	ALA	3.0
1	A	10	ILE	2.9
1	A	127	GLY	2.9
1	A	59	GLN	2.8
1	A	116	CYS	2.8
1	A	117	GLN	2.6
1	A	26	ASN	2.6
1	A	78	LYS	2.5
1	A	120	VAL	2.5
1	A	65	CYS	2.5
1	A	118	HIS	2.5
1	A	66	SER	2.4
1	A	68	ARG	2.4
1	A	51	ASP	2.4
1	A	38	ARG	2.3
1	A	70	LYS	2.3
1	A	43	SER	2.3
1	A	7	SER	2.2
1	A	9	ALA	2.1
1	A	131	LEU	2.1
1	A	64	TYR	2.1
1	A	24	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 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($\text{\AA}^2$)	Q<0.9
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	S07	A	201	18/18	0.44	0.45	27,33,39,39	18
4	DMS	A	205	4/4	0.58	0.35	105,112,112,112	0
4	DMS	A	203	4/4	0.60	0.32	106,108,112,113	0
4	DMS	A	206	4/4	0.66	0.30	69,76,81,84	0
4	DMS	A	204	4/4	0.68	0.24	62,67,71,71	0
5	SO4	A	207	5/5	0.68	0.23	141,145,154,161	0
3	ZN	A	202	1/1	0.95	0.09	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.