



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 11:28 am BST

PDB ID : 3IEK
Title : Crystal Structure of native TTHA0252 from *Thermus thermophilus* HB8
Authors : Ishikawa, H.; Nakagawa, N.; Kuramitsu, S.; Yokoyama, S.; Masui, R.
Deposited on : 2009-07-22
Resolution : 2.05 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 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)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

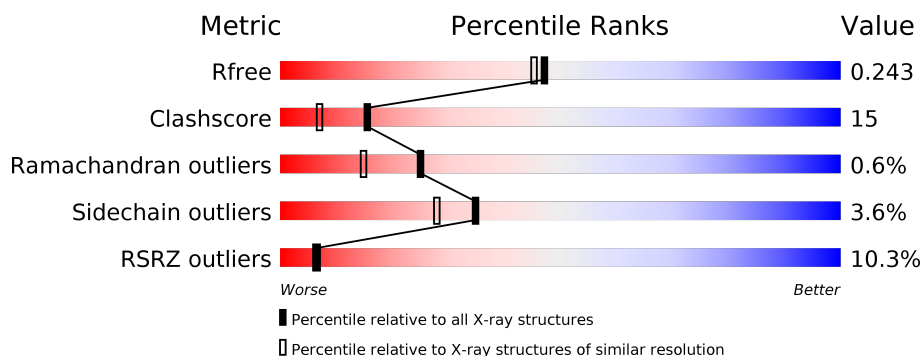
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 on 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	431	<div> <div>84%</div> <div>15%</div> <div>.</div> </div>
1	B	431	<div> <div>77%</div> <div>22%</div> </div>
1	C	431	<div> <div>14%</div> <div>67%</div> <div>31%</div> <div>.</div> </div>
1	D	431	<div> <div>25%</div> <div>61%</div> <div>35%</div> <div>.</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	450	-	-	X	X
2	SO4	A	451	-	-	X	-
2	SO4	B	453	-	-	X	-
2	SO4	C	448	-	-	-	X
2	SO4	C	450	-	-	-	X
2	SO4	C	454	-	-	X	-
2	SO4	D	434	-	-	-	X
3	FLC	A	460	-	-	X	-
3	FLC	B	463	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 14435 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 Ribonuclease TTHA0252.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	0	0
			3326	2127	597	594	8			
1	B	431	Total	C	N	O	S	0	0	0
			3326	2127	597	594	8			
1	C	431	Total	C	N	O	S	0	0	0
			3326	2127	597	594	8			
1	D	431	Total	C	N	O	S	0	0	0
			3326	2127	597	594	8			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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

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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

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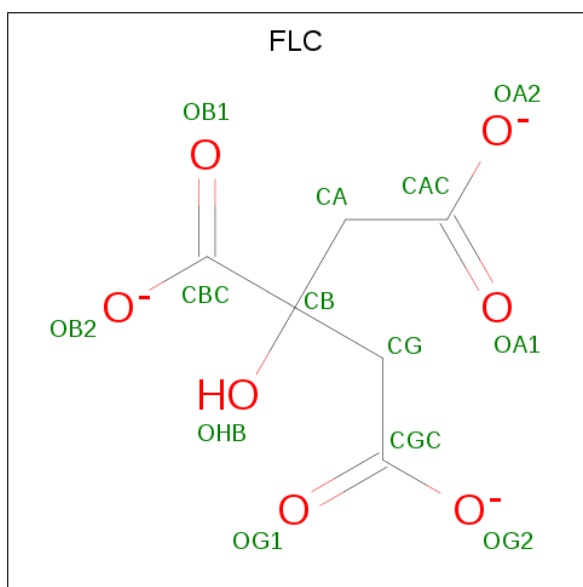
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: C₆H₅O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Zn	0	0
			2	2		
4	A	2	Total	Zn	0	0
			2	2		
4	D	2	Total	Zn	0	0
			2	2		
4	C	2	Total	Zn	0	0
			2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	244	Total	O	0	0
			244	244		
5	B	196	Total	O	0	0
			196	196		
5	C	78	Total	O	0	0
			78	78		

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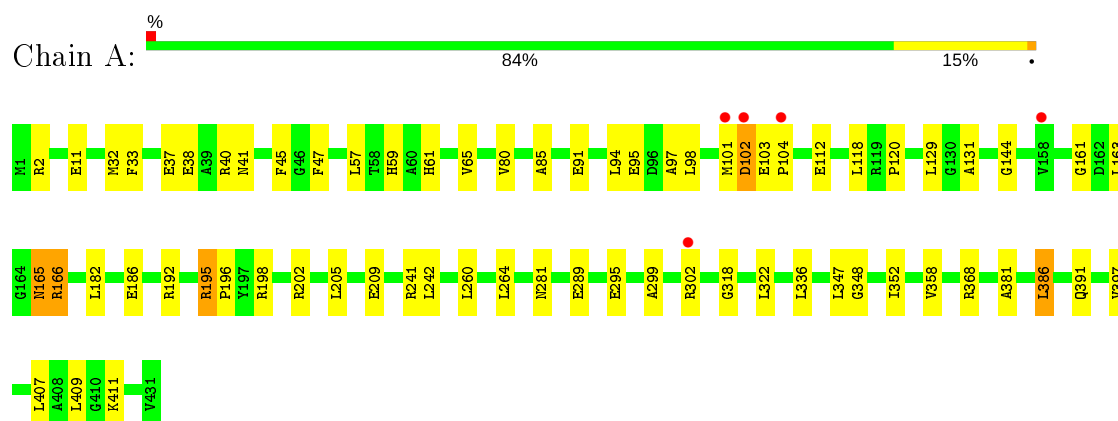
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	79	Total	O	0	0
			79	79		

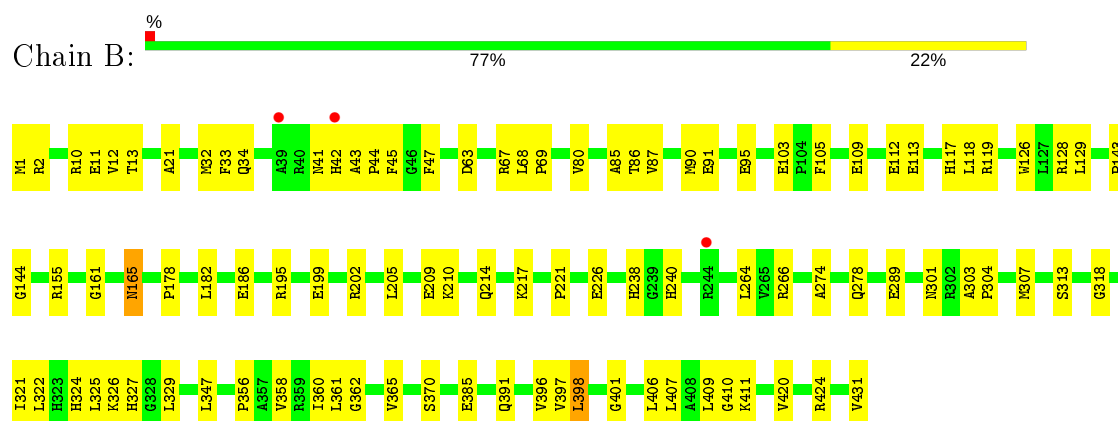
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

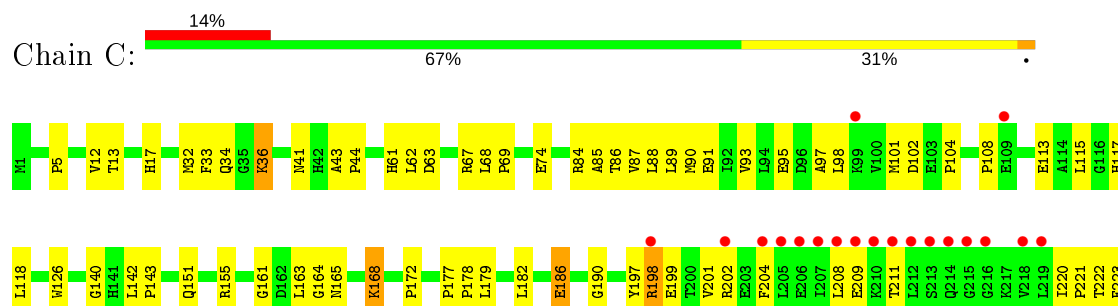
• Molecule 1: Ribonuclease TTHA0252

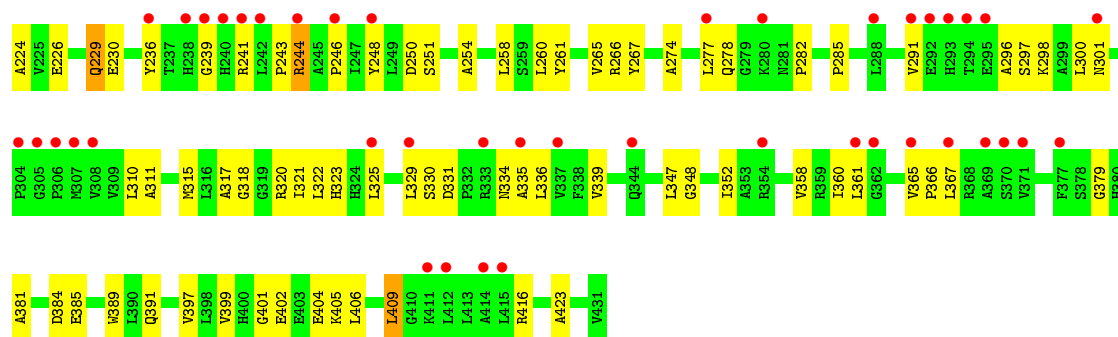


• Molecule 1: Ribonuclease TTHA0252

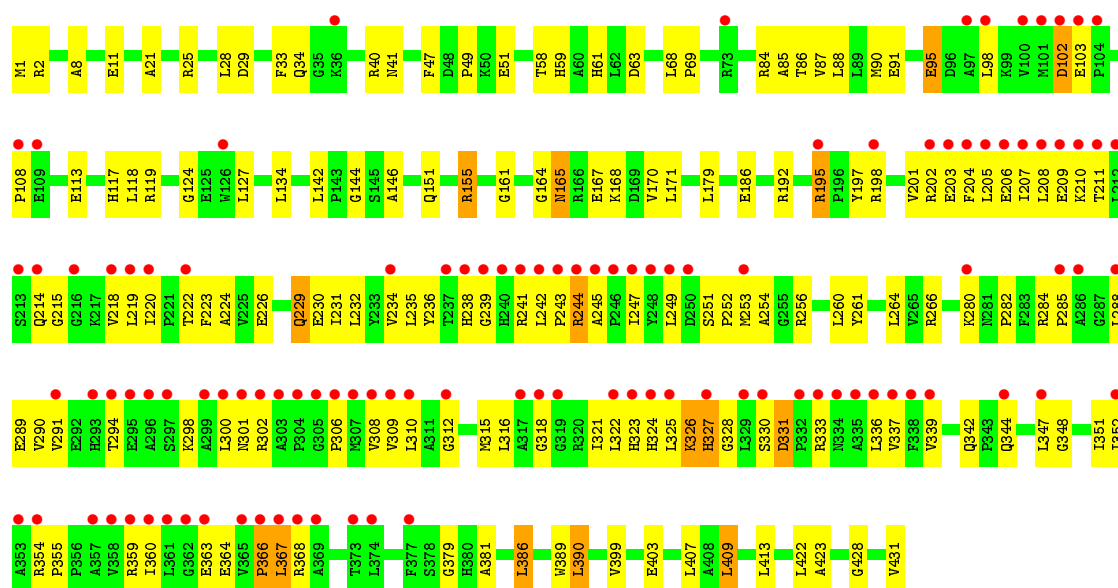


• Molecule 1: Ribonuclease TTHA0252





● Molecule 1: Ribonuclease TTHA0252



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	145.22Å 145.70Å 119.65Å 90.00° 110.52° 90.00°	Depositor
Resolution (Å)	50.00 – 2.05 49.71 – 2.05	Depositor EDS
% Data completeness (in resolution range)	94.3 (50.00-2.05) 94.4 (49.71-2.05)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.57 (at 2.05Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.218 , 0.250 0.212 , 0.243	Depositor DCC
R_{free} test set	14389 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	28.1	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 50.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14435	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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: FLC, ZN, 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	0.34	0/3407	0.65	1/4621 (0.0%)
1	B	0.33	0/3407	0.62	1/4621 (0.0%)
1	C	0.29	0/3407	0.57	1/4621 (0.0%)
1	D	0.28	0/3407	0.56	1/4621 (0.0%)
All	All	0.31	0/13628	0.60	4/18484 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	161	GLY	N-CA-C	-5.92	98.30	113.10
1	B	161	GLY	N-CA-C	-5.48	99.41	113.10
1	D	161	GLY	N-CA-C	-5.42	99.54	113.10
1	C	161	GLY	N-CA-C	-5.00	100.60	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3326	0	3351	59	0
1	B	3326	0	3351	81	0
1	C	3326	0	3351	127	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3326	0	3351	144	0
2	A	140	0	0	5	0
2	B	155	0	0	9	0
2	C	115	0	0	6	0
2	D	90	0	0	3	0
3	A	13	0	5	4	0
3	B	13	0	5	5	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	244	0	0	7	0
5	B	196	0	0	6	0
5	C	78	0	0	1	0
5	D	79	0	0	3	0
All	All	14435	0	13414	404	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 15.

All (404) 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:391:GLN:HG3	5:A:700:HOH:O	1.34	1.24
1:B:10:ARG:HH12	1:B:424:ARG:HG2	1.01	1.10
1:B:2:ARG:HG3	2:B:453:SO4:O1	1.55	1.06
1:A:120:PRO:HB2	2:A:451:SO4:O3	1.59	1.02
1:D:363:GLU:HG2	1:D:364:GLU:H	1.25	1.01
1:D:33:PHE:H	1:D:41:ASN:HD21	1.05	0.98
1:C:244:ARG:HD3	1:C:244:ARG:H	1.26	0.97
1:A:195:ARG:HB2	1:A:195:ARG:HH11	1.30	0.97
1:A:195:ARG:HB2	1:A:195:ARG:NH1	1.81	0.96
1:B:10:ARG:HH12	1:B:424:ARG:CG	1.80	0.94
1:C:33:PHE:H	1:C:41:ASN:HD21	1.14	0.94
1:B:10:ARG:NH1	1:B:424:ARG:HG2	1.83	0.92
1:A:302:ARG:NH2	1:B:303:ALA:HB1	1.84	0.92
1:A:33:PHE:H	1:A:41:ASN:HD21	1.12	0.90
1:B:33:PHE:H	1:B:41:ASN:HD21	0.89	0.88
1:B:33:PHE:N	1:B:41:ASN:HD21	1.71	0.86
1:B:33:PHE:H	1:B:41:ASN:ND2	1.72	0.86
1:C:44:PRO:CB	2:C:454:SO4:O4	2.24	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:ARG:HH22	1:B:303:ALA:HB1	1.40	0.85
1:B:411:LYS:HB2	3:B:463:FLC:HA2	1.56	0.85
1:C:97:ALA:O	1:C:101:MET:HB2	1.78	0.84
1:C:44:PRO:HB3	2:C:454:SO4:O4	1.78	0.84
1:D:209:GLU:HG2	1:D:243:PRO:HD3	1.60	0.82
1:D:222:THR:HG22	1:D:339:VAL:HG21	1.62	0.81
1:D:168:LYS:HE3	1:D:230:GLU:OE1	1.80	0.81
1:D:231:ILE:O	1:D:234:VAL:HG22	1.81	0.79
1:D:235:LEU:HD13	1:D:247:ILE:HD13	1.65	0.78
1:B:391:GLN:HG3	5:B:655:HOH:O	1.82	0.77
1:B:313:SER:HA	2:B:457:SO4:O2	1.84	0.77
1:D:2:ARG:HG3	2:D:435:SO4:O1	1.87	0.75
1:A:129:LEU:HD21	5:A:470:HOH:O	1.87	0.74
1:D:91:GLU:O	1:D:95:GLU:HB2	1.86	0.74
1:C:198:ARG:HE	1:C:198:ARG:HA	1.53	0.74
1:D:331:ASP:N	1:D:368:ARG:HB2	2.03	0.74
1:C:360:ILE:HG22	1:C:361:LEU:HD13	1.70	0.74
1:A:120:PRO:CB	2:A:451:SO4:O3	2.35	0.73
1:C:209:GLU:HG2	1:C:243:PRO:HD3	1.69	0.72
1:C:229:GLN:CD	1:C:229:GLN:H	1.90	0.72
1:D:331:ASP:H	1:D:368:ARG:HB2	1.54	0.72
1:D:298:LYS:HA	1:D:301:ASN:HD22	1.54	0.72
1:B:358:VAL:O	1:B:365:VAL:HG12	1.91	0.71
1:C:244:ARG:HD3	1:C:244:ARG:N	2.05	0.71
1:A:299:ALA:O	1:A:302:ARG:HD2	1.91	0.71
1:C:198:ARG:NE	1:C:198:ARG:HA	2.05	0.71
1:D:318:GLY:HA2	1:D:322:LEU:HD11	1.73	0.71
1:D:222:THR:HG22	1:D:339:VAL:CG2	2.20	0.71
1:D:1:MET:HG3	1:D:21:ALA:HB2	1.72	0.70
1:D:363:GLU:HG2	1:D:364:GLU:N	2.04	0.69
1:D:309:VAL:HG11	1:D:324:HIS:NE2	2.07	0.69
1:A:131:ALA:HB1	2:A:450:SO4:O1	1.93	0.69
1:C:244:ARG:CD	1:C:244:ARG:H	2.05	0.69
1:D:207:ILE:O	1:D:211:THR:HG22	1.91	0.69
1:A:368:ARG:NH2	2:A:435:SO4:O1	2.26	0.68
1:B:2:ARG:CG	2:B:453:SO4:O1	2.39	0.68
1:B:87:VAL:HA	1:B:90:MET:CE	2.24	0.68
1:C:199:GLU:HA	1:C:202:ARG:HD2	1.75	0.68
1:D:211:THR:HG21	1:D:218:VAL:HG22	1.74	0.68
1:D:33:PHE:H	1:D:41:ASN:ND2	1.87	0.67
1:B:411:LYS:N	3:B:463:FLC:HG2	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:GLU:HG3	5:B:527:HOH:O	1.93	0.67
1:C:168:LYS:HE3	1:C:230:GLU:OE1	1.94	0.67
1:D:239:GLY:HA2	1:D:242:LEU:HG	1.76	0.67
1:D:336:LEU:HD23	1:D:337:VAL:N	2.10	0.66
1:B:347:LEU:HD11	1:B:358:VAL:HG11	1.78	0.66
1:B:87:VAL:HA	1:B:90:MET:HE3	1.78	0.65
1:D:229:GLN:H	1:D:229:GLN:CD	1.99	0.65
1:D:34:GLN:NE2	1:D:63:ASP:HB3	2.11	0.65
1:C:329:LEU:HD23	1:C:367:LEU:HD13	1.77	0.64
1:D:205:LEU:HD13	1:D:241:ARG:HD2	1.77	0.64
1:D:33:PHE:N	1:D:41:ASN:HD21	1.87	0.64
1:D:195:ARG:H	1:D:195:ARG:HD2	1.62	0.64
1:D:316:LEU:HD13	1:D:347:LEU:HD12	1.78	0.64
1:A:381:ALA:HB3	1:A:386:LEU:HD13	1.79	0.64
1:A:59:HIS:HD2	1:A:61:HIS:H	1.46	0.63
1:C:331:ASP:HB3	1:C:334:ASN:ND2	2.14	0.63
1:D:294:THR:HG22	1:D:298:LYS:NZ	2.14	0.63
1:D:61:HIS:CE1	1:D:142:LEU:HD11	2.34	0.62
1:B:90:MET:HE3	1:B:118:LEU:HD13	1.82	0.62
1:B:411:LYS:HA	3:B:463:FLC:OB2	1.98	0.62
1:D:326:LYS:O	1:D:326:LYS:HG2	2.00	0.62
1:C:229:GLN:HG3	1:C:261:TYR:CZ	2.35	0.62
1:A:33:PHE:H	1:A:41:ASN:ND2	1.93	0.61
1:D:215:GLY:HA2	1:D:306:PRO:HD3	1.81	0.61
1:A:102:ASP:CG	1:A:103:GLU:H	2.03	0.61
1:C:86:THR:HG22	1:C:90:MET:CE	2.29	0.61
1:D:34:GLN:HE21	1:D:63:ASP:HB3	1.65	0.61
1:C:33:PHE:H	1:C:41:ASN:ND2	1.93	0.61
1:A:295:GLU:HG3	5:A:693:HOH:O	1.99	0.61
1:D:291:VAL:HG21	1:D:300:LEU:HD11	1.83	0.61
1:A:318:GLY:HA2	1:A:322:LEU:HD11	1.83	0.61
1:C:250:ASP:HA	1:C:291:VAL:HB	1.83	0.61
1:D:348:GLY:O	1:D:352:ILE:HG13	2.00	0.61
1:C:34:GLN:NE2	1:C:63:ASP:HB3	2.15	0.61
1:B:182:LEU:HD11	1:B:397:VAL:HG23	1.82	0.60
1:C:220:ILE:HG22	1:C:222:THR:HG23	1.84	0.60
1:D:170:VAL:HG12	1:D:171:LEU:HD12	1.83	0.60
1:C:91:GLU:OE2	1:C:115:LEU:HD13	2.01	0.60
1:A:11:GLU:OE2	1:A:40:ARG:NH1	2.34	0.60
1:C:85:ALA:HB2	1:C:267:TYR:CD2	2.36	0.60
1:B:356:PRO:HG2	5:B:536:HOH:O	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:GLN:HE21	1:B:63:ASP:HB3	1.67	0.59
1:C:274:ALA:O	1:C:277:LEU:HB3	2.02	0.59
1:D:204:PHE:O	1:D:208:LEU:HG	2.03	0.59
1:D:229:GLN:H	1:D:229:GLN:NE2	1.99	0.59
1:C:74:GLU:OE2	2:C:454:SO4:O1	2.21	0.59
1:D:298:LYS:HA	1:D:301:ASN:ND2	2.18	0.59
1:D:389:TRP:HE3	1:D:390:LEU:HD13	1.67	0.58
1:C:197:TYR:O	1:C:201:VAL:HG23	2.03	0.58
1:C:61:HIS:CD2	1:C:142:LEU:HD11	2.39	0.58
1:C:33:PHE:N	1:C:41:ASN:HD21	1.93	0.58
1:C:44:PRO:HB2	2:C:454:SO4:O4	2.03	0.58
1:A:318:GLY:HA2	1:A:322:LEU:CD1	2.33	0.58
1:D:309:VAL:C	1:D:310:LEU:HD12	2.24	0.58
1:B:326:LYS:HD2	1:B:361:LEU:HB2	1.86	0.57
1:D:155:ARG:NH2	2:D:449:SO4:O1	2.33	0.57
1:A:347:LEU:HD11	1:A:358:VAL:HG11	1.87	0.57
1:D:239:GLY:HA2	1:D:242:LEU:CG	2.34	0.57
1:D:309:VAL:HG11	1:D:324:HIS:CD2	2.39	0.57
1:B:221:PRO:HB3	1:B:321:ILE:HG12	1.86	0.57
1:D:155:ARG:HD3	1:D:431:VAL:O	2.05	0.57
1:A:260:LEU:HD22	1:A:264:LEU:HD11	1.85	0.56
1:A:281:ASN:HB2	3:A:460:FLC:OB2	2.05	0.56
1:D:98:LEU:HD21	1:D:108:PRO:HB3	1.85	0.56
1:B:86:THR:O	1:B:90:MET:HG3	2.05	0.56
1:C:404:GLU:CD	1:C:404:GLU:H	2.08	0.56
1:D:202:ARG:O	1:D:206:GLU:HG3	2.05	0.56
1:D:223:PHE:HZ	1:D:315:MET:HG3	1.71	0.56
1:A:205:LEU:O	1:A:209:GLU:HG3	2.04	0.56
1:C:61:HIS:NE2	1:C:142:LEU:HD11	2.21	0.56
1:B:80:VAL:HB	1:B:118:LEU:HD23	1.87	0.55
1:B:266:ARG:HG2	5:B:573:HOH:O	2.06	0.55
1:D:223:PHE:CZ	1:D:315:MET:HG3	2.41	0.55
1:D:90:MET:HE3	1:D:118:LEU:HD13	1.88	0.55
1:B:396:VAL:HG12	1:B:398:LEU:HD13	1.88	0.55
1:D:236:TYR:OH	1:D:280:LYS:HD3	2.05	0.55
1:B:91:GLU:O	1:B:95:GLU:HG2	2.07	0.55
1:C:182:LEU:HD11	1:C:397:VAL:HG23	1.88	0.55
1:A:182:LEU:HD11	1:A:397:VAL:HG23	1.88	0.55
1:C:322:LEU:HB3	1:C:361:LEU:HD11	1.87	0.55
1:A:289:GLU:HG3	5:A:603:HOH:O	2.07	0.55
1:C:211:THR:HG21	1:C:335:ALA:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:LEU:O	1:B:209:GLU:HG3	2.07	0.55
1:B:401:GLY:HA3	1:B:406:LEU:HD13	1.88	0.55
1:B:202:ARG:NE	2:B:458:SO4:O3	2.35	0.54
1:D:302:ARG:HG2	1:D:302:ARG:HH21	1.70	0.54
1:C:221:PRO:HB3	1:C:321:ILE:HG12	1.90	0.54
1:D:407:LEU:HD22	1:D:422:LEU:HD21	1.88	0.54
1:C:236:TYR:HD1	1:C:285:PRO:HA	1.73	0.54
1:D:224:ALA:HB3	1:D:253:MET:CE	2.38	0.54
1:B:362:GLY:N	2:B:451:SO4:O1	2.41	0.54
1:D:325:LEU:C	1:D:327:HIS:H	2.11	0.53
1:D:244:ARG:HD2	1:D:244:ARG:N	2.24	0.53
1:D:84:ARG:HD2	1:D:266:ARG:HH12	1.73	0.53
1:B:128:ARG:O	1:B:129:LEU:HD23	2.07	0.53
1:B:385:GLU:CD	5:B:551:HOH:O	2.47	0.53
1:C:87:VAL:HG13	1:C:118:LEU:HD13	1.90	0.53
1:C:321:ILE:O	1:C:325:LEU:HD13	2.09	0.53
1:D:381:ALA:HB3	1:D:386:LEU:HD13	1.91	0.53
1:D:229:GLN:HG3	1:D:261:TYR:CE1	2.43	0.53
1:C:325:LEU:HG	1:C:329:LEU:HD11	1.91	0.53
1:D:88:LEU:HB3	1:D:260:LEU:HD21	1.91	0.53
1:B:238:HIS:HA	1:B:240:HIS:CE1	2.43	0.53
1:C:199:GLU:HA	1:C:202:ARG:CD	2.40	0.53
1:D:359:ARG:HA	1:D:363:GLU:O	2.09	0.52
1:B:155:ARG:HD2	1:B:431:VAL:O	2.09	0.52
1:C:211:THR:HG21	1:C:335:ALA:CB	2.39	0.52
1:C:86:THR:O	1:C:90:MET:HB2	2.10	0.52
1:D:87:VAL:HA	1:D:90:MET:CE	2.40	0.52
2:A:450:SO4:O2	1:D:179:LEU:HD21	2.09	0.52
1:C:358:VAL:O	1:C:365:VAL:HG22	2.09	0.52
1:C:318:GLY:HA2	1:C:322:LEU:HD11	1.92	0.52
1:A:195:ARG:HG3	1:A:196:PRO:HD2	1.92	0.52
1:C:401:GLY:HA3	1:C:406:LEU:HD11	1.90	0.52
1:D:219:LEU:N	1:D:219:LEU:HD12	2.24	0.52
1:B:327:HIS:O	2:B:438:SO4:O4	2.28	0.52
1:C:402:GLU:HB2	1:C:405:LYS:HG2	1.92	0.52
1:C:86:THR:HG22	1:C:90:MET:HE3	1.91	0.52
1:D:218:VAL:HB	1:D:308:VAL:HG22	1.92	0.52
1:D:321:ILE:O	1:D:325:LEU:HD13	2.11	0.51
1:C:236:TYR:CA	1:C:285:PRO:HB3	2.40	0.51
1:D:285:PRO:HD2	1:D:288:LEU:HD22	1.92	0.51
1:A:166:ARG:HB2	1:A:166:ARG:NH2	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:ARG:HH11	1:C:179:LEU:HA	1.76	0.51
1:B:1:MET:HG3	1:B:21:ALA:HB2	1.93	0.51
1:D:119:ARG:HD2	5:D:585:HOH:O	2.11	0.51
1:D:229:GLN:HG3	1:D:261:TYR:CZ	2.46	0.51
1:C:236:TYR:HA	1:C:285:PRO:HB3	1.91	0.51
1:D:68:LEU:HB3	1:D:69:PRO:HD3	1.93	0.51
1:B:370:SER:HA	2:B:455:SO4:O2	2.10	0.51
1:C:43:ALA:HB1	1:C:44:PRO:HD2	1.93	0.51
1:C:204:PHE:O	1:C:208:LEU:HG	2.12	0.50
1:C:297:SER:OG	1:C:320:ARG:HD3	2.11	0.50
1:B:68:LEU:HB3	1:B:69:PRO:HD3	1.93	0.50
1:D:85:ALA:HB3	1:D:144:GLY:HA3	1.94	0.50
1:D:1:MET:HG3	1:D:21:ALA:CB	2.41	0.50
1:D:47:PHE:O	1:D:49:PRO:HD3	2.12	0.50
1:C:391:GLN:HA	1:C:416:ARG:NH2	2.26	0.50
1:D:326:LYS:HB2	1:D:360:ILE:HG21	1.93	0.50
1:D:102:ASP:CG	1:D:103:GLU:H	2.14	0.50
1:D:171:LEU:HD11	1:D:226:GLU:OE1	2.11	0.50
1:D:325:LEU:HD12	1:D:325:LEU:N	2.26	0.50
1:B:401:GLY:HA3	1:B:406:LEU:CD1	2.42	0.49
1:D:164:GLY:HA2	1:D:379:GLY:O	2.12	0.49
1:C:34:GLN:HE21	1:C:63:ASP:HB3	1.78	0.49
1:B:87:VAL:HA	1:B:90:MET:HE2	1.94	0.49
1:B:210:LYS:O	1:B:214:GLN:HG2	2.13	0.49
1:D:234:VAL:O	1:D:238:HIS:HB2	2.12	0.49
1:D:224:ALA:HB3	1:D:253:MET:HE2	1.94	0.49
1:D:409:LEU:HD22	1:D:413:LEU:HG	1.93	0.49
1:C:360:ILE:CG2	1:C:361:LEU:HD13	2.41	0.49
1:C:402:GLU:HB3	1:C:404:GLU:OE2	2.12	0.49
1:D:88:LEU:HD13	1:D:260:LEU:HD11	1.95	0.49
1:A:59:HIS:CD2	1:A:61:HIS:HB2	2.48	0.48
1:D:61:HIS:CD2	1:D:142:LEU:HD11	2.48	0.48
1:A:260:LEU:HD22	1:A:264:LEU:CD1	2.43	0.48
1:A:281:ASN:HD22	3:A:460:FLC:HA2	1.78	0.48
1:C:236:TYR:CE2	1:C:282:PRO:HA	2.48	0.48
1:C:399:VAL:HG12	1:C:423:ALA:CB	2.44	0.48
1:C:164:GLY:HA2	1:C:379:GLY:O	2.12	0.48
1:C:61:HIS:CE1	1:C:142:LEU:HD11	2.49	0.48
1:C:318:GLY:HA2	1:C:322:LEU:CD1	2.43	0.48
1:C:348:GLY:O	1:C:352:ILE:HG13	2.13	0.48
1:B:113:GLU:OE2	1:B:117:HIS:HE1	1.97	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:318:GLY:HA2	1:B:322:LEU:CD1	2.43	0.48
1:B:398:LEU:HB3	1:B:406:LEU:HG	1.95	0.48
1:C:68:LEU:HB3	1:C:69:PRO:HD3	1.96	0.48
1:D:171:LEU:N	1:D:171:LEU:HD12	2.28	0.48
1:C:190:GLY:HA3	1:C:409:LEU:HB2	1.96	0.48
1:A:11:GLU:CD	1:A:40:ARG:HH12	2.17	0.48
1:A:33:PHE:N	1:A:41:ASN:HD21	1.94	0.48
1:A:101:MET:HE2	1:A:104:PRO:HA	1.96	0.48
1:B:360:ILE:HD12	1:B:365:VAL:HG11	1.96	0.47
1:C:298:LYS:HA	1:C:301:ASN:ND2	2.29	0.47
1:D:203:GLU:O	1:D:207:ILE:HG13	2.13	0.47
1:A:97:ALA:O	1:A:101:MET:HB2	2.14	0.47
1:B:165:ASN:C	1:B:165:ASN:HD22	2.16	0.47
1:D:102:ASP:OD2	1:D:103:GLU:HG2	2.14	0.47
1:C:246:PRO:HG2	1:C:248:TYR:HE1	1.80	0.47
1:C:36:LYS:NZ	1:C:36:LYS:HB2	2.29	0.47
1:D:253:MET:HA	1:D:256:ARG:NH1	2.29	0.47
1:D:249:LEU:HD23	1:D:290:VAL:HG22	1.96	0.47
1:D:33:PHE:CD2	1:D:40:ARG:HB2	2.50	0.47
1:A:209:GLU:HG2	1:A:242:LEU:HD23	1.96	0.47
1:C:84:ARG:HB3	1:C:267:TYR:OH	2.15	0.47
1:D:165:ASN:HD22	1:D:165:ASN:C	2.18	0.47
1:C:88:LEU:HB3	1:C:260:LEU:HD21	1.96	0.47
1:B:411:LYS:CB	3:B:463:FLC:HA2	2.37	0.47
1:C:402:GLU:HB2	1:C:405:LYS:CG	2.45	0.47
1:C:91:GLU:O	1:C:95:GLU:HG2	2.15	0.47
1:D:354:ARG:N	1:D:355:PRO:CD	2.78	0.47
1:D:428:GLY:HA3	2:D:446:SO4:O1	2.14	0.46
1:C:140:GLY:O	1:C:164:GLY:HA3	2.15	0.46
1:C:163:LEU:HD11	1:C:389:TRP:CE3	2.51	0.46
1:C:88:LEU:HD13	1:C:260:LEU:HD11	1.96	0.46
1:D:1:MET:HB3	1:D:431:VAL:HB	1.97	0.46
1:D:252:PRO:HD2	5:D:495:HOH:O	2.16	0.46
1:D:315:MET:HA	1:D:342:GLN:HE22	1.80	0.46
1:C:221:PRO:HA	1:C:311:ALA:O	2.15	0.46
1:A:198:ARG:HG3	1:A:198:ARG:HH21	1.80	0.46
1:B:85:ALA:HB3	1:B:144:GLY:HA3	1.98	0.46
1:D:403:GLU:O	1:D:407:LEU:HD23	2.15	0.46
1:C:265:VAL:HG23	1:C:266:ARG:N	2.31	0.46
1:A:198:ARG:NH2	1:A:198:ARG:HG3	2.31	0.46
1:A:209:GLU:OE2	1:A:241:ARG:NH2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:PRO:HD3	1:B:226:GLU:HG3	1.99	0.45
1:D:321:ILE:C	1:D:323:HIS:H	2.19	0.45
1:A:59:HIS:NE2	1:A:61:HIS:HB2	2.30	0.45
1:C:62:LEU:HD13	1:C:93:VAL:HG12	1.99	0.45
1:B:12:VAL:HG23	1:B:13:THR:HG23	1.98	0.45
1:C:222:THR:HG22	1:C:339:VAL:CG2	2.46	0.45
1:C:89:LEU:O	1:C:93:VAL:HG23	2.16	0.45
1:D:363:GLU:CG	1:D:364:GLU:H	2.09	0.45
1:B:396:VAL:O	1:B:420:VAL:HA	2.17	0.45
1:B:410:GLY:C	3:B:463:FLC:HG2	2.36	0.45
1:C:320:ARG:HA	1:C:323:HIS:HD2	1.81	0.45
1:C:325:LEU:O	1:C:329:LEU:HD13	2.16	0.45
1:D:58:THR:HB	1:D:146:ALA:O	2.17	0.45
1:B:109:GLU:O	1:B:112:GLU:HG2	2.17	0.45
1:C:204:PHE:CE1	1:C:208:LEU:HD11	2.51	0.45
1:D:211:THR:CG2	1:D:218:VAL:HG22	2.44	0.45
1:D:244:ARG:O	1:D:245:ALA:HB2	2.17	0.45
1:D:288:LEU:HD12	1:D:289:GLU:H	1.81	0.45
1:D:310:LEU:N	1:D:310:LEU:HD12	2.32	0.45
1:A:281:ASN:HB3	3:A:460:FLC:HG2	1.99	0.45
1:A:59:HIS:CD2	1:A:61:HIS:H	2.30	0.45
1:D:61:HIS:NE2	1:D:142:LEU:HD11	2.31	0.45
1:D:336:LEU:C	1:D:336:LEU:HD23	2.36	0.45
1:D:347:LEU:HD13	1:D:347:LEU:O	2.17	0.45
1:D:280:LYS:O	1:D:282:PRO:HD3	2.17	0.45
1:A:102:ASP:CG	1:A:103:GLU:N	2.70	0.45
1:B:109:GLU:HA	1:B:112:GLU:HG2	1.99	0.45
1:B:128:ARG:NH2	1:C:391:GLN:O	2.50	0.45
1:D:165:ASN:ND2	1:D:167:GLU:H	2.15	0.45
1:D:197:TYR:O	1:D:201:VAL:HG23	2.17	0.45
1:B:34:GLN:NE2	1:B:63:ASP:HB3	2.30	0.44
1:B:43:ALA:HB1	1:B:44:PRO:HD2	1.98	0.44
1:C:172:PRO:HA	2:C:442:SO4:O3	2.17	0.44
1:C:32:MET:HA	1:C:67:ARG:HG3	1.98	0.44
1:C:98:LEU:HD23	1:C:98:LEU:O	2.16	0.44
1:C:209:GLU:HG2	1:C:243:PRO:CD	2.42	0.44
1:C:143:PRO:HD3	1:C:226:GLU:HG3	1.98	0.44
1:C:32:MET:SD	1:C:62:LEU:HG	2.56	0.44
1:D:381:ALA:HB3	1:D:386:LEU:CD1	2.47	0.44
1:C:85:ALA:HB2	1:C:267:TYR:CE2	2.53	0.44
1:C:296:ALA:O	1:C:300:LEU:HD13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:ALA:HB3	1:A:144:GLY:HA3	1.99	0.44
1:B:195:ARG:CZ	1:B:199:GLU:HG2	2.48	0.44
1:B:217:LYS:HG2	1:B:307:MET:HG2	1.99	0.44
1:C:88:LEU:O	1:C:91:GLU:HB3	2.18	0.44
1:D:28:LEU:O	1:D:29:ASP:HB2	2.17	0.44
1:D:86:THR:O	1:D:90:MET:HG3	2.18	0.44
1:B:301:ASN:OD1	1:B:324:HIS:HA	2.18	0.44
1:C:223:PHE:CZ	1:C:315:MET:HG3	2.53	0.44
1:C:98:LEU:HD23	1:C:98:LEU:C	2.37	0.44
1:C:248:TYR:CD2	1:C:300:LEU:HD21	2.52	0.44
1:A:101:MET:CE	1:A:104:PRO:HA	2.48	0.44
1:A:2:ARG:NH2	5:A:618:HOH:O	2.49	0.44
1:A:91:GLU:O	1:A:95:GLU:HG2	2.17	0.44
1:D:312:GLY:O	1:D:321:ILE:HB	2.18	0.44
1:D:399:VAL:HG12	1:D:423:ALA:HB3	2.00	0.44
1:A:45:PHE:HB3	1:A:47:PHE:CE1	2.53	0.44
1:A:80:VAL:HB	1:A:118:LEU:HD23	2.00	0.44
1:D:318:GLY:HA2	1:D:322:LEU:CD1	2.46	0.43
1:D:220:ILE:HG23	1:D:339:VAL:HG13	2.00	0.43
1:D:88:LEU:HD12	1:D:264:LEU:HD21	2.01	0.43
1:A:281:ASN:CB	3:A:460:FLC:HG2	2.48	0.43
1:C:229:GLN:CD	1:C:229:GLN:N	2.66	0.43
1:D:327:HIS:O	1:D:327:HIS:ND1	2.50	0.43
1:B:42:HIS:ND1	1:B:105:PHE:HB3	2.33	0.43
1:B:32:MET:HA	1:B:67:ARG:HG3	1.99	0.43
1:C:381:ALA:HB1	1:C:385:GLU:HB2	1.99	0.43
1:C:163:LEU:HD11	1:C:389:TRP:CD2	2.53	0.43
1:D:86:THR:HG22	1:D:90:MET:HE2	1.99	0.43
1:B:424:ARG:HA	2:B:454:SO4:O3	2.18	0.43
1:C:399:VAL:HG12	1:C:423:ALA:HB3	2.01	0.43
1:D:251:SER:HB3	1:D:254:ALA:HB3	2.01	0.43
1:A:37:GLU:HG3	1:A:40:ARG:HH11	1.83	0.43
1:B:45:PHE:HB3	1:B:47:PHE:CE1	2.54	0.43
1:C:5:PRO:HA	1:C:17:HIS:HD2	1.83	0.43
1:C:365:VAL:O	1:C:365:VAL:HG23	2.18	0.43
1:D:210:LYS:HG3	1:D:210:LYS:O	2.19	0.43
1:B:126:TRP:CE3	1:C:178:PRO:HB3	2.53	0.43
1:D:239:GLY:HA2	1:D:242:LEU:CD1	2.49	0.42
1:C:224:ALA:HB1	1:C:254:ALA:HA	2.02	0.42
1:C:310:LEU:HD12	1:C:310:LEU:N	2.33	0.42
1:A:411:LYS:NZ	5:A:488:HOH:O	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1:MET:N	2:B:453:SO4:O3	2.43	0.42
1:B:178:PRO:HB3	1:C:126:TRP:CE3	2.54	0.42
1:C:317:ALA:HB2	5:C:494:HOH:O	2.18	0.42
1:D:214:GLN:NE2	1:D:333:ARG:HA	2.34	0.42
1:B:318:GLY:HA2	1:B:322:LEU:HD11	2.01	0.42
1:C:113:GLU:OE2	1:C:117:HIS:HE1	2.03	0.42
1:C:186:GLU:HA	1:C:399:VAL:O	2.19	0.42
1:C:98:LEU:HD11	1:C:108:PRO:HB3	2.01	0.42
1:D:124:GLY:C	5:D:526:HOH:O	2.57	0.42
1:D:326:LYS:HD2	1:D:360:ILE:HG22	2.01	0.42
1:A:32:MET:HE2	1:A:32:MET:HB3	1.93	0.42
1:B:109:GLU:HA	1:B:112:GLU:OE2	2.20	0.42
1:B:365:VAL:HG13	1:B:365:VAL:O	2.19	0.42
1:D:244:ARG:CD	1:D:244:ARG:N	2.83	0.42
1:A:166:ARG:CB	1:A:166:ARG:HH21	2.33	0.42
1:B:10:ARG:NH1	1:B:424:ARG:HA	2.34	0.42
1:C:177:PRO:HD3	1:C:389:TRP:CE2	2.55	0.42
1:B:274:ALA:O	1:B:278:GLN:HG3	2.19	0.42
1:A:202:ARG:NH2	5:A:479:HOH:O	2.53	0.41
1:C:384:ASP:N	1:C:384:ASP:OD2	2.53	0.41
1:D:87:VAL:HA	1:D:90:MET:HE2	2.00	0.41
1:A:348:GLY:O	1:A:352:ILE:HG13	2.19	0.41
1:B:266:ARG:NE	5:B:622:HOH:O	2.34	0.41
1:D:198:ARG:HB3	1:D:202:ARG:NH2	2.36	0.41
1:D:253:MET:HA	1:D:256:ARG:CZ	2.50	0.41
1:D:366:PRO:O	1:D:367:LEU:HB2	2.20	0.41
1:C:12:VAL:HG23	1:C:13:THR:HG23	2.01	0.41
1:D:389:TRP:CE3	1:D:390:LEU:HD13	2.52	0.41
1:C:98:LEU:HD11	1:C:108:PRO:CA	2.50	0.41
1:C:347:LEU:HD11	1:C:358:VAL:HG11	2.03	0.41
1:C:224:ALA:HB1	1:C:254:ALA:CA	2.50	0.41
1:C:322:LEU:HB3	1:C:361:LEU:CD1	2.51	0.41
1:C:101:MET:HE2	1:C:104:PRO:HB3	2.01	0.41
1:C:151:GLN:HB2	2:C:448:SO4:O3	2.21	0.41
1:C:251:SER:HB3	1:C:254:ALA:HB3	2.02	0.41
1:C:330:SER:HA	1:C:366:PRO:O	2.20	0.41
1:D:284:ARG:HD3	1:D:288:LEU:HD23	2.03	0.41
1:D:25:ARG:NH1	1:D:51:GLU:HB3	2.36	0.41
1:D:232:LEU:HB3	1:D:285:PRO:HD3	2.03	0.41
1:D:285:PRO:HG2	1:D:288:LEU:HB2	2.03	0.41
1:D:316:LEU:CD1	1:D:347:LEU:HD12	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:8:ALA:HA	1:D:11:GLU:HG3	2.03	0.41
1:A:165:ASN:C	1:A:165:ASN:HD22	2.24	0.41
1:B:165:ASN:C	1:B:165:ASN:ND2	2.74	0.41
1:C:274:ALA:O	1:C:278:GLN:HG3	2.21	0.41
1:D:302:ARG:HG2	1:D:302:ARG:NH2	2.35	0.41
1:D:330:SER:O	1:D:331:ASP:HB2	2.21	0.41
1:C:236:TYR:CD2	1:C:282:PRO:HA	2.56	0.40
1:C:360:ILE:HD12	1:C:365:VAL:HG21	2.03	0.40
1:D:209:GLU:HG2	1:D:243:PRO:CD	2.41	0.40
1:D:347:LEU:CD1	1:D:351:ILE:HD11	2.51	0.40
1:D:59:HIS:CD2	1:D:61:HIS:HB2	2.55	0.40
1:A:302:ARG:HD3	1:B:304:PRO:HD2	2.02	0.40
1:D:87:VAL:HA	1:D:90:MET:HE3	2.03	0.40
1:A:57:LEU:HD13	1:A:65:VAL:HG12	2.03	0.40
1:C:229:GLN:HG3	1:C:261:TYR:CE1	2.56	0.40
1:C:239:GLY:C	1:C:241:ARG:H	2.23	0.40
1:D:113:GLU:OE2	1:D:117:HIS:HE1	2.04	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	A	429/431 (100%)	418 (97%)	10 (2%)	1 (0%)	47	39
1	B	429/431 (100%)	416 (97%)	13 (3%)	0	100	100
1	C	429/431 (100%)	400 (93%)	26 (6%)	3 (1%)	22	12
1	D	429/431 (100%)	394 (92%)	28 (6%)	7 (2%)	9	2
All	All	1716/1724 (100%)	1628 (95%)	77 (4%)	11 (1%)	25	15

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	ASP
1	D	102	ASP
1	D	366	PRO
1	C	102	ASP
1	D	327	HIS
1	D	367	LEU
1	C	198	ARG
1	D	326	LYS
1	C	168	LYS
1	D	328	GLY
1	D	331	ASP

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	342/342 (100%)	328 (96%)	14 (4%)	30	23
1	B	342/342 (100%)	331 (97%)	11 (3%)	39	32
1	C	342/342 (100%)	333 (97%)	9 (3%)	46	39
1	D	342/342 (100%)	327 (96%)	15 (4%)	28	21
All	All	1368/1368 (100%)	1319 (96%)	49 (4%)	35	28

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	GLU
1	A	94	LEU
1	A	98	LEU
1	A	112	GLU
1	A	163	LEU
1	A	165	ASN
1	A	166	ARG
1	A	186	GLU
1	A	192	ARG
1	A	195	ARG
1	A	336	LEU

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Mol	Chain	Res	Type
1	A	386	LEU
1	A	407	LEU
1	A	409	LEU
1	B	11	GLU
1	B	103	GLU
1	B	119	ARG
1	B	165	ASN
1	B	186	GLU
1	B	264	LEU
1	B	325	LEU
1	B	329	LEU
1	B	398	LEU
1	B	407	LEU
1	B	409	LEU
1	C	36	LYS
1	C	155	ARG
1	C	165	ASN
1	C	186	GLU
1	C	229	GLN
1	C	244	ARG
1	C	258	LEU
1	C	336	LEU
1	C	409	LEU
1	D	95	GLU
1	D	127	LEU
1	D	134	LEU
1	D	151	GLN
1	D	155	ARG
1	D	165	ASN
1	D	186	GLU
1	D	192	ARG
1	D	195	ARG
1	D	229	GLN
1	D	244	ARG
1	D	344	GLN
1	D	386	LEU
1	D	390	LEU
1	D	409	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	59	HIS
1	A	165	ASN
1	A	275	HIS
1	A	344	GLN
1	B	34	GLN
1	B	41	ASN
1	B	165	ASN
1	B	238	HIS
1	C	17	HIS
1	C	34	GLN
1	C	41	ASN
1	C	59	HIS
1	C	165	ASN
1	C	214	GLN
1	C	301	ASN
1	C	323	HIS
1	D	17	HIS
1	D	34	GLN
1	D	41	ASN
1	D	165	ASN
1	D	214	GLN
1	D	229	GLN
1	D	301	ASN
1	D	323	HIS
1	D	383	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 110 ligands modelled in this entry, 8 are monoatomic - leaving 102 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	$\# Z > 2$
2	SO4	D	434	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	A	436	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	C	441	-	4,4,4	1.00	0	6,6,6	0.65	0
2	SO4	C	439	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	A	459	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	B	448	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	C	447	-	4,4,4	1.02	0	6,6,6	0.67	0
2	SO4	B	458	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	A	458	-	4,4,4	0.99	0	6,6,6	0.68	0
2	SO4	A	455	-	4,4,4	1.00	0	6,6,6	0.67	0
2	SO4	B	442	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	B	456	-	4,4,4	0.93	0	6,6,6	0.63	0
2	SO4	A	454	-	4,4,4	0.99	0	6,6,6	0.66	0
2	SO4	B	452	-	4,4,4	0.99	0	6,6,6	0.64	0
2	SO4	B	455	-	4,4,4	0.99	0	6,6,6	0.67	0
2	SO4	C	444	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	B	453	-	4,4,4	1.00	0	6,6,6	0.64	0
2	SO4	D	447	-	4,4,4	1.00	0	6,6,6	0.65	0
2	SO4	A	445	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	B	435	-	4,4,4	1.03	0	6,6,6	0.65	0
2	SO4	D	437	-	4,4,4	0.98	0	6,6,6	0.66	0
2	SO4	A	434	-	4,4,4	1.00	0	6,6,6	0.65	0
2	SO4	A	441	-	4,4,4	0.98	0	6,6,6	0.66	0
2	SO4	B	439	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	A	448	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	C	434	-	4,4,4	1.02	0	6,6,6	0.63	0
2	SO4	B	445	-	4,4,4	1.02	0	6,6,6	0.65	0
2	SO4	B	441	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	B	446	-	4,4,4	0.98	0	6,6,6	0.63	0
2	SO4	C	438	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	A	453	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	B	440	-	4,4,4	1.02	0	6,6,6	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	456	-	4,4,4	1.02	0	6,6,6	0.65	0
2	SO4	A	435	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	D	441	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	C	453	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	C	436	-	4,4,4	1.02	0	6,6,6	0.65	0
2	SO4	C	443	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	B	437	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	B	433	-	4,4,4	1.01	0	6,6,6	0.66	0
3	FLC	B	463	-	3,12,12	0.62	0	3,17,17	0.28	0
2	SO4	C	452	-	4,4,4	1.02	0	6,6,6	0.65	0
2	SO4	C	442	-	4,4,4	1.02	0	6,6,6	0.66	0
3	FLC	A	460	-	3,12,12	1.06	0	3,17,17	0.66	0
2	SO4	D	445	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	B	438	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	C	454	-	4,4,4	1.00	0	6,6,6	0.65	0
2	SO4	B	451	-	4,4,4	0.98	0	6,6,6	0.67	0
2	SO4	A	447	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	B	460	-	4,4,4	0.99	0	6,6,6	0.67	0
2	SO4	A	444	-	4,4,4	1.04	0	6,6,6	0.62	0
2	SO4	D	439	-	4,4,4	0.98	0	6,6,6	0.66	0
2	SO4	B	447	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	A	432	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	B	443	-	4,4,4	0.98	0	6,6,6	0.68	0
2	SO4	A	449	-	4,4,4	0.90	0	6,6,6	0.64	0
2	SO4	A	442	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	C	437	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	B	457	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	C	449	-	4,4,4	0.99	0	6,6,6	0.65	0
2	SO4	C	433	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	A	440	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	C	445	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	B	434	-	4,4,4	0.99	0	6,6,6	0.67	0
2	SO4	A	451	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	D	446	-	4,4,4	1.02	0	6,6,6	0.64	0
2	SO4	B	444	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	D	438	-	4,4,4	1.00	0	6,6,6	0.67	0
2	SO4	D	449	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	C	432	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	D	436	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	C	450	-	4,4,4	1.01	0	6,6,6	0.64	0
2	SO4	C	451	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	D	432	-	4,4,4	1.01	0	6,6,6	0.67	0
2	SO4	D	435	-	4,4,4	1.01	0	6,6,6	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	443	-	4,4,4	0.98	0	6,6,6	0.67	0
2	SO4	A	457	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	A	438	-	4,4,4	1.00	0	6,6,6	0.67	0
2	SO4	D	433	-	4,4,4	1.00	0	6,6,6	0.68	0
2	SO4	D	443	-	4,4,4	0.97	0	6,6,6	0.63	0
2	SO4	B	461	-	4,4,4	1.01	0	6,6,6	0.67	0
2	SO4	B	432	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	C	448	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	D	442	-	4,4,4	1.01	0	6,6,6	0.64	0
2	SO4	B	449	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	439	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	A	450	-	4,4,4	1.01	0	6,6,6	0.64	0
2	SO4	D	444	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	D	448	-	4,4,4	0.99	0	6,6,6	0.66	0
2	SO4	B	459	-	4,4,4	0.99	0	6,6,6	0.66	0
2	SO4	B	454	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	D	440	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	B	450	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	437	-	4,4,4	1.04	0	6,6,6	0.65	0
2	SO4	C	446	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	B	436	-	4,4,4	1.02	0	6,6,6	0.65	0
2	SO4	B	462	-	4,4,4	1.00	0	6,6,6	0.67	0
2	SO4	C	440	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	452	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	C	435	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	446	-	4,4,4	0.99	0	6,6,6	0.65	0
2	SO4	A	433	-	4,4,4	1.01	0	6,6,6	0.66	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
3	FLC	B	463	-	-	0/6/16/16	-
3	FLC	A	460	-	-	0/6/16/16	-

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.

18 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	458	SO4	1	0
2	B	455	SO4	1	0
2	B	453	SO4	3	0
2	A	435	SO4	1	0
3	B	463	FLC	5	0
2	C	442	SO4	1	0
3	A	460	FLC	4	0
2	B	438	SO4	1	0
2	C	454	SO4	4	0
2	B	451	SO4	1	0
2	B	457	SO4	1	0
2	A	451	SO4	2	0
2	D	446	SO4	1	0
2	D	449	SO4	1	0
2	D	435	SO4	1	0
2	C	448	SO4	1	0
2	A	450	SO4	2	0
2	B	454	SO4	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, 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	431/431 (100%)	-0.03	5 (1%) 79 81	13, 22, 39, 65	0
1	B	431/431 (100%)	-0.04	3 (0%) 87 89	14, 26, 44, 62	0
1	C	431/431 (100%)	0.76	61 (14%) 2 2	17, 45, 75, 91	0
1	D	431/431 (100%)	1.15	109 (25%) 0 0	16, 42, 92, 103	0
All	All	1724/1724 (100%)	0.46	178 (10%) 6 6	13, 31, 78, 103	0

All (178) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	329	LEU	8.8
1	D	300	LEU	8.0
1	D	306	PRO	7.9
1	C	242	LEU	7.6
1	D	242	LEU	7.6
1	D	212	LEU	7.6
1	D	325	LEU	7.3
1	C	277	LEU	6.7
1	C	415	LEU	6.1
1	D	304	PRO	5.9
1	D	362	GLY	5.8
1	D	324	HIS	5.7
1	D	332	PRO	5.6
1	D	297	SER	5.5
1	C	335	ALA	5.5
1	D	104	PRO	5.5
1	C	216	GLY	5.5
1	D	239	GLY	5.5
1	D	299	ALA	5.4
1	D	241	ARG	5.2
1	C	212	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
1	D	208	LEU	5.2
1	D	335	ALA	5.2
1	C	213	SER	5.2
1	D	286	ALA	5.1
1	C	306	PRO	5.1
1	D	244	ARG	5.1
1	C	333	ARG	5.1
1	D	240	HIS	5.1
1	D	334	ASN	5.1
1	D	327	HIS	5.0
1	D	210	LYS	5.0
1	D	213	SER	4.9
1	D	368	ARG	4.8
1	D	333	ARG	4.7
1	D	296	ALA	4.7
1	C	205	LEU	4.4
1	C	208	LEU	4.4
1	D	248	TYR	4.4
1	D	211	THR	4.2
1	D	366	PRO	4.2
1	C	204	PHE	4.1
1	B	42	HIS	4.1
1	D	247	ILE	4.1
1	C	209	GLU	4.1
1	D	249	LEU	4.1
1	C	354	ARG	4.0
1	C	207	ILE	4.0
1	D	310	LEU	3.9
1	D	98	LEU	3.9
1	D	317	ALA	3.9
1	D	361	LEU	3.9
1	D	209	GLU	3.8
1	D	357	ALA	3.7
1	C	244	ARG	3.7
1	D	365	VAL	3.7
1	D	245	ALA	3.7
1	D	359	ARG	3.7
1	D	101	MET	3.6
1	D	234	VAL	3.6
1	C	295	GLU	3.6
1	C	308	VAL	3.6
1	C	305	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	243	PRO	3.6
1	C	239	GLY	3.6
1	D	36	LYS	3.5
1	D	293	HIS	3.5
1	C	210	LYS	3.5
1	C	240	HIS	3.5
1	D	285	PRO	3.5
1	C	241	ARG	3.5
1	D	354	ARG	3.5
1	C	215	GLY	3.4
1	D	219	LEU	3.4
1	D	367	LEU	3.4
1	C	288	LEU	3.4
1	D	358	VAL	3.4
1	D	220	ILE	3.3
1	C	198	ARG	3.3
1	D	309	VAL	3.3
1	D	238	HIS	3.3
1	D	207	ILE	3.2
1	D	108	PRO	3.2
1	C	325	LEU	3.2
1	D	322	LEU	3.2
1	D	336	LEU	3.2
1	D	374	LEU	3.2
1	D	214	GLN	3.2
1	C	202	ARG	3.2
1	D	218	VAL	3.2
1	D	294	THR	3.2
1	D	250	ASP	3.1
1	D	198	ARG	3.1
1	D	302	ARG	3.1
1	C	206	GLU	3.1
1	D	360	ILE	3.1
1	D	100	VAL	3.1
1	D	330	SER	3.0
1	D	102	ASP	3.0
1	C	211	THR	3.0
1	D	369	ALA	3.0
1	C	248	TYR	2.9
1	D	307	MET	2.9
1	B	244	ARG	2.9
1	C	293	HIS	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	214	GLN	2.9
1	D	373	THR	2.9
1	D	319	GLY	2.9
1	D	308	VAL	2.8
1	C	294	THR	2.8
1	C	238	HIS	2.8
1	D	301	ASN	2.8
1	D	205	LEU	2.8
1	D	318	GLY	2.8
1	D	288	LEU	2.8
1	C	280	LYS	2.8
1	C	370	SER	2.8
1	A	302	ARG	2.7
1	D	305	GLY	2.7
1	C	369	ALA	2.7
1	D	295	GLU	2.7
1	D	303	ALA	2.7
1	D	253	MET	2.7
1	D	206	GLU	2.6
1	D	291	VAL	2.6
1	C	377	PHE	2.6
1	D	97	ALA	2.6
1	D	237	THR	2.6
1	D	363	GLU	2.6
1	C	99	LYS	2.6
1	D	204	PHE	2.6
1	C	329	LEU	2.6
1	C	304	PRO	2.6
1	C	301	ASN	2.6
1	D	312	GLY	2.6
1	A	104	PRO	2.6
1	C	365	VAL	2.6
1	C	344	GLN	2.6
1	C	307	MET	2.6
1	C	246	PRO	2.6
1	C	411	LYS	2.5
1	A	158	VAL	2.5
1	C	218	VAL	2.5
1	D	222	THR	2.5
1	D	109	GLU	2.5
1	C	414	ALA	2.5
1	C	367	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	338	PHE	2.4
1	D	344	GLN	2.4
1	D	377	PHE	2.3
1	C	291	VAL	2.3
1	C	337	VAL	2.3
1	D	195	ARG	2.3
1	D	347	LEU	2.3
1	D	73	ARG	2.3
1	D	203	GLU	2.3
1	C	109	GLU	2.2
1	D	352	ILE	2.2
1	B	39	ALA	2.2
1	D	202	ARG	2.2
1	D	323	HIS	2.2
1	C	361	LEU	2.2
1	C	362	GLY	2.2
1	D	216	GLY	2.2
1	A	102	ASP	2.2
1	C	412	LEU	2.2
1	C	292	GLU	2.2
1	D	246	PRO	2.2
1	D	337	VAL	2.1
1	D	339	VAL	2.1
1	C	236	TYR	2.1
1	D	103	GLU	2.1
1	C	371	VAL	2.0
1	D	353	ALA	2.0
1	C	219	LEU	2.0
1	A	101	MET	2.0
1	D	126	TRP	2.0
1	D	280	LYS	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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(Å ²)	Q<0.9
3	FLC	A	460	13/13	0.55	0.35	69,73,75,75	0
2	SO4	B	457	5/5	0.66	0.36	128,128,128,128	0
2	SO4	B	449	5/5	0.66	0.32	84,86,86,86	0
2	SO4	A	433	5/5	0.66	0.17	116,116,117,117	0
2	SO4	B	439	5/5	0.67	0.22	105,105,106,106	0
2	SO4	D	434	5/5	0.69	0.49	103,103,103,103	0
2	SO4	B	433	5/5	0.69	0.34	128,128,128,129	0
2	SO4	C	448	5/5	0.71	0.56	122,122,123,123	0
2	SO4	C	451	5/5	0.72	0.29	121,121,121,121	0
2	SO4	C	432	5/5	0.72	0.34	140,140,141,141	0
2	SO4	D	449	5/5	0.74	0.20	125,125,125,125	0
2	SO4	D	444	5/5	0.74	0.30	137,137,138,138	0
2	SO4	A	445	5/5	0.74	0.21	90,91,91,92	0
2	SO4	A	440	5/5	0.75	0.21	107,107,107,107	0
2	SO4	B	440	5/5	0.75	0.29	108,108,108,109	0
2	SO4	B	438	5/5	0.76	0.29	113,113,113,113	0
2	SO4	B	453	5/5	0.76	0.26	129,129,129,130	0
2	SO4	C	450	5/5	0.77	0.51	120,120,120,121	0
2	SO4	D	437	5/5	0.77	0.33	102,102,103,103	0
2	SO4	A	450	5/5	0.79	0.58	131,131,131,131	0
2	SO4	B	437	5/5	0.79	0.31	113,113,114,114	0
2	SO4	B	450	5/5	0.79	0.27	121,121,121,121	0
2	SO4	A	451	5/5	0.79	0.32	118,118,118,119	0
2	SO4	C	454	5/5	0.80	0.30	90,90,90,92	0
3	FLC	B	463	13/13	0.80	0.52	96,97,98,99	0
2	SO4	A	438	5/5	0.81	0.21	101,101,101,101	0
2	SO4	D	433	5/5	0.81	0.30	107,107,108,108	0
2	SO4	B	445	5/5	0.82	0.19	99,100,100,100	0
2	SO4	A	459	5/5	0.82	0.19	114,114,114,114	0
2	SO4	A	456	5/5	0.82	0.18	104,104,104,105	0
2	SO4	B	436	5/5	0.82	0.32	124,124,124,124	0
2	SO4	B	444	5/5	0.82	0.36	69,70,71,73	0
2	SO4	C	438	5/5	0.83	0.35	128,128,128,128	0
2	SO4	A	453	5/5	0.83	0.22	125,125,125,125	0
2	SO4	A	448	5/5	0.83	0.15	101,101,101,101	0
2	SO4	C	446	5/5	0.84	0.27	136,136,137,137	0
2	SO4	A	434	5/5	0.85	0.18	118,118,118,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	A	454	5/5	0.85	0.21	77,78,78,79	0
2	SO4	B	448	5/5	0.85	0.32	99,99,99,100	0
2	SO4	D	445	5/5	0.85	0.14	124,124,124,124	0
2	SO4	C	452	5/5	0.86	0.17	91,91,91,91	0
2	SO4	D	435	5/5	0.86	0.15	99,99,100,100	0
2	SO4	A	442	5/5	0.86	0.16	87,88,88,88	0
2	SO4	C	440	5/5	0.86	0.25	123,124,124,124	0
2	SO4	A	435	5/5	0.86	0.15	105,105,105,105	0
2	SO4	D	440	5/5	0.87	0.19	118,118,118,118	0
2	SO4	C	442	5/5	0.87	0.14	84,84,84,84	0
2	SO4	D	442	5/5	0.87	0.20	89,89,89,90	0
2	SO4	B	455	5/5	0.87	0.25	79,79,80,80	0
2	SO4	A	447	5/5	0.87	0.19	95,96,96,96	0
2	SO4	B	447	5/5	0.87	0.21	126,126,126,126	0
2	SO4	D	439	5/5	0.88	0.24	98,98,98,98	0
2	SO4	A	436	5/5	0.88	0.15	94,94,95,95	0
2	SO4	A	432	5/5	0.88	0.29	118,118,118,118	0
2	SO4	D	441	5/5	0.88	0.15	101,101,101,102	0
2	SO4	D	448	5/5	0.88	0.20	85,85,86,86	0
2	SO4	A	446	5/5	0.88	0.18	95,95,96,96	0
2	SO4	B	454	5/5	0.88	0.22	90,91,91,92	0
2	SO4	B	442	5/5	0.89	0.13	110,110,110,110	0
2	SO4	C	436	5/5	0.89	0.24	108,108,108,108	0
2	SO4	C	437	5/5	0.89	0.13	115,115,115,115	0
4	ZN	C	455	1/1	0.89	0.06	65,65,65,65	0
2	SO4	C	453	5/5	0.90	0.19	101,101,101,101	0
2	SO4	D	436	5/5	0.90	0.16	89,90,90,90	0
2	SO4	C	435	5/5	0.90	0.11	92,92,92,92	0
2	SO4	C	441	5/5	0.90	0.20	78,78,79,79	0
2	SO4	B	462	5/5	0.90	0.17	93,93,93,93	0
2	SO4	B	461	5/5	0.91	0.16	76,76,76,77	0
2	SO4	B	458	5/5	0.91	0.30	102,102,102,102	0
2	SO4	D	447	5/5	0.91	0.17	66,66,67,68	0
2	SO4	B	459	5/5	0.92	0.14	64,64,66,66	0
2	SO4	C	444	5/5	0.92	0.17	114,114,114,114	0
2	SO4	C	439	5/5	0.92	0.13	91,91,91,91	0
2	SO4	A	455	5/5	0.93	0.09	69,69,70,70	0
2	SO4	A	437	5/5	0.93	0.14	68,68,69,69	0
2	SO4	A	439	5/5	0.93	0.12	100,100,101,101	0
2	SO4	A	452	5/5	0.93	0.12	65,65,66,66	0
2	SO4	C	447	5/5	0.93	0.10	72,72,73,73	0
4	ZN	D	450	1/1	0.94	0.06	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	A	444	5/5	0.94	0.21	56,57,57,57	0
2	SO4	D	446	5/5	0.94	0.14	73,73,74,74	0
2	SO4	B	441	5/5	0.94	0.17	79,79,79,79	0
2	SO4	C	434	5/5	0.94	0.15	65,65,66,66	0
2	SO4	B	435	5/5	0.94	0.13	67,67,68,68	0
2	SO4	B	434	5/5	0.94	0.10	56,56,57,58	0
2	SO4	B	443	5/5	0.95	0.19	53,54,55,56	0
2	SO4	C	445	5/5	0.95	0.23	97,97,97,97	0
2	SO4	B	451	5/5	0.95	0.11	68,68,68,69	0
4	ZN	A	462	1/1	0.96	0.09	50,50,50,50	0
2	SO4	C	443	5/5	0.96	0.10	64,64,65,65	0
2	SO4	D	432	5/5	0.96	0.12	51,51,52,53	0
4	ZN	C	456	1/1	0.96	0.06	61,61,61,61	0
2	SO4	C	433	5/5	0.96	0.08	50,50,51,52	0
2	SO4	B	460	5/5	0.96	0.07	70,71,72,72	0
2	SO4	D	443	5/5	0.97	0.08	42,43,45,46	0
2	SO4	B	452	5/5	0.97	0.12	48,49,50,51	0
2	SO4	A	441	5/5	0.97	0.10	53,53,54,56	0
2	SO4	B	432	5/5	0.97	0.12	48,48,49,50	0
2	SO4	D	438	5/5	0.97	0.10	50,50,51,51	0
2	SO4	A	457	5/5	0.98	0.10	48,48,49,49	0
4	ZN	D	451	1/1	0.98	0.05	54,54,54,54	0
4	ZN	A	461	1/1	0.98	0.06	47,47,47,47	0
2	SO4	C	449	5/5	0.98	0.13	42,43,44,44	0
2	SO4	A	458	5/5	0.99	0.13	35,37,39,40	0
2	SO4	B	446	5/5	0.99	0.09	31,32,33,34	0
4	ZN	B	464	1/1	0.99	0.09	46,46,46,46	0
2	SO4	A	449	5/5	0.99	0.10	18,23,25,25	0
4	ZN	B	465	1/1	0.99	0.10	53,53,53,53	0
2	SO4	A	443	5/5	0.99	0.12	32,32,35,35	0
2	SO4	B	456	5/5	0.99	0.11	20,22,23,23	0

6.5 Other polymers

There are no such residues in this entry.