



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:52 AM GMT

PDB ID : 3NE1  
Title : Mycobacterium tuberculosis Acyl Carrier Protein Synthase in complex with sulfate ion  
Authors : Gokulan, K.  
Deposited on : 2010-06-08  
Resolution : 2.51 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

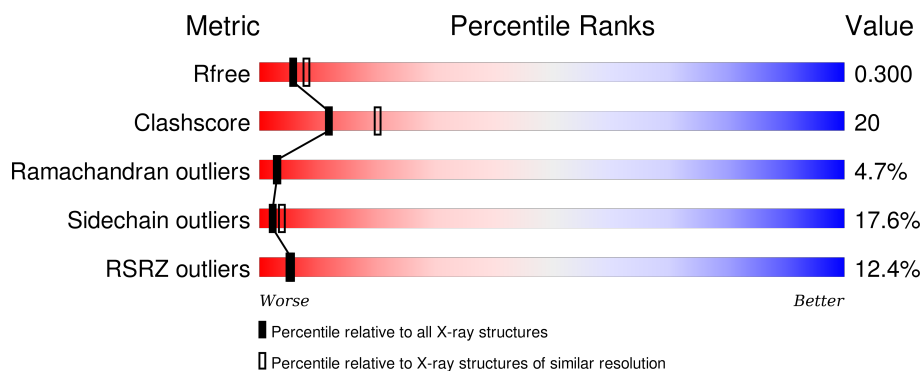
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.51 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))
$R_{free}$	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	130	<div> <div>9%</div> <div>32%</div> <div>41%</div> <div>23%</div> <div>..</div> </div>
1	B	130	<div> <div>12%</div> <div>37%</div> <div>36%</div> <div>18%</div> <div>8%</div> <div>.</div> </div>
1	C	130	<div> <div>15%</div> <div>35%</div> <div>38%</div> <div>25%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	131	-	X	-	-
2	SO4	C	131	-	-	X	-

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2986 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 Holo-[acyl-carrier-protein] synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	0	0
			970	606	176	187	1			
1	B	129	Total	C	N	O	S	0	0	0
			970	606	176	187	1			
1	C	129	Total	C	N	O	S	0	0	0
			970	606	176	187	1			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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		

*Continued on next page...*

*Continued from previous page...*

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

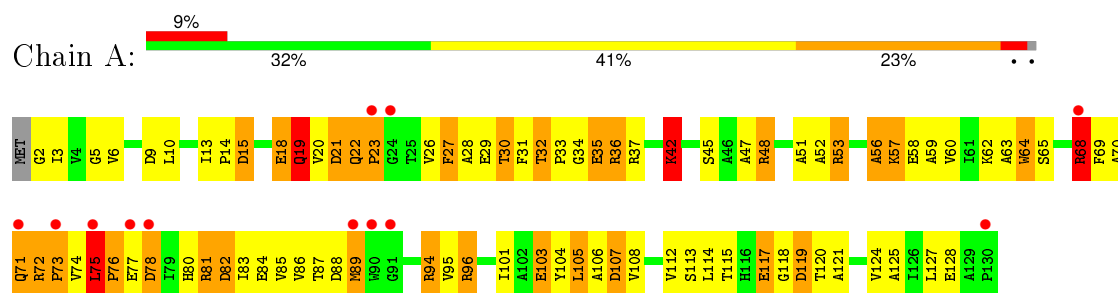
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	19	Total	O	0	0
			19	19		
3	B	25	Total	O	0	0
			25	25		
3	C	12	Total	O	0	0
			12	12		

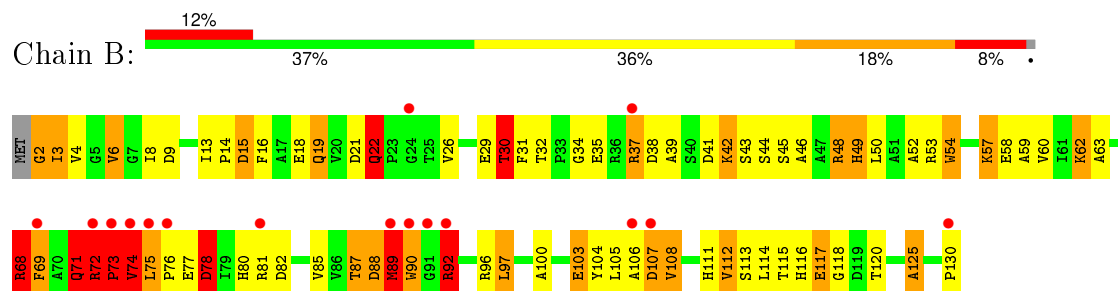
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

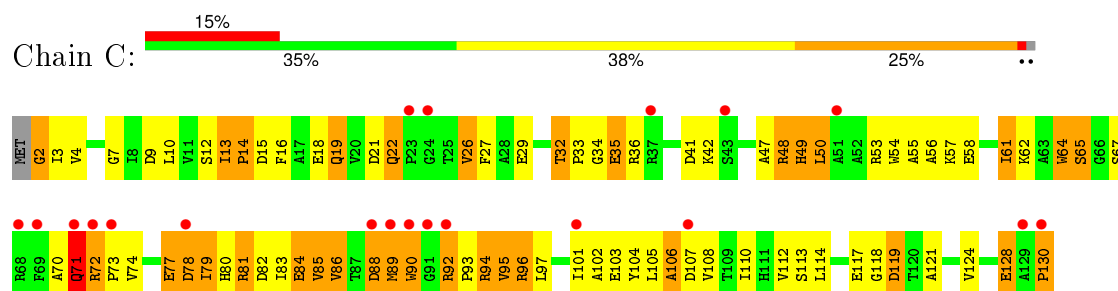
#### • Molecule 1: Holo-[acyl-carrier-protein] synthase



#### • Molecule 1: Holo-[acyl-carrier-protein] synthase



#### • Molecule 1: Holo-[acyl-carrier-protein] synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.12Å 104.87Å 105.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.07 – 2.51 20.07 – 2.51	Depositor EDS
% Data completeness (in resolution range)	95.7 (20.07-2.51) 96.0 (20.07-2.51)	Depositor EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.09 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.228 , 0.301 0.239 , 0.300	Depositor DCC
$R_{free}$ test set	761 reflections (5.18%)	DCC
Wilson B-factor (Å <sup>2</sup> )	63.0	Xtriage
Anisotropy	0.431	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 65.0	EDS
Estimated twinning fraction	0.019 for -h,-l,-k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 15465 reflections (0.006%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2986	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.87% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	2.34	43/991 (4.3%)	1.78	26/1354 (1.9%)
1	B	2.50	57/991 (5.8%)	1.87	30/1354 (2.2%)
1	C	2.65	70/991 (7.1%)	1.94	28/1354 (2.1%)
All	All	2.50	170/2973 (5.7%)	1.87	84/4062 (2.1%)

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	B	0	2
1	C	0	1
All	All	0	3

All (170) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	26	VAL	CB-CG1	13.13	1.80	1.52
1	B	31	PHE	CG-CD2	10.23	1.54	1.38
1	C	35	GLU	CD-OE2	-10.05	1.14	1.25
1	C	90	TRP	CB-CG	10.04	1.68	1.50
1	A	27	PHE	CD1-CE1	9.94	1.59	1.39
1	C	64	TRP	CG-CD1	-9.80	1.23	1.36
1	A	96	ARG	CG-CD	9.34	1.75	1.51
1	B	90	TRP	CB-CG	9.25	1.66	1.50
1	C	121	ALA	CA-CB	9.23	1.71	1.52
1	A	57	LYS	CD-CE	8.81	1.73	1.51
1	C	19	GLN	CG-CD	8.74	1.71	1.51
1	B	54	TRP	CB-CG	8.65	1.65	1.50
1	B	18	GLU	CD-OE2	8.64	1.35	1.25

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	60	VAL	CB-CG2	8.61	1.71	1.52
1	C	58	GLU	CD-OE2	-8.52	1.16	1.25
1	C	94	ARG	NE-CZ	8.51	1.44	1.33
1	B	107	ASP	CB-CG	8.39	1.69	1.51
1	B	125	ALA	CA-CB	-8.39	1.34	1.52
1	A	56	ALA	N-CA	8.39	1.63	1.46
1	B	29	GLU	CG-CD	8.37	1.64	1.51
1	B	74	VAL	CA-CB	8.36	1.72	1.54
1	C	7	GLY	CA-C	-8.19	1.38	1.51
1	B	29	GLU	CD-OE1	8.18	1.34	1.25
1	A	94	ARG	NE-CZ	8.18	1.43	1.33
1	A	29	GLU	CD-OE1	8.17	1.34	1.25
1	B	89	MET	SD-CE	7.99	2.22	1.77
1	C	81	ARG	NE-CZ	7.94	1.43	1.33
1	B	63	ALA	CA-CB	-7.89	1.35	1.52
1	C	113	SER	CB-OG	7.87	1.52	1.42
1	B	48	ARG	NE-CZ	7.78	1.43	1.33
1	B	62	LYS	CE-NZ	7.77	1.68	1.49
1	A	36	ARG	CG-CD	-7.65	1.32	1.51
1	C	96	ARG	C-O	7.60	1.37	1.23
1	C	53	ARG	NE-CZ	7.58	1.43	1.33
1	C	96	ARG	CG-CD	7.55	1.70	1.51
1	A	107	ASP	CB-CG	7.45	1.67	1.51
1	B	42	LYS	CD-CE	7.28	1.69	1.51
1	C	103	GLU	CD-OE1	7.25	1.33	1.25
1	C	86	VAL	CB-CG1	7.12	1.67	1.52
1	B	39	ALA	CA-CB	-7.09	1.37	1.52
1	B	29	GLU	CB-CG	7.06	1.65	1.52
1	A	42	LYS	CE-NZ	7.02	1.66	1.49
1	A	18	GLU	CD-OE1	6.94	1.33	1.25
1	B	59	ALA	CA-CB	-6.90	1.38	1.52
1	C	94	ARG	CZ-NH1	6.90	1.42	1.33
1	B	16	PHE	CB-CG	6.87	1.63	1.51
1	B	21	ASP	C-O	-6.85	1.10	1.23
1	C	18	GLU	CG-CD	6.83	1.62	1.51
1	A	64	TRP	CG-CD1	6.82	1.46	1.36
1	B	6	VAL	C-O	-6.80	1.10	1.23
1	A	27	PHE	CD2-CE2	6.76	1.52	1.39
1	C	47	ALA	C-O	-6.76	1.10	1.23
1	B	115	THR	N-CA	-6.76	1.32	1.46
1	B	37	ARG	CG-CD	6.75	1.68	1.51
1	C	64	TRP	CZ3-CH2	-6.74	1.29	1.40

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	47	ALA	CA-CB	6.72	1.66	1.52
1	A	65	SER	CB-OG	-6.72	1.33	1.42
1	C	29	GLU	CD-OE1	6.71	1.33	1.25
1	C	95	VAL	CB-CG1	-6.70	1.38	1.52
1	C	62	LYS	CD-CE	-6.58	1.34	1.51
1	C	2	GLY	N-CA	6.56	1.55	1.46
1	B	52	ALA	N-CA	-6.47	1.33	1.46
1	A	21	ASP	CB-CG	6.45	1.65	1.51
1	C	19	GLN	CB-CG	6.41	1.69	1.52
1	B	108	VAL	CB-CG2	-6.40	1.39	1.52
1	B	103	GLU	CG-CD	6.37	1.61	1.51
1	C	4	VAL	C-O	-6.37	1.11	1.23
1	C	104	TYR	CE2-CZ	6.35	1.46	1.38
1	A	18	GLU	CG-CD	6.29	1.61	1.51
1	A	35	GLU	CD-OE2	-6.29	1.18	1.25
1	C	117	GLU	C-O	6.28	1.35	1.23
1	A	125	ALA	C-O	-6.28	1.11	1.23
1	B	4	VAL	CB-CG1	6.26	1.66	1.52
1	A	103	GLU	CD-OE2	6.26	1.32	1.25
1	A	62	LYS	C-O	-6.25	1.11	1.23
1	C	48	ARG	CZ-NH1	6.24	1.41	1.33
1	A	53	ARG	CG-CD	6.22	1.67	1.51
1	C	81	ARG	CZ-NH1	6.22	1.41	1.33
1	A	96	ARG	NE-CZ	-6.22	1.25	1.33
1	C	112	VAL	CB-CG1	-6.18	1.39	1.52
1	B	118	GLY	C-O	-6.13	1.13	1.23
1	C	112	VAL	CB-CG2	6.08	1.65	1.52
1	B	89	MET	CG-SD	6.08	1.97	1.81
1	C	33	PRO	CG-CD	6.07	1.70	1.50
1	A	121	ALA	CA-CB	6.06	1.65	1.52
1	B	53	ARG	CZ-NH2	6.05	1.41	1.33
1	A	62	LYS	CE-NZ	-6.05	1.33	1.49
1	C	18	GLU	CD-OE1	6.02	1.32	1.25
1	B	57	LYS	CD-CE	6.00	1.66	1.51
1	A	59	ALA	CA-C	-5.96	1.37	1.52
1	A	118	GLY	C-O	5.96	1.33	1.23
1	A	56	ALA	CA-CB	-5.93	1.40	1.52
1	C	89	MET	SD-CE	5.92	2.11	1.77
1	B	85	VAL	CA-CB	-5.90	1.42	1.54
1	A	19	GLN	CG-CD	5.88	1.64	1.51
1	C	103	GLU	CG-CD	5.88	1.60	1.51
1	A	83	ILE	CA-CB	5.83	1.68	1.54

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	100	ALA	CA-CB	5.81	1.64	1.52
1	A	31	PHE	CD1-CE1	5.80	1.50	1.39
1	C	110	ILE	CA-CB	5.79	1.68	1.54
1	B	19	GLN	CB-CG	-5.79	1.36	1.52
1	C	89	MET	CG-SD	5.78	1.96	1.81
1	B	48	ARG	CG-CD	5.78	1.66	1.51
1	B	6	VAL	CB-CG1	-5.74	1.40	1.52
1	B	42	LYS	C-O	5.73	1.34	1.23
1	C	16	PHE	C-O	-5.72	1.12	1.23
1	B	42	LYS	CE-NZ	5.72	1.63	1.49
1	B	112	VAL	C-O	-5.72	1.12	1.23
1	C	53	ARG	CZ-NH1	5.70	1.40	1.33
1	A	29	GLU	CD-OE2	5.69	1.31	1.25
1	C	84	GLU	CD-OE1	5.67	1.31	1.25
1	B	59	ALA	N-CA	-5.66	1.35	1.46
1	C	72	ARG	N-CA	5.66	1.57	1.46
1	B	16	PHE	CE2-CZ	-5.65	1.26	1.37
1	C	71	GLN	CA-C	5.63	1.67	1.52
1	C	49	HIS	C-O	5.62	1.34	1.23
1	C	130	PRO	CB-CG	5.55	1.77	1.50
1	B	73	PRO	CB-CG	5.55	1.77	1.50
1	A	6	VAL	CB-CG2	-5.54	1.41	1.52
1	C	93	PRO	CB-CG	-5.54	1.22	1.50
1	C	15	ASP	CG-OD1	5.53	1.38	1.25
1	B	77	GLU	CG-CD	5.53	1.60	1.51
1	C	62	LYS	CB-CG	5.51	1.67	1.52
1	C	57	LYS	CD-CE	5.50	1.65	1.51
1	B	18	GLU	CD-OE1	5.50	1.31	1.25
1	C	58	GLU	CA-CB	-5.48	1.41	1.53
1	C	119	ASP	CB-CG	-5.47	1.40	1.51
1	B	54	TRP	CG-CD1	-5.45	1.29	1.36
1	C	55	ALA	N-CA	-5.44	1.35	1.46
1	A	22	GLN	C-O	5.44	1.33	1.23
1	C	108	VAL	CB-CG1	-5.43	1.41	1.52
1	C	83	ILE	CA-CB	5.42	1.67	1.54
1	B	22	GLN	CD-NE2	5.42	1.46	1.32
1	A	51	ALA	CA-CB	-5.41	1.41	1.52
1	C	13	ILE	C-O	-5.41	1.13	1.23
1	C	85	VAL	CA-CB	5.39	1.66	1.54
1	C	88	ASP	C-O	5.39	1.33	1.23
1	C	58	GLU	CA-C	5.39	1.67	1.52
1	C	85	VAL	CB-CG1	5.39	1.64	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	53	ARG	CZ-NH1	5.39	1.40	1.33
1	A	58	GLU	CD-OE2	5.38	1.31	1.25
1	C	74	VAL	CB-CG2	5.37	1.64	1.52
1	A	45	SER	CB-OG	5.36	1.49	1.42
1	B	113	SER	N-CA	-5.36	1.35	1.46
1	B	116	HIS	C-O	-5.33	1.13	1.23
1	B	2	GLY	C-O	-5.32	1.15	1.23
1	C	106	ALA	CA-CB	5.27	1.63	1.52
1	C	10	LEU	CB-CG	5.26	1.67	1.52
1	C	36	ARG	NE-CZ	5.25	1.39	1.33
1	C	117	GLU	CD-OE2	5.23	1.31	1.25
1	A	42	LYS	CD-CE	5.23	1.64	1.51
1	A	89	MET	SD-CE	5.23	2.07	1.77
1	A	57	LYS	CE-NZ	5.22	1.62	1.49
1	C	77	GLU	CG-CD	5.22	1.59	1.51
1	C	84	GLU	CA-C	-5.19	1.39	1.52
1	B	31	PHE	CD1-CE1	5.19	1.49	1.39
1	A	10	LEU	CG-CD2	5.18	1.71	1.51
1	B	48	ARG	CZ-NH2	5.17	1.39	1.33
1	B	68	ARG	CG-CD	5.16	1.64	1.51
1	A	5	GLY	C-O	5.16	1.31	1.23
1	C	34	GLY	C-O	5.15	1.31	1.23
1	A	115	THR	CA-CB	-5.14	1.40	1.53
1	B	26	VAL	CB-CG2	5.13	1.63	1.52
1	B	85	VAL	C-O	-5.09	1.13	1.23
1	C	16	PHE	CG-CD2	-5.08	1.31	1.38
1	B	57	LYS	N-CA	-5.08	1.36	1.46
1	A	6	VAL	CA-CB	5.03	1.65	1.54
1	C	113	SER	C-O	-5.02	1.13	1.23
1	B	43	SER	C-O	-5.01	1.13	1.23
1	C	83	ILE	C-O	5.00	1.32	1.23

All (84) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	78	ASP	CB-CG-OD2	12.38	129.44	118.30
1	C	41	ASP	CB-CG-OD2	11.98	129.09	118.30
1	C	94	ARG	NE-CZ-NH1	11.94	126.27	120.30
1	A	15	ASP	CB-CG-OD2	11.67	128.80	118.30
1	C	82	ASP	CB-CG-OD2	11.57	128.72	118.30
1	A	94	ARG	NE-CZ-NH1	11.03	125.81	120.30
1	C	48	ARG	NE-CZ-NH2	-10.47	115.06	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	96	ARG	NE-CZ-NH2	-10.39	115.10	120.30
1	C	9	ASP	CB-CG-OD2	-9.76	109.52	118.30
1	B	82	ASP	CB-CG-OD2	9.72	127.05	118.30
1	A	37	ARG	NE-CZ-NH2	9.68	125.14	120.30
1	C	81	ARG	NE-CZ-NH1	9.67	125.13	120.30
1	B	9	ASP	CB-CG-OD1	9.44	126.79	118.30
1	C	15	ASP	CB-CG-OD2	-9.06	110.14	118.30
1	C	50	LEU	CA-CB-CG	8.98	135.96	115.30
1	C	21	ASP	CB-CG-OD2	8.87	126.28	118.30
1	A	48	ARG	NE-CZ-NH2	-8.82	115.89	120.30
1	A	37	ARG	NE-CZ-NH1	-8.60	116.00	120.30
1	B	88	ASP	CB-CG-OD2	8.52	125.97	118.30
1	C	81	ARG	NE-CZ-NH2	-8.50	116.05	120.30
1	B	62	LYS	CD-CE-NZ	8.16	130.47	111.70
1	B	31	PHE	CB-CG-CD2	8.06	126.44	120.80
1	A	88	ASP	CB-CG-OD2	7.98	125.48	118.30
1	B	68	ARG	NE-CZ-NH2	7.94	124.27	120.30
1	C	9	ASP	CB-CG-OD1	7.74	125.27	118.30
1	B	75	LEU	CA-CB-CG	7.64	132.88	115.30
1	B	112	VAL	CG1-CB-CG2	-7.61	98.73	110.90
1	A	48	ARG	CG-CD-NE	-7.60	95.84	111.80
1	C	119	ASP	CB-CG-OD1	-7.54	111.51	118.30
1	B	41	ASP	CB-CG-OD2	7.27	124.84	118.30
1	A	119	ASP	CB-CG-OD2	7.20	124.78	118.30
1	C	94	ARG	NE-CZ-NH2	-7.20	116.70	120.30
1	B	112	VAL	CA-CB-CG1	-7.20	100.11	110.90
1	A	75	LEU	CA-CB-CG	7.15	131.75	115.30
1	A	3	ILE	CG1-CB-CG2	-7.02	95.95	111.40
1	B	31	PHE	CB-CG-CD1	-6.92	115.96	120.80
1	B	92	ARG	NE-CZ-NH1	6.87	123.74	120.30
1	B	78	ASP	CB-CG-OD1	6.87	124.48	118.30
1	B	30	THR	OG1-CB-CG2	-6.82	94.31	110.00
1	A	62	LYS	CD-CE-NZ	-6.70	96.29	111.70
1	B	48	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	B	15	ASP	CB-CG-OD2	6.56	124.20	118.30
1	A	2	GLY	N-CA-C	-6.46	96.95	113.10
1	A	9	ASP	CB-CG-OD1	-6.41	112.53	118.30
1	A	78	ASP	N-CA-C	-6.39	93.75	111.00
1	C	92	ARG	NE-CZ-NH2	6.38	123.49	120.30
1	C	36	ARG	NE-CZ-NH2	6.35	123.47	120.30
1	A	9	ASP	CB-CG-OD2	6.29	123.96	118.30
1	C	112	VAL	CG1-CB-CG2	-6.28	100.85	110.90

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	97	LEU	CA-CB-CG	6.20	129.56	115.30
1	B	73	PRO	CA-C-N	-6.16	103.66	117.20
1	A	30	THR	OG1-CB-CG2	-6.09	95.99	110.00
1	B	38	ASP	CB-CG-OD2	6.04	123.74	118.30
1	A	15	ASP	OD1-CG-OD2	-5.93	112.03	123.30
1	B	89	MET	CG-SD-CE	5.92	109.66	100.20
1	B	73	PRO	C-N-CA	5.91	136.47	121.70
1	A	48	ARG	NE-CZ-NH1	5.80	123.20	120.30
1	B	72	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	B	77	GLU	OE1-CD-OE2	-5.76	116.38	123.30
1	B	72	ARG	CB-CA-C	5.70	121.79	110.40
1	B	2	GLY	N-CA-C	-5.69	98.88	113.10
1	C	118	GLY	N-CA-C	-5.62	99.04	113.10
1	C	124	VAL	CG1-CB-CG2	-5.55	102.02	110.90
1	C	58	GLU	OE1-CD-OE2	-5.54	116.65	123.30
1	C	82	ASP	CB-CG-OD1	-5.53	113.32	118.30
1	A	68	ARG	NE-CZ-NH1	-5.52	117.54	120.30
1	C	88	ASP	CB-CG-OD2	5.50	123.25	118.30
1	C	61	ILE	CA-CB-CG1	5.50	121.45	111.00
1	B	9	ASP	CB-CG-OD2	-5.42	113.42	118.30
1	A	117	GLU	OE1-CD-OE2	-5.40	116.82	123.30
1	B	60	VAL	CG1-CB-CG2	-5.40	102.27	110.90
1	A	82	ASP	CB-CG-OD2	5.39	123.15	118.30
1	A	124	VAL	CG1-CB-CG2	-5.37	102.31	110.90
1	C	61	ILE	CG1-CB-CG2	-5.36	99.62	111.40
1	A	112	VAL	CG1-CB-CG2	-5.26	102.49	110.90
1	C	88	ASP	O-C-N	5.21	131.03	122.70
1	A	60	VAL	CG1-CB-CG2	-5.19	102.60	110.90
1	C	114	LEU	CB-CG-CD1	5.15	119.75	111.00
1	A	42	LYS	CD-CE-NZ	5.14	123.52	111.70
1	A	96	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	C	48	ARG	N-CA-C	5.13	124.84	111.00
1	C	128	GLU	OE1-CD-OE2	5.12	129.44	123.30
1	B	87	THR	OG1-CB-CG2	-5.08	98.32	110.00
1	B	103	GLU	OE1-CD-OE2	-5.06	117.23	123.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	71	GLN	Peptide
1	B	72	ARG	Peptide

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Group
1	C	71	GLN	Peptide

## 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	970	0	918	43	0
1	B	970	0	918	42	1
1	C	970	0	918	35	0
2	A	5	0	0	1	0
2	B	10	0	0	0	0
2	C	5	0	0	3	0
3	A	19	0	0	0	0
3	B	25	0	0	3	1
3	C	12	0	0	2	0
All	All	2986	0	2754	114	2

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 20.

All (114) 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:96:ARG:CG	1:A:96:ARG:CD	1.75	1.61
1:C:26:VAL:CG1	1:C:26:VAL:CB	1.80	1.56
1:B:73:PRO:CG	1:B:73:PRO:CB	1.77	1.53
1:B:62:LYS:CE	1:B:62:LYS:NZ	1.68	1.53
1:C:130:PRO:CG	1:C:130:PRO:CB	1.77	1.52
1:A:89:MET:SD	1:A:89:MET:CE	2.07	1.43
1:C:89:MET:CE	1:C:89:MET:SD	2.11	1.37
1:B:89:MET:SD	1:B:89:MET:CE	2.22	1.26
1:A:101:ILE:HG22	1:A:105:LEU:HD23	1.67	0.76
1:B:32:THR:HG21	3:B:138:HOH:O	1.86	0.75
1:A:57:LYS:HD3	1:A:80:HIS:O	1.88	0.72
1:A:64:TRP:O	1:A:70:ALA:HB2	1.91	0.70
1:C:32:THR:HG21	3:C:144:HOH:O	1.90	0.70

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:ASP:O	1:A:19:GLN:HG2	1.91	0.69
1:A:71:GLN:O	1:A:74:VAL:HG13	1.93	0.69
1:A:104:TYR:C	1:A:106:ALA:H	1.95	0.69
1:C:32:THR:HG22	1:C:35:GLU:H	1.57	0.68
1:C:107:ASP:O	1:C:130:PRO:HD3	1.93	0.68
1:C:13:ILE:HB	1:C:14:PRO:HD3	1.75	0.68
1:A:108:VAL:HB	1:A:128:GLU:O	1.95	0.66
1:C:70:ALA:O	1:C:71:GLN:HG3	1.94	0.66
1:A:56:ALA:HB2	1:A:114:LEU:HD21	1.77	0.66
1:B:81:ARG:NH2	3:B:163:HOH:O	2.29	0.65
1:A:103:GLU:O	1:A:106:ALA:HB2	1.97	0.65
1:B:45:SER:HA	1:B:48:ARG:NH1	2.12	0.64
1:C:84:GLU:HB2	1:C:96:ARG:HB3	1.80	0.63
1:B:44:SER:O	1:B:46:ALA:N	2.32	0.63
1:C:22:GLN:N	1:C:22:GLN:HE21	1.97	0.63
1:C:79:ILE:O	1:C:80:HIS:HB2	2.00	0.61
1:B:71:GLN:O	1:B:72:ARG:C	2.39	0.61
1:B:105:LEU:HB3	1:B:108:VAL:HG22	1.82	0.61
1:A:32:THR:HG22	1:A:34:GLY:H	1.66	0.61
1:C:70:ALA:C	1:C:71:GLN:HG3	2.22	0.60
1:C:79:ILE:HG23	1:C:80:HIS:ND1	2.17	0.60
1:B:32:THR:HG22	1:B:34:GLY:H	1.68	0.59
1:B:30:THR:HB	1:B:57:LYS:HZ2	1.69	0.58
1:A:96:ARG:CB	1:A:96:ARG:CD	2.77	0.57
1:B:15:ASP:O	1:B:19:GLN:HG2	2.04	0.56
1:C:26:VAL:CA	1:C:26:VAL:CG1	2.78	0.55
1:A:101:ILE:CG2	1:A:105:LEU:HD23	2.36	0.55
1:B:35:GLU:HB3	1:B:50:LEU:HD11	1.89	0.55
1:B:92:ARG:NH1	1:C:67:SER:O	2.40	0.54
1:C:102:ALA:O	1:C:106:ALA:HA	2.07	0.54
1:A:70:ALA:HB1	1:A:74:VAL:HG11	1.89	0.54
1:C:27:PHE:HE1	1:C:54:TRP:CE2	2.26	0.53
1:B:62:LYS:NZ	3:B:147:HOH:O	2.41	0.53
1:B:72:ARG:HD3	1:B:74:VAL:HG12	1.91	0.53
1:A:32:THR:HG22	1:A:35:GLU:H	1.74	0.52
1:A:56:ALA:HB2	1:A:114:LEU:CD2	2.40	0.52
1:C:101:ILE:HG22	1:C:105:LEU:HD12	1.92	0.52
1:A:20:VAL:HA	1:A:27:PHE:CD2	2.45	0.52
1:B:6:VAL:O	1:B:6:VAL:HG13	2.09	0.52
1:B:111:HIS:O	1:B:125:ALA:HA	2.09	0.52
1:B:2:GLY:O	1:B:3:ILE:C	2.49	0.52

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ARG:CG	1:A:96:ARG:NE	2.64	0.50
1:A:104:TYR:C	1:A:106:ALA:N	2.62	0.50
1:A:28:ALA:HA	1:A:36:ARG:NH1	2.27	0.50
1:C:49:HIS:HE1	2:C:131:SO4:S	2.35	0.50
1:B:37:ARG:O	1:B:37:ARG:HD3	2.12	0.50
1:A:53:ARG:O	1:A:85:VAL:HG11	2.12	0.50
1:A:26:VAL:O	1:A:30:THR:HG22	2.11	0.49
1:B:2:GLY:O	1:B:3:ILE:O	2.31	0.49
1:A:72:ARG:HG3	1:C:90:TRP:CZ3	2.47	0.49
1:B:13:ILE:N	1:B:14:PRO:CD	2.76	0.49
1:B:92:ARG:HH22	1:C:72:ARG:NH1	2.10	0.49
1:C:49:HIS:CE1	2:C:131:SO4:O1	2.67	0.48
1:B:76:PRO:HB2	1:B:78:ASP:HB2	1.96	0.48
1:C:22:GLN:N	1:C:22:GLN:NE2	2.60	0.48
1:A:52:ALA:O	1:A:114:LEU:HD22	2.14	0.48
1:B:92:ARG:HH22	1:C:72:ARG:HH12	1.61	0.48
1:A:14:PRO:CG	1:A:119:ASP:HB3	2.44	0.47
1:A:72:ARG:N	1:A:73:PRO:CD	2.77	0.47
1:A:13:ILE:N	1:A:14:PRO:CD	2.77	0.47
1:C:77:GLU:O	1:C:78:ASP:HB2	2.14	0.47
1:A:14:PRO:CD	1:A:119:ASP:HB3	2.44	0.47
1:B:45:SER:CA	1:B:48:ARG:NH1	2.78	0.46
1:A:113:SER:HB3	1:B:8:ILE:HG22	1.98	0.46
1:A:86:VAL:HG22	1:A:87:THR:N	2.30	0.46
1:A:105:LEU:HD12	1:A:108:VAL:HG21	1.98	0.46
1:B:6:VAL:CG1	1:B:6:VAL:O	2.63	0.45
1:B:68:ARG:HG3	1:B:69:PHE:N	2.29	0.45
1:B:30:THR:CB	1:B:57:LYS:HZ2	2.28	0.45
1:A:81:ARG:NH1	1:A:84:GLU:HG3	2.32	0.45
1:B:54:TRP:O	1:B:58:GLU:HG2	2.17	0.44
1:C:79:ILE:O	1:C:81:ARG:N	2.44	0.44
1:B:117:GLU:CD	1:B:117:GLU:O	2.55	0.44
1:C:49:HIS:HE1	2:C:131:SO4:O1	2.00	0.44
1:B:30:THR:HG21	1:B:54:TRP:HZ3	1.82	0.44
1:A:32:THR:HG22	1:A:34:GLY:N	2.30	0.44
1:A:14:PRO:HD3	1:A:119:ASP:HB3	2.00	0.43
1:C:95:VAL:HG12	1:C:96:ARG:N	2.33	0.43
1:B:117:GLU:HG3	1:C:12:SER:N	2.34	0.43
1:C:61:ILE:O	1:C:65:SER:HB2	2.18	0.43
1:B:103:GLU:O	1:B:106:ALA:HB2	2.18	0.43
1:B:73:PRO:CB	1:B:104:TYR:OH	2.67	0.43

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:PRO:O	1:B:76:PRO:HD3	2.19	0.42
1:B:45:SER:O	1:B:49:HIS:ND1	2.53	0.42
1:C:2:GLY:O	1:C:3:ILE:C	2.53	0.42
1:C:56:ALA:HB3	1:C:85:VAL:HG21	2.02	0.42
1:A:68:ARG:C	1:A:70:ALA:N	2.73	0.42
1:A:30:THR:OG1	1:A:57:LYS:HE3	2.20	0.42
1:A:14:PRO:HB3	1:A:42:LYS:HE2	2.02	0.42
1:A:75:LEU:O	1:A:76:PRO:O	2.38	0.42
1:A:82:ASP:N	1:A:82:ASP:OD1	2.53	0.42
1:A:48:ARG:NH1	2:A:131:SO4:O1	2.48	0.42
1:B:72:ARG:C	1:B:74:VAL:N	2.73	0.41
1:C:26:VAL:HG12	3:C:136:HOH:O	2.21	0.41
1:B:57:LYS:NZ	1:B:80:HIS:O	2.43	0.41
1:C:64:TRP:HD1	1:C:105:LEU:HD21	1.85	0.41
1:C:105:LEU:HA	1:C:105:LEU:HD23	1.93	0.41
1:A:21:ASP:O	1:A:22:GLN:CG	2.69	0.41
1:B:107:ASP:O	1:B:130:PRO:HD3	2.21	0.40
1:A:63:ALA:HB1	1:A:127:LEU:HD13	2.03	0.40
1:B:71:GLN:O	1:B:71:GLN:HG3	2.20	0.40

All (2) 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)
3:B:139:HOH:O	3:B:139:HOH:O[2_565]	2.08	0.12
1:B:22:GLN:NE2	1:B:22:GLN:NE2[2_565]	2.14	0.06

## 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	127/130 (98%)	110 (87%)	10 (8%)	7 (6%)	2 2

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	127/130 (98%)	109 (86%)	11 (9%)	7 (6%)	2	2
1	C	127/130 (98%)	108 (85%)	15 (12%)	4 (3%)	5	7
All	All	381/390 (98%)	327 (86%)	36 (9%)	18 (5%)	3	3

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	76	PRO
1	A	77	GLU
1	B	3	ILE
1	B	42	LYS
1	B	72	ARG
1	B	73	PRO
1	B	74	VAL
1	A	69	PHE
1	B	71	GLN
1	B	88	ASP
1	C	42	LYS
1	A	71	GLN
1	A	105	LEU
1	C	48	ARG
1	C	79	ILE
1	A	23	PRO
1	A	73	PRO
1	C	73	PRO

### 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	91/101 (90%)	75 (82%)	16 (18%)	2	4
1	B	91/101 (90%)	73 (80%)	18 (20%)	1	3
1	C	91/101 (90%)	77 (85%)	14 (15%)	3	6
All	All	273/303 (90%)	225 (82%)	48 (18%)	2	4

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	GLU
1	A	19	GLN
1	A	23	PRO
1	A	32	THR
1	A	33	PRO
1	A	42	LYS
1	A	68	ARG
1	A	72	ARG
1	A	75	LEU
1	A	78	ASP
1	A	81	ARG
1	A	94	ARG
1	A	95	VAL
1	A	107	ASP
1	A	117	GLU
1	A	120	THR
1	B	22	GLN
1	B	30	THR
1	B	49	HIS
1	B	68	ARG
1	B	69	PHE
1	B	73	PRO
1	B	74	VAL
1	B	75	LEU
1	B	78	ASP
1	B	87	THR
1	B	89	MET
1	B	90	TRP
1	B	92	ARG
1	B	97	LEU
1	B	112	VAL
1	B	114	LEU
1	B	117	GLU
1	B	120	THR
1	C	14	PRO
1	C	19	GLN
1	C	22	GLN
1	C	32	THR
1	C	50	LEU
1	C	65	SER
1	C	71	GLN
1	C	86	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	88	ASP
1	C	92	ARG
1	C	94	ARG
1	C	97	LEU
1	C	119	ASP
1	C	128	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	80	HIS
1	C	22	GLN
1	C	49	HIS
1	C	111	HIS

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

4 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
2	SO4	A	131	-	4,4,4	0.74	0	6,6,6	1.22	1 (16%)
2	SO4	B	131	-	4,4,4	1.24	1 (25%)	6,6,6	2.70	3 (50%)
2	SO4	B	132	-	4,4,4	0.76	0	6,6,6	1.19	1 (16%)
2	SO4	C	131	-	4,4,4	0.54	0	6,6,6	1.52	1 (16%)

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	SO4	A	131	-	-	0/0/0/0	0/0/0/0
2	SO4	B	131	-	-	0/0/0/0	0/0/0/0
2	SO4	B	132	-	-	0/0/0/0	0/0/0/0
2	SO4	C	131	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	131	SO4	O3-S	-2.09	1.39	1.47

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	131	SO4	O3-S-O1	-2.45	87.37	110.19
2	A	131	SO4	O4-S-O3	-2.28	99.72	108.98
2	B	132	SO4	O2-S-O1	2.37	117.01	109.50
2	C	131	SO4	O4-S-O3	3.05	121.39	108.98
2	B	131	SO4	O2-S-O1	4.24	122.92	109.50
2	B	131	SO4	O4-S-O3	4.26	126.32	108.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	131	SO4	1	0
2	C	131	SO4	3	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	129/130 (99%)	0.50	12 (9%)	11 11	43, 73, 137, 154	0
1	B	129/130 (99%)	0.51	16 (12%)	5 5	41, 69, 131, 153	0
1	C	129/130 (99%)	0.77	20 (15%)	3 3	38, 71, 117, 143	0
All	All	387/390 (99%)	0.59	48 (12%)	5 5	38, 71, 131, 154	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	71	GLN	8.8
1	A	90	TRP	8.6
1	A	75	LEU	8.4
1	A	73	PRO	7.3
1	C	73	PRO	7.2
1	A	89	MET	7.1
1	C	72	ARG	6.9
1	C	89	MET	6.4
1	B	73	PRO	5.5
1	B	74	VAL	5.3
1	B	130	PRO	5.1
1	A	71	GLN	5.0
1	A	77	GLU	4.7
1	B	72	ARG	4.6
1	B	24	GLY	4.6
1	C	90	TRP	4.5
1	B	89	MET	4.5
1	C	68	ARG	4.4
1	B	90	TRP	4.2
1	C	130	PRO	4.0
1	B	107	ASP	4.0
1	C	88	ASP	3.9
1	B	75	LEU	3.9

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	C	69	PHE	3.8
1	B	91	GLY	3.3
1	B	37	ARG	3.3
1	C	107	ASP	3.3
1	C	78	ASP	3.1
1	A	130	PRO	3.0
1	B	76	PRO	2.9
1	C	37	ARG	2.9
1	C	92	ARG	2.9
1	A	91	GLY	2.9
1	B	69	PHE	2.9
1	C	101	ILE	2.8
1	B	81	ARG	2.7
1	A	78	ASP	2.6
1	B	92	ARG	2.5
1	C	23	PRO	2.5
1	C	91	GLY	2.4
1	C	51	ALA	2.4
1	A	68	ARG	2.3
1	A	24	GLY	2.2
1	C	24	GLY	2.2
1	C	129	ALA	2.1
1	C	43	SER	2.1
1	A	23	PRO	2.0
1	B	106	ALA	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	B	132	5/5	0.95	0.17	-	99,102,103,105	0
2	SO4	C	131	5/5	0.95	0.21	-	98,103,109,113	0
2	SO4	A	131	5/5	0.99	0.20	-	67,77,82,84	0
2	SO4	B	131	5/5	0.98	0.13	-	78,79,81,83	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.