



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 19, 2019 – 10:43 AM EDT

PDB ID : 6AC8  
Title : Crystal structure of Mycobacterium smegmatis Mfd at 2.75 Å resolution  
Authors : Putta, S.; Fox, G.C.; Walsh, M.A.; Rao, D.N.; Nagaraja, V.; Natesh, R.  
Deposited on : 2018-07-25  
Resolution : 2.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : 2.4  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

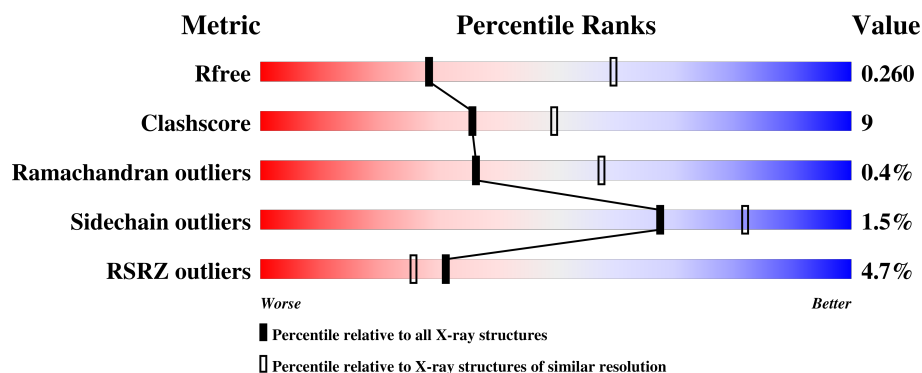
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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))
$R_{free}$	111664	4013 (2.80-2.72)
Clashscore	122126	1029 (2.78-2.74)
Ramachandran outliers	120053	1013 (2.78-2.74)
Sidechain outliers	120020	1013 (2.78-2.74)
RSRZ outliers	108989	3920 (2.80-2.72)

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	1235	<div> <div>3%</div> <div>78%</div> <div>16%</div> <div>5%</div> </div>
1	B	1235	<div> <div>6%</div> <div>74%</div> <div>20%</div> <div>5%</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	A	1307	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17331 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 Mycobacterium smegmatis Mfd.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1171	Total	C	N	O	S	0	0	0
			8590	5395	1526	1639	30			
1	B	1174	Total	C	N	O	S	0	0	0
			8566	5391	1519	1626	30			

There are 40 discrepancies between the modelled and reference sequences:

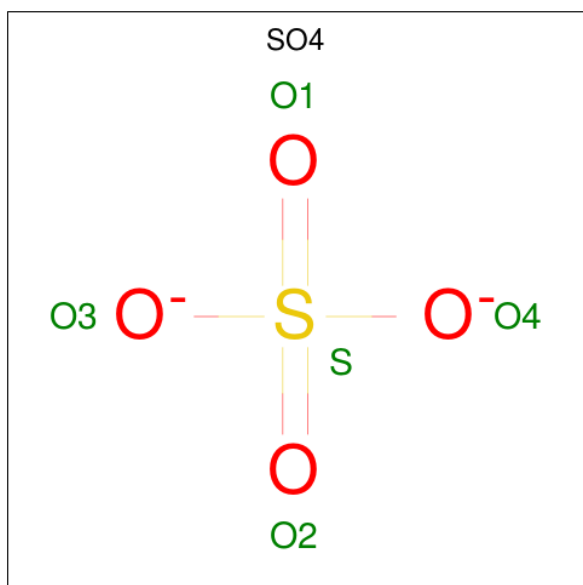
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP I7G7M2
A	-18	GLY	-	expression tag	UNP I7G7M2
A	-17	SER	-	expression tag	UNP I7G7M2
A	-16	SER	-	expression tag	UNP I7G7M2
A	-15	HIS	-	expression tag	UNP I7G7M2
A	-14	HIS	-	expression tag	UNP I7G7M2
A	-13	HIS	-	expression tag	UNP I7G7M2
A	-12	HIS	-	expression tag	UNP I7G7M2
A	-11	HIS	-	expression tag	UNP I7G7M2
A	-10	HIS	-	expression tag	UNP I7G7M2
A	-9	SER	-	expression tag	UNP I7G7M2
A	-8	SER	-	expression tag	UNP I7G7M2
A	-7	GLY	-	expression tag	UNP I7G7M2
A	-6	LEU	-	expression tag	UNP I7G7M2
A	-5	VAL	-	expression tag	UNP I7G7M2
A	-4	PRO	-	expression tag	UNP I7G7M2
A	-3	ARG	-	expression tag	UNP I7G7M2
A	-2	GLY	-	expression tag	UNP I7G7M2
A	-1	SER	-	expression tag	UNP I7G7M2
A	0	HIS	-	expression tag	UNP I7G7M2
B	-19	MET	-	initiating methionine	UNP I7G7M2
B	-18	GLY	-	expression tag	UNP I7G7M2
B	-17	SER	-	expression tag	UNP I7G7M2
B	-16	SER	-	expression tag	UNP I7G7M2
B	-15	HIS	-	expression tag	UNP I7G7M2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP I7G7M2
B	-13	HIS	-	expression tag	UNP I7G7M2
B	-12	HIS	-	expression tag	UNP I7G7M2
B	-11	HIS	-	expression tag	UNP I7G7M2
B	-10	HIS	-	expression tag	UNP I7G7M2
B	-9	SER	-	expression tag	UNP I7G7M2
B	-8	SER	-	expression tag	UNP I7G7M2
B	-7	GLY	-	expression tag	UNP I7G7M2
B	-6	LEU	-	expression tag	UNP I7G7M2
B	-5	VAL	-	expression tag	UNP I7G7M2
B	-4	PRO	-	expression tag	UNP I7G7M2
B	-3	ARG	-	expression tag	UNP I7G7M2
B	-2	GLY	-	expression tag	UNP I7G7M2
B	-1	SER	-	expression tag	UNP I7G7M2
B	0	HIS	-	expression tag	UNP I7G7M2

- 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	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 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

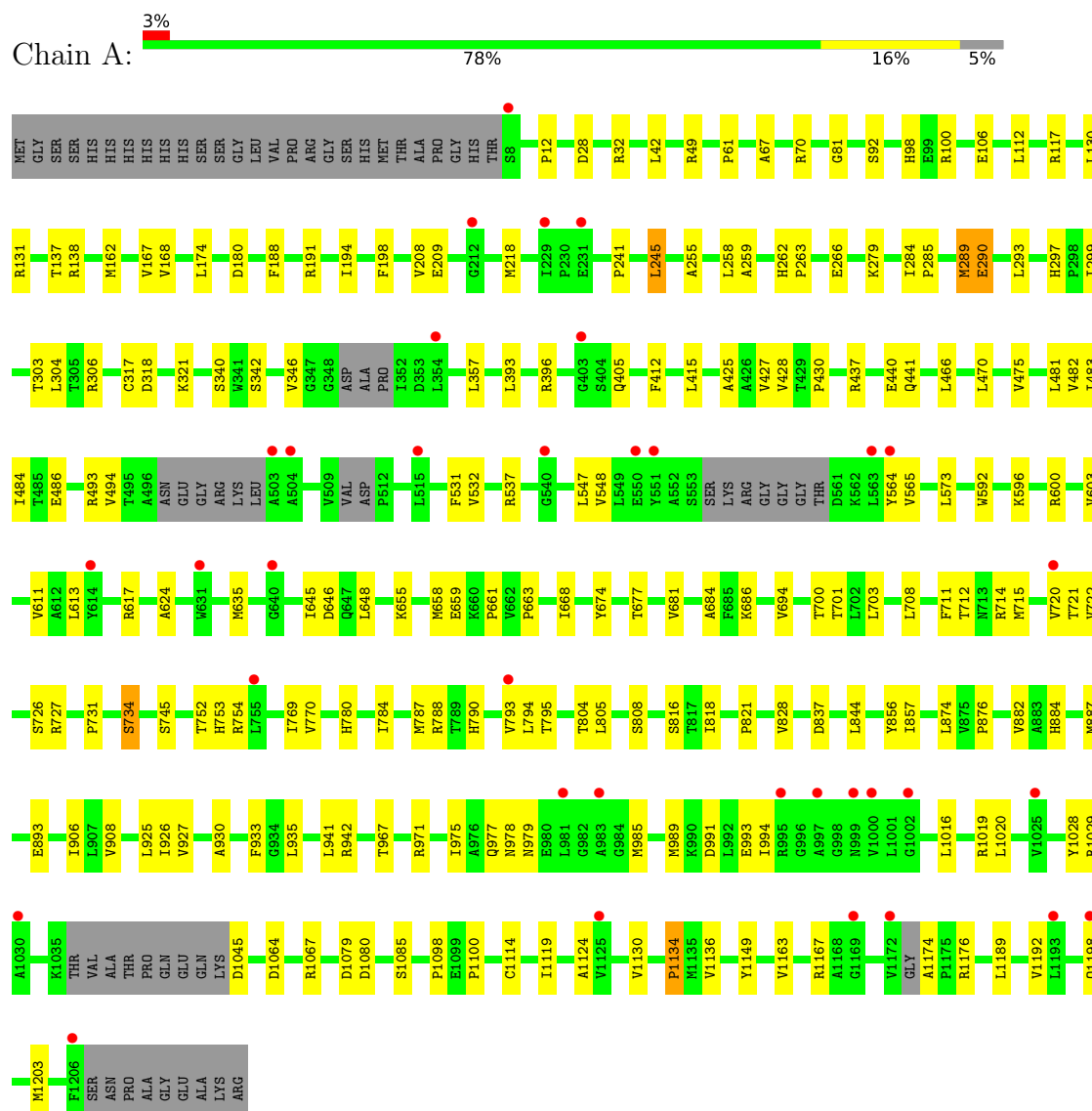
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	51	Total O 51 51	0	0
3	B	69	Total O 69 69	0	0

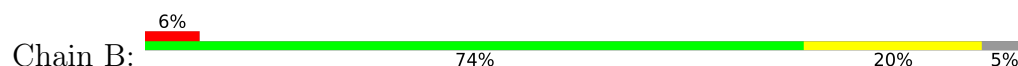
### 3 Residue-property plots

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: *Mycobacterium smegmatis* Mfd



- Molecule 1: *Mycobacterium smegmatis* Mfd







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.86Å 162.03Å 215.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.51 – 2.75 40.51 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.3 (40.51-2.75) 99.3 (40.51-2.75)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.68 (at 2.77Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575:000)	Depositor
R, $R_{free}$	0.224 , 0.259 0.224 , 0.260	Depositor DCC
$R_{free}$ test set	3815 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	80.9	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 49.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	17331	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.57% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.27	0/8744	0.45	1/11944 (0.0%)
1	B	0.27	0/8721	0.46	0/11924
All	All	0.27	0/17465	0.46	1/23868 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	245	LEU	CB-CG-CD1	5.64	120.58	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8590	0	8318	126	0
1	B	8566	0	8336	168	0
2	A	35	0	0	3	0
2	B	20	0	0	0	0
3	A	51	0	0	0	0
3	B	69	0	0	2	0
All	All	17331	0	16654	293	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (293) 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:712:THR:HG22	1:A:722:VAL:HG21	1.54	0.90
1:B:712:THR:HG22	1:B:722:VAL:HG21	1.53	0.89
1:A:635:MET:SD	1:A:714:ARG:NH2	2.48	0.87
1:B:825:ARG:HD2	1:B:947:ARG:O	1.81	0.81
1:A:942:ARG:HH22	1:A:978:ASN:HB2	1.47	0.79
1:A:727:ARG:NH2	1:A:893:GLU:OE2	2.19	0.75
1:B:730:ASP:HB2	1:B:733:GLU:H	1.51	0.73
1:A:92:SER:HB2	1:A:138:ARG:HD2	1.71	0.72
1:B:92:SER:HB2	1:B:138:ARG:HD2	1.72	0.71
1:B:545:GLU:HB2	1:B:567:MET:CE	2.21	0.70
1:A:668:ILE:HG22	1:A:816:SER:HB2	1.73	0.70
1:A:971:ARG:NH1	2:A:1307:SO4:O4	2.24	0.69
1:A:318:ASP:HB3	1:A:321:LYS:HD2	1.74	0.68
1:A:770:VAL:HB	1:A:795:THR:HG22	1.76	0.68
1:B:708:LEU:HD22	1:B:724:GLY:HA3	1.74	0.68
1:A:28:ASP:O	1:A:32:ARG:HG3	1.94	0.68
1:B:933:PHE:O	1:B:971:ARG:NH2	2.27	0.67
1:A:437:ARG:NH1	1:A:440:GLU:OE1	2.27	0.67
1:B:654:VAL:HG12	1:B:666:ARG:HD2	1.76	0.67
1:A:991:ASP:HA	1:A:994:ILE:HG12	1.76	0.66
1:B:765:LEU:HD21	1:B:768:ILE:HD11	1.77	0.66
1:B:438:VAL:O	1:B:441:GLN:N	2.29	0.66
1:B:601:ARG:HA	1:B:604:ARG:HD2	1.77	0.66
1:B:696:VAL:HG22	1:B:769:ILE:HB	1.79	0.65
1:A:100:ARG:NH2	1:A:340:SER:O	2.29	0.65
1:B:752:THR:OG1	1:B:753:HIS:N	2.30	0.65
1:A:727:ARG:NH1	2:A:1304:SO4:O3	2.30	0.64
1:B:943:GLY:O	1:B:947:ARG:NE	2.29	0.64
1:B:701:THR:HG23	1:B:726:SER:HB3	1.79	0.64
1:A:194:ILE:HG12	1:A:209:GLU:HG2	1.80	0.63
1:A:658:MET:HE3	1:A:686:LYS:HD3	1.80	0.63
1:B:439:VAL:HA	1:B:442:LEU:HD23	1.80	0.63
1:A:430:PRO:HD2	1:A:486:GLU:HG2	1.80	0.63
1:B:694:VAL:HG22	1:B:767:LEU:HB3	1.80	0.63
1:B:720:VAL:HG23	1:B:747:ASP:OD2	1.97	0.63
1:B:532:VAL:HG23	1:B:533:GLU:HG2	1.81	0.62
1:B:436:HIS:HA	1:B:439:VAL:HG22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:LEU:HD13	1:A:241:PRO:HG2	1.81	0.62
1:A:208:VAL:HG12	1:A:218:MET:HG2	1.82	0.62
1:B:664:MET:HB3	1:B:792:ASP:HB3	1.82	0.62
1:B:276:MET:HG3	1:B:286:VAL:HG21	1.80	0.61
1:B:540:GLY:O	1:B:1178:ARG:NH2	2.32	0.61
1:B:545:GLU:HB2	1:B:567:MET:HE3	1.83	0.61
1:A:1079:ASP:OD2	1:A:1080:ASP:N	2.33	0.60
1:A:117:ARG:HB3	1:A:130:LEU:HD21	1.82	0.60
1:A:708:LEU:O	1:A:712:THR:HG23	2.02	0.60
1:B:942:ARG:NH1	1:B:975:ILE:O	2.32	0.60
1:A:977:GLN:OE1	1:A:977:GLN:N	2.33	0.60
1:A:1149:TYR:HE2	1:A:1192:VAL:HG21	1.66	0.60
1:A:645:ILE:HD12	1:A:648:LEU:HD11	1.84	0.59
1:A:437:ARG:NH1	1:A:441:GLN:HG3	2.18	0.59
1:A:857:ILE:HD13	1:A:941:LEU:HD13	1.84	0.59
1:B:708:LEU:O	1:B:712:THR:HG23	2.01	0.59
1:A:255:ALA:O	1:A:259:ALA:N	2.36	0.59
1:B:414:MET:O	1:B:417:ALA:N	2.36	0.58
1:B:611:VAL:HG11	1:B:1028:TYR:HB3	1.86	0.58
1:B:448:ALA:HB1	1:B:462:VAL:HA	1.86	0.58
1:B:148:LEU:HA	1:B:151:ILE:CD1	2.34	0.58
1:B:475:VAL:HG22	1:B:482:VAL:HG13	1.85	0.57
1:B:188:PHE:HB3	1:B:197:VAL:HG23	1.87	0.57
1:A:715:MET:HB3	1:A:720:VAL:HG21	1.85	0.57
1:A:1064:ASP:OD1	1:A:1067:ARG:NH2	2.37	0.57
1:B:292:LEU:HD21	1:B:341:TRP:CH2	2.40	0.57
1:B:426:ALA:HB2	1:B:458:PRO:HG3	1.88	0.56
1:B:151:ILE:N	1:B:151:ILE:HD12	2.20	0.56
1:B:148:LEU:HA	1:B:151:ILE:HD13	1.88	0.56
1:B:725:LEU:HD21	1:B:754:ARG:HE	1.71	0.56
1:A:285:PRO:HB3	1:A:289:MET:HE1	1.87	0.56
1:A:290:GLU:HA	1:A:293:LEU:HD13	1.87	0.56
1:B:832:VAL:HG12	1:B:956:PHE:HB2	1.87	0.56
1:B:154:VAL:HB	1:B:239:ALA:HB3	1.87	0.55
1:A:787:MET:HA	1:A:790:HIS:ND1	2.21	0.55
1:B:730:ASP:HB2	1:B:733:GLU:HB2	1.88	0.55
1:A:405:GLN:OE1	1:A:405:GLN:N	2.39	0.55
1:B:513:LEU:HD22	1:B:1068:LEU:HD13	1.89	0.55
1:B:923:ASN:HA	1:B:945:VAL:HG22	1.89	0.55
1:A:788:ARG:HH21	1:A:795:THR:HG21	1.72	0.54
1:B:841:ALA:HB2	1:B:874:LEU:HD22	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:607:ALA:O	1:B:611:VAL:HG12	2.08	0.53
1:B:848:LEU:HD11	1:B:878:ALA:HB2	1.90	0.53
1:B:51:LEU:HD11	1:B:474:VAL:HG11	1.89	0.53
1:B:712:THR:HG22	1:B:722:VAL:CG2	2.32	0.53
1:B:137:THR:HB	1:B:322:VAL:HG13	1.91	0.53
1:A:967:THR:HG23	2:A:1307:SO4:O4	2.08	0.53
1:A:731:PRO:HA	1:A:734:SER:HB3	1.91	0.53
1:B:147:ASP:O	1:B:151:ILE:HD12	2.09	0.53
1:B:78:GLU:HG2	1:B:470:LEU:HA	1.90	0.52
1:B:924:THR:HG22	1:B:953:TYR:HD2	1.75	0.52
1:B:799:THR:OG1	1:B:992:LEU:O	2.27	0.52
1:A:303:THR:OG1	1:A:304:LEU:N	2.43	0.52
1:B:185:ARG:NH2	1:B:202:ALA:O	2.42	0.52
1:A:162:MET:HE2	1:A:167:VAL:HG21	1.92	0.52
1:A:475:VAL:HG13	1:A:482:VAL:HG22	1.90	0.52
1:B:531:PHE:HE1	1:B:547:LEU:HD11	1.74	0.52
1:B:536:GLU:HG2	1:B:543:ARG:NH2	2.25	0.52
1:B:970:ASP:O	1:B:974:THR:HG23	2.09	0.52
1:B:531:PHE:CE1	1:B:547:LEU:HD11	2.44	0.52
1:B:545:GLU:CB	1:B:567:MET:CE	2.87	0.52
1:B:439:VAL:HG12	1:B:449:ALA:HB1	1.92	0.52
1:A:49:ARG:HE	1:A:317:CYS:HB3	1.74	0.52
1:A:168:VAL:HG23	1:A:188:PHE:HE2	1.75	0.51
1:B:12:PRO:HD2	1:B:81:GLY:HA2	1.91	0.51
1:B:884:HIS:CE1	1:B:887:MET:HG2	2.45	0.51
1:A:415:LEU:HD22	1:A:425:ALA:HB1	1.92	0.51
1:B:56:LEU:HB2	1:B:62:LEU:HD11	1.92	0.51
1:A:12:PRO:HD2	1:A:81:GLY:HA2	1.91	0.51
1:A:884:HIS:CE1	1:A:887:MET:HG3	2.45	0.51
1:B:111:ARG:NH1	1:B:244:GLU:OE2	2.43	0.51
1:B:708:LEU:HA	1:B:750:ILE:HD12	1.91	0.51
1:B:931:ASP:N	1:B:931:ASP:OD1	2.43	0.51
1:A:646:ASP:HB2	1:A:818:ILE:HG23	1.92	0.51
1:A:180:ASP:O	1:A:191:ARG:NH1	2.33	0.51
1:A:684:ALA:HB1	1:A:694:VAL:HG21	1.92	0.51
1:B:48:ALA:HB2	1:B:395:ILE:HG21	1.93	0.51
1:B:653:GLU:OE1	1:B:666:ARG:NH1	2.44	0.50
1:A:721:THR:OG1	1:A:745:SER:O	2.27	0.50
1:A:828:VAL:HG22	1:A:942:ARG:HD3	1.94	0.50
1:B:1130:VAL:HG11	1:B:1185:TRP:HZ3	1.77	0.50
1:B:685:PHE:HA	1:B:688:VAL:HG22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1098:PRO:HB2	1:A:1100:PRO:HD2	1.94	0.50
1:A:681:VAL:HG12	1:A:711:PHE:CE1	2.47	0.50
1:A:787:MET:HA	1:A:790:HIS:CE1	2.47	0.50
1:A:481:LEU:HD21	1:A:483:ILE:HD11	1.94	0.50
1:B:847:GLU:OE1	1:B:924:THR:HG23	2.11	0.50
1:A:412:PHE:HE2	1:A:441:GLN:HB3	1.77	0.50
1:A:701:THR:HB	1:A:726:SER:HB3	1.93	0.50
1:B:164:PHE:CZ	1:B:190:VAL:HG23	2.47	0.50
1:B:27:GLN:O	1:B:31:ARG:HG2	2.11	0.50
1:B:1046:VAL:HB	1:B:1111:ARG:HG2	1.93	0.50
1:A:168:VAL:HG23	1:A:188:PHE:CE2	2.46	0.49
1:A:592:TRP:NE1	1:A:596:LYS:HD2	2.27	0.49
1:B:959:PRO:HB2	1:B:962:LYS:HG2	1.94	0.49
1:A:297:HIS:CE1	1:A:299:ILE:HD11	2.47	0.49
1:A:42:LEU:HB3	1:A:393:LEU:HD11	1.95	0.49
1:B:1054:ALA:HB1	1:B:1104:LEU:HA	1.94	0.49
1:B:270:PRO:O	1:B:958:TYR:OH	2.26	0.49
1:B:43:VAL:HG11	1:B:386:SER:HA	1.94	0.49
1:B:545:GLU:HB2	1:B:567:MET:HE2	1.95	0.49
1:B:734:SER:HB2	1:B:754:ARG:HH21	1.77	0.49
1:B:624:ALA:HB2	1:B:661:PRO:HA	1.95	0.49
1:B:1121:GLU:HG2	1:B:1133:SER:HB3	1.95	0.48
1:A:734:SER:OG	1:A:754:ARG:NH2	2.46	0.48
1:B:137:THR:HG21	1:B:325:ARG:HG2	1.95	0.48
1:B:747:ASP:OD1	1:B:747:ASP:N	2.36	0.48
1:B:802:PRO:HG3	1:B:993:GLU:HB3	1.95	0.48
1:A:266:GLU:H	1:A:266:GLU:CD	2.17	0.48
1:A:780:HIS:O	1:A:784:ILE:HG13	2.12	0.48
1:A:857:ILE:HD12	1:A:927:VAL:HG22	1.95	0.48
1:B:882:VAL:HA	1:B:908:VAL:O	2.13	0.48
1:A:1198:GLN:N	1:A:1198:GLN:OE1	2.43	0.48
1:B:1061:ILE:HB	1:B:1067:ARG:HG3	1.95	0.48
1:B:1079:ASP:OD1	1:B:1080:ASP:N	2.46	0.48
1:B:148:LEU:O	1:B:151:ILE:HD13	2.14	0.48
1:A:655:LYS:O	1:A:659:GLU:HG2	2.12	0.48
1:A:752:THR:OG1	1:A:753:HIS:N	2.45	0.48
1:B:600:ARG:HA	1:B:603:VAL:HG22	1.96	0.48
1:A:844:LEU:HD13	1:A:906:ILE:HD13	1.96	0.48
1:B:536:GLU:HG3	1:B:545:GLU:HG2	1.95	0.48
1:A:1167:ARG:NH1	1:A:1174:ALA:O	2.42	0.47
1:A:844:LEU:HD21	1:A:926:ILE:HG13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:684:ALA:HA	1:B:694:VAL:HG21	1.96	0.47
1:A:342:SER:O	1:A:346:VAL:HG23	2.14	0.47
1:B:67:ALA:O	1:B:137:THR:HG22	2.15	0.47
1:B:401:ALA:N	1:B:488:ASP:O	2.47	0.47
1:B:576:TYR:CZ	1:B:582:PRO:HG3	2.49	0.47
1:B:1029:ARG:HB2	1:B:1029:ARG:CZ	2.44	0.47
1:B:535:THR:HG21	1:B:537:ARG:CZ	2.44	0.47
1:A:162:MET:HE2	1:A:167:VAL:CG2	2.45	0.47
1:B:414:MET:HE2	1:B:418:HIS:HB2	1.97	0.47
1:B:837:ASP:HB3	1:B:874:LEU:HD21	1.96	0.47
1:A:935:LEU:H	1:A:935:LEU:HD12	1.79	0.47
1:A:882:VAL:HA	1:A:908:VAL:O	2.14	0.47
1:B:544:ARG:NH1	3:B:1402:HOH:O	2.47	0.47
1:A:1167:ARG:HD2	1:A:1174:ALA:HB3	1.97	0.47
1:A:788:ARG:HG2	1:A:793:VAL:HG11	1.97	0.47
1:B:66:ALA:O	1:B:136:THR:HA	2.15	0.47
1:A:700:THR:HG23	1:A:703:LEU:H	1.80	0.46
1:B:536:GLU:HG2	1:B:543:ARG:HH21	1.79	0.46
1:A:106:GLU:CD	1:A:106:GLU:H	2.18	0.46
1:B:1064:ASP:OD1	1:B:1067:ARG:NH2	2.48	0.46
1:B:470:LEU:HD23	1:B:485:THR:CG2	2.45	0.46
1:B:929:ARG:HG3	1:B:931:ASP:OD1	2.14	0.46
1:A:611:VAL:HG21	1:A:1028:TYR:HB3	1.98	0.46
1:A:1045:ASP:N	1:A:1045:ASP:OD1	2.47	0.46
1:A:174:LEU:HB3	1:A:241:PRO:HA	1.97	0.46
1:B:452:LEU:HD23	1:B:456:THR:HG23	1.97	0.46
1:B:836:ASP:OD2	1:B:838:LYS:N	2.49	0.46
1:A:266:GLU:OE1	1:A:266:GLU:N	2.40	0.46
1:A:856:TYR:O	1:A:908:VAL:HA	2.15	0.46
1:B:989:MET:HA	1:B:992:LEU:HD13	1.97	0.46
1:A:856:TYR:HB3	1:A:908:VAL:HG22	1.97	0.46
1:B:515:LEU:HD23	1:B:515:LEU:HA	1.79	0.46
1:A:677:THR:O	1:A:681:VAL:HG13	2.16	0.46
1:B:985:MET:O	1:B:989:MET:HG2	2.15	0.46
1:B:191:ARG:HB2	1:B:194:ILE:HB	1.97	0.46
1:B:355:GLU:N	1:B:355:GLU:OE2	2.35	0.46
1:B:545:GLU:C	1:B:567:MET:CE	2.84	0.46
1:B:674:TYR:CE1	1:B:821:PRO:HB3	2.51	0.45
1:B:185:ARG:HB3	1:B:200:PRO:HA	1.97	0.45
1:A:1016:LEU:O	1:A:1020:LEU:HG	2.17	0.45
1:B:227:ARG:HD3	1:B:1089:GLU:HG3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:354:LEU:HD23	1:B:354:LEU:HA	1.63	0.45
1:B:944:ARG:HA	1:B:944:ARG:HH21	1.80	0.45
1:A:67:ALA:O	1:A:137:THR:HG23	2.17	0.45
1:A:837:ASP:HB3	1:A:874:LEU:HD21	1.99	0.45
1:B:1012:VAL:HG22	1:B:1016:LEU:HD23	1.97	0.45
1:B:514:ALA:HB2	1:B:1065:ARG:HD3	1.98	0.45
1:A:531:PHE:HE1	1:A:547:LEU:HG	1.82	0.45
1:A:548:VAL:HG12	1:A:564:TYR:CD1	2.52	0.44
1:A:70:ARG:HH22	1:A:493:ARG:HD3	1.82	0.44
1:B:1091:ILE:HA	1:B:1095:GLY:O	2.17	0.44
1:B:1167:ARG:NH1	1:B:1173:GLY:H	2.15	0.44
1:B:991:ASP:HA	1:B:994:ILE:HB	1.98	0.44
1:B:63:LEU:HD22	1:B:308:LEU:HD11	1.99	0.44
1:B:164:PHE:HZ	1:B:190:VAL:HG23	1.82	0.44
1:B:545:GLU:O	1:B:567:MET:HE2	2.17	0.44
1:B:650:ALA:O	1:B:654:VAL:HG13	2.17	0.44
1:B:294:PRO:HG3	1:B:360:SER:HB2	2.00	0.44
1:B:417:ALA:O	1:B:421:THR:OG1	2.22	0.44
1:B:600:ARG:O	1:B:604:ARG:NE	2.51	0.44
1:B:143:PRO:HB2	1:B:301:PRO:HB2	1.99	0.44
1:A:61:PRO:HA	1:A:131:ARG:O	2.18	0.44
1:A:396:ARG:CZ	1:A:396:ARG:HB3	2.47	0.44
1:A:674:TYR:CZ	1:A:821:PRO:HB3	2.53	0.44
1:B:543:ARG:HB3	1:B:1055:HIS:CD2	2.52	0.43
1:B:1080:ASP:HA	1:B:1083:VAL:HG22	2.01	0.43
1:B:606:ILE:O	1:B:610:LEU:HD23	2.18	0.43
1:A:218:MET:HB3	1:A:218:MET:HE2	1.49	0.43
1:A:857:ILE:CD1	1:A:925:LEU:HD11	2.47	0.43
1:A:804:THR:OG1	1:A:805:LEU:N	2.50	0.43
1:B:725:LEU:C	1:B:725:LEU:HD23	2.39	0.43
1:A:547:LEU:HB3	1:A:565:VAL:HG22	2.00	0.43
1:A:989:MET:O	1:A:993:GLU:HG3	2.18	0.43
1:B:1149:TYR:CE1	1:B:1192:VAL:HG21	2.54	0.43
1:A:930:ALA:HA	1:A:933:PHE:HD2	1.82	0.43
1:A:975:ILE:HD12	1:A:975:ILE:HA	1.89	0.43
1:B:106:GLU:HG3	1:B:185:ARG:HD2	2.00	0.43
1:B:856:TYR:OH	1:B:928:GLU:OE2	2.32	0.43
1:A:600:ARG:O	1:A:603:VAL:HG12	2.18	0.42
1:B:923:ASN:O	1:B:952:GLY:HA2	2.19	0.42
1:A:98:HIS:NE2	1:A:357:LEU:O	2.51	0.42
1:B:909:CYS:HB2	1:B:913:VAL:CG1	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:ALA:HB3	1:B:148:LEU:HG	2.00	0.42
1:B:884:HIS:CE1	1:B:886:GLN:HB2	2.54	0.42
1:A:279:LYS:HB3	1:A:284:ILE:HG13	2.02	0.42
1:B:183:GLY:HA2	1:B:223:ILE:HD12	2.00	0.42
1:B:693:GLN:HB3	1:B:747:ASP:HA	2.01	0.42
1:A:428:VAL:HA	1:A:466:LEU:O	2.19	0.42
1:A:770:VAL:O	1:A:795:THR:HA	2.20	0.42
1:A:828:VAL:CG2	1:A:942:ARG:HD3	2.49	0.42
1:B:1149:TYR:HE1	1:B:1192:VAL:HG21	1.85	0.42
1:A:769:ILE:HA	1:A:794:LEU:O	2.20	0.42
1:B:449:ALA:HA	1:B:463:VAL:O	2.20	0.42
1:A:1114:CYS:HB3	1:A:1119:ILE:HB	2.02	0.42
1:A:412:PHE:CE2	1:A:441:GLN:HB3	2.54	0.42
1:A:624:ALA:HB2	1:A:661:PRO:HA	2.00	0.42
1:B:100:ARG:HH21	1:B:276:MET:HE3	1.85	0.42
1:B:576:TYR:CE2	1:B:582:PRO:HG3	2.55	0.42
1:A:1163:VAL:HG21	1:A:1189:LEU:HD22	2.01	0.41
1:B:618:GLN:HE21	1:B:662:VAL:HG21	1.84	0.41
1:B:152:GLU:O	1:B:170:ARG:NH2	2.47	0.41
1:B:262:HIS:ND1	1:B:348:GLY:HA3	2.35	0.41
1:A:532:VAL:HB	1:A:548:VAL:HG23	2.02	0.41
1:A:258:LEU:HD23	1:A:258:LEU:HA	1.89	0.41
1:A:405:GLN:CD	1:A:405:GLN:N	2.73	0.41
1:B:302:THR:OG1	1:B:306:ARG:HD2	2.20	0.41
1:B:61:PRO:HD2	3:B:1416:HOH:O	2.20	0.41
1:B:651:ILE:HG13	1:B:679:ILE:HG12	2.03	0.41
1:B:727:ARG:NH2	1:B:889:GLU:HG3	2.36	0.41
1:B:888:ASN:ND2	1:B:891:THR:HG23	2.35	0.41
1:A:1124:ALA:HA	1:A:1130:VAL:HA	2.03	0.41
1:B:1129:THR:HG21	1:B:1162:GLN:HG3	2.03	0.41
1:B:711:PHE:CG	1:B:750:ILE:HD11	2.56	0.41
1:A:1119:ILE:HA	1:A:1134:PRO:HG2	2.03	0.41
1:A:245:LEU:CD2	1:A:293:LEU:HD11	2.51	0.41
1:B:545:GLU:CB	1:B:567:MET:HE3	2.50	0.41
1:A:617:ARG:HG3	1:A:663:PRO:HG2	2.02	0.41
1:B:448:ALA:O	1:B:463:VAL:N	2.54	0.41
1:A:805:LEU:HA	1:A:808:SER:OG	2.21	0.41
1:B:859:ASN:HA	1:B:910:THR:HG22	2.02	0.41
1:B:845:ARG:NE	1:B:877:GLU:OE2	2.52	0.41
1:A:428:VAL:HG11	1:A:470:LEU:HB2	2.03	0.40
1:A:857:ILE:HD12	1:A:925:LEU:HD11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:565:VAL:HG21	1:A:573:LEU:HD11	2.03	0.40
1:A:427:VAL:HA	1:A:484:ILE:O	2.20	0.40
1:B:604:ARG:HG2	1:B:604:ARG:H	1.62	0.40
1:B:734:SER:OG	1:B:735:ARG:N	2.54	0.40
1:B:855:PHE:HE1	1:B:907:LEU:HD23	1.87	0.40
1:A:49:ARG:NH2	1:A:318:ASP:OD2	2.55	0.40
1:B:198:PHE:CD2	1:B:205:PRO:HG3	2.56	0.40
1:B:521:VAL:HG11	1:B:549:LEU:HD22	2.03	0.40
1:B:825:ARG:CD	1:B:947:ARG:O	2.62	0.40
1:A:876:PRO:HB3	1:B:872:ARG:NH2	2.37	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	1157/1235 (94%)	1096 (95%)	56 (5%)	5 (0%)	36	58
1	B	1166/1235 (94%)	1102 (94%)	60 (5%)	4 (0%)	43	65
All	All	2323/2470 (94%)	2198 (95%)	116 (5%)	9 (0%)	36	58

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	494	VAL
1	B	737	VAL
1	A	263	PRO
1	A	979	ASN
1	A	734	SER
1	B	446	ASP
1	A	1134	PRO
1	B	438	VAL

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Mol	Chain	Res	Type
1	B	1134	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	848/988 (86%)	834 (98%)	14 (2%)	63	80
1	B	847/988 (86%)	836 (99%)	11 (1%)	71	84
All	All	1695/1976 (86%)	1670 (98%)	25 (2%)	67	82

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	198	PHE
1	A	262	HIS
1	A	289	MET
1	A	290	GLU
1	A	306	ARG
1	A	537	ARG
1	A	613	LEU
1	A	985	MET
1	A	1019	ARG
1	A	1029	ARG
1	A	1085	SER
1	A	1136	VAL
1	A	1176	ARG
1	A	1203	MET
1	B	191	ARG
1	B	198	PHE
1	B	388	GLU
1	B	619	SER
1	B	641	PHE
1	B	690	ASP
1	B	692	LYS
1	B	815	MET

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Mol	Chain	Res	Type
1	B	929	ARG
1	B	1005	GLN
1	B	1029	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

11 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	1301	-	4,4,4	0.17	0	6,6,6	0.08	0
2	SO4	A	1302	-	4,4,4	0.18	0	6,6,6	0.08	0
2	SO4	A	1303	-	4,4,4	0.18	0	6,6,6	0.08	0
2	SO4	A	1304	-	4,4,4	0.17	0	6,6,6	0.04	0
2	SO4	A	1305	-	4,4,4	0.16	0	6,6,6	0.08	0
2	SO4	A	1306	-	4,4,4	0.18	0	6,6,6	0.10	0
2	SO4	A	1307	-	4,4,4	0.19	0	6,6,6	0.04	0
2	SO4	B	1301	-	4,4,4	0.18	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	B	1302	-	4,4,4	0.16	0	6,6,6	0.07	0
2	SO4	B	1303	-	4,4,4	0.16	0	6,6,6	0.07	0
2	SO4	B	1304	-	4,4,4	0.17	0	6,6,6	0.06	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	1171/1235 (94%)	0.23	35 (2%)	50	46	47, 80, 117, 143	0
1	B	1174/1235 (95%)	0.34	76 (6%)	19	14	48, 86, 126, 141	0
All	All	2345/2470 (94%)	0.28	111 (4%)	31	26	47, 82, 123, 143	0

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	8	SER	7.9
1	A	8	SER	5.5
1	B	215	ILE	5.5
1	B	630	PRO	5.2
1	B	260	ALA	5.2
1	B	403	GLY	5.2
1	A	229	ILE	5.1
1	B	231	GLU	5.0
1	B	269	VAL	4.9
1	B	210	PHE	4.6
1	A	354	LEU	4.4
1	B	641	PHE	4.3
1	B	450	THR	4.1
1	A	504	ALA	4.1
1	B	415	LEU	4.1
1	B	717	GLY	4.0
1	B	463	VAL	3.9
1	A	564	TYR	3.9
1	B	347	GLY	3.8
1	B	349	ASP	3.8
1	A	1172	VAL	3.7
1	A	1169	GLY	3.7
1	B	587	LEU	3.6
1	B	716	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	640	GLY	3.6
1	B	719	PRO	3.6
1	A	563	LEU	3.5
1	B	354	LEU	3.5
1	B	158	VAL	3.5
1	B	755	LEU	3.5
1	B	162	MET	3.4
1	B	884	HIS	3.3
1	A	540	GLY	3.3
1	A	1030	ALA	3.2
1	B	581	ALA	3.2
1	B	237	VAL	3.2
1	B	580	GLU	3.2
1	B	258	LEU	3.2
1	B	391	VAL	3.1
1	B	194	ILE	3.0
1	B	208	VAL	3.0
1	A	1002	GLY	3.0
1	B	426	ALA	2.9
1	B	510	VAL	2.9
1	B	423	GLY	2.9
1	A	515	LEU	2.9
1	B	156	LEU	2.9
1	B	551	TYR	2.8
1	A	631	TRP	2.8
1	B	648	LEU	2.8
1	B	236	THR	2.8
1	B	645	ILE	2.8
1	B	431	GLY	2.8
1	B	424	TYR	2.8
1	B	350	ALA	2.8
1	A	999	ASN	2.8
1	B	265	THR	2.7
1	A	995	ARG	2.7
1	B	348	GLY	2.7
1	B	447	THR	2.7
1	A	1198	GLN	2.6
1	B	642	THR	2.6
1	B	159	GLY	2.6
1	B	767	LEU	2.6
1	B	960	PRO	2.6
1	A	1193	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	440	GLU	2.6
1	A	983	ALA	2.6
1	B	164	PHE	2.5
1	A	997	ALA	2.5
1	B	563	LEU	2.5
1	A	212	GLY	2.5
1	B	678	GLU	2.5
1	B	1125	VAL	2.5
1	A	403	GLY	2.4
1	A	231	GLU	2.4
1	B	157	SER	2.4
1	A	1206	PHE	2.4
1	B	564	TYR	2.4
1	A	550	GLU	2.4
1	B	29	VAL	2.4
1	B	214	GLU	2.3
1	A	640	GLY	2.3
1	A	981	LEU	2.3
1	B	961	ASN	2.3
1	B	9	VAL	2.3
1	B	234	VAL	2.3
1	B	515	LEU	2.3
1	A	755	LEU	2.3
1	B	552	ALA	2.3
1	A	614	TYR	2.3
1	A	551	TYR	2.2
1	B	193	GLY	2.2
1	B	977	GLN	2.2
1	A	720	VAL	2.2
1	B	694	VAL	2.2
1	B	709	GLN	2.2
1	B	784	ILE	2.2
1	B	632	GLN	2.2
1	B	639	PHE	2.2
1	A	1000	VAL	2.1
1	B	582	PRO	2.1
1	A	503	ALA	2.1
1	B	484	ILE	2.1
1	B	441	GLN	2.1
1	A	1025	VAL	2.1
1	A	1125	VAL	2.1
1	B	603	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	211	TRP	2.1
1	B	345	ALA	2.0
1	A	793	VAL	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	SO4	B	1303	5/5	0.67	0.36	131,134,139,147	0
2	SO4	A	1304	5/5	0.85	0.33	119,121,129,134	0
2	SO4	B	1304	5/5	0.88	0.21	132,133,141,145	0
2	SO4	A	1307	5/5	0.90	0.30	121,129,135,139	0
2	SO4	A	1306	5/5	0.95	0.35	92,97,101,120	0
2	SO4	B	1302	5/5	0.95	0.12	91,94,97,98	0
2	SO4	A	1305	5/5	0.96	0.09	99,104,111,120	0
2	SO4	A	1303	5/5	0.96	0.17	58,67,73,73	0
2	SO4	A	1302	5/5	0.98	0.17	67,69,74,75	0
2	SO4	A	1301	5/5	0.99	0.11	68,70,74,80	0
2	SO4	B	1301	5/5	0.99	0.13	65,68,73,75	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.