



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 08:36 PM GMT

PDB ID : 3IFZ  
Title : crystal structure of the first part of the Mycobacterium tuberculosis DNA gyrase reaction core: the breakage and reunion domain at 2.7 Å resolution  
Authors : Piton, J.; Aubry, A.; Delarue, M.; Mayer, C.  
Deposited on : 2009-07-27  
Resolution : 2.70 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

---

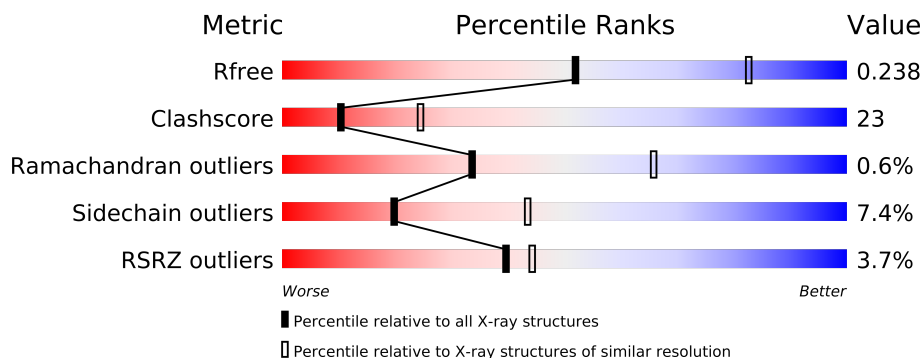
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	508	
1	B	508	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	MPD	A	509	-	X
2	MPD	B	509	-	X
3	NA	A	510	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7774 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA gyrase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	487	Total	C	N	O	S	0	0	0
			3834	2386	701	734	13			
1	B	473	Total	C	N	O	S	0	0	0
			3700	2303	682	703	12			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	502	GLU	-	EXPRESSION TAG	UNP Q07702
A	503	HIS	-	EXPRESSION TAG	UNP Q07702
A	504	HIS	-	EXPRESSION TAG	UNP Q07702
A	505	HIS	-	EXPRESSION TAG	UNP Q07702
A	506	HIS	-	EXPRESSION TAG	UNP Q07702
A	507	HIS	-	EXPRESSION TAG	UNP Q07702
A	508	HIS	-	EXPRESSION TAG	UNP Q07702
B	502	GLU	-	EXPRESSION TAG	UNP Q07702
B	503	HIS	-	EXPRESSION TAG	UNP Q07702
B	504	HIS	-	EXPRESSION TAG	UNP Q07702
B	505	HIS	-	EXPRESSION TAG	UNP Q07702
B	506	HIS	-	EXPRESSION TAG	UNP Q07702
B	507	HIS	-	EXPRESSION TAG	UNP Q07702
B	508	HIS	-	EXPRESSION TAG	UNP Q07702

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Na	0	0
			1	1		
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is water.

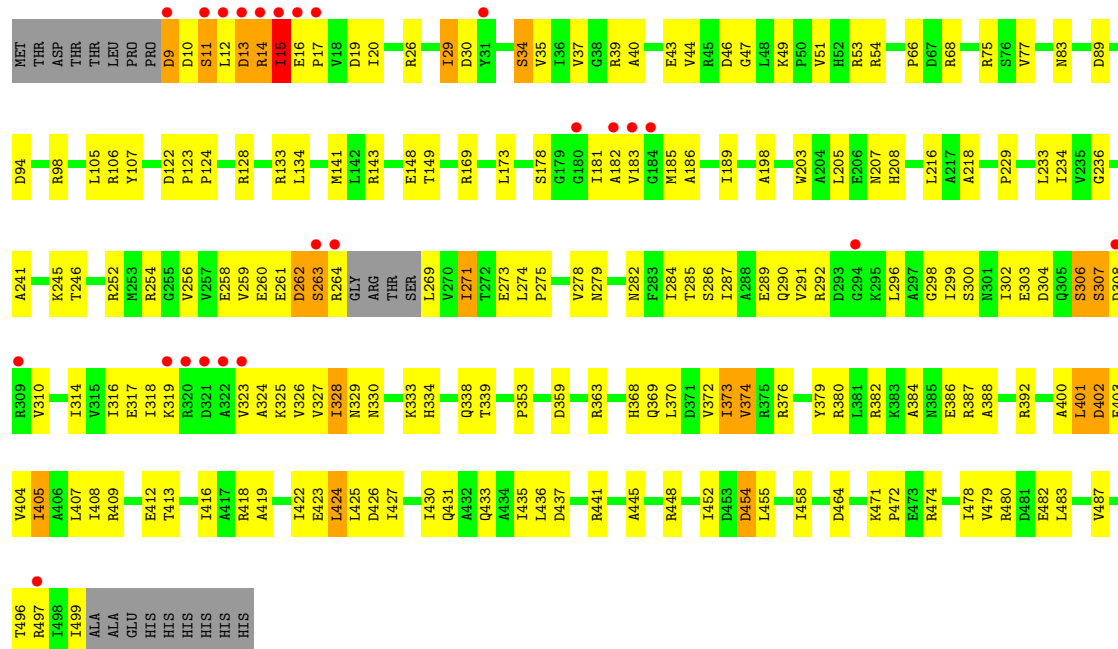
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	104	Total	O	0	0
			104	104		
4	B	118	Total	O	0	0
			118	118		

### 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.

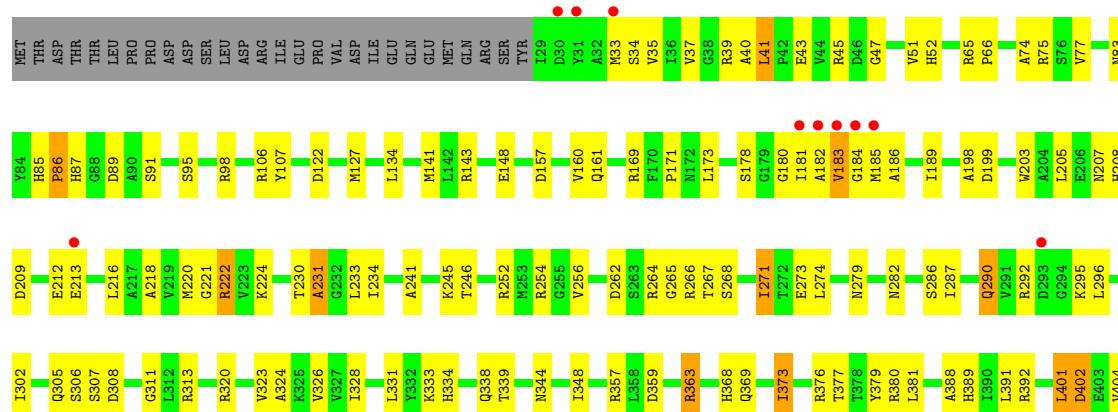
#### • Molecule 1: DNA gyrase subunit A

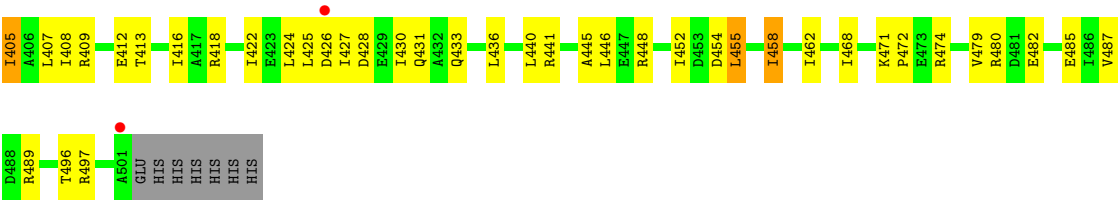
Chain A: 



#### • Molecule 1: DNA gyrase subunit A

Chain B: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	163.91Å 109.66Å 102.00Å 90.00° 120.40° 90.00°	Depositor
Resolution (Å)	19.90 – 2.70 19.90 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.90-2.70) 99.2 (19.90-2.70)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.46 (at 2.71Å)	Xtriage
Refinement program	BUSTER-TNT 2.5.1	Depositor
R, $R_{free}$	0.192 , 0.233 0.200 , 0.238	Depositor DCC
$R_{free}$ test set	2125 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	51.2	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 45.6	EDS
Estimated twinning fraction	0.009 for -1/2*h+1/2*k+l,1/2*h-1/2*k+l,1/2*h+1/2*k 0.015 for -1/2*h-1/2*k+l,-1/2*h-1/2*k-l,1/2*h-1/2*k	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 42396 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7774	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, MPD

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	0.26	0/3892	0.48	0/5271
1	B	0.27	0/3757	0.49	0/5090
All	All	0.26	0/7649	0.48	0/10361

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3834	0	3838	199	0
1	B	3700	0	3715	154	0
2	A	8	0	14	9	0
2	B	8	0	14	9	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	104	0	0	4	0
4	B	118	0	0	0	0
All	All	7774	0	7581	352	0



Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 23.

All (352) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:509:MPD:C5	2:B:509:MPD:H12	1.61	1.22
2:B:509:MPD:C1	2:B:509:MPD:H53	1.57	1.21
1:A:298:GLY:HA2	1:A:319:LYS:HG2	1.32	1.08
1:A:259:VAL:HG12	1:A:269:LEU:HA	1.33	1.07
1:A:318:ILE:HD12	1:A:323:VAL:HA	1.39	1.05
2:A:509:MPD:H53	2:A:509:MPD:H12	1.40	1.03
2:B:509:MPD:C1	2:B:509:MPD:C5	2.30	0.98
1:A:424:LEU:HD13	1:A:425:LEU:HG	1.46	0.97
2:B:509:MPD:O2	2:B:509:MPD:H52	1.58	0.97
1:A:274:LEU:HB3	1:A:278:VAL:HG21	1.45	0.96
1:A:262:ASP:HB2	1:A:264:ARG:N	1.82	0.94
1:A:9:ASP:N	1:A:26:ARG:HD3	1.85	0.91
1:A:205:LEU:HD11	1:A:479:VAL:HG22	1.50	0.91
1:A:418:ARG:HH11	1:A:433:GLN:HE22	1.18	0.91
1:B:205:LEU:HD11	1:B:479:VAL:HG22	1.52	0.91
1:B:418:ARG:HH11	1:B:433:GLN:HE22	1.18	0.90
1:A:16:GLU:HG3	1:A:17:PRO:HD2	1.54	0.89
1:B:373:ILE:HD11	1:B:376:ARG:HH21	1.38	0.88
1:A:284:ILE:HD11	1:A:314:ILE:CD1	2.04	0.88
2:A:509:MPD:H53	2:A:509:MPD:C1	1.99	0.87
1:A:324:ALA:HB3	1:A:326:VAL:HG12	1.58	0.85
1:A:284:ILE:HD11	1:A:314:ILE:HD12	1.60	0.83
1:B:241:ALA:O	1:B:245:LYS:HG2	1.79	0.82
1:B:74:ALA:HA	1:B:127:MET:CE	2.09	0.82
1:A:324:ALA:CB	1:A:326:VAL:HG12	2.10	0.82
1:A:291:VAL:CG2	1:A:299:ILE:HD12	2.10	0.81
1:A:287:ILE:HG22	1:A:302:ILE:HD11	1.60	0.81
1:A:292:ARG:HG3	1:A:292:ARG:HH11	1.45	0.80
1:A:424:LEU:CD1	1:A:425:LEU:HG	2.12	0.80
2:B:509:MPD:O2	2:B:509:MPD:C5	2.30	0.80
1:A:16:GLU:CG	1:A:17:PRO:HD2	2.12	0.80
1:B:485:GLU:HG2	1:B:489:ARG:HH22	1.47	0.80
2:A:509:MPD:O2	2:A:509:MPD:C5	2.30	0.79
1:B:405:ILE:O	1:B:409:ARG:HG3	1.81	0.79
1:A:405:ILE:O	1:A:409:ARG:HG3	1.83	0.79
1:B:373:ILE:CD1	1:B:376:ARG:HH21	1.96	0.78
1:A:274:LEU:HB3	1:A:278:VAL:CG2	2.12	0.78
1:A:83:ASN:ND2	1:B:75:ARG:HH12	1.82	0.77
1:A:318:ILE:CD1	1:A:323:VAL:HA	2.13	0.77

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:241:ALA:O	1:A:245:LYS:HG2	1.85	0.76
1:A:254:ARG:HH21	1:A:338:GLN:NE2	1.84	0.76
1:B:264:ARG:N	1:B:265:GLY:HA2	1.99	0.75
1:A:298:GLY:HA2	1:A:319:LYS:CG	2.14	0.75
1:B:148:GLU:HG3	1:B:379:TYR:CD1	2.21	0.75
1:A:275:PRO:O	1:A:278:VAL:HG22	1.86	0.75
1:A:262:ASP:HA	1:A:263:SER:CB	2.15	0.75
1:A:205:LEU:HD11	1:A:479:VAL:CG2	2.16	0.75
1:B:305:GLN:HB2	1:B:313:ARG:HG2	1.68	0.75
1:A:448:ARG:HD3	4:A:606:HOH:O	1.86	0.75
1:B:323:VAL:HB	1:B:326:VAL:HG13	1.69	0.74
1:B:254:ARG:HH21	1:B:338:GLN:NE2	1.86	0.74
1:B:205:LEU:HD11	1:B:479:VAL:CG2	2.18	0.74
1:B:74:ALA:HA	1:B:127:MET:HE2	1.68	0.74
1:A:148:GLU:HG3	1:A:379:TYR:CD1	2.23	0.74
1:A:259:VAL:CG1	1:A:269:LEU:HD12	2.17	0.73
1:A:424:LEU:O	1:A:424:LEU:HD22	1.88	0.73
1:A:12:LEU:H	1:A:12:LEU:HD23	1.53	0.73
1:A:259:VAL:HG11	1:A:269:LEU:HD12	1.72	0.72
2:A:509:MPD:C5	2:A:509:MPD:H12	2.06	0.72
1:A:330:ASN:HA	1:A:333:LYS:HD2	1.71	0.72
1:A:94:ASP:O	1:A:98:ARG:HG3	1.90	0.71
1:A:236:GLY:H	1:A:499:ILE:HD13	1.54	0.71
1:B:418:ARG:HH11	1:B:433:GLN:NE2	1.89	0.71
1:B:169:ARG:HE	1:B:369:GLN:HE22	1.37	0.71
1:A:169:ARG:HE	1:A:369:GLN:HE22	1.38	0.70
1:A:105:LEU:HD21	2:A:509:MPD:H53	1.73	0.70
1:A:14:ARG:O	1:A:15:ILE:HG22	1.91	0.69
1:A:418:ARG:HH11	1:A:433:GLN:NE2	1.89	0.69
1:A:236:GLY:H	1:A:499:ILE:CD1	2.06	0.69
1:A:413:THR:HG22	1:B:446:LEU:HD12	1.74	0.69
1:B:182:ALA:HB3	1:B:185:MET:CG	2.22	0.68
1:A:30:ASP:O	1:A:34:SER:HB3	1.94	0.68
1:A:271:ILE:O	1:A:271:ILE:HG13	1.94	0.68
1:A:14:ARG:HD3	1:A:19:ASP:CG	2.14	0.67
1:A:40:ALA:HB3	1:A:182:ALA:HB2	1.77	0.67
1:A:284:ILE:HD11	1:A:314:ILE:HD11	1.76	0.67
1:B:77:VAL:HB	1:B:127:MET:CE	2.25	0.67
1:A:287:ILE:HG22	1:A:302:ILE:CD1	2.24	0.66
1:B:271:ILE:HD11	1:B:274:LEU:HG	1.77	0.66
1:B:77:VAL:HB	1:B:127:MET:HE2	1.77	0.66
1:A:437:ASP:OD1	1:B:441:ARG:NH1	2.28	0.66

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:298:GLY:CA	1:A:319:LYS:HG2	2.19	0.66
2:A:509:MPD:O4	2:A:509:MPD:H12	1.95	0.66
1:A:419:ALA:O	1:A:423:GLU:HG3	1.96	0.66
1:B:74:ALA:HA	1:B:127:MET:HE1	1.77	0.66
1:A:445:ALA:HB3	1:B:412:GLU:HA	1.76	0.66
1:A:271:ILE:HD11	1:A:274:LEU:HG	1.79	0.65
1:A:37:VAL:HG22	1:A:182:ALA:HB1	1.79	0.65
1:A:441:ARG:NH1	1:B:433:GLN:OE1	2.30	0.65
1:A:75:ARG:NH1	1:B:157:ASP:OD1	2.30	0.65
1:A:234:ILE:CD1	1:A:496:THR:HG21	2.26	0.64
2:A:509:MPD:O2	2:A:509:MPD:H53	1.97	0.64
1:B:87:HIS:C	1:B:89:ASP:H	1.99	0.64
1:B:37:VAL:HG12	1:B:348:ILE:HD11	1.80	0.64
1:B:271:ILE:HG13	1:B:271:ILE:O	1.96	0.63
1:A:307:SER:O	1:A:310:VAL:HG12	1.99	0.63
1:A:263:SER:O	1:A:264:ARG:HG3	1.97	0.63
1:B:264:ARG:NH2	1:B:267:THR:O	2.31	0.63
1:A:286:SER:HA	1:A:289:GLU:OE1	1.98	0.63
1:B:389:HIS:CE1	1:B:430:ILE:HD11	2.34	0.63
1:A:291:VAL:HG22	1:A:299:ILE:HD12	1.80	0.63
1:B:182:ALA:HB3	1:B:185:MET:HG2	1.81	0.62
1:B:33:MET:HE1	1:B:183:VAL:HG11	1.81	0.62
1:B:307:SER:O	1:B:311:GLY:N	2.30	0.62
1:A:40:ALA:HB3	1:A:182:ALA:CB	2.29	0.62
1:A:292:ARG:HG3	1:A:292:ARG:NH1	2.13	0.62
1:B:391:LEU:HD12	1:B:458:ILE:HD12	1.82	0.62
1:A:169:ARG:HE	1:A:369:GLN:NE2	1.98	0.61
1:B:169:ARG:HE	1:B:369:GLN:NE2	1.98	0.61
2:A:509:MPD:O4	2:A:509:MPD:C1	2.48	0.61
1:B:287:ILE:HG22	1:B:302:ILE:CD1	2.31	0.61
1:A:256:VAL:HB	1:A:273:GLU:HB2	1.82	0.61
1:A:424:LEU:HD13	1:A:425:LEU:CG	2.27	0.60
1:A:262:ASP:HA	1:A:263:SER:OG	2.01	0.60
1:B:324:ALA:O	1:B:328:ILE:HG13	2.01	0.60
1:B:41:LEU:HD21	1:B:182:ALA:HB2	1.84	0.60
1:A:16:GLU:HG3	1:A:17:PRO:CD	2.30	0.60
1:A:106:ARG:HG3	1:A:107:TYR:CE2	2.37	0.60
2:A:509:MPD:O2	2:A:509:MPD:H52	2.03	0.59
1:A:106:ARG:HA	1:A:229:PRO:HB3	1.86	0.58
1:A:298:GLY:O	1:A:318:ILE:HA	2.03	0.58
1:B:256:VAL:HB	1:B:273:GLU:HB2	1.84	0.58
1:A:285:THR:HG22	1:A:289:GLU:OE1	2.03	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:33:MET:CE	1:B:183:VAL:HG11	2.34	0.58
1:B:106:ARG:HG3	1:B:107:TYR:CE2	2.38	0.58
1:A:234:ILE:HD12	1:A:496:THR:CG2	2.34	0.58
1:B:468:ILE:HG13	1:B:474:ARG:NH1	2.19	0.57
1:A:234:ILE:HD12	1:A:496:THR:HG21	1.87	0.57
1:B:182:ALA:HB3	1:B:185:MET:HG3	1.85	0.57
1:A:262:ASP:HA	1:A:263:SER:HB3	1.86	0.57
1:B:485:GLU:CG	1:B:489:ARG:HH22	2.16	0.57
1:A:418:ARG:HD3	1:A:433:GLN:NE2	2.19	0.57
1:B:418:ARG:HD3	1:B:433:GLN:NE2	2.20	0.56
1:A:169:ARG:NH2	1:A:373:ILE:HD11	2.20	0.56
1:A:323:VAL:HG12	1:A:323:VAL:O	2.04	0.56
1:B:252:ARG:NH1	1:B:252:ARG:HG3	2.20	0.56
2:B:509:MPD:HO2	2:B:509:MPD:H52	1.68	0.56
1:A:12:LEU:N	1:A:12:LEU:HD23	2.20	0.56
1:A:499:ILE:HD12	4:A:599:HOH:O	2.06	0.56
1:B:160:VAL:HG12	1:B:161:GLN:N	2.21	0.56
1:A:15:ILE:HG23	1:A:15:ILE:O	2.05	0.56
1:B:485:GLU:HG2	1:B:489:ARG:NH2	2.20	0.55
1:A:252:ARG:NH1	1:A:252:ARG:HG3	2.21	0.55
1:B:373:ILE:HD11	1:B:376:ARG:NH2	2.17	0.55
1:B:266:ARG:HG3	1:B:320:ARG:HG2	1.89	0.55
1:A:412:GLU:HA	1:B:445:ALA:HB3	1.87	0.55
1:B:39:ARG:HH12	1:B:51:VAL:HG22	1.71	0.55
1:B:422:ILE:HG23	1:B:427:ILE:O	2.07	0.55
1:B:404:VAL:O	1:B:408:ILE:HG13	2.07	0.54
1:B:216:LEU:O	1:B:220:MET:HG3	2.07	0.54
2:B:509:MPD:H53	2:B:509:MPD:H12	0.69	0.54
1:A:296:LEU:HG	1:A:299:ILE:HD11	1.88	0.54
1:A:422:ILE:HG23	1:A:427:ILE:O	2.08	0.54
1:A:404:VAL:O	1:A:408:ILE:HG13	2.08	0.54
1:A:40:ALA:CB	1:A:182:ALA:HA	2.38	0.54
1:A:12:LEU:O	1:A:13:ASP:HB3	2.08	0.53
1:A:269:LEU:HD21	1:A:327:VAL:HG12	1.91	0.53
1:A:10:ASP:CG	1:A:11:SER:H	2.10	0.53
1:B:183:VAL:O	1:B:183:VAL:HG13	2.08	0.53
1:B:287:ILE:HG22	1:B:302:ILE:HD13	1.90	0.53
1:B:373:ILE:O	1:B:377:THR:HG23	2.09	0.53
1:A:254:ARG:HE	1:A:338:GLN:HE21	1.56	0.53
1:A:169:ARG:HG3	1:A:169:ARG:HH11	1.73	0.53
1:A:300:SER:N	1:A:317:GLU:O	2.34	0.53
1:A:290:GLN:HE22	1:A:334:HIS:HB3	1.74	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:16:GLU:CD	1:A:17:PRO:HD2	2.29	0.53
1:B:295:LYS:HE3	1:B:334:HIS:CD2	2.44	0.53
1:A:17:PRO:HA	1:A:20:ILE:HD12	1.91	0.52
1:B:323:VAL:HB	1:B:326:VAL:CG1	2.39	0.52
1:B:182:ALA:HB3	1:B:185:MET:O	2.09	0.52
1:B:407:LEU:HD23	1:B:407:LEU:C	2.29	0.52
1:A:183:VAL:C	1:A:185:MET:H	2.12	0.52
1:A:260:GLU:O	1:A:261:GLU:HG3	2.09	0.52
1:B:233:LEU:HD23	1:B:497:ARG:HB2	1.91	0.52
1:A:39:ARG:HH22	1:A:54:ARG:HH12	1.58	0.52
1:B:254:ARG:HE	1:B:338:GLN:HE21	1.55	0.52
1:A:304:ASP:OD1	1:A:306:SER:OG	2.28	0.52
1:A:324:ALA:HB3	1:A:326:VAL:CG1	2.35	0.52
1:B:328:ILE:O	1:B:331:LEU:HB2	2.09	0.52
1:A:291:VAL:HG22	1:A:296:LEU:O	2.10	0.51
1:A:83:ASN:HD21	1:B:75:ARG:HH12	1.57	0.51
1:B:262:ASP:O	1:B:265:GLY:HA2	2.10	0.51
1:A:407:LEU:HD23	1:A:407:LEU:C	2.30	0.51
1:B:402:ASP:N	1:B:402:ASP:OD2	2.43	0.51
1:A:269:LEU:HB2	1:A:316:ILE:O	2.11	0.51
1:B:198:ALA:CB	1:B:487:VAL:HG21	2.40	0.51
1:A:183:VAL:HG12	1:A:183:VAL:O	2.09	0.51
1:B:407:LEU:HD13	1:B:424:LEU:HD22	1.93	0.51
1:B:262:ASP:OD2	1:B:266:ARG:N	2.44	0.51
1:B:287:ILE:HG22	1:B:302:ILE:HD11	1.93	0.51
1:A:203:TRP:CE2	1:A:207:ASN:ND2	2.79	0.51
1:A:448:ARG:NH1	4:A:606:HOH:O	2.24	0.50
1:A:402:ASP:OD2	1:A:402:ASP:N	2.44	0.50
1:A:455:LEU:O	1:A:458:ILE:HG22	2.11	0.50
1:B:203:TRP:CE2	1:B:207:ASN:ND2	2.79	0.50
1:B:169:ARG:HG3	1:B:169:ARG:HH11	1.76	0.50
1:A:233:LEU:HD23	1:A:497:ARG:HB2	1.94	0.50
1:B:418:ARG:NH1	1:B:433:GLN:HE22	1.99	0.50
1:A:325:LYS:O	1:A:328:ILE:HB	2.12	0.50
1:A:373:ILE:CG1	1:A:376:ARG:HH21	2.25	0.50
1:A:373:ILE:HG13	1:A:376:ARG:HH21	1.76	0.50
1:B:391:LEU:CD1	1:B:458:ILE:HD12	2.42	0.50
1:B:45:ARG:HG2	1:B:368:HIS:HB2	1.94	0.50
1:B:252:ARG:HH11	1:B:252:ARG:HG3	1.76	0.50
1:A:205:LEU:CD1	1:A:479:VAL:HG22	2.33	0.49
1:A:259:VAL:HG12	1:A:269:LEU:CA	2.24	0.49
1:A:259:VAL:CG1	1:A:269:LEU:HA	2.24	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:359:ASP:O	1:B:363:ARG:HG3	2.12	0.49
1:A:75:ARG:NH2	1:B:83:ASN:ND2	2.60	0.49
1:B:290:GLN:HB3	1:B:296:LEU:HD12	1.93	0.49
1:A:205:LEU:HD13	1:A:480:ARG:HB2	1.95	0.49
1:A:284:ILE:CD1	1:A:314:ILE:HD12	2.39	0.49
1:A:262:ASP:HB2	1:A:263:SER:C	2.33	0.49
1:A:252:ARG:HG3	1:A:252:ARG:HH11	1.77	0.49
1:B:37:VAL:CG1	1:B:348:ILE:HD11	2.42	0.49
1:B:212:GLU:OE1	1:B:357:ARG:NH2	2.42	0.49
1:A:216:LEU:HD13	1:A:359:ASP:OD1	2.13	0.49
1:B:39:ARG:NH2	1:B:85:HIS:HE1	2.11	0.48
1:A:401:LEU:O	1:A:405:ILE:HG13	2.12	0.48
1:A:169:ARG:HG3	1:A:169:ARG:NH1	2.28	0.48
1:A:455:LEU:HD12	1:A:455:LEU:O	2.13	0.48
1:B:40:ALA:HB1	1:B:181:ILE:O	2.14	0.48
1:B:47:GLY:CA	1:B:173:LEU:HB2	2.43	0.48
1:B:407:LEU:CD1	1:B:424:LEU:HD22	2.44	0.48
1:A:368:HIS:HD2	4:A:544:HOH:O	1.95	0.48
1:A:173:LEU:HD11	1:A:189:ILE:HD13	1.96	0.48
1:B:455:LEU:HD12	1:B:455:LEU:O	2.13	0.48
1:A:425:LEU:O	1:A:426:ASP:HB3	2.14	0.48
1:A:412:GLU:HG3	1:B:446:LEU:HG	1.96	0.48
1:A:258:GLU:HG3	1:A:258:GLU:O	2.13	0.48
1:A:262:ASP:CA	1:A:263:SER:CB	2.89	0.48
1:B:182:ALA:O	1:B:184:GLY:N	2.47	0.48
1:A:286:SER:O	1:A:290:GLN:HB2	2.13	0.48
1:B:205:LEU:CD1	1:B:479:VAL:HG22	2.35	0.47
1:B:389:HIS:ND1	1:B:430:ILE:HD11	2.29	0.47
1:A:37:VAL:HG22	1:A:182:ALA:CB	2.43	0.47
1:B:454:ASP:O	1:B:458:ILE:HG13	2.14	0.47
1:A:66:PRO:HG3	1:A:134:LEU:O	2.13	0.47
1:A:149:THR:HB	1:A:372:VAL:HG13	1.97	0.47
1:B:205:LEU:HD13	1:B:480:ARG:HB2	1.97	0.47
1:B:173:LEU:HD11	1:B:189:ILE:HD13	1.97	0.47
1:B:401:LEU:O	1:B:405:ILE:HG13	2.15	0.47
1:A:328:ILE:HG22	1:A:329:ASN:N	2.29	0.47
1:B:286:SER:O	1:B:290:GLN:HB2	2.14	0.47
1:B:254:ARG:HH21	1:B:338:GLN:HE22	1.59	0.47
1:A:435:ILE:O	1:B:440:LEU:HD12	2.14	0.47
1:B:448:ARG:O	1:B:452:ILE:HD12	2.15	0.47
1:A:436:LEU:HB3	1:B:441:ARG:HB3	1.97	0.46
1:B:425:LEU:O	1:B:426:ASP:HB3	2.14	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:387:ARG:NH2	1:A:454:ASP:OD2	2.47	0.46
1:B:230:THR:O	1:B:231:ALA:HB3	2.15	0.46
1:A:37:VAL:HG11	1:A:353:PRO:HG3	1.97	0.46
1:A:278:VAL:HG23	1:A:278:VAL:O	2.15	0.46
1:A:252:ARG:CG	1:A:252:ARG:HH11	2.29	0.46
1:A:471:LYS:HA	1:A:472:PRO:HD2	1.72	0.46
1:A:430:ILE:CG2	1:A:431:GLN:N	2.78	0.46
1:A:324:ALA:HB1	1:A:326:VAL:HG12	1.90	0.46
1:B:52:HIS:CD2	1:B:95:SER:HB3	2.51	0.46
1:A:75:ARG:NH2	1:B:83:ASN:HD22	2.14	0.46
1:B:160:VAL:CG1	1:B:161:GLN:N	2.78	0.45
1:A:474:ARG:O	1:A:478:ILE:HG13	2.16	0.45
1:B:376:ARG:O	1:B:380:ARG:HG3	2.17	0.45
1:B:87:HIS:C	1:B:89:ASP:N	2.69	0.45
1:A:77:VAL:HG11	1:A:89:ASP:HB2	1.99	0.45
1:A:441:ARG:HB3	1:B:436:LEU:HB3	1.98	0.45
1:A:198:ALA:CB	1:A:487:VAL:HG21	2.47	0.45
1:A:303:GLU:HA	1:A:303:GLU:OE1	2.17	0.45
1:A:329:ASN:O	1:A:333:LYS:HG3	2.16	0.45
1:B:252:ARG:HH11	1:B:252:ARG:CG	2.29	0.45
1:B:234:ILE:CD1	1:B:496:THR:HG21	2.47	0.45
1:A:424:LEU:C	1:A:424:LEU:HD22	2.37	0.44
1:A:448:ARG:O	1:A:452:ILE:HD12	2.17	0.44
1:B:98:ARG:HE	2:B:509:MPD:HM3	1.82	0.44
1:A:455:LEU:HA	1:A:458:ILE:HG22	1.98	0.44
1:B:381:LEU:HD11	1:B:462:ILE:HG23	2.00	0.44
1:A:413:THR:OG1	1:A:416:ILE:HD12	2.17	0.44
1:B:290:GLN:NE2	1:B:334:HIS:HB3	2.33	0.44
1:A:384:ALA:HA	1:A:458:ILE:HD11	1.99	0.44
1:A:47:GLY:CA	1:A:173:LEU:HB2	2.47	0.44
1:A:483:LEU:O	1:A:487:VAL:HG23	2.18	0.44
1:A:208:HIS:H	1:A:208:HIS:CD2	2.35	0.44
1:B:279:ASN:HB3	1:B:282:ASN:HB2	2.00	0.44
1:A:254:ARG:HH21	1:A:338:GLN:HE22	1.59	0.44
1:B:203:TRP:CE2	1:B:218:ALA:CB	3.01	0.43
1:A:418:ARG:NH1	1:A:433:GLN:HE22	1.99	0.43
1:B:373:ILE:HD12	1:B:373:ILE:HA	1.78	0.43
1:A:259:VAL:HG11	1:A:269:LEU:CD1	2.46	0.43
1:B:413:THR:OG1	1:B:416:ILE:HD12	2.18	0.43
1:A:271:ILE:HD12	1:A:273:GLU:O	2.19	0.43
1:B:169:ARG:HG3	1:B:169:ARG:NH1	2.32	0.43
1:B:271:ILE:HD12	1:B:273:GLU:O	2.19	0.43

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:290:GLN:HG3	1:B:295:LYS:HB3	2.00	0.43
1:B:65:ARG:HB2	1:B:66:PRO:HD2	2.01	0.43
1:B:66:PRO:HG3	1:B:134:LEU:O	2.19	0.43
1:A:291:VAL:CG2	1:A:296:LEU:HB3	2.49	0.43
1:A:254:ARG:HH21	1:A:338:GLN:HE21	1.65	0.43
1:B:169:ARG:NH2	1:B:482:GLU:OE1	2.41	0.43
1:B:376:ARG:HD3	1:B:380:ARG:CZ	2.49	0.42
1:A:29:ILE:HG22	1:A:30:ASP:N	2.33	0.42
1:A:9:ASP:HB3	1:A:10:ASP:H	1.60	0.42
1:B:306:SER:O	1:B:307:SER:HB3	2.18	0.42
1:B:471:LYS:HA	1:B:472:PRO:HD2	1.76	0.42
1:A:40:ALA:O	1:A:49:LYS:HD3	2.19	0.42
1:B:221:GLY:O	1:B:224:LYS:NZ	2.47	0.42
1:A:279:ASN:HB3	1:A:282:ASN:HB2	2.00	0.42
1:A:388:ALA:O	1:A:392:ARG:HG3	2.19	0.42
1:A:181:ILE:HD12	1:A:186:ALA:HB2	2.01	0.42
1:A:430:ILE:HG23	1:A:431:GLN:N	2.34	0.42
1:A:169:ARG:NH2	1:A:482:GLU:OE1	2.41	0.42
1:B:391:LEU:CD1	1:B:458:ILE:CD1	2.98	0.42
1:A:128:ARG:HB3	1:B:86:PRO:HB2	2.00	0.42
1:A:376:ARG:O	1:A:380:ARG:HG3	2.20	0.42
1:A:412:GLU:O	1:B:446:LEU:HG	2.19	0.42
1:B:198:ALA:HB2	1:B:487:VAL:HG21	2.02	0.42
1:B:52:HIS:HD2	1:B:95:SER:HB3	1.85	0.42
1:B:74:ALA:CA	1:B:127:MET:HE1	2.46	0.42
1:B:216:LEU:HD12	1:B:216:LEU:O	2.20	0.42
1:B:208:HIS:CD2	1:B:208:HIS:H	2.36	0.42
1:B:388:ALA:O	1:B:392:ARG:HG3	2.20	0.42
1:A:68:ARG:O	1:A:133:ARG:NH1	2.43	0.41
1:B:333:LYS:HG2	1:B:334:HIS:CE1	2.54	0.41
1:A:236:GLY:CA	1:A:499:ILE:HD11	2.50	0.41
1:B:262:ASP:OD2	1:B:264:ARG:HB2	2.20	0.41
1:A:46:ASP:OD1	1:A:53:ARG:NH1	2.53	0.41
1:B:430:ILE:HG13	1:B:431:GLN:N	2.35	0.41
1:A:370:LEU:O	1:A:374:VAL:HG13	2.20	0.41
1:A:262:ASP:HB2	1:A:264:ARG:HB2	2.01	0.41
1:B:216:LEU:HA	1:B:359:ASP:HB3	2.03	0.41
1:B:199:ASP:HB3	1:B:222:ARG:HG2	2.02	0.41
1:B:98:ARG:HE	2:B:509:MPD:CM	2.34	0.41
1:B:234:ILE:HD12	1:B:496:THR:CG2	2.50	0.41
1:B:65:ARG:HB2	1:B:66:PRO:CD	2.51	0.41
1:A:259:VAL:HG12	1:A:269:LEU:HD12	1.97	0.41

*Continued on next page...*



Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:77:VAL:HB	1:B:127:MET:HE3	1.99	0.41
1:A:262:ASP:HB2	1:A:264:ARG:H	1.73	0.41
1:A:376:ARG:HD3	1:A:380:ARG:CZ	2.51	0.41
1:A:252:ARG:NH1	1:A:252:ARG:CG	2.84	0.41
1:A:123:PRO:HA	1:A:124:PRO:HD3	1.89	0.41
1:B:180:GLY:O	1:B:186:ALA:HB1	2.21	0.41
1:A:262:ASP:CB	1:A:264:ARG:HB2	2.51	0.41
1:A:234:ILE:HD12	1:A:496:THR:HG22	2.03	0.41
1:B:389:HIS:HE1	1:B:428:ASP:OD2	2.03	0.41
1:A:400:ALA:O	1:A:404:VAL:HG13	2.21	0.40
1:A:203:TRP:CE2	1:A:218:ALA:CB	3.04	0.40
1:A:464:ASP:OD1	1:A:474:ARG:NH2	2.38	0.40
1:A:260:GLU:HG2	1:A:261:GLU:H	1.85	0.40
1:A:16:GLU:HB3	1:A:19:ASP:OD2	2.22	0.40
1:B:77:VAL:CG1	1:B:127:MET:HE3	2.52	0.40
1:B:313:ARG:O	1:B:313:ARG:HG2	2.20	0.40
1:B:471:LYS:O	1:B:474:ARG:HB2	2.21	0.40
1:A:382:ARG:O	1:A:386:GLU:HG3	2.22	0.40
1:A:203:TRP:CE2	1:A:218:ALA:HB1	2.57	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	483/508 (95%)	449 (93%)	32 (7%)	2 (0%)	43	76
1	B	471/508 (93%)	445 (94%)	22 (5%)	4 (1%)	27	58
All	All	954/1016 (94%)	894 (94%)	54 (6%)	6 (1%)	33	66

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	ASP

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	171	PRO
1	B	86	PRO
1	B	231	ALA
1	B	183	VAL
1	A	15	ILE

### 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	409/427 (96%)	377 (92%)	32 (8%)	18	40
1	B	391/427 (92%)	364 (93%)	27 (7%)	22	48
All	All	800/854 (94%)	741 (93%)	59 (7%)	20	43

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ASP
1	A	11	SER
1	A	14	ARG
1	A	15	ILE
1	A	29	ILE
1	A	34	SER
1	A	35	VAL
1	A	43	GLU
1	A	44	VAL
1	A	51	VAL
1	A	122	ASP
1	A	141	MET
1	A	143	ARG
1	A	178	SER
1	A	246	THR
1	A	262	ASP
1	A	263	SER
1	A	271	ILE
1	A	306	SER
1	A	307	SER

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	308	ASP
1	A	328	ILE
1	A	339	THR
1	A	363	ARG
1	A	373	ILE
1	A	374	VAL
1	A	401	LEU
1	A	402	ASP
1	A	403	GLU
1	A	405	ILE
1	A	424	LEU
1	A	454	ASP
1	B	34	SER
1	B	35	VAL
1	B	41	LEU
1	B	43	GLU
1	B	91	SER
1	B	122	ASP
1	B	141	MET
1	B	143	ARG
1	B	178	SER
1	B	209	ASP
1	B	213	GLU
1	B	222	ARG
1	B	246	THR
1	B	268	SER
1	B	271	ILE
1	B	290	GLN
1	B	292	ARG
1	B	308	ASP
1	B	339	THR
1	B	344	ASN
1	B	363	ARG
1	B	373	ILE
1	B	401	LEU
1	B	402	ASP
1	B	405	ILE
1	B	455	LEU
1	B	458	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	83	ASN
1	A	85	HIS
1	A	208	HIS
1	A	338	GLN
1	A	368	HIS
1	A	369	GLN
1	A	389	HIS
1	A	433	GLN
1	A	475	GLN
1	B	52	HIS
1	B	83	ASN
1	B	85	HIS
1	B	208	HIS
1	B	238	GLN
1	B	290	GLN
1	B	329	ASN
1	B	338	GLN
1	B	344	ASN
1	B	368	HIS
1	B	369	GLN
1	B	389	HIS
1	B	475	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	MPD	A	509	-	7,7,7	0.51	0	10,10,10	0.97	1 (10%)
2	MPD	B	509	-	7,7,7	0.61	0	10,10,10	0.76	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MPD	A	509	-	-	0/5/5/5	0/0/0/0
2	MPD	B	509	-	-	0/5/5/5	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	509	MPD	C2-C3-C4	-2.03	105.61	116.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	487/508 (95%)	0.01	24 (4%)	28 31	29, 56, 109, 144	0
1	B	473/508 (93%)	-0.22	12 (2%)	54 61	26, 50, 80, 121	0
All	All	960/1016 (94%)	-0.10	36 (3%)	39 43	26, 53, 103, 144	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	14	ARG	5.0
1	B	183	VAL	4.9
1	A	182	ALA	4.8
1	A	322	ALA	4.7
1	A	321	ASP	4.4
1	A	13	ASP	4.3
1	A	16	GLU	4.3
1	A	9	ASP	4.2
1	A	320	ARG	4.1
1	B	182	ALA	4.1
1	A	264	ARG	4.1
1	A	15	ILE	4.1
1	A	309	ARG	4.0
1	A	319	LYS	4.0
1	A	12	LEU	3.9
1	B	185	MET	3.8
1	A	183	VAL	3.6
1	B	181	ILE	3.5
1	B	184	GLY	3.3
1	A	180	GLY	3.3
1	B	31	TYR	3.3
1	A	11	SER	3.3
1	B	33	MET	3.1
1	A	263	SER	3.0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	501	ALA	2.8
1	B	213	GLU	2.7
1	A	184	GLY	2.7
1	A	31	TYR	2.6
1	B	30	ASP	2.4
1	A	294	GLY	2.4
1	B	426	ASP	2.2
1	B	293	ASP	2.1
1	A	17	PRO	2.1
1	A	497	ARG	2.1
1	A	323	VAL	2.1
1	A	308	ASP	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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	MPD	A	509	8/8	0.41	13.62	96,97,99,99	0
3	NA	A	510	1/1	0.30	4.99	54,54,54,54	0
2	MPD	B	509	8/8	0.26	2.79	63,65,67,67	0
3	NA	B	510	1/1	0.22	0.37	77,77,77,77	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.