



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:46 AM GMT

PDB ID : 2BNP  
Title : Lipidic cubic phase grown reaction centre from Rhodobacter sphaeroides, ground state  
Authors : Katona, G.; Snijder, A.; Gourdon, P.; Andreasson, U.; Hansson, O.; Andreasson, L.E.; Neutze, R.  
Deposited on : 2005-03-31  
Resolution : 2.70 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.

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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 : 1.7 (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

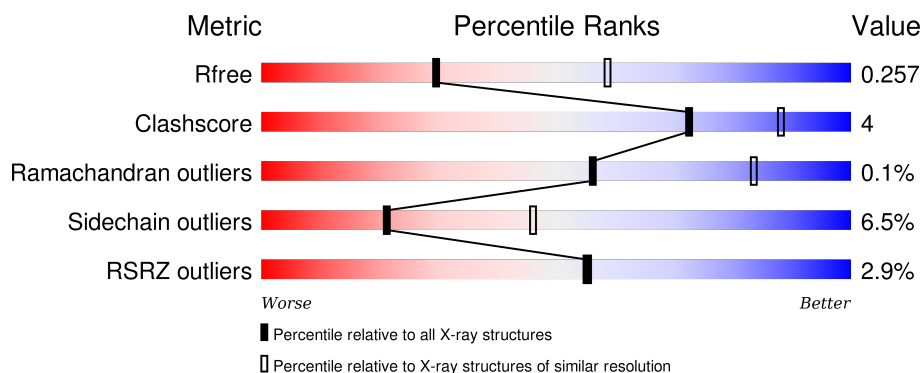
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (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. 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	281	<div> <div>3%</div> <div>87%</div> <div>12%</div> <div>.</div> </div>
2	B	307	<div> <div>3%</div> <div>86%</div> <div>11%</div> <div>..</div> </div>
3	C	260	<div> <div>2%</div> <div>80%</div> <div>10%</div> <div>9%</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
10	PO4	B	1308	-	-	-	X
4	BCL	B	1302	-	-	-	X
4	BCL	B	1303	-	-	-	X
5	BPH	A	1284	-	-	-	X
5	BPH	B	1304	-	-	-	X
6	MST	A	1285	-	-	X	X
8	U10	B	1306	-	-	-	X
9	CL	B	1307	-	-	-	X

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 6935 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 REACTION CENTRE PROTEIN L CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	4	0	0
			2232	1507	355	362	8			

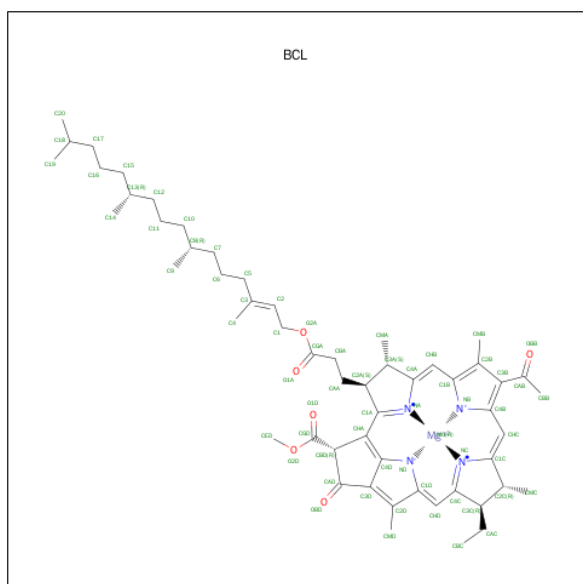
- Molecule 2 is a protein called REACTION CENTRE PROTEIN M CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	302	Total	C	N	O	S	19	0	1
			2405	1605	394	396	10			

- Molecule 3 is a protein called REACTION CENTRE PROTEIN H CHAIN.

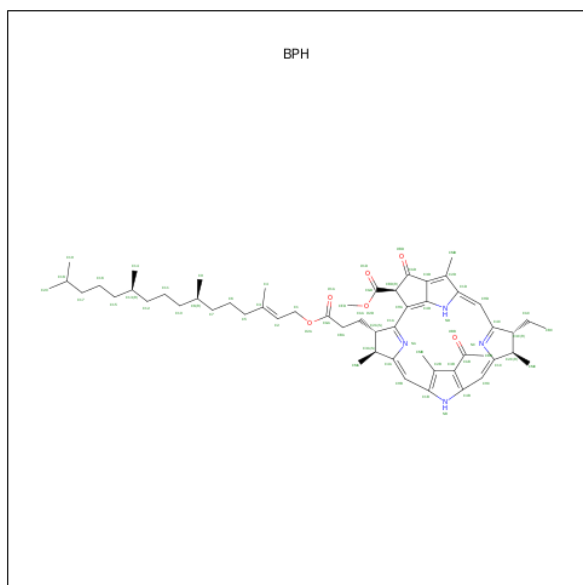
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	237	Total	C	N	O	S	31	0	0
			1803	1154	307	333	9			

- Molecule 4 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula:  $C_{55}H_{74}MgN_4O_6$ ).



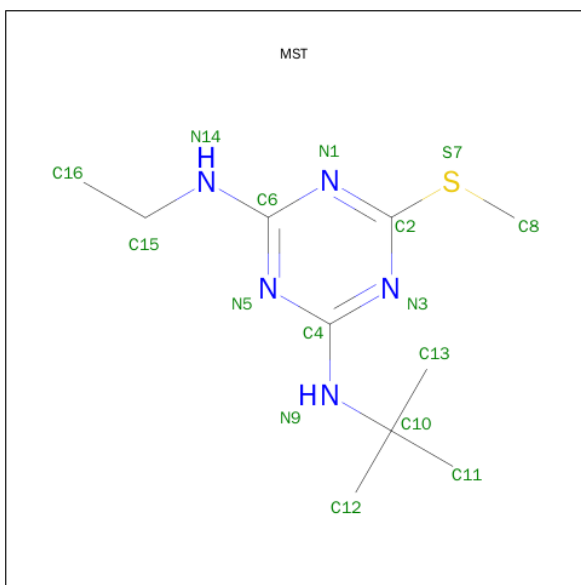
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
4	A	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
4	B	1	Total	C	Mg	N	O	0	0
			51	40	1	4	6		
4	B	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 5 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula:  $C_{55}H_{76}N_4O_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			65	55	4	6		
5	B	1	Total	C	N	O	0	0
			51	41	4	6		

- Molecule 6 is 2-T-BUTYLAMINO-4-ETHYLAMINO-6-METHYLTHIO-S-TRIAZINE (three-letter code: MST) (formula:  $C_{10}H_{19}N_5S$ ).

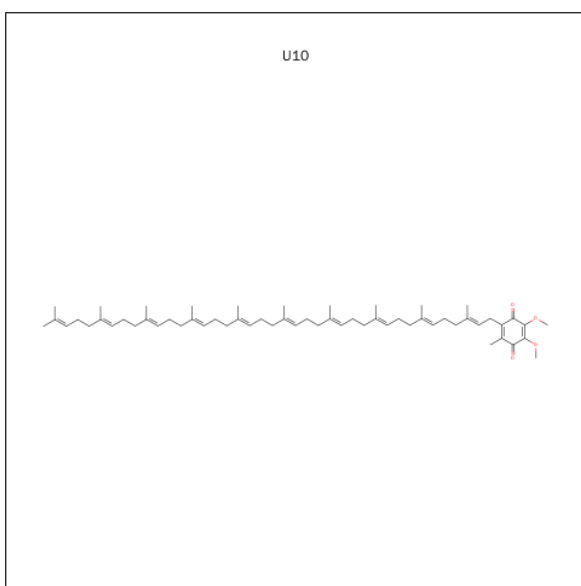


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	S	0	0
			16	10	5	1		

- Molecule 7 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Fe	0	0
			1	1		

- Molecule 8 is UBIQUINONE-10 (three-letter code: U10) (formula: C<sub>59</sub>H<sub>90</sub>O<sub>4</sub>).

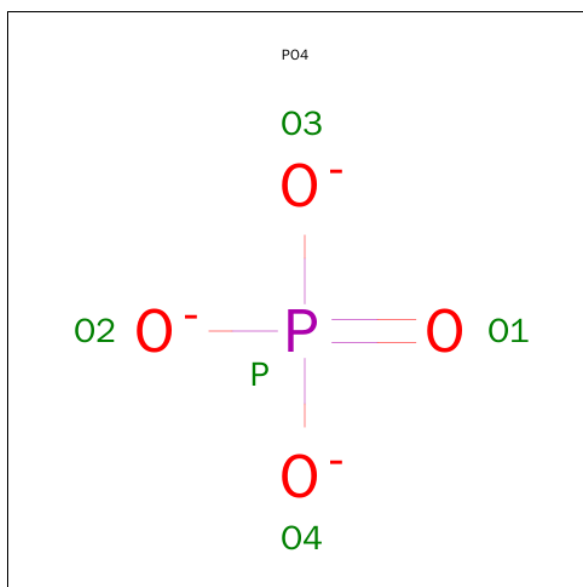


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			38	34	4		

- Molecule 9 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	Cl		0	0
			1	1			

- Molecule 10 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	O	P	0	0
			5	4	1		
10	B	1	Total	O	P	0	0
			5	4	1		

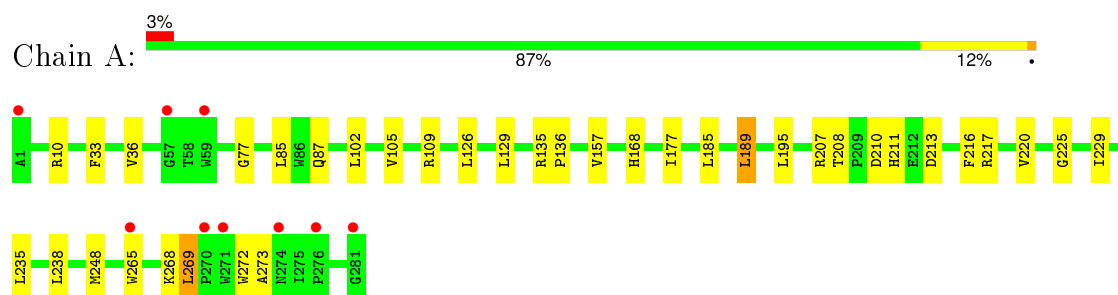
- Molecule 11 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	22	Total	O		0	0
			22	22			
11	B	22	Total	O		0	0
			22	22			
11	C	20	Total	O		0	0
			20	20			

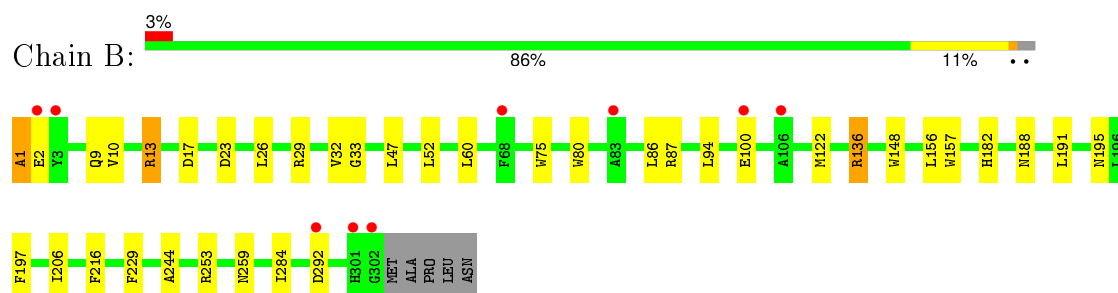
### 3 Residue-property plots [i](#)

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.

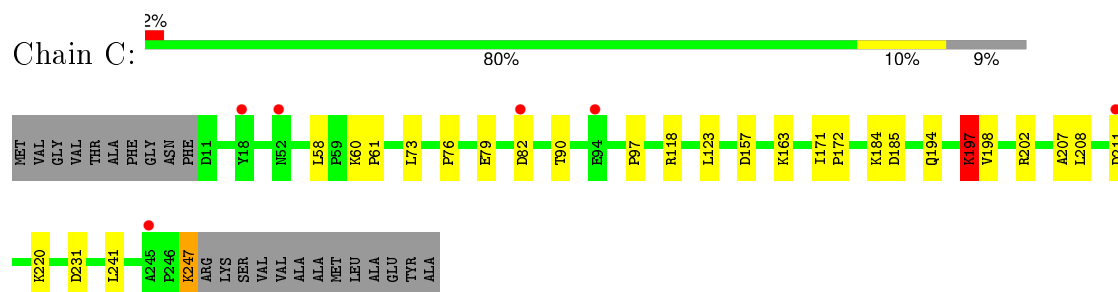
#### • Molecule 1: REACTION CENTRE PROTEIN L CHAIN



#### • Molecule 2: REACTION CENTRE PROTEIN M CHAIN



#### • Molecule 3: REACTION CENTRE PROTEIN H CHAIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.14Å 100.14Å 238.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.53 – 2.70 39.50 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (39.53-2.70) 99.4 (39.50-2.70)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.85 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.210 , 0.249 0.226 , 0.257	Depositor DCC
$R_{free}$ test set	1696 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.8	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 37.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 33951 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6935	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% 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: BCL, CL, BPH, PO4, MST, FE2, U10

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	0.65	2/2320 (0.1%)	0.72	3/3175 (0.1%)
2	B	0.84	4/2497 (0.2%)	0.91	7/3410 (0.2%)
3	C	0.99	4/1851 (0.2%)	0.87	6/2520 (0.2%)
All	All	0.83	10/6668 (0.1%)	0.84	16/9105 (0.2%)

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
2	B	0	3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	247	LYS	CB-CG	25.81	2.22	1.52
3	C	60	LYS	CG-CD	-17.83	0.91	1.52
2	B	52	LEU	CB-CG	-16.69	1.04	1.52
2	B	13	ARG	CD-NE	-14.32	1.22	1.46
2	B	1	ALA	C-N	-13.25	1.03	1.34
2	B	188	ASN	CB-CG	-10.26	1.27	1.51
3	C	197	LYS	CG-CD	-10.00	1.18	1.52
1	A	265	TRP	CB-CG	6.40	1.61	1.50
1	A	268	LYS	CB-CG	-5.33	1.38	1.52
3	C	118	ARG	CB-CG	5.27	1.66	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	ALA	O-C-N	-24.84	82.96	122.70
2	B	1	ALA	C-N-CA	16.64	163.31	121.70
2	B	1	ALA	CA-C-N	16.53	153.56	117.20
3	C	184	LYS	CA-CB-CG	-16.21	77.74	113.40
1	A	268	LYS	CA-CB-CG	11.79	139.35	113.40
3	C	60	LYS	CB-CG-CD	10.09	137.84	111.60
2	B	13	ARG	CD-NE-CZ	-9.35	110.52	123.60
3	C	220	LYS	CB-CG-CD	-7.34	92.53	111.60
1	A	210	ASP	CB-CG-OD2	7.09	124.69	118.30
2	B	13	ARG	CG-CD-NE	-7.00	97.09	111.80
1	A	213	ASP	CB-CG-OD2	6.97	124.57	118.30
3	C	185	ASP	CB-CG-OD2	5.70	123.43	118.30
3	C	211	ASP	CB-CG-OD2	5.59	123.33	118.30
3	C	157	ASP	CB-CG-OD2	5.59	123.33	118.30
2	B	292	ASP	CB-CG-OD2	5.40	123.16	118.30
2	B	23	ASP	CB-CG-OD2	5.31	123.08	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	1	ALA	Mainchain,Peptide
2	B	13	ARG	Sidechain

## 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	2232	0	2187	19	0
2	B	2405	0	2317	14	0
3	C	1803	0	1805	7	0
4	A	132	0	148	7	0
4	B	117	0	115	9	0
5	A	65	0	76	3	0
5	B	51	0	45	8	0
6	A	16	0	19	8	0
7	B	1	0	0	0	0
8	B	38	0	47	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	B	1	0	0	0	0
10	B	10	0	0	0	0
11	A	22	0	0	0	0
11	B	22	0	0	1	0
11	C	20	0	0	0	0
All	All	6935	0	6759	57	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 4.

All (57) 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)
6:A:1285:MST:H81	6:A:1285:MST:H121	1.65	0.78
6:A:1285:MST:C8	6:A:1285:MST:H121	2.14	0.77
2:B:9:GLN:HE22	3:C:197:LYS:HA	1.53	0.71
4:B:1302:BCL:HHC	4:B:1302:BCL:HBB3	1.74	0.70
1:A:177:ILE:HG12	4:A:1282:BCL:HMB3	1.76	0.67
1:A:216:PHE:CE2	6:A:1285:MST:H132	2.32	0.64
2:B:197:PHE:CZ	4:B:1303:BCL:HBB2	2.34	0.62
2:B:136:ARG:HA	2:B:136:ARG:NE	2.16	0.61
4:A:1282:BCL:HMB1	4:A:1282:BCL:HBB3	1.85	0.57
3:C:90:THR:HB	3:C:97:PRO:O	2.05	0.56
1:A:135:ARG:HB3	1:A:136:PRO:HD3	1.87	0.56
4:A:1283:BCL:HMB1	4:A:1283:BCL:HBB2	1.88	0.56
2:B:32:VAL:HG12	2:B:33:GLY:O	2.06	0.55
2:B:9:GLN:NE2	3:C:198:VAL:H	2.04	0.55
1:A:208:THR:H	1:A:211:HIS:HD2	1.54	0.55
4:A:1283:BCL:HBB3	5:A:1284:BPH:H141	1.88	0.55
3:C:171:ILE:HB	3:C:172:PRO:HD3	1.89	0.55
5:A:1284:BPH:ND	5:A:1284:BPH:NC	2.55	0.54
6:A:1285:MST:H121	6:A:1285:MST:H82	1.89	0.54
6:A:1285:MST:N3	6:A:1285:MST:H121	2.23	0.54
1:A:189:LEU:CD1	5:B:1304:BPH:HMD2	2.38	0.54
5:B:1304:BPH:HBC3	5:B:1304:BPH:HHB	1.92	0.52
2:B:75:TRP:HB3	2:B:80:TRP:CZ3	2.45	0.52
1:A:217:ARG:HD2	11:B:2007:HOH:O	2.10	0.51
1:A:269:LEU:O	1:A:273:ALA:HB2	2.11	0.50
2:B:197:PHE:HZ	4:B:1303:BCL:HBB2	1.76	0.50
1:A:157:VAL:HG11	4:B:1303:BCL:HBB1	1.93	0.50
1:A:168:HIS:NE2	4:A:1282:BCL:OB	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:PHE:O	1:A:36:VAL:HG22	2.11	0.49
4:B:1303:BCL:CBB	4:B:1303:BCL:HHC	2.43	0.48
1:A:229:ILE:HD13	6:A:1285:MST:H81	1.94	0.48
2:B:197:PHE:CE1	4:B:1303:BCL:HBB2	2.49	0.47
4:B:1303:BCL:H2	5:B:1304:BPH:HHC	1.95	0.47
1:A:105:VAL:O	1:A:109:ARG:HG3	2.14	0.47
4:A:1282:BCL:NC	4:B:1303:BCL:HBB3	2.30	0.47
1:A:189:LEU:HG	1:A:216:PHE:HZ	1.80	0.46
2:B:9:GLN:HE22	3:C:198:VAL:H	1.61	0.46
5:B:1304:BPH:ND	5:B:1304:BPH:NC	2.64	0.46
2:B:122:MET:HE3	2:B:157:TRP:HE1	1.80	0.46
2:B:284:ILE:HG12	4:B:1303:BCL:HED3	1.98	0.46
5:A:1284:BPH:CMB	5:A:1284:BPH:HBB3	2.46	0.45
5:B:1304:BPH:HMB3	5:B:1304:BPH:HBB3	1.98	0.45
1:A:208:THR:H	1:A:211:HIS:CD2	2.33	0.45
2:B:253:ARG:HD2	2:B:259:ASN:OD1	2.17	0.45
1:A:185:LEU:HD13	5:B:1304:BPH:ND	2.33	0.44
4:A:1283:BCL:HMD1	2:B:206:ILE:HD13	2.00	0.44
1:A:135:ARG:HD2	1:A:248:MET:O	2.18	0.43
1:A:225:GLY:C	6:A:1285:MST:H151	2.38	0.43
5:B:1304:BPH:CMB	5:B:1304:BPH:HBB3	2.48	0.43
1:A:77:GLY:HA2	1:A:87:GLN:HE22	1.84	0.43
8:B:1306:U10:C3M	8:B:1306:U10:H4M2	2.50	0.42
6:A:1285:MST:C12	6:A:1285:MST:N3	2.81	0.42
2:B:229:PHE:HB2	2:B:244:ALA:HB2	2.02	0.42
3:C:61:PRO:HA	3:C:76:PRO:HD2	2.02	0.41
1:A:189:LEU:HD13	5:B:1304:BPH:HMD2	2.01	0.41
8:B:1306:U10:O3	8:B:1306:U10:H4M2	2.20	0.41
3:C:207:ALA:HA	3:C:241:LEU:HD23	2.03	0.41

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	279/281 (99%)	268 (96%)	11 (4%)	0	100	100
2	B	300/307 (98%)	291 (97%)	8 (3%)	1 (0%)	46	75
3	C	235/260 (90%)	226 (96%)	9 (4%)	0	100	100
All	All	814/848 (96%)	785 (96%)	28 (3%)	1 (0%)	56	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	2	GLU

### 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	220/220 (100%)	207 (94%)	13 (6%)	24	51
2	B	236/240 (98%)	219 (93%)	17 (7%)	18	41
3	C	192/208 (92%)	180 (94%)	12 (6%)	22	48
All	All	648/668 (97%)	606 (94%)	42 (6%)	21	46

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ARG
1	A	85	LEU
1	A	102	LEU
1	A	126	LEU
1	A	129	LEU
1	A	189	LEU
1	A	195	LEU
1	A	207	ARG
1	A	220	VAL
1	A	235	LEU
1	A	238	LEU
1	A	269	LEU

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Mol	Chain	Res	Type
1	A	272	TRP
2	B	10	VAL
2	B	17	ASP
2	B	26	LEU
2	B	29	ARG
2	B	47	LEU
2	B	60	LEU
2	B	86	LEU
2	B	87	ARG
2	B	94	LEU
2	B	100	GLU
2	B	136	ARG
2	B	148	TRP
2	B	156	LEU
2	B	182	HIS
2	B	191	LEU
2	B	195	ASN
2	B	216	PHE
3	C	58	LEU
3	C	73	LEU
3	C	79	GLU
3	C	82	ASP
3	C	123	LEU
3	C	163	LYS
3	C	194	GLN
3	C	197	LYS
3	C	202	ARG
3	C	208	LEU
3	C	231	ASP
3	C	247	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	211	HIS
2	B	9	GLN
2	B	195	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	BCL	A	1282	1	53,74,74	1.30	5 (9%)	57,115,115	1.56	11 (19%)
4	BCL	A	1283	1	53,74,74	1.30	5 (9%)	57,115,115	1.69	11 (19%)
5	BPH	A	1284	-	64,70,70	1.99	13 (20%)	73,101,101	1.50	9 (12%)
6	MST	A	1285	-	16,16,16	3.27	3 (18%)	21,22,22	3.62	6 (28%)
4	BCL	B	1302	2	38,59,74	1.50	5 (13%)	40,97,115	1.89	9 (22%)
4	BCL	B	1303	2	53,74,74	1.31	4 (7%)	57,115,115	1.91	12 (21%)
5	BPH	B	1304	-	50,56,70	2.34	14 (28%)	56,84,101	1.88	12 (21%)
8	U10	B	1306	-	38,38,63	3.05	11 (28%)	46,49,79	1.46	5 (10%)
10	PO4	B	1308	-	4,4,4	0.87	0	6,6,6	0.28	0
10	PO4	B	1309	-	4,4,4	0.22	0	6,6,6	0.28	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
4	BCL	A	1282	1	-	0/37/137/137	0/0/9/9
4	BCL	A	1283	1	-	0/37/137/137	0/0/9/9
5	BPH	A	1284	-	-	0/54/105/105	0/1/6/6
6	MST	A	1285	-	-	0/10/10/10	0/1/1/1
4	BCL	B	1302	2	-	0/19/119/137	0/0/9/9
4	BCL	B	1303	2	-	0/37/137/137	0/0/9/9
5	BPH	B	1304	-	-	0/38/89/105	0/1/6/6
8	U10	B	1306	-	-	0/33/57/87	0/1/1/1
10	PO4	B	1308	-	-	0/0/0/0	0/0/0/0
10	PO4	B	1309	-	-	0/0/0/0	0/0/0/0

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1285	MST	C2-S7	-11.10	1.66	1.75
5	B	1304	BPH	C3D-C4D	-5.61	1.34	1.41
5	A	1284	BPH	C3D-C4D	-5.31	1.34	1.41
8	B	1306	U10	O3-C3	-5.03	1.23	1.37
5	A	1284	BPH	C1C-NC	-5.00	1.26	1.37
8	B	1306	U10	O4-C4	-4.77	1.24	1.37
5	B	1304	BPH	C1C-NC	-4.68	1.27	1.37
5	B	1304	BPH	C1A-NA	-4.58	1.27	1.37
5	A	1284	BPH	C1A-NA	-4.43	1.27	1.37
4	B	1303	BCL	C3C-C4C	-3.85	1.46	1.51
5	A	1284	BPH	CHB-C4A	-3.21	1.34	1.40
8	B	1306	U10	C3-C2	-3.18	1.39	1.48
4	B	1302	BCL	C2A-C1A	-3.10	1.45	1.52
4	A	1282	BCL	C3C-C4C	-3.07	1.47	1.51
8	B	1306	U10	C4-C5	-3.07	1.40	1.48
5	B	1304	BPH	CHB-C4A	-2.92	1.35	1.40
4	A	1283	BCL	C3C-C4C	-2.80	1.48	1.51
4	A	1283	BCL	C2A-C1A	-2.70	1.46	1.52
4	A	1282	BCL	C2A-C1A	-2.66	1.46	1.52
4	B	1302	BCL	C3C-C4C	-2.65	1.48	1.51
5	A	1284	BPH	C1B-C2B	-2.47	1.40	1.45
5	B	1304	BPH	C4C-NC	-2.15	1.32	1.37
5	B	1304	BPH	C1B-C2B	-2.14	1.41	1.45
8	B	1306	U10	C6-C5	-2.13	1.40	1.46
5	B	1304	BPH	C3B-C4B	-2.08	1.38	1.43
5	A	1284	BPH	C1D-CHD	2.11	1.48	1.40
8	B	1306	U10	C6-C1	2.40	1.40	1.35
5	B	1304	BPH	CHC-C4B	2.61	1.46	1.40
4	B	1303	BCL	OBD-CAD	2.70	1.26	1.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1284	BPH	CHC-C4B	3.18	1.48	1.40
4	B	1302	BCL	OBD-CAD	3.34	1.27	1.22
5	A	1284	BPH	O2A-CGA	3.48	1.43	1.33
4	A	1283	BCL	OBD-CAD	3.60	1.27	1.22
5	B	1304	BPH	OBD-CAD	3.61	1.27	1.22
4	A	1282	BCL	O2A-CGA	3.70	1.44	1.33
6	A	1285	MST	C4-N9	3.75	1.39	1.34
4	A	1283	BCL	O2D-CGD	3.86	1.43	1.33
5	A	1284	BPH	OBD-CAD	3.87	1.28	1.22
4	B	1302	BCL	O2D-CGD	3.99	1.43	1.33
4	A	1282	BCL	OBD-CAD	4.00	1.28	1.22
5	A	1284	BPH	O2D-CGD	4.04	1.43	1.33
5	A	1284	BPH	CHA-C1A	4.24	1.47	1.37
4	B	1303	BCL	O2A-CGA	4.31	1.46	1.33
5	B	1304	BPH	O2A-CGA	4.40	1.46	1.33
4	A	1283	BCL	O2A-CGA	4.41	1.46	1.33
4	B	1302	BCL	O2A-CGA	4.58	1.47	1.33
4	A	1282	BCL	O2D-CGD	4.60	1.44	1.33
5	B	1304	BPH	CHC-C1C	4.69	1.45	1.36
4	B	1303	BCL	O2D-CGD	4.72	1.45	1.33
5	B	1304	BPH	CHA-C1A	4.82	1.48	1.37
6	A	1285	MST	C10-N9	4.83	1.55	1.48
5	A	1284	BPH	CHC-C1C	5.10	1.46	1.36
8	B	1306	U10	C28-C29	5.24	1.48	1.32
5	A	1284	BPH	CHB-C1B	5.31	1.49	1.38
5	B	1304	BPH	O2D-CGD	5.50	1.47	1.33
5	B	1304	BPH	CHB-C1B	6.16	1.50	1.38
8	B	1306	U10	C23-C24	7.16	1.47	1.33
8	B	1306	U10	C13-C14	7.38	1.47	1.33
8	B	1306	U10	C18-C19	7.63	1.47	1.33
8	B	1306	U10	C8-C9	8.01	1.48	1.33

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1285	MST	N5-C4-N3	-7.37	114.89	126.22
4	B	1303	BCL	C1D-CHD-C4C	-5.47	117.72	126.07
4	B	1302	BCL	CMB-C2B-C1B	-4.93	120.21	128.36
4	B	1303	BCL	CMB-C2B-C1B	-4.83	120.37	128.36
4	A	1282	BCL	CMB-C2B-C1B	-4.58	120.79	128.36
4	A	1283	BCL	CMB-C2B-C1B	-4.51	120.90	128.36
4	B	1302	BCL	C1D-CHD-C4C	-4.32	119.47	126.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1283	BCL	C1D-CHD-C4C	-4.23	119.61	126.07
8	B	1306	U10	C17-C18-C19	-3.78	119.54	127.76
4	A	1283	BCL	CAC-C3C-C2C	-3.28	105.88	114.13
5	A	1284	BPH	C7-C6-C5	-3.07	104.00	113.06
6	A	1285	MST	N5-C6-N1	-3.03	121.56	126.22
4	A	1282	BCL	CHA-C1A-NA	-3.02	118.62	126.06
5	B	1304	BPH	O1D-CGD-CBD	-2.90	120.47	124.62
5	A	1284	BPH	O2A-CGA-O1A	-2.87	116.08	123.49
4	A	1283	BCL	CAA-C2A-C3A	-2.72	105.41	113.22
8	B	1306	U10	C22-C23-C24	-2.64	122.02	127.76
4	B	1302	BCL	O1D-CGD-CBD	-2.59	120.91	124.62
5	B	1304	BPH	O2D-CGD-O1D	-2.59	118.45	123.79
4	B	1303	BCL	CAC-C3C-C2C	-2.57	107.66	114.13
4	B	1303	BCL	CHA-C1A-NA	-2.52	119.87	126.06
4	A	1282	BCL	C1D-CHD-C4C	-2.51	122.25	126.07
8	B	1306	U10	C12-C13-C14	-2.44	122.47	127.76
4	A	1283	BCL	C4A-NA-C1A	-2.38	103.28	106.36
5	B	1304	BPH	C3A-C4A-NA	-2.28	109.58	113.57
4	B	1302	BCL	C4A-NA-C1A	-2.26	103.42	106.36
4	B	1303	BCL	OBb-CAB-CBB	-2.22	114.82	120.13
4	A	1282	BCL	CAA-C2A-C3A	-2.20	106.89	113.22
4	B	1303	BCL	C4A-NA-C1A	-2.19	103.52	106.36
4	A	1282	BCL	C4A-NA-C1A	-2.19	103.53	106.36
4	B	1302	BCL	O2D-CGD-O1D	-2.16	119.32	123.79
4	A	1283	BCL	C5-C3-C2	-2.15	116.96	121.05
5	A	1284	BPH	O2D-CGD-O1D	-2.10	119.46	123.79
4	B	1303	BCL	O2D-CGD-O1D	-2.06	119.54	123.79
4	B	1302	BCL	O2A-CGA-O1A	-2.06	118.19	123.49
5	B	1304	BPH	CMD-C2D-C3D	-2.03	121.12	125.09
5	A	1284	BPH	O2A-CGA-CBA	2.03	118.09	111.90
8	B	1306	U10	C31-C29-C30	2.15	119.92	114.64
4	A	1282	BCL	CHB-C4A-NA	2.29	127.68	124.51
5	B	1304	BPH	C2B-C1B-NB	2.32	113.21	109.73
4	B	1302	BCL	O2A-CGA-CBA	2.43	119.29	111.90
4	A	1282	BCL	C4-C3-C5	2.44	119.13	115.41
6	A	1285	MST	S7-C2-N1	2.47	124.50	115.89
5	A	1284	BPH	C2B-C1B-NB	2.55	113.55	109.73
4	A	1283	BCL	C2C-C3C-C4C	2.61	105.92	101.50
4	A	1282	BCL	OBb-CAB-C3B	2.63	124.17	120.00
5	A	1284	BPH	C4A-NA-C1A	2.64	110.57	108.21
5	B	1304	BPH	C4A-NA-C1A	2.70	110.62	108.21
4	A	1282	BCL	CED-O2D-CGD	2.83	122.63	115.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1283	BCL	CHB-C4A-NA	2.84	128.43	124.51
5	B	1304	BPH	CMB-C2B-C1B	2.90	129.77	125.06
5	B	1304	BPH	C4-C3-C5	2.90	118.97	115.68
4	A	1283	BCL	O2D-CGD-CBD	2.91	115.29	111.30
4	B	1303	BCL	CED-O2D-CGD	2.92	122.84	115.99
6	A	1285	MST	N9-C4-N5	3.05	126.43	117.48
4	A	1282	BCL	O2A-CGA-CBA	3.14	121.46	111.90
5	B	1304	BPH	C2D-C1D-ND	3.19	115.52	110.29
5	A	1284	BPH	C2D-C1D-ND	3.31	115.71	110.29
5	B	1304	BPH	CED-O2D-CGD	3.41	123.98	115.99
4	A	1283	BCL	CMB-C2B-C3B	3.43	131.79	125.09
4	B	1302	BCL	CMB-C2B-C3B	3.72	132.37	125.09
4	A	1283	BCL	CHC-C1C-NC	3.88	129.88	124.51
4	B	1303	BCL	CMB-C2B-C3B	3.94	132.80	125.09
4	B	1303	BCL	O2A-CGA-CBA	4.03	124.19	111.90
4	A	1282	BCL	CMB-C2B-C3B	4.07	133.05	125.09
5	A	1284	BPH	O2D-CGD-CBD	4.55	117.55	111.30
5	B	1304	BPH	C3C-C4C-NC	4.61	112.55	107.93
4	B	1303	BCL	CHC-C1C-NC	4.65	130.94	124.51
8	B	1306	U10	C25-C24-C26	4.83	122.79	115.41
5	A	1284	BPH	C3C-C4C-NC	4.89	112.83	107.93
4	B	1303	BCL	O2D-CGD-CBD	4.92	118.05	111.30
6	A	1285	MST	C6-N5-C4	5.66	122.29	113.99
4	B	1302	BCL	O2D-CGD-CBD	6.17	119.76	111.30
5	B	1304	BPH	O2D-CGD-CBD	7.12	121.07	111.30
6	A	1285	MST	C2-N3-C4	12.26	121.64	113.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1282	BCL	4	0
4	A	1283	BCL	3	0
5	A	1284	BPH	3	0
6	A	1285	MST	8	0
4	B	1302	BCL	1	0
4	B	1303	BCL	8	0
5	B	1304	BPH	8	0
8	B	1306	U10	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	281/281 (100%)	-0.12	9 (3%)	51	51	20, 29, 53, 58	1 (0%)
2	B	301/307 (98%)	-0.02	9 (2%)	54	54	19, 27, 44, 53	4 (1%)
3	C	237/260 (91%)	0.06	6 (2%)	61	61	23, 36, 43, 53	8 (3%)
All	All	819/848 (96%)	-0.03	24 (2%)	55	55	19, 30, 45, 58	13 (1%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	302	GLY	5.4
1	A	270	PRO	4.8
2	B	3	TYR	3.9
2	B	301	HIS	3.8
1	A	274	ASN	3.2
2	B	106	ALA	2.9
1	A	57	GLY	2.9
3	C	94	GLU	2.8
1	A	265	TRP	2.8
2	B	2	GLU	2.8
1	A	59	TRP	2.8
2	B	292	ASP	2.7
3	C	52	ASN	2.7
1	A	271	TRP	2.6
1	A	281	GLY	2.6
3	C	18	TYR	2.5
3	C	82	ASP	2.4
3	C	211	ASP	2.3
2	B	68	PHE	2.3
1	A	1	ALA	2.3
1	A	276	PRO	2.2
3	C	245	ALA	2.2
2	B	100	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	83	ALA	2.1

## 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. 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(Å <sup>2</sup> )	Q<0.9
6	MST	A	1285	16/16	0.80	0.32	5.18	52,56,58,60	0
9	CL	B	1307	1/1	0.91	0.25	3.54	52,52,52,52	0
8	U10	B	1306	38/63	0.91	0.27	3.15	43,47,60,60	0
5	BPH	A	1284	65/65	0.93	0.27	3.00	35,37,46,48	0
4	BCL	B	1302	51/66	0.94	0.26	2.86	38,42,48,50	0
5	BPH	B	1304	51/65	0.93	0.27	2.52	43,46,52,54	0
10	PO4	B	1308	5/5	0.98	0.18	2.48	35,36,38,39	0
4	BCL	B	1303	66/66	0.92	0.27	2.18	37,40,49,51	0
4	BCL	A	1282	66/66	0.91	0.26	1.99	39,41,47,49	0
4	BCL	A	1283	66/66	0.94	0.24	1.39	37,40,50,50	0
10	PO4	B	1309	5/5	0.97	0.16	0.30	55,56,56,56	0
7	FE2	B	1305	1/1	0.99	0.13	-1.50	30,30,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.