



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:48 AM GMT

PDB ID : 2UWT
Title : X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC
REACTION CENTER FROM RB. SPHAEROIDES AT PH 6.5 IN THE
CHARGE-SEPARATED STATE 2ND DATASET
Authors : Koepke, J.; Diehm, R.; Fritzsche, G.
Deposited on : 2007-03-23
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

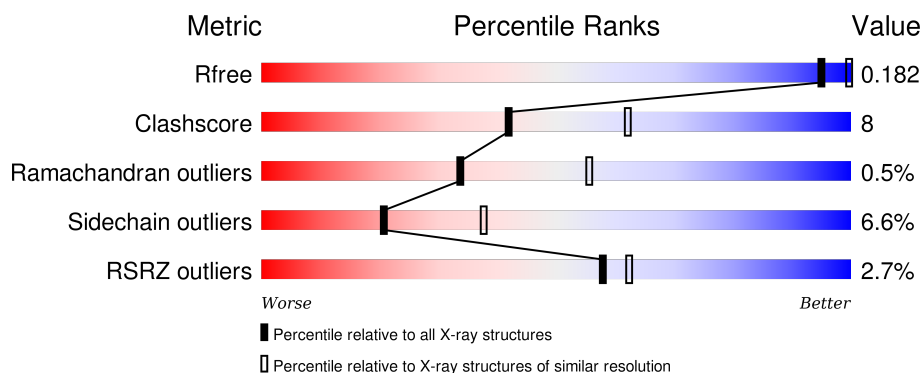
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	H	260	<div> <div>3%</div> <div>77%</div> <div>13%</div> <div>7%</div> </div>
2	L	281	<div> <div>2%</div> <div>86%</div> <div>12%</div> <div>•</div> </div>
3	M	307	<div> <div>3%</div> <div>81%</div> <div>15%</div> <div>••</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	LDA	M	1305	-	-	-	X
10	LDA	M	1306	-	-	-	X
10	LDA	M	1307	-	-	-	X
10	LDA	M	1308	-	-	-	X
10	LDA	M	1309	-	-	-	X
10	LDA	M	1310	-	-	-	X
13	SPO	M	1314	-	-	-	X
4	GOL	H	1251	-	-	-	X
5	BCL	L	1282	X	-	-	-
5	BCL	L	1283	X	-	-	-
5	BCL	M	1303	X	-	-	-
5	BCL	M	1304	X	-	-	-
7	UQ2	L	1285[A]	-	-	-	X
7	UQ2	L	1285[B]	-	-	-	X
9	HTO	L	1287	-	-	-	X

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 7512 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 CENTER PROTEIN H CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	241	Total	C	N	O	S	0	0	1
			1830	1169	315	337	9			

- Molecule 2 is a protein called REACTION CENTER PROTEIN L CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	281	Total	C	N	O	S	0	0	0
			2232	1507	355	362	8			

- Molecule 3 is a protein called REACTION CENTER PROTEIN M CHAIN.

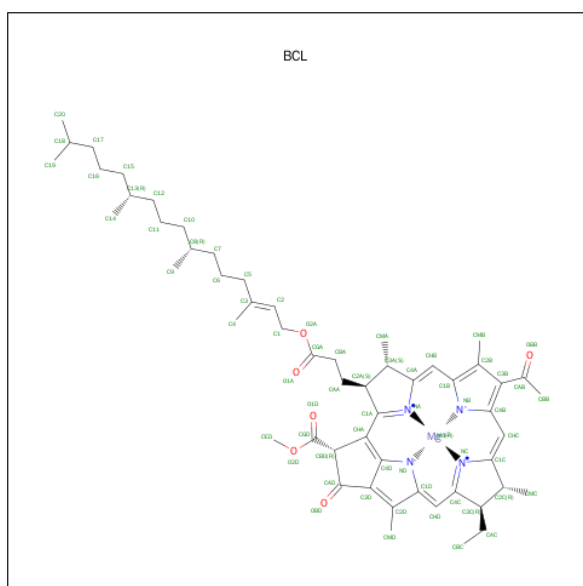
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	303	Total	C	N	O	S	0	0	1
			2409	1607	395	397	10			

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



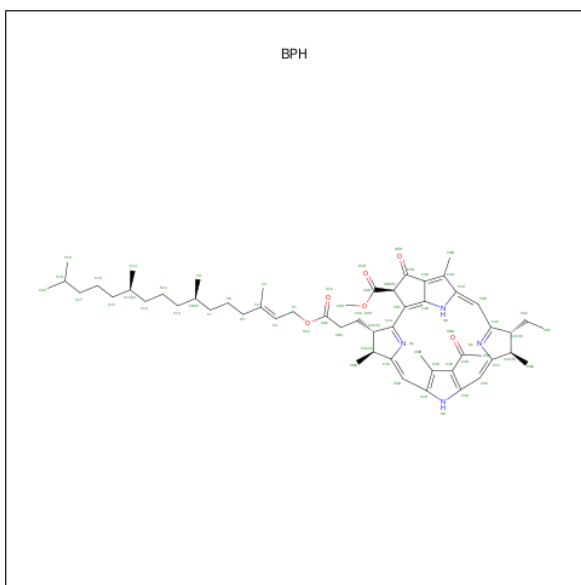
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total C O 6 3 3	0	0
4	H	1	Total C O 6 3 3	0	0
4	H	1	Total C O 6 3 3	0	0
4	L	1	Total C O 6 3 3	0	0
4	M	1	Total C O 6 3 3	0	0

- Molecule 5 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



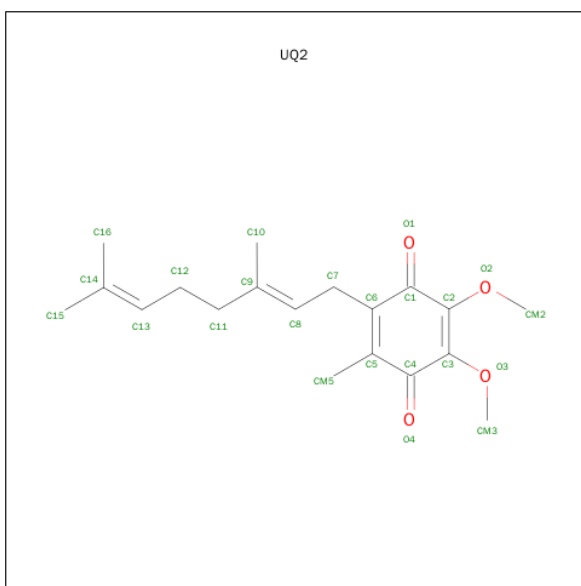
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	L	1	Total C Mg N O 66 55 1 4 6	0	0
5	L	1	Total C Mg N O 66 55 1 4 6	0	0
5	M	1	Total C Mg N O 66 55 1 4 6	0	0
5	M	1	Total C Mg N O 66 55 1 4 6	0	0

- Molecule 6 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: $C_{55}H_{76}N_4O_6$).



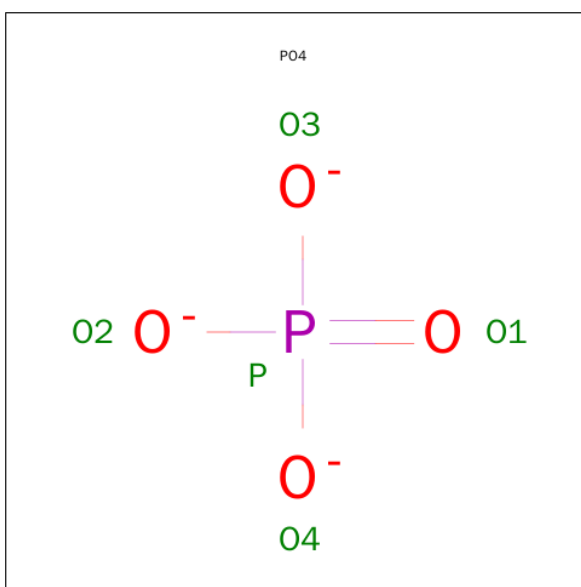
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	L	1	Total	C	N	O	0	0
			65	55	4	6		
6	M	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 7 is UBIQUINONE-2 (three-letter code: UQ2) (formula: $C_{19}H_{26}O_4$).



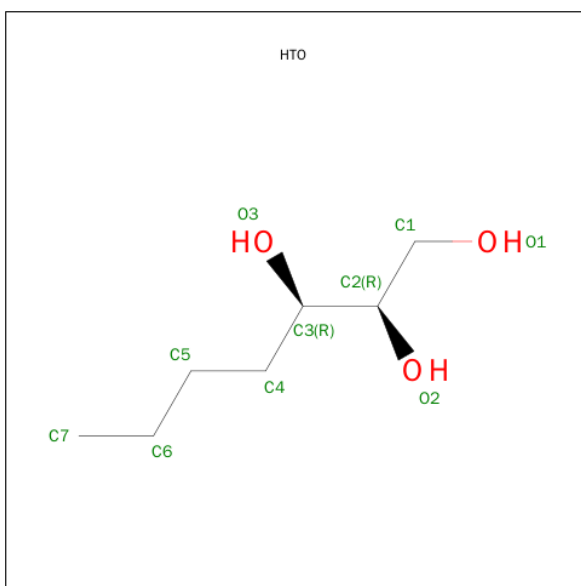
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	L	1	Total	C	O	0	1
			46	38	8		

- Molecule 8 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



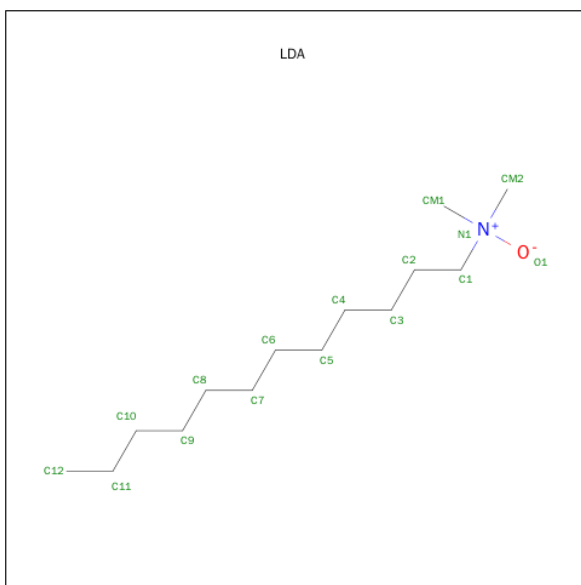
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	L	1	Total	O	P	0	0
			5	4	1		

- Molecule 9 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula: $C_7H_{16}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	L	1	Total	C	O	0	0
			10	7	3		

- Molecule 10 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).

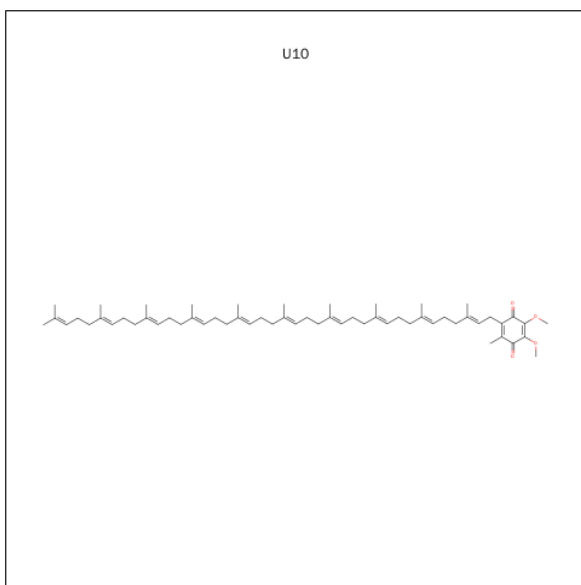


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	M	1	Total C N O 16 14 1 1	0	0
10	M	1	Total C N O 16 14 1 1	0	0
10	M	1	Total C N O 16 14 1 1	0	0
10	M	1	Total C N O 16 14 1 1	0	0
10	M	1	Total C N O 16 14 1 1	0	0
10	M	1	Total C N O 16 14 1 1	0	0

- Molecule 11 is FE (III) ION (three-letter code: FE) (formula: Fe).

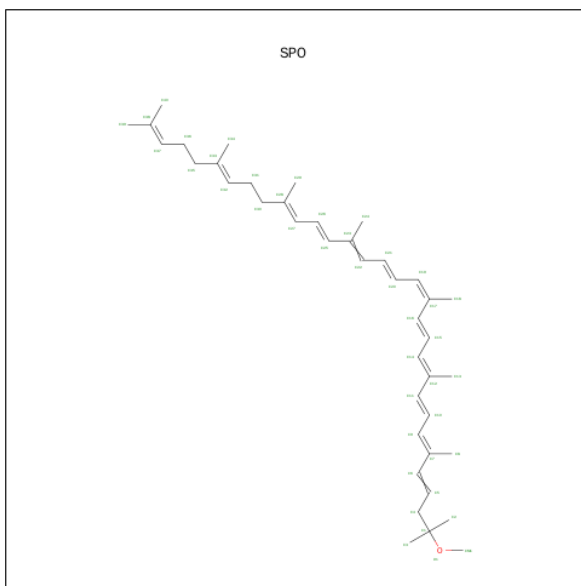
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	M	1	Total Fe 1 1	0	0

- Molecule 12 is UBIQUINONE-10 (three-letter code: U10) (formula: C₅₉H₉₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	M	1	Total	C	O	0	0
			48	44	4		

- Molecule 13 is SPHEROIDENE (three-letter code: SPO) (formula: $C_{41}H_{60}O$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	M	1	Total	C	O	0	0
			42	41	1		

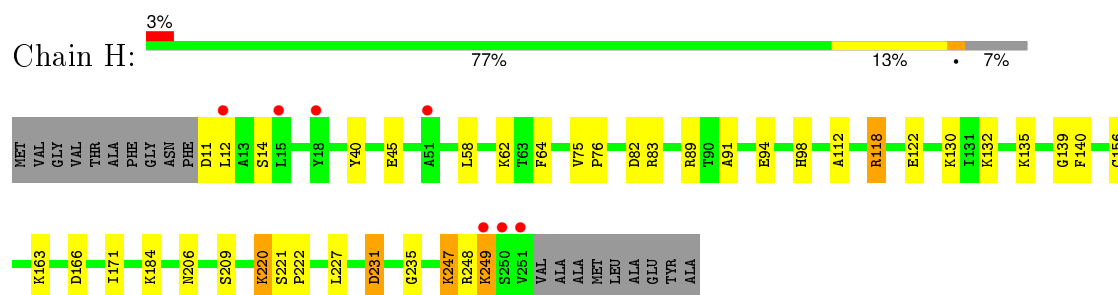
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	H	151	Total 151	O 151	0	0
14	L	113	Total 113	O 113	0	0
14	M	105	Total 105	O 105	0	0

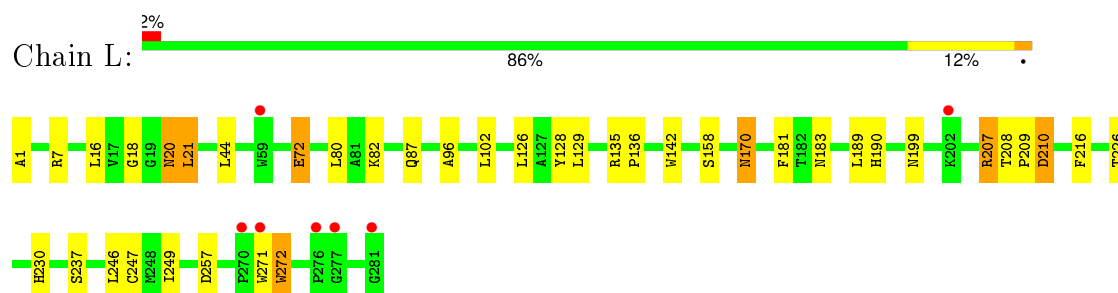
3 Residue-property plots [i](#)

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.

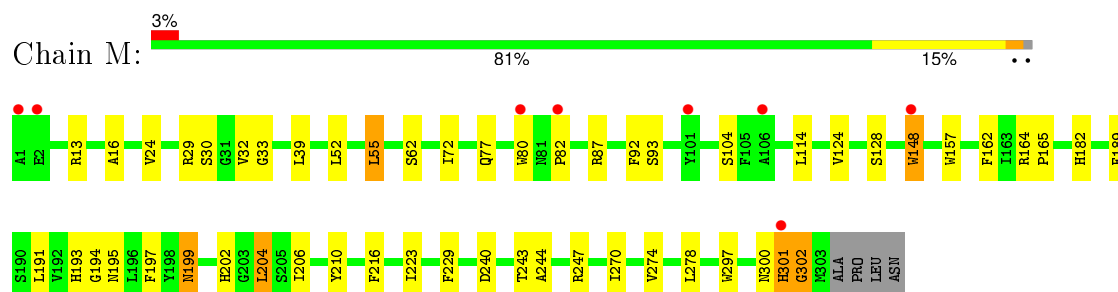
• Molecule 1: REACTION CENTER PROTEIN H CHAIN



• Molecule 2: REACTION CENTER PROTEIN L CHAIN



• Molecule 3: REACTION CENTER PROTEIN M CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	139.53Å 139.53Å 184.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	121.27 – 2.50 29.81 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.7 (121.27-2.50) 93.8 (29.81-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.50 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.196 , 0.219 0.183 , 0.182	Depositor DCC
R_{free} test set	3578 reflections (5.54%)	DCC
Wilson B-factor (Å ²)	43.6	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.7	EDS
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 71530 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7512	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 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, GOL, LDA, HTO, BPH, PO4, FE, SPO, U10, UQ2

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	H	0.77	0/1878	0.84	4/2555 (0.2%)
2	L	0.77	0/2320	0.74	3/3175 (0.1%)
3	M	0.72	0/2501	0.73	1/3415 (0.0%)
All	All	0.75	0/6699	0.77	8/9145 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	H	139	GLY	N-CA-C	-6.94	95.76	113.10
1	H	82	ASP	CB-CG-OD2	6.76	124.38	118.30
1	H	231	ASP	CB-CG-OD2	6.71	124.34	118.30
2	L	257	ASP	CB-CG-OD2	6.49	124.14	118.30
1	H	166	ASP	CB-CG-OD2	5.75	123.47	118.30
2	L	207	ARG	NE-CZ-NH2	-5.32	117.64	120.30
2	L	207	ARG	NE-CZ-NH1	5.14	122.87	120.30
3	M	240	ASP	CB-CG-OD2	5.04	122.83	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1830	0	1836	24	0
2	L	2232	0	2187	24	0
3	M	2409	0	2321	37	0
4	H	18	0	24	3	0
4	L	6	0	8	1	0
4	M	6	0	8	0	0
5	L	132	0	148	9	0
5	M	132	0	148	15	0
6	L	65	0	76	6	0
6	M	65	0	76	9	0
7	L	46	0	52	6	0
8	L	5	0	0	0	0
9	L	10	0	16	0	0
10	M	96	0	186	12	0
11	M	1	0	0	0	0
12	M	48	0	63	1	0
13	M	42	0	60	3	0
14	H	151	0	0	5	1
14	L	113	0	0	1	0
14	M	105	0	0	0	0
All	All	7512	0	7209	120	1

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 8.

All (120) 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:L:1284:BPH:HBB3	6:L:1284:BPH:HHC	1.46	0.93
3:M:197:PHE:CZ	5:M:1304:BCL:HBB2	2.10	0.87
3:M:197:PHE:HZ	5:M:1304:BCL:HBB2	1.43	0.81
6:L:1284:BPH:HBB2	3:M:210:TYR:HB3	1.64	0.80
4:H:1251:GOL:H31	14:H:2003:HOH:O	1.81	0.79
2:L:181:PHE:CD2	6:M:1312:BPH:HBB1	2.18	0.78
5:M:1304:BCL:HBB2	5:M:1304:BCL:HHC	1.66	0.77
3:M:16:ALA:HB1	3:M:32:VAL:HG11	1.66	0.76
10:M:1307:LDA:C4	10:M:1308:LDA:H41	2.15	0.76
3:M:300:ASN:C	3:M:302:GLY:H	1.88	0.76
6:L:1284:BPH:HHC	6:L:1284:BPH:CBB	2.14	0.76
5:M:1304:BCL:CBB	5:M:1304:BCL:HHC	2.16	0.76
6:M:1312:BPH:HBB3	6:M:1312:BPH:HHC	1.70	0.73
1:H:118:ARG:HH11	1:H:118:ARG:CG	2.04	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:98:HIS:CD2	2:L:7:ARG:HH21	2.08	0.71
10:M:1307:LDA:H41	10:M:1308:LDA:H41	1.74	0.69
3:M:77:GLN:HE22	3:M:93:SER:H	1.42	0.67
2:L:170:ASN:C	2:L:170:ASN:HD22	2.00	0.65
1:H:98:HIS:HD2	2:L:7:ARG:HH21	1.42	0.65
2:L:181:PHE:HB3	6:M:1312:BPH:HBB2	1.78	0.65
6:M:1312:BPH:HHC	6:M:1312:BPH:CBB	2.28	0.64
10:M:1305:LDA:H101	10:M:1307:LDA:H121	1.78	0.63
5:M:1304:BCL:CBB	5:M:1304:BCL:CHC	2.75	0.63
3:M:157:TRP:HB2	5:M:1304:BCL:H71	1.81	0.62
3:M:62:SER:OG	3:M:124:VAL:HG22	1.98	0.62
2:L:226:THR:HG22	7:L:1285[A]:UQ2:H3M3	1.82	0.60
10:M:1305:LDA:H92	10:M:1307:LDA:C12	2.32	0.60
1:H:118:ARG:HH11	1:H:118:ARG:HG3	1.67	0.59
3:M:189:PHE:O	3:M:193:HIS:HD2	1.86	0.58
3:M:197:PHE:HZ	5:M:1304:BCL:CBB	2.13	0.58
2:L:208:THR:HB	2:L:209:PRO:HD2	1.87	0.57
6:L:1284:BPH:HBB1	3:M:210:TYR:CD2	2.39	0.56
1:H:220:LYS:NZ	14:H:2138:HOH:O	2.37	0.56
1:H:248:ARG:HA	1:H:249:LYS:CB	2.37	0.55
3:M:300:ASN:C	3:M:302:GLY:N	2.59	0.55
3:M:162:PHE:HB2	13:M:1314:SPO:H312	1.89	0.54
3:M:202:HIS:CE1	3:M:206:ILE:HD11	2.42	0.54
2:L:135:ARG:HB3	2:L:136:PRO:HD3	1.88	0.54
5:M:1303:BCL:HBB2	5:M:1303:BCL:HHC	1.90	0.53
5:L:1282:BCL:H193	5:L:1283:BCL:H102	1.90	0.53
5:M:1303:BCL:HBB3	5:M:1304:BCL:H41	1.90	0.53
3:M:297:TRP:CE2	3:M:302:GLY:HA2	2.43	0.53
2:L:18:GLY:O	2:L:21:LEU:HB2	2.08	0.53
6:M:1312:BPH:HBB3	6:M:1312:BPH:CHC	2.38	0.53
1:H:118:ARG:CG	1:H:118:ARG:NH1	2.71	0.52
3:M:55:LEU:HD22	3:M:128:SER:HB2	1.90	0.52
2:L:199:ASN:HA	4:L:1288:GOL:H31	1.91	0.52
3:M:199:ASN:C	3:M:199:ASN:HD22	2.11	0.52
2:L:181:PHE:HB3	6:M:1312:BPH:CBB	2.40	0.52
3:M:197:PHE:CE1	5:M:1304:BCL:HBB2	2.44	0.52
7:L:1285[A]:UQ2:H153	10:M:1309:LDA:C12	2.41	0.51
5:M:1304:BCL:HAA2	5:M:1304:BCL:HBD	1.91	0.51
3:M:24:VAL:HG21	3:M:29:ARG:NH1	2.26	0.50
3:M:77:GLN:NE2	3:M:93:SER:H	2.10	0.50
1:H:130:LYS:HD2	14:L:2093:HOH:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:112:ALA:HA	1:H:235:GLY:O	2.12	0.50
2:L:189:LEU:HB3	7:L:1285[B]:UQ2:H3M3	1.93	0.49
10:M:1305:LDA:H92	10:M:1307:LDA:H123	1.94	0.49
2:L:272:TRP:CD1	3:M:87:ARG:HG3	2.48	0.48
2:L:190:HIS:HA	7:L:1285[A]:UQ2:O4	2.13	0.48
2:L:96:ALA:HB1	6:L:1284:BPH:H2	1.95	0.48
3:M:300:ASN:O	3:M:302:GLY:N	2.46	0.48
1:H:209:SER:OG	1:H:247:LYS:HD3	2.14	0.48
1:H:122:GLU:HB2	1:H:227:LEU:HD21	1.96	0.47
5:M:1304:BCL:HBB3	5:M:1304:BCL:CHC	2.44	0.47
5:L:1282:BCL:CBB	5:L:1282:BCL:HMB1	2.45	0.47
1:H:140:PHE:HA	3:M:13:ARG:O	2.15	0.47
3:M:80:TRP:O	3:M:82:PRO:HD3	2.14	0.47
1:H:156:CYS:HB3	1:H:206:ASN:O	2.15	0.47
1:H:45:GLU:HG3	1:H:94:GLU:OE1	2.15	0.46
14:H:2068:HOH:O	2:L:1:ALA:HB1	2.16	0.46
2:L:20:ASN:C	2:L:20:ASN:HD22	2.19	0.46
10:M:1307:LDA:H51	10:M:1307:LDA:H81	1.69	0.46
5:M:1303:BCL:H102	5:M:1303:BCL:H13	1.65	0.45
1:H:75:VAL:HA	1:H:76:PRO:C	2.37	0.45
3:M:189:PHE:O	3:M:193:HIS:CD2	2.69	0.44
1:H:132:LYS:HB2	1:H:171:ILE:HD11	1.99	0.44
1:H:40:TYR:HB3	1:H:58:LEU:HD21	1.98	0.44
1:H:248:ARG:HA	1:H:249:LYS:HB3	1.99	0.44
3:M:164:ARG:HB3	3:M:165:PRO:HD3	1.99	0.44
2:L:230:HIS:CD2	3:M:223:ILE:HG13	2.53	0.44
2:L:210:ASP:OD1	2:L:210:ASP:N	2.50	0.44
3:M:148:TRP:HA	3:M:148:TRP:CE3	2.54	0.43
6:M:1312:BPH:CHC	6:M:1312:BPH:CBB	2.96	0.43
3:M:270:ILE:O	3:M:274:VAL:HG13	2.18	0.43
3:M:33:GLY:HA2	10:M:1309:LDA:H12	1.99	0.43
5:L:1282:BCL:H142	5:L:1283:BCL:HMB1	2.00	0.43
6:L:1284:BPH:CHC	6:L:1284:BPH:CBB	2.90	0.43
1:H:220:LYS:HE3	14:H:2086:HOH:O	2.18	0.43
3:M:243:THR:O	3:M:247:ARG:HG3	2.18	0.42
5:M:1303:BCL:HBB2	13:M:1314:SPO:H243	2.00	0.42
5:M:1303:BCL:CBB	13:M:1314:SPO:H243	2.49	0.42
5:L:1283:BCL:H142	5:L:1283:BCL:H161	1.86	0.42
3:M:194:GLY:O	3:M:195:ASN:HB3	2.18	0.42
5:L:1282:BCL:H52	5:L:1283:BCL:HBB3	2.01	0.42
5:L:1283:BCL:HHC	5:L:1283:BCL:CBB	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:128:TYR:HD1	5:L:1283:BCL:HBB1	1.85	0.42
1:H:62:LYS:HE2	1:H:64:PHE:CZ	2.55	0.42
3:M:204:LEU:HD13	10:M:1305:LDA:H22	2.01	0.42
5:L:1283:BCL:HBB2	5:L:1283:BCL:HHC	2.02	0.42
10:M:1308:LDA:HM21	10:M:1308:LDA:H21	1.78	0.42
4:H:1251:GOL:C3	14:H:2003:HOH:O	2.53	0.41
2:L:183:ASN:ND2	2:L:237:SER:HB3	2.36	0.41
2:L:72:GLU:H	2:L:72:GLU:HG3	1.49	0.41
6:M:1312:BPH:H2	6:M:1312:BPH:H6C2	1.87	0.41
3:M:274:VAL:HA	6:M:1312:BPH:HBC1	2.02	0.41
1:H:156:CYS:SG	1:H:248:ARG:HB2	2.61	0.41
1:H:62:LYS:HE3	4:H:1251:GOL:H11	2.03	0.41
7:L:1285[B]:UQ2:H71	7:L:1285[B]:UQ2:H5M1	1.90	0.41
7:L:1285[A]:UQ2:H153	10:M:1309:LDA:H121	2.03	0.41
1:H:221:SER:HA	1:H:222:PRO:HD3	1.89	0.41
2:L:249:ILE:HA	2:L:249:ILE:HD12	1.96	0.41
12:M:1313:U10:H372	12:M:1313:U10:H351	1.90	0.40
3:M:229:PHE:HB2	3:M:244:ALA:HB2	2.02	0.40
3:M:274:VAL:HG23	3:M:278:LEU:HD12	2.02	0.40
10:M:1307:LDA:H31	10:M:1307:LDA:H61	1.72	0.40
5:L:1283:BCL:HMB1	5:L:1283:BCL:OBB	2.21	0.40
1:H:89:ARG:HD3	1:H:91:ALA:O	2.21	0.40
2:L:87:GLN:NE2	2:L:142:TRP:CD1	2.90	0.40
3:M:77:GLN:HE21	3:M:92:PHE:HB3	1.87	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:H:2049:HOH:O	14:H:2049:HOH:O[4_555]	2.19	0.01

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	H	239/260 (92%)	230 (96%)	8 (3%)	1 (0%)	39	61
2	L	279/281 (99%)	271 (97%)	8 (3%)	0	100	100
3	M	301/307 (98%)	284 (94%)	14 (5%)	3 (1%)	19	34
All	All	819/848 (97%)	785 (96%)	30 (4%)	4 (0%)	34	55

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	249	LYS
3	M	301	HIS
3	M	30	SER
3	M	302	GLY

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	H	195/208 (94%)	184 (94%)	11 (6%)	26	47
2	L	220/220 (100%)	201 (91%)	19 (9%)	13	24
3	M	236/240 (98%)	223 (94%)	13 (6%)	27	48
All	All	651/668 (98%)	608 (93%)	43 (7%)	21	38

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	11	ASP
1	H	12	LEU
1	H	14	SER
1	H	83	ARG
1	H	118	ARG
1	H	135	LYS
1	H	163	LYS

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Mol	Chain	Res	Type
1	H	184	LYS
1	H	220	LYS
1	H	231	ASP
1	H	247	LYS
2	L	16	LEU
2	L	20	ASN
2	L	21	LEU
2	L	44	LEU
2	L	72	GLU
2	L	80	LEU
2	L	82	LYS
2	L	102	LEU
2	L	126	LEU
2	L	129	LEU
2	L	158	SER
2	L	170	ASN
2	L	207	ARG
2	L	210	ASP
2	L	216	PHE
2	L	246	LEU
2	L	247	CYS
2	L	271	TRP
2	L	272	TRP
3	M	39	LEU
3	M	52	LEU
3	M	55	LEU
3	M	72	ILE
3	M	104	SER
3	M	114	LEU
3	M	148	TRP
3	M	182	HIS
3	M	191	LEU
3	M	199	ASN
3	M	204	LEU
3	M	216	PHE
3	M	301	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	98	HIS
1	H	141	HIS

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Mol	Chain	Res	Type
2	L	20	ASN
2	L	159	ASN
2	L	170	ASN
2	L	183	ASN
3	M	77	GLN
3	M	187	ASN
3	M	193	HIS
3	M	199	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 1 is monoatomic - leaving 23 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	GOL	H	1251	-	5,5,5	0.50	0	5,5,5	0.90	0
4	GOL	H	1252	-	5,5,5	0.41	0	5,5,5	0.46	0
4	GOL	H	1253	-	5,5,5	0.32	0	5,5,5	0.37	0
5	BCL	L	1282	2	53,74,74	2.12	4 (7%)	57,115,115	1.96	13 (22%)
5	BCL	L	1283	2	53,74,74	2.04	6 (11%)	57,115,115	1.95	16 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	BPH	L	1284	-	64,70,70	2.92	19 (29%)	73,101,101	1.85	14 (19%)
7	UQ2	L	1285[A]	-	23,23,23	2.66	8 (34%)	28,31,31	1.63	7 (25%)
7	UQ2	L	1285[B]	-	23,23,23	2.71	7 (30%)	28,31,31	1.21	2 (7%)
8	PO4	L	1286	-	4,4,4	0.38	0	6,6,6	0.27	0
9	HTO	L	1287	-	9,9,9	0.47	0	8,10,10	0.50	0
4	GOL	L	1288	-	5,5,5	0.32	0	5,5,5	0.91	0
5	BCL	M	1303	3	53,74,74	2.10	6 (11%)	57,115,115	1.85	12 (21%)
5	BCL	M	1304	3	53,74,74	2.07	6 (11%)	57,115,115	2.08	15 (26%)
10	LDA	M	1305	-	15,15,15	3.86	1 (6%)	16,17,17	1.25	2 (12%)
10	LDA	M	1306	-	15,15,15	3.63	1 (6%)	16,17,17	0.93	1 (6%)
10	LDA	M	1307	-	15,15,15	3.34	2 (13%)	16,17,17	0.75	0
10	LDA	M	1308	-	15,15,15	3.84	2 (13%)	16,17,17	0.87	0
10	LDA	M	1309	-	15,15,15	3.70	2 (13%)	16,17,17	0.69	0
10	LDA	M	1310	-	15,15,15	3.76	1 (6%)	16,17,17	0.72	0
6	BPH	M	1312	-	64,70,70	2.92	19 (29%)	73,101,101	1.77	13 (17%)
12	U10	M	1313	-	48,48,63	3.13	11 (22%)	58,61,79	1.74	10 (17%)
13	SPO	M	1314	-	40,41,41	4.04	12 (30%)	45,50,50	2.22	14 (31%)
4	GOL	M	1315	-	5,5,5	0.34	0	5,5,5	0.33	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	GOL	H	1251	-	-	0/4/4/4	0/0/0/0
4	GOL	H	1252	-	-	0/4/4/4	0/0/0/0
4	GOL	H	1253	-	-	0/4/4/4	0/0/0/0
5	BCL	L	1282	2	2/2/21/25	0/37/137/137	0/0/9/9
5	BCL	L	1283	2	2/2/21/25	0/37/137/137	0/0/9/9
6	BPH	L	1284	-	-	0/54/105/105	0/1/6/6
7	UQ2	L	1285[A]	-	-	0/15/39/39	0/1/1/1
7	UQ2	L	1285[B]	-	-	0/15/39/39	0/1/1/1
8	PO4	L	1286	-	-	0/0/0/0	0/0/0/0
9	HTO	L	1287	-	-	0/10/10/10	0/0/0/0
4	GOL	L	1288	-	-	0/4/4/4	0/0/0/0
5	BCL	M	1303	3	2/2/21/25	0/37/137/137	0/0/9/9
5	BCL	M	1304	3	2/2/21/25	0/37/137/137	0/0/9/9

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	LDA	M	1305	-	-	0/13/13/13	0/0/0/0
10	LDA	M	1306	-	-	0/13/13/13	0/0/0/0
10	LDA	M	1307	-	-	0/13/13/13	0/0/0/0
10	LDA	M	1308	-	-	0/13/13/13	0/0/0/0
10	LDA	M	1309	-	-	0/13/13/13	0/0/0/0
10	LDA	M	1310	-	-	0/13/13/13	0/0/0/0
6	BPH	M	1312	-	-	0/54/105/105	0/1/6/6
12	U10	M	1313	-	-	0/45/69/87	0/1/1/1
13	SPO	M	1314	-	-	0/47/47/47	0/0/0/0
4	GOL	M	1315	-	-	0/4/4/4	0/0/0/0

All (107) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	1305	LDA	O1-N1	-14.67	1.25	1.39
10	M	1308	LDA	O1-N1	-14.64	1.25	1.39
10	M	1310	LDA	O1-N1	-14.32	1.25	1.39
10	M	1309	LDA	O1-N1	-14.03	1.26	1.39
10	M	1306	LDA	O1-N1	-13.89	1.26	1.39
10	M	1307	LDA	O1-N1	-12.65	1.27	1.39
7	L	1285[B]	UQ2	O2-C2	-4.75	1.24	1.37
7	L	1285[A]	UQ2	O2-C2	-4.71	1.24	1.37
7	L	1285[B]	UQ2	O3-C3	-4.64	1.24	1.37
12	M	1313	U10	O4-C4	-4.15	1.26	1.37
6	L	1284	BPH	C3D-CAD	-3.70	1.39	1.46
6	M	1312	BPH	C3D-C4D	-3.62	1.36	1.41
7	L	1285[A]	UQ2	O3-C3	-3.61	1.27	1.37
6	L	1284	BPH	C3D-C4D	-3.60	1.36	1.41
12	M	1313	U10	O3-C3	-3.52	1.27	1.37
6	M	1312	BPH	C3D-CAD	-3.46	1.39	1.46
7	L	1285[B]	UQ2	C3-C4	-3.13	1.39	1.48
6	M	1312	BPH	C1B-C2B	-3.06	1.39	1.45
6	M	1312	BPH	O2D-CGD	-3.02	1.25	1.33
12	M	1313	U10	C4-C5	-2.96	1.40	1.48
6	M	1312	BPH	O2A-CGA	-2.90	1.24	1.33
7	L	1285[A]	UQ2	C3-C4	-2.87	1.40	1.48
7	L	1285[B]	UQ2	C2-C1	-2.83	1.40	1.48
5	M	1303	BCL	O2D-CGD	-2.52	1.26	1.33
10	M	1309	LDA	C1-N1	-2.47	1.46	1.51
10	M	1307	LDA	C1-N1	-2.45	1.46	1.51
6	L	1284	BPH	O2D-CGD	-2.41	1.27	1.33
5	L	1283	BCL	C3D-CAD	-2.40	1.39	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	1282	BCL	O2D-CGD	-2.34	1.27	1.33
5	M	1304	BCL	O2D-CGD	-2.34	1.27	1.33
7	L	1285[A]	UQ2	C6-C1	-2.34	1.39	1.46
5	M	1304	BCL	O2A-CGA	-2.33	1.26	1.33
6	L	1284	BPH	C1B-C2B	-2.32	1.40	1.45
5	L	1283	BCL	O2D-CGD	-2.18	1.27	1.33
5	L	1283	BCL	O2A-CGA	-2.17	1.26	1.33
6	L	1284	BPH	C3B-C4B	-2.16	1.38	1.43
6	L	1284	BPH	O2D-CED	-2.12	1.40	1.45
6	L	1284	BPH	O2A-CGA	-2.11	1.26	1.33
10	M	1308	LDA	C1-N1	-2.09	1.47	1.51
5	M	1304	BCL	C3D-CAD	-2.07	1.39	1.45
5	M	1303	BCL	C3D-CAD	-2.05	1.40	1.45
7	L	1285[A]	UQ2	C2-C1	-2.03	1.43	1.48
6	M	1312	BPH	C1C-NC	-2.01	1.33	1.37
6	M	1312	BPH	C4C-NC	-2.00	1.33	1.37
5	M	1303	BCL	O1D-CGD	2.09	1.26	1.21
7	L	1285[A]	UQ2	C6-C5	2.29	1.40	1.35
7	L	1285[B]	UQ2	C6-C5	2.38	1.40	1.35
6	L	1284	BPH	C1D-CHD	2.53	1.49	1.40
12	M	1313	U10	C6-C1	2.63	1.41	1.35
6	M	1312	BPH	C1D-CHD	3.09	1.52	1.40
6	L	1284	BPH	CHD-C4C	3.18	1.46	1.38
6	M	1312	BPH	CHB-C4A	3.26	1.46	1.40
5	M	1304	BCL	C2-C3	3.35	1.39	1.33
6	M	1312	BPH	C3D-C2D	3.54	1.48	1.40
6	L	1284	BPH	CHC-C4B	3.54	1.49	1.40
6	M	1312	BPH	CHD-C4C	3.59	1.47	1.38
6	L	1284	BPH	CHB-C4A	3.72	1.47	1.40
6	M	1312	BPH	CHC-C4B	3.76	1.49	1.40
6	L	1284	BPH	C3D-C2D	3.82	1.49	1.40
13	M	1314	SPO	C21-C20	3.96	1.46	1.35
5	L	1283	BCL	C2-C3	4.11	1.41	1.33
13	M	1314	SPO	C26-C25	4.17	1.45	1.34
5	M	1303	BCL	C2-C3	4.20	1.41	1.33
13	M	1314	SPO	C15-C16	4.34	1.45	1.34
5	L	1282	BCL	C2-C3	4.36	1.41	1.33
6	L	1284	BPH	CHC-C1C	4.48	1.45	1.36
13	M	1314	SPO	C10-C11	4.52	1.46	1.34
13	M	1314	SPO	C6-C5	4.84	1.45	1.31
7	L	1285[B]	UQ2	C13-C14	5.02	1.47	1.32
12	M	1313	U10	C38-C39	5.37	1.48	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	1312	BPH	CHC-C1C	5.63	1.47	1.36
5	L	1282	BCL	O1A-CGA	5.64	1.39	1.22
13	M	1314	SPO	C37-C38	5.66	1.49	1.32
6	M	1312	BPH	O1A-CGA	5.69	1.39	1.22
6	M	1312	BPH	CHB-C1B	5.73	1.49	1.38
5	L	1283	BCL	O1A-CGA	5.75	1.39	1.22
5	M	1303	BCL	O1A-CGA	5.77	1.39	1.22
7	L	1285[A]	UQ2	C13-C14	5.85	1.50	1.32
5	M	1304	BCL	O1A-CGA	5.90	1.40	1.22
6	L	1284	BPH	O1A-CGA	6.31	1.41	1.22
6	L	1284	BPH	CHB-C1B	6.54	1.51	1.38
6	L	1284	BPH	O1D-CGD	6.80	1.38	1.21
6	M	1312	BPH	O1D-CGD	7.10	1.39	1.21
12	M	1313	U10	C23-C24	7.26	1.47	1.33
12	M	1313	U10	C18-C19	7.34	1.47	1.33
12	M	1313	U10	C8-C9	7.52	1.47	1.33
6	L	1284	BPH	C2-C3	7.61	1.47	1.33
13	M	1314	SPO	C32-C33	7.69	1.48	1.33
7	L	1285[A]	UQ2	C8-C9	7.70	1.48	1.33
12	M	1313	U10	C28-C29	7.71	1.48	1.33
7	L	1285[B]	UQ2	C8-C9	7.77	1.48	1.33
6	M	1312	BPH	C2-C3	7.78	1.48	1.33
13	M	1314	SPO	C22-C23	7.79	1.46	1.35
6	M	1312	BPH	OBB-CAB	8.05	1.40	1.23
12	M	1313	U10	C13-C14	8.08	1.48	1.33
6	L	1284	BPH	OBB-CAB	8.56	1.42	1.23
13	M	1314	SPO	C14-C12	8.67	1.47	1.35
13	M	1314	SPO	C19-C17	8.97	1.47	1.35
12	M	1313	U10	C33-C34	9.05	1.50	1.33
13	M	1314	SPO	C9-C7	9.33	1.48	1.35
6	M	1312	BPH	OBD-CAD	11.36	1.39	1.22
6	L	1284	BPH	OBD-CAD	11.60	1.40	1.22
5	L	1283	BCL	OBD-CAD	11.63	1.40	1.22
5	M	1303	BCL	OBD-CAD	11.88	1.40	1.22
5	M	1304	BCL	OBD-CAD	11.90	1.40	1.22
13	M	1314	SPO	C27-C28	12.44	1.47	1.34
5	L	1282	BCL	OBD-CAD	12.44	1.41	1.22

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	1303	BCL	CMB-C2B-C1B	-7.15	116.53	128.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1282	BCL	CMB-C2B-C1B	-7.09	116.64	128.36
5	M	1304	BCL	CMB-C2B-C1B	-6.89	116.97	128.36
13	M	1314	SPO	C21-C22-C23	-5.39	119.41	127.20
6	M	1312	BPH	OBD-CAD-CBD	-5.39	117.81	125.94
6	L	1284	BPH	O1D-CGD-CBD	-5.36	116.94	124.62
13	M	1314	SPO	C15-C14-C12	-5.06	119.89	127.20
5	L	1283	BCL	CMB-C2B-C1B	-4.82	120.39	128.36
13	M	1314	SPO	C10-C9-C7	-4.63	120.51	127.20
13	M	1314	SPO	C4-C5-C6	-4.49	118.28	124.67
5	L	1283	BCL	C1D-CHD-C4C	-3.99	119.98	126.07
6	M	1312	BPH	O1D-CGD-CBD	-3.95	118.97	124.62
5	M	1304	BCL	C1D-CHD-C4C	-3.86	120.17	126.07
6	M	1312	BPH	CHC-C4B-NB	-3.78	117.72	124.91
5	L	1283	BCL	O1D-CGD-CBD	-3.73	119.28	124.62
10	M	1305	LDA	CM2-N1-CM1	-3.66	104.70	108.83
12	M	1313	U10	C30-C29-C28	-3.60	116.44	123.50
13	M	1314	SPO	C20-C19-C17	-3.34	122.38	127.20
7	L	1285[A]	UQ2	O1-C1-C6	-3.31	115.45	121.68
12	M	1313	U10	C22-C23-C24	-3.27	120.66	127.76
5	L	1283	BCL	C6-C5-C3	-3.24	105.38	112.48
5	L	1282	BCL	OBD-CAD-CBD	-3.09	121.28	125.94
6	L	1284	BPH	C1C-NC-C4C	-3.09	107.27	110.44
7	L	1285[A]	UQ2	C7-C8-C9	-2.97	121.67	126.70
5	M	1304	BCL	O2D-CGD-O1D	-2.96	117.68	123.79
12	M	1313	U10	C17-C18-C19	-2.94	121.36	127.76
6	M	1312	BPH	OBD-CAD-C3D	-2.84	122.56	128.35
5	L	1282	BCL	C3C-C4C-CHD	-2.82	117.04	123.33
13	M	1314	SPO	C5-C6-C7	-2.77	121.53	125.75
12	M	1313	U10	C26-C27-C28	-2.69	104.64	111.69
5	M	1303	BCL	C1D-CHD-C4C	-2.68	121.98	126.07
5	L	1282	BCL	O1D-CGD-CBD	-2.67	120.79	124.62
5	M	1303	BCL	O1D-CGD-CBD	-2.56	120.95	124.62
7	L	1285[A]	UQ2	CM5-C5-C6	-2.55	118.65	124.10
5	M	1303	BCL	C3C-C4C-CHD	-2.54	117.66	123.33
6	L	1284	BPH	O2A-CGA-O1A	-2.54	116.93	123.49
5	M	1303	BCL	CAA-C2A-C3A	-2.52	105.96	113.22
5	M	1304	BCL	C16-C15-C13	-2.44	107.40	115.49
5	L	1283	BCL	O2A-CGA-O1A	-2.43	117.21	123.49
5	L	1282	BCL	C1D-CHD-C4C	-2.43	122.36	126.07
5	L	1282	BCL	CHB-C4A-NA	-2.37	121.24	124.51
6	L	1284	BPH	OBD-CAD-CBD	-2.37	122.37	125.94
6	L	1284	BPH	C1B-NB-C4B	-2.36	101.85	106.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1283	BCL	OBD-CAD-CBD	-2.32	122.44	125.94
5	M	1303	BCL	OBD-CAD-CBD	-2.31	122.45	125.94
5	L	1283	BCL	C3C-C4C-CHD	-2.31	118.17	123.33
5	M	1304	BCL	O2A-CGA-O1A	-2.29	117.59	123.49
13	M	1314	SPO	C21-C20-C19	-2.28	118.35	123.39
12	M	1313	U10	C11-C9-C8	-2.27	116.75	121.05
5	L	1282	BCL	O2D-CGD-O1D	-2.25	119.14	123.79
7	L	1285[B]	UQ2	C10-C9-C8	-2.25	119.08	123.50
7	L	1285[A]	UQ2	C10-C9-C8	-2.25	119.09	123.50
5	L	1282	BCL	CMA-C3A-C2A	-2.24	104.44	114.35
13	M	1314	SPO	C14-C15-C16	-2.24	116.31	123.13
5	L	1283	BCL	CHC-C1C-NC	-2.23	121.43	124.51
5	M	1304	BCL	CMD-C2D-C3D	-2.23	120.73	125.09
6	M	1312	BPH	C3B-C2B-C1B	-2.22	102.20	105.77
7	L	1285[A]	UQ2	O4-C4-C3	-2.22	115.98	120.79
6	L	1284	BPH	C7-C6-C5	-2.18	106.63	113.06
5	M	1303	BCL	O2D-CGD-O1D	-2.17	119.31	123.79
5	M	1303	BCL	CHA-C1A-NA	-2.16	120.74	126.06
5	M	1304	BCL	C3C-C4C-CHD	-2.12	118.60	123.33
5	M	1303	BCL	O2A-CGA-O1A	-2.09	118.09	123.49
10	M	1306	LDA	O1-N1-CM2	-2.09	106.26	109.05
5	L	1283	BCL	CAA-C2A-C3A	-2.07	107.27	113.22
6	L	1284	BPH	OBD-CAD-C3D	-2.06	124.16	128.35
6	M	1312	BPH	C1C-NC-C4C	-2.03	108.35	110.44
5	M	1304	BCL	O1D-CGD-CBD	-2.03	121.72	124.62
5	L	1283	BCL	CHA-C1A-NA	-2.01	121.11	126.06
5	L	1283	BCL	O2D-CGD-O1D	-2.01	119.63	123.79
6	L	1284	BPH	C4A-NA-C1A	2.08	110.07	108.21
6	M	1312	BPH	C4-C3-C5	2.10	118.61	115.41
13	M	1314	SPO	C24-C23-C25	2.10	121.60	118.10
5	L	1282	BCL	C14-C13-C12	2.16	119.36	111.08
5	L	1283	BCL	CED-O2D-CGD	2.16	121.06	115.99
5	L	1283	BCL	C4-C3-C5	2.36	119.02	115.41
5	M	1304	BCL	OBB-CAB-C3B	2.36	123.75	120.00
12	M	1313	U10	C35-C34-C36	2.37	119.02	115.41
6	M	1312	BPH	CED-O2D-CGD	2.38	121.56	115.99
5	L	1282	BCL	CED-O2D-CGD	2.38	121.56	115.99
6	L	1284	BPH	CED-O2D-CGD	2.42	121.66	115.99
13	M	1314	SPO	C8-C7-C6	2.42	122.12	118.10
6	M	1312	BPH	O2A-CGA-CBA	2.42	119.28	111.90
5	L	1283	BCL	CMB-C2B-C3B	2.46	129.89	125.09
13	M	1314	SPO	C13-C12-C11	2.50	122.26	118.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	1304	BCL	C4-C3-C5	2.56	119.31	115.41
13	M	1314	SPO	C18-C17-C16	2.62	122.45	118.10
10	M	1305	LDA	O1-N1-C1	2.71	113.33	110.27
6	L	1284	BPH	CMB-C2B-C1B	2.73	129.51	125.06
13	M	1314	SPO	C34-C33-C35	2.76	119.62	115.41
6	M	1312	BPH	CAC-C3C-C4C	2.81	119.90	112.67
5	M	1304	BCL	CHD-C4C-NC	2.87	128.38	125.06
6	M	1312	BPH	C2B-C1B-NB	2.92	114.10	109.73
6	L	1284	BPH	O2A-CGA-CBA	2.98	120.99	111.90
6	L	1284	BPH	C2B-C1B-NB	3.06	114.31	109.73
5	L	1283	BCL	O2A-CGA-CBA	3.13	121.43	111.90
7	L	1285[B]	UQ2	C10-C9-C11	3.13	120.19	115.41
12	M	1313	U10	C15-C14-C16	3.15	120.22	115.41
5	M	1304	BCL	CED-O2D-CGD	3.18	123.45	115.99
7	L	1285[A]	UQ2	C10-C9-C11	3.19	120.28	115.41
7	L	1285[A]	UQ2	CM3-O3-C3	3.21	128.03	116.61
5	M	1303	BCL	O2A-CGA-CBA	3.37	122.18	111.90
12	M	1313	U10	C25-C24-C26	3.52	120.78	115.41
5	L	1282	BCL	O2A-CGA-CBA	3.53	122.64	111.90
5	M	1304	BCL	O2A-CGA-CBA	3.85	123.64	111.90
13	M	1314	SPO	C29-C28-C30	3.87	121.32	115.41
12	M	1313	U10	C10-C9-C11	4.18	121.80	115.41
5	L	1282	BCL	CMB-C2B-C3B	4.24	133.38	125.09
6	M	1312	BPH	C3C-C4C-NC	4.32	112.26	107.93
5	M	1304	BCL	CMB-C2B-C3B	4.57	134.03	125.09
5	M	1303	BCL	CMB-C2B-C3B	4.61	134.10	125.09
12	M	1313	U10	C30-C29-C31	5.18	123.32	115.41
6	L	1284	BPH	C3C-C4C-NC	5.40	113.34	107.93
5	M	1303	BCL	O2D-CGD-CBD	6.15	119.74	111.30
5	L	1282	BCL	O2D-CGD-CBD	6.39	120.07	111.30
5	M	1304	BCL	O2D-CGD-CBD	6.78	120.60	111.30
5	L	1283	BCL	O2D-CGD-CBD	7.11	121.05	111.30
6	M	1312	BPH	O2D-CGD-CBD	7.18	121.14	111.30
6	L	1284	BPH	O2D-CGD-CBD	8.69	123.22	111.30

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	L	1283	BCL	C8
5	L	1283	BCL	C13
5	L	1282	BCL	C8
5	L	1282	BCL	C13

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Mol	Chain	Res	Type	Atom
5	M	1303	BCL	C8
5	M	1303	BCL	C13
5	M	1304	BCL	C8
5	M	1304	BCL	C13

There are no torsion outliers.

There are no ring outliers.

16 monomers are involved in 61 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	1251	GOL	3	0
5	L	1282	BCL	4	0
5	L	1283	BCL	8	0
6	L	1284	BPH	6	0
7	L	1285[A]	UQ2	4	0
7	L	1285[B]	UQ2	2	0
4	L	1288	GOL	1	0
5	M	1303	BCL	5	0
5	M	1304	BCL	11	0
10	M	1305	LDA	4	0
10	M	1307	LDA	7	0
10	M	1308	LDA	3	0
10	M	1309	LDA	3	0
6	M	1312	BPH	9	0
12	M	1313	U10	1	0
13	M	1314	SPO	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	H	241/260 (92%)	-0.32	7 (2%)	55	60	28, 36, 48, 83	0
2	L	281/281 (100%)	-0.46	7 (2%)	61	65	25, 34, 59, 69	0
3	M	303/307 (98%)	-0.29	8 (2%)	59	63	24, 39, 62, 74	0
All	All	825/848 (97%)	-0.36	22 (2%)	58	62	24, 37, 60, 83	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	M	1	ALA	7.3
1	H	250	SER	7.1
1	H	251	VAL	5.4
2	L	59	TRP	5.0
1	H	249	LYS	4.3
2	L	276	PRO	4.2
2	L	281	GLY	4.1
3	M	148	TRP	3.4
2	L	277	GLY	2.9
3	M	80	TRP	2.8
1	H	15	LEU	2.7
2	L	271	TRP	2.7
1	H	51	ALA	2.7
3	M	101	TYR	2.6
3	M	106	ALA	2.5
1	H	18	TYR	2.4
3	M	2	GLU	2.3
3	M	82	PRO	2.3
3	M	301	HIS	2.2
2	L	270	PRO	2.1
2	L	202	LYS	2.0
1	H	12	LEU	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. 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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
9	HTO	L	1287	10/10	0.78	0.38	13.13	82,84,85,86	0
10	LDA	M	1308	16/16	0.40	0.49	12.11	106,110,119,120	0
10	LDA	M	1309	16/16	0.47	0.34	10.97	95,101,111,111	0
4	GOL	H	1251	6/6	0.80	0.23	8.11	54,60,62,63	0
7	UQ2	L	1285[B]	23/23	0.87	0.26	7.25	8,12,17,18	23
7	UQ2	L	1285[A]	23/23	0.87	0.26	6.69	45,50,73,75	23
10	LDA	M	1310	16/16	0.26	0.52	6.29	91,99,109,110	0
10	LDA	M	1306	16/16	0.83	0.36	5.90	61,65,84,85	0
10	LDA	M	1305	16/16	0.81	0.28	5.69	42,65,72,72	0
13	SPO	M	1314	42/42	0.87	0.22	2.77	32,46,70,74	0
10	LDA	M	1307	16/16	0.78	0.23	2.71	53,57,66,66	0
12	U10	M	1313	48/63	0.91	0.18	1.30	25,39,71,73	0
4	GOL	L	1288	6/6	0.90	0.21	0.95	40,48,49,54	0
6	BPH	M	1312	65/65	0.95	0.14	0.84	27,38,100,103	0
5	BCL	M	1303	66/66	0.97	0.13	0.81	23,30,83,85	0
6	BPH	L	1284	65/65	0.98	0.12	0.39	22,28,40,42	0
5	BCL	M	1304	66/66	0.98	0.14	0.36	24,28,54,63	0
5	BCL	L	1282	66/66	0.97	0.12	0.30	22,29,46,52	0
5	BCL	L	1283	66/66	0.97	0.13	0.11	21,27,55,58	0
8	PO4	L	1286	5/5	0.97	0.11	-0.80	62,63,63,65	0
11	FE	M	1311	1/1	0.99	0.03	-2.99	26,26,26,26	0
4	GOL	M	1315	6/6	0.70	0.25	-	97,98,99,99	0
4	GOL	H	1253	6/6	0.42	0.41	-	92,96,96,96	0
4	GOL	H	1252	6/6	0.67	0.40	-	80,81,81,82	0

6.5 Other polymers

There are no such residues in this entry.