



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:26 PM GMT

PDB ID : 1FNQ  
Title : CRYSTAL STRUCTURE ANALYSIS OF THE MUTANT REACTION CENTER PRO L209-> GLU FROM THE PHOTOSYNTHETIC PURPLE BACTERIUM RHODOBACTER SPHAEROIDES  
Authors : Kuglstatter, A.; Ermler, U.; Michel, H.; Baciou, L.; Fritzsche, G.  
Deposited on : 2000-08-23  
Resolution : 2.60 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

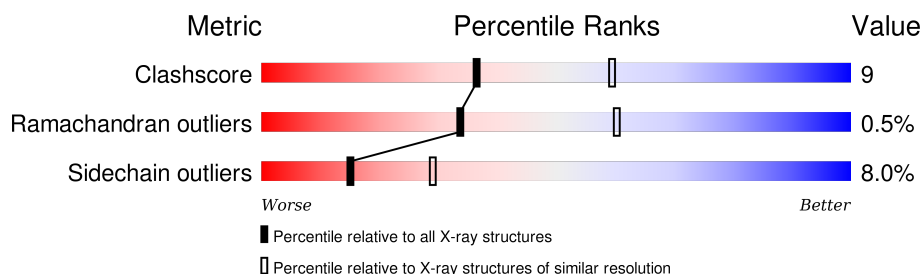
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	281	
2	M	307	
3	H	260	

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
6	BCL	L	304	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	BCL	M	801	X	-	-	-

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 7248 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 L CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	281	Total	C	N	O	S	0	0	0
			2234	1507	355	364	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	209	GLU	PRO	ENGINEERED	UNP P02954

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	302	Total	C	N	O	S	0	0	0
			2404	1603	394	397	10			

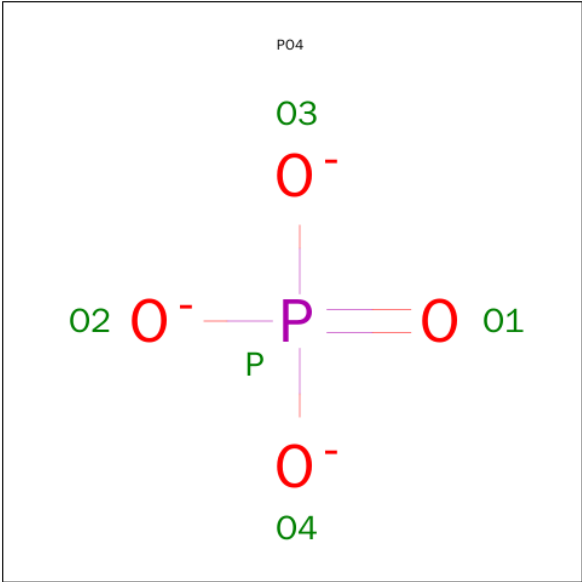
- Molecule 3 is a protein called REACTION CENTER PROTEIN H CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	239	Total	C	N	O	S	0	0	0
			1823	1166	313	335	9			

- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

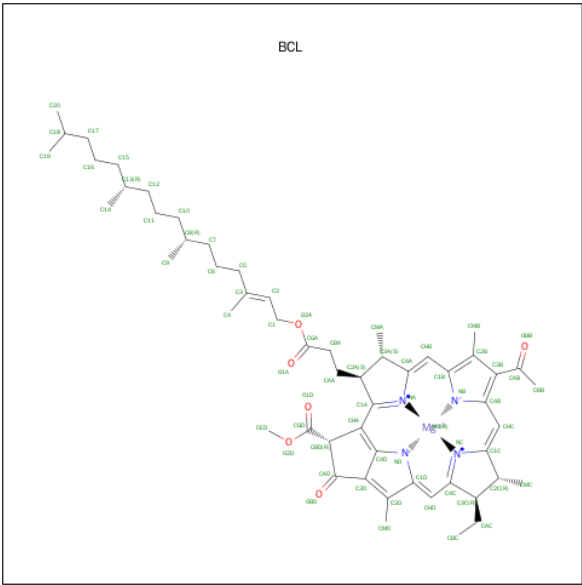
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	M	1	Total	Fe	0	0
			1	1		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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

- Molecule 6 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: C<sub>55</sub>H<sub>74</sub>MgN<sub>4</sub>O<sub>6</sub>).



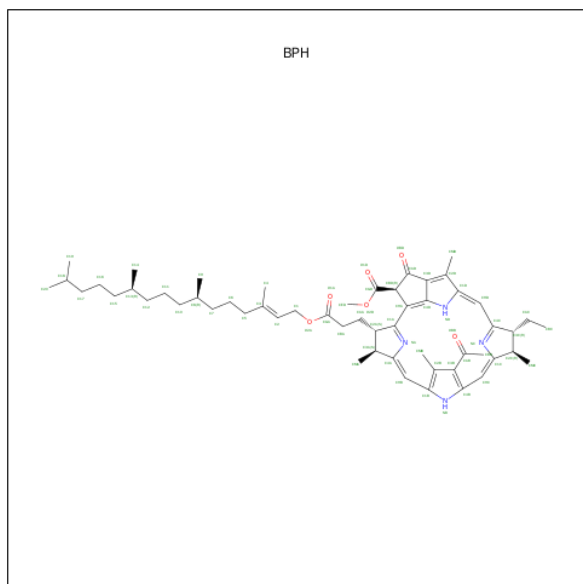
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
6	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
6	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

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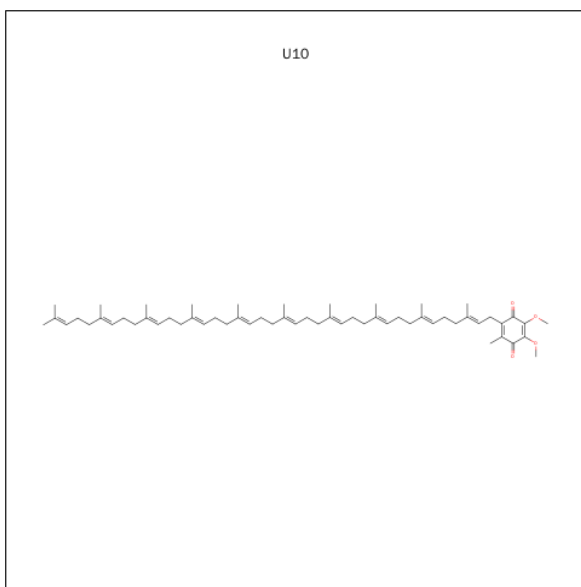
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 7 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula:  $C_{55}H_{76}N_4O_6$ ).



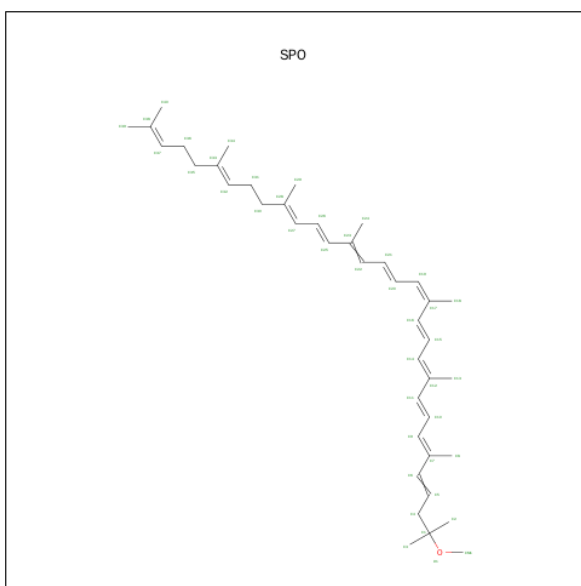
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	M	1	Total	C	N	O	0	0
			65	55	4	6		
7	L	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 8 is UBIQUINONE-10 (three-letter code: U10) (formula:  $C_{59}H_{90}O_4$ ).



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

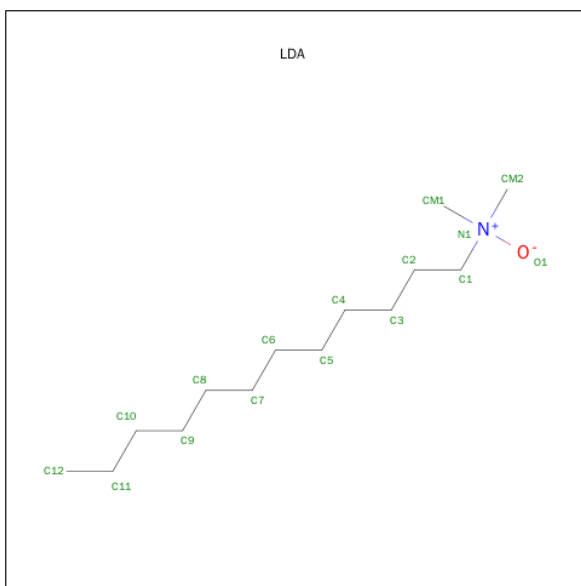
- Molecule 9 is SPHEROIDENE (three-letter code: SPO) (formula:  $C_{41}H_{60}O$ ).



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

- Molecule 10 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula:

C<sub>14</sub>H<sub>31</sub>NO).



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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	H	64	Total O 64 64	0	0
11	L	34	Total O 34 34	0	0
11	M	39	Total O 39 39	0	0

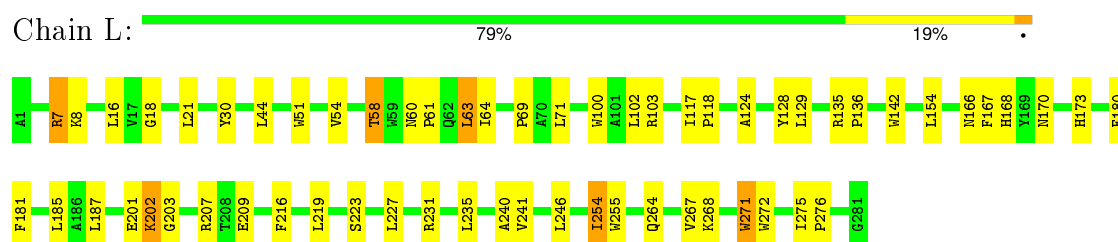


### 3 Residue-property plots

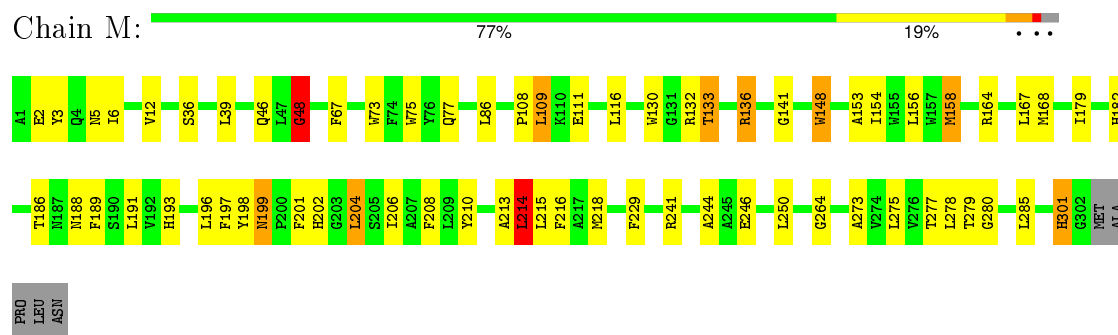
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

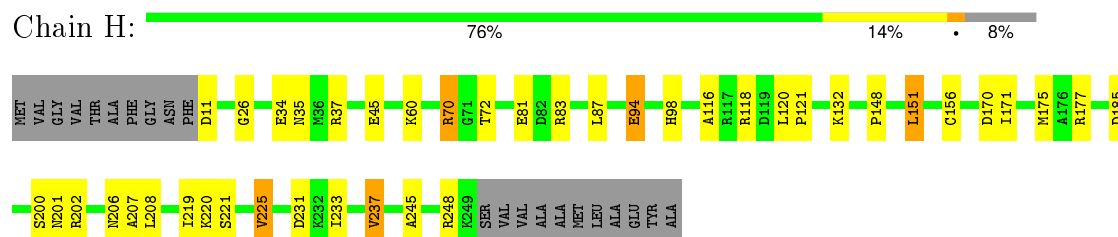
#### • Molecule 1: REACTION CENTER PROTEIN L CHAIN



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



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



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	141.53Å 141.53Å 187.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.60	Depositor
% Data completeness (in resolution range)	93.1 (50.00-2.60)	Depositor
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 0.3	Depositor
R, $R_{free}$	0.217 , 0.247	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7248	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCL, LDA, BPH, PO4, FE, SPO, 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	L	0.44	0/2321	0.49	0/3175
2	M	0.44	0/2496	0.49	1/3407 (0.0%)
3	H	0.41	0/1871	0.51	0/2545
All	All	0.43	0/6688	0.50	1/9127 (0.0%)

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	M	0	2
3	H	0	1
All	All	0	3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	214	LEU	CA-CB-CG	5.86	128.78	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	H	118	ARG	Sidechain
2	M	198	TYR	Sidechain
2	M	48	GLY	Peptide

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	2234	0	2186	39	0
2	M	2404	0	2311	47	0
3	H	1823	0	1831	27	0
4	M	1	0	0	0	0
5	M	5	0	0	0	0
6	L	132	0	148	12	0
6	M	132	0	148	17	0
7	L	65	0	76	8	0
7	M	65	0	76	11	0
8	L	48	0	63	2	0
8	M	48	0	63	2	0
9	M	42	0	60	2	0
10	H	32	0	62	3	0
10	L	16	0	31	0	0
10	M	64	0	124	4	0
11	H	64	0	0	5	0
11	L	34	0	0	1	0
11	M	39	0	0	1	0
All	All	7248	0	7179	135	0

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

All (135) 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:304:BCL:HBB2	6:L:304:BCL:HHC	1.43	1.01
6:M:801:BCL:HHC	6:M:801:BCL:HBB2	1.43	0.98
7:L:402:BPH:HHC	7:L:402:BPH:HBB3	1.51	0.92
1:L:202:LYS:HG3	1:L:203:GLY:H	1.36	0.90
1:L:241:VAL:HG21	7:L:402:BPH:HAC2	1.57	0.85
6:M:802:BCL:HHC	6:M:802:BCL:HBB2	1.62	0.81
2:M:153:ALA:HB2	7:M:401:BPH:HAC1	1.62	0.81
6:L:302:BCL:HBB3	6:L:302:BCL:HHC	1.63	0.80
6:L:302:BCL:HHC	6:L:302:BCL:CBB	2.12	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:802:BCL:HHC	6:M:802:BCL:CBB	2.15	0.77
2:M:204:LEU:HB3	2:M:279:THR:HG21	1.67	0.76
2:M:46:GLN:HG2	2:M:48:GLY:H	1.49	0.75
1:L:168:HIS:NE2	6:L:302:BCL:HBB2	2.03	0.73
1:L:264:GLN:HA	1:L:267:VAL:HG12	1.70	0.73
1:L:124:ALA:HB2	7:L:402:BPH:HAC1	1.74	0.69
2:M:188:ASN:HB2	11:M:836:HOH:O	1.93	0.68
6:L:304:BCL:CBB	6:L:304:BCL:HHC	2.22	0.67
1:L:167:PHE:HB3	6:L:302:BCL:HMC3	1.77	0.66
2:M:109:LEU:H	2:M:109:LEU:HD22	1.61	0.66
7:L:402:BPH:HBB2	2:M:210:TYR:HB3	1.78	0.65
1:L:69:PRO:HG2	1:L:142:TRP:HB2	1.78	0.65
1:L:7:ARG:HH21	3:H:98:HIS:CD2	2.15	0.65
6:L:304:BCL:H61	8:M:501:U10:H203	1.79	0.64
2:M:46:GLN:HE21	2:M:48:GLY:HA3	1.63	0.63
10:M:704:LDA:HM12	10:H:706:LDA:HM11	1.80	0.62
3:H:148:PRO:HA	3:H:151:LEU:HD22	1.81	0.62
6:M:801:BCL:HHC	6:M:801:BCL:CBB	2.23	0.61
7:M:401:BPH:HHC	7:M:401:BPH:HBB3	1.85	0.58
2:M:275:LEU:HD23	2:M:278:LEU:HD23	1.86	0.58
1:L:181:PHE:CD2	7:M:401:BPH:HBB1	2.39	0.58
1:L:30:TYR:O	1:L:103:ARG:NH2	2.37	0.57
2:M:46:GLN:HG2	2:M:48:GLY:N	2.19	0.57
1:L:223:SER:HA	8:L:502:U10:O2	2.05	0.57
1:L:58:THR:HG21	1:L:63:LEU:HD23	1.87	0.57
1:L:202:LYS:HG3	1:L:203:GLY:N	2.14	0.56
2:M:197:PHE:CZ	6:M:802:BCL:HBB2	2.40	0.56
3:H:148:PRO:O	3:H:151:LEU:HB2	2.06	0.56
2:M:241:ARG:HD3	2:M:246:GLU:HG2	1.88	0.56
2:M:130:TRP:O	2:M:133:THR:HG22	2.05	0.55
7:L:402:BPH:HHC	7:L:402:BPH:CBB	2.32	0.55
1:L:135:ARG:HB3	1:L:136:PRO:HD3	1.88	0.55
2:M:197:PHE:HZ	6:M:802:BCL:HBB2	1.71	0.55
3:H:94:GLU:HG3	11:H:752:HOH:O	2.06	0.55
6:M:801:BCL:HBB3	6:M:802:BCL:H41	1.89	0.55
2:M:199:ASN:HD22	2:M:199:ASN:C	2.09	0.55
2:M:199:ASN:ND2	2:M:201:PHE:H	2.05	0.54
3:H:45:GLU:HG3	11:H:752:HOH:O	2.06	0.54
2:M:3:TYR:CZ	2:M:5:ASN:HA	2.42	0.54
1:L:271:TRP:N	1:L:271:TRP:CD1	2.75	0.54
7:L:402:BPH:HMC3	2:M:213:ALA:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:199:ASN:HD22	2:M:201:PHE:H	1.55	0.54
1:L:187:LEU:HD23	2:M:273:ALA:HB2	1.90	0.53
1:L:7:ARG:NH2	3:H:98:HIS:CD2	2.77	0.53
1:L:170:ASN:HB3	1:L:173:HIS:HB3	1.91	0.53
3:H:11:ASP:HB2	11:H:731:HOH:O	2.09	0.52
3:H:70:ARG:NH1	3:H:121:PRO:O	2.42	0.52
1:L:181:PHE:HB3	7:M:401:BPH:CBB	2.40	0.52
1:L:103:ARG:HG3	11:L:709:HOH:O	2.09	0.52
7:L:402:BPH:CHC	7:L:402:BPH:HBB3	2.33	0.51
7:L:402:BPH:HMC3	2:M:213:ALA:CB	2.41	0.50
3:H:70:ARG:NH1	3:H:120:LEU:HB3	2.26	0.50
1:L:60:ASN:HD22	1:L:61:PRO:HD2	1.76	0.50
1:L:117:ILE:HB	1:L:118:PRO:HD3	1.93	0.50
3:H:34:GLU:O	3:H:37:ARG:HG3	2.12	0.50
2:M:73:TRP:NE1	2:M:77:GLN:NE2	2.60	0.50
6:M:801:BCL:H93	6:M:802:BCL:H191	1.93	0.50
10:M:704:LDA:CM1	10:H:706:LDA:HM11	2.42	0.50
6:L:302:BCL:C1C	6:M:802:BCL:HBB3	2.43	0.49
2:M:154:ILE:O	2:M:158:MET:HB2	2.13	0.49
7:M:401:BPH:H121	7:M:401:BPH:H7C1	1.94	0.49
1:L:71:LEU:H	1:L:71:LEU:HD12	1.77	0.49
3:H:26:GLY:HA3	10:H:706:LDA:H71	1.94	0.49
1:L:231:ARG:HD3	2:M:5:ASN:O	2.12	0.48
1:L:219:LEU:HD12	2:M:132:ARG:NH2	2.28	0.48
3:H:156:CYS:HB3	3:H:206:ASN:O	2.13	0.47
2:M:229:PHE:HB2	2:M:244:ALA:HB2	1.95	0.47
3:H:156:CYS:HB2	3:H:248:ARG:HG3	1.95	0.47
2:M:179:ILE:HG23	6:M:801:BCL:HED1	1.97	0.47
2:M:208:PHE:HE2	10:M:701:LDA:H101	1.80	0.46
2:M:214:LEU:HD22	2:M:218:MET:SD	2.56	0.46
1:L:60:ASN:O	1:L:64:ILE:HG13	2.14	0.46
2:M:136:ARG:HA	2:M:136:ARG:NE	2.31	0.46
2:M:148:TRP:HA	2:M:148:TRP:CE3	2.51	0.46
3:H:245:ALA:HB2	3:H:248:ARG:HH11	1.80	0.46
1:L:8:LYS:HA	3:H:87:LEU:HD11	1.98	0.46
1:L:18:GLY:O	1:L:21:LEU:HB2	2.15	0.46
3:H:233:ILE:O	3:H:237:VAL:HG13	2.17	0.45
1:L:268:LYS:HD3	1:L:268:LYS:HA	1.79	0.45
6:L:302:BCL:HBB3	6:M:802:BCL:HAC2	1.98	0.45
1:L:128:TYR:HD1	6:L:304:BCL:HBB1	1.82	0.45
3:H:34:GLU:OE2	3:H:37:ARG:NH2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:148:TRP:HA	2:M:148:TRP:HE3	1.81	0.45
2:M:277:THR:HG21	7:M:401:BPH:HAC2	1.97	0.45
2:M:204:LEU:CB	2:M:279:THR:HG21	2.43	0.44
3:H:206:ASN:HD21	3:H:248:ARG:HD3	1.82	0.44
7:M:401:BPH:H4C1	7:M:401:BPH:H6C1	1.57	0.44
6:M:801:BCL:HBB2	6:M:801:BCL:CHC	2.29	0.44
2:M:186:THR:HG23	6:M:802:BCL:HMD2	2.00	0.44
3:H:132:LYS:HB2	3:H:171:ILE:HD11	2.00	0.44
9:M:600:SPO:H131	9:M:600:SPO:H15	1.75	0.44
1:L:227:LEU:O	1:L:231:ARG:HG3	2.18	0.44
2:M:264:GLY:HA3	3:H:35:ASN:OD1	2.18	0.43
2:M:36:SER:HB3	2:M:39:LEU:HB2	2.00	0.43
3:H:201:ASN:HD21	3:H:202:ARG:NH1	2.16	0.43
6:L:304:BCL:CHC	6:L:304:BCL:HBB2	2.30	0.43
2:M:164:ARG:O	2:M:168:MET:HG2	2.19	0.43
8:L:502:U10:H1M1	8:L:502:U10:C8	2.47	0.43
2:M:153:ALA:CB	7:M:401:BPH:HAC1	2.43	0.43
2:M:189:PHE:O	2:M:193:HIS:HD2	2.01	0.42
3:H:37:ARG:NH1	3:H:60:LYS:O	2.51	0.42
1:L:254:ILE:HG13	1:L:255:TRP:N	2.33	0.42
3:H:170:ASP:OD1	3:H:177:ARG:HD2	2.18	0.42
6:L:302:BCL:NC	6:M:802:BCL:HBB3	2.33	0.42
1:L:51:TRP:O	1:L:54:VAL:HG22	2.19	0.42
2:M:67:PHE:CD2	7:M:401:BPH:H9C1	2.54	0.42
10:M:704:LDA:HM21	11:H:744:HOH:O	2.19	0.42
1:L:275:ILE:HA	1:L:276:PRO:HD3	1.91	0.42
2:M:280:GLY:HA2	6:M:802:BCL:HED3	2.01	0.42
1:L:201:GLU:HG3	2:M:141:GLY:O	2.19	0.42
2:M:201:PHE:HD2	2:M:279:THR:HG23	1.85	0.42
3:H:220:LYS:HE2	11:H:754:HOH:O	2.20	0.42
1:L:231:ARG:HD2	2:M:6:ILE:O	2.19	0.42
2:M:108:PRO:HG2	2:M:111:GLU:HB2	2.01	0.41
2:M:277:THR:CG2	7:M:401:BPH:HAC2	2.50	0.41
7:M:401:BPH:H3A	7:M:401:BPH:HBA2	1.81	0.41
3:H:207:ALA:HB1	3:H:237:VAL:O	2.21	0.41
9:M:600:SPO:H5	9:M:600:SPO:HM13	2.02	0.41
2:M:202:HIS:O	2:M:206:ILE:HG13	2.21	0.41
1:L:100:TRP:CH2	8:M:501:U10:H251	2.55	0.41
6:M:801:BCL:CBB	6:M:801:BCL:CHC	2.92	0.41
1:L:166:ASN:HD21	1:L:168:HIS:HD1	1.68	0.40
6:M:802:BCL:HAA2	6:M:802:BCL:HBD	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:180:PHE:CE2	1:L:240:ALA:HB1	2.57	0.40
3:H:219:ILE:HG21	3:H:225:VAL:HG13	2.03	0.40
3:H:81:GLU:O	3:H:83:ARG:HG2	2.22	0.40

There are no symmetry-related clashes.

## 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	L	279/281 (99%)	266 (95%)	12 (4%)	1 (0%)	39	65
2	M	300/307 (98%)	281 (94%)	17 (6%)	2 (1%)	26	51
3	H	237/260 (91%)	227 (96%)	9 (4%)	1 (0%)	39	65
All	All	816/848 (96%)	774 (95%)	38 (5%)	4 (0%)	34	60

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	M	301	HIS
3	H	116	ALA
1	L	202	LYS
2	M	48	GLY

### 5.3.2 Protein sidechains [i](#)

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	L	220/220 (100%)	203 (92%)	17 (8%)	16	31
2	M	235/240 (98%)	212 (90%)	23 (10%)	10	19
3	H	194/208 (93%)	182 (94%)	12 (6%)	23	45
All	All	649/668 (97%)	597 (92%)	52 (8%)	15	29

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	7	ARG
1	L	16	LEU
1	L	44	LEU
1	L	58	THR
1	L	63	LEU
1	L	102	LEU
1	L	129	LEU
1	L	154	LEU
1	L	185	LEU
1	L	207	ARG
1	L	209	GLU
1	L	216	PHE
1	L	235	LEU
1	L	246	LEU
1	L	254	ILE
1	L	271	TRP
1	L	272	TRP
2	M	2	GLU
2	M	12	VAL
2	M	75	TRP
2	M	86	LEU
2	M	109	LEU
2	M	116	LEU
2	M	133	THR
2	M	136	ARG
2	M	148	TRP
2	M	156	LEU
2	M	158	MET
2	M	167	LEU
2	M	182	HIS
2	M	191	LEU
2	M	196	LEU
2	M	199	ASN
2	M	204	LEU

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Mol	Chain	Res	Type
2	M	214	LEU
2	M	215	LEU
2	M	216	PHE
2	M	250	LEU
2	M	285	LEU
2	M	301	HIS
3	H	70	ARG
3	H	72	THR
3	H	94	GLU
3	H	151	LEU
3	H	175	MET
3	H	185	ASP
3	H	200	SER
3	H	208	LEU
3	H	221	SER
3	H	225	VAL
3	H	231	ASP
3	H	237	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	62	GLN
1	L	159	ASN
1	L	183	ASN
2	M	25	ASN
2	M	44	ASN
2	M	193	HIS
2	M	199	ASN
3	H	98	HIS
3	H	206	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 18 ligands modelled in this entry, 1 is monoatomic - leaving 17 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	$\# Z  > 2$
10	LDA	H	702	-	15,15,15	4.69	3 (20%)	16,17,17	0.60	0
10	LDA	H	706	-	15,15,15	4.36	3 (20%)	16,17,17	0.55	0
6	BCL	L	302	1	53,74,74	1.22	5 (9%)	57,115,115	1.61	9 (15%)
6	BCL	L	304	1	53,74,74	1.35	4 (7%)	57,115,115	2.08	7 (12%)
7	BPH	L	402	-	64,70,70	1.22	5 (7%)	73,101,101	1.77	10 (13%)
8	U10	L	502	-	48,48,63	1.87	13 (27%)	58,61,79	1.04	5 (8%)
10	LDA	L	705	-	15,15,15	4.36	1 (6%)	16,17,17	0.49	0
7	BPH	M	401	-	64,70,70	1.19	6 (9%)	73,101,101	1.80	12 (16%)
8	U10	M	501	-	48,48,63	2.07	14 (29%)	58,61,79	1.01	3 (5%)
9	SPO	M	600	-	40,41,41	3.16	21 (52%)	45,50,50	2.11	12 (26%)
10	LDA	M	701	-	15,15,15	4.45	2 (13%)	16,17,17	0.52	0
10	LDA	M	703	-	15,15,15	4.25	1 (6%)	16,17,17	0.56	0
10	LDA	M	704	-	15,15,15	4.43	4 (26%)	16,17,17	0.72	0
10	LDA	M	707	-	15,15,15	3.44	1 (6%)	16,17,17	0.68	0
5	PO4	M	800	-	4,4,4	1.41	0	6,6,6	0.30	0
6	BCL	M	801	2	53,74,74	1.23	4 (7%)	57,115,115	2.00	7 (12%)
6	BCL	M	802	2	53,74,74	1.18	4 (7%)	57,115,115	1.92	8 (14%)

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
10	LDA	H	702	-	-	0/13/13/13	0/0/0/0
10	LDA	H	706	-	-	0/13/13/13	0/0/0/0
6	BCL	L	302	1	-	0/37/137/137	0/0/9/9
6	BCL	L	304	1	1/1/21/25	0/37/137/137	0/0/9/9
7	BPH	L	402	-	-	0/54/105/105	0/1/6/6
8	U10	L	502	-	-	0/45/69/87	0/1/1/1
10	LDA	L	705	-	-	0/13/13/13	0/0/0/0
7	BPH	M	401	-	-	0/54/105/105	0/1/6/6
8	U10	M	501	-	-	0/45/69/87	0/1/1/1
9	SPO	M	600	-	-	0/47/47/47	0/0/0/0
10	LDA	M	701	-	-	0/13/13/13	0/0/0/0
10	LDA	M	703	-	-	0/13/13/13	0/0/0/0
10	LDA	M	704	-	-	0/13/13/13	0/0/0/0
10	LDA	M	707	-	-	0/13/13/13	0/0/0/0
5	PO4	M	800	-	-	0/0/0/0	0/0/0/0
6	BCL	M	801	2	1/1/21/25	0/37/137/137	0/0/9/9
6	BCL	M	802	2	-	0/37/137/137	0/0/9/9

All (91) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	H	702	LDA	O1-N1	-17.61	1.22	1.39
10	M	701	LDA	O1-N1	-16.87	1.23	1.39
10	L	705	LDA	O1-N1	-16.60	1.23	1.39
10	H	706	LDA	O1-N1	-16.47	1.23	1.39
10	M	703	LDA	O1-N1	-16.34	1.24	1.39
10	M	704	LDA	O1-N1	-16.24	1.24	1.39
10	M	707	LDA	O1-N1	-13.19	1.27	1.39
8	M	501	U10	C7-C8	-6.36	1.40	1.50
10	M	704	LDA	CM1-N1	-3.85	1.43	1.49
6	L	302	BCL	O2D-CED	-3.74	1.36	1.45
7	M	401	BPH	O2D-CED	-3.21	1.37	1.45
10	H	702	LDA	C1-N1	-3.17	1.45	1.51
8	L	502	U10	O4-C4M	-3.13	1.37	1.45
9	M	600	SPO	C25-C23	-3.08	1.39	1.45
6	M	801	BCL	O2D-CED	-2.99	1.38	1.45
10	M	704	LDA	CM2-N1	-2.98	1.44	1.49
6	M	802	BCL	O2D-CED	-2.96	1.38	1.45
9	M	600	SPO	C11-C12	-2.88	1.39	1.45
9	M	600	SPO	C16-C17	-2.82	1.39	1.45
8	M	501	U10	O4-C4M	-2.74	1.38	1.45
9	M	600	SPO	C6-C7	-2.69	1.39	1.45
10	H	702	LDA	CM1-N1	-2.56	1.45	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	701	LDA	CM1-N1	-2.54	1.45	1.49
9	M	600	SPO	C31-C32	-2.54	1.43	1.50
8	L	502	U10	C7-C8	-2.48	1.46	1.50
8	M	501	U10	O3-C3M	-2.45	1.39	1.45
10	M	704	LDA	C1-N1	-2.44	1.46	1.51
10	H	706	LDA	CM1-N1	-2.34	1.45	1.49
8	L	502	U10	O3-C3M	-2.32	1.39	1.45
7	L	402	BPH	O2D-CED	-2.32	1.39	1.45
10	H	706	LDA	CM2-N1	-2.11	1.46	1.49
6	L	304	BCL	C1-C2	-2.10	1.42	1.49
9	M	600	SPO	C22-C23	2.04	1.38	1.35
7	M	401	BPH	CHC-C1C	2.04	1.40	1.36
7	L	402	BPH	C3D-C4D	2.10	1.44	1.41
8	M	501	U10	C31-C29	2.10	1.56	1.51
9	M	600	SPO	C26-C27	2.11	1.50	1.43
7	M	401	BPH	C3D-C4D	2.14	1.44	1.41
8	M	501	U10	C30-C29	2.18	1.56	1.50
8	L	502	U10	C7-C6	2.23	1.55	1.51
6	L	302	BCL	C4-C3	2.32	1.56	1.50
8	L	502	U10	C38-C39	2.50	1.39	1.32
9	M	600	SPO	C15-C14	2.53	1.51	1.43
8	L	502	U10	O4-C4	2.54	1.43	1.37
9	M	600	SPO	C37-C38	2.64	1.40	1.32
8	M	501	U10	C8-C9	2.74	1.38	1.33
9	M	600	SPO	C10-C9	2.74	1.52	1.43
9	M	600	SPO	C14-C12	2.84	1.39	1.35
8	M	501	U10	C38-C39	2.86	1.41	1.32
6	M	802	BCL	C2-C3	2.87	1.38	1.33
9	M	600	SPO	C9-C7	3.00	1.39	1.35
9	M	600	SPO	C19-C17	3.01	1.39	1.35
8	L	502	U10	O3-C3	3.02	1.45	1.37
7	M	401	BPH	O2D-CGD	3.04	1.40	1.33
6	L	302	BCL	O2A-CGA	3.07	1.42	1.33
8	M	501	U10	O4-C4	3.10	1.45	1.37
6	L	302	BCL	C2-C3	3.23	1.39	1.33
9	M	600	SPO	C32-C33	3.25	1.39	1.33
7	M	401	BPH	O2A-CGA	3.27	1.43	1.33
8	M	501	U10	C18-C19	3.28	1.39	1.33
6	M	802	BCL	O2A-CGA	3.32	1.43	1.33
7	L	402	BPH	O2A-CGA	3.32	1.43	1.33
6	L	304	BCL	C2-C3	3.32	1.39	1.33
8	M	501	U10	C23-C24	3.34	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	L	502	U10	C18-C19	3.35	1.39	1.33
7	M	401	BPH	C2-C3	3.38	1.39	1.33
7	L	402	BPH	C2-C3	3.38	1.39	1.33
8	L	502	U10	C8-C9	3.38	1.39	1.33
8	L	502	U10	C33-C34	3.49	1.39	1.33
6	M	801	BCL	C2-C3	3.49	1.39	1.33
8	L	502	U10	C28-C29	3.50	1.39	1.33
8	M	501	U10	C33-C34	3.52	1.39	1.33
8	M	501	U10	C13-C14	3.52	1.39	1.33
9	M	600	SPO	O1-CM1	3.52	1.54	1.43
8	M	501	U10	C28-C29	3.54	1.39	1.33
8	L	502	U10	C23-C24	3.54	1.39	1.33
8	L	502	U10	C13-C14	3.56	1.40	1.33
6	M	801	BCL	O2D-CGD	3.72	1.42	1.33
6	L	304	BCL	O2A-CGA	4.22	1.46	1.33
7	L	402	BPH	O2D-CGD	4.22	1.44	1.33
6	L	302	BCL	O2D-CGD	4.29	1.44	1.33
6	M	801	BCL	O2A-CGA	4.46	1.46	1.33
6	M	802	BCL	O2D-CGD	4.47	1.44	1.33
9	M	600	SPO	C27-C28	4.64	1.39	1.34
8	M	501	U10	O3-C3	4.97	1.50	1.37
9	M	600	SPO	C26-C25	5.08	1.47	1.34
9	M	600	SPO	C21-C20	5.15	1.49	1.35
6	L	304	BCL	O2D-CGD	6.24	1.49	1.33
9	M	600	SPO	C15-C16	7.19	1.53	1.34
9	M	600	SPO	C10-C11	7.83	1.55	1.34
9	M	600	SPO	C6-C5	7.99	1.54	1.31

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	304	BCL	O1D-CGD-CBD	-7.99	113.17	124.62
6	M	801	BCL	O1D-CGD-CBD	-7.48	113.90	124.62
7	M	401	BPH	O1D-CGD-CBD	-7.30	114.16	124.62
7	L	402	BPH	O1D-CGD-CBD	-7.29	114.17	124.62
6	M	802	BCL	O1D-CGD-CBD	-7.22	114.28	124.62
9	M	600	SPO	C15-C14-C12	-6.52	117.78	127.20
9	M	600	SPO	C4-C5-C6	-4.46	118.32	124.67
6	L	302	BCL	O1D-CGD-CBD	-4.43	118.27	124.62
9	M	600	SPO	C20-C19-C17	-3.97	121.46	127.20
9	M	600	SPO	C21-C22-C23	-3.69	121.86	127.20
9	M	600	SPO	C25-C23-C22	-3.58	113.22	118.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	M	600	SPO	C20-C21-C22	-3.56	115.52	123.39
6	M	802	BCL	OBD-CAD-CBD	-3.44	120.75	125.94
7	L	402	BPH	OBD-CAD-CBD	-3.25	121.04	125.94
6	M	801	BCL	OBD-CAD-CBD	-3.25	121.04	125.94
9	M	600	SPO	C15-C16-C17	-3.24	116.78	126.32
9	M	600	SPO	C10-C9-C7	-3.19	122.58	127.20
7	M	401	BPH	OBD-CAD-CBD	-3.13	121.22	125.94
6	L	302	BCL	OBD-CAD-CBD	-3.05	121.34	125.94
6	L	304	BCL	CMB-C2B-C1B	-2.86	123.64	128.36
6	L	304	BCL	OBD-CAD-CBD	-2.82	121.68	125.94
6	M	802	BCL	CMB-C2B-C1B	-2.75	123.82	128.36
7	M	401	BPH	CBB-CAB-C3B	-2.61	114.71	120.52
6	L	302	BCL	CMB-C2B-C1B	-2.58	124.10	128.36
7	L	402	BPH	C3A-C4A-NA	-2.56	109.09	113.57
9	M	600	SPO	C6-C7-C9	-2.49	114.98	118.98
7	L	402	BPH	O2A-CGA-O1A	-2.36	117.40	123.49
7	M	401	BPH	C3A-C4A-NA	-2.35	109.47	113.57
7	M	401	BPH	O2A-CGA-O1A	-2.34	117.45	123.49
9	M	600	SPO	C34-C33-C35	-2.30	111.89	115.41
6	L	302	BCL	O2A-CGA-O1A	-2.28	117.60	123.49
8	L	502	U10	C15-C14-C16	-2.11	112.19	115.41
8	M	501	U10	C20-C19-C21	-2.10	112.20	115.41
7	L	402	BPH	C2A-C1A-NA	-2.10	109.39	112.08
9	M	600	SPO	C10-C11-C12	-2.10	120.14	126.32
6	M	802	BCL	CAC-C3C-C4C	-2.09	107.94	112.58
6	M	801	BCL	CAC-C3C-C4C	-2.08	107.96	112.58
7	M	401	BPH	C2A-C1A-NA	-2.04	109.46	112.08
6	L	302	BCL	CAC-C3C-C4C	-2.04	108.06	112.58
7	L	402	BPH	CED-O2D-CGD	2.01	120.70	115.99
8	L	502	U10	C3M-O3-C3	2.01	123.77	116.61
7	L	402	BPH	C3A-C4A-CHB	2.05	125.65	121.84
8	L	502	U10	C32-C33-C34	2.09	132.31	127.76
8	M	501	U10	C4M-O4-C4	2.12	124.16	116.61
8	L	502	U10	C7-C8-C9	2.16	130.35	126.70
6	M	801	BCL	CMD-C2D-C3D	2.16	129.31	125.09
7	M	401	BPH	CMD-C2D-C3D	2.22	129.43	125.09
7	M	401	BPH	C4A-NA-C1A	2.23	110.20	108.21
7	M	401	BPH	CED-O2D-CGD	2.26	121.29	115.99
8	L	502	U10	C17-C18-C19	2.35	132.87	127.76
6	L	304	BCL	CMD-C2D-C3D	2.36	129.71	125.09
7	L	402	BPH	C4A-NA-C1A	2.39	110.34	108.21
6	M	802	BCL	CED-O2D-CGD	2.45	121.73	115.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	M	401	BPH	OBB-CAB-C3B	2.45	125.04	120.31
8	M	501	U10	C7-C8-C9	2.61	131.12	126.70
9	M	600	SPO	C8-C7-C6	2.67	122.54	118.10
6	L	302	BCL	CED-O2D-CGD	2.71	122.34	115.99
6	L	304	BCL	C4A-NA-C1A	2.84	110.03	106.36
6	M	802	BCL	C4A-NA-C1A	2.87	110.07	106.36
6	L	302	BCL	C4A-NA-C1A	3.06	110.32	106.36
6	L	304	BCL	O2A-CGA-CBA	3.10	121.34	111.90
6	M	801	BCL	C4A-NA-C1A	3.14	110.42	106.36
6	M	802	BCL	O2A-CGA-CBA	3.39	122.24	111.90
7	L	402	BPH	O2A-CGA-CBA	3.43	122.36	111.90
6	L	302	BCL	O2A-CGA-CBA	3.45	122.41	111.90
6	M	801	BCL	O2A-CGA-CBA	3.51	122.58	111.90
7	M	401	BPH	O2A-CGA-CBA	3.64	123.00	111.90
6	L	302	BCL	O2D-CGD-CBD	6.53	120.26	111.30
6	M	802	BCL	O2D-CGD-CBD	8.50	122.96	111.30
7	M	401	BPH	O2D-CGD-CBD	8.94	123.57	111.30
7	L	402	BPH	O2D-CGD-CBD	9.23	123.96	111.30
6	M	801	BCL	O2D-CGD-CBD	9.36	124.14	111.30
6	L	304	BCL	O2D-CGD-CBD	9.85	124.81	111.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	M	801	BCL	C8
6	L	304	BCL	C13

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 55 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	H	706	LDA	3	0
6	L	302	BCL	7	0
6	L	304	BCL	5	0
7	L	402	BPH	8	0
8	L	502	U10	2	0
7	M	401	BPH	11	0
8	M	501	U10	2	0
9	M	600	SPO	2	0
10	M	701	LDA	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	M	704	LDA	3	0
6	M	801	BCL	7	0
6	M	802	BCL	12	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.