

Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 01:32 pm GMT

PDB ID	:	8C87
Title	:	Double mutant $A(L172)C/L(L246)C$ structure of Photosynthetic Reaction
		Center From Cereibacter sphaeroides strain RV
Authors	:	Gabdulkhakov, A.; Selikhanov, G.; Fufina, T.; Vasilieva, L.; Atamas, A.;
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Deposited on	:	2023-01-19
Resolution	:	2.45 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 https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.45 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	Similar resolution
	$(\# { m Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
R_{free}	130704	$1544 \ (2.48-2.44)$
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	Н	251	3% 68%	25%	• •
2	L	281	70%	28%	
3	М	303	73%	25%	

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
4	LDA	М	410	-	-	-	Х



2 Entry composition (i)

There are 15 unique types of molecules in this entry. The entry contains 7434 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		At	oms			ZeroOcc	AltConf	Trace
1	Н	240	Total 1845	C 1184	N 314	O 338	S 9	0	2	0

• Molecule 2 is a protein called Reaction center protein L chain.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	L	281	Total 2240	C 1511	N 356	O 363	S 10	0	1	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	172	CYS	ALA	engineered mutation	UNP P0C0Y8
L	178	THR	SER	engineered mutation	UNP P0C0Y8
L	246	CYS	LEU	engineered mutation	UNP P0C0Y8

• Molecule 3 is a protein called Reaction center protein M chain.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
3	М	302	Total 2414	C 1613	N 394	O 397	S 10	0	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
М	8	THR	SER	engineered mutation	UNP P0C0Y9

• Molecule 4 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
4	Ц	1	Total C N O	0	0	
4	п	L	16 14 1 1	0	0	
4	Ц	1	Total C N O	0	0	
4	11	T	16 14 1 1	0	0	
4	н	1	Total C N O	0	0	
4	11	T	16 14 1 1	0	0	
4	н	1	Total C N O	0	0	
4	11	T	16 14 1 1	0	0	
1	L	1	Total C N O	0	0	
	Ľ	I	16 14 1 1	0	0	
4	L	1	Total C N O	0	0	
1		1	16 14 1 1	0	0	
4	М	1	Total C N O	0	0	
		T	16 14 1 1	0	Ŭ	
4	М	1	Total C N O	0	0	
-		-	16 14 1 1	Ŭ	Ŭ	
4	М	1	Total C N O	0	0	
		-	16 14 1 1	Ŭ	Ŭ	
4	М	1	Total C N O	0	0	
		1	16 14 1 1	0	0	
4	М	1	Total C N O	0	0	
		-		Ŭ,		
4	М	1	Total C N O	0	0	
	111	±	16 14 1 1	Ŭ		

 $\bullet\,$ Molecule 5 is UNKNOWN LIGAND (three-letter code: UNL) (formula:).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	Н	2	$\begin{array}{cc} \text{Total} & \text{C} \\ 27 & 27 \end{array}$	0	0
5	L	2	Total C 22 22	0	0
5	М	1	Total C 12 12	0	0

• Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	Н	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
6	М	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0

• Molecule 7 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: $C_{21}H_{40}O_4$) (labeled as "Ligand of Interest" by depositor).



OLC

Mol	Chain	Residues	At	\mathbf{oms}		ZeroOcc	AltConf
7	L	1	Total 25	C 21	0 4	0	0

• Molecule 8 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: $C_{55}H_{74}MgN_4O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		At	oms			ZeroOcc	AltConf
8	т	1	Total	С	Mg	Ν	Ο	0	0
0		T	66	55	1	4	6	0	0
8	т	1	Total	С	Mg	Ν	Ο	0	0
0			66	55	1	4	6	0	



α \cdots 1	C		
Continued	from	previous	page
	9	1	1 0

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf
0	о т	1	Total	С	Mg	Ν	Ο	0	0
0		L	66	55	1	4	6		
0	М	1	Total	С	Mg	Ν	Ο	0	0
0	111		66	55	1	4	6	0	0

• Molecule 9 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: $C_{55}H_{76}N_4O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	A	Aton	ns		ZeroOcc	AltConf
9	L	1	Total 65	$\begin{array}{c} \mathrm{C} \\ 55 \end{array}$	N 4	O 6	0	0
9	М	1	Total 65	$\begin{array}{c} \mathrm{C} \\ 55 \end{array}$	N 4	O 6	0	0

• Molecule 10 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula: C₇H₁₆O₃).





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

• Molecule 11 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	М	1	Total 81	C 62	O 17	Р 2	0	0

• Molecule 12 is FE (III) ION (three-letter code: FE) (formula: Fe) (labeled as "Ligand of



Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	М	1	Total Fe 1 1	0	0

• Molecule 13 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
13	М	1	Total 48	C 44	0 4	0	0

• Molecule 14 is SPEROIDENONE (three-letter code: SPN) (formula: $C_{41}H_{70}O_2$) (labeled as "Ligand of Interest" by depositor).



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01	7	

Mo	Chain	Residues	Atoms		ZeroOcc	AltConf	
14	М	1	Total 43	C 41	O 2	0	0

• Molecule 15 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	Н	28	TotalO2828	0	0
15	L	12	Total O 12 12	0	0
15	М	22	TotalO2222	0	0



Residue-property plots (i) 3

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.



• Molecule 1: Reaction center protein H chain





• Molecule 3: Reaction center protein M chain





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants	99.72Å 99.72Å 239.11Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
$\mathbf{P}_{\text{ascolution}}\left(\mathring{\mathbf{A}}\right)$	23.45 - 2.45	Depositor
Resolution (A)	23.45 - 2.30	EDS
% Data completeness	99.3 (23.45-2.45)	Depositor
(in resolution range)	$96.8\ (23.45 ext{-}2.30)$	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.37 (at 2.31 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0352, PHENIX 1.20.1_4487	Depositor
B B a	0.259 , 0.308	Depositor
It, Itfree	0.266 , 0.311	DCC
R_{free} test set	2688 reflections $(5.06%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	22.2	Xtriage
Anisotropy	0.292	Xtriage
Bulk solvent $k_{sol}(e/A^3), B_{sol}(A^2)$	0.35 , 53.7	EDS
L-test for $twinning^2$	$< L > = 0.40, < L^2 > = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	7434	wwPDB-VP
Average B, all atoms $(Å^2)$	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.24% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SPN, UNL, FE, HTO, LDA, OLC, CDL, EDO, BPH, BCL, 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).

Mal	Chain	Bond	lengths	Bo	nd angles
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	Н	0.49	0/1900	0.72	1/2584~(0.0%)
2	L	0.51	0/2328	0.67	0/3186
3	М	0.48	0/2509	0.63	0/3426
All	All	0.49	0/6737	0.67	1/9196~(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
3	М	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	Н	98	HIS	C-N-CA	-5.69	107.48	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	М	267	ARG	Sidechain

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Н	1845	0	1857	58	0
2	L	2240	0	2193	66	0
3	М	2414	0	2334	74	0
4	Н	64	0	124	13	0
4	L	32	0	62	2	0
4	М	96	0	186	8	0
5	Н	27	0	0	0	0
5	L	22	0	0	0	0
5	М	12	0	0	0	0
6	Н	4	0	6	0	0
6	М	4	0	6	2	0
7	L	25	0	40	5	0
8	L	198	0	222	17	0
8	М	66	0	74	6	0
9	L	65	0	76	2	0
9	М	65	0	76	4	0
10	L	20	0	32	3	0
11	М	81	0	106	11	0
12	М	1	0	0	0	0
13	М	48	0	63	4	0
14	М	43	0	70	8	0
15	Н	28	0	0	1	0
15	L	12	0	0	0	0
15	М	22	0	0	0	0
All	All	7434	0	7527	202	0

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.

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 14.

All (202) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
11:M:401:CDL:H312	11:M:401:CDL:H521	1.54	0.88
1:H:25:ALA:HB1	4:H:305:LDA:H72	1.55	0.88
2:L:56:GLN:HG2	2:L:58:THR:HG22	1.69	0.75
3:M:13:ARG:NH2	3:M:37:THR:OG1	2.20	0.74
4:H:305:LDA:H42	11:M:401:CDL:H232	1.71	0.71
8:L:302:BCL:HBB2	8:M:402:BCL:H111	1.73	0.71
1:H:171:ILE:HB	1:H:172:PRO:HD3	1.74	0.70



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:H:12:LEU:HD23	3:M:290:VAL:HG21	1.72	0.70
1:H:156:CYS:HB2	1:H:248:ARG:HG3	1.79	0.65
1:H:152:PRO:HB2	1:H:160:ILE:HD12	1.78	0.64
1:H:58:LEU:HD22	1:H:59:PRO:HD2	1.78	0.63
2:L:200:PRO:HB3	2:L:207:ARG:HD3	1.80	0.63
3:M:271:TRP:HH2	11:M:401:CDL:H362	1.63	0.63
1:H:168:TRP:HB2	1:H:178:PHE:HB2	1.80	0.62
4:H:307:LDA:H92	2:L:105:VAL:HG21	1.81	0.62
1:H:118:ARG:HG3	1:H:118:ARG:HH11	1.63	0.62
3:M:218:MET:HG2	3:M:252:TRP:CH2	2.35	0.62
1:H:29:TYR:HB2	4:H:305:LDA:H61	1.82	0.61
3:M:70:ILE:HD13	3:M:177:TYR:HB3	1.83	0.61
1:H:87:LEU:HD23	1:H:100:PRO:HA	1.82	0.61
1:H:148:PRO:HD2	1:H:167:ILE:HD11	1.82	0.60
2:L:77:GLY:HA2	2:L:87:GLN:HE22	1.66	0.60
1:H:56:PHE:HE2	4:H:301:LDA:H42	1.67	0.60
2:L:269:LEU:HD13	2:L:271:TRP:CZ2	2.37	0.60
2:L:69:PRO:HG2	2:L:142:TRP:HB2	1.84	0.60
2:L:272:TRP:CD1	3:M:87:ARG:HG3	2.37	0.60
1:H:170:ASP:O	1:H:174:GLN:N	2.34	0.60
2:L:265:TRP:O	2:L:269:LEU:HG	2.02	0.59
3:M:21:THR:HG23	3:M:26:LEU:HD21	1.85	0.59
2:L:264:GLN:NE2	2:L:268:LYS:HE2	2.17	0.58
1:H:11:ASP:H	1:H:14:SER:HB2	1.69	0.58
2:L:231:ARG:NE	3:M:5:ASN:O	2.35	0.57
3:M:148:TRP:CD2	11:M:401:CDL:H542	2.40	0.57
2:L:75:LEU:HD21	2:L:137:VAL:HA	1.87	0.57
3:M:148:TRP:NE1	11:M:401:CDL:H511	2.20	0.57
2:L:241:VAL:HG21	9:L:305:BPH:HBC3	1.87	0.56
3:M:108:PRO:HG2	3:M:111:GLU:HB2	1.86	0.56
4:H:305:LDA:H82	4:H:306:LDA:H111	1.88	0.55
2:L:16:LEU:HD11	2:L:105:VAL:HG12	1.88	0.55
8:L:302:BCL:CAB	14:M:406:SPN:H162	2.37	0.55
2:L:33:PHE:O	2:L:36:VAL:HB	2.07	0.54
1:H:73:LEU:HD22	3:M:239:ALA:O	2.08	0.54
3:M:117:ILE:HG12	4:M:409:LDA:H72	1.90	0.54
1:H:171:ILE:O	1:H:173:GLU:N	2.41	0.53
3:M:157:TRP:CE2	14:M:406:SPN:HM73	2.44	0.53
1:H:148:PRO:HA	1:H:151:LEU:HD12	1.90	0.53
3:M:274:VAL:HG11	11:M:401:CDL:H731	1.91	0.53
1:H:122:GLU:HB2	1:H:227:LEU:HD21	1.90	0.53



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:L:244:SER:HB3	8:L:303:BCL:HED3	1.91	0.52
1:H:220:LYS:HD2	1:H:220:LYS:C	2.30	0.52
3:M:34:PRO:O	3:M:47:LEU:HB2	2.09	0.52
11:M:401:CDL:OB7	11:M:401:CDL:O1	2.28	0.52
3:M:120:PHE:CD2	4:M:409:LDA:H111	2.44	0.52
2:L:117:ILE:HD11	3:M:222:THR:OG1	2.10	0.52
1:H:89:ARG:O	1:H:89:ARG:HG3	2.10	0.52
3:M:93:SER:OG	3:M:95:GLU:OE2	2.23	0.52
1:H:112:ALA:HA	1:H:235:GLY:O	2.09	0.51
1:H:56:PHE:CE2	4:H:301:LDA:H42	2.44	0.51
1:H:163:LYS:HE3	1:H:182:GLU:OE2	2.10	0.51
3:M:129:TRP:O	3:M:133:THR:HG23	2.10	0.51
1:H:194:GLN:HB3	6:M:412:EDO:H21	1.93	0.51
1:H:29:TYR:CE2	4:H:305:LDA:H12	2.46	0.50
3:M:186:THR:HG23	8:M:402:BCL:HMD2	1.92	0.50
8:M:402:BCL:H2	9:M:403:BPH:HHC	1.92	0.50
3:M:13:ARG:HD3	3:M:35:PHE:CD2	2.47	0.50
1:H:197:LYS:HE3	3:M:1:ALA:O	2.12	0.50
4:H:307:LDA:H12	2:L:109:ARG:HH12	1.77	0.49
2:L:158:SER:HA	8:L:303:BCL:HBC1	1.94	0.49
3:M:256:MET:HB2	13:M:405:U10:H262	1.93	0.49
3:M:2:GLU:O	3:M:4:GLN:NE2	2.45	0.49
1:H:87:LEU:HD12	2:L:8:LYS:HA	1.95	0.49
2:L:180:PHE:CD2	2:L:240:ALA:HB1	2.48	0.49
3:M:162:PHE:CE1	14:M:406:SPN:HM83	2.47	0.49
1:H:62:LYS:HE2	1:H:64:PHE:CZ	2.48	0.48
1:H:220:LYS:HG3	1:H:229:GLU:OE2	2.14	0.48
3:M:55:LEU:HD12	3:M:55:LEU:HA	1.69	0.48
2:L:193:LEU:HD23	7:L:301:OLC:H21A	1.95	0.47
3:M:162:PHE:CD1	14:M:406:SPN:HM83	2.50	0.47
3:M:134:TYR:CE2	3:M:144:LYS:HD2	2.50	0.47
3:M:16:ALA:HB1	3:M:32:VAL:HG21	1.95	0.47
3:M:229:PHE:HB2	3:M:244:ALA:HB2	1.97	0.47
1:H:22:ILE:HG23	11:M:401:CDL:H222	1.97	0.47
2:L:211:HIS:NE2	3:M:22:GLU:OE2	2.24	0.47
3:M:67:PHE:HB2	9:M:403:BPH:H9C3	1.96	0.47
4:M:410:LDA:HM21	4:M:410:LDA:H22	1.61	0.47
3:M:66:TRP:CD1	3:M:122:MET:HB2	2.49	0.47
3:M:81:ASN:HB3	3:M:84:VAL:HB	1.96	0.47
3:M:100:GLU:H	3:M:100:GLU:CD	2.18	0.47
1:H:197:LYS:HD3	3:M:3:TYR:HB2	1.97	0.46



Atom_1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
2:L:153:HIS:O	2:L:157:VAL:HG23	2.15	0.46
2:L:192:ALA:HA	3:M:270:ILE:HD12	1.96	0.46
1:H:63:THR:HA	1:H:73:LEU:O	2.16	0.46
1:H:194:GLN:O	6:M:412:EDO:H12	2.16	0.46
13:M:405:U10:H23	4:M:413:LDA:H42	1.96	0.46
2:L:74:GLY:O	2:L:141:ALA:HA	2.16	0.46
8:L:303:BCL:NA	8:M:402:BCL:HBB2	2.31	0.46
2:L:41:PHE:O	2:L:92:CYS:HB3	2.16	0.46
2:L:269:LEU:HD23	2:L:269:LEU:HA	1.80	0.46
3:M:78:ALA:HB2	3:M:92:PHE:CZ	2.51	0.46
3:M:150:PHE:CZ	9:M:403:BPH:HAA2	2.51	0.46
1:H:35:ASN:OD1	3:M:264:GLY:HA3	2.16	0.46
2:L:85:LEU:HA	2:L:85:LEU:HD23	1.71	0.46
2:L:149:GLY:HA3	2:L:152:THR:OG1	2.15	0.46
2:L:264:GLN:NE2	2:L:264:GLN:HA	2.31	0.46
3:M:148:TRP:HA	3:M:148:TRP:CE3	2.51	0.46
1:H:140:PHE:CE2	1:H:171:ILE:HD12	2.51	0.46
1:H:157:ASP:OD1	1:H:157:ASP:N	2.48	0.46
2:L:56:GLN:HE22	2:L:65:SER:H	1.64	0.46
3:M:275:LEU:HD23	3:M:275:LEU:HA	1.77	0.45
1:H:68:HIS:NE2	15:H:405:HOH:O	2.33	0.45
2:L:190:HIS:HA	7:L:301:OLC:O19	2.16	0.45
3:M:59:SER:OG	9:M:403:BPH:H4C2	2.16	0.45
2:L:52:SER:HA	2:L:55:LEU:HD12	1.98	0.45
1:H:133:PRO:HB2	1:H:166:ASP:OD2	2.16	0.45
1:H:115:VAL:O	1:H:117:ARG:N	2.50	0.45
1:H:171:ILE:HB	1:H:172:PRO:CD	2.45	0.45
4:H:306:LDA:HM13	4:H:306:LDA:H21	1.64	0.45
1:H:81:GLU:O	1:H:83:ARG:HG2	2.16	0.45
2:L:51:TRP:O	2:L:55:LEU:HD12	2.16	0.45
2:L:131:LEU:HD21	2:L:248:MET:HG3	1.99	0.45
3:M:120:PHE:CE2	4:M:409:LDA:H111	2.52	0.44
3:M:208:PHE:O	3:M:212:SER:N	2.45	0.44
1:H:182:GLU:HA	1:H:188:THR:HG22	1.99	0.44
3:M:222:THR:O	3:M:226:VAL:HG22	2.17	0.44
3:M:272:MET:HE2	4:M:407:LDA:H112	1.99	0.44
3:M:284:ILE:HG12	8:M:402:BCL:HED3	1.98	0.44
1:H:85[B]:ILE:HD12	2:L:8:LYS:HD3	1.99	0.44
2:L:239:SER:O	2:L:243:PHE:HD2	2.00	0.44
2:L:135:ARG:HB3	2:L:136:PRO:HD3	2.00	0.44
3:M:234:GLU:HG2	3:M:262:MET:SD	2.58	0.44



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
2:L:142:TRP:CH2	4:L:311:LDA:H71	2.52	0.44
1:H:146:LYS:HE3	1:H:151:LEU:HD11	1.98	0.44
2:L:135:ARG:O	2:L:139:MET:HG3	2.18	0.44
1:H:118:ARG:HG3	1:H:118:ARG:NH1	2.29	0.43
7:L:301:OLC:H8A	7:L:301:OLC:H5	1.79	0.43
3:M:148:TRP:CH2	11:M:401:CDL:H561	2.53	0.43
11:M:401:CDL:HB61	11:M:401:CDL:HA4	2.00	0.43
1:H:29:TYR:CD2	4:H:305:LDA:H12	2.52	0.43
4:H:307:LDA:H12	2:L:109:ARG:NH1	2.33	0.43
2:L:51:TRP:HA	2:L:54:VAL:HG22	2.00	0.43
2:L:60:ASN:O	2:L:64:ILE:HG13	2.17	0.43
8:L:303:BCL:HBD	8:L:304:BCL:HAC1	2.01	0.43
3:M:256:MET:CE	13:M:405:U10:H102	2.47	0.43
2:L:52:SER:HA	2:L:55:LEU:CD1	2.49	0.43
1:H:118:ARG:HG2	1:H:120:LEU:HB2	2.00	0.43
2:L:111:LEU:HG	3:M:254:TRP:CZ3	2.54	0.43
2:L:200:PRO:HA	3:M:143:GLY:H	1.82	0.43
11:M:401:CDL:H811	11:M:401:CDL:H782	1.57	0.43
2:L:177:ILE:HG12	8:L:303:BCL:HMB3	2.00	0.43
1:H:87:LEU:CD1	2:L:8:LYS:HA	2.49	0.42
1:H:233:ILE:O	1:H:237:VAL:HG23	2.19	0.42
2:L:46:ILE:HG12	8:L:304:BCL:H191	2.01	0.42
3:M:45:ALA:O	3:M:47:LEU:HD13	2.19	0.42
3:M:157:TRP:NE1	14:M:406:SPN:H211	2.35	0.42
2:L:158:SER:HA	8:L:303:BCL:CBC	2.49	0.42
1:H:212:LEU:HD23	1:H:212:LEU:HA	1.82	0.42
2:L:38:THR:HG21	2:L:100:TRP:HE3	1.84	0.42
8:L:302:BCL:OBB	8:L:302:BCL:HHC	2.20	0.42
8:L:304:BCL:H203	10:L:310:HTO:H11	2.01	0.42
1:H:118:ARG:HH11	1:H:118:ARG:CG	2.29	0.42
2:L:231:ARG:HB3	3:M:42:PHE:CE1	2.54	0.42
2:L:91:ILE:HG12	4:L:311:LDA:H123	2.02	0.42
3:M:52[B]:LEU:HD23	3:M:52[B]:LEU:HA	1.65	0.42
2:L:189:LEU:HD12	7:L:301:OLC:H7A	2.01	0.42
2:L:208:THR:HB	2:L:209:PRO:HD2	2.02	0.42
3:M:157:TRP:HE1	14:M:406:SPN:H211	1.84	0.42
3:M:157:TRP:CZ2	14:M:406:SPN:HM73	2.55	0.42
1:H:118:ARG:C	1:H:120:LEU:H	2.23	0.41
2:L:229:ILE:HD13	7:L:301:OLC:H3	2.02	0.41
2:L:238:LEU:HD23	9:L:305:BPH:HBC1	2.01	0.41
3:M:66:TRP:O	3:M:70:ILE:HG13	2.20	0.41



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
14:M:406:SPN:HM51	14:M:406:SPN:H152	1.64	0.41
2:L:201:GLU:CG	3:M:144:LYS:HZ1	2.34	0.41
2:L:256:PHE:CE2	10:L:309:HTO:H72	2.56	0.41
8:L:303:BCL:HBB3	8:L:303:BCL:HMB1	2.01	0.41
8:L:304:BCL:H172	10:L:310:HTO:H42	2.02	0.41
4:H:307:LDA:H92	2:L:105:VAL:CG2	2.50	0.41
8:L:302:BCL:H111	8:L:302:BCL:H91	1.65	0.41
3:M:155:TRP:NE1	3:M:281:GLY:HA3	2.35	0.41
3:M:251:PHE:CD1	3:M:251:PHE:C	2.94	0.41
1:H:135:LYS:HG2	1:H:166:ASP:OD2	2.21	0.41
2:L:227:LEU:HD11	3:M:5:ASN:ND2	2.35	0.41
8:L:302:BCL:HBC1	8:M:402:BCL:HAA2	2.01	0.41
3:M:148:TRP:HA	3:M:148:TRP:HE3	1.85	0.41
1:H:58:LEU:CD2	1:H:59:PRO:HD2	2.48	0.41
1:H:96:PHE:HB3	1:H:97:PRO:HD2	2.03	0.41
2:L:117:ILE:HG21	3:M:251:PHE:CZ	2.55	0.41
3:M:13:ARG:HH12	4:M:410:LDA:H11	1.86	0.41
3:M:66:TRP:CG	3:M:122:MET:HB2	2.56	0.41
3:M:155:TRP:O	3:M:159:VAL:HG23	2.21	0.41
3:M:249:ALA:HB2	13:M:405:U10:H4M1	2.03	0.41
3:M:268:TRP:HZ3	4:M:407:LDA:H111	1.86	0.41
1:H:40:TYR:HA	1:H:41:PRO:C	2.42	0.41
2:L:129:LEU:HD23	2:L:129:LEU:HA	1.88	0.41
1:H:208:LEU:HD23	1:H:240:GLY:HA3	2.02	0.40
2:L:169:TYR:OH	3:M:184:ASP:OD1	2.28	0.40
3:M:110:LYS:HE2	3:M:110:LYS:HB2	1.89	0.40
8:L:304:BCL:OBB	8:L:304:BCL:HHC	2.21	0.40
2:L:236:LEU:HD23	2:L:236:LEU:HA	1.90	0.40
1:H:157:ASP:OD2	1:H:210:SER:OG	2.25	0.40
2:L:277:GLY:N	2:L:281:GLY:O	2.39	0.40
8:L:302:BCL:H111	8:L:302:BCL:H152	1.89	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.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
1	Н	240/251~(96%)	224~(93%)	14 (6%)	2(1%)	19	22
2	L	280/281~(100%)	260~(93%)	18 (6%)	2(1%)	22	25
3	М	301/303~(99%)	282 (94%)	19 (6%)	0	100	100
All	All	821/835~(98%)	766 (93%)	51 (6%)	4 (0%)	29	34

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Н	55	PRO
1	Н	171	ILE
2	L	200	PRO
2	L	31	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Н	197/202~(98%)	188~(95%)	9~(5%)	27	35	
2	L	$222/221 \ (100\%)$	213~(96%)	9 (4%)	30	40	
3	М	237/237~(100%)	229~(97%)	8 (3%)	37	48	
All	All	656/660~(99%)	630 (96%)	26 (4%)	33	41	

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Н	11	ASP
1	Н	14	SER
1	Н	58	LEU
1	Н	89	ARG
1	Н	92	VAL
1	Н	118	ARG



Mol	Chain	Res	Type
1	Н	163	LYS
1	Н	220	LYS
1	Н	231	ASP
2	L	167	PHE
2	L	202	LYS
2	L	207	ARG
2	L	210	ASP
2	L	216	PHE
2	L	237	SER
2	L	247	CYS
2	L	258	GLN
2	L	272	TRP
3	М	47	LEU
3	М	52[A]	LEU
3	М	52[B]	LEU
3	М	62	SER
3	М	148	TRP
3	М	162	PHE
3	М	182	HIS
3	М	216	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	Н	206	ASN
2	L	56	GLN
2	L	264	GLN

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 monosaccharides in this entry.



5.6 Ligand geometry (i)

Of 32 ligands modelled in this entry, 5 are unknown and 1 is monoatomic - leaving 26 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	Dog	Link	Bond lengths		Bond angles			
	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
4	LDA	Н	306	-	$12,\!15,\!15$	2.06	1 (8%)	$14,\!17,\!17$	0.58	0
8	BCL	L	304	-	64,74,74	1.44	7 (10%)	78,115,115	1.61	16 (20%)
14	SPN	М	406	-	40,42,42	0.43	0	$50,\!52,\!52$	0.76	1 (2%)
4	LDA	Н	307	-	12,15,15	2.10	1 (8%)	14,17,17	0.55	0
4	LDA	L	306	-	12,15,15	2.04	1 (8%)	14,17,17	0.42	0
4	LDA	Н	301	-	12,15,15	2.02	1 (8%)	14,17,17	0.46	0
4	LDA	М	408	-	12,15,15	2.07	1 (8%)	14,17,17	0.58	0
4	LDA	М	409	-	12,15,15	2.07	1 (8%)	14,17,17	0.58	0
4	LDA	М	410	-	12,15,15	2.06	1 (8%)	14,17,17	0.51	0
6	EDO	М	412	-	3,3,3	0.55	0	2,2,2	0.22	0
10	HTO	L	310	-	9,9,9	0.48	0	10,10,10	0.84	0
8	BCL	L	303	-	64,74,74	1.60	9 (14%)	78,115,115	1.53	10 (12%)
9	BPH	М	403	-	51,70,70	1.12	3 (5%)	52,101,101	1.54	9 (17%)
4	LDA	L	311	-	12,15,15	2.05	1 (8%)	14,17,17	0.57	0
8	BCL	М	402	-	64,74,74	1.35	5 (7%)	78,115,115	1.69	13 (16%)
9	BPH	L	305	-	51,70,70	1.21	5 (9%)	52,101,101	1.33	8 (15%)
8	BCL	L	302	-	64,74,74	1.35	8 (12%)	78,115,115	1.77	16 (20%)
4	LDA	М	414	-	12,15,15	2.00	1 (8%)	14,17,17	0.50	0
4	LDA	Н	305	-	12,15,15	2.05	1 (8%)	14,17,17	0.83	0
11	CDL	М	401	-	80,80,99	0.40	0	86,92,111	0.35	0
13	U10	М	405	-	48,48,63	2.71	13 (27%)	58,61,79	1.62	13 (22%)
4	LDA	М	407	_	12,15,15	1.95	1 (8%)	14,17,17	0.78	0
6	EDO	Н	304	-	3,3,3	0.43	0	2,2,2	0.39	0
4	LDA	М	413	-	12,15,15	2.03	1 (8%)	14,17,17	0.49	0
7	OLC	L	301	-	24,24,24	0.83	1 (4%)	$25,\!25,\!25$	0.97	2 (8%)
10	HTO	L	309	-	9,9,9	0.27	0	10,10,10	0.96	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	LDA	Н	306	-	-	10/13/13/13	-
8	BCL	L	304	-	-	6/37/137/137	-
14	SPN	М	406	-	-	15/50/51/51	-
4	LDA	Н	307	-	-	11/13/13/13	-
4	LDA	L	306	-	-	8/13/13/13	-
4	LDA	Н	301	-	-	9/13/13/13	-
4	LDA	М	408	-	-	5/13/13/13	-
4	LDA	М	409	-	-	9/13/13/13	-
4	LDA	М	410	-	-	7/13/13/13	-
6	EDO	М	412	-	_	1/1/1/1	-
10	HTO	L	310	-	-	9/10/10/10	-
8	BCL	L	303	-	-	2/37/137/137	-
9	BPH	М	403	-	-	6/37/105/105	0/5/6/6
4	LDA	L	311	-	-	8/13/13/13	-
8	BCL	М	402	-	-	2/37/137/137	-
9	BPH	L	305	-	-	4/37/105/105	0/5/6/6
8	BCL	L	302	-	-	8/37/137/137	-
4	LDA	М	414	-	-	9/13/13/13	-
4	LDA	Н	305	-	-	10/13/13/13	-
11	CDL	М	401	-	-	50/91/91/110	-
13	U10	М	405	-	-	15/45/69/87	0/1/1/1
4	LDA	М	407	-	-	4/13/13/13	-
6	EDO	Н	304	-	-	0/1/1/1	-
4	LDA	М	413	-	_	10/13/13/13	-
7	OLC	L	301	-	-	12/24/24/24	-
10	HTO	L	309	-	-	5/10/10/10	-

All (63) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms		Observed(Å)	Ideal(Å)
4	Н	307	LDA	O1-N1	-7.15	1.25	1.42
4	М	408	LDA	O1-N1	-7.07	1.25	1.42
4	М	409	LDA	O1-N1	-7.06	1.25	1.42



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	М	410	LDA	01-N1	-7.06	1.25	1.42
4	Н	306	LDA	O1-N1	-7.06	1.25	1.42
4	Н	305	LDA	O1-N1	-7.05	1.25	1.42
4	L	311	LDA	O1-N1	-7.05	1.25	1.42
4	М	413	LDA	O1-N1	-6.95	1.25	1.42
4	L	306	LDA	01-N1	-6.93	1.26	1.42
4	Н	301	LDA	01-N1	-6.88	1.26	1.42
4	М	414	LDA	O1-N1	-6.75	1.26	1.42
4	М	407	LDA	O1-N1	-6.67	1.26	1.42
13	М	405	U10	C13-C14	6.42	1.48	1.33
13	М	405	U10	C8-C9	6.35	1.48	1.33
13	М	405	U10	C33-C34	6.21	1.47	1.33
13	М	405	U10	C18-C19	6.09	1.47	1.33
8	L	304	BCL	C1B-NB	6.01	1.40	1.35
13	М	405	U10	C28-C29	5.76	1.46	1.33
13	М	405	U10	C23-C24	5.75	1.46	1.33
8	L	303	BCL	MG-NA	5.69	2.19	2.06
8	М	402	BCL	MG-NA	5.63	2.19	2.06
13	М	405	U10	C38-C39	5.38	1.47	1.32
13	М	405	U10	O3-C3	-5.32	1.23	1.36
13	М	405	U10	O4-C4	-5.10	1.24	1.36
8	L	302	BCL	MG-NA	4.94	2.18	2.06
8	L	303	BCL	MG-NC	4.60	2.17	2.06
8	L	302	BCL	C1B-NB	4.51	1.39	1.35
8	М	402	BCL	C1B-NB	4.40	1.39	1.35
8	L	304	BCL	MG-NA	4.38	2.16	2.06
8	L	303	BCL	C1B-NB	4.32	1.39	1.35
9	L	305	BPH	CBD-CGD	-4.10	1.46	1.52
9	М	403	BPH	CBD-CGD	-4.07	1.46	1.52
13	М	405	U10	C3-C2	-3.66	1.38	1.48
8	L	303	BCL	CAC-C3C	3.61	1.61	1.54
7	L	301	OLC	O20-C1	3.61	1.43	1.33
8	L	304	BCL	MG-NC	3.34	2.14	2.06
9	L	305	BPH	CAC-C3C	3.25	1.60	1.53
8	L	303	BCL	C4B-NB	3.16	1.38	1.35
8	L	302	BCL	MG-NC	3.01	2.13	2.06
8	L	303	BCL	C1D-ND	2.87	1.41	1.37
13	М	405	U10	C4-C5	-2.77	1.40	1.48
8	L	304	BCL	OBD-CAD	2.76	1.27	1.22
8	М	402	BCL	MG-NC	2.68	2.12	2.06
8	L	303	BCL	O1A-CGA	-2.66	1.14	1.22
8	L	302	BCL	01A-CGA	-2.65	1.14	1.22



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	L	302	BCL	C5-C3	2.55	1.56	1.51
13	М	405	U10	C1-C2	-2.49	1.38	1.47
9	L	305	BPH	O2A-CGA	-2.45	1.26	1.33
8	L	303	BCL	CHD-C1D	2.45	1.43	1.38
8	L	303	BCL	C4-C3	2.43	1.56	1.50
8	М	402	BCL	C4B-NB	2.40	1.37	1.35
8	L	304	BCL	C1D-ND	2.37	1.40	1.37
9	L	305	BPH	C2C-C3C	-2.33	1.52	1.54
9	М	403	BPH	OBD-CAD	2.30	1.25	1.22
8	L	304	BCL	C1D-C2D	-2.29	1.40	1.45
8	L	304	BCL	CHD-C1D	2.25	1.42	1.38
8	L	302	BCL	C4B-NB	2.20	1.37	1.35
8	L	302	BCL	OBD-CAD	2.18	1.26	1.22
9	М	403	BPH	C1C-C2C	-2.15	1.47	1.51
9	L	305	BPH	C14-C13	2.10	1.59	1.52
13	М	405	U10	C6-C5	-2.07	1.40	1.46
8	L	302	BCL	C1D-ND	2.04	1.40	1.37
8	М	402	BCL	C3B-C2B	2.03	1.43	1.39

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
8	L	302	BCL	C1-C2-C3	5.67	135.85	126.04
8	М	402	BCL	CHD-C1D-ND	-5.51	119.39	124.45
8	L	302	BCL	CHD-C1D-ND	-5.21	119.67	124.45
8	L	304	BCL	CHD-C1D-ND	-5.02	119.84	124.45
8	L	303	BCL	CHD-C1D-ND	-4.83	120.01	124.45
8	М	402	BCL	CMB-C2B-C1B	-4.83	121.04	128.46
8	М	402	BCL	C4D-CHA-C1A	4.66	126.92	121.25
8	L	303	BCL	C4D-CHA-C1A	4.66	126.92	121.25
8	L	302	BCL	C4D-CHA-C1A	4.53	126.76	121.25
8	L	304	BCL	C4D-CHA-C1A	4.49	126.72	121.25
8	L	304	BCL	C1D-ND-C4D	-4.28	103.30	106.33
13	М	405	U10	C30-C29-C31	4.19	122.32	115.27
8	L	303	BCL	CMB-C2B-C1B	-4.10	122.17	128.46
8	L	303	BCL	C1D-ND-C4D	-4.07	103.45	106.33
9	М	403	BPH	CAA-CBA-CGA	4.01	124.97	113.25
9	М	403	BPH	CAC-C3C-C4C	-4.00	104.78	113.73
8	L	302	BCL	CMB-C2B-C1B	-4.00	122.31	128.46
8	М	402	BCL	C1D-ND-C4D	-3.88	103.58	106.33
9	L	305	BPH	C1-C2-C3	-3.74	119.57	126.04
8	М	402	BCL	CHA-C1A-NA	-3.68	117.97	126.40



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Mol	Chain	\mathbf{Res}	Type	Atoms		$Observed(^{o})$	$Ideal(^{o})$
8	L	302	BCL	C1D-ND-C4D	-3.66	103.74	106.33
9	L	305	BPH	C11-C10-C8	-3.65	104.13	115.92
8	М	402	BCL	CMB-C2B-C3B	3.65	131.50	124.68
13	М	405	U10	C20-C19-C21	3.60	121.33	115.27
13	М	405	U10	C22-C23-C24	-3.56	119.10	127.66
8	L	302	BCL	C2A-C1A-CHA	3.49	129.97	123.86
8	L	304	BCL	CMB-C2B-C1B	-3.45	123.16	128.46
8	М	402	BCL	O2D-CGD-CBD	3.39	117.30	111.27
8	L	304	BCL	C16-C17-C18	-3.38	100.04	115.98
9	М	403	BPH	CMC-C2C-C1C	-3.27	107.22	114.38
9	М	403	BPH	OBD-CAD-CBD	-3.13	121.23	125.82
9	L	305	BPH	OBD-CAD-CBD	-3.10	121.27	125.82
8	L	303	BCL	C2A-C1A-CHA	3.08	129.25	123.86
8	L	303	BCL	CHA-C1A-NA	-3.04	119.45	126.40
8	L	302	BCL	C6-C7-C8	3.03	125.71	115.92
8	L	302	BCL	CHA-C1A-NA	-3.02	119.49	126.40
13	М	405	U10	C17-C18-C19	-3.01	120.41	127.66
8	L	304	BCL	CMB-C2B-C3B	2.93	130.17	124.68
9	М	403	BPH	C1-O2A-CGA	2.93	124.13	116.44
8	L	304	BCL	C4B-C3B-CAB	-2.92	121.50	127.13
13	М	405	U10	C41-C39-C40	2.92	121.04	114.60
8	L	304	BCL	C2A-C1A-CHA	2.87	128.87	123.86
8	L	302	BCL	OBB-CAB-CBB	-2.83	113.80	120.17
8	L	303	BCL	CMB-C2B-C3B	2.83	129.97	124.68
8	L	303	BCL	C16-C15-C13	2.82	125.02	115.92
8	L	302	BCL	CMB-C2B-C3B	2.79	129.89	124.68
8	L	304	BCL	C2D-C1D-ND	2.77	112.15	110.10
8	L	304	BCL	CHA-C1A-NA	-2.74	120.13	126.40
8	L	302	BCL	O2A-C1-C2	-2.68	101.59	108.64
13	М	405	U10	C37-C38-C39	-2.66	118.67	127.75
8	М	402	BCL	C17-C16-C15	-2.61	101.23	113.24
8	L	302	BCL	C2D-C1D-ND	2.60	112.02	110.10
8	L	304	BCL	C11-C10-C8	-2.58	107.59	115.92
9	М	403	BPH	CMB-C2B-C3B	2.53	129.42	124.68
8	М	402	BCL	OBB-CAB-CBB	-2.52	114.49	120.17
14	М	406	SPN	C24-C23-C22	-2.50	107.12	115.76
8	L	302	BCL	C1-O2A-CGA	2.49	122.98	116.44
9	L	305	BPH	CMD-C2D-C3D	2.47	129.30	124.68
13	М	405	U10	C32-C33-C34	-2.40	121.88	127.66
8	L	304	BCL	O2A-C1-C2	-2.39	102.34	108.64
8	М	402	BCL	C1-C2-C3	-2.37	121.95	126.04

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124.68

129.04



2.33

CMB-C2B-C3B

BPH

L

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
8	L	303	BCL	C4B-C3B-CAB	-2.33	122.63	127.13
8	L	304	BCL	O2D-CGD-O1D	-2.32	119.29	123.84
7	L	301	OLC	O20-C1-C2	2.30	119.12	111.91
9	М	403	BPH	C16-C15-C13	2.30	123.35	115.92
8	L	302	BCL	C4B-C3B-CAB	-2.30	122.69	127.13
8	М	402	BCL	O2D-CGD-O1D	-2.28	119.39	123.84
13	М	405	U10	C25-C24-C26	2.28	119.10	115.27
9	L	305	BPH	CAA-CBA-CGA	-2.27	106.63	113.25
7	L	301	OLC	O20-C1-O19	-2.27	117.87	123.59
8	L	303	BCL	O2A-C1-C2	-2.25	102.72	108.64
8	L	304	BCL	O2A-CGA-CBA	-2.24	104.89	111.91
8	L	304	BCL	CHC-C1C-NC	-2.23	121.43	124.51
8	L	304	BCL	C4-C3-C5	-2.21	111.55	115.27
9	L	305	BPH	C4C-C3C-C2C	-2.17	100.77	102.84
13	М	405	U10	C35-C34-C36	2.17	118.92	115.27
9	М	403	BPH	O2A-C1-C2	-2.16	102.95	108.64
9	L	305	BPH	OBB-CAB-CBB	-2.13	115.39	120.17
8	М	402	BCL	C1-O2A-CGA	-2.12	110.88	116.44
8	L	302	BCL	C6-C5-C3	2.12	119.01	113.45
9	М	403	BPH	CMD-C2D-C3D	2.12	128.64	124.68
13	М	405	U10	C10-C9-C11	2.11	118.83	115.27
8	Μ	402	BCL	C2A-C1A-CHA	2.11	127.56	123.86
13	Μ	405	U10	C6-C1-C2	2.08	120.83	119.18
13	М	405	U10	C31-C29-C28	-2.05	116.96	121.12
8	L	302	BCL	C4A-NA-C1A	2.05	107.63	106.71
13	М	405	U10	C7-C6-C5	2.02	120.91	118.48

There are no chirality outliers.

All (235) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	Н	301	LDA	C2-C1-N1-O1
4	Н	301	LDA	C2-C1-N1-CM1
4	Н	305	LDA	C2-C1-N1-O1
4	Н	305	LDA	C2-C1-N1-CM1
4	Н	305	LDA	C2-C1-N1-CM2
4	Н	306	LDA	C2-C1-N1-O1
4	Н	306	LDA	C2-C1-N1-CM1
4	Н	306	LDA	C2-C1-N1-CM2
4	Н	306	LDA	N1-C1-C2-C3
4	Н	307	LDA	C2-C1-N1-CM1
4	Н	307	LDA	C2-C1-N1-CM2



Mol	Chain	Res	Type	Atoms
4	L	306	LDA	C2-C1-N1-CM2
4	М	409	LDA	C2-C1-N1-CM1
4	М	409	LDA	C2-C1-N1-CM2
4	М	413	LDA	C2-C1-N1-O1
4	М	413	LDA	C2-C1-N1-CM1
4	М	414	LDA	C2-C1-N1-CM1
4	М	414	LDA	C2-C1-N1-CM2
4	М	414	LDA	N1-C1-C2-C3
7	L	301	OLC	O20-C21-C22-C24
7	L	301	OLC	O20-C21-C22-O23
8	L	303	BCL	C4C-C3C-CAC-CBC
9	М	403	BPH	C4C-C3C-CAC-CBC
10	L	310	HTO	O1-C1-C2-O2
10	L	310	НТО	C1-C2-C3-O3
10	L	310	HTO	C1-C2-C3-C4
10	L	310	HTO	O2-C2-C3-O3
10	L	310	HTO	O2-C2-C3-C4
10	L	310	HTO	O3-C3-C4-C5
11	М	401	CDL	CA2-C1-CB2-OB2
11	М	401	CDL	CA3-OA5-PA1-OA4
11	М	401	CDL	CB2-OB2-PB2-OB3
11	М	401	CDL	CB3-OB5-PB2-OB3
13	М	405	U10	C27-C28-C29-C30
13	М	405	U10	C27-C28-C29-C31
14	М	406	SPN	C2-C1-O1-CMA
14	М	406	SPN	C12-C13-C14-C15
14	М	406	SPN	CM5-C13-C14-C15
14	М	406	SPN	C16-C17-C18-CM6
14	М	406	SPN	C16-C17-C18-C19
11	М	401	CDL	C31-CA7-OA8-CA6
10	L	309	HTO	O1-C1-C2-O2
11	М	401	CDL	OA9-CA7-OA8-CA6
11	М	401	CDL	O1-C1-CA2-OA2
11	М	401	CDL	O1-C1-CB2-OB2
14	М	406	SPN	C9-C10-C11-C12
14	М	406	SPN	C26-C27-C28-C29
4	Н	301	LDA	C5-C6-C7-C8
14	М	406	SPN	C14-C15-C16-C17
11	М	401	CDL	C78-C79-C80-C81
11	М	401	CDL	CA7-C31-C32-C33
9	М	403	BPH	C8-C10-C11-C12
10	L	310	HTO	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
13	М	405	U10	C24-C26-C27-C28
13	М	405	U10	C34-C36-C37-C38
13	М	405	U10	C37-C38-C39-C40
9	М	403	BPH	C10-C11-C12-C13
13	М	405	U10	C20-C19-C21-C22
8	L	304	BCL	C15-C16-C17-C18
11	М	401	CDL	C20-C21-C22-C23
4	L	311	LDA	C4-C5-C6-C7
4	М	408	LDA	C7-C8-C9-C10
4	М	414	LDA	C6-C7-C8-C9
7	L	301	OLC	C11-C12-C13-C14
11	М	401	CDL	C37-C38-C39-C40
11	М	401	CDL	C76-C77-C78-C79
4	М	408	LDA	C4-C5-C6-C7
4	Н	307	LDA	C5-C6-C7-C8
4	М	410	LDA	C4-C5-C6-C7
14	М	406	SPN	CM1-C1-O1-CMA
14	М	406	SPN	CM2-C1-O1-CMA
4	Н	307	LDA	C7-C8-C9-C10
4	М	413	LDA	C9-C10-C11-C12
4	М	408	LDA	C11-C10-C9-C8
11	М	401	CDL	C13-C14-C15-C16
11	М	401	CDL	C14-C15-C16-C17
11	М	401	CDL	C38-C39-C40-C41
10	L	310	HTO	C2-C3-C4-C5
4	Н	307	LDA	C3-C4-C5-C6
4	L	311	LDA	C3-C4-C5-C6
4	М	410	LDA	C7-C8-C9-C10
11	М	401	CDL	C11-C12-C13-C14
11	М	401	CDL	C32-C33-C34-C35
11	M	401	CDL	C51-C52-C53-C54
4	H	307	LDA	C4-C5-C6-C7
11	М	401	CDL	C18-C19-C20-C21
11	М	401	CDL	C73-C74-C75-C76
4	Н	306	LDA	C11-C10-C9-C8
4	L	311	LDA	C6-C7-C8-C9
11	М	401	CDL	C19-C20-C21-C22
11	М	401	CDL	C33-C34-C35-C36
4	H	306	LDA	C7-C8-C9-C10
4	L	306	LDA	C7-C8-C9-C10
4	М	414	LDA	$C4-\overline{C5-C6}-\overline{C7}$
4	L	306	LDA	C4-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
7	L	301	OLC	C3-C4-C5-C6
4	Н	306	LDA	C1-C2-C3-C4
11	М	401	CDL	C12-C13-C14-C15
4	Н	305	LDA	C2-C3-C4-C5
7	L	301	OLC	C1-C2-C3-C4
4	L	311	LDA	C2-C3-C4-C5
4	М	414	LDA	C11-C10-C9-C8
13	М	405	U10	C37-C38-C39-C41
4	Н	305	LDA	C11-C10-C9-C8
11	М	401	CDL	C75-C76-C77-C78
14	М	406	SPN	CM8-C26-C27-C28
9	L	305	BPH	C11-C10-C8-C7
4	Н	307	LDA	C9-C10-C11-C12
4	М	414	LDA	C1-C2-C3-C4
4	М	409	LDA	C1-C2-C3-C4
4	М	410	LDA	C2-C3-C4-C5
8	L	302	BCL	C8-C10-C11-C12
4	Н	307	LDA	C6-C7-C8-C9
4	Н	301	LDA	C7-C8-C9-C10
4	L	311	LDA	C5-C6-C7-C8
4	М	408	LDA	C5-C6-C7-C8
13	М	405	U10	C18-C19-C21-C22
4	М	408	LDA	C1-C2-C3-C4
9	М	403	BPH	C2C-C3C-CAC-CBC
11	М	401	CDL	CB3-OB5-PB2-OB2
4	Н	301	LDA	C1-C2-C3-C4
4	М	407	LDA	C1-C2-C3-C4
4	М	413	LDA	C5-C6-C7-C8
4	М	407	LDA	C3-C4-C5-C6
4	Н	305	LDA	C4-C5-C6-C7
4	М	410	LDA	C11-C10-C9-C8
4	М	413	LDA	C11-C10-C9-C8
11	М	401	CDL	C39-C40-C41-C42
11	М	401	CDL	C80-C81-C82-C83
11	М	401	CDL	C55-C56-C57-C58
4	L	306	LDA	C3-C4-C5-C6
4	L	306	LDA	C9-C10-C11-C12
4	М	413	LDA	C6-C7-C8-C9
4	Н	305	LDA	C9-C10-C11-C12
4	М	409	LDA	C5-C6-C7-C8
7	L	301	OLC	C15-C16-C17-C18
4	Н	307	LDA	C1-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
11	М	401	CDL	OA6-CA4-CA6-OA8
7	L	301	OLC	C13-C14-C15-C16
4	М	413	LDA	C7-C8-C9-C10
8	L	302	BCL	C15-C16-C17-C18
11	М	401	CDL	C16-C17-C18-C19
4	Н	305	LDA	N1-C1-C2-C3
4	L	311	LDA	N1-C1-C2-C3
4	Н	306	LDA	C4-C5-C6-C7
4	L	306	LDA	C1-C2-C3-C4
4	Н	301	LDA	C9-C10-C11-C12
14	М	406	SPN	C25-C26-C27-C28
4	М	409	LDA	C11-C10-C9-C8
4	М	409	LDA	C6-C7-C8-C9
10	L	309	HTO	C1-C2-C3-O3
11	М	401	CDL	CA3-CA4-CA6-OA8
8	L	302	BCL	C4-C3-C5-C6
4	М	413	LDA	C4-C5-C6-C7
4	М	410	LDA	C1-C2-C3-C4
8	L	304	BCL	C16-C17-C18-C19
4	L	311	LDA	C9-C10-C11-C12
11	М	401	CDL	C53-C54-C55-C56
8	L	302	BCL	C2-C1-O2A-CGA
9	L	305	BPH	C11-C10-C8-C9
11	М	401	CDL	C72-C73-C74-C75
6	М	412	EDO	O1-C1-C2-O2
8	L	302	BCL	C4C-C3C-CAC-CBC
10	L	309	HTO	O1-C1-C2-C3
8	М	402	BCL	CAD-CBD-CGD-O2D
9	L	305	BPH	CAD-CBD-CGD-O2D
11	М	401	CDL	C17-C18-C19-C20
4	Н	306	LDA	C2-C3-C4-C5
13	М	405	U10	C25-C24-C26-C27
4	М	407	LDA	C11-C10-C9-C8
8	L	302	BCL	C2-C3-C5-C6
7	L	301	OLC	C4-C5-C6-C7
14	М	406	SPN	C22-C23-C24-C25
4	Н	301	LDA	C2-C1-N1-CM2
4	L	306	LDA	C2-C1-N1-CM1
4	М	413	LDA	C2-C1-N1-CM2
8	М	402	BCL	CHA-CBD-CGD-O1D
11	М	401	CDL	C74-C75-C76-C77
11	М	401	CDL	C81-C82-C83-C84

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Mol	Chain	Res	Type	Atoms
4	Н	305	LDA	C7-C8-C9-C10
10	L	309	HTO	C3-C4-C5-C6
4	М	409	LDA	C7-C8-C9-C10
11	М	401	CDL	CA3-OA5-PA1-OA3
11	М	401	CDL	CB3-OB5-PB2-OB4
4	М	414	LDA	C2-C3-C4-C5
4	Н	307	LDA	C2-C3-C4-C5
4	L	306	LDA	C2-C1-N1-O1
7	L	301	OLC	C10-C11-C12-C13
4	М	410	LDA	C6-C7-C8-C9
8	L	304	BCL	C16-C17-C18-C20
11	М	401	CDL	C35-C36-C37-C38
13	М	405	U10	C23-C24-C26-C27
4	М	409	LDA	C9-C10-C11-C12
7	L	301	OLC	C6-C7-C8-C9
11	М	401	CDL	CA3-OA5-PA1-OA2
11	М	401	CDL	CB2-C1-CA2-OA2
9	М	403	BPH	C15-C16-C17-C18
10	L	310	HTO	C3-C4-C5-C6
8	L	302	BCL	C11-C10-C8-C9
11	М	401	CDL	CB2-OB2-PB2-OB5
4	М	413	LDA	C2-C3-C4-C5
11	М	401	CDL	CB7-C71-C72-C73
4	Н	306	LDA	C5-C6-C7-C8
11	М	401	CDL	C54-C55-C56-C57
4	L	311	LDA	C1-C2-C3-C4
13	М	405	U10	C14-C16-C17-C18
8	L	303	BCL	C2C-C3C-CAC-CBC
8	L	304	BCL	C14-C13-C15-C16
4	М	407	LDA	C9-C10-C11-C12
4	Н	305	LDA	C1-C2-C3-C4
13	М	405	U10	C35-C34-C36-C37
7	L	301	OLC	C14-C15-C16-C17
7	L	301	OLC	C9-C10-C11-C12
13	М	405	U10	C5-C4-O4-C4M
11	М	401	CDL	C79-C80-C81-C82
8	L	302	BCL	CAD-CBD-CGD-O2D
8	L	304	BCL	CAD-CBD-CGD-O2D
4	Н	301	LDA	C11-C10-C9-C8
13	М	405	U10	C33-C34-C36-C37
9	L	305	BPH	O2A-C1-C2-C3
10	L	309	HTO	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
9	М	403	BPH	CHA-CBD-CGD-O1D
11	М	401	CDL	C32-C31-CA7-OA8
14	М	406	SPN	C2-C3-C4-C5
4	М	410	LDA	C5-C6-C7-C8
11	М	401	CDL	CB2-OB2-PB2-OB4
11	М	401	CDL	OA5-CA3-CA4-CA6
13	М	405	U10	C16-C17-C18-C19
4	Н	307	LDA	C2-C1-N1-O1
4	М	409	LDA	C2-C1-N1-O1
4	М	414	LDA	C2-C1-N1-O1
11	М	401	CDL	C32-C31-CA7-OA9
8	Ĺ	304	BCL	C13-C15-C16-C17
4	Н	301	LDA	C3-C4-C5-C6
14	М	406	SPN	C21-C22-C23-C24

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There are no ring outliers.

22	monomers	are	involve	d in	76	short	contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	Н	306	LDA	2	0
8	L	304	BCL	5	0
14	М	406	SPN	8	0
4	Н	307	LDA	4	0
4	Н	301	LDA	2	0
4	М	409	LDA	3	0
4	М	410	LDA	2	0
6	М	412	EDO	2	0
10	L	310	HTO	2	0
8	L	303	BCL	7	0
9	М	403	BPH	4	0
4	L	311	LDA	2	0
8	М	402	BCL	6	0
9	L	305	BPH	2	0
8	L	302	BCL	6	0
4	Н	305	LDA	6	0
11	М	401	CDL	11	0
13	М	405	U10	4	0
4	М	407	LDA	2	0
4	М	413	LDA	1	0
7	L	301	OLC	5	0
10	L	309	HTO	1	0



The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and sufficient must be highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



















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)

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^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	Н	240/251~(95%)	0.10	7 (2%) 51 47	7, 18, 31, 61	0
2	L	281/281 (100%)	0.18	12 (4%) 35 32	3, 15, 39, 68	0
3	М	302/303~(99%)	0.03	7 (2%) 60 56	4, 15, 37, 62	0
All	All	823/835~(98%)	0.10	26 (3%) 47 44	3, 16, 37, 68	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	271	TRP	6.7
2	L	270	PRO	4.8
3	М	1	ALA	4.5
2	L	281	GLY	4.4
1	Н	249	LYS	4.2
2	L	277	GLY	3.5
2	L	59	TRP	3.3
3	М	106	ALA	3.1
1	Н	186	GLY	3.0
2	L	276	PRO	3.0
3	М	76	TYR	2.9
1	Н	221	SER	2.8
2	L	269	LEU	2.8
3	М	108	PRO	2.7
2	L	273	ALA	2.6
2	L	54	VAL	2.6
1	Н	246	PRO	2.5
2	L	58	THR	2.5
1	Н	245	ALA	2.4
1	Н	92	VAL	2.4
1	Н	200	SER	2.3
2	L	260	VAL	2.3
2	L	21[A]	LEU	2.2



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Mol	Chain	Res	Type	RSRZ
3	М	301	HIS	2.1
3	М	80	TRP	2.0
3	М	300	ASN	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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
4	LDA	М	410	16/16	0.40	0.54	$23,\!53,\!90,\!94$	0
5	UNL	L	307	10/-	0.47	0.36	$13,\!36,\!53,\!59$	0
4	LDA	М	407	16/16	0.61	0.28	6,22,33,38	0
4	LDA	М	414	16/16	0.63	0.31	23,39,49,51	0
4	LDA	М	409	16/16	0.63	0.28	22,35,60,64	0
10	HTO	L	309	10/10	0.70	0.32	14,23,33,36	10
5	UNL	Н	302	12/-	0.72	0.33	12,33,42,45	0
5	UNL	L	308	12/-	0.73	0.29	24,39,48,52	0
5	UNL	Н	303	15/-	0.74	0.30	18,41,54,58	0
4	LDA	Н	306	16/16	0.75	0.39	$23,\!38,\!51,\!53$	0
10	HTO	L	310	10/10	0.76	0.26	$23,\!34,\!44,\!57$	0
4	LDA	L	306	16/16	0.77	0.18	$5,\!23,\!42,\!48$	0
4	LDA	Н	307	16/16	0.78	0.24	$8,\!39,\!58,\!72$	0
14	SPN	М	406	43/43	0.79	0.25	8,24,48,50	0
11	CDL	М	401	81/100	0.80	0.23	7,23,43,47	81
4	LDA	L	311	16/16	0.80	0.24	11,29,57,66	0
4	LDA	М	413	16/16	0.81	0.22	12,29,42,46	0
7	OLC	L	301	25/25	0.81	0.23	5,25,44,53	0
4	LDA	М	408	16/16	0.83	0.25	10,23,37,57	0
4	LDA	Н	305	16/16	0.85	0.29	20,33,50,58	0



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
4	LDA	Н	301	16/16	0.86	0.20	8,14,30,33	0
6	EDO	М	412	4/4	0.87	0.21	13,17,19,20	0
13	U10	М	405	48/63	0.88	0.17	3,8,28,36	0
9	BPH	М	403	65/65	0.88	0.17	$2,\!11,\!38,\!47$	0
5	UNL	М	411	12/-	0.89	0.14	8,20,32,36	0
8	BCL	L	303	66/66	0.89	0.17	3,12,22,24	0
8	BCL	М	402	66/66	0.90	0.17	3,11,20,39	0
8	BCL	L	304	66/66	0.91	0.14	$5,\!11,\!25,\!30$	0
8	BCL	L	302	66/66	0.91	0.14	$5,\!14,\!29,\!44$	0
6	EDO	Н	304	4/4	0.92	0.26	23,32,34,38	0
9	BPH	L	305	65/65	0.92	0.15	3,8,15,27	0
12	FE	М	404	1/1	0.99	0.06	$15,\!15,\!15,\!15$	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.































6.5 Other polymers (i)

There are no such residues in this entry.

