



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:32 AM GMT

PDB ID : 2HJ6  
Title : Reaction centre from Rhodobacter sphaeroides strain R-26.1 complexed with dibrominated phosphatidylserine  
Authors : Roszak, A.W.; Gardiner, A.T.; Isaacs, N.W.; Cogdell, R.J.  
Deposited on : 2006-06-30  
Resolution : 3.00 Å(reported)

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

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

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

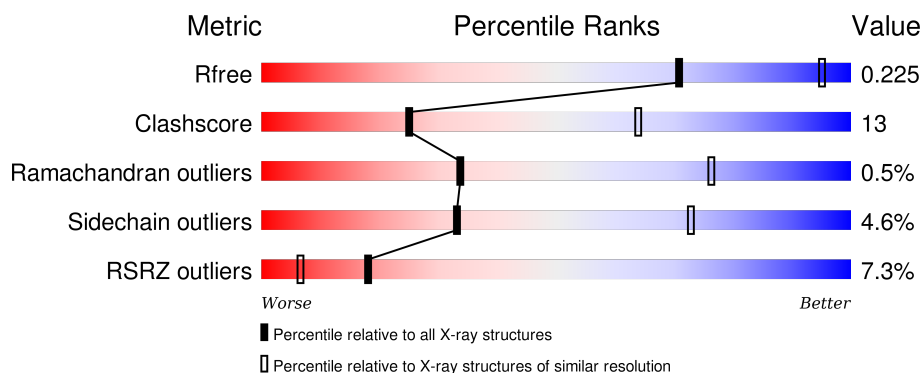
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L	281	<div> <div>7%</div> <div> <div></div> <div>75%</div> <div>21%</div> <div>.</div> </div> </div>
2	M	307	<div> <div>6%</div> <div> <div></div> <div>76%</div> <div>20%</div> <div>..</div> </div> </div>
3	H	260	<div> <div>8%</div> <div> <div></div> <div>71%</div> <div>20%</div> <div>. 7%</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
11	CDL	M	800	-	-	-	X
12	PS2	M	802	-	-	-	X
13	LDA	H	902	-	-	-	X
13	LDA	H	905	-	-	-	X
13	LDA	M	903	-	-	-	X
13	LDA	M	906	-	-	-	X
13	LDA	M	907	-	-	-	X
13	LDA	M	920	-	-	X	X
14	GOL	M	704	-	-	-	X
9	U10	L	502	-	-	-	X

## 2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 7685 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	3	0
			2249	1520	357	364	8			

- 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	5	0
			2452	1637	403	402	10			

- Molecule 3 is a protein called Reaction center protein H chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	241	Total	C	N	O	S	0	5	0
			1846	1180	316	339	11			

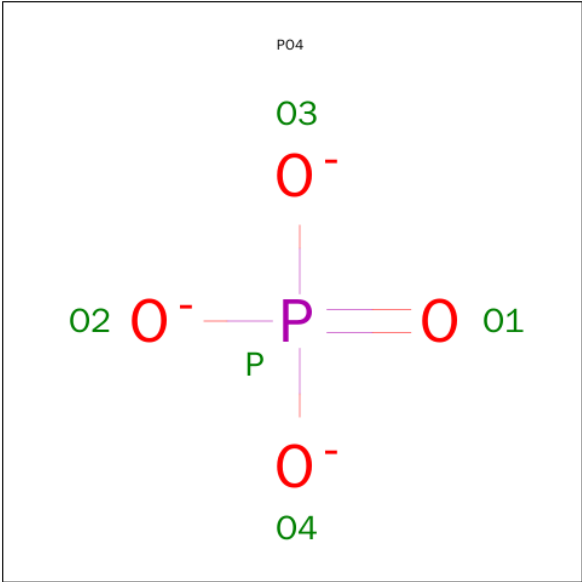
- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

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

- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

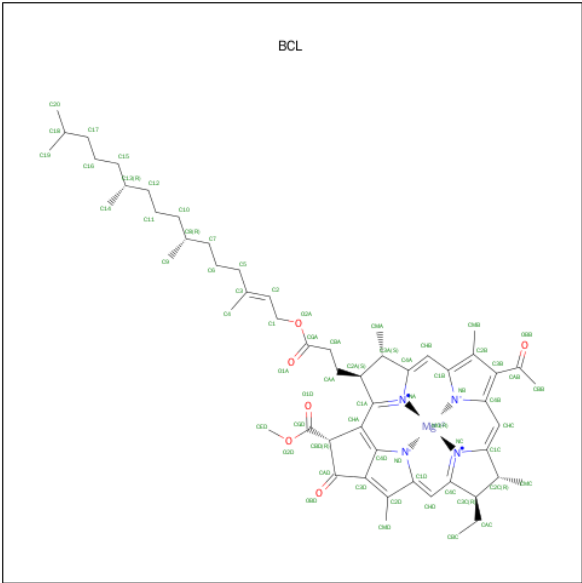
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	K	0	0
			1	1		

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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

- Molecule 7 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: C<sub>55</sub>H<sub>74</sub>MgN<sub>4</sub>O<sub>6</sub>).



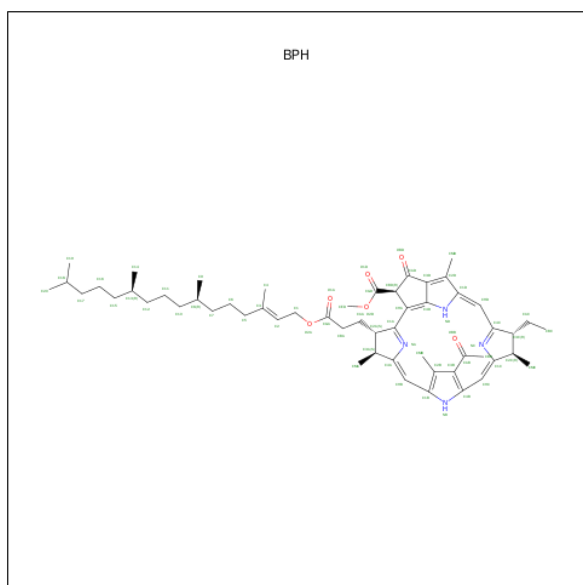
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	M	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	L	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

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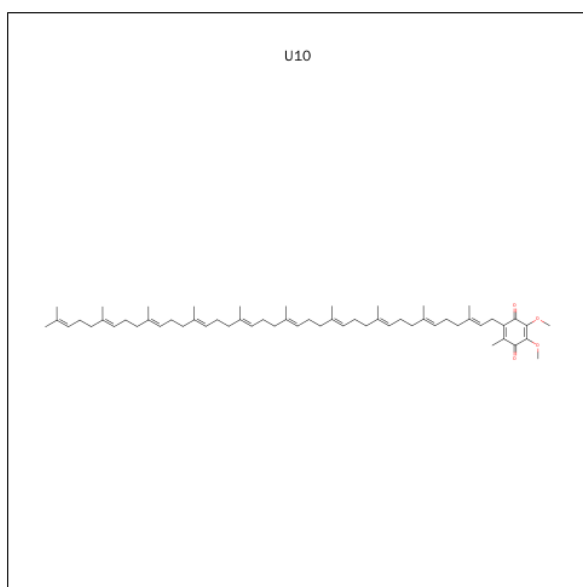
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
7	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 8 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula:  $C_{55}H_{76}N_4O_6$ ).



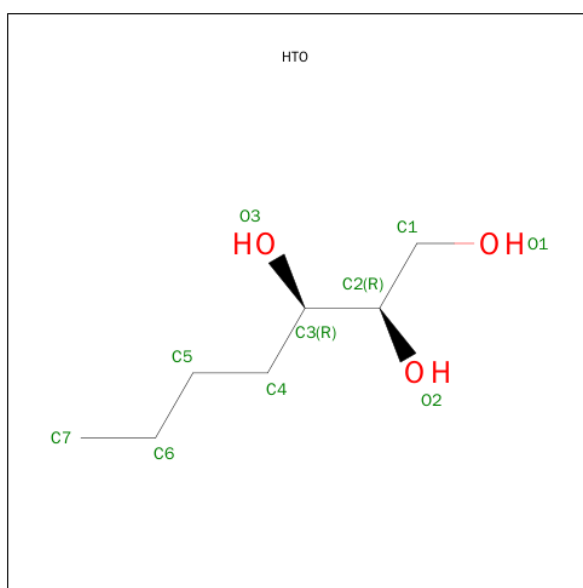
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	M	1	Total	C	N	O	0	0
			65	55	4	6		
8	L	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 9 is UBIQUINONE-10 (three-letter code: U10) (formula:  $C_{59}H_{90}O_4$ ).



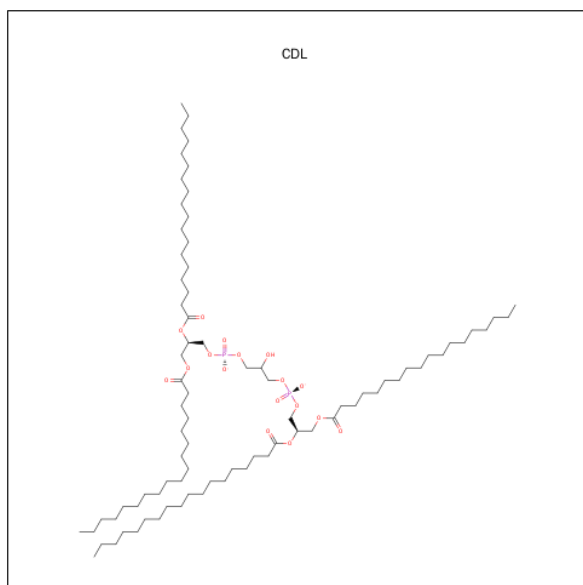
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	M	1	Total	C	O	0	0
			48	44	4		
9	L	1	Total	C	O	0	0
			48	44	4		

- Molecule 10 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula:  $C_7H_{16}O_3$ ).



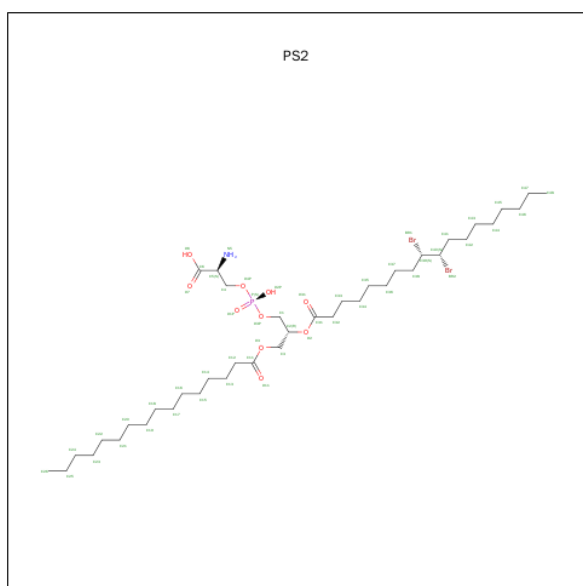
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	M	1	Total	C	O	0	0
			10	7	3		

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



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

- Molecule 12 is O-[[[(2R)-2-[[[(9S,10S)-9,10-DIBROMOOCTADECANOYL]OXY}-3-(PALM ITOYLOXY)PROPYL]OXY}(HYDROXY)PHOSPHORYL]-L-SERINE (three-letter code: PS2) (formula:  $C_{40}H_{76}Br_2NO_{10}P$ ).

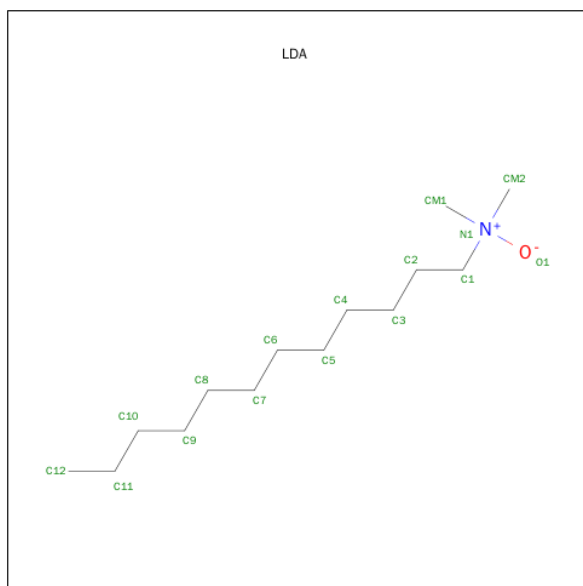


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
12	M	1	Total	Br	C	N	O	P	0	0
			54	2	40	1	10	1		

- Molecule 13 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
13	M	1	Total	C	N	O	0	0
			16	14	1	1		
13	H	1	Total	C	N	O	0	0
			16	14	1	1		
13	M	1	Total	C	N	O	0	0
			16	14	1	1		
13	H	1	Total	C	N	O	0	0
			16	14	1	1		
13	H	1	Total	C	N	O	0	0
			16	14	1	1		
13	M	1	Total	C	N	O	0	0
			16	14	1	1		
13	M	1	Total	C	N	O	0	0
			16	14	1	1		
13	M	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 14 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

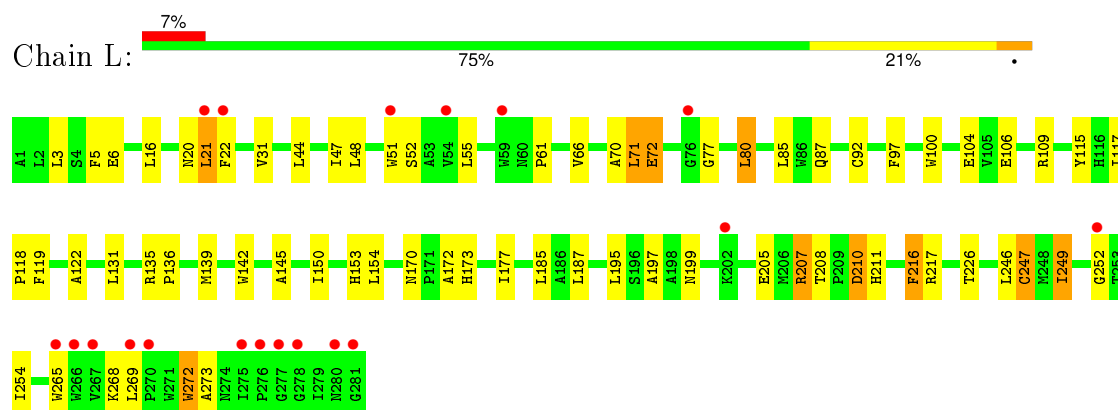
- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	H	165	Total	O	0	0
			165	165		
15	L	78	Total	O	0	0
			78	78		
15	M	108	Total	O	0	0
			108	108		

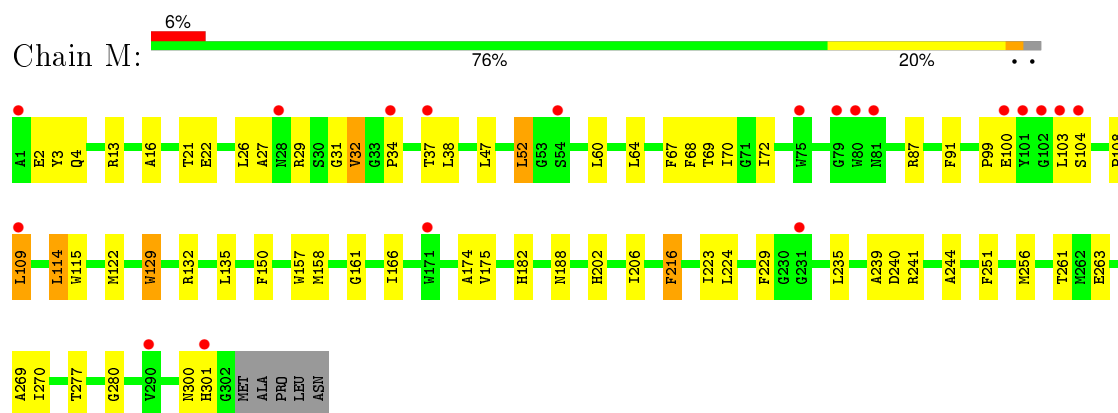
### 3 Residue-property plots [i](#)

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.

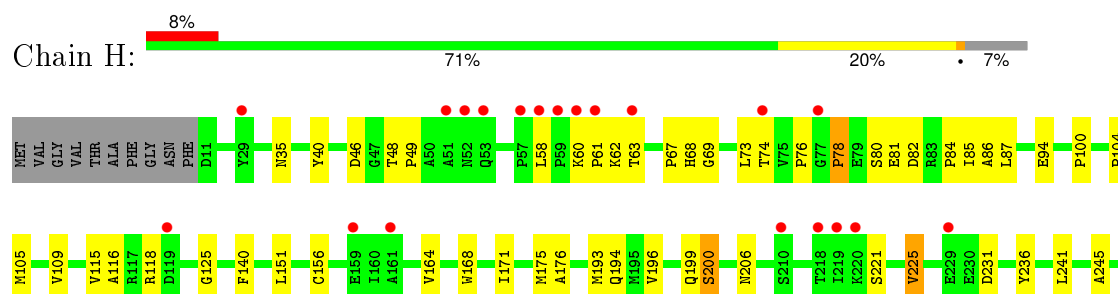
#### • Molecule 1: Reaction center protein L chain



#### • Molecule 2: Reaction center protein M chain



#### • Molecule 3: Reaction center protein H chain



R248			
R249			
S250			
V251			
VAL			
ALA			
ALA			
MET			
LEU			
ALA			
GLU			
TYR			
ALA			

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	139.35Å 139.35Å 183.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.29 – 3.00 38.27 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (39.29-3.00) 99.4 (38.27-3.00)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.77 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.174 , 0.227 0.178 , 0.225	Depositor DCC
$R_{free}$ test set	2083 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	75.3	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 103.6	EDS
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 41494 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7685	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: BCL, GOL, LDA, CDL, BPH, K, HTO, FE, PS2, U10, PO4

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	0.85	0/2350	0.79	0/3216
2	M	0.87	1/2552 (0.0%)	0.85	4/3482 (0.1%)
3	H	0.88	1/1921 (0.1%)	0.89	0/2612
All	All	0.86	2/6823 (0.0%)	0.84	4/9310 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	129	TRP	CB-CG	-5.74	1.40	1.50
3	H	94	GLU	CG-CD	5.52	1.60	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	241	ARG	NE-CZ-NH1	-5.62	117.49	120.30
2	M	3	TYR	CB-CG-CD2	-5.47	117.72	121.00
2	M	3	TYR	CB-CG-CD1	5.18	124.11	121.00
2	M	29	ARG	NE-CZ-NH1	5.11	122.86	120.30

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	L	2249	0	2210	53	0
2	M	2452	0	2357	65	0
3	H	1846	0	1866	42	0
4	M	1	0	0	0	0
5	H	1	0	0	0	0
6	M	10	0	0	0	0
7	L	132	0	148	12	0
7	M	132	0	148	14	0
8	L	65	0	76	2	0
8	M	65	0	76	5	0
9	L	48	0	63	9	0
9	M	48	0	63	4	0
10	M	10	0	16	0	0
11	M	81	0	106	3	0
12	M	54	0	72	8	0
13	H	48	0	93	1	0
13	M	80	0	155	21	0
14	H	6	0	8	0	0
14	M	6	0	8	2	0
15	H	165	0	0	8	0
15	L	78	0	0	1	0
15	M	108	0	0	5	0
All	All	7685	0	7465	188	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 13.

The worst 5 of 188 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)
9:L:502:U10:H4M3	9:L:502:U10:H3M2	1.31	1.12
3:H:250:SER:O	3:H:251:VAL:CG2	2.11	0.99
2:M:16:ALA:HB1	2:M:32:VAL:HG11	1.46	0.97
3:H:250:SER:O	3:H:251:VAL:HG23	1.64	0.97
7:M:311:BCL:HBB2	7:M:311:BCL:HMB1	1.51	0.91

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	282/281 (100%)	263 (93%)	18 (6%)	1 (0%)	39	80
2	M	305/307 (99%)	283 (93%)	21 (7%)	1 (0%)	46	84
3	H	244/260 (94%)	237 (97%)	5 (2%)	2 (1%)	24	66
All	All	831/848 (98%)	783 (94%)	44 (5%)	4 (0%)	34	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	M	109	LEU
1	L	31	VAL
3	H	86	ALA
3	H	78	PRO

### 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	L	223/220 (101%)	210 (94%)	13 (6%)	25	63
2	M	241/240 (100%)	230 (95%)	11 (5%)	33	73
3	H	201/208 (97%)	194 (96%)	7 (4%)	43	80
All	All	665/668 (100%)	634 (95%)	31 (5%)	33	72

5 of 31 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
2	M	37	THR
2	M	72	ILE
3	H	221[B]	SER
2	M	38	LEU
2	M	104	SER

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

Mol	Chain	Res	Type
1	L	20	ASN
2	M	202	HIS
3	H	68	HIS
3	H	141	HIS

### 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 25 ligands modelled in this entry, 2 are 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	$\# Z  > 2$
14	GOL	H	705	-	5,5,5	0.36	0	5,5,5	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	LDA	H	902	-	15,15,15	3.44	1 (6%)	16,17,17	1.18	2 (12%)
13	LDA	H	904	-	15,15,15	3.63	1 (6%)	16,17,17	0.74	0
13	LDA	H	905	-	15,15,15	3.80	2 (13%)	16,17,17	0.50	0
7	BCL	L	312	1	53,74,74	0.73	0	57,115,115	1.32	9 (15%)
7	BCL	L	314	1	53,74,74	1.03	4 (7%)	57,115,115	1.93	18 (31%)
8	BPH	L	402	-	64,70,70	0.68	0	73,101,101	1.39	8 (10%)
9	U10	L	502	-	48,48,63	1.13	4 (8%)	58,61,79	1.73	13 (22%)
7	BCL	M	311	2	53,74,74	0.98	2 (3%)	57,115,115	1.81	14 (24%)
7	BCL	M	313	2	53,74,74	0.86	0	57,115,115	1.36	10 (17%)
8	BPH	M	401	-	64,70,70	0.79	1 (1%)	73,101,101	1.60	11 (15%)
9	U10	M	501	-	48,48,63	1.18	7 (14%)	58,61,79	1.50	12 (20%)
6	PO4	M	701	-	4,4,4	0.26	0	6,6,6	0.32	0
6	PO4	M	702	-	4,4,4	0.32	0	6,6,6	0.30	0
10	HTO	M	703	-	9,9,9	0.84	0	8,10,10	1.79	3 (37%)
14	GOL	M	704	-	5,5,5	0.46	0	5,5,5	0.45	0
11	CDL	M	800	-	80,80,99	1.23	5 (6%)	82,92,111	1.37	9 (10%)
12	PS2	M	802	-	50,53,53	1.10	4 (8%)	52,62,62	2.54	11 (21%)
13	LDA	M	901	-	15,15,15	4.07	1 (6%)	16,17,17	1.08	2 (12%)
13	LDA	M	903	-	15,15,15	3.51	1 (6%)	16,17,17	1.76	2 (12%)
13	LDA	M	906	-	15,15,15	2.68	1 (6%)	16,17,17	1.43	2 (12%)
13	LDA	M	907	-	15,15,15	3.00	1 (6%)	16,17,17	1.16	2 (12%)
13	LDA	M	920	-	15,15,15	3.11	1 (6%)	16,17,17	0.96	1 (6%)

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
14	GOL	H	705	-	-	0/4/4/4	0/0/0/0
13	LDA	H	902	-	-	0/13/13/13	0/0/0/0
13	LDA	H	904	-	-	0/13/13/13	0/0/0/0
13	LDA	H	905	-	-	0/13/13/13	0/0/0/0
7	BCL	L	312	1	-	0/37/137/137	0/0/9/9
7	BCL	L	314	1	-	0/37/137/137	0/0/9/9
8	BPH	L	402	-	-	0/54/105/105	0/1/6/6
9	U10	L	502	-	-	0/45/69/87	0/1/1/1
7	BCL	M	311	2	-	0/37/137/137	0/0/9/9

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	BCL	M	313	2	-	0/37/137/137	0/0/9/9
8	BPH	M	401	-	-	0/54/105/105	0/1/6/6
9	U10	M	501	-	-	0/45/69/87	0/1/1/1
6	PO4	M	701	-	-	0/0/0/0	0/0/0/0
6	PO4	M	702	-	-	0/0/0/0	0/0/0/0
10	HTO	M	703	-	-	0/10/10/10	0/0/0/0
14	GOL	M	704	-	-	0/4/4/4	0/0/0/0
11	CDL	M	800	-	-	0/91/91/110	0/0/0/0
12	PS2	M	802	-	-	0/58/62/62	0/0/0/0
13	LDA	M	901	-	-	0/13/13/13	0/0/0/0
13	LDA	M	903	-	-	0/13/13/13	0/0/0/0
13	LDA	M	906	-	-	0/13/13/13	0/0/0/0
13	LDA	M	907	-	-	0/13/13/13	0/0/0/0
13	LDA	M	920	-	-	0/13/13/13	0/0/0/0

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	M	901	LDA	O1-N1	-15.58	1.24	1.39
13	H	905	LDA	O1-N1	-14.48	1.25	1.39
13	H	904	LDA	O1-N1	-13.83	1.26	1.39
13	M	903	LDA	O1-N1	-13.26	1.27	1.39
13	H	902	LDA	O1-N1	-13.12	1.27	1.39

The worst 5 of 129 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	M	802	PS2	C3-C2-C1	-6.53	96.81	112.07
12	M	802	PS2	BR1-C39-C40	-5.76	98.40	110.23
7	L	314	BCL	O1D-CGD-CBD	-5.46	116.79	124.62
13	M	903	LDA	O1-N1-CM2	-4.95	102.43	109.05
8	M	401	BPH	OBD-CAD-CBD	-4.87	118.58	125.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

17 monomers are involved in 73 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	H	905	LDA	1	0
7	L	312	BCL	8	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	L	314	BCL	5	0
8	L	402	BPH	2	0
9	L	502	U10	9	0
7	M	311	BCL	9	0
7	M	313	BCL	6	0
8	M	401	BPH	5	0
9	M	501	U10	4	0
14	M	704	GOL	2	0
11	M	800	CDL	3	0
12	M	802	PS2	8	0
13	M	901	LDA	6	0
13	M	903	LDA	6	0
13	M	906	LDA	1	0
13	M	907	LDA	1	0
13	M	920	LDA	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](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	L	281/281 (100%)	0.18	19 (6%) 20 7	61, 70, 78, 86	0
2	M	302/307 (98%)	0.31	19 (6%) 23 9	62, 69, 78, 113	0
3	H	241/260 (92%)	0.38	22 (9%) 11 4	59, 69, 80, 100	0
All	All	824/848 (97%)	0.28	60 (7%) 18 6	59, 69, 79, 113	0

The worst 5 of 60 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	77	GLY	4.8
2	M	1	ALA	3.9
3	H	219	ILE	3.8
3	H	218	THR	3.7
2	M	104	SER	3.7

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
13	LDA	M	906	16/16	0.72	0.58	13.26	57,61,68,70	16
14	GOL	M	704	6/6	0.71	1.21	11.68	68,71,72,74	6
13	LDA	M	903	16/16	0.83	0.50	5.25	41,60,71,72	16
13	LDA	M	907	16/16	0.75	0.56	4.99	63,67,78,78	16
11	CDL	M	800	81/100	0.61	0.52	4.16	57,70,81,82	81
13	LDA	H	905	16/16	0.50	0.58	3.80	65,69,74,75	16
13	LDA	M	920	16/16	0.69	0.48	3.50	65,70,85,87	16
13	LDA	H	902	16/16	0.55	0.73	3.03	55,59,73,73	16
12	PS2	M	802	54/54	0.48	0.62	2.84	48,62,75,77	54
9	U10	L	502	48/63	0.70	0.44	2.75	52,57,69,71	48
9	U10	M	501	48/63	0.83	0.38	1.26	64,72,91,92	0
8	BPH	M	401	65/65	0.84	0.31	1.12	61,71,110,111	0
7	BCL	L	312	66/66	0.89	0.26	1.02	60,66,77,82	0
13	LDA	M	901	16/16	0.84	0.33	0.65	67,70,73,74	16
7	BCL	M	313	66/66	0.95	0.24	0.53	55,65,80,84	0
7	BCL	M	311	66/66	0.95	0.23	0.17	52,66,113,114	0
6	PO4	M	701	5/5	0.92	0.33	0.10	61,62,63,64	5
8	BPH	L	402	65/65	0.94	0.22	0.08	61,71,74,75	0
7	BCL	L	314	66/66	0.95	0.21	0.02	62,69,74,78	0
5	K	H	700	1/1	0.97	0.10	-1.27	63,63,63,63	0
4	FE	M	500	1/1	0.99	0.19	-1.52	70,70,70,70	0
10	HTO	M	703	10/10	0.53	0.52	-	58,61,63,63	10
6	PO4	M	702	5/5	0.62	0.39	-	64,66,68,68	5
13	LDA	H	904	16/16	0.32	1.04	-	53,57,61,62	16
14	GOL	H	705	6/6	0.58	0.23	-	56,58,60,61	6

## 6.5 Other polymers [i](#)

There are no such residues in this entry.