



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:15 PM GMT

PDB ID : 1JGZ
Title : Photosynthetic Reaction Center Mutant With Tyr M 76 Replaced With Lys
Authors : Camara-Artigas, A.; Magee, C.L.; Williams, J.C.; Allen, J.P.
Deposited on : 2001-06-27
Resolution : 2.70 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtrriage (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

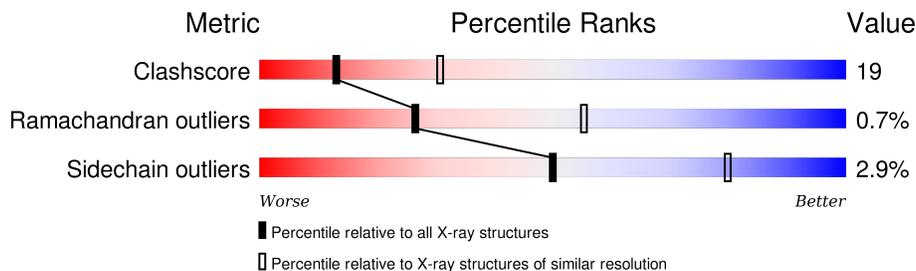
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 7096 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 Photosynthetic Reaction Center L subunit.

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

- Molecule 2 is a protein called Photosynthetic Reaction Center M subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	M	302	2405	1604	395	396	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	76	LYS	TYR	ENGINEERED	UNP P02953

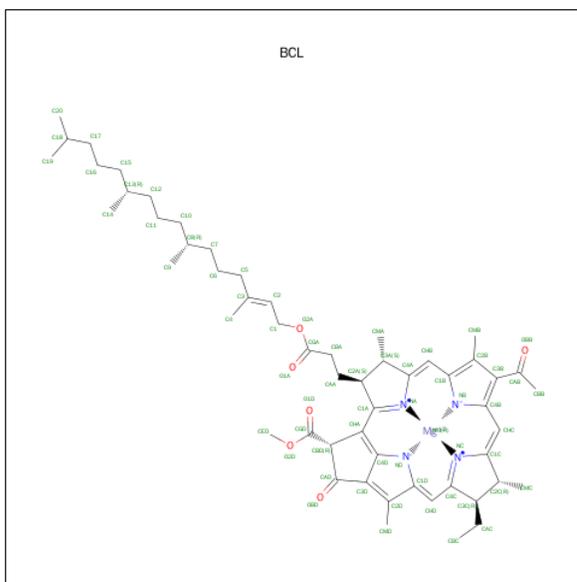
- Molecule 3 is a protein called Photosynthetic Reaction Center H subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	236	1794	1148	305	332	9	0	0	0

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

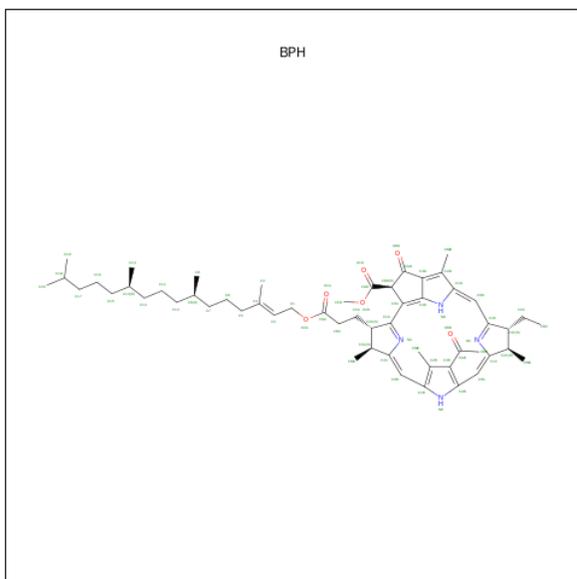
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	M	1	Total	Fe	0	0
			1	1		

- Molecule 5 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: C₅₅H₇₄MgN₄O₆).



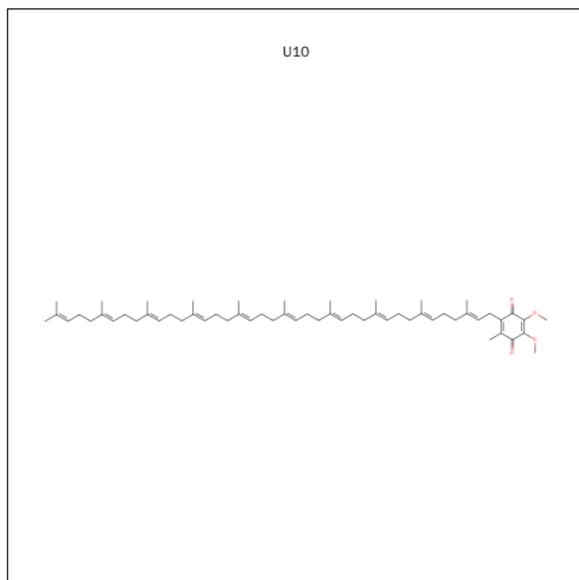
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Mg	N			O
5	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

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



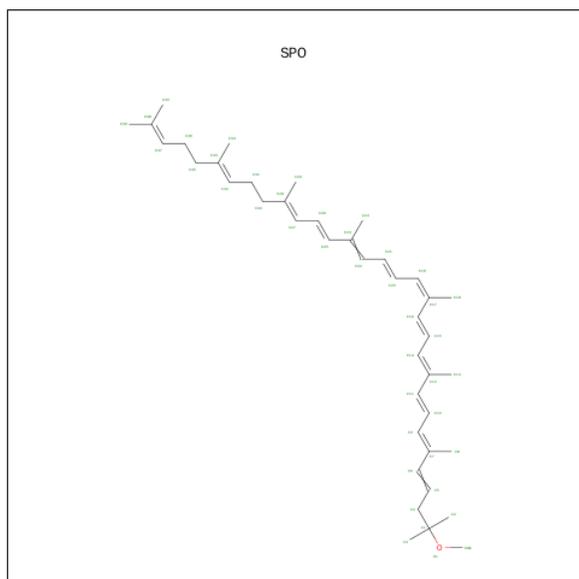
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	M	1	Total	C	N	O	0	0
			65	55	4	6		
6	L	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 7 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$).



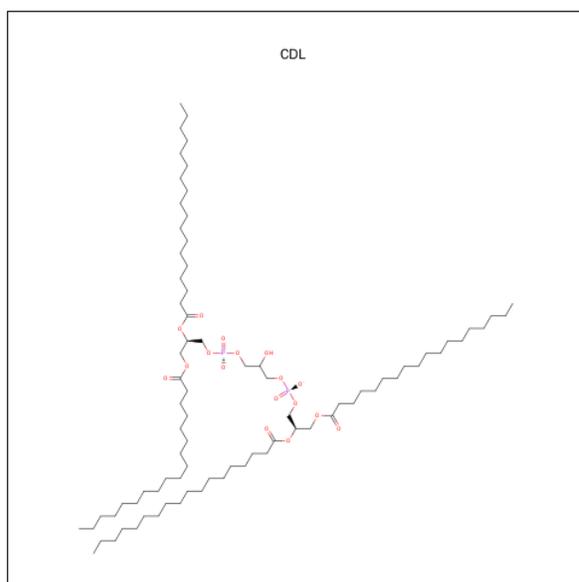
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	M	1	Total	C	O	0	0
			48	44	4		

- Molecule 8 is SPHEROIDENE (three-letter code: SPO) (formula: $C_{41}H_{60}O$).



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

- Molecule 9 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



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

- Molecule 10 is water.

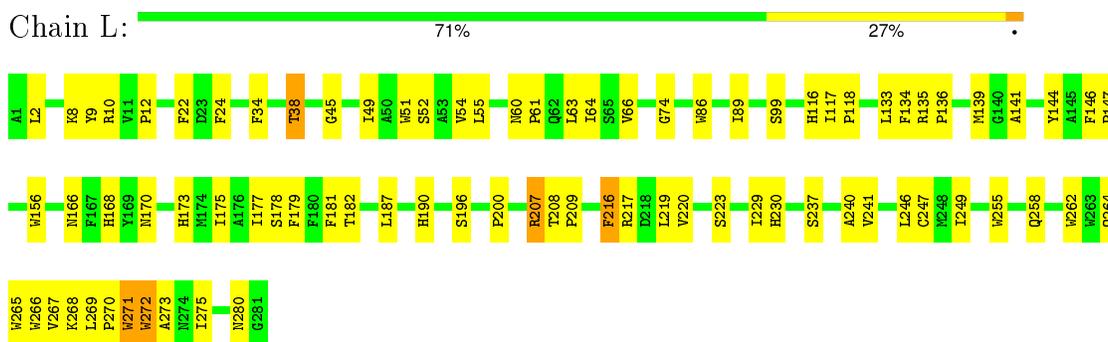
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	H	38	Total	O	0	0
			38	38		
10	L	25	Total	O	0	0
			25	25		
10	M	36	Total	O	0	0
			36	36		

3 Residue-property plots

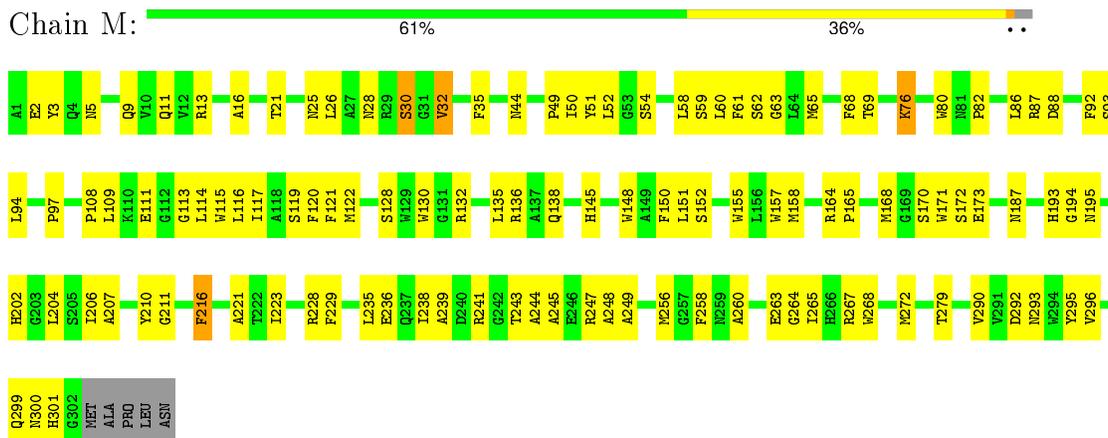
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

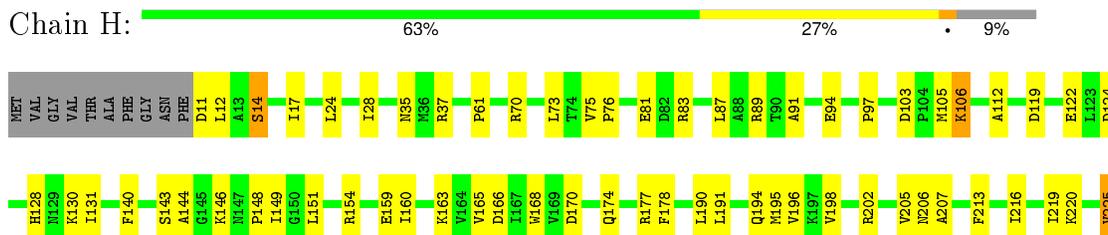
- Molecule 1: Photosynthetic Reaction Center L subunit



- Molecule 2: Photosynthetic Reaction Center M subunit



- Molecule 3: Photosynthetic Reaction Center H subunit



T226		
E229		
E230		
D231		
K232		
I233		
C234		
G235		
Y236		
Y237		
L241		
R242		
Y243		
A244		
A245		
P246		
LYS		
ARG		
LYS		
LYS		
SER		
VAL		
VAL		
ALA		
ALA		
ALA		
MET		
LEU		
ALA		
GLU		
TYR		
ALA		

4 Data and refinement statistics

Xtrriage (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, α , β , γ	142.61Å 142.61Å 187.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.64 – 2.70	Depositor
% Data completeness (in resolution range)	72.4 (28.64-2.70)	Depositor
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.215 , 0.249	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	7096	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

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: BCL, CDL, BPH, 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	0.46	0/2320	0.63	0/3175
2	M	0.46	0/2496	0.61	0/3406
3	H	0.43	0/1842	0.67	0/2509
All	All	0.45	0/6658	0.63	0/9090

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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 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	2232	0	2187	93	0
2	M	2405	0	2325	130	0
3	H	1794	0	1792	59	0
4	M	1	0	0	0	0
5	L	132	0	148	9	0
5	M	132	0	148	12	0
6	L	65	0	76	6	0
6	M	65	0	76	4	0
7	M	48	0	63	6	0
8	M	42	0	60	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	M	81	0	106	3	0
10	H	38	0	0	7	0
10	L	25	0	0	3	0
10	M	36	0	0	4	0
All	All	7096	0	6981	266	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 19.

The worst 5 of 266 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)
2:M:243:THR:CG2	2:M:247:ARG:HE	1.71	1.03
2:M:21:THR:HG23	2:M:26:LEU:HD21	1.51	0.93
2:M:279:THR:HB	10:M:1024:HOH:O	1.70	0.91
3:H:148:PRO:HA	3:H:151:LEU:HD12	1.53	0.90
3:H:245:ALA:HB3	3:H:246:PRO:HD3	1.56	0.87

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%)	247 (88%)	30 (11%)	2 (1%)	26	55
2	M	300/307 (98%)	268 (89%)	29 (10%)	3 (1%)	19	45
3	H	234/260 (90%)	212 (91%)	21 (9%)	1 (0%)	39	69
All	All	813/848 (96%)	727 (89%)	80 (10%)	6 (1%)	26	55

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	245	ALA
2	M	54	SER
2	M	30	SER
1	L	237	SER
1	L	200	PRO

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%)	214 (97%)	6 (3%)	52	82
2	M	236/240 (98%)	229 (97%)	7 (3%)	48	79
3	H	191/208 (92%)	185 (97%)	6 (3%)	47	78
All	All	647/668 (97%)	628 (97%)	19 (3%)	50	80

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	M	86	LEU
2	M	216	PHE
3	H	106	LYS
2	M	76	LYS
3	H	206	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	M	28	ASN
3	H	206	ASN
2	M	202	HIS
2	M	5	ASN
2	M	299	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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
5	BCL	L	850	2	53,74,74	1.46	8 (15%)	57,115,115	1.83	11 (19%)
5	BCL	L	851	1	53,74,74	1.32	6 (11%)	57,115,115	1.60	8 (14%)
6	BPH	L	855	-	64,70,70	1.35	10 (15%)	73,101,101	1.99	16 (21%)
9	CDL	M	3000	-	80,80,99	0.75	2 (2%)	82,92,111	0.95	5 (6%)
5	BCL	M	852	2	53,74,74	1.43	8 (15%)	57,115,115	1.78	10 (17%)
5	BCL	M	853	1	53,74,74	1.53	6 (11%)	57,115,115	1.98	11 (19%)
6	BPH	M	854	-	64,70,70	1.42	11 (17%)	73,101,101	1.65	16 (21%)
7	U10	M	857	-	48,48,63	2.33	14 (29%)	58,61,79	2.39	22 (37%)
8	SPO	M	859	-	40,41,41	3.58	24 (60%)	45,50,50	2.69	16 (35%)

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
5	BCL	L	850	2	-	0/37/137/137	0/0/9/9
5	BCL	L	851	1	-	0/37/137/137	0/0/9/9
6	BPH	L	855	-	-	0/54/105/105	0/1/6/6
9	CDL	M	3000	-	-	0/91/91/110	0/0/0/0
5	BCL	M	852	2	-	0/37/137/137	0/0/9/9
5	BCL	M	853	1	-	0/37/137/137	0/0/9/9
6	BPH	M	854	-	-	0/54/105/105	0/1/6/6
7	U10	M	857	-	-	0/45/69/87	0/1/1/1
8	SPO	M	859	-	-	0/47/47/47	0/0/0/0

The worst 5 of 89 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	857	U10	C7-C8	-3.68	1.45	1.50
8	M	859	SPO	C4-C5	-3.68	1.44	1.50
6	L	855	BPH	C3D-CAD	-3.14	1.40	1.46
8	M	859	SPO	C31-C32	-3.11	1.41	1.50
6	M	854	BPH	C3D-CAD	-2.82	1.41	1.46

The worst 5 of 115 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	M	859	SPO	C25-C23-C22	-10.99	101.28	118.98
5	L	850	BCL	CMB-C2B-C1B	-6.14	118.20	128.36
5	M	852	BCL	CMB-C2B-C1B	-5.91	118.58	128.36
5	L	851	BCL	CMB-C2B-C1B	-5.81	118.75	128.36
7	M	857	U10	C10-C9-C8	-5.72	112.28	123.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	850	BCL	4	0
5	L	851	BCL	5	0
6	L	855	BPH	6	0
9	M	3000	CDL	3	0
5	M	852	BCL	6	0
5	M	853	BCL	7	0
6	M	854	BPH	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	M	857	U10	6	0
8	M	859	SPO	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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