



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 10:40 PM GMT

PDB ID : 1E6D
Title : PHOTOSYNTHETIC REACTION CENTER MUTANT WITH TRP M115 REPLACED WITH PHE (CHAIN M, WM115F) PHE M197 REPLACED WITH ARG (CHAIN M, FM197R)
Authors : Ridge, J.P.; Fyfe, P.K.; Mcauley, K.E.; Van Brederode, M.E.; Robert, B.; Van Grondelle, R.; Isaacs, N.W.; Cogdell, R.J.; Jones, M.R.
Deposited on : 2000-08-11
Resolution : 2.30 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

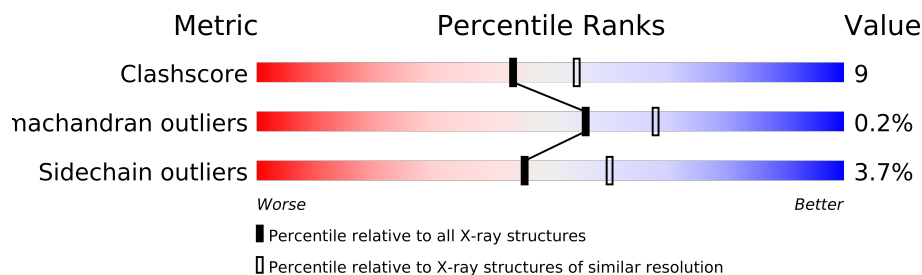
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.30 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	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

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

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 7334 atoms, of which 0 are hydrogen and 0 are deuterium.

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 H SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	240	Total	C	N	O	S	0	0	0
			1829	1169	314	337	9			

- Molecule 2 is a protein called PHOTOSYNTHETIC REACTION CENTER L SUBUNIT.

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

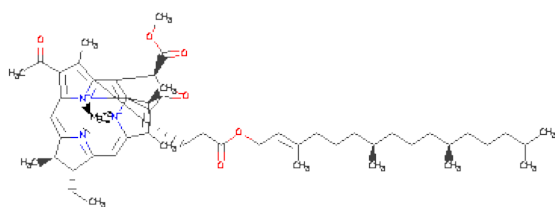
- Molecule 3 is a protein called PHOTOSYNTHETIC REACTION CENTER M SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	302	Total	C	N	O	S	0	0	0
			2405	1602	396	397	10			

There are 2 discrepancies between the modelled and reference sequences:

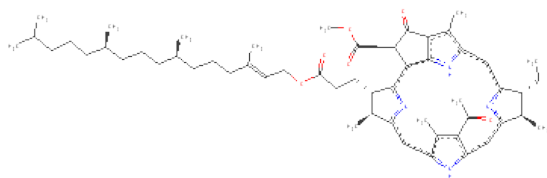
Chain	Residue	Modelled	Actual	Comment	Reference
M	197	ARG	PHE	ENGINEERED MUTATION	UNP P02953
M	115	PHE	TRP	ENGINEERED MUTATION	UNP P02953

- Molecule 4 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: C₅₅H₇₄MgN₄O₆).



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

- Molecule 5 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: $C_{55}H_{76}N_4O_6$).

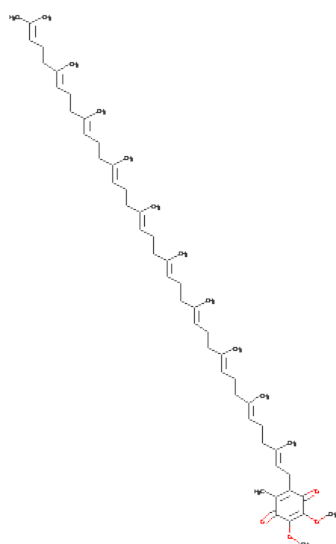


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	M	1	Total	C	N	O	0	0
			65	55	4	6		
5	L	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 6 is FE (III) ION (three-letter code: FE) (formula: Fe).

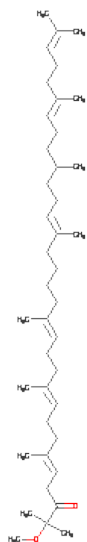
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	M	1	Total	Fe	0	0
			1	1		

- Molecule 7 is UBIQUINONE-10 (three-letter code: U10) (formula: C₅₉H₉₀O₄).



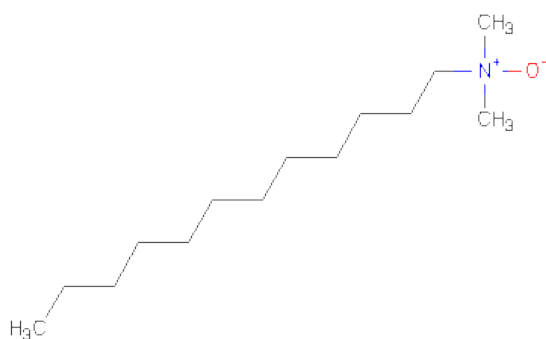
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	M	1	Total	C	O	0	0
			48	44	4		
7	L	1	Total	C	O	0	0
			48	44	4		

- Molecule 8 is SPEROIDENONE (three-letter code: SPN) (formula: C₄₁H₇₀O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	M	1	Total	C	O	0	0
			43	41	2		

- Molecule 9 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).



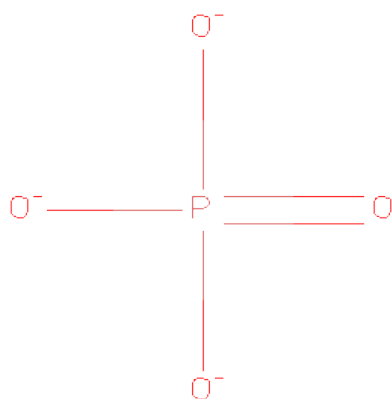
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	M	1	Total	C	N	O	0	0
			16	14	1	1		
9	M	1	Total	C	N	O	0	0
			16	14	1	1		

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

- Molecule 10 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	L	1	Total	O	0	0
			1	1		
11	M	2	Total	O	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	L	1	Total 1	O 1	0	0
11	H	1	Total 1	O 1	0	0
11	M	1	Total 1	O 1	0	0
11	H	94	Total 94	O 94	0	0
11	L	47	Total 47	O 47	0	0
11	M	65	Total 65	O 65	0	0

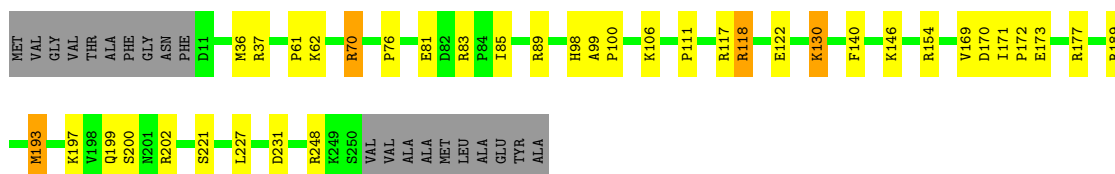
3 Residue-property plots

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.

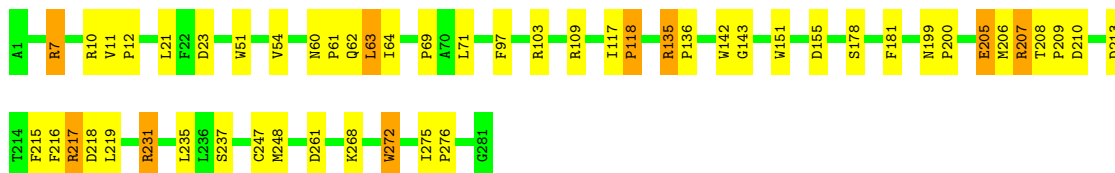
• Molecule 1: PHOTOSYNTHETIC REACTION CENTER H SUBUNIT

Chain H: 



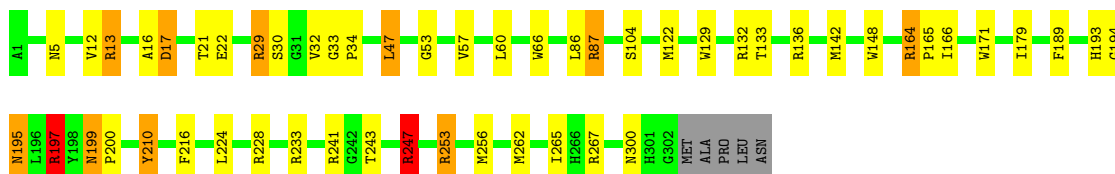
• Molecule 2: PHOTOSYNTHETIC REACTION CENTER L SUBUNIT

Chain L: 



• Molecule 3: PHOTOSYNTHETIC REACTION CENTER M SUBUNIT

Chain M: 



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, α , β , γ	141.20Å 141.20Å 187.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	26.40 – 2.30	Depositor
% Data completeness (in resolution range)	94.5 (26.40-2.30)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.174 , 0.200	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7334	wwPDB-VP
Average B, all atoms (Å ²)	42.0	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, SPN, 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	H	0.74	0/1877	1.29	14/2553 (0.5%)
2	L	0.73	1/2320 (0.0%)	1.12	15/3175 (0.5%)
3	M	0.70	0/2495	1.11	17/3404 (0.5%)
All	All	0.72	1/6692 (0.0%)	1.17	46/9132 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	237	SER	CA-CB	5.00	1.60	1.52

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	70	ARG	CD-NE-CZ	18.85	149.99	123.60
2	L	135	ARG	NE-CZ-NH2	-10.14	115.23	120.30
3	M	210	TYR	CB-CG-CD1	8.25	125.95	121.00
3	M	247	ARG	NE-CZ-NH2	7.74	124.17	120.30
1	H	117	ARG	NE-CZ-NH2	7.22	123.91	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1829	0	1836	17	0
2	L	2232	0	2187	36	0
3	M	2405	0	2324	44	0
4	L	132	0	148	5	0
4	M	132	0	148	14	0
5	L	65	0	75	6	0
5	M	65	0	76	10	0
6	M	1	0	0	0	0
7	L	48	0	63	9	0
7	M	48	0	63	3	0
8	M	43	0	69	2	0
9	H	32	0	62	0	0
9	M	80	0	155	11	0
10	M	10	0	0	3	0
11	H	95	0	0	1	0
11	L	49	0	0	8	0
11	M	68	0	0	1	0
All	All	7334	0	7206	124	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

The worst 5 of 124 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:M:243:THR:O	3:M:247:ARG:HG2	1.58	1.02
4:M:1303:BCL:H191	9:M:1706:LDA:H121	1.47	0.97
5:L:1402:BPH:HHC	5:L:1402:BPH:HBB3	1.51	0.93
2:L:215:PHE:HB2	3:M:142:MET:HE1	1.50	0.93
9:M:1701:LDA:H91	9:M:1702:LDA:H121	1.54	0.88

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	H	238/260 (92%)	233 (98%)	5 (2%)	0	100	100
2	L	279/281 (99%)	271 (97%)	8 (3%)	0	100	100
3	M	300/307 (98%)	290 (97%)	8 (3%)	2 (1%)	30	34
All	All	817/848 (96%)	794 (97%)	21 (3%)	2 (0%)	56	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	M	30	SER
3	M	195	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	195/208 (94%)	189 (97%)	6 (3%)	52	68
2	L	220/220 (100%)	211 (96%)	9 (4%)	41	55
3	M	236/240 (98%)	227 (96%)	9 (4%)	44	59
All	All	651/668 (98%)	627 (96%)	24 (4%)	45	60

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	216	PHE
2	L	268	LYS
3	M	247	ARG
2	L	235	LEU
2	L	247	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	M	28	ASN
3	M	299	GLN
3	M	193	HIS

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Mol	Chain	Res	Type
2	L	199	ASN
3	M	187	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 19 ligands modelled in this entry, 1 is monoatomic - leaving 18 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	$\# Z > 2$
9	LDA	H	1704	-	15,15,15	4.36	2 (13%)	17,17,17	4.15	2 (11%)
9	LDA	H	1707	-	15,15,15	4.34	2 (13%)	17,17,17	1.95	1 (5%)
4	BCL	L	1302	2	74,74,74	1.58	13 (17%)	97,115,115	1.87	27 (27%)
4	BCL	L	1304	2	74,74,74	1.66	11 (14%)	97,115,115	1.97	26 (26%)
5	BPH	L	1402	-	70,70,70	1.58	13 (18%)	94,101,101	1.91	25 (26%)
7	U10	L	1502	-	48,48,63	2.12	16 (33%)	59,61,79	1.77	10 (16%)
4	BCL	M	1301	3	74,74,74	1.63	13 (17%)	97,115,115	1.90	25 (25%)
4	BCL	M	1303	3	74,74,74	1.51	14 (18%)	97,115,115	1.73	21 (21%)
5	BPH	M	1401	-	70,70,70	1.55	13 (18%)	94,101,101	1.95	23 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	U10	M	1501	-	48,48,63	2.01	18 (37%)	59,61,79	1.66	12 (20%)
8	SPN	M	1600	-	42,42,42	4.20	18 (42%)	52,52,52	2.55	20 (38%)
9	LDA	M	1701	-	15,15,15	4.38	3 (20%)	17,17,17	3.98	2 (11%)
9	LDA	M	1702	-	15,15,15	4.87	3 (20%)	17,17,17	2.52	2 (11%)
9	LDA	M	1703	-	15,15,15	4.35	3 (20%)	17,17,17	2.91	3 (17%)
9	LDA	M	1705	-	15,15,15	4.32	3 (20%)	17,17,17	2.49	2 (11%)
9	LDA	M	1706	-	15,15,15	4.72	2 (13%)	17,17,17	2.48	2 (11%)
10	PO4	M	1800	-	4,4,4	1.35	1 (25%)	6,6,6	0.42	0
10	PO4	M	1801	-	4,4,4	0.80	0	6,6,6	0.37	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
9	LDA	H	1704	-	-	0/13/13/13	0/0/0/0
9	LDA	H	1707	-	-	0/13/13/13	0/0/0/0
4	BCL	L	1302	2	-	0/41/137/137	0/0/9/9
4	BCL	L	1304	2	1/1/21/25	0/41/137/137	0/0/9/9
5	BPH	L	1402	-	2/2/18/22	0/49/105/105	0/0/6/6
7	U10	L	1502	-	-	0/45/69/87	0/1/1/1
4	BCL	M	1301	3	1/1/21/25	0/41/137/137	0/0/9/9
4	BCL	M	1303	3	-	0/41/137/137	0/0/9/9
5	BPH	M	1401	-	1/1/18/22	0/49/105/105	0/0/6/6
7	U10	M	1501	-	-	0/45/69/87	0/1/1/1
8	SPN	M	1600	-	-	0/51/51/51	0/0/0/0
9	LDA	M	1701	-	-	0/13/13/13	0/0/0/0
9	LDA	M	1702	-	-	0/13/13/13	0/0/0/0
9	LDA	M	1703	-	-	0/13/13/13	0/0/0/0
9	LDA	M	1705	-	-	0/13/13/13	0/0/0/0
9	LDA	M	1706	-	-	0/13/13/13	0/0/0/0
10	PO4	M	1800	-	-	0/0/0/0	0/0/0/0
10	PO4	M	1801	-	-	0/0/0/0	0/0/0/0

The worst 5 of 148 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	M	1702	LDA	O1-N1	-18.35	1.22	1.39
9	M	1706	LDA	O1-N1	-17.88	1.22	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	M	1703	LDA	O1-N1	-16.43	1.23	1.39
9	H	1707	LDA	O1-N1	-16.40	1.23	1.39
9	M	1701	LDA	O1-N1	-16.35	1.23	1.39

The worst 5 of 203 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	H	1704	LDA	C2-C1-N1	16.75	142.67	113.80
9	M	1701	LDA	C2-C1-N1	15.97	141.33	113.80
9	M	1703	LDA	C2-C1-N1	11.23	133.15	113.80
9	M	1702	LDA	C2-C1-N1	9.90	130.86	113.80
9	M	1706	LDA	C2-C1-N1	9.50	130.18	113.80

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	M	1301	BCL	C13
4	L	1304	BCL	C13
5	M	1401	BPH	C13
5	L	1402	BPH	C8
5	L	1402	BPH	C13

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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.