



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:36 PM GMT

PDB ID : 1PST
Title : CRYSTALLOGRAPHIC ANALYSES OF SITE-DIRECTED MUTANTS OF
THE PHOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER
SPHAEROIDES
Authors : Chirino, A.J.; Feher, G.; Rees, D.C.
Deposited on : 1993-12-13
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
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)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

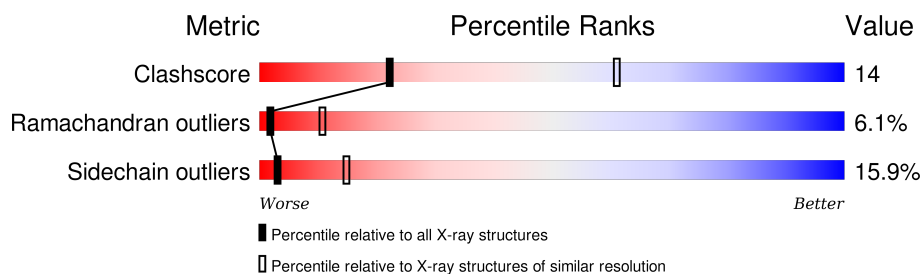
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (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 ≥ 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	266	 62% 30% 8% •
2	M	296	 56% 32% 9% •
3	H	237	 53% 33% 10% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	BPH	M	5	X	-	-	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6786 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	266	Total	C	N	O	S	0	0	0
			2121	1433	336	344	8			

- Molecule 2 is a protein called PHOTOSYNTHETIC REACTION CENTER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	296	Total	C	N	O	S	0	0	0
			2360	1579	384	387	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	202	LEU	HIS	CONFLICT	UNP P02953

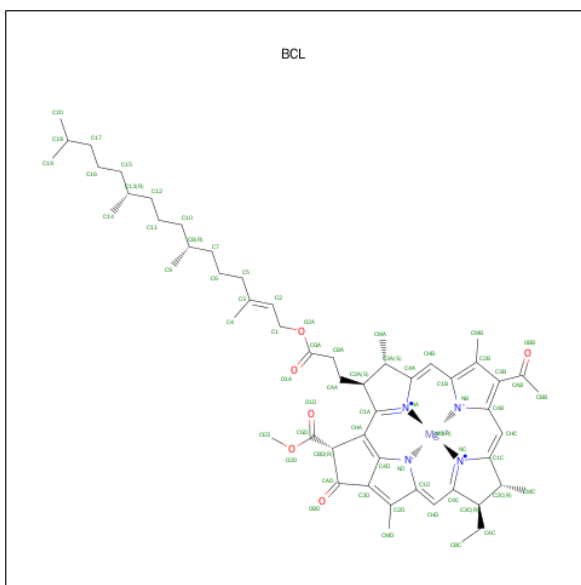
- Molecule 3 is a protein called PHOTOSYNTHETIC REACTION CENTER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	237	Total	C	N	O	S	0	0	0
			1807	1156	310	332	9			

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

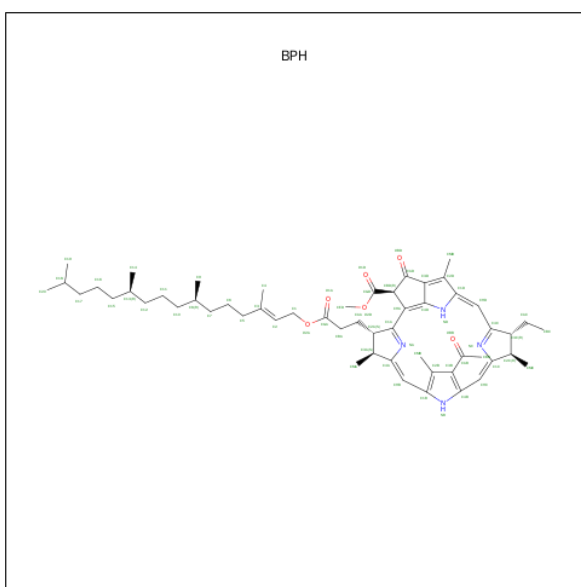
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	M	1	Total	Fe	0	0
			1	1		

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	M	1	Total 51	C 40	Mg 1	N 4	O 6	0	0
5	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
5	L	1	Total 51	C 40	Mg 1	N 4	O 6	0	0

- Molecule 6 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: $\text{C}_{55}\text{H}_{76}\text{N}_4\text{O}_6$).



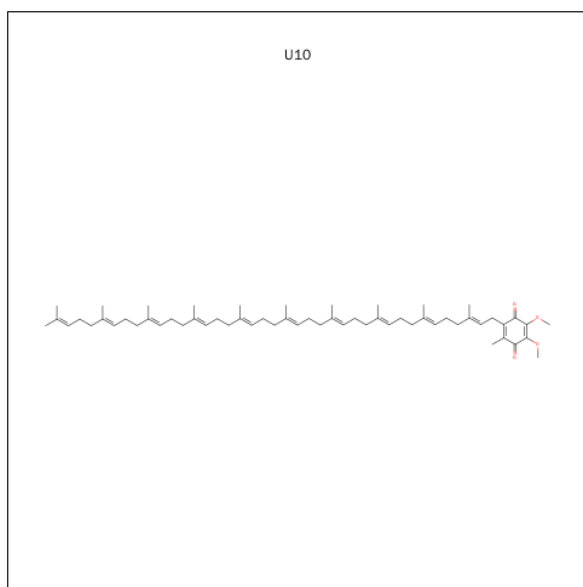
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	M	1	Total	C	N	O	0	0
			65	55	4	6		

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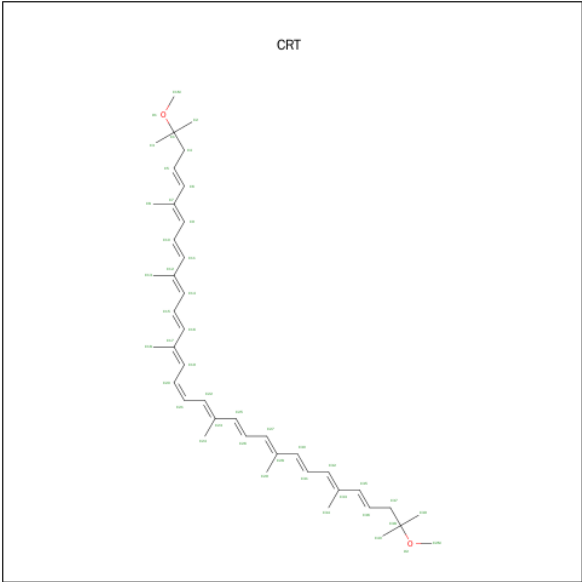
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	M	1	Total	C	N	O	0	0
			65	55	4	6		
6	L	1	Total	C	N	O	0	0
			65	55	4	6		

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	M	1	Total	C	O	0	0
			51	47	4		
7	L	1	Total	C	O	0	0
			41	37	4		

- Molecule 8 is SPIRILLOXANTHIN (three-letter code: CRT) (formula: C₄₂H₆₀O₂).



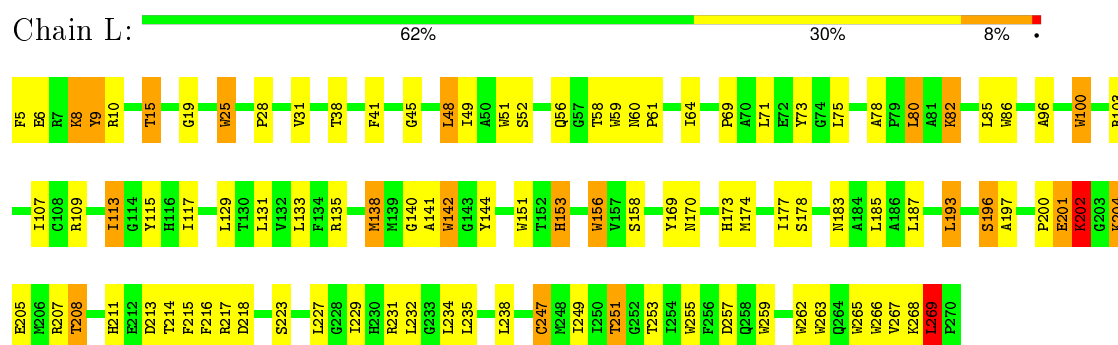
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	M	1	Total	C	O	0	0
			42	41	1		

3 Residue-property plots

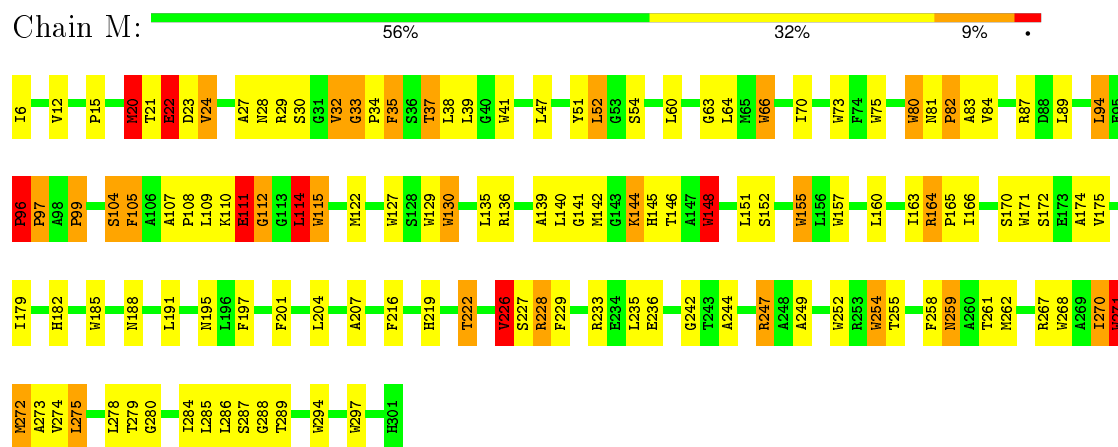
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

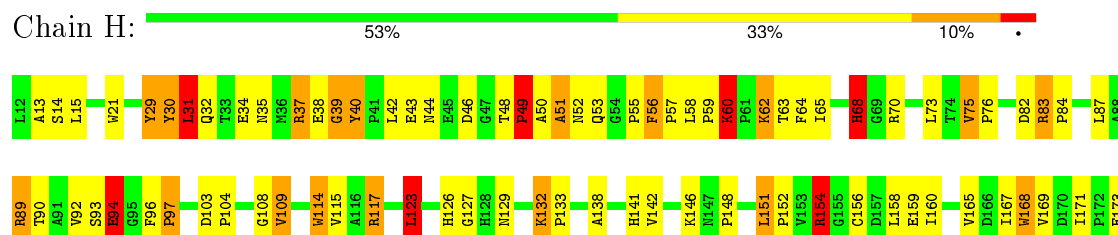
• Molecule 1: PHOTOSYNTHETIC REACTION CENTER



• Molecule 2: PHOTOSYNTHETIC REACTION CENTER



• Molecule 3: PHOTOSYNTHETIC REACTION CENTER



R177	F178	K184	D185	T188	R189	L190	L191	P192	M193	R202	V205	N206	A207	L208	S209	S210	D211	L212	F213	A214	G215	P217	T218	I219	K220	S221	E224	L228	T233	V237	L241	P246	K247	R248
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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	138.00 Å 77.50 Å 141.80 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.218 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6786	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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, BPH, FE, CRT, 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	0.83	0/2204	1.66	54/3014 (1.8%)
2	M	0.90	0/2450	1.77	81/3344 (2.4%)
3	H	0.80	0/1855	1.56	30/2523 (1.2%)
All	All	0.85	0/6509	1.67	165/8881 (1.9%)

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
1	L	0	1
2	M	0	2
3	H	0	4
All	All	0	7

There are no bond length outliers.

The worst 5 of 165 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	100	TRP	CD1-CG-CD2	10.03	114.33	106.30
3	H	168	TRP	CD1-CG-CD2	9.15	113.62	106.30
2	M	171	TRP	CD1-CG-CD2	9.08	113.56	106.30
1	L	86	TRP	CD1-CG-CD2	9.04	113.53	106.30
2	M	157	TRP	CD1-CG-CD2	8.71	113.27	106.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	H	40	TYR	Peptide
3	H	56	PHE	Peptide
1	L	269	LEU	Peptide
2	M	81	ASN	Peptide
2	M	96	PRO	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	2121	0	2077	53	0
2	M	2360	0	2285	75	0
3	H	1807	0	1814	60	0
4	M	1	0	0	0	0
5	L	117	0	115	11	0
5	M	51	0	41	8	0
6	L	65	0	76	7	0
6	M	130	0	152	7	0
7	L	41	0	52	5	0
7	M	51	0	68	5	0
8	M	42	0	57	2	0
All	All	6786	0	6737	187	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 14.

The worst 5 of 187 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)
3:H:154:ARG:HD2	3:H:160:ILE:HG12	1.52	0.92
2:M:229:PHE:HB2	2:M:244:ALA:HB2	1.58	0.84
1:L:205:GLU:HA	3:H:65:ILE:HG13	1.63	0.79
2:M:261:THR:HG22	3:H:40:TYR:HD1	1.49	0.76
2:M:27:ALA:HB2	2:M:51:TYR:HD1	1.50	0.74

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	264/266 (99%)	237 (90%)	20 (8%)	7 (3%)	6	32
2	M	294/296 (99%)	242 (82%)	30 (10%)	22 (8%)	1	6
3	H	235/237 (99%)	188 (80%)	28 (12%)	19 (8%)	1	5
All	All	793/799 (99%)	667 (84%)	78 (10%)	48 (6%)	2	11

5 of 48 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	71	LEU
1	L	115	TYR
1	L	201	GLU
1	L	269	LEU
2	M	22	GLU

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	210/210 (100%)	180 (86%)	30 (14%)	4	19
2	M	232/232 (100%)	197 (85%)	35 (15%)	3	17
3	H	192/192 (100%)	156 (81%)	36 (19%)	2	10
All	All	634/634 (100%)	533 (84%)	101 (16%)	3	15

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	M	114	LEU
2	M	258	PHE
3	H	212	LEU
2	M	148	TRP
2	M	216	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	173	HIS
1	L	211	HIS
2	M	11	GLN
3	H	141	HIS
3	H	204	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 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	2	1	53,74,74	1.12	6 (11%)	57,115,115	1.56	10 (17%)
6	BPH	L	271	-	64,70,70	1.09	6 (9%)	73,101,101	1.83	8 (10%)
7	U10	L	272	-	41,41,63	1.85	10 (24%)	49,52,79	1.70	12 (24%)
5	BCL	L	4	1	38,59,74	1.30	5 (13%)	40,97,115	2.22	9 (22%)
5	BCL	M	1	2	38,59,74	1.21	4 (10%)	40,97,115	2.02	10 (25%)
6	BPH	M	3	-	64,70,70	1.17	7 (10%)	73,101,101	1.70	12 (16%)
7	U10	M	303	-	51,51,63	1.69	13 (25%)	61,64,79	1.77	16 (26%)
8	CRT	M	304	-	40,41,43	4.05	26 (65%)	44,50,54	2.91	16 (36%)
6	BPH	M	5	-	64,70,70	1.15	8 (12%)	73,101,101	1.71	9 (12%)

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	2	1	-	0/37/137/137	0/0/9/9
6	BPH	L	271	-	-	0/54/105/105	0/1/6/6
7	U10	L	272	-	-	0/37/61/87	0/1/1/1
5	BCL	L	4	1	-	0/19/119/137	0/0/9/9
5	BCL	M	1	2	-	0/19/119/137	0/0/9/9
6	BPH	M	3	-	-	0/54/105/105	0/1/6/6
7	U10	M	303	-	-	0/49/73/87	0/1/1/1
8	CRT	M	304	-	-	1/47/47/51	0/0/0/0
6	BPH	M	5	-	2/2/18/22	1/54/105/105	0/1/6/6

The worst 5 of 85 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	M	304	CRT	C37-C38	-5.21	1.37	1.54
6	M	3	BPH	C3D-CAD	-4.39	1.37	1.46
7	L	272	U10	C7-C8	-4.13	1.44	1.50
8	M	304	CRT	C25-C23	-4.12	1.36	1.45
8	M	304	CRT	C30-C28	-3.97	1.37	1.45

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	M	304	CRT	C37-C36-C35	-8.56	106.03	125.67
6	L	271	BPH	O1D-CGD-CBD	-6.67	115.06	124.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	M	304	CRT	C36-C35-C33	-6.58	115.70	125.75
5	L	4	BCL	O1D-CGD-CBD	-6.32	115.57	124.62
8	M	304	CRT	C26-C27-C28	-6.09	118.41	127.20

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	M	5	BPH	C8
6	M	5	BPH	C13

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	M	5	BPH	OBB-CAB-C3B-C4B
8	M	304	CRT	C32-C31-C30-C28

There are no ring outliers.

9 monomers are involved in 39 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	2	BCL	8	0
6	L	271	BPH	7	0
7	L	272	U10	5	0
5	L	4	BCL	6	0
5	M	1	BCL	8	0
6	M	3	BPH	6	0
7	M	303	U10	5	0
8	M	304	CRT	2	0
6	M	5	BPH	1	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.