



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:58 PM GMT

PDB ID : 1Z9J
Title : Photosynthetic Reaction Center from Rhodobacter sphaeroides
Authors : Thielges, M.; Uyeda, G.; Camara-Artigas, A.; Kalman, L.; Williams, J.C.; Allen, J.P.
Deposited on : 2005-04-02
Resolution : 4.50 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) : 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

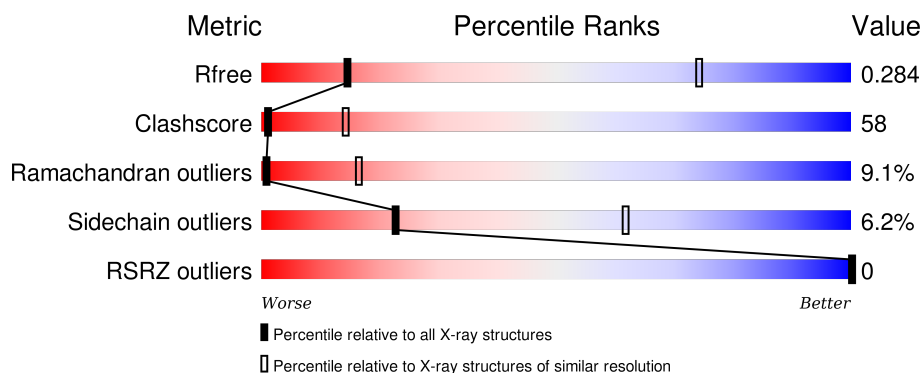
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.50 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	1071 (5.40-3.60)
Clashscore	102246	1003 (5.30-3.62)
Ramachandran outliers	100387	1117 (5.40-3.60)
Sidechain outliers	100360	1099 (5.40-3.60)
RSRZ outliers	91569	1075 (5.40-3.60)

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.

Mol	Chain	Length	Quality of chain
1	A	281	<div> <div>25%</div> <div>62%</div> <div>12%</div> <div>.</div> </div>
2	B	307	<div> <div>26%</div> <div>62%</div> <div>10%</div> <div>..</div> </div>
3	C	260	<div> <div>36%</div> <div>49%</div> <div>7%</div> <div>8%</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
6	BCL	A	850	-	-	-	X
6	BCL	A	851	-	-	-	X
7	BPH	B	854	-	-	-	X
8	U10	A	857	-	-	-	X
8	U10	B	856	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6957 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	A	281	Total	C	N	O	S	0	0	0
			2234	1507	357	362	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	131	HIS	LEU	ENGINEERED	UNP P02954

- Molecule 2 is a protein called Reaction center protein M chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	302	Total	C	N	O	S	0	0	0
			2415	1609	395	402	9			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	160	HIS	LEU	ENGINEERED	UNP P02953
B	164	TYR	ARG	ENGINEERED	UNP P02953
B	168	GLU	MET	ENGINEERED	UNP P02953
B	197	HIS	PHE	ENGINEERED	UNP P02953
B	288	ASP	GLY	ENGINEERED	UNP P02953

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	238	Total	C	N	O	S	0	0	0
			1814	1160	311	334	9			

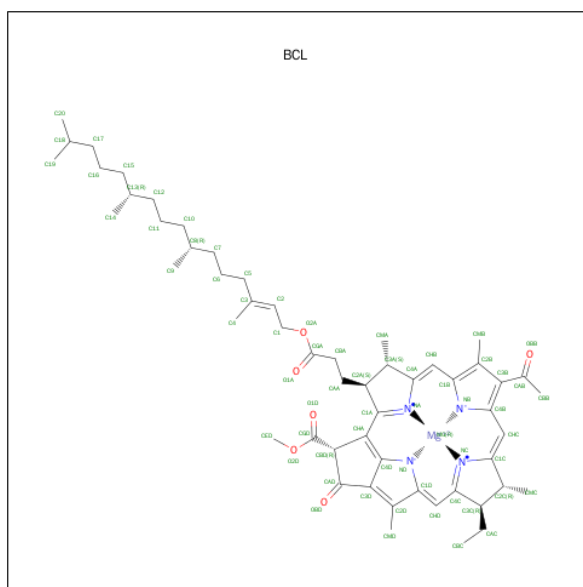
- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

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

- Molecule 5 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

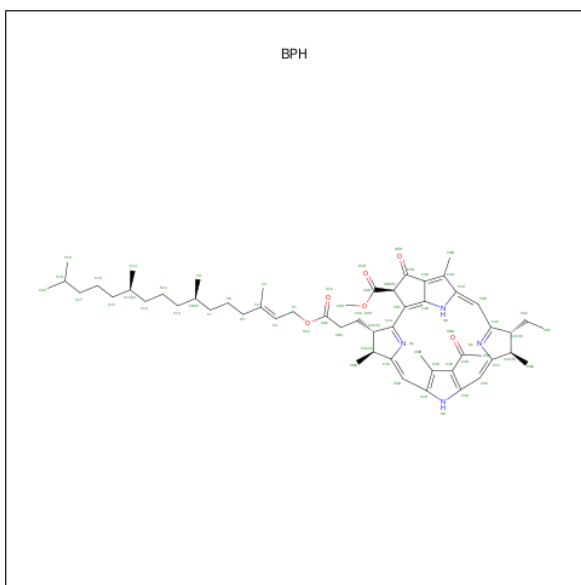
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Mn 1 1	0	0

- Molecule 6 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: C₅₅H₇₄MgN₄O₆).



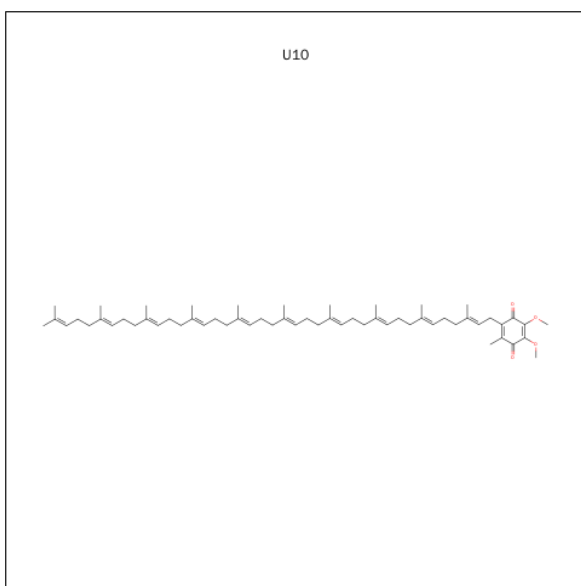
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C Mg N O 66 55 1 4 6	0	0
6	A	1	Total C Mg N O 66 55 1 4 6	0	0
6	B	1	Total C Mg N O 66 55 1 4 6	0	0
6	B	1	Total C Mg N O 66 55 1 4 6	0	0

- Molecule 7 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: C₅₅H₇₆N₄O₆).



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

- Molecule 8 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			48	44	4		
8	A	1	Total	C	O	0	0
			48	44	4		

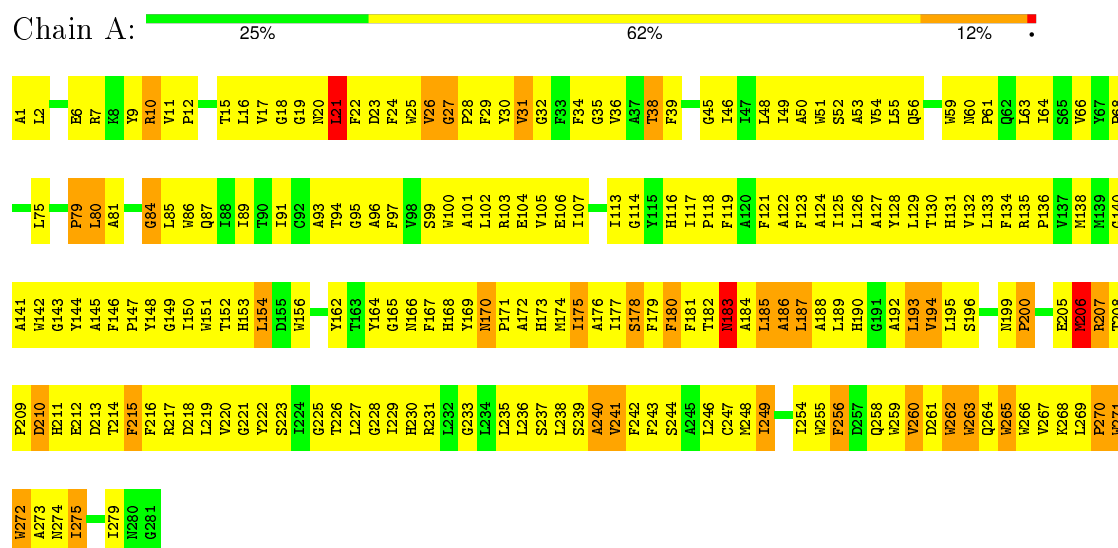
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	2	Total	O	0	0
			2	2		

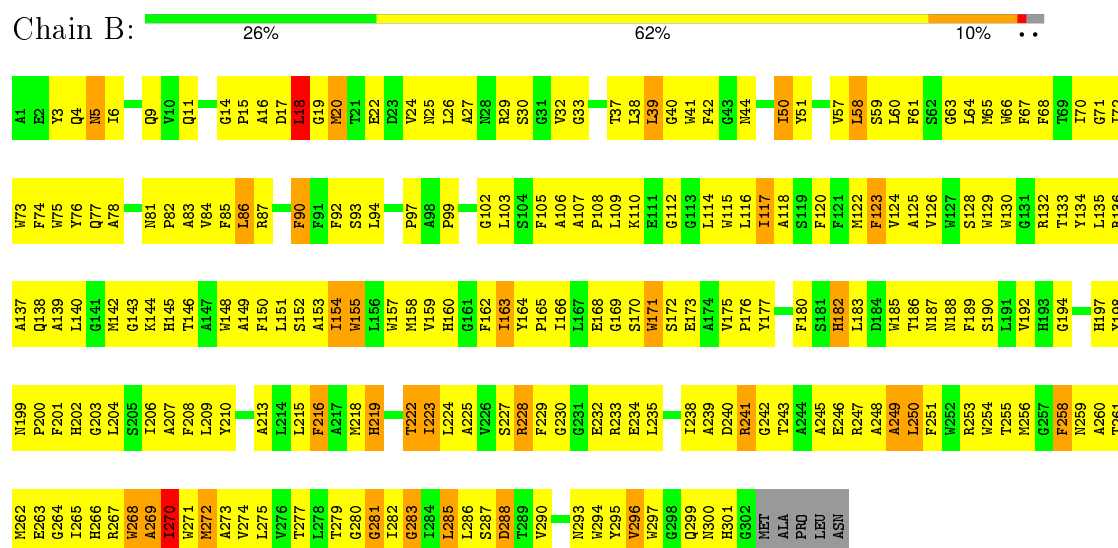
3 Residue-property plots

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.

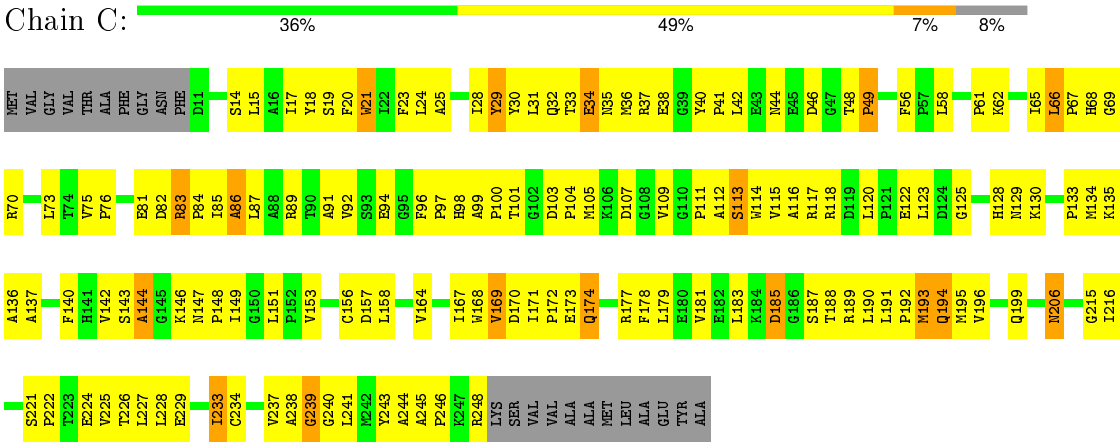
• Molecule 1: Reaction center protein L chain



• Molecule 2: Reaction center protein M chain



• Molecule 3: Reaction center protein H chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 2 2	Depositor
Cell constants a, b, c, α , β , γ	203.84Å 203.84Å 119.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 4.50 24.90 – 4.30	Depositor EDS
% Data completeness (in resolution range)	79.9 (19.96-4.50) 80.7 (24.90-4.30)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 4.24Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.299 , 0.338 0.227 , 0.284	Depositor DCC
R_{free} test set	613 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	145.2	Xtriage
Anisotropy	0.494	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.19 , -0.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 14195 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6957	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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, BPH, MN, FE, 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	A	0.63	0/2323	0.80	1/3179 (0.0%)
2	B	0.63	0/2509	0.79	1/3428 (0.0%)
3	C	0.62	1/1862 (0.1%)	0.80	0/2534
All	All	0.62	1/6694 (0.0%)	0.80	2/9141 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	21	TRP	CB-CG	-5.17	1.41	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	27	GLY	N-CA-C	-5.09	100.38	113.10
2	B	285	LEU	CA-CB-CG	-5.03	103.73	115.30

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	A	2234	0	2183	329	0
2	B	2415	0	2309	368	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1814	0	1818	187	1
4	B	1	0	0	0	0
5	B	1	0	0	0	0
6	A	132	0	148	20	0
6	B	132	0	148	18	0
7	A	65	0	76	19	0
7	B	65	0	76	14	0
8	A	48	0	63	7	0
8	B	48	0	63	15	0
9	B	2	0	0	1	0
All	All	6957	0	6884	802	1

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 58.

The worst 5 of 802 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:B:64:LEU:HD21	7:B:854:BPH:H112	1.32	1.10
2:B:267:ARG:O	2:B:270:ILE:HG22	1.65	0.96
1:A:171:PRO:HA	1:A:174:MET:HG3	1.48	0.95
2:B:242:GLY:HA2	3:C:117:ARG:HD2	1.49	0.94
1:A:114:GLY:H	2:B:225:ALA:HB1	1.32	0.93

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:128:HIS:NE2	3:C:128:HIS:NE2[5_656]	2.18	0.02

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	A	279/281 (99%)	199 (71%)	51 (18%)	29 (10%)	1	12
2	B	300/307 (98%)	202 (67%)	69 (23%)	29 (10%)	1	14
3	C	236/260 (91%)	175 (74%)	45 (19%)	16 (7%)	1	24
All	All	815/848 (96%)	576 (71%)	165 (20%)	74 (9%)	1	16

5 of 74 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	10	ARG
1	A	80	LEU
1	A	186	ALA
1	A	200	PRO
1	A	215	PHE

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	A	220/220 (100%)	201 (91%)	19 (9%)	13	49
2	B	237/241 (98%)	223 (94%)	14 (6%)	24	63
3	C	193/208 (93%)	186 (96%)	7 (4%)	42	75
All	All	650/669 (97%)	610 (94%)	40 (6%)	23	62

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	272	TRP
2	B	86	LEU
3	C	185	ASP
2	B	42	PHE
2	B	90	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	202	HIS
2	B	259	ASN
3	C	68	HIS
2	B	188	ASN
3	C	44	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	$\# Z > 2$
6	BCL	A	850	-	53,74,74	1.48	12 (22%)	57,115,115	1.85	10 (17%)
6	BCL	A	851	1	53,74,74	1.37	10 (18%)	57,115,115	1.60	7 (12%)
7	BPH	A	855	-	64,70,70	1.23	8 (12%)	73,101,101	1.63	13 (17%)
8	U10	A	857	-	48,48,63	2.69	16 (33%)	58,61,79	2.32	20 (34%)
6	BCL	B	852	2	53,74,74	1.38	8 (15%)	57,115,115	1.88	12 (21%)
6	BCL	B	853	1	53,74,74	1.38	9 (16%)	57,115,115	2.05	14 (24%)
7	BPH	B	854	-	64,70,70	1.50	11 (17%)	73,101,101	1.80	16 (21%)
8	U10	B	856	-	48,48,63	2.36	15 (31%)	58,61,79	2.29	19 (32%)

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
6	BCL	A	850	-	-	0/37/137/137	0/0/9/9
6	BCL	A	851	1	-	0/37/137/137	0/0/9/9
7	BPH	A	855	-	-	0/54/105/105	0/1/6/6
8	U10	A	857	-	-	0/45/69/87	0/1/1/1
6	BCL	B	852	2	-	0/37/137/137	0/0/9/9
6	BCL	B	853	1	-	0/37/137/137	0/0/9/9
7	BPH	B	854	-	-	0/54/105/105	0/1/6/6
8	U10	B	856	-	-	0/45/69/87	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	854	BPH	C3D-CAD	-3.96	1.38	1.46
8	A	857	U10	C7-C8	-3.93	1.44	1.50
8	B	856	U10	C7-C8	-3.27	1.45	1.50
6	B	853	BCL	C3C-C4C	-3.00	1.47	1.51
6	A	850	BCL	C3C-C4C	-2.99	1.47	1.51

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	853	BCL	CAA-C2A-C1A	-6.34	90.10	112.47
6	B	853	BCL	CMB-C2B-C1B	-6.34	117.88	128.36
6	A	850	BCL	CMB-C2B-C1B	-6.17	118.16	128.36
6	A	851	BCL	CMB-C2B-C1B	-6.11	118.25	128.36
6	B	852	BCL	CMB-C2B-C1B	-5.90	118.61	128.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 87 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	850	BCL	11	0
6	A	851	BCL	11	0
7	A	855	BPH	19	0
8	A	857	U10	7	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	852	BCL	9	0
6	B	853	BCL	11	0
7	B	854	BPH	14	0
8	B	856	U10	15	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, 95th 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 ²)	Q<0.9
1	A	281/281 (100%)	-0.88	0 100 100	90, 90, 90, 90	0
2	B	302/307 (98%)	-0.83	0 100 100	90, 90, 90, 90	0
3	C	238/260 (91%)	-0.69	0 100 100	90, 90, 90, 90	0
All	All	821/848 (96%)	-0.81	0 100 100	90, 90, 90, 90	0

There are no RSRZ outliers to report.

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, 95th 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 ²)	Q<0.9
8	U10	A	857	48/63	0.81	0.39	4.98	90,90,90,90	13
7	BPH	B	854	65/65	0.89	0.30	3.67	90,90,90,90	0
8	U10	B	856	48/63	0.85	0.35	2.94	90,90,90,90	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	BCL	A	850	66/66	0.92	0.27	2.60	90,90,90,90	0
6	BCL	A	851	66/66	0.93	0.23	2.49	90,90,90,90	0
5	MN	B	900	1/1	0.98	0.18	1.92	90,90,90,90	0
6	BCL	B	853	66/66	0.92	0.24	1.59	90,90,90,90	0
7	BPH	A	855	65/65	0.95	0.19	0.52	90,90,90,90	0
6	BCL	B	852	66/66	0.95	0.18	0.39	90,90,90,90	0
4	FE	B	858	1/1	1.00	0.05	-2.85	90,90,90,90	0

6.5 Other polymers

There are no such residues in this entry.