



wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 11:13 AM GMT

PDB ID : 1DV3
Title : PHOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER
SPHAEROIDES IN THE CHARGE-SEPARATED D+QAQB-STATE WITH
THE PROTON TRANSFER INHIBITOR CD2+
Authors : Axelrod, H.L.; Abresch, E.C.; Paddock, M.L.; Okamura, M.Y.; Feher, G.
Deposited on : 2000-01-19
Resolution : 2.50 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>

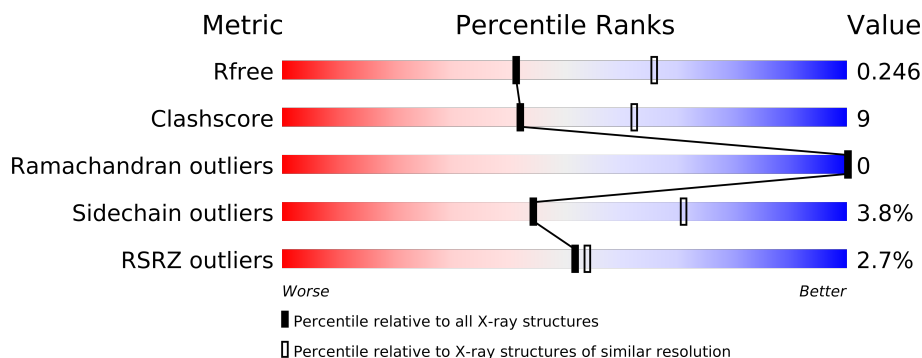
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
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 2.50 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}	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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.

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

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
10	LDA	M	1012	-	X
10	LDA	M	1013	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 14271 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 REACTION CENTER.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	299	Total	C	N	O	S	0	0	0
			2390	1597	391	392	10			
2	S	299	Total	C	N	O	S	0	0	0
			2390	1597	391	392	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	307	ALA	ASN	CONFLICT	UNP P02953
S	307	ALA	ASN	CONFLICT	UNP P02953

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	246	Total	C	N	O	S	0	0	0
			1869	1196	320	343	10			
3	T	246	Total	C	N	O	S	0	0	0
			1869	1196	320	343	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	8	GLN	GLY	CONFLICT	UNP P11846
T	8	GLN	GLY	CONFLICT	UNP P11846

- Molecule 4 is FE (II) ION (three-letter code: FE2) (formula: Fe).

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

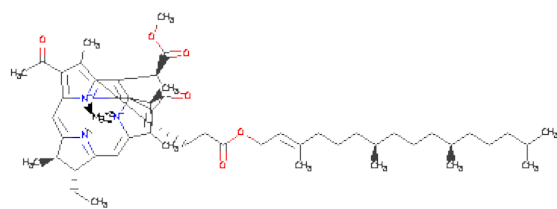
- Molecule 5 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	1	Total Cd 1 1	0	0
5	T	1	Total Cd 1 1	0	0

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

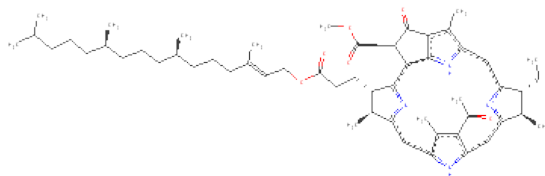
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	S	1	Total Cl 1 1	0	0
6	M	1	Total Cl 1 1	0	0

- Molecule 7 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: C₅₅H₇₄MgN₄O₆).



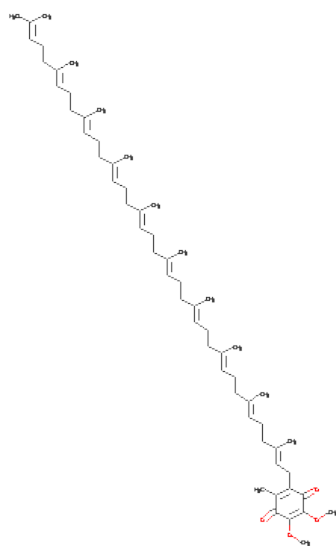
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	L	1	Total	C	Mg	N	O	0	0
			51	40	1	4	6		
7	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
7	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
7	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
7	S	1	Total	C	Mg	N	O	0	0
			52	41	1	4	6		
7	R	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
7	S	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
7	R	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 8 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: C₅₅H₇₆N₄O₆).



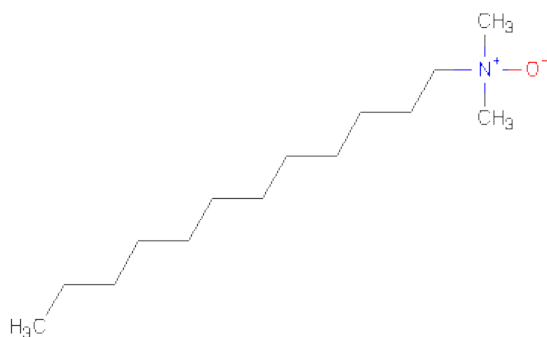
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	M	1	Total	C	N	O	0	0
			50	40	4	6		
8	L	1	Total	C	N	O	0	0
			65	55	4	6		
8	S	1	Total	C	N	O	0	0
			52	42	4	6		
8	R	1	Total	C	N	O	0	0
			65	55	4	6		

- 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
			38	34	4		
9	L	1	Total	C	O	0	0
			26	22	4		
9	S	1	Total	C	O	0	0
			31	27	4		
9	R	1	Total	C	O	0	0
			19	15	4		

- Molecule 10 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).



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

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	H	84	Total	O	0	0
			84	84		
11	L	52	Total	O	0	0
			52	52		
11	M	88	Total	O	0	0
			88	88		

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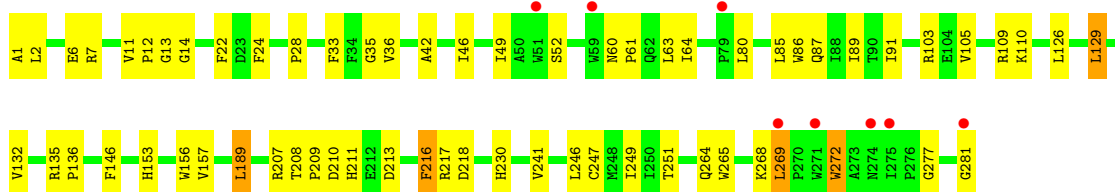
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	R	44	Total 44	O 44	0	0
11	S	72	Total 72	O 72	0	0
11	T	66	Total 66	O 66	0	0

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.

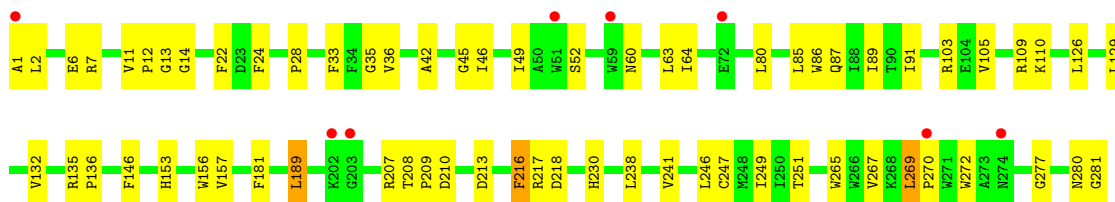
- Molecule 1: PHOTOSYNTHETIC REACTION CENTER REACTION CENTER

Chain L: 



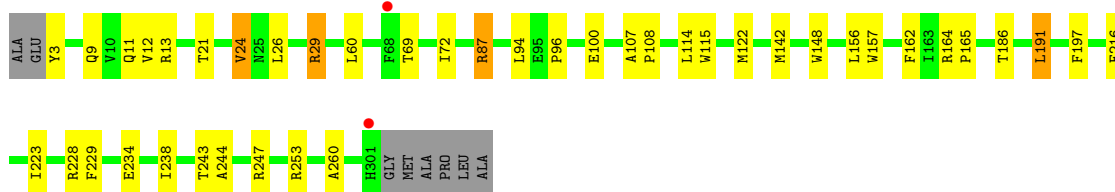
- Molecule 1: PHOTOSYNTHETIC REACTION CENTER REACTION CENTER

Chain R: 



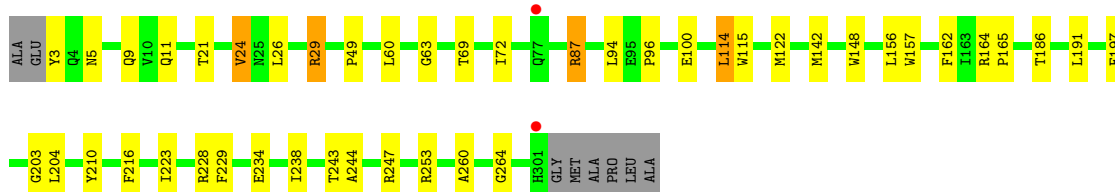
- Molecule 2: PHOTOSYNTHETIC REACTION CENTER REACTION CENTER

Chain M: 



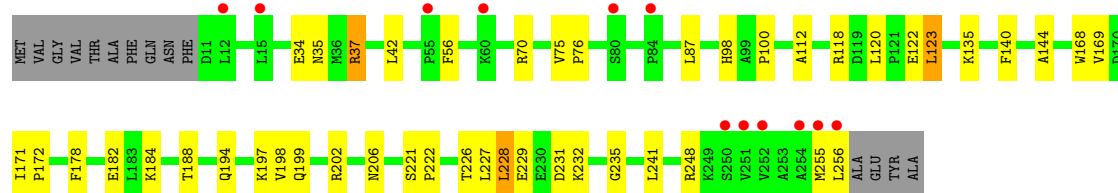
- Molecule 2: PHOTOSYNTHETIC REACTION CENTER REACTION CENTER

Chain S: 



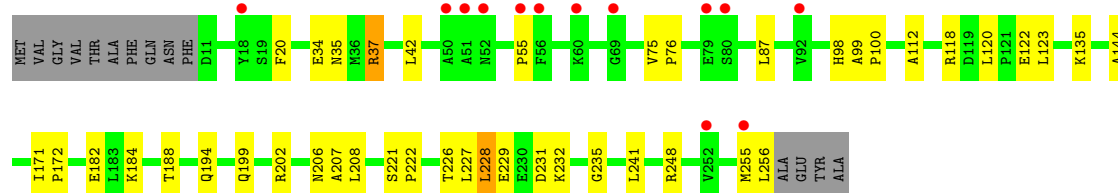
- Molecule 3: PHOTOSYNTHETIC REACTION CENTER REACTION CENTER

Chain H: 



- Molecule 3: PHOTOSYNTHETIC REACTION CENTER REACTION CENTER

Chain T: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	141.25Å 141.25Å 275.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.80 – 2.50 27.76 – 2.49	Depositor EDS
% Data completeness (in resolution range)	95.2 (27.80-2.50) 94.6 (27.76-2.49)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.51Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.226 , 0.252 0.220 , 0.246	Depositor DCC
R_{free} test set	4394 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	41.7	Xtriage
Anisotropy	0.361	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 92258 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14271	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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, CL, BPH, CD, FE2, 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	0.40	0/2320	0.55	0/3175
1	R	0.40	0/2320	0.55	0/3175
2	M	0.41	0/2482	0.53	0/3389
2	S	0.42	0/2482	0.53	0/3389
3	H	0.34	0/1917	0.59	0/2608
3	T	0.34	0/1917	0.59	0/2608
All	All	0.39	0/13438	0.56	0/18344

There are no bond length outliers.

There are no bond angle outliers.

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	L	2232	0	2187	46	0
1	R	2232	0	2187	48	0
2	M	2390	0	2304	36	0
2	S	2390	0	2304	40	0
3	H	1869	0	1884	38	0
3	T	1869	0	1884	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	M	1	0	0	0	0
4	S	1	0	0	0	0
5	H	1	0	0	0	0
5	T	1	0	0	0	0
6	M	1	0	0	0	0
6	S	1	0	0	0	0
7	L	117	0	115	8	0
7	M	132	0	148	10	0
7	R	132	0	148	10	0
7	S	118	0	117	12	0
8	L	65	0	76	4	0
8	M	50	0	43	0	0
8	R	65	0	76	8	0
8	S	52	0	47	6	0
9	L	26	0	28	0	0
9	M	38	0	47	2	0
9	R	19	0	17	1	0
9	S	31	0	36	0	0
10	M	32	0	62	1	0
11	H	84	0	0	0	0
11	L	52	0	0	2	0
11	M	88	0	0	0	0
11	R	44	0	0	1	0
11	S	72	0	0	2	0
11	T	66	0	0	2	0
All	All	14271	0	13710	247	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 247 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:S:228:ARG:HA	3:T:194:GLN:CG	2.07	0.84
8:S:2005:BPH:HBB3	8:S:2005:BPH:HHC	1.61	0.83
2:M:197:PHE:HZ	7:M:1003:BCL:HBB2	1.45	0.81
1:R:181:PHE:HB3	8:S:2005:BPH:HBB2	1.63	0.79
2:S:21:THR:O	2:S:24:VAL:HG13	1.86	0.76

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	279/281 (99%)	263 (94%)	16 (6%)	0	100	100
1	R	279/281 (99%)	264 (95%)	15 (5%)	0	100	100
2	M	297/307 (97%)	287 (97%)	10 (3%)	0	100	100
2	S	297/307 (97%)	289 (97%)	8 (3%)	0	100	100
3	H	244/260 (94%)	235 (96%)	9 (4%)	0	100	100
3	T	244/260 (94%)	236 (97%)	8 (3%)	0	100	100
All	All	1640/1696 (97%)	1574 (96%)	66 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	220/220 (100%)	211 (96%)	9 (4%)	41	67
1	R	220/220 (100%)	211 (96%)	9 (4%)	41	67
2	M	235/239 (98%)	225 (96%)	10 (4%)	40	65
2	S	235/239 (98%)	225 (96%)	10 (4%)	40	65
3	H	199/209 (95%)	193 (97%)	6 (3%)	53	80
3	T	199/209 (95%)	193 (97%)	6 (3%)	53	80
All	All	1308/1336 (98%)	1258 (96%)	50 (4%)	44	71

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	184	LYS
1	R	129	LEU
3	T	135	LYS
3	H	228	LEU
1	R	7	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	206	ASN
1	R	87	GLN
3	T	194	GLN
3	H	199	GLN
2	S	300	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 24 ligands modelled in this entry, 6 are 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
7	BCL	L	1001	2	59,59,74	1.33	10 (16%)	77,97,115	1.79	23 (29%)
7	BCL	L	1002	1	74,74,74	1.25	8 (10%)	97,115,115	1.63	20 (20%)
8	BPH	L	1006	-	70,70,70	1.24	7 (10%)	94,101,101	1.56	20 (21%)
9	U10	L	1009	-	25,26,63	1.63	4 (16%)	33,34,79	1.43	7 (21%)
7	BCL	M	1003	2	74,74,74	1.15	8 (10%)	97,115,115	1.65	21 (21%)
7	BCL	M	1004	1	74,74,74	1.14	7 (9%)	97,115,115	1.82	29 (29%)
8	BPH	M	1005	-	55,55,70	1.47	9 (16%)	74,83,101	1.89	19 (25%)
9	U10	M	1008	-	38,38,63	1.89	8 (21%)	47,49,79	1.20	3 (6%)
10	LDA	M	1012	-	15,15,15	4.82	3 (20%)	17,17,17	2.97	2 (11%)
10	LDA	M	1013	-	15,15,15	4.72	3 (20%)	17,17,17	3.02	5 (29%)
7	BCL	R	2002	1	74,74,74	1.25	7 (9%)	97,115,115	1.68	22 (22%)
7	BCL	R	2004	1	74,74,74	1.15	7 (9%)	97,115,115	1.66	19 (19%)
8	BPH	R	2006	-	70,70,70	1.16	6 (8%)	94,101,101	1.55	19 (20%)
9	U10	R	2009	-	19,19,63	2.23	5 (26%)	25,26,79	1.31	3 (12%)
7	BCL	S	2001	2	60,60,74	1.46	10 (16%)	79,98,115	1.83	18 (22%)
7	BCL	S	2003	2	74,74,74	1.14	7 (9%)	97,115,115	1.65	21 (21%)
8	BPH	S	2005	-	57,57,70	1.44	7 (12%)	78,85,101	1.60	18 (23%)
9	U10	S	2008	-	30,31,63	1.76	4 (13%)	39,40,79	1.03	2 (5%)

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
7	BCL	L	1001	2	-	0/23/119/137	0/0/9/9
7	BCL	L	1002	1	-	0/41/137/137	0/0/9/9
8	BPH	L	1006	-	2/2/18/22	0/49/105/105	0/0/6/6
9	U10	L	1009	-	-	0/19/43/87	0/1/1/1
7	BCL	M	1003	2	1/1/21/25	0/41/137/137	0/0/9/9
7	BCL	M	1004	1	-	0/41/137/137	0/0/9/9
8	BPH	M	1005	-	-	0/31/87/105	0/0/6/6
9	U10	M	1008	-	-	0/33/57/87	0/1/1/1
10	LDA	M	1012	-	-	0/13/13/13	0/0/0/0
10	LDA	M	1013	-	-	0/13/13/13	0/0/0/0
7	BCL	R	2002	1	-	0/41/137/137	0/0/9/9
7	BCL	R	2004	1	-	0/41/137/137	0/0/9/9
8	BPH	R	2006	-	2/2/18/22	0/49/105/105	0/0/6/6

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	U10	R	2009	-	-	0/11/35/87	0/1/1/1
7	BCL	S	2001	2	-	0/25/121/137	0/0/9/9
7	BCL	S	2003	2	-	0/41/137/137	0/0/9/9
8	BPH	S	2005	-	-	0/34/90/105	0/0/6/6
9	U10	S	2008	-	-	0/25/49/87	0/1/1/1

The worst 5 of 120 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	1012	LDA	O1-N1	-18.23	1.22	1.39
10	M	1013	LDA	O1-N1	-17.67	1.22	1.39
8	M	1005	BPH	C1D-CHD	6.43	1.42	1.35
9	R	2009	U10	C12-C11	-5.22	1.53	1.55
8	S	2005	BPH	C1D-CHD	5.14	1.41	1.35

The worst 5 of 271 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	M	1012	LDA	CM2-N1-CM1	-10.96	96.33	108.85
10	M	1013	LDA	CM2-N1-CM1	-10.91	96.38	108.85
7	L	1002	BCL	C4D-C3D-C2D	-6.40	99.60	107.42
7	M	1003	BCL	C4D-C3D-C2D	-6.18	99.87	107.42
7	M	1004	BCL	C4D-C3D-C2D	-6.11	99.95	107.42

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	M	1003	BCL	C13
8	R	2006	BPH	C8
8	R	2006	BPH	C13
8	L	1006	BPH	C8
8	L	1006	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 ⓘ

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	L	281/281 (100%)	-0.06	8 (2%) 50 53	23, 40, 62, 70	0
1	R	281/281 (100%)	-0.14	8 (2%) 50 53	25, 42, 62, 69	0
2	M	299/307 (97%)	-0.14	2 (0%) 84 86	25, 34, 50, 69	0
2	S	299/307 (97%)	-0.28	2 (0%) 84 86	27, 36, 50, 70	0
3	H	246/260 (94%)	-0.09	12 (4%) 28 29	29, 41, 66, 81	0
3	T	246/260 (94%)	-0.02	13 (5%) 25 26	31, 42, 67, 82	0
All	All	1652/1696 (97%)	-0.13	45 (2%) 52 54	23, 39, 62, 82	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	T	92	VAL	5.4
3	H	255	MET	5.2
3	T	80	SER	5.1
3	H	80	SER	4.5
3	H	252	VAL	4.4

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
10	LDA	M	1013	16/16	0.40	11.01	62,65,70,71	0
10	LDA	M	1012	16/16	0.35	8.51	67,72,78,78	0
8	BPH	R	2006	65/65	0.15	1.88	34,42,49,50	0
9	U10	S	2008	31/63	0.15	1.56	41,42,44,45	0
7	BCL	S	2003	66/66	0.15	1.25	29,32,44,46	0
7	BCL	R	2002	66/66	0.14	1.24	30,34,42,46	0
9	U10	M	1008	38/63	0.18	1.07	24,30,47,49	0
7	BCL	L	1002	66/66	0.15	1.06	24,31,33,35	0
6	CL	S	2011	1/1	0.12	1.02	51,51,51,51	0
9	U10	R	2009	19/63	0.15	0.98	42,45,49,49	0
7	BCL	M	1003	66/66	0.15	0.87	23,29,38,43	0
9	U10	L	1009	26/63	0.14	0.50	35,37,39,39	0
8	BPH	L	1006	65/65	0.13	0.24	17,30,40,40	0
7	BCL	R	2004	66/66	0.13	-0.03	21,29,56,58	0
8	BPH	S	2005	52/65	0.12	-0.06	27,31,49,52	0
7	BCL	S	2001	52/66	0.10	-0.14	26,31,40,42	0
6	CL	M	1011	1/1	0.11	-0.15	38,38,38,38	0
7	BCL	M	1004	66/66	0.15	-0.22	20,26,50,55	0
7	BCL	L	1001	51/66	0.11	-0.58	24,27,37,39	0
8	BPH	M	1005	50/65	0.10	-1.03	20,24,30,31	0
4	FE2	S	2007	1/1	0.06	-1.94	29,29,29,29	0
4	FE2	M	1007	1/1	0.07	-2.86	24,24,24,24	0
5	CD	H	1010	1/1	0.04	-13.55	43,43,43,43	0
5	CD	T	2010	1/1	0.03	-20.03	56,56,56,56	0

6.5 Other polymers ⓘ

There are no such residues in this entry.