



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 03:40 AM GMT

PDB ID : 2UX3
Title : X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC
REACTION CENTER FROM RB. SPHAEROIDES AT PH 9 IN THE NEU-
TRAL STATE
Authors : Koepke, J.; Diehm, R.; Fritzsche, G.
Deposited on : 2007-03-26
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>

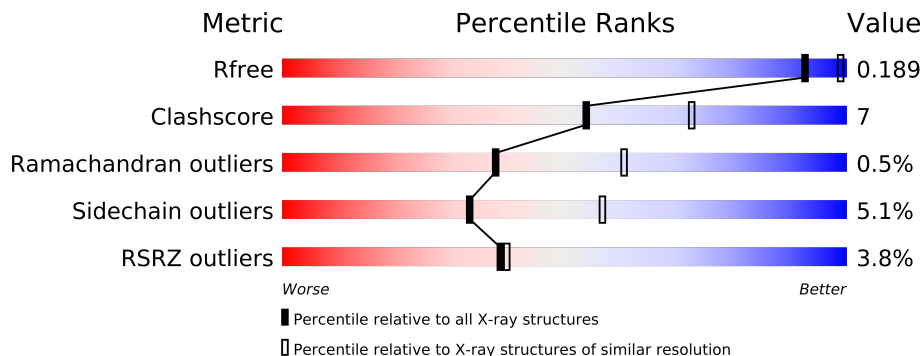
The following versions of software and data (see [references](#)) were used in the production of this report:

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	H	260	
2	L	281	
3	M	307	

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	HTO	L	1288	-	X
13	SPO	M	1315	-	X
14	CDL	M	1316	-	X
4	GOL	H	1251	-	X
4	GOL	H	1252	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	GOL	H	1253	-	X
4	GOL	L	1290	-	X
6	LDA	L	1283	-	X
6	LDA	L	1711	-	X
6	LDA	M	1305	-	X
6	LDA	M	1306	-	X
6	LDA	M	1308	-	X
6	LDA	M	1309	-	X
6	LDA	M	1310	-	X
6	LDA	M	1311	-	X
8	UQ2	L	1285[A]	-	X
8	UQ2	L	1285[B]	-	X

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 7606 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 REACTION CENTER PROTEIN H CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	241	Total	C	N	O	S	0	3	1
			1846	1181	319	337	9			

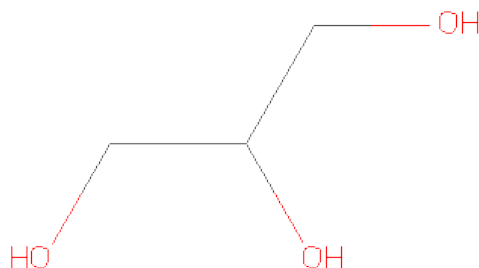
- Molecule 2 is a protein called REACTION CENTER PROTEIN L CHAIN.

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 REACTION CENTER PROTEIN M CHAIN.

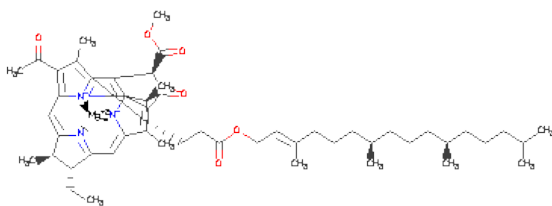
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	303	Total	C	N	O	S	0	1	1
			2419	1616	396	397	10			

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



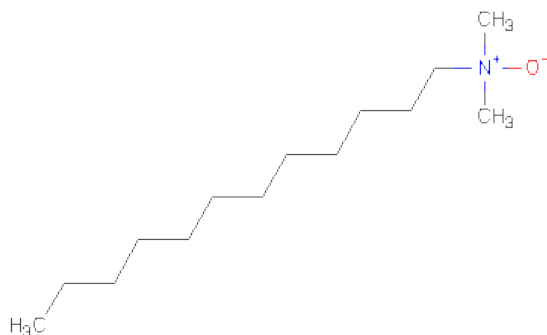
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



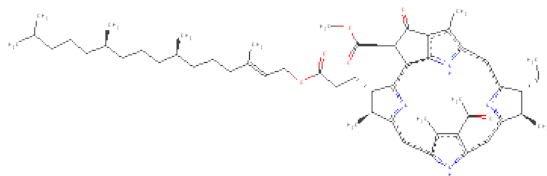
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 6 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).



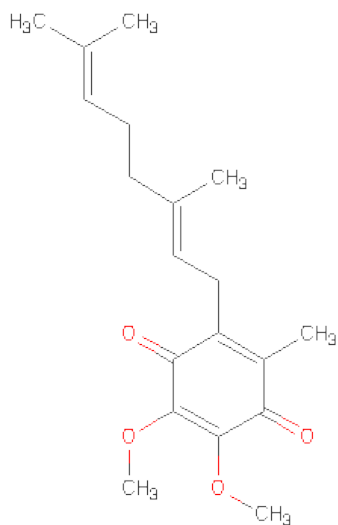
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	L	1	Total	C	N	O	0	0
			16	14	1	1		
6	L	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1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

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



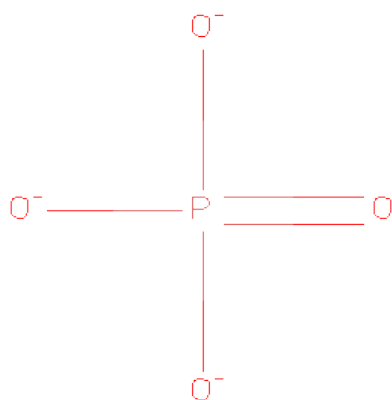
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	L	1	Total	C	N	O	0	0
			65	55	4	6		
7	M	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 8 is UBIQUINONE-2 (three-letter code: UQ2) (formula: $C_{19}H_{26}O_4$).



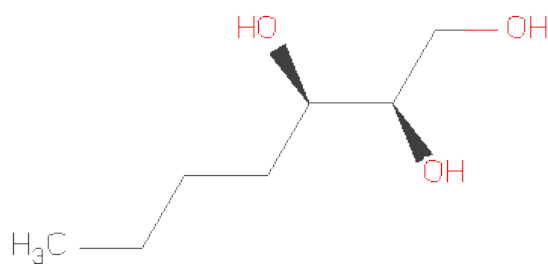
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	L	1	Total	C	O	0	1
			46	38	8		

- Molecule 9 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	L	1	Total	O	P	0	0
			5	4	1		

- Molecule 10 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula: C₇H₁₆O₃).

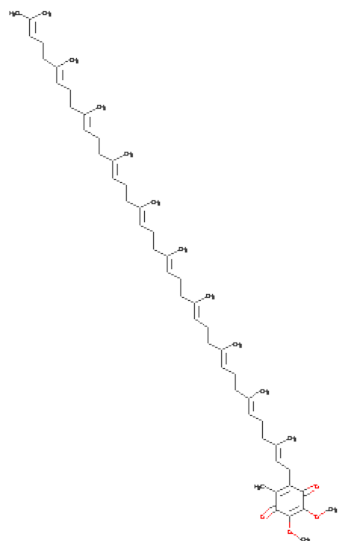


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	L	1	Total	C	O	0	0
			10	7	3		

- Molecule 11 is FE (III) ION (three-letter code: FE) (formula: Fe).

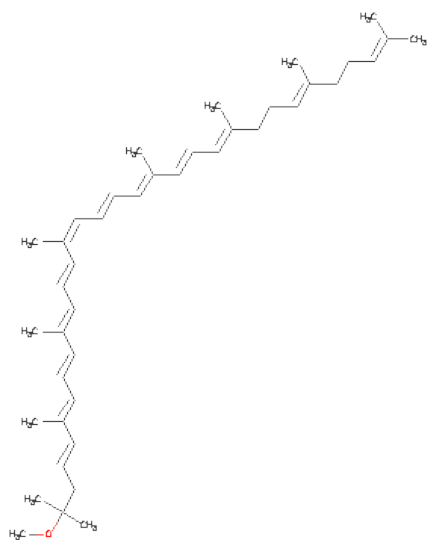
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	M	1	Total	Fe	0	0
			1	1		

- Molecule 12 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$).



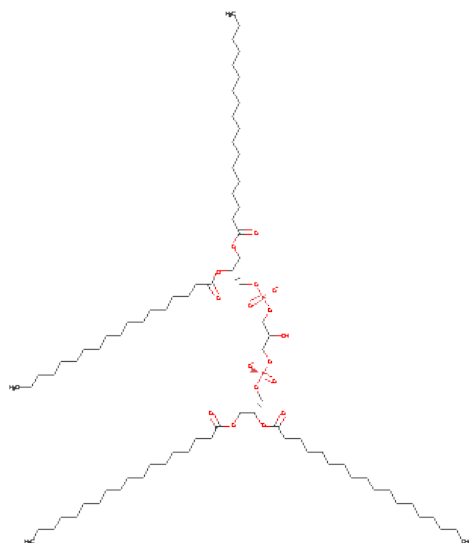
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	M	1	Total	C	O	0	0
			48	44	4		

- Molecule 13 is SPHEROIDENE (three-letter code: SPO) (formula: $C_{41}H_{60}O$).



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

- Molecule 14 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



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

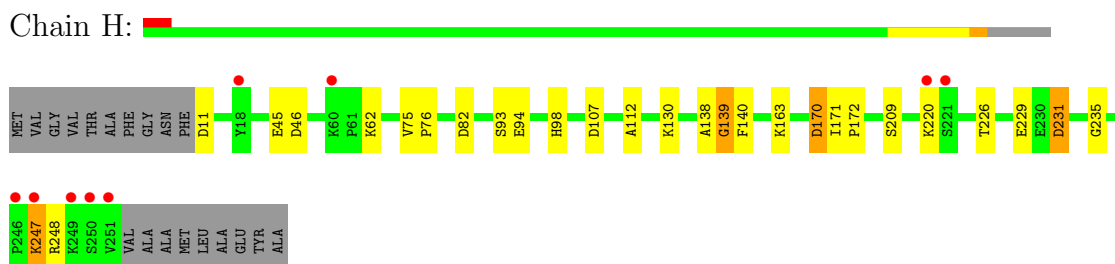
- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	H	114	Total	O	0	0
			114	114		
15	L	92	Total	O	0	0
			92	92		
15	M	96	Total	O	0	0
			96	96		

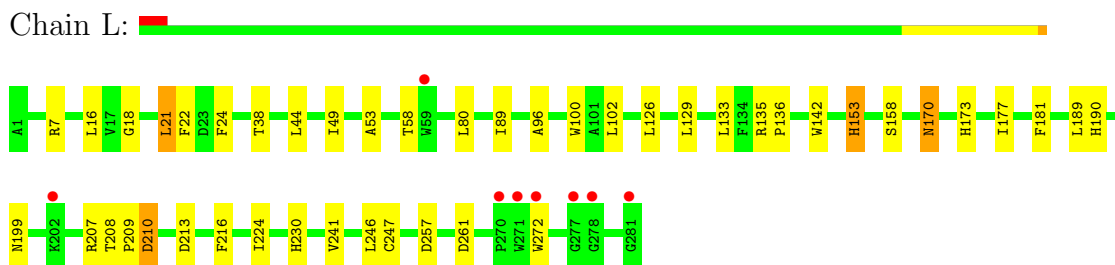
3 Residue-property plots

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.

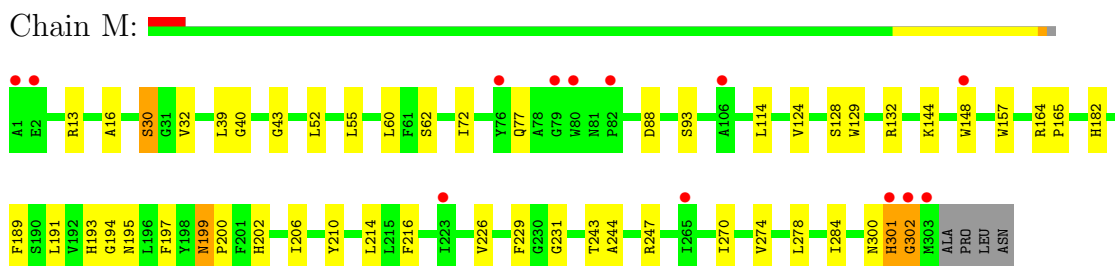
- Molecule 1: REACTION CENTER PROTEIN H CHAIN



- Molecule 2: REACTION CENTER PROTEIN L CHAIN



- Molecule 3: REACTION CENTER PROTEIN M CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	139.45Å 139.45Å 184.58Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	119.52 – 2.50 36.90 – 2.50	Depositor EDS
% Data completeness (in resolution range)	92.1 (119.52-2.50) 86.6 (36.90-2.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.79 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.185 , 0.221 0.182 , 0.189	Depositor DCC
R_{free} test set	1904 reflections (3.14%)	DCC
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.190	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.6	EDS
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 66473 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7606	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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, GOL, LDA, CDL, BPH, PO4, HTO, FE, SPO, U10, UQ2

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	0.63	0/1906	0.78	7/2591 (0.3%)
2	L	0.66	0/2320	0.68	4/3175 (0.1%)
3	M	0.61	0/2517	0.68	2/3438 (0.1%)
All	All	0.63	0/6743	0.71	13/9204 (0.1%)

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
3	M	0	1

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	82	ASP	CB-CG-OD2	7.62	125.16	118.30
1	H	11	ASP	CB-CG-OD2	7.00	124.60	118.30
2	L	213	ASP	CB-CG-OD2	6.80	124.42	118.30
1	H	139	GLY	N-CA-C	-5.99	98.13	113.10
2	L	210	ASP	CB-CG-OD1	5.96	123.67	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	M	300	ASN	Peptide

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	1846	0	1861	13	0
2	L	2232	0	2187	28	0
3	M	2419	0	2327	28	0
4	H	24	0	32	1	0
4	L	12	0	16	1	0
5	L	132	0	148	8	0
5	M	132	0	148	18	0
6	L	32	0	62	2	0
6	M	112	0	217	2	0
7	L	65	0	76	9	0
7	M	65	0	76	14	0
8	L	46	0	52	8	0
9	L	5	0	0	0	0
10	L	10	0	16	2	0
11	M	1	0	0	0	0
12	M	48	0	63	2	0
13	M	42	0	60	3	0
14	M	81	0	82	3	0
15	H	114	0	0	0	1
15	L	92	0	0	0	0
15	M	96	0	0	0	0
All	All	7606	0	7423	101	1

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 7.

The worst 5 of 101 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:L:224:ILE:HG22	8:L:1285[A]:UQ2:H8	1.61	0.83
8:L:1285[A]:UQ2:H161	6:L:1711:LDA:H121	1.62	0.81
3:M:197:PHE:HZ	5:M:1304:BCL:HBB2	1.46	0.79
2:L:181:PHE:CD2	7:M:1313:BPH:HBB1	2.18	0.78
3:M:197:PHE:CZ	5:M:1304:BCL:HBB2	2.18	0.78

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:H:2033:HOH:O	15:H:2033:HOH:O[4_555]	2.10	0.10

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	242/260 (93%)	234 (97%)	7 (3%)	1 (0%)	43	66
2	L	279/281 (99%)	270 (97%)	9 (3%)	0	100	100
3	M	302/307 (98%)	286 (95%)	13 (4%)	3 (1%)	22	38
All	All	823/848 (97%)	790 (96%)	29 (4%)	4 (0%)	38	60

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	M	301	HIS
1	H	248	ARG
3	M	30	SER
3	M	302	GLY

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	198/208 (95%)	192 (97%)	6 (3%)	53	80
2	L	220/220 (100%)	204 (93%)	16 (7%)	20	36
3	M	237/240 (99%)	225 (95%)	12 (5%)	33	57
All	All	655/668 (98%)	621 (95%)	34 (5%)	33	55

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	170	ASN
2	L	246	LEU
3	M	216	PHE
2	L	210	ASP
2	L	16	LEU

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

Mol	Chain	Res	Type
2	L	183	ASN
3	M	199	ASN
3	M	187	ASN
2	L	170	ASN
3	M	77	GLN

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 29 ligands modelled in this entry, 1 is monoatomic - leaving 28 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
4	GOL	H	1251	-	5,5,5	0.49	0	5,5,5	0.69	0
4	GOL	H	1252	-	5,5,5	0.35	0	5,5,5	0.40	0
4	GOL	H	1253	-	5,5,5	0.30	0	5,5,5	0.40	0
4	GOL	H	1254	-	5,5,5	0.31	0	5,5,5	0.31	0
5	BCL	L	1282	2	74,74,74	2.12	11 (14%)	97,115,115	2.03	27 (27%)
6	LDA	L	1283	-	15,15,15	3.76	1 (6%)	17,17,17	0.69	0
7	BPH	L	1284	-	70,70,70	2.89	14 (20%)	94,101,101	1.70	16 (17%)
8	UQ2	L	1285[A]	-	23,23,23	2.64	6 (26%)	31,31,31	1.70	6 (19%)
8	UQ2	L	1285[B]	-	23,23,23	2.73	7 (30%)	31,31,31	1.21	3 (9%)
5	BCL	L	1286	2	74,74,74	2.11	11 (14%)	97,115,115	2.07	26 (26%)
9	PO4	L	1287	-	4,4,4	0.27	0	6,6,6	0.31	0
10	HTO	L	1288	-	9,9,9	0.41	0	10,10,10	0.80	0
4	GOL	L	1289	-	5,5,5	0.31	0	5,5,5	0.41	0
4	GOL	L	1290	-	5,5,5	0.32	0	5,5,5	0.35	0
6	LDA	L	1711	-	15,15,15	3.94	2 (13%)	17,17,17	0.87	0
5	BCL	M	1303	3	74,74,74	2.11	11 (14%)	97,115,115	2.02	25 (25%)
5	BCL	M	1304	3	74,74,74	2.07	12 (16%)	97,115,115	1.85	21 (21%)
6	LDA	M	1305	-	15,15,15	3.69	1 (6%)	17,17,17	0.99	2 (11%)
6	LDA	M	1306	-	15,15,15	3.70	2 (13%)	17,17,17	0.65	0
6	LDA	M	1307	-	15,15,15	3.76	2 (13%)	17,17,17	1.09	1 (5%)
6	LDA	M	1308	-	15,15,15	3.78	2 (13%)	17,17,17	0.70	0
6	LDA	M	1309	-	15,15,15	3.84	2 (13%)	17,17,17	0.60	0
6	LDA	M	1310	-	15,15,15	3.77	2 (13%)	17,17,17	0.73	0
6	LDA	M	1311	-	15,15,15	3.74	2 (13%)	17,17,17	0.67	0
7	BPH	M	1313	-	70,70,70	3.05	18 (25%)	94,101,101	1.84	18 (19%)
12	U10	M	1314	-	48,48,63	3.09	13 (27%)	59,61,79	1.71	15 (25%)
13	SPO	M	1315	-	41,41,41	4.11	12 (29%)	50,50,50	2.16	13 (26%)
14	CDL	M	1316	-	80,80,99	2.81	22 (27%)	92,92,111	3.51	14 (15%)

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
4	GOL	H	1251	-	-	0/4/4/4	0/0/0/0
4	GOL	H	1252	-	-	0/4/4/4	0/0/0/0
4	GOL	H	1253	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	H	1254	-	-	0/4/4/4	0/0/0/0
5	BCL	L	1282	2	2/2/21/25	0/41/137/137	0/0/9/9
6	LDA	L	1283	-	-	0/13/13/13	0/0/0/0
7	BPH	L	1284	-	2/2/18/22	0/49/105/105	0/0/6/6
8	UQ2	L	1285[A]	-	-	0/15/39/39	0/1/1/1
8	UQ2	L	1285[B]	-	-	0/15/39/39	0/1/1/1
5	BCL	L	1286	2	2/2/21/25	0/41/137/137	0/0/9/9
9	PO4	L	1287	-	-	0/0/0/0	0/0/0/0
10	HTO	L	1288	-	-	0/10/10/10	0/0/0/0
4	GOL	L	1289	-	-	0/4/4/4	0/0/0/0
4	GOL	L	1290	-	-	0/4/4/4	0/0/0/0
6	LDA	L	1711	-	-	0/13/13/13	0/0/0/0
5	BCL	M	1303	3	2/2/21/25	0/41/137/137	0/0/9/9
5	BCL	M	1304	3	2/2/21/25	0/41/137/137	0/0/9/9
6	LDA	M	1305	-	-	0/13/13/13	0/0/0/0
6	LDA	M	1306	-	-	0/13/13/13	0/0/0/0
6	LDA	M	1307	-	-	0/13/13/13	0/0/0/0
6	LDA	M	1308	-	-	0/13/13/13	0/0/0/0
6	LDA	M	1309	-	-	0/13/13/13	0/0/0/0
6	LDA	M	1310	-	-	0/13/13/13	0/0/0/0
6	LDA	M	1311	-	-	0/13/13/13	0/0/0/0
7	BPH	M	1313	-	2/2/18/22	0/49/105/105	0/0/6/6
12	U10	M	1314	-	-	0/45/69/87	0/1/1/1
13	SPO	M	1315	-	-	0/47/47/47	0/0/0/0
14	CDL	M	1316	-	1/1/9/9	0/91/91/110	0/0/0/0

The worst 5 of 153 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	L	1711	LDA	O1-N1	-15.01	1.25	1.39
6	M	1309	LDA	O1-N1	-14.58	1.25	1.39
7	M	1313	BPH	C1D-CHD	14.50	1.51	1.35
6	M	1308	LDA	O1-N1	-14.37	1.25	1.39
6	L	1283	LDA	O1-N1	-14.34	1.25	1.39

The worst 5 of 187 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	M	1316	CDL	C33-C32-C31	17.02	177.43	113.28
14	M	1316	CDL	C12-C11-CA5	12.22	161.41	113.51
14	M	1316	CDL	C17-C16-C15	11.05	174.41	114.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	M	1316	CDL	C20-C19-C18	10.79	173.01	114.61
14	M	1316	CDL	C13-C12-C11	10.35	152.29	113.28

5 of 13 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	M	1313	BPH	C8
7	M	1313	BPH	C13
14	M	1316	CDL	CA4
5	M	1303	BCL	C8
5	M	1303	BCL	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	H	241/260 (92%)	-0.25	9 (3%) 39 41	38, 48, 61, 105	0
2	L	281/281 (100%)	-0.30	8 (2%) 50 53	35, 44, 69, 77	0
3	M	303/307 (98%)	0.04	13 (4%) 34 35	33, 50, 73, 86	0
All	All	825/848 (97%)	-0.16	30 (3%) 38 42	33, 47, 72, 105	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	M	1	ALA	6.4
1	H	249	LYS	5.8
1	H	250	SER	5.7
3	M	303	MET	5.6
1	H	246	PRO	4.5

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
6	LDA	M	1311	16/16	0.59	23.88	115,118,122,122	0
4	GOL	H	1253	6/6	0.39	14.99	103,104,106,106	0
6	LDA	L	1711	16/16	0.48	14.30	108,112,117,117	0
6	LDA	L	1283	16/16	0.39	14.13	78,103,114,115	0
6	LDA	M	1308	16/16	0.37	12.19	96,99,107,108	0
10	HTO	L	1288	10/10	0.42	9.71	83,85,85,86	0
6	LDA	M	1310	16/16	0.64	8.69	101,111,118,118	0
6	LDA	M	1309	16/16	0.53	8.63	118,120,126,126	0
4	GOL	H	1251	6/6	0.32	8.32	70,75,76,76	0
4	GOL	L	1290	6/6	0.33	6.04	98,99,99,100	0
6	LDA	M	1306	16/16	0.45	5.06	70,74,86,87	0
14	CDL	M	1316	81/100	0.45	3.54	91,107,125,126	0
4	GOL	H	1252	6/6	0.32	3.46	93,94,94,95	0
6	LDA	M	1305	16/16	0.29	3.09	70,80,85,85	0
8	UQ2	L	1285[B]	23/23	0.31	2.57	42,47,53,54	23
13	SPO	M	1315	42/42	0.22	2.41	44,57,77,80	0
8	UQ2	L	1285[A]	23/23	0.31	2.38	38,44,54,55	23
4	GOL	L	1289	6/6	0.29	1.64	65,69,70,73	0
12	U10	M	1314	48/63	0.24	1.27	36,47,75,78	0
7	BPH	M	1313	65/65	0.23	1.24	38,45,98,99	0
6	LDA	M	1307	16/16	0.18	0.69	68,70,76,77	0
5	BCL	M	1303	66/66	0.15	0.67	30,36,89,90	0
5	BCL	M	1304	66/66	0.16	0.56	30,36,58,65	0
5	BCL	L	1286	66/66	0.12	0.21	30,38,51,56	0
7	BPH	L	1284	65/65	0.12	0.02	29,36,45,48	0
9	PO4	L	1287	5/5	0.13	-0.09	100,100,101,101	0
5	BCL	L	1282	66/66	0.12	-0.19	29,35,58,61	0
11	FE	M	1312	1/1	0.09	-4.24	34,34,34,34	0
4	GOL	H	1254	6/6	0.23	-	92,93,93,93	0

6.5 Other polymers ⓘ

There are no such residues in this entry.