



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 12:00 AM GMT

PDB ID : 3EOJ
Title : Fmo protein from Prosthecochloris Aestuarii 2K AT 1.3A Resolution
Authors : Tronrud, D.E.; Wen, J.; Gay, L.; Blankenship, R.E.
Deposited on : 2008-09-27
Resolution : 1.30 Å(reported)

This is a full wwPDB validation 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>

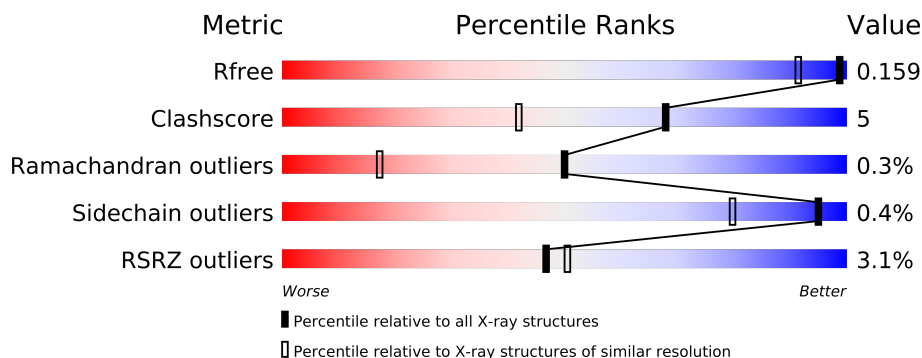
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.30 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))
R_{free}	66092	1025 (1.34-1.26)
Clashscore	79885	1140 (1.34-1.26)
Ramachandran outliers	78287	1093 (1.34-1.26)
Sidechain outliers	78261	1092 (1.34-1.26)
RSRZ outliers	66119	1025 (1.34-1.26)

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	A	366	

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

Mol	Type	Chain	Res	Geometry	Electron density
2	BCL	A	376[C]	-	X
2	BCL	A	376[D]	-	X
2	BCL	A	377[E]	-	X
2	BCL	A	377[F]	-	X
2	BCL	A	378[B]	-	X
3	EDO	A	380	-	X
3	EDO	A	382	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	EDO	A	384	-	X
3	EDO	A	387	-	X
3	EDO	A	388[A]	-	X
3	EDO	A	390	-	X
3	EDO	A	391[A]	-	X
3	EDO	A	392	-	X
4	NA	A	1232	-	X

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 4115 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.

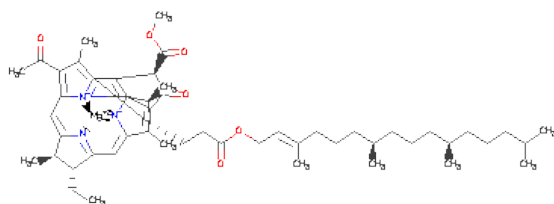
- Molecule 1 is a protein called Bacteriochlorophyll a protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	60	1
			3082	1974	527	573	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	117	SER	GLN	SEE REMARK 999	UNP P11741

- Molecule 2 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



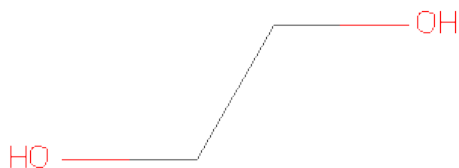
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Mg	N	O	0	1
			71	60	1	4	6		
2	A	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
2	A	1	Total	C	Mg	N	O	0	1
			79	68	1	4	6		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
2	A	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
2	A	1	Total	C	Mg	N	O	0	1
			84	69	1	5	9		
2	A	1	Total	C	Mg	N	O	0	1
			83	71	1	4	7		
2	A	1	Total	C	Mg	N	O	0	1
			47	36	1	4	6		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	1
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	1
3	A	1	Total C O 4 2 2	0	1
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	1

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0

- Molecule 5 is AMMONIUM ION (three-letter code: NH4) (formula: H₄N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total N 2 2	0	1

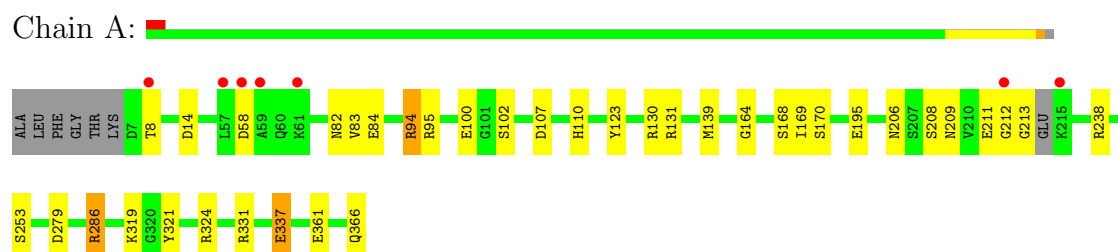
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	406	Total O 408 408	0	50

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: Bacteriochlorophyll a protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	111.24Å 111.24Å 98.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.30 48.40 – 1.30	Depositor EDS
% Data completeness (in resolution range)	94.9 (50.00-1.30) 92.4 (48.40-1.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 1.30Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.135 , 0.161 0.144 , 0.159	Depositor DCC
R_{free} test set	7749 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	11.5	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.6	EDS
Estimated twinning fraction	0.027 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 168127 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	4115	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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, NH4, EDO, NA

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	6.77	4/3302 (0.1%)	1.65	38/4466 (0.9%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	213[A]	GLY	CA-C	271.60	5.86	1.51
1	A	213[B]	GLY	CA-C	271.60	5.86	1.51
1	A	139[A]	MET	SD-CE	33.99	3.68	1.77
1	A	139[B]	MET	SD-CE	33.99	3.68	1.77

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	213[A]	GLY	CA-C-O	-36.76	54.43	120.60
1	A	213[B]	GLY	CA-C-O	-36.76	54.43	120.60
1	A	139[A]	MET	CG-SD-CE	-29.38	53.19	100.20
1	A	139[B]	MET	CG-SD-CE	-29.38	53.19	100.20
1	A	94[A]	ARG	NE-CZ-NH2	15.73	128.16	120.30
1	A	94[B]	ARG	NE-CZ-NH2	15.73	128.16	120.30
1	A	107	ASP	CB-CG-OD1	14.56	131.41	118.30
1	A	131	ARG	NE-CZ-NH1	13.63	127.11	120.30
1	A	130[A]	ARG	CD-NE-CZ	9.47	136.86	123.60
1	A	130[B]	ARG	CD-NE-CZ	9.47	136.86	123.60
1	A	107	ASP	CB-CG-OD2	-8.61	110.55	118.30
1	A	94[A]	ARG	NE-CZ-NH1	-7.99	116.30	120.30
1	A	94[B]	ARG	NE-CZ-NH1	-7.99	116.30	120.30
1	A	123[A]	TYR	CB-CG-CD1	7.92	125.75	121.00
1	A	123[B]	TYR	CB-CG-CD1	7.92	125.75	121.00
1	A	58	ASP	C-N-CA	-6.91	104.42	121.70
1	A	123[A]	TYR	CB-CG-CD2	-6.85	116.89	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	123[B]	TYR	CB-CG-CD2	-6.85	116.89	121.00
1	A	83	VAL	CA-CB-CG2	6.82	121.12	110.90
1	A	279	ASP	CB-CG-OD1	6.82	124.44	118.30
1	A	238	ARG	NE-CZ-NH1	-6.67	116.96	120.30
1	A	286[A]	ARG	NE-CZ-NH1	6.59	123.60	120.30
1	A	286[B]	ARG	NE-CZ-NH1	6.59	123.60	120.30
1	A	366	GLN	CA-CB-CG	6.55	127.82	113.40
1	A	110	HIS	CA-CB-CG	6.17	124.09	113.60
1	A	331[A]	ARG	NE-CZ-NH2	-5.87	117.36	120.30
1	A	331[B]	ARG	NE-CZ-NH2	-5.87	117.36	120.30
1	A	337[A]	GLU	OE1-CD-OE2	5.58	130.00	123.30
1	A	337[B]	GLU	OE1-CD-OE2	5.58	130.00	123.30
1	A	130[A]	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	130[B]	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	321	TYR	CB-CG-CD2	5.45	124.27	121.00
1	A	95	ARG	NE-CZ-NH2	-5.23	117.69	120.30
1	A	130[A]	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	A	130[B]	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	A	212[A]	GLY	C-N-CA	5.15	133.11	122.30
1	A	212[B]	GLY	C-N-CA	5.15	133.11	122.30
1	A	95	ARG	NE-CZ-NH1	5.11	122.86	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	A	3082	0	0	17	0
2	A	562	0	0	1	0
3	A	60	0	0	4	0
4	A	1	0	0	0	0
5	A	2	0	0	1	0
6	A	408	0	0	6	0
All	All	4115	0	0	18	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 5.

All (18) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:208[A]:SER:O	1:A:209[A]:ASN:ND2	1.93	1.01
1:A:195[B]:GLU:OE2	5:A:2378[B]:NH4:N	2.06	0.88
1:A:208[A]:SER:C	1:A:209[A]:ASN:ND2	2.31	0.84
1:A:206[B]:ASN:ND2	6:A:1149:HOH:O	2.22	0.73
1:A:164[B]:GLY:O	1:A:168[B]:SER:N	2.26	0.68
1:A:8:THR:O	6:A:1230:HOH:O	2.18	0.56
1:A:337[B]:GLU:CG	6:A:1100:HOH:O	2.53	0.56
1:A:253:SER:OG	3:A:382:EDO:C1	2.55	0.55
1:A:100[B]:GLU:OE2	3:A:385:EDO:O1	2.24	0.55
1:A:94[A]:ARG:NE	6:A:2351[A]:HOH:O	2.43	0.50
1:A:286[B]:ARG:NH1	1:A:361:GLU:OE2	2.45	0.50
1:A:169[B]:ILE:CG1	6:A:1191:HOH:O	2.61	0.48
1:A:209[B]:ASN:ND2	1:A:211[B]:GLU:CG	2.81	0.44
1:A:14:ASP:OD2	3:A:386:EDO:O1	2.38	0.41
2:A:377[E]:BCL:C15	2:A:377[E]:BCL:C19	2.98	0.41
1:A:82[B]:ASN:OD1	1:A:102:SER:OG	2.38	0.41
1:A:84:GLU:OE1	3:A:385:EDO:O1	2.38	0.41
1:A:319:LYS:NZ	6:A:1094:HOH:O	2.55	0.40

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	A	413/366 (113%)	408 (99%)	3 (1%)	2 (0%)	38 8

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	170[A]	SER
1	A	170[B]	SER

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	335/303 (111%)	333 (99%)	2 (1%)	92 72

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	324[A]	ARG
1	A	324[B]	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 36 ligands modelled in this entry, 2 are modelled with single atom and 1 is monoatomic - leaving 33 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	$\# Z > 2$
2	BCL	A	371[A]	-	4,4,74	2.75	1 (25%)	3,4,115	0.99	0
2	BCL	A	371[B]	-	4,4,74	3.43	1 (25%)	3,4,115	0.53	0
2	BCL	A	372	6	74,74,74	1.25	10 (13%)	97,115,115	1.29	12 (12%)
2	BCL	A	373[A]	-	12,12,74	1.11	1 (8%)	12,13,115	0.90	0
2	BCL	A	373[B]	-	12,12,74	1.20	1 (8%)	12,13,115	1.26	1 (8%)
2	BCL	A	374	1	74,74,74	1.16	8 (10%)	97,115,115	1.32	12 (12%)
2	BCL	A	375	1	74,74,74	1.23	8 (10%)	97,115,115	1.27	12 (12%)
2	BCL	A	376[A]	-	4,8,74	0.86	0	3,10,115	0.93	0
2	BCL	A	376[B]	-	4,8,74	0.72	0	3,10,115	1.02	0
2	BCL	A	376[C]	-	6,10,74	0.60	0	6,13,115	1.49	1 (16%)
2	BCL	A	376[D]	-	6,10,74	0.73	0	6,13,115	1.81	2 (33%)
2	BCL	A	377[A]	-	3,3,74	0.74	0	2,3,115	0.78	0
2	BCL	A	377[B]	-	3,3,74	0.48	0	2,3,115	0.67	0
2	BCL	A	377[C]	-	6,6,74	0.69	0	3,7,115	1.84	1 (33%)
2	BCL	A	377[D]	-	6,6,74	0.71	0	3,7,115	1.26	0
2	BCL	A	377[E]	-	5,5,74	1.66	1 (20%)	5,5,115	1.55	1 (20%)
2	BCL	A	377[F]	-	5,5,74	7.05	1 (20%)	5,5,115	0.50	0
2	BCL	A	378[B]	1	54,55,74	1.36	6 (11%)	73,92,115	1.70	18 (24%)
3	EDO	A	379	-	3,3,3	0.44	0	2,2,2	0.22	0
3	EDO	A	380	-	3,3,3	0.48	0	2,2,2	0.17	0
3	EDO	A	381	-	3,3,3	0.26	0	2,2,2	1.93	1 (50%)
3	EDO	A	382	-	3,3,3	0.67	0	2,2,2	0.50	0
3	EDO	A	383[A]	-	3,3,3	0.33	0	2,2,2	0.52	0
3	EDO	A	384	-	3,3,3	0.62	0	2,2,2	0.35	0
3	EDO	A	385	-	3,3,3	0.79	0	2,2,2	0.30	0
3	EDO	A	386	-	3,3,3	0.44	0	2,2,2	0.55	0
3	EDO	A	387	-	3,3,3	0.69	0	2,2,2	0.75	0
3	EDO	A	388[A]	-	3,3,3	0.76	0	2,2,2	0.47	0
3	EDO	A	389	-	3,3,3	0.78	0	2,2,2	1.48	0
3	EDO	A	390	-	3,3,3	0.66	0	2,2,2	0.36	0
3	EDO	A	391[A]	-	3,3,3	0.35	0	2,2,2	0.77	0
3	EDO	A	392	-	3,3,3	0.71	0	2,2,2	0.36	0
3	EDO	A	393[B]	-	3,3,3	0.64	0	2,2,2	0.56	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. '-' means

no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BCL	A	371[A]	-	-	0/2/2/137	0/0/0/9
2	BCL	A	371[B]	-	-	0/2/2/137	0/0/0/9
2	BCL	A	372	6	-	0/41/137/137	0/0/9/9
2	BCL	A	373[A]	-	-	0/10/11/137	0/0/0/9
2	BCL	A	373[B]	-	-	0/10/11/137	0/0/0/9
2	BCL	A	374	1	-	0/41/137/137	0/0/9/9
2	BCL	A	375	1	-	0/41/137/137	0/0/9/9
2	BCL	A	376[A]	-	-	0/2/12/137	0/1/1/9
2	BCL	A	376[B]	-	-	0/2/12/137	0/1/1/9
2	BCL	A	376[C]	-	-	0/6/15/137	0/1/1/9
2	BCL	A	376[D]	-	-	0/6/15/137	0/1/1/9
2	BCL	A	377[A]	-	-	0/0/0/137	0/0/0/9
2	BCL	A	377[B]	-	-	0/0/0/137	0/0/0/9
2	BCL	A	377[C]	-	-	0/6/6/137	0/0/0/9
2	BCL	A	377[D]	-	-	0/6/6/137	0/0/0/9
2	BCL	A	377[E]	-	-	0/3/3/137	0/0/0/9
2	BCL	A	377[F]	-	-	0/3/3/137	0/0/0/9
2	BCL	A	378[B]	1	-	0/19/115/137	0/0/9/9
3	EDO	A	379	-	-	0/1/1/1	0/0/0/0
3	EDO	A	380	-	-	0/1/1/1	0/0/0/0
3	EDO	A	381	-	-	0/1/1/1	0/0/0/0
3	EDO	A	382	-	-	0/1/1/1	0/0/0/0
3	EDO	A	383[A]	-	-	0/1/1/1	0/0/0/0
3	EDO	A	384	-	-	0/1/1/1	0/0/0/0
3	EDO	A	385	-	-	0/1/1/1	0/0/0/0
3	EDO	A	386	-	-	0/1/1/1	0/0/0/0
3	EDO	A	387	-	-	0/1/1/1	0/0/0/0
3	EDO	A	388[A]	-	-	0/1/1/1	0/0/0/0
3	EDO	A	389	-	-	0/1/1/1	0/0/0/0
3	EDO	A	390	-	-	0/1/1/1	0/0/0/0
3	EDO	A	391[A]	-	-	0/1/1/1	0/0/0/0
3	EDO	A	392	-	-	0/1/1/1	0/0/0/0
3	EDO	A	393[B]	-	-	0/1/1/1	0/0/0/0

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	377[F]	BCL	C15-C16	-15.73	1.48	1.55
2	A	371[B]	BCL	C16-C17	-6.83	1.52	1.55
2	A	371[A]	BCL	C16-C17	-5.41	1.53	1.55
2	A	374	BCL	C4B-NB	4.57	1.40	1.34
2	A	378[B]	BCL	C1B-NB	3.95	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	373[B]	BCL	C9-C8	3.76	1.55	1.49
2	A	375	BCL	C4B-NB	3.60	1.39	1.34
2	A	377[E]	BCL	C15-C16	-3.59	1.53	1.55
2	A	373[A]	BCL	C9-C8	3.56	1.55	1.49
2	A	375	BCL	C1B-C2B	3.56	1.44	1.40
2	A	372	BCL	C1B-C2B	3.49	1.44	1.40
2	A	378[B]	BCL	C3B-C4B	3.33	1.45	1.40
2	A	372	BCL	C1B-NB	3.21	1.38	1.34
2	A	372	BCL	C1A-NA	3.19	1.39	1.32
2	A	375	BCL	C1B-NB	3.13	1.38	1.34
2	A	375	BCL	MG-NA	3.11	2.16	2.07
2	A	374	BCL	C1A-NA	3.08	1.39	1.32
2	A	374	BCL	MG-NA	2.92	2.15	2.07
2	A	378[B]	BCL	C4C-NC	2.92	1.38	1.32
2	A	374	BCL	C3B-C4B	2.88	1.44	1.40
2	A	374	BCL	C1B-C2B	2.83	1.43	1.40
2	A	378[B]	BCL	C1A-NA	2.80	1.38	1.32
2	A	372	BCL	C3B-C4B	2.70	1.44	1.40
2	A	372	BCL	MG-NA	2.66	2.15	2.07
2	A	374	BCL	C1B-NB	2.64	1.37	1.34
2	A	372	BCL	C4C-NC	2.61	1.38	1.32
2	A	375	BCL	C3B-C4B	2.58	1.44	1.40
2	A	374	BCL	C4C-NC	2.56	1.37	1.32
2	A	372	BCL	C4B-NB	2.51	1.37	1.34
2	A	378[B]	BCL	MG-NA	2.50	2.14	2.07
2	A	372	BCL	C3D-CAD	-2.40	1.42	1.47
2	A	375	BCL	C1A-NA	2.39	1.37	1.32
2	A	375	BCL	MG-NC	2.35	2.14	2.07
2	A	374	BCL	CHC-C1C	2.15	1.41	1.36
2	A	372	BCL	C1C-NC	-2.14	1.34	1.39
2	A	378[B]	BCL	C3D-CAD	-2.06	1.43	1.47
2	A	375	BCL	C4C-NC	2.05	1.36	1.32
2	A	372	BCL	C1D-CHD	2.03	1.44	1.38

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	374	BCL	C2D-C1D-ND	5.07	113.24	109.41
2	A	378[B]	BCL	CMB-C2B-C1B	-4.68	121.42	128.62
2	A	374	BCL	C1D-C2D-C3D	-4.25	103.31	106.78
2	A	375	BCL	C4-C3-C5	-3.88	109.49	115.39
2	A	378[B]	BCL	CBA-CAA-C2A	3.83	125.37	114.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	378[B]	BCL	O2A-CGA-O1A	-3.77	115.17	122.96
2	A	374	BCL	CMD-C2D-C3D	3.76	130.90	124.97
2	A	372	BCL	CMB-C2B-C3B	3.58	130.62	124.97
2	A	378[B]	BCL	O2A-CGA-CBA	3.53	121.38	110.52
2	A	373[B]	BCL	C17-C16-C15	3.49	130.92	113.02
2	A	376[D]	BCL	OBD-CAD-CBD	-3.44	119.56	125.97
2	A	374	BCL	CMB-C2B-C3B	3.28	130.13	124.97
2	A	378[B]	BCL	OBD-CAD-CBD	-3.26	121.02	125.94
2	A	372	BCL	CMB-C2B-C1B	-3.25	123.62	128.62
2	A	375	BCL	C4-C3-C2	3.24	129.94	123.52
2	A	374	BCL	CMB-C2B-C1B	-3.19	123.71	128.62
2	A	372	BCL	C2C-C1C-NC	3.19	114.83	110.95
2	A	375	BCL	C2D-C1D-ND	3.15	111.79	109.41
2	A	375	BCL	CMB-C2B-C1B	-3.14	123.79	128.62
2	A	377[C]	BCL	CAC-C3C-C2C	3.13	117.40	111.71
2	A	374	BCL	OBD-CAD-CBD	-3.12	121.23	125.94
2	A	374	BCL	C4D-ND-C1D	-3.02	102.92	106.57
2	A	377[E]	BCL	C16-C17-C18	-3.01	104.21	114.88
2	A	374	BCL	C2B-C1B-NB	3.01	111.68	109.41
2	A	372	BCL	CMD-C2D-C3D	3.00	129.70	124.97
2	A	375	BCL	CHA-C1A-NA	-2.85	120.38	126.22
2	A	378[B]	BCL	CMD-C2D-C3D	2.85	129.45	124.97
2	A	375	BCL	C1D-C2D-C3D	-2.82	104.48	106.78
2	A	375	BCL	CMB-C2B-C3B	2.73	129.27	124.97
2	A	372	BCL	CHA-C1A-NA	-2.71	120.66	126.22
3	A	381	EDO	O1-C1-C2	2.69	130.91	112.13
2	A	375	BCL	OBD-CAD-CBD	-2.68	121.89	125.94
2	A	372	BCL	C1-C2-C3	-2.67	121.44	126.19
2	A	378[B]	BCL	C2C-C1C-NC	2.61	114.13	110.95
2	A	378[B]	BCL	C4D-ND-C1D	-2.59	103.44	106.57
2	A	378[B]	BCL	C4D-C3D-CAD	-2.57	104.90	108.05
2	A	372	BCL	OBB-CAB-C3B	2.52	123.86	120.07
2	A	372	BCL	OBD-CAD-CBD	-2.49	122.18	125.94
2	A	378[B]	BCL	C2A-C3A-C4A	2.48	105.22	101.40
2	A	376[C]	BCL	O2D-CGD-O1D	-2.43	118.86	123.79
2	A	375	BCL	CMD-C2D-C3D	2.38	128.72	124.97
2	A	372	BCL	C4D-CHA-CBD	-2.38	103.78	109.37
2	A	378[B]	BCL	C3B-C4B-NB	2.37	110.95	108.64
2	A	372	BCL	C2D-C1D-ND	2.36	111.20	109.41
2	A	378[B]	BCL	C4D-CHA-CBD	-2.36	103.81	109.37
2	A	378[B]	BCL	C4A-NA-C1A	2.36	109.77	106.52
2	A	372	BCL	O2A-C1-C2	-2.36	103.44	108.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	375	BCL	C4D-ND-C1D	-2.35	103.73	106.57
2	A	375	BCL	C3B-C4B-NB	2.32	110.90	108.64
2	A	372	BCL	C4D-CHA-C1A	2.32	127.04	120.32
2	A	376[D]	BCL	O2D-CGD-CBD	2.32	114.77	111.16
2	A	374	BCL	CHA-C1A-NA	-2.26	121.58	126.22
2	A	375	BCL	O2A-CGA-O1A	-2.24	117.32	123.43
2	A	374	BCL	C2A-C1A-CHA	2.23	127.70	123.83
2	A	378[B]	BCL	CHD-C4C-NC	-2.23	122.64	125.86
2	A	378[B]	BCL	C1D-C2D-C3D	-2.20	104.98	106.78
2	A	378[B]	BCL	C2D-C1D-ND	2.19	111.07	109.41
2	A	378[B]	BCL	C4B-C3B-C2B	-2.06	104.48	106.97
2	A	374	BCL	C4A-NA-C1A	2.03	109.32	106.52
2	A	374	BCL	C4D-CHA-CBD	-2.01	104.64	109.37
2	A	378[B]	BCL	CHA-C1A-NA	-2.00	122.11	126.22

There are no chirality outliers.

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	A	359/366 (98%)	-0.25	7 (1%) 64 69	8, 14, 26, 48	14 (3%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	8	THR	4.8
1	A	59	ALA	4.3
1	A	212[A]	GLY	3.3
1	A	58	ASP	2.7
1	A	61	LYS	2.5
1	A	215[A]	LYS	2.2
1	A	57	LEU	2.1

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(\AA^2)	Q<0.9
4	NA	A	1232	1/1	0.30	72.30	27,27,27,27	0
2	BCL	A	377[F]	6/66	0.09	20.50	22,25,29,31	6
3	EDO	A	391[A]	4/4	0.32	17.53	29,29,39,39	4
3	EDO	A	388[A]	4/4	0.23	11.49	17,19,21,22	4
3	EDO	A	382	4/4	0.22	7.73	64,72,72,77	0
3	EDO	A	380	4/4	0.16	4.19	34,35,38,60	0
2	BCL	A	376[D]	10/66	0.07	4.13	9,10,12,12	10
2	BCL	A	376[C]	10/66	0.07	4.13	9,10,12,12	10
3	EDO	A	387	4/4	0.18	3.63	23,27,33,45	0
3	EDO	A	392	4/4	0.34	3.51	39,41,44,55	0
2	BCL	A	378[B]	47/66	0.17	3.41	13,19,26,33	47
3	EDO	A	384	4/4	0.19	3.30	25,27,38,47	0
3	EDO	A	390	4/4	0.13	2.93	19,20,30,32	0
3	EDO	A	385	4/4	0.14	1.92	34,35,37,42	0
3	EDO	A	393[B]	4/4	0.15	1.63	24,27,28,32	4
3	EDO	A	383[A]	4/4	0.12	1.54	20,25,28,30	4
3	EDO	A	389	4/4	0.12	1.03	15,17,28,29	0
3	EDO	A	379	4/4	0.11	0.93	28,41,43,50	0
3	EDO	A	386	4/4	0.09	0.82	25,27,32,39	0
2	BCL	A	374	66/66	0.06	0.32	8,11,14,18	0
2	BCL	A	377[C]	7/66	0.09	0.29	8,9,11,11	7
2	BCL	A	377[B]	4/66	0.09	0.29	9,9,9,10	4
2	BCL	A	377[E]	6/66	0.09	0.29	21,25,27,27	6
2	BCL	A	377[A]	4/66	0.09	0.29	8,9,10,12	4
2	BCL	A	377[D]	7/66	0.09	0.29	8,9,10,12	7
2	BCL	A	376[B]	8/66	0.07	0.13	8,9,10,12	8
2	BCL	A	376[A]	8/66	0.07	0.02	8,9,10,12	8
2	BCL	A	375	66/66	0.05	-0.16	9,12,22,30	0
2	BCL	A	372	66/66	0.06	-0.29	9,11,18,21	0
2	BCL	A	371[B]	5/66	0.05	-0.43	12,14,16,19	5
2	BCL	A	371[A]	5/66	0.05	-0.44	14,15,16,16	5
3	EDO	A	381	4/4	0.09	-0.58	13,19,20,25	0
2	BCL	A	373[B]	13/66	0.06	-1.27	13,15,18,19	13
2	BCL	A	373[A]	13/66	0.06	-1.27	12,14,16,17	13
5	NH4	A	2378[B]	1/1	0.84	-	6,6,6,6	1
5	NH4	A	2378[A]	1/1	0.84	-	27,27,27,27	1

6.5 Other polymers ⓘ

There are no such residues in this entry.