



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 04:03 PM GMT

PDB ID : 3GL2
Title : Crystal structure of dicamba monooxygenase bound to dicamba
Authors : Wilson, M.A.; Dumitru, R.; Jiang, W.Z.; Weeks, D.P.
Deposited on : 2009-03-11
Resolution : 2.10 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>

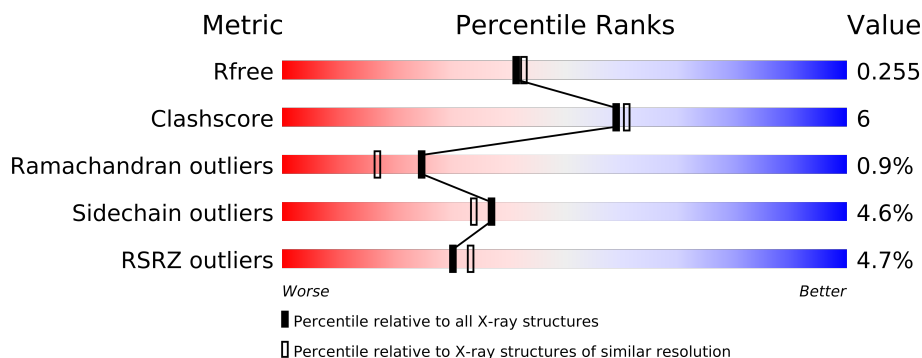
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.10 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	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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	349	
1	B	349	
1	C	349	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8156 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 DdmC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2633	1659	473	488	13			
1	B	334	Total	C	N	O	S	0	0	0
			2590	1634	463	480	13			
1	C	315	Total	C	N	O	S	0	1	0
			2440	1545	428	454	13			

There are 33 discrepancies between the modelled and reference sequences:

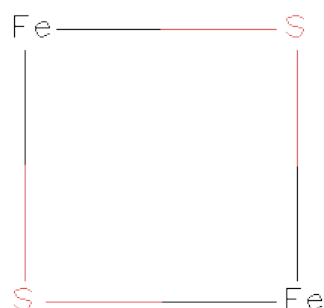
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INSERTION	UNP Q5S3I3
A	2	ALA	-	INSERTION	UNP Q5S3I3
A	341	ARG	-	INSERTION	UNP Q5S3I3
A	342	LEU	-	EXPRESSION TAG	UNP Q5S3I3
A	343	GLU	-	EXPRESSION TAG	UNP Q5S3I3
A	344	HIS	-	EXPRESSION TAG	UNP Q5S3I3
A	345	HIS	-	EXPRESSION TAG	UNP Q5S3I3
A	346	HIS	-	EXPRESSION TAG	UNP Q5S3I3
A	347	HIS	-	EXPRESSION TAG	UNP Q5S3I3
A	348	HIS	-	EXPRESSION TAG	UNP Q5S3I3
A	349	HIS	-	EXPRESSION TAG	UNP Q5S3I3
B	1	MET	-	INSERTION	UNP Q5S3I3
B	2	ALA	-	INSERTION	UNP Q5S3I3
B	341	ARG	-	INSERTION	UNP Q5S3I3
B	342	LEU	-	EXPRESSION TAG	UNP Q5S3I3
B	343	GLU	-	EXPRESSION TAG	UNP Q5S3I3
B	344	HIS	-	EXPRESSION TAG	UNP Q5S3I3
B	345	HIS	-	EXPRESSION TAG	UNP Q5S3I3
B	346	HIS	-	EXPRESSION TAG	UNP Q5S3I3
B	347	HIS	-	EXPRESSION TAG	UNP Q5S3I3
B	348	HIS	-	EXPRESSION TAG	UNP Q5S3I3
B	349	HIS	-	EXPRESSION TAG	UNP Q5S3I3
C	1	MET	-	INSERTION	UNP Q5S3I3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	2	ALA	-	INSERTION	UNP Q5S3I3
C	341	ARG	-	INSERTION	UNP Q5S3I3
C	342	LEU	-	EXPRESSION TAG	UNP Q5S3I3
C	343	GLU	-	EXPRESSION TAG	UNP Q5S3I3
C	344	HIS	-	EXPRESSION TAG	UNP Q5S3I3
C	345	HIS	-	EXPRESSION TAG	UNP Q5S3I3
C	346	HIS	-	EXPRESSION TAG	UNP Q5S3I3
C	347	HIS	-	EXPRESSION TAG	UNP Q5S3I3
C	348	HIS	-	EXPRESSION TAG	UNP Q5S3I3
C	349	HIS	-	EXPRESSION TAG	UNP Q5S3I3

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe S 4 2 2	0	0
2	B	1	Total Fe S 4 2 2	0	0
2	C	1	Total Fe S 4 2 2	0	0

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

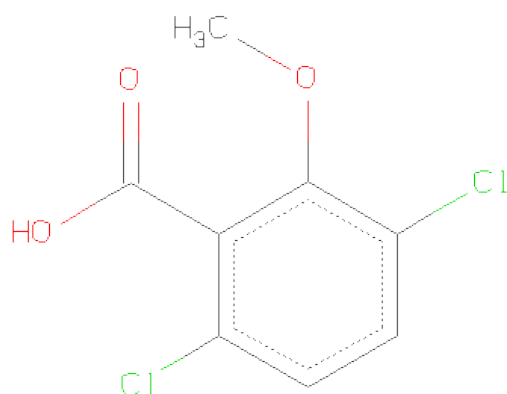
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Fe 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Fe	0	0
			1	1		

- Molecule 4 is 3,6-DICHLORO-2-METHOXYBENZOICACID (three-letter code: D3M) (formula: C₈H₆Cl₂O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	Cl	O	0	0
			13	8	2	3		
4	B	1	Total	C	Cl	O	0	0
			13	8	2	3		

- Molecule 5 is water.

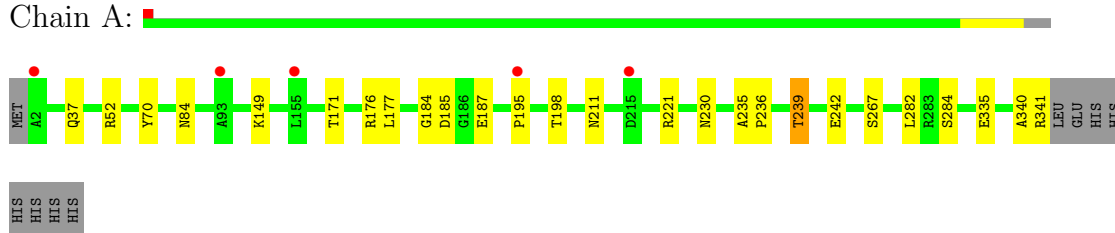
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	155	Total	O	0	0
			155	155		
5	B	142	Total	O	0	0
			142	142		
5	C	156	Total	O	0	0
			156	156		

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.

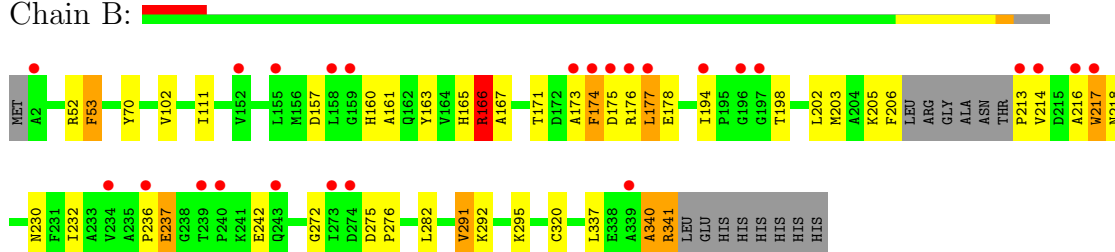
• Molecule 1: DdmC

Chain A:



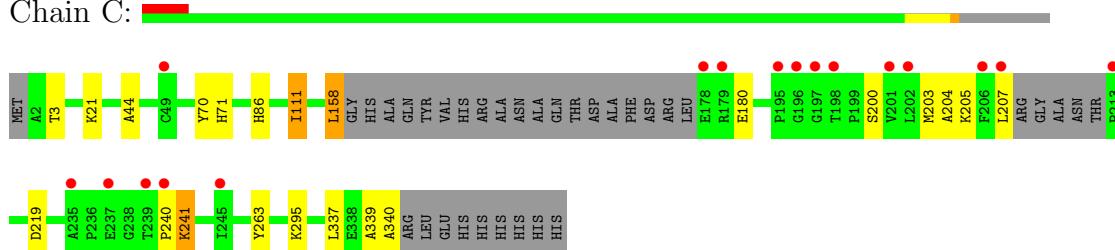
• Molecule 1: DdmC

Chain B:



• Molecule 1: DdmC

Chain C:



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	81.32Å 81.32Å 159.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.00 – 2.10 36.21 – 2.11	Depositor EDS
% Data completeness (in resolution range)	98.4 (36.00-2.10) 98.4 (36.21-2.11)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.190 , 0.247 0.201 , 0.255	Depositor DCC
R_{free} test set	3338 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	49.9	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.3	EDS
Estimated twinning fraction	0.000 for -h,-k,l 0.034 for h,-h-k,-l 0.013 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 67158 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8156	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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: D3M, FE, FES

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	0.46	0/2698	0.53	0/3674
1	B	0.47	0/2654	0.55	0/3612
1	C	0.45	0/2502	0.54	0/3405
All	All	0.46	0/7854	0.54	0/10691

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
1	C	0	1
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	340	ALA	Peptide
1	B	205	LYS	Peptide
1	B	213	PRO	Peptide
1	C	339	ALA	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	A	2633	0	0	13	0
1	B	2590	0	0	26	0
1	C	2440	0	0	8	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	13	0	5	0	0
4	B	13	0	5	0	0
5	A	155	0	0	4	0
5	B	142	0	0	4	0
5	C	156	0	0	3	0
All	All	8156	0	10	47	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 6.

All (47) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:158:LEU:CD1	1:C:158:LEU:C	2.19	1.10
1:A:236:PRO:O	1:A:239:THR:CG2	2.28	0.81
1:B:291:VAL:CG1	1:B:291:VAL:O	2.29	0.81
1:B:174:PHE:CA	1:B:177:LEU:CD2	2.62	0.78
1:C:295:LYS:NZ	5:C:395:HOH:O	2.18	0.77
1:B:206:PHE:O	5:B:355:HOH:O	2.07	0.73
1:C:340:ALA:CB	5:C:461:HOH:O	2.36	0.72
1:B:217:TRP:CD1	1:B:217:TRP:N	2.60	0.68
1:B:157:ASP:O	5:B:482:HOH:O	2.11	0.67
1:B:340:ALA:O	1:B:341:ARG:C	2.39	0.61
1:B:174:PHE:O	1:B:177:LEU:CD2	2.50	0.60
1:A:267:SER:OG	1:A:282:LEU:CD2	2.51	0.58
1:B:174:PHE:O	1:B:177:LEU:CG	2.52	0.58
1:B:236:PRO:O	1:B:237:GLU:C	2.42	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:160:HIS:O	1:B:163:TYR:N	2.40	0.55
1:B:218:ASN:OD1	1:B:232:ILE:CD1	2.55	0.55
1:A:176:ARG:NH2	5:A:474:HOH:O	2.39	0.54
1:A:52:ARG:NH2	5:A:410:HOH:O	2.40	0.54
1:B:203:MET:O	1:B:206:PHE:C	2.47	0.53
1:B:165:HIS:O	1:B:167:ALA:N	2.42	0.52
1:B:174:PHE:C	1:B:177:LEU:CD2	2.81	0.49
1:A:84:ASN:C	1:A:84:ASN:OD1	2.50	0.49
1:C:340:ALA:CB	5:C:399:HOH:O	2.60	0.49
1:A:176:ARG:NH1	1:A:195:PRO:O	2.46	0.48
1:C:219:ASP:OD2	1:C:241:LYS:NZ	2.47	0.48
1:C:71:HIS:O	1:C:86:HIS:NE2	2.48	0.47
1:A:149:LYS:NZ	1:A:335:GLU:OE2	2.47	0.47
1:B:272:GLY:O	1:B:275:ASP:CB	2.64	0.45
1:B:194:ILE:N	1:B:216:ALA:O	2.49	0.45
1:B:165:HIS:CD2	5:B:366:HOH:O	2.69	0.45
1:C:203:MET:O	1:C:204:ALA:C	2.55	0.45
1:B:340:ALA:O	1:B:341:ARG:O	2.35	0.45
1:A:211:ASN:OD1	1:A:211:ASN:N	2.50	0.45
1:A:184:GLY:N	1:A:187:GLU:O	2.50	0.44
1:A:221:ARG:NH1	5:A:372:HOH:O	2.50	0.44
1:B:175:ASP:OD2	1:B:175:ASP:N	2.50	0.44
1:C:44:ALA:CB	1:C:111:ILE:CD1	2.96	0.44
1:A:37:GLN:NE2	5:A:467:HOH:O	2.50	0.44
1:B:173:ALA:O	1:B:176:ARG:N	2.51	0.44
1:A:230:ASN:C	1:A:230:ASN:OD1	2.57	0.43
1:B:102:VAL:CG1	1:B:111:ILE:CD1	2.96	0.42
1:B:165:HIS:O	1:B:166:ARG:C	2.57	0.42
1:A:235:ALA:O	1:A:236:PRO:C	2.58	0.41
1:B:206:PHE:CD1	1:B:206:PHE:C	2.94	0.41
1:B:52:ARG:O	1:B:53:PHE:CB	2.69	0.40
1:B:52:ARG:NH1	5:B:420:HOH:O	2.55	0.40
1:B:230:ASN:OD1	1:B:230:ASN:C	2.60	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	338/349 (97%)	324 (96%)	14 (4%)	0	100	100
1	B	330/349 (95%)	303 (92%)	20 (6%)	7 (2%)	11	4
1	C	310/349 (89%)	292 (94%)	16 (5%)	2 (1%)	33	28
All	All	978/1047 (93%)	919 (94%)	50 (5%)	9 (1%)	25	17

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	166	ARG
1	B	340	ALA
1	B	237	GLU
1	B	292	LYS
1	C	180	GLU
1	B	53	PHE
1	B	161	ALA
1	B	291	VAL
1	C	240	PRO

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	275/284 (97%)	266 (97%)	9 (3%)	50	51
1	B	271/284 (95%)	254 (94%)	17 (6%)	25	21
1	C	258/284 (91%)	247 (96%)	11 (4%)	40	37
All	All	804/852 (94%)	767 (95%)	37 (5%)	37	34

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	TYR
1	A	171	THR
1	A	177	LEU

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Mol	Chain	Res	Type
1	A	185	ASP
1	A	198	THR
1	A	239	THR
1	A	242	GLU
1	A	284	SER
1	A	341	ARG
1	B	70	TYR
1	B	166	ARG
1	B	171	THR
1	B	174	PHE
1	B	177	LEU
1	B	178	GLU
1	B	198	THR
1	B	202	LEU
1	B	214	VAL
1	B	217	TRP
1	B	242	GLU
1	B	276	PRO
1	B	282	LEU
1	B	295	LYS
1	B	320	CYS
1	B	337	LEU
1	B	341	ARG
1	C	3	THR
1	C	21	LYS
1	C	70	TYR
1	C	111	ILE
1	C	158	LEU
1	C	200	SER
1	C	205	LYS
1	C	207	LEU
1	C	241	LYS
1	C	263	TYR
1	C	337	LEU

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 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	FES	A	500	1	0,4,4	0.00	-	0,4,4	0.00	-
4	D3M	A	600	-	13,13,13	1.06	1 (7%)	18,18,18	0.96	1 (5%)
2	FES	B	500	1	0,4,4	0.00	-	0,4,4	0.00	-
4	D3M	B	600	-	13,13,13	1.08	2 (15%)	18,18,18	1.06	2 (11%)
2	FES	C	500	1	0,4,4	0.00	-	0,4,4	0.00	-

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
2	FES	A	500	1	-	0/0/4/4	0/0/1/1
4	D3M	A	600	-	-	0/6/6/6	0/1/1/1
2	FES	B	500	1	-	0/0/4/4	0/0/1/1
4	D3M	B	600	-	-	0/6/6/6	0/1/1/1
2	FES	C	500	1	-	0/0/4/4	0/0/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	600	D3M	C5-CL1	2.59	1.80	1.73
4	A	600	D3M	C5-CL1	2.13	1.79	1.73
4	B	600	D3M	C2-CL2	2.08	1.78	1.73

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	600	D3M	C8-O3-C6	2.93	122.92	114.90
4	B	600	D3M	C6-C5-CL1	2.29	121.28	118.45
4	A	600	D3M	C2-C1-C7	-2.20	119.28	121.20

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	340/349 (97%)	-0.03	5 (1%) 70 74	41, 56, 86, 110	0
1	B	334/349 (95%)	0.26	25 (7%) 14 16	39, 57, 112, 138	0
1	C	315/349 (90%)	0.16	17 (5%) 25 27	39, 55, 116, 145	0
All	All	989/1047 (94%)	0.13	47 (4%) 30 32	39, 56, 107, 145	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	198	THR	5.8
1	C	201	VAL	5.4
1	C	207	LEU	4.9
1	B	214	VAL	4.7
1	C	195	PRO	4.3
1	B	339	ALA	4.3
1	A	2	ALA	3.8
1	B	194	ILE	3.7
1	C	196	GLY	3.6
1	B	216	ALA	3.6
1	B	213	PRO	3.6
1	B	243	GLN	3.4
1	C	213	PRO	3.1
1	C	197	GLY	3.1
1	B	273	ILE	3.1
1	C	178	GLU	3.0
1	C	237	GLU	3.0
1	B	155	LEU	2.9
1	B	239	THR	2.9
1	B	2	ALA	2.9
1	B	234	VAL	2.8
1	C	179	ARG	2.8
1	A	195	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	177	LEU	2.8
1	C	206	PHE	2.8
1	B	176	ARG	2.8
1	B	274	ASP	2.6
1	B	174	PHE	2.6
1	A	215	ASP	2.6
1	B	173	ALA	2.5
1	C	240	PRO	2.4
1	B	240	PRO	2.4
1	B	152	VAL	2.4
1	C	235	ALA	2.4
1	B	159	GLY	2.4
1	C	202	LEU	2.3
1	A	93	ALA	2.3
1	B	217	TRP	2.3
1	B	236	PRO	2.2
1	B	196	GLY	2.2
1	B	158	LEU	2.2
1	B	175	ASP	2.2
1	A	155	LEU	2.2
1	B	197	GLY	2.1
1	C	49	CYS	2.1
1	C	245	ILE	2.1
1	C	239	THR	2.0

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
2	FES	A	500	4/4	0.10	-0.02	46,47,49,53	0
3	FE	B	501	1/1	0.15	-0.16	64,64,64,64	0
3	FE	A	501	1/1	0.17	-0.41	48,48,48,48	0
4	D3M	A	600	13/13	0.10	-0.54	46,53,60,69	0
2	FES	B	500	4/4	0.08	-0.58	41,44,44,47	0
2	FES	C	500	4/4	0.16	-0.90	41,43,44,50	0
4	D3M	B	600	13/13	0.10	-1.00	57,72,76,79	0

6.5 Other polymers ⓘ

There are no such residues in this entry.