



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2017 – 10:27 AM EDT

PDB ID : 5ERM
Title : Crystal structure of cyclization domain of Phomopsis amygdali fusicoccadiene synthase complexed with magnesium ions and pamidronate
Authors : Chen, M.; Christianson, D.W.
Deposited on : unknown
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure 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/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

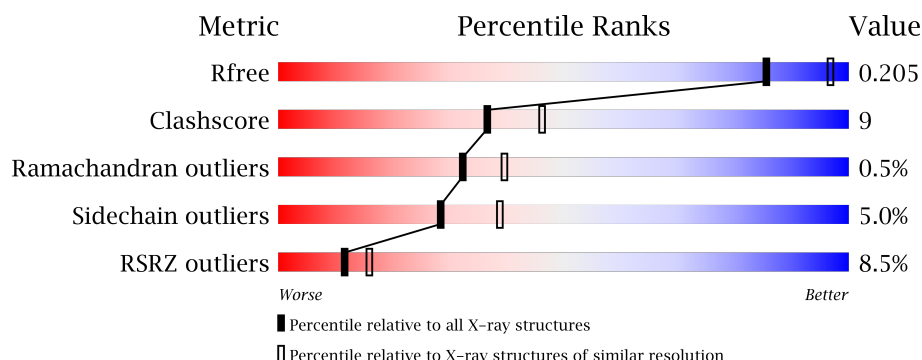
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	363	<div> <div>7%</div> <div> <div></div> <div>66%</div> <div>15%</div> <div>•</div> <div>17%</div> </div> </div>
1	B	363	<div> <div>7%</div> <div> <div></div> <div>70%</div> <div>15%</div> <div>•</div> <div>13%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5218 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Fusicoccadiene synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	301	Total	C	N	O	S	0	2	0
			2450	1573	407	454	16			
1	B	314	Total	C	N	O	S	0	0	0
			2550	1627	433	474	16			

There are 40 discrepancies between the modelled and reference sequences:

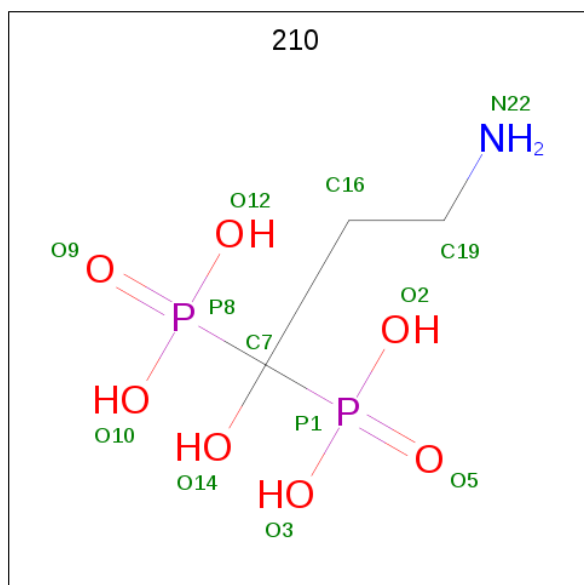
Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP A2PZA5
A	-17	GLY	-	expression tag	UNP A2PZA5
A	-16	SER	-	expression tag	UNP A2PZA5
A	-15	SER	-	expression tag	UNP A2PZA5
A	-14	HIS	-	expression tag	UNP A2PZA5
A	-13	HIS	-	expression tag	UNP A2PZA5
A	-12	HIS	-	expression tag	UNP A2PZA5
A	-11	HIS	-	expression tag	UNP A2PZA5
A	-10	HIS	-	expression tag	UNP A2PZA5
A	-9	HIS	-	expression tag	UNP A2PZA5
A	-8	SER	-	expression tag	UNP A2PZA5
A	-7	SER	-	expression tag	UNP A2PZA5
A	-6	GLY	-	expression tag	UNP A2PZA5
A	-5	LEU	-	expression tag	UNP A2PZA5
A	-4	VAL	-	expression tag	UNP A2PZA5
A	-3	PRO	-	expression tag	UNP A2PZA5
A	-2	ARG	-	expression tag	UNP A2PZA5
A	-1	GLY	-	expression tag	UNP A2PZA5
A	0	SER	-	expression tag	UNP A2PZA5
A	53	ARG	GLY	conflict	UNP A2PZA5
B	-18	MET	-	initiating methionine	UNP A2PZA5
B	-17	GLY	-	expression tag	UNP A2PZA5
B	-16	SER	-	expression tag	UNP A2PZA5
B	-15	SER	-	expression tag	UNP A2PZA5
B	-14	HIS	-	expression tag	UNP A2PZA5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	HIS	-	expression tag	UNP A2PZA5
B	-12	HIS	-	expression tag	UNP A2PZA5
B	-11	HIS	-	expression tag	UNP A2PZA5
B	-10	HIS	-	expression tag	UNP A2PZA5
B	-9	HIS	-	expression tag	UNP A2PZA5
B	-8	SER	-	expression tag	UNP A2PZA5
B	-7	SER	-	expression tag	UNP A2PZA5
B	-6	GLY	-	expression tag	UNP A2PZA5
B	-5	LEU	-	expression tag	UNP A2PZA5
B	-4	VAL	-	expression tag	UNP A2PZA5
B	-3	PRO	-	expression tag	UNP A2PZA5
B	-2	ARG	-	expression tag	UNP A2PZA5
B	-1	GLY	-	expression tag	UNP A2PZA5
B	0	SER	-	expression tag	UNP A2PZA5
B	53	ARG	GLY	conflict	UNP A2PZA5

- Molecule 2 is PAMIDRONATE (three-letter code: 210) (formula: $C_3H_{11}NO_7P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			13	3	1	7	2		
2	B	1	Total	C	N	O	P	0	0
			13	3	1	7	2		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	3	Total	Mg	0	0
			3	3		
4	A	3	Total	Mg	0	0
			3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	82	Total	O	0	0
			82	82		
5	B	102	Total	O	0	0
			102	102		

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.29Å 143.29Å 118.26Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.90 – 2.30 46.90 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.90-2.30) 95.3 (46.90-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 2.29Å)	Xtriage
Refinement program	PHENIX dev_1839	Depositor
R, R_{free}	0.178 , 0.206 0.178 , 0.205	Depositor DCC
R_{free} test set	3027 reflections (5.10%)	DCC
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.378 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5218	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: MG, 210, CL

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	0.32	2/2515 (0.1%)	0.50	6/3405 (0.2%)
1	B	0.23	0/2611	0.39	0/3533
All	All	0.28	2/5126 (0.0%)	0.45	6/6938 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	68[A]	VAL	CA-C	5.46	1.67	1.52
1	A	68[B]	VAL	CA-C	5.46	1.67	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	220[A]	LEU	CB-CA-C	-6.43	97.97	110.20
1	A	220[B]	LEU	CB-CA-C	-6.43	97.97	110.20
1	A	220[A]	LEU	N-CA-C	5.93	127.02	111.00
1	A	220[B]	LEU	N-CA-C	5.93	127.02	111.00
1	A	68[A]	VAL	CA-C-O	5.50	131.66	120.10
1	A	68[B]	VAL	CA-C-O	5.50	131.66	120.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2450	0	2398	49	0
1	B	2550	0	2479	40	0
2	A	13	0	7	3	0
2	B	13	0	7	2	0
3	A	1	0	0	1	0
3	B	1	0	0	1	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
5	A	82	0	0	3	0
5	B	102	0	0	4	0
All	All	5218	0	4891	89	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (89) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:HIS:CE1	1:B:239:LYS:HD2	1.93	1.03
1:B:190:MET:SD	5:B:842:HOH:O	2.32	0.88
1:A:64:SER:O	1:A:68[B]:VAL:HG22	1.75	0.87
1:A:216:LEU:HD12	1:A:216:LEU:O	1.79	0.82
1:A:216:LEU:O	1:A:220[A]:LEU:HD13	1.84	0.77
1:B:100:HIS:CE1	1:B:239:LYS:CD	2.68	0.77
2:B:704:210:O9	5:B:801:HOH:O	2.08	0.71
1:B:189:ILE:HG12	1:B:225:TRP:HD1	1.56	0.71
1:B:100:HIS:ND1	1:B:239:LYS:HD2	2.06	0.70
1:A:344:LEU:OXT	1:B:5:TYR:OH	2.11	0.69
1:B:66:ILE:HD13	1:B:81:ILE:HG22	1.75	0.68
3:A:402:CL:CL	5:A:545:HOH:O	2.48	0.67
3:B:705:CL:CL	5:B:824:HOH:O	2.48	0.67
1:B:295:ASP:O	1:B:303:ARG:NH2	2.28	0.67
1:A:216:LEU:CD1	1:A:220[A]:LEU:HD11	2.27	0.65
1:A:232:ASN:ND2	1:A:326:TYR:OH	2.29	0.65
1:A:76:GLU:CD	1:B:36:ARG:HH21	2.01	0.63
2:A:401:210:O2	5:A:501:HOH:O	2.15	0.63
1:A:300:LEU:HG	1:A:304:LYS:HE3	1.82	0.62
1:A:216:LEU:HD12	1:A:220[A]:LEU:CD1	2.31	0.60
1:A:66:ILE:HD13	1:A:81:ILE:HG22	1.81	0.60
1:B:243:ALA:O	1:B:247:HIS:ND1	2.29	0.59
1:B:100:HIS:CE1	1:B:239:LYS:HZ3	2.20	0.59
1:A:216:LEU:HD11	1:A:220[A]:LEU:HD11	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:LEU:HD22	1:B:259:LEU:HD21	1.86	0.58
1:B:232:ASN:ND2	1:B:326:TYR:OH	2.37	0.57
1:A:141:SER:HA	1:A:144:PHE:HD2	1.71	0.56
1:B:100:HIS:NE2	1:B:239:LYS:NZ	2.46	0.56
1:A:42:HIS:NE2	1:A:86:GLU:OE1	2.27	0.56
1:B:81:ILE:HD11	1:B:203:PHE:HD2	1.71	0.55
1:A:220[B]:LEU:HD12	1:A:306:LEU:HD21	1.89	0.54
1:B:98:VAL:HG13	1:B:243:ALA:HB2	1.89	0.54
1:B:224:ALA:HB2	1:B:285:TYR:CG	2.43	0.53
1:A:216:LEU:HD12	1:A:216:LEU:C	2.30	0.52
1:A:66:ILE:HD11	1:A:85:ASN:HB2	1.92	0.52
1:A:216:LEU:CD1	1:A:220[A]:LEU:CD1	2.88	0.51
1:A:207:LEU:HB3	1:A:301:ASP:HB3	1.92	0.51
1:A:289:ILE:HG13	1:A:310:LEU:HD11	1.91	0.51
1:B:66:ILE:HD12	1:B:82:SER:HA	1.93	0.50
1:A:76:GLU:OE1	1:B:36:ARG:NH2	2.42	0.50
1:A:213:GLU:HG3	1:A:216:LEU:HD23	1.95	0.49
1:A:216:LEU:O	1:A:220[A]:LEU:CD1	2.59	0.48
1:B:298:ILE:HG23	1:B:302:LEU:HD23	1.94	0.48
1:A:223:ASN:HB2	1:A:285:TYR:HB2	1.96	0.47
1:A:188:ARG:NH2	2:A:401:210:O5	2.41	0.47
1:A:36:ARG:NE	1:B:76:GLU:OE2	2.26	0.47
1:B:211:ASP:HA	1:B:214:LEU:HG	1.96	0.47
1:B:100:HIS:CE1	1:B:239:LYS:NZ	2.82	0.47
1:B:339:TRP:HB3	1:B:344:LEU:HD23	1.96	0.47
1:B:136:LYS:HD2	1:B:139:ILE:HG13	1.95	0.47
1:B:188:ARG:NH1	5:B:820:HOH:O	2.47	0.47
1:B:232:ASN:OD1	2:B:704:210:O2	2.33	0.46
1:A:144:PHE:HA	1:A:147:MET:HE3	1.97	0.46
1:A:247:HIS:HB2	1:A:249:LYS:HG2	1.97	0.46
1:A:66:ILE:HD12	1:A:82:SER:HA	1.98	0.46
1:B:17:GLU:OE1	1:B:275:ARG:NH2	2.49	0.46
1:B:100:HIS:CE1	1:B:239:LYS:CG	2.99	0.46
1:B:98:VAL:HG13	1:B:243:ALA:CB	2.46	0.46
1:A:343:GLY:HA2	5:A:506:HOH:O	2.16	0.45
1:A:329:ASP:N	1:A:329:ASP:OD2	2.42	0.45
1:A:49:ILE:HG13	1:A:50:GLY:N	2.31	0.45
1:A:11:PRO:HA	1:A:14:TYR:CZ	2.52	0.45
1:A:339:TRP:O	1:A:343:GLY:HA2	2.16	0.45
1:A:325:ARG:NH2	2:A:401:210:O12	2.50	0.44
1:B:168:VAL:O	1:B:171:SER:OG	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:LEU:HD22	1:A:259:LEU:HD21	1.98	0.44
1:B:232:ASN:O	1:B:236:SER:OG	2.36	0.44
1:B:45:TRP:HD1	1:B:52:CYS:HB2	1.82	0.44
1:A:77:ARG:NH1	1:A:203:PHE:O	2.46	0.44
1:B:66:ILE:HD11	1:B:85:ASN:HB2	2.00	0.43
1:A:257:TRP:O	1:A:261:GLN:HG2	2.18	0.43
1:A:208:HIS:N	1:A:301:ASP:OD2	2.38	0.43
1:A:289:ILE:O	1:A:293:LYS:HG2	2.19	0.42
1:A:148:LEU:HD12	1:A:152:PRO:HA	2.02	0.42
1:A:216:LEU:HD12	1:A:220[A]:LEU:HD13	1.98	0.42
1:A:211:ASP:N	1:A:211:ASP:OD1	2.52	0.42
1:B:59:LEU:HA	1:B:59:LEU:HD12	1.88	0.42
1:A:213:GLU:CG	1:A:216:LEU:HD23	2.50	0.42
1:B:100:HIS:CD2	1:B:325:ARG:CZ	3.03	0.42
1:A:45:TRP:CD1	1:A:52:CYS:HB2	2.55	0.41
1:A:77:ARG:O	1:A:81:ILE:HG12	2.21	0.41
1:A:59:LEU:HD12	1:A:59:LEU:HA	1.86	0.41
1:A:286:LEU:HA	1:A:286:LEU:HD12	1.92	0.41
1:B:310:LEU:HA	1:B:310:LEU:HD12	1.92	0.41
1:A:45:TRP:HD1	1:A:52:CYS:HB2	1.86	0.41
1:B:68:VAL:HG22	1:B:315:GLY:HA2	2.03	0.41
1:B:271:MET:O	1:B:275:ARG:HG3	2.21	0.40
1:A:285:TYR:HE2	1:A:310:LEU:HD12	1.86	0.40
1:B:188:ARG:HA	1:B:191:ASP:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	297/363 (82%)	283 (95%)	11 (4%)	3 (1%)	18 20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	308/363 (85%)	290 (94%)	18 (6%)	0	100	100
All	All	605/726 (83%)	573 (95%)	29 (5%)	3 (0%)	32	39

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	177	ARG
1	A	139	ILE
1	A	253	VAL

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	266/317 (84%)	255 (96%)	11 (4%)	35	48
1	B	275/317 (87%)	259 (94%)	16 (6%)	23	31
All	All	541/634 (85%)	514 (95%)	27 (5%)	28	39

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ILE
1	A	59	LEU
1	A	138	ARG
1	A	146	GLU
1	A	148	LEU
1	A	153	GLU
1	A	211	ASP
1	A	213	GLU
1	A	306	LEU
1	A	307	ASP
1	A	341	ARG
1	B	21	GLU
1	B	49	ILE

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Mol	Chain	Res	Type
1	B	56	ARG
1	B	59	LEU
1	B	96	ASP
1	B	98	VAL
1	B	100	HIS
1	B	130	ASP
1	B	132	ARG
1	B	133	ARG
1	B	137	LYS
1	B	164	ARG
1	B	187	TYR
1	B	296	GLU
1	B	341	ARG
1	B	344	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	232	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	210	A	401	4	12,12,12	1.95	2 (16%)	17,20,20	1.03	1 (5%)
2	210	B	704	4	12,12,12	2.07	2 (16%)	17,20,20	1.06	1 (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
2	210	A	401	4	-	0/22/22/22	0/0/0/0
2	210	B	704	4	-	0/22/22/22	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	704	210	P8-C7	-4.46	1.82	1.85
2	B	704	210	P1-C7	-4.05	1.82	1.85
2	A	401	210	P8-C7	-3.94	1.82	1.85
2	A	401	210	P1-C7	-3.78	1.82	1.85

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	210	O5-P1-C7	-2.09	104.37	109.92
2	B	704	210	O12-P8-O10	2.20	114.27	108.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	210	3	0
2	B	704	210	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	301/363 (82%)	0.79	27 (8%)	10 14	39, 55, 98, 170	0
1	B	314/363 (86%)	0.78	25 (7%)	13 17	33, 50, 105, 162	0
All	All	615/726 (84%)	0.78	52 (8%)	11 16	33, 53, 105, 170	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	167	GLU	9.3
1	B	167	GLU	6.6
1	B	100	HIS	6.4
1	B	101	ASP	5.2
1	A	138	ARG	5.1
1	B	172	ARG	4.9
1	A	164	ARG	4.7
1	B	134	ALA	4.7
1	A	168	VAL	4.3
1	B	168	VAL	4.1
1	B	102	THR	4.0
1	B	133	ARG	3.9
1	A	214	LEU	3.8
1	B	131	ILE	3.6
1	A	136	LYS	3.5
1	B	170	SER	3.5
1	B	225	TRP	3.3
1	B	175	GLU	3.3
1	B	130	ASP	3.2
1	A	156	LYS	3.1
1	B	99	GLY	3.1
1	B	144	PHE	3.1
1	B	98	VAL	3.0
1	A	247	HIS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	166	VAL	2.8
1	A	190	MET	2.7
1	A	294	ASN	2.7
1	B	138	ARG	2.7
1	A	160	LYS	2.7
1	A	210	PRO	2.6
1	B	97	HIS	2.5
1	A	248	GLY	2.5
1	A	297	SER	2.5
1	B	176	THR	2.5
1	A	216	LEU	2.5
1	B	164	ARG	2.3
1	A	211	ASP	2.3
1	B	166	VAL	2.3
1	A	296	GLU	2.3
1	A	142	GLN	2.2
1	A	180	GLU	2.2
1	B	344	LEU	2.2
1	B	145	LEU	2.2
1	B	50	GLY	2.2
1	A	145	LEU	2.1
1	A	137	LYS	2.1
1	B	343	GLY	2.1
1	A	144	PHE	2.1
1	A	163	ALA	2.1
1	A	195	MET	2.0
1	A	193	GLY	2.0
1	A	218	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	MG	A	405	1/1	0.99	0.18	1.50	49,49,49,49	0
2	210	A	401	13/13	0.95	0.17	0.68	50,55,65,65	0
2	210	B	704	13/13	0.93	0.17	-0.25	48,57,67,71	0
4	MG	A	404	1/1	0.89	0.14	-0.53	52,52,52,52	0
4	MG	B	701	1/1	0.76	0.14	-1.10	56,56,56,56	0
3	CL	B	705	1/1	0.91	0.12	-1.55	61,61,61,61	0
4	MG	B	703	1/1	0.92	0.12	-1.63	53,53,53,53	0
3	CL	A	402	1/1	0.93	0.10	-2.35	59,59,59,59	0
4	MG	B	702	1/1	0.53	0.09	-	73,73,73,73	0
4	MG	A	403	1/1	0.92	0.14	-	70,70,70,70	0

6.5 Other polymers

There are no such residues in this entry.