



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 30, 2017 – 11:02 PM EDT

PDB ID : 5BP2
Title : Dehydratase domain (DH) of a mycocerosic acid synthase-like (MAS-like) PKS, crystal form 1
Authors : Herbst, D.A.; Jakob, P.R.; Zaehring, F.; Maier, T.
Deposited on : unknown
Resolution : 1.75 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

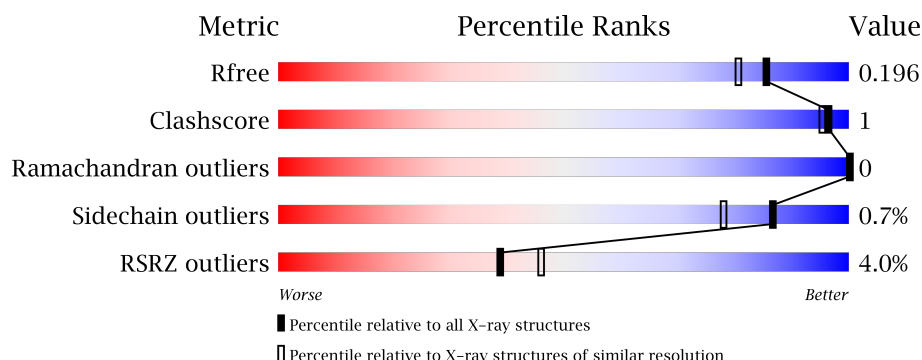
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	1762 (1.76-1.76)
Clashscore	112137	1889 (1.76-1.76)
Ramachandran outliers	110173	1868 (1.76-1.76)
Sidechain outliers	110143	1868 (1.76-1.76)
RSRZ outliers	101464	1770 (1.76-1.76)

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	305	<div> <div>4%</div> <div>90%</div> <div>7%</div> </div>
1	B	305	<div> <div>5%</div> <div>90%</div> <div>7%</div> </div>
1	C	305	<div> <div>4%</div> <div>89%</div> <div>8%</div> </div>
1	D	305	<div> <div>3%</div> <div>90%</div> <div>7%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	A	1203	-	-	-	X
3	EDO	A	1204	-	-	-	X
3	EDO	A	1206	-	-	-	X
3	EDO	A	1207[B]	-	-	-	X
3	EDO	A	1208	-	-	-	X
3	EDO	A	1212	-	-	-	X
3	EDO	A	1213	-	-	-	X
3	EDO	B	1201	-	-	-	X
3	EDO	B	1202	-	-	-	X
3	EDO	C	1202	-	-	-	X
3	EDO	C	1203	-	-	-	X
3	EDO	C	1204	-	-	-	X
3	EDO	C	1205	-	-	-	X
3	EDO	C	1206	-	-	-	X
3	EDO	C	1207	-	-	-	X
3	EDO	C	1209	-	-	-	X
3	EDO	D	1203	-	-	-	X
3	EDO	D	1204	-	-	-	X
3	EDO	D	1205	-	-	-	X
3	EDO	D	1206	-	-	-	X
3	EDO	D	1207	-	-	-	X
3	EDO	D	1208	-	-	-	X
3	EDO	D	1209	-	-	-	X
3	EDO	D	1210	-	-	-	X
4	GOL	A	1214	-	-	-	X
4	GOL	B	1203	-	-	-	X
4	GOL	C	1210	-	-	-	X
4	GOL	D	1211	-	-	-	X
4	GOL	D	1212	-	-	-	X
6	PG4	C	1212	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 18419 atoms, of which 8782 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 Mycocerosic acid synthase-like polyketide synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	285	Total	C	H	N	O	S	0	22	0
			4388	1396	2157	402	424	9			
1	B	284	Total	C	H	N	O	S	0	17	0
			4303	1360	2137	389	407	10			
1	C	282	Total	C	H	N	O	S	0	14	0
			4253	1346	2111	385	403	8			
1	D	283	Total	C	H	N	O	S	0	19	0
			4329	1369	2145	393	414	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	882	SER	-	expression tag	UNP A0R1E8
A	883	MET	-	expression tag	UNP A0R1E8
B	882	SER	-	expression tag	UNP A0R1E8
B	883	MET	-	expression tag	UNP A0R1E8
C	882	SER	-	expression tag	UNP A0R1E8
C	883	MET	-	expression tag	UNP A0R1E8
D	882	SER	-	expression tag	UNP A0R1E8
D	883	MET	-	expression tag	UNP A0R1E8

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	D	1	Total	Mg	0	0
			1	1		

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	1
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	1
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		

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

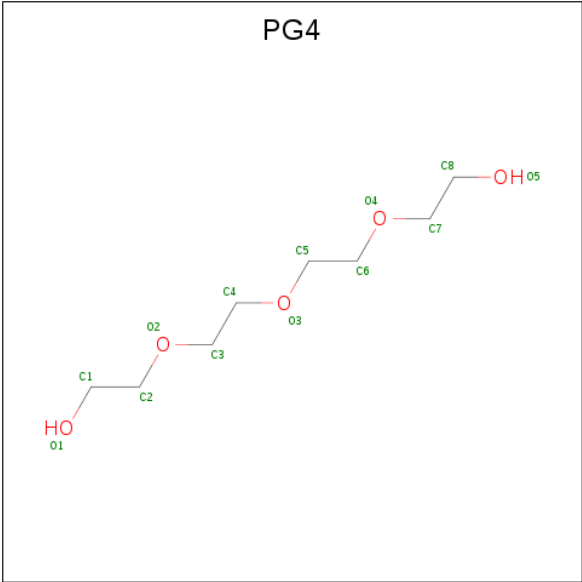


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	B	1	Total	C	H	O	0	0
			14	3	8	3		
4	C	1	Total	C	H	O	0	0
			14	3	8	3		
4	D	1	Total	C	H	O	0	0
			14	3	8	3		
4	D	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		
5	D	1	Total	Cl	0	0
			1	1		
5	C	1	Total	Cl	0	0
			1	1		

- Molecule 6 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			13	8	5		

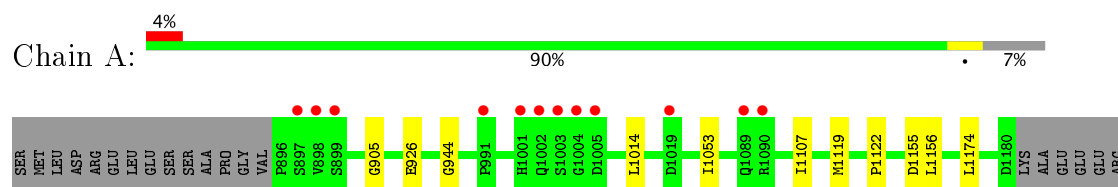
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	193	Total	O	0	4
			193	193		
7	B	163	Total	O	0	3
			163	163		
7	C	177	Total	O	0	1
			177	177		
7	D	205	Total	O	0	2
			205	205		

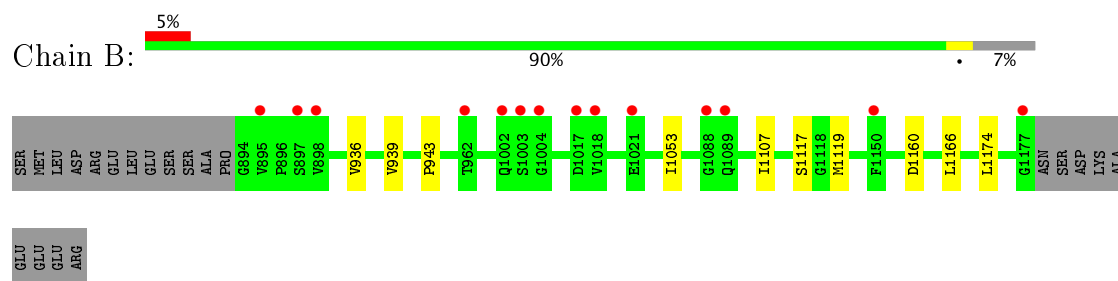
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

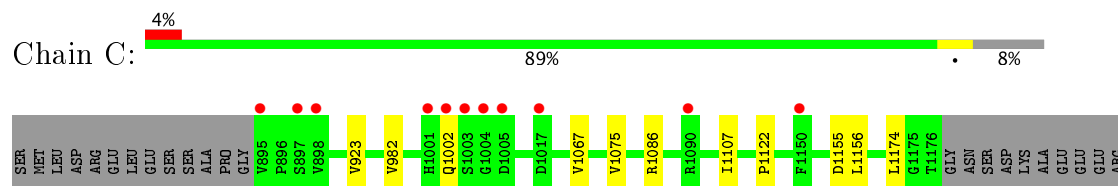
- Molecule 1: Mycocerosic acid synthase-like polyketide synthase



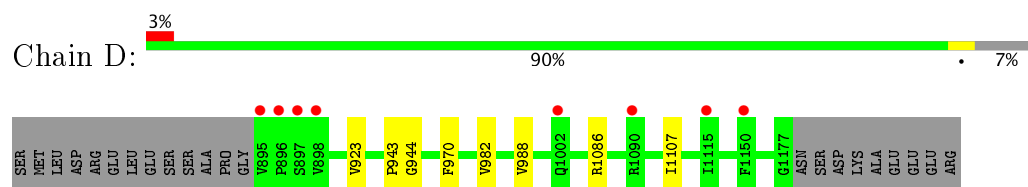
- Molecule 1: Mycocerosic acid synthase-like polyketide synthase



- Molecule 1: Mycocerosic acid synthase-like polyketide synthase



- Molecule 1: Mycocerosic acid synthase-like polyketide synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.65Å 162.40Å 66.62Å 90.00° 91.38° 90.00°	Depositor
Resolution (Å)	66.60 – 1.75 66.60 – 1.75	Depositor EDS
% Data completeness (in resolution range)	96.9 (66.60-1.75) 96.8 (66.60-1.75)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 1.75Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.183 , 0.203 0.177 , 0.196	Depositor DCC
R_{free} test set	2012 reflections (1.66%)	DCC
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.237 for h,-k,-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	18419	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.98% 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: PG4, GOL, MG, EDO, 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	0.50	0/2340	0.66	0/3197
1	B	0.49	0/2282	0.62	0/3120
1	C	0.50	0/2249	0.66	2/3077 (0.1%)
1	D	0.52	0/2289	0.66	0/3130
All	All	0.50	0/9160	0.65	2/12524 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1086[A]	ARG	C-N-CA	6.37	137.63	121.70
1	C	1086[B]	ARG	C-N-CA	6.37	137.63	121.70

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	2231	2157	2130	6	0
1	B	2166	2137	2064	5	0
1	C	2142	2111	2057	5	0
1	D	2184	2145	2089	5	0
2	A	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1	0	0	0	0
3	A	48	72	72	0	0
3	B	8	12	12	0	0
3	C	36	54	54	0	0
3	D	36	54	54	1	0
4	A	6	8	8	2	0
4	B	6	8	8	1	0
4	C	6	8	8	1	0
4	D	12	16	16	2	0
5	A	1	0	0	1	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	C	13	0	18	0	0
7	A	193	0	0	0	0
7	B	163	0	0	0	0
7	C	177	0	0	0	0
7	D	205	0	0	0	0
All	All	9637	8782	8590	21	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 1.

All (21) 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:C:1067:VAL:HG12	1:C:1075[B]:VAL:HG12	1.45	0.99
1:D:988:VAL:HG12	3:D:1208:EDO:H22	1.83	0.60
1:D:943:PRO:HA	4:D:1212:GOL:H32	1.83	0.59
1:A:1107[A]:ILE:HD11	1:A:1174:LEU:HD13	1.83	0.59
1:B:943:PRO:HA	4:B:1203:GOL:H32	1.87	0.56
1:C:1122:PRO:HD2	4:C:1210:GOL:C1	2.42	0.49
1:C:1107[A]:ILE:HD11	1:C:1174:LEU:HD13	1.95	0.48
1:B:1160:ASP:HB3	1:B:1166:LEU:HD11	1.96	0.46
1:D:944:GLY:H	4:D:1212:GOL:C3	2.29	0.46
1:A:905:GLY:O	5:A:1215:CL:CL	2.73	0.44
1:D:923:VAL:HG22	1:D:982[B]:VAL:CG2	2.48	0.44
1:B:1053:ILE:HD11	1:B:1119:MET:CG	2.48	0.43
1:C:923:VAL:HG22	1:C:982[A]:VAL:CG2	2.49	0.42
1:A:944:GLY:H	4:A:1214:GOL:C1	2.33	0.41
1:A:1053:ILE:HD11	1:A:1119:MET:HG2	2.03	0.41
1:B:936:VAL:O	1:B:939:VAL:HG22	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1107[A]:ILE:HD11	1:B:1174:LEU:HD13	2.02	0.41
1:A:1122:PRO:HD2	4:A:1214:GOL:C1	2.51	0.41
1:C:1155:ASP:C	1:C:1156:LEU:HD12	2.41	0.41
1:A:1155:ASP:C	1:A:1156:LEU:HD12	2.41	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	305/305 (100%)	298 (98%)	7 (2%)	0	100	100
1	B	299/305 (98%)	293 (98%)	6 (2%)	0	100	100
1	C	294/305 (96%)	287 (98%)	7 (2%)	0	100	100
1	D	300/305 (98%)	297 (99%)	3 (1%)	0	100	100
All	All	1198/1220 (98%)	1175 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	236/234 (101%)	233 (99%)	3 (1%)	73	58
1	B	230/234 (98%)	229 (100%)	1 (0%)	93	89

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	227/234 (97%)	226 (100%)	1 (0%)	93	89
1	D	231/234 (99%)	229 (99%)	2 (1%)	82	71
All	All	924/936 (99%)	917 (99%)	7 (1%)	87	75

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	926[A]	GLU
1	A	926[B]	GLU
1	A	1014	LEU
1	B	1117	SER
1	C	1002	GLN
1	D	970	PHE
1	D	1086	ARG

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

Mol	Chain	Res	Type
1	A	907	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 43 ligands modelled in this entry, 5 are monoatomic - leaving 38 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	$\# Z > 2$
3	EDO	A	1202	-	3,3,3	0.64	0	2,2,2	0.31	0
3	EDO	A	1203	-	3,3,3	0.64	0	2,2,2	0.29	0
3	EDO	A	1204	-	3,3,3	0.64	0	2,2,2	0.12	0
3	EDO	A	1205[A]	-	3,3,3	0.42	0	2,2,2	0.26	0
3	EDO	A	1206	-	3,3,3	0.53	0	2,2,2	0.42	0
3	EDO	A	1207[B]	-	3,3,3	0.55	0	2,2,2	0.36	0
3	EDO	A	1208	-	3,3,3	0.52	0	2,2,2	0.43	0
3	EDO	A	1209	-	3,3,3	0.53	0	2,2,2	0.28	0
3	EDO	A	1210	-	3,3,3	0.65	0	2,2,2	0.23	0
3	EDO	A	1211	-	3,3,3	0.48	0	2,2,2	0.34	0
3	EDO	A	1212	-	3,3,3	0.66	0	2,2,2	0.29	0
3	EDO	A	1213	-	3,3,3	0.56	0	2,2,2	0.11	0
4	GOL	A	1214	-	5,5,5	0.15	0	5,5,5	1.14	1 (20%)
3	EDO	B	1201	-	3,3,3	0.66	0	2,2,2	0.35	0
3	EDO	B	1202	-	3,3,3	0.72	0	2,2,2	0.37	0
4	GOL	B	1203	-	5,5,5	0.48	0	5,5,5	0.53	0
3	EDO	C	1201	-	3,3,3	0.57	0	2,2,2	0.17	0
3	EDO	C	1202	-	3,3,3	0.64	0	2,2,2	0.16	0
3	EDO	C	1203	-	3,3,3	0.70	0	2,2,2	0.10	0
3	EDO	C	1204	-	3,3,3	0.58	0	2,2,2	0.39	0
3	EDO	C	1205	-	3,3,3	0.46	0	2,2,2	0.24	0
3	EDO	C	1206	-	3,3,3	0.72	0	2,2,2	0.29	0
3	EDO	C	1207	-	3,3,3	0.54	0	2,2,2	0.33	0
3	EDO	C	1208	-	3,3,3	0.51	0	2,2,2	0.63	0
3	EDO	C	1209	-	3,3,3	0.62	0	2,2,2	0.36	0
4	GOL	C	1210	-	5,5,5	0.18	0	5,5,5	0.95	0
6	PG4	C	1212	-	12,12,12	0.59	0	11,11,11	0.66	0
3	EDO	D	1202	-	3,3,3	0.59	0	2,2,2	0.55	0
3	EDO	D	1203	-	3,3,3	0.78	0	2,2,2	0.16	0
3	EDO	D	1204	-	3,3,3	0.64	0	2,2,2	0.40	0
3	EDO	D	1205	-	3,3,3	0.67	0	2,2,2	0.47	0
3	EDO	D	1206	-	3,3,3	0.56	0	2,2,2	0.26	0
3	EDO	D	1207	-	3,3,3	0.68	0	2,2,2	0.17	0
3	EDO	D	1208	-	3,3,3	0.66	0	2,2,2	2.15	1 (50%)
3	EDO	D	1209	-	3,3,3	0.48	0	2,2,2	0.67	0
3	EDO	D	1210	-	3,3,3	0.97	0	2,2,2	0.40	0
4	GOL	D	1211	-	5,5,5	0.12	0	5,5,5	0.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	D	1212	-	5,5,5	0.48	0	5,5,5	0.61	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. 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
3	EDO	A	1202	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1203	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1204	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1205[A]	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1206	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1207[B]	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1208	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1209	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1210	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1211	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1212	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1213	-	-	0/1/1/1	0/0/0/0
4	GOL	A	1214	-	-	0/4/4/4	0/0/0/0
3	EDO	B	1201	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1202	-	-	0/1/1/1	0/0/0/0
4	GOL	B	1203	-	-	0/4/4/4	0/0/0/0
3	EDO	C	1201	-	-	0/1/1/1	0/0/0/0
3	EDO	C	1202	-	-	0/1/1/1	0/0/0/0
3	EDO	C	1203	-	-	0/1/1/1	0/0/0/0
3	EDO	C	1204	-	-	0/1/1/1	0/0/0/0
3	EDO	C	1205	-	-	0/1/1/1	0/0/0/0
3	EDO	C	1206	-	-	0/1/1/1	0/0/0/0
3	EDO	C	1207	-	-	0/1/1/1	0/0/0/0
3	EDO	C	1208	-	-	0/1/1/1	0/0/0/0
3	EDO	C	1209	-	-	0/1/1/1	0/0/0/0
4	GOL	C	1210	-	-	0/4/4/4	0/0/0/0
6	PG4	C	1212	-	-	0/10/10/10	0/0/0/0
3	EDO	D	1202	-	-	0/1/1/1	0/0/0/0
3	EDO	D	1203	-	-	0/1/1/1	0/0/0/0
3	EDO	D	1204	-	-	0/1/1/1	0/0/0/0
3	EDO	D	1205	-	-	0/1/1/1	0/0/0/0
3	EDO	D	1206	-	-	0/1/1/1	0/0/0/0
3	EDO	D	1207	-	-	0/1/1/1	0/0/0/0
3	EDO	D	1208	-	-	0/1/1/1	0/0/0/0
3	EDO	D	1209	-	-	0/1/1/1	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	D	1210	-	-	0/1/1/1	0/0/0/0
4	GOL	D	1211	-	-	0/4/4/4	0/0/0/0
4	GOL	D	1212	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1214	GOL	C3-C2-C1	-2.02	103.50	111.52
3	D	1208	EDO	O2-C2-C1	3.02	133.70	112.08

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1214	GOL	2	0
4	B	1203	GOL	1	0
4	C	1210	GOL	1	0
3	D	1208	EDO	1	0
4	D	1212	GOL	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	285/305 (93%)	0.17	12 (4%)	37 44	41, 53, 87, 129	0
1	B	284/305 (93%)	0.28	14 (4%)	30 36	44, 55, 90, 117	0
1	C	282/305 (92%)	0.22	11 (3%)	40 47	43, 53, 87, 118	0
1	D	283/305 (92%)	0.16	8 (2%)	53 60	41, 50, 84, 107	0
All	All	1134/1220 (92%)	0.21	45 (3%)	39 46	41, 53, 87, 129	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1003	SER	9.0
1	B	1003	SER	8.8
1	C	898	VAL	7.9
1	A	1003	SER	7.9
1	C	895	VAL	7.7
1	A	1002	GLN	7.0
1	A	898	VAL	6.4
1	D	898	VAL	5.7
1	B	895	VAL	5.6
1	C	1150	PHE	5.5
1	B	898	VAL	5.5
1	D	895	VAL	5.4
1	B	962	THR	5.2
1	B	1002	GLN	5.0
1	C	1002	GLN	4.7
1	B	1021	GLU	4.6
1	C	1090	ARG	4.3
1	D	1150	PHE	4.2
1	A	1005	ASP	4.0
1	D	896	PRO	4.0
1	B	1150	PHE	4.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	1001	HIS	3.8
1	A	1090	ARG	3.7
1	B	897	SER	3.7
1	D	1002	GLN	3.5
1	A	1004	GLY	3.5
1	B	1177	GLY	3.3
1	D	1090	ARG	3.3
1	D	1115[A]	ILE	3.0
1	C	897	SER	2.7
1	C	1001	HIS	2.7
1	B	1089	GLN	2.7
1	C	1017	ASP	2.7
1	B	1004	GLY	2.6
1	A	897	SER	2.6
1	A	899	SER	2.5
1	A	1019	ASP	2.5
1	C	1005	ASP	2.5
1	A	1089	GLN	2.4
1	C	1004	GLY	2.3
1	D	897	SER	2.3
1	B	1088	GLY	2.2
1	B	1017	ASP	2.2
1	B	1018	VAL	2.2
1	A	991	PRO	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(\AA^2)	Q<0.9
3	EDO	A	1204	4/4	0.79	0.39	36.49	72,75,77,78	0
3	EDO	C	1209	4/4	0.79	0.30	30.69	56,62,67,68	0
3	EDO	C	1202	4/4	0.69	0.43	23.77	64,70,79,80	0
3	EDO	C	1205	4/4	0.87	0.34	22.86	73,75,78,78	0
6	PG4	C	1212	13/13	0.66	0.40	21.68	87,89,90,90	0
3	EDO	D	1207	4/4	0.92	0.62	15.90	67,75,79,79	0
4	GOL	C	1210	6/6	0.91	0.26	14.18	45,68,83,84	0
3	EDO	D	1208	4/4	0.88	0.40	13.79	76,79,81,81	0
3	EDO	A	1206	4/4	0.90	0.46	13.67	93,95,95,95	0
3	EDO	D	1210	4/4	0.81	0.26	12.73	65,68,71,71	0
4	GOL	A	1214	6/6	0.76	0.35	12.52	47,70,78,79	0
3	EDO	A	1207[B]	4/4	0.85	0.40	12.11	63,66,67,67	10
3	EDO	C	1204	4/4	0.77	0.26	11.93	89,90,91,91	0
3	EDO	D	1203	4/4	0.81	0.31	11.15	64,71,73,73	0
3	EDO	A	1213	4/4	0.90	0.27	10.55	54,63,67,67	0
3	EDO	C	1207	4/4	0.78	0.40	10.35	82,82,84,84	0
3	EDO	A	1203	4/4	0.91	0.24	9.44	78,79,84,85	0
4	GOL	D	1212	6/6	0.76	0.29	9.34	43,64,71,72	0
3	EDO	B	1202	4/4	0.87	0.27	9.11	58,61,71,71	0
3	EDO	C	1206	4/4	0.83	0.35	8.76	57,70,76,76	0
3	EDO	D	1204	4/4	0.90	0.25	8.50	67,70,74,74	0
4	GOL	B	1203	6/6	0.71	0.31	8.29	44,65,75,76	0
3	EDO	B	1201	4/4	0.80	0.32	7.51	81,83,85,85	0
3	EDO	C	1203	4/4	0.81	0.29	6.18	68,70,78,78	0
3	EDO	D	1205	4/4	0.77	0.17	5.65	78,79,81,81	0
3	EDO	A	1208	4/4	0.47	0.78	4.70	102,105,107,107	0
4	GOL	D	1211	6/6	0.93	0.24	4.06	79,85,89,89	0
3	EDO	D	1209	4/4	0.94	0.18	3.91	62,66,69,69	0
3	EDO	D	1206	4/4	0.87	0.22	3.74	58,71,77,77	0
3	EDO	A	1212	4/4	0.92	0.14	2.67	60,70,75,75	0
3	EDO	A	1202	4/4	0.87	0.16	1.74	84,86,87,87	0
3	EDO	D	1202	4/4	0.84	0.13	1.14	58,63,66,67	0
3	EDO	A	1210	4/4	0.79	0.10	0.90	88,89,90,90	0
3	EDO	A	1211	4/4	0.74	0.18	0.22	101,102,104,104	0
3	EDO	A	1205[A]	4/4	0.95	0.13	0.13	78,78,80,80	10
5	CL	A	1215	1/1	0.98	0.09	-0.32	68,68,68,68	0
3	EDO	C	1201	4/4	0.91	0.09	-1.11	90,91,94,94	0
2	MG	A	1201	1/1	0.77	0.11	-	88,88,88,88	0
3	EDO	A	1209	4/4	0.70	0.44	-	60,69,71,71	0
3	EDO	C	1208	4/4	0.67	0.47	-	81,85,89,89	0
5	CL	D	1213	1/1	0.79	0.23	-	98,98,98,98	0
5	CL	C	1211	1/1	0.78	0.09	-	99,99,99,99	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	MG	D	1201	1/1	0.95	0.04	-	63,63,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.