WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Feb 3, 2024 – 03:31 PM EST

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PDB ID	:	1M2X
Title	:	Crystal Structure of the metallo-beta-lactamase BlaB of Chryseobacterium meningosepticum in complex with the inhibitor D-captopril
Authors	:	Garcia-Saez, I.; Dideberg, O.
Deposited on	:	2002-06-26
Resolution	:	1.50 Å(reported)

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 1.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.
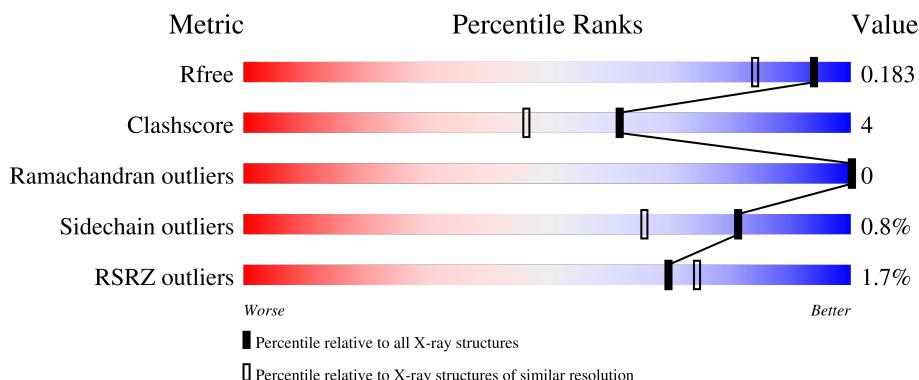
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	223	2% 88% 9% •
1	B	223	.% 86% 13% •
1	C	223	2% 87% 9% •
1	D	223	.% 87% 11% •
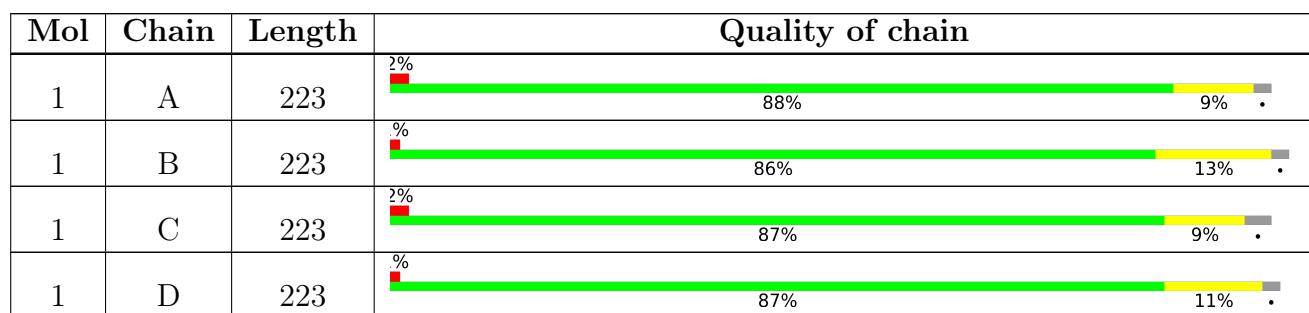
2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 8034 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 class B carbapenemase BlaB-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	8	8	0
			1821	1163	306	348	4			
1	B	219	Total	C	N	O	S	12	8	0
			1822	1163	307	348	4			
1	C	217	Total	C	N	O	S	6	4	0
			1774	1134	297	339	4			
1	D	219	Total	C	N	O	S	4	6	0
			1804	1153	302	345	4			

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Zn	0	0
			3	3		
3	B	3	Total	Zn	0	0
			3	3		
3	C	3	Total	Zn	0	0
			3	3		
3	D	3	Total	Zn	0	0
			3	3		

- Molecule 4 is 1-(3-MERCAPTO-2-METHYL-PROPIONYL)-PYRROLIDINE-2-CARBOX YLIC ACID (three-letter code: MCO) (formula: $C_9H_{15}NO_3S$).
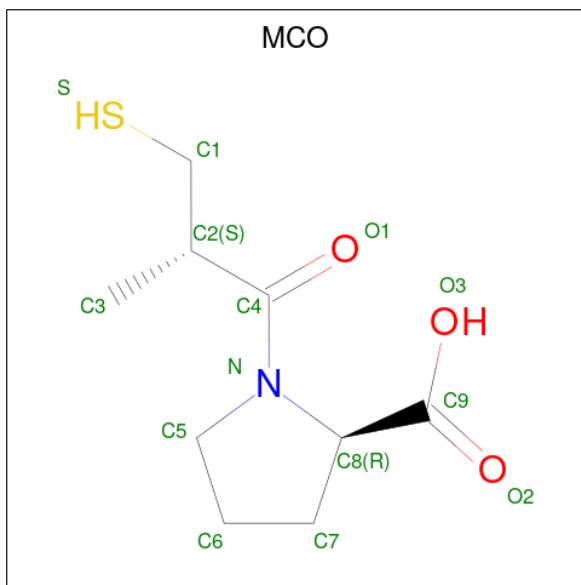
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
4	B	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
4	C	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
4	D	1	Total	C	N	O	S	0	0
			14	9	1	3	1		

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).
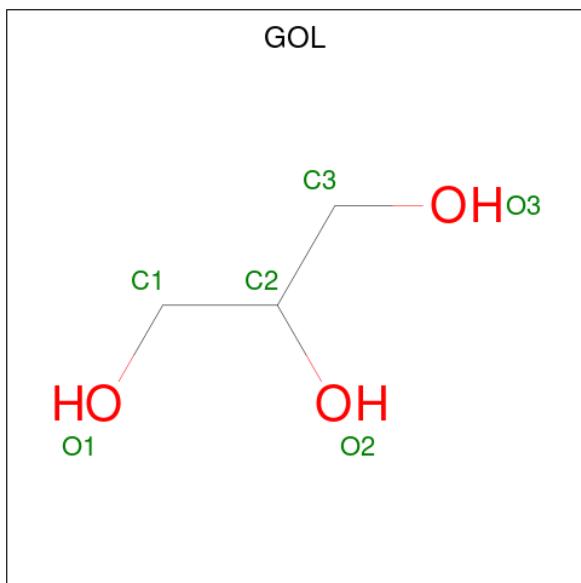
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 6	C 3	O 3	0	0
5	B	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0
5	D	1	Total 6	C 3	O 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	185	Total 185	O 185	0	0
6	B	169	Total 169	O 169	0	0
6	C	173	Total 173	O 173	0	0
6	D	192	Total 193	O 193	0	1

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: class B carbapenemase BlaB-1
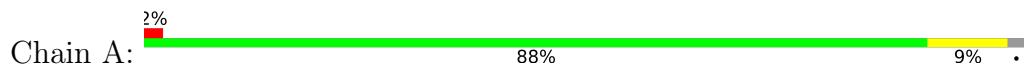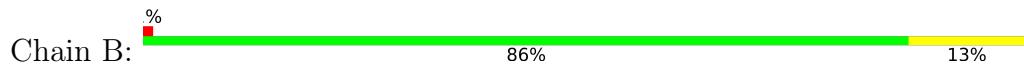
Chain A:

- Molecule 1: class B carbapenemase BlaB-1

Chain B:

- Molecule 1: class B carbapenemase BlaB-1

Chain C:

- Molecule 1: class B carbapenemase BlaB-1

Chain D:
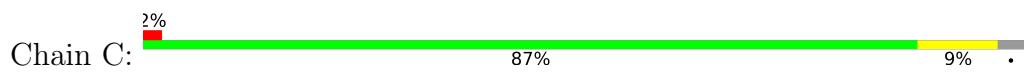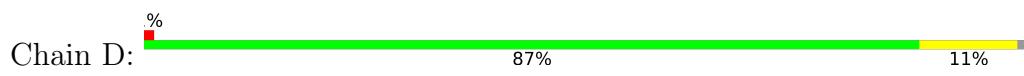
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	159.69Å　　159.69Å　　97.81Å 90.00°　　　90.00°　　　120.00°	Depositor
Resolution (Å)	10.00　–　1.50 9.98　–　1.50	Depositor EDS
% Data completeness (in resolution range)	90.0 (10.00-1.50) 90.1 (9.98-1.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	3.09 (at 1.50Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.190　,　0.208 0.185　,　0.183	Depositor DCC
R_{free} test set	12239 reflections (9.14%)	wwPDB-VP
Wilson B-factor (Å^2)	11.4	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 51.8	EDS
L-test for twinning[2]	$< \lvert L \rvert > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.019 for -1/3*h+1/3*k+4/3*l,-k,2/3*h+1/3*k+1/3*l 0.023 for -2/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+4/3*l,-1/3*h+1/3*k+1/3*l 0.014 for -h,1/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+1/3*l 0.430 for -1/3*h-2/3*k+4/3*l,-2/3*h-1/3*k-4/3*l,1/3*h-1/3*k-1/3*l 0.418 for -h,2/3*h+1/3*k+4/3*l,1/3*h+2/3*k-1/3*l 0.417 for 1/3*h+2/3*k-4/3*l,-k,-2/3*h-1/3*k-1/3*l 0.025 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8034	wwPDB-VP
Average B, all atoms (Å^2)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ 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: MCO, ZN, NA, GOL

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	0.29	0/1863	0.59	0/2515
1	B	0.29	0/1864	0.60	0/2515
1	C	0.30	0/1816	0.60	0/2452
1	D	0.29	0/1846	0.60	0/2493
All	All	0.29	0/7389	0.60	0/9975

There are no bond length outliers.

There are no bond angle outliers.

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	1821	0	1774	13	0
1	B	1822	0	1776	22	0
1	C	1774	0	1726	15	0
1	D	1804	0	1757	15	0
2	A	1	0	0	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	14	0	13	1	0
4	B	14	0	13	1	0
4	C	14	0	13	1	0
4	D	14	0	13	1	0
5	A	6	0	8	0	0
5	B	6	0	8	0	0
5	C	6	0	8	0	0
5	D	6	0	8	0	0
6	A	185	0	0	1	0
6	B	169	0	0	0	0
6	C	173	0	0	0	0
6	D	193	0	0	0	0
All	All	8034	0	7117	63	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 4.

All (63) 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:292:GLU:HA	1:B:295:GLN:HE21	1.34	0.90
1:D:219:GLY:HA3	1:D:223[B]:ILE:HD12	1.75	0.68
1:B:181:LYS:HD3	1:B:186:GLU:HG2	1.74	0.68
1:B:250:GLN:CG	1:B:283:ILE:HG21	2.28	0.62
1:B:292:GLU:O	1:B:295:GLN:HG2	2.02	0.58
1:A:184:LYS:NZ	1:A:184:LYS:HB2	2.21	0.56
1:C:49:LYS:HB2	1:C:49:LYS:NZ	2.21	0.55
1:C:181:LYS:HE2	1:C:183:GLY:O	2.07	0.55
1:B:184:LYS:HB2	1:B:184:LYS:NZ	2.22	0.55
1:C:58:TYR:O	1:C:91:LYS:NZ	2.38	0.55
1:C:184:LYS:HB2	1:C:184:LYS:NZ	2.21	0.55
1:D:181:LYS:HE2	1:D:183:GLY:O	2.07	0.54
1:C:247:HIS:CD2	1:D:250:GLN:HG2	2.43	0.54
1:C:118:HIS:HB3	4:C:813:MCO:HC12	1.90	0.53
1:A:254:SER:OG	1:B:247:HIS:HD2	1.91	0.52
1:D:184:LYS:HB2	1:D:184:LYS:NZ	2.24	0.51
1:A:49:LYS:HB2	1:A:49:LYS:NZ	2.25	0.51
1:D:118:HIS:HB3	4:D:814:MCO:HC12	1.93	0.51
1:B:77:ASP:OD1	1:B:78:LYS:HG3	2.10	0.51
1:B:118:HIS:HB3	4:B:812:MCO:HC12	1.92	0.51
1:B:250:GLN:CD	1:B:283:ILE:HG21	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:250:GLN:HG2	1:B:283:ILE:HD13	1.93	0.50
1:C:181:LYS:HD3	1:C:186:GLU:HG2	1.94	0.49
1:C:49:LYS:HB2	1:C:49:LYS:HZ3	1.74	0.49
1:A:89:GLU:HA	1:A:92:PHE:CE2	2.47	0.49
1:A:232:GLY:HA2	6:A:1033:HOH:O	2.11	0.49
1:B:250:GLN:HG3	1:B:283:ILE:HG21	1.93	0.49
1:D:77:ASP:OD1	1:D:78:LYS:HG2	2.14	0.48
1:A:55:TYR:CZ	1:A:71:ALA:HB3	2.49	0.47
1:A:118:HIS:HB3	4:A:811:MCO:HC12	1.97	0.46
1:B:55:TYR:CZ	1:B:71:ALA:HB3	2.50	0.46
1:C:89:GLU:HA	1:C:92:PHE:CE2	2.51	0.46
1:D:288:ASP:O	1:D:292:GLU:HG3	2.15	0.46
1:B:184:LYS:HB2	1:B:184:LYS:HZ2	1.80	0.46
1:C:77:ASP:OD1	1:C:78:LYS:HG2	2.16	0.46
1:B:57:THR:HG21	1:B:86:PRO:HB3	1.99	0.45
1:B:288:ASP:O	1:B:292:GLU:HG3	2.16	0.45
1:C:55:TYR:CZ	1:C:71:ALA:HB3	2.51	0.45
1:C:291:ASN:O	1:C:295:GLN:HG3	2.17	0.45
1:D:116:HIS:CE1	1:D:121:ARG:HG3	2.51	0.45
1:C:116:HIS:CE1	1:C:121:ARG:HG3	2.51	0.45
1:A:116:HIS:CE1	1:A:121:ARG:HG3	2.52	0.45
1:D:89:GLU:HA	1:D:92:PHE:CE2	2.52	0.45
1:D:181:LYS:HD3	1:D:186:GLU:HG2	1.99	0.44
1:B:116:HIS:CE1	1:B:121:ARG:HG3	2.52	0.44
1:C:184:LYS:HB2	1:C:184:LYS:HZ2	1.83	0.43
1:D:55:TYR:CZ	1:D:71:ALA:HB3	2.54	0.43
1:A:181:LYS:HE2	1:A:183:GLY:O	2.18	0.43
1:B:181:LYS:HE2	1:B:183:GLY:O	2.17	0.43
1:B:284:GLN:HA	1:B:287:LEU:HD12	1.99	0.43
1:D:138:SER:O	1:D:173:THR:HA	2.19	0.43
1:A:291:ASN:O	1:A:295:GLN:HG3	2.19	0.43
1:B:138:SER:O	1:B:173:THR:HA	2.19	0.42
1:B:225[B]:SER:OG	1:B:227:ASP:OD1	2.37	0.42
1:A:138:SER:O	1:A:173:THR:HA	2.19	0.42
1:C:138:SER:O	1:C:173:THR:HA	2.19	0.42
1:D:227:ASP:OD2	1:D:265:ASP:HB3	2.20	0.42
1:A:219:GLY:HA3	1:A:223[B]:ILE:HD12	2.00	0.42
1:B:184:LYS:HG2	1:B:184:LYS:O	2.19	0.42
1:B:89:GLU:HA	1:B:92:PHE:CE2	2.55	0.41
1:A:288:ASP:O	1:A:292:GLU:HG3	2.21	0.40
1:D:57:THR:HG21	1:D:86:PRO:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:116:HIS:ND1	1:D:121:ARG:HG3	2.36	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	225/223 (101%)	214 (95%)	11 (5%)	0	100	100
1	B	225/223 (101%)	215 (96%)	10 (4%)	0	100	100
1	C	219/223 (98%)	209 (95%)	10 (5%)	0	100	100
1	D	223/223 (100%)	213 (96%)	10 (4%)	0	100	100
All	All	892/892 (100%)	851 (95%)	41 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	197/192 (103%)	195 (99%)	2 (1%)	76	57
1	B	197/192 (103%)	196 (100%)	1 (0%)	88	78
1	C	191/192 (100%)	189 (99%)	2 (1%)	76	57
1	D	195/192 (102%)	194 (100%)	1 (0%)	88	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	780/768 (102%)	774 (99%)	6 (1%)	81 66

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	LYS
1	A	200	ASN
1	B	200	ASN
1	C	49	LYS
1	C	200	ASN
1	D	200	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	188	GLN
1	B	176	ASN
1	B	247	HIS
1	B	295	GLN
1	C	176	ASN
1	C	188	GLN
1	D	176	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 21 ligands modelled in this entry, 13 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
4	MCO	C	813	3	14,14,14	0.93	0	18,19,19	0.88	0
5	GOL	A	801	-	5,5,5	0.46	0	5,5,5	1.63	1 (20%)
5	GOL	C	803	-	5,5,5	0.50	0	5,5,5	1.63	1 (20%)
4	MCO	A	811	3	14,14,14	0.87	0	18,19,19	0.89	0
5	GOL	B	802	-	5,5,5	0.46	0	5,5,5	1.65	1 (20%)
4	MCO	D	814	3	14,14,14	0.86	0	18,19,19	0.91	0
4	MCO	B	812	3	14,14,14	0.88	0	18,19,19	0.85	0
5	GOL	D	804	-	5,5,5	0.48	0	5,5,5	1.66	1 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MCO	C	813	3	-	2/14/24/24	0/1/1/1
5	GOL	A	801	-	-	0/4/4/4	-
5	GOL	C	803	-	-	1/4/4/4	-
4	MCO	A	811	3	-	2/14/24/24	0/1/1/1
5	GOL	B	802	-	-	1/4/4/4	-
4	MCO	D	814	3	-	2/14/24/24	0/1/1/1
4	MCO	B	812	3	-	2/14/24/24	0/1/1/1
5	GOL	D	804	-	-	1/4/4/4	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	801	GOL	O1-C1-C2	2.97	124.44	110.20
5	D	804	GOL	O1-C1-C2	2.96	124.37	110.20
5	B	802	GOL	O1-C1-C2	2.95	124.37	110.20
5	C	803	GOL	O1-C1-C2	2.88	124.02	110.20

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	804	GOL	C1-C2-C3-O3
5	B	802	GOL	O1-C1-C2-C3
4	A	811	MCO	C7-C8-C9-O2
4	A	811	MCO	C7-C8-C9-O3
4	B	812	MCO	C7-C8-C9-O2
4	B	812	MCO	C7-C8-C9-O3
4	C	813	MCO	C7-C8-C9-O2
4	C	813	MCO	C7-C8-C9-O3
4	D	814	MCO	C7-C8-C9-O2
4	D	814	MCO	C7-C8-C9-O3
5	C	803	GOL	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	813	MCO	1	0
4	A	811	MCO	1	0
4	D	814	MCO	1	0
4	B	812	MCO	1	0

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	219/223 (98%)	-0.07	5 (2%)	60	65	7, 12, 23, 35	25 (11%)
1	B	219/223 (98%)	-0.09	3 (1%)	75	79	7, 12, 24, 36	25 (11%)
1	C	217/223 (97%)	-0.08	5 (2%)	60	65	7, 12, 22, 31	23 (10%)
1	D	219/223 (98%)	-0.08	2 (0%)	84	87	7, 12, 24, 36	26 (11%)
All	All	874/892 (97%)	-0.08	15 (1%)	70	75	7, 12, 23, 36	99 (11%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	48	LEU	3.2
1	A	296	LYS	2.6
1	C	41	ASP	2.5
1	B	297	GLN	2.5
1	C	48	LEU	2.4
1	C	88	GLY	2.4
1	B	41	ASP	2.4
1	D	226	ALA	2.3
1	A	281	ARG	2.2
1	C	90	ASP	2.2
1	A	229	LYS	2.2
1	D	88	GLY	2.1
1	A	41	ASP	2.1
1	B	184	LYS	2.1
1	C	227	ASP	2.1

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 ⓘ

There are no monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
5	GOL	C	803	6/6	0.69	0.20	37,39,40,40	0
5	GOL	D	804	6/6	0.70	0.16	36,38,39,39	0
5	GOL	A	801	6/6	0.79	0.14	30,35,35,37	0
5	GOL	B	802	6/6	0.86	0.11	31,35,36,37	0
2	NA	A	302	1/1	0.94	0.10	28,28,28,28	0
4	MCO	C	813	14/14	0.95	0.12	11,16,17,18	2
4	MCO	A	811	14/14	0.96	0.13	11,16,19,19	2
4	MCO	B	812	14/14	0.96	0.11	11,15,17,18	3
3	ZN	A	900	1/1	0.96	0.06	21,21,21,21	1
4	MCO	D	814	14/14	0.96	0.12	10,16,18,19	2
3	ZN	C	900	1/1	0.97	0.07	20,20,20,20	1
3	ZN	B	900	1/1	0.98	0.06	21,21,21,21	1
3	ZN	D	900	1/1	0.98	0.05	22,22,22,22	1
3	ZN	C	902	1/1	0.99	0.04	8,8,8,8	1
3	ZN	A	902	1/1	0.99	0.03	9,9,9,9	1
3	ZN	D	902	1/1	0.99	0.06	9,9,9,9	1
3	ZN	C	901	1/1	0.99	0.04	8,8,8,8	0
3	ZN	A	901	1/1	1.00	0.02	8,8,8,8	0
3	ZN	D	901	1/1	1.00	0.03	8,8,8,8	0
3	ZN	B	901	1/1	1.00	0.04	8,8,8,8	0
3	ZN	B	902	1/1	1.00	0.05	9,9,9,9	1

6.5 Other polymers ⓘ

There are no such residues in this entry.