



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 08:39 am BST

PDB ID : 4X4W
Title : Crystal structure of the full-length human mitochondrial CCA-adding enzyme
Authors : Kuhn, C.-D.; Joshua-Tor, L.
Deposited on : 2014-12-03
Resolution : 1.90 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

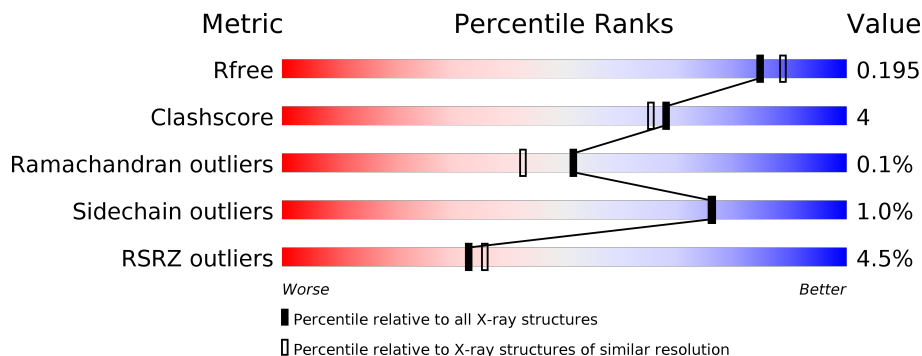
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 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 $\leq 5\%$. 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	416	<p>4% 90% 5% . .</p>
1	B	416	<p>5% 86% 9% 5%</p>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13908 atoms, of which 6560 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 CCA tRNA nucleotidyltransferase 1, mitochondrial.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	398	6454	2051	3244	544	605	10	0	1	0
1	B	397	6468	2056	3258	542	602	10	0	2	0

There are 18 discrepancies between the modelled and reference sequences:

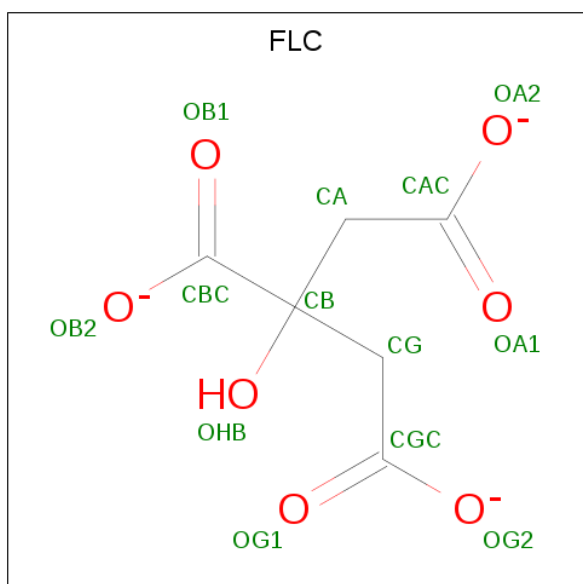
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q96Q11
A	409	LEU	-	expression tag	UNP Q96Q11
A	410	GLU	-	expression tag	UNP Q96Q11
A	411	HIS	-	expression tag	UNP Q96Q11
A	412	HIS	-	expression tag	UNP Q96Q11
A	413	HIS	-	expression tag	UNP Q96Q11
A	414	HIS	-	expression tag	UNP Q96Q11
A	415	HIS	-	expression tag	UNP Q96Q11
A	416	HIS	-	expression tag	UNP Q96Q11
B	1	MET	-	initiating methionine	UNP Q96Q11
B	409	LEU	-	expression tag	UNP Q96Q11
B	410	GLU	-	expression tag	UNP Q96Q11
B	411	HIS	-	expression tag	UNP Q96Q11
B	412	HIS	-	expression tag	UNP Q96Q11
B	413	HIS	-	expression tag	UNP Q96Q11
B	414	HIS	-	expression tag	UNP Q96Q11
B	415	HIS	-	expression tag	UNP Q96Q11
B	416	HIS	-	expression tag	UNP Q96Q11

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



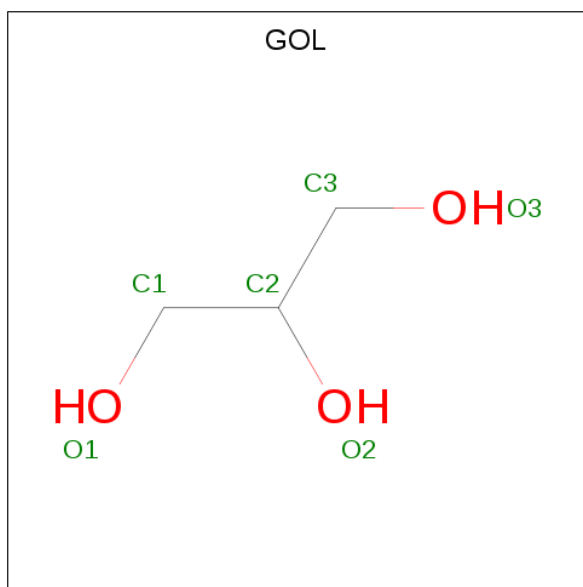
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			18	6	5	7		
3	B	1	Total	C	H	O	0	0
			18	6	5	7		

- 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	A	1	Total	C	H	O	0	0
			14	3	8	3		
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	B	1	Total	C	H	O	0	0
			14	3	8	3		
4	B	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	B	3	Total	Cl	0	0
			3	3		
5	A	5	Total	Cl	0	0
			5	5		

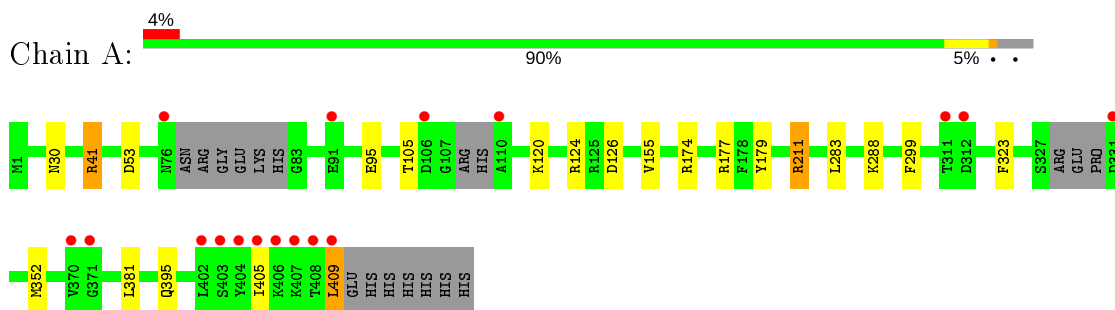
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	424	Total 424	O 424	0	0
6	B	409	Total 409	O 409	0	0

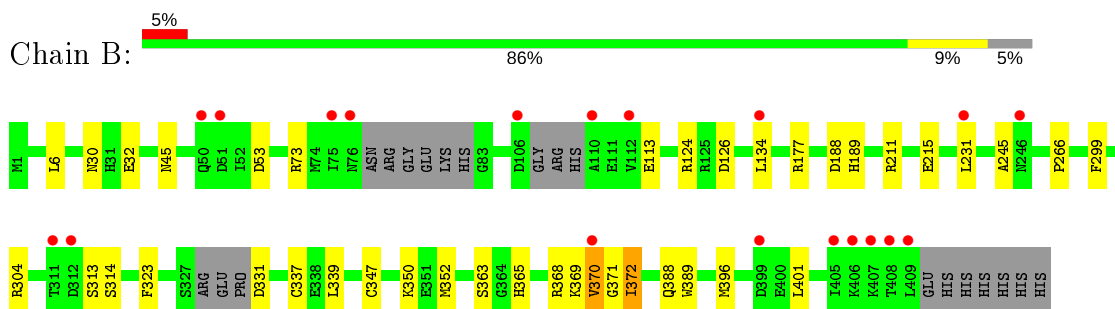
3 Residue-property plots [i](#)

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: CCA tRNA nucleotidyltransferase 1, mitochondrial



- Molecule 1: CCA tRNA nucleotidyltransferase 1, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	40.97Å 142.36Å 100.59Å 90.00° 94.64° 90.00°	Depositor
Resolution (Å)	29.08 – 1.90 29.08 – 1.85	Depositor EDS
% Data completeness (in resolution range)	98.9 (29.08-1.90) 98.9 (29.08-1.85)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 1.85Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.154 , 0.196 0.155 , 0.195	Depositor DCC
R_{free} test set	4829 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.198	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 53.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13908	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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: GOL, FLC, SO4, 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	0.81	0/3268	0.79	4/4399 (0.1%)
1	B	0.84	4/3275 (0.1%)	0.81	3/4411 (0.1%)
All	All	0.83	4/6543 (0.1%)	0.80	7/8810 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	32	GLU	CG-CD	5.42	1.60	1.51
1	B	215	GLU	CD-OE2	-5.40	1.19	1.25
1	B	126	ASP	CB-CG	5.21	1.62	1.51
1	B	337	CYS	CB-SG	5.03	1.90	1.82

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	126	ASP	CB-CG-OD1	9.37	126.73	118.30
1	B	352	MET	CG-SD-CE	-8.84	86.05	100.20
1	B	126	ASP	CB-CG-OD1	8.70	126.13	118.30
1	B	188	ASP	CB-CG-OD1	6.26	123.94	118.30
1	A	41	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	A	211	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	352	MET	CG-SD-CE	-5.06	92.10	100.20

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	3210	3244	3235	14	0
1	B	3210	3258	3249	29	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
3	A	13	5	5	3	0
3	B	13	5	5	1	0
4	A	18	24	24	1	0
4	B	18	24	24	3	0
5	A	5	0	0	2	0
5	B	3	0	0	2	0
6	A	424	0	0	8	4
6	B	409	0	0	15	4
All	All	7348	6560	6542	49	4

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 (49) 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)
5:A:505:CL:CL	6:A:950:HOH:O	2.04	1.11
5:B:509:CL:CL	6:B:982:HOH:O	2.04	1.10
5:B:505:CL:CL	6:B:977:HOH:O	2.23	0.94
5:A:510:CL:CL	6:A:1004:HOH:O	2.25	0.89
1:B:177:ARG:NH2	3:B:501:FLC:OB1	2.22	0.72
4:B:506:GOL:O3	4:B:506:GOL:O1	2.07	0.71
1:B:53:ASP:OD1	6:B:928:HOH:O	2.09	0.70
1:B:45:ASN:ND2	6:B:938:HOH:O	2.24	0.70
1:B:314:SER:O	6:B:601:HOH:O	2.09	0.69
1:A:124:ARG:HH12	4:A:502:GOL:H2	1.61	0.65
1:A:95:GLU:OE2	6:A:874:HOH:O	2.13	0.64
1:B:388:GLN:O	1:B:396:MET:HE1	1.96	0.64
1:A:30:ASN:HB3	6:A:685:HOH:O	1.98	0.62
1:B:347:CYS:N	6:B:604:HOH:O	2.24	0.62
1:A:174:ARG:HH12	3:A:501:FLC:HA2	1.63	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:502:GOL:O3	6:B:960:HOH:O	2.17	0.56
1:B:211:ARG:NH1	6:B:982:HOH:O	2.26	0.55
1:B:368:ARG:O	1:B:371:GLY:N	2.40	0.54
1:B:113:GLU:OE1	6:B:602:HOH:O	2.18	0.53
1:B:371:GLY:HA2	1:B:372:ILE:HG12	1.90	0.52
1:B:350:LYS:NZ	6:B:611:HOH:O	2.45	0.50
1:A:211:ARG:NH1	6:A:950:HOH:O	2.40	0.49
1:B:313:SER:O	6:B:603:HOH:O	2.19	0.49
1:B:369:LYS:O	1:B:370:VAL:HG12	2.13	0.49
1:B:389:TRP:HA	1:B:396:MET:HE2	1.94	0.48
1:B:30:ASN:HB3	6:B:684:HOH:O	2.12	0.47
1:B:189:HIS:CE1	1:B:231[B]:LEU:HD11	2.49	0.47
1:B:396:MET:HE3	1:B:401:LEU:HD21	1.96	0.46
1:B:73:ARG:NH2	6:B:613:HOH:O	2.46	0.45
1:A:409:LEU:O	6:A:1020:HOH:O	2.21	0.45
1:B:299:PHE:HE1	1:B:323:PHE:CZ	2.35	0.45
1:B:363:SER:HG	1:B:365:HIS:CD2	2.35	0.45
1:A:395:GLN:O	1:A:395:GLN:NE2	2.50	0.44
1:A:177:ARG:NH2	3:A:501:FLC:OB2	2.42	0.44
1:A:120:LYS:NZ	6:A:608:HOH:O	2.50	0.44
1:B:396:MET:HE2	1:B:396:MET:HB2	1.85	0.44
1:A:41:ARG:HH12	3:A:501:FLC:HG1	1.83	0.43
1:B:245:ALA:HA	6:B:859:HOH:O	2.18	0.43
1:B:124:ARG:HH12	4:B:502:GOL:C2	2.31	0.43
1:B:6:LEU:HD23	1:B:134[A]:LEU:HD21	2.00	0.43
1:A:381:LEU:HD22	1:A:405:ILE:HD11	2.00	0.43
1:B:370:VAL:HG13	1:B:370:VAL:O	2.19	0.43
1:B:304:ARG:HA	1:B:339:LEU:HD11	2.00	0.43
1:A:299:PHE:HE1	1:A:323:PHE:CZ	2.37	0.42
1:B:368:ARG:O	1:B:371:GLY:HA3	2.19	0.42
1:A:53:ASP:OD2	6:A:1023:HOH:O	2.21	0.42
1:B:389:TRP:HA	1:B:396:MET:CE	2.50	0.42
1:A:155:VAL:HG21	1:A:179:TYR:HA	2.02	0.41
1:B:245:ALA:HA	6:B:878:HOH:O	2.19	0.41

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:627:HOH:O	6:B:639:HOH:O 2_746	2.02	0.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:688:HOH:O	6:B:678:HOH:O[2_746]	2.03	0.17
6:A:704:HOH:O	6:B:715:HOH:O[2_646]	2.18	0.02
6:A:675:HOH:O	6:B:687:HOH:O[2_746]	2.19	0.01

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	390/416 (94%)	385 (99%)	5 (1%)	0	100	100
1	B	391/416 (94%)	385 (98%)	5 (1%)	1 (0%)	41	31
All	All	781/832 (94%)	770 (99%)	10 (1%)	1 (0%)	51	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	372	ILE

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	352/368 (96%)	348 (99%)	4 (1%)	73	73
1	B	353/368 (96%)	350 (99%)	3 (1%)	81	82
All	All	705/736 (96%)	698 (99%)	7 (1%)	76	76

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

Mol	Chain	Res	Type
1	A	105	THR
1	A	283	LEU
1	A	288	LYS
1	A	409	LEU
1	B	266	PRO
1	B	331	ASP
1	B	370	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	395	GLN
1	B	365	HIS

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 21 ligands modelled in this entry, 8 are monoatomic - leaving 13 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	GOL	B	507	-	5,5,5	0.36	0	5,5,5	0.25	0
2	SO4	B	500	-	4,4,4	0.30	0	6,6,6	0.78	0
4	GOL	B	502	-	5,5,5	0.55	0	5,5,5	1.02	0
4	GOL	A	507	-	5,5,5	0.37	0	5,5,5	0.67	0
4	GOL	B	506	-	5,5,5	0.39	0	5,5,5	0.75	0
2	SO4	A	503	-	4,4,4	0.15	0	6,6,6	0.09	0
2	SO4	B	503	-	4,4,4	0.11	0	6,6,6	0.44	0
2	SO4	B	504	-	4,4,4	0.25	0	6,6,6	0.36	0
4	GOL	A	502	-	5,5,5	0.58	0	5,5,5	0.84	0
2	SO4	A	500	-	4,4,4	0.34	0	6,6,6	0.59	0
4	GOL	A	506	-	5,5,5	0.52	0	5,5,5	1.18	0
3	FLC	A	501	-	3,12,12	2.43	1 (33%)	3,17,17	1.80	1 (33%)
3	FLC	B	501	-	3,12,12	2.41	3 (100%)	3,17,17	2.81	1 (33%)

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	GOL	B	507	-	-	2/4/4/4	-
4	GOL	A	507	-	-	0/4/4/4	-
4	GOL	B	502	-	-	2/4/4/4	-
4	GOL	B	506	-	-	2/4/4/4	-
4	GOL	A	502	-	-	2/4/4/4	-
4	GOL	A	506	-	-	0/4/4/4	-
3	FLC	A	501	-	-	3/6/16/16	-
3	FLC	B	501	-	-	1/6/16/16	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	FLC	CA-CB	-3.52	1.49	1.54
3	B	501	FLC	OHB-CB	-2.78	1.38	1.43
3	B	501	FLC	CA-CB	-2.33	1.51	1.54
3	B	501	FLC	CG-CB	-2.05	1.52	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	501	FLC	CB-CG-CGC	-4.56	107.69	114.98
3	A	501	FLC	CB-CA-CAC	2.99	119.77	114.98

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	507	GOL	C1-C2-C3-O3
4	B	502	GOL	O1-C1-C2-C3
4	B	506	GOL	O1-C1-C2-O2
4	A	502	GOL	O1-C1-C2-C3
3	A	501	FLC	CA-CB-CG-CGC
3	A	501	FLC	CBC-CB-CG-CGC
3	A	501	FLC	OHB-CB-CG-CGC
4	B	507	GOL	O2-C2-C3-O3
4	B	506	GOL	O1-C1-C2-C3
4	B	502	GOL	O1-C1-C2-O2
4	A	502	GOL	O1-C1-C2-O2
3	B	501	FLC	CA-CB-CG-CGC

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	502	GOL	2	0
4	B	506	GOL	1	0
4	A	502	GOL	1	0
3	A	501	FLC	3	0
3	B	501	FLC	1	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 [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	398/416 (95%)	0.04	17 (4%) 35 38	16, 28, 56, 97	0
1	B	397/416 (95%)	0.06	19 (4%) 30 33	16, 28, 55, 85	0
All	All	795/832 (95%)	0.05	36 (4%) 33 36	16, 28, 55, 97	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	312	ASP	7.8
1	A	409	LEU	7.5
1	B	370	VAL	7.0
1	B	409	LEU	6.8
1	B	311	THR	5.9
1	B	312	ASP	5.7
1	A	407	LYS	5.1
1	B	407	LYS	4.9
1	A	311	THR	4.6
1	A	405	ILE	4.6
1	A	406	LYS	4.5
1	B	408	THR	4.5
1	A	371	GLY	4.1
1	A	110	ALA	4.1
1	B	106	ASP	4.1
1	A	408	THR	3.8
1	A	76	ASN	3.7
1	B	110	ALA	3.4
1	A	370	VAL	3.4
1	B	406	LYS	3.1
1	B	75	ILE	3.1
1	A	91	GLU	3.0
1	B	50	GLN	2.9
1	B	405	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	403	SER	2.8
1	A	404	TYR	2.7
1	A	402	LEU	2.7
1	B	76	ASN	2.6
1	B	134[A]	LEU	2.5
1	B	231[A]	LEU	2.5
1	B	112	VAL	2.5
1	B	246	ASN	2.3
1	A	106	ASP	2.2
1	A	331	ASP	2.1
1	B	51	ASP	2.1
1	B	399	ASP	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. 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
3	FLC	B	501	13/13	0.80	0.24	47,65,87,87	0
4	GOL	A	502	6/6	0.85	0.20	42,58,73,77	0
3	FLC	A	501	13/13	0.86	0.21	38,50,65,70	0
4	GOL	B	507	6/6	0.86	0.21	42,59,66,70	0
4	GOL	B	502	6/6	0.88	0.17	47,57,71,71	0
5	CL	A	509	1/1	0.88	0.06	70,70,70,70	0
5	CL	A	508	1/1	0.89	0.22	57,57,57,57	0
4	GOL	B	506	6/6	0.91	0.12	56,67,71,79	0
5	CL	A	504	1/1	0.93	0.05	71,71,71,71	0
5	CL	A	510	1/1	0.93	0.18	61,61,61,61	0
4	GOL	A	507	6/6	0.94	0.12	37,45,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	CL	B	505	1/1	0.94	0.20	61,61,61,61	0
2	SO4	B	503	5/5	0.94	0.16	69,78,81,82	0
4	GOL	A	506	6/6	0.95	0.14	36,43,51,55	0
2	SO4	A	503	5/5	0.95	0.13	89,89,90,91	0
5	CL	B	508	1/1	0.96	0.16	55,55,55,55	0
2	SO4	B	504	5/5	0.97	0.15	49,56,60,63	0
5	CL	B	509	1/1	0.97	0.08	47,47,47,47	0
5	CL	A	505	1/1	0.98	0.10	48,48,48,48	0
2	SO4	A	500	5/5	0.99	0.09	24,30,32,34	0
2	SO4	B	500	5/5	0.99	0.09	25,29,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.