



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 3, 2024 – 05:28 am GMT

PDB ID : 6G60
Title : Choline sulfatase from Ensifer (Sinorhizobium) meliloti cocrystallized with choline
Authors : Martinez-Rodriguez, S.; Camara-Artigas, A.
Deposited on : 2018-03-30
Resolution : 1.84 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

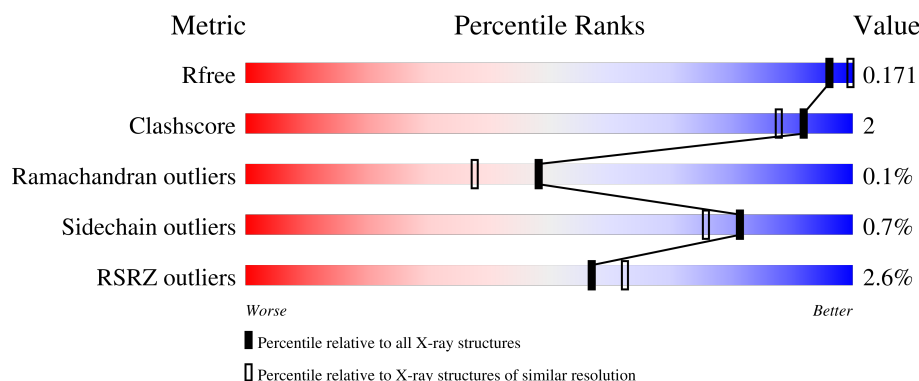
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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}	164625	1150 (1.84-1.84)
Clashscore	180529	1248 (1.84-1.84)
Ramachandran outliers	177936	1240 (1.84-1.84)
Sidechain outliers	177891	1240 (1.84-1.84)
RSRZ outliers	164620	1149 (1.84-1.84)

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 $\leq 5\%$. 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	508	<div> <div>%</div> <div> <div></div> <div>95%</div> <div>5%</div> </div> </div>
1	B	508	<div> <div>4%</div> <div> <div></div> <div>97%</div> <div>.</div> </div> </div>
1	C	508	<div> <div>%</div> <div> <div></div> <div>96%</div> <div>..</div> </div> </div>
1	D	508	<div> <div>5%</div> <div> <div></div> <div>93%</div> <div>6% .</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17304 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.

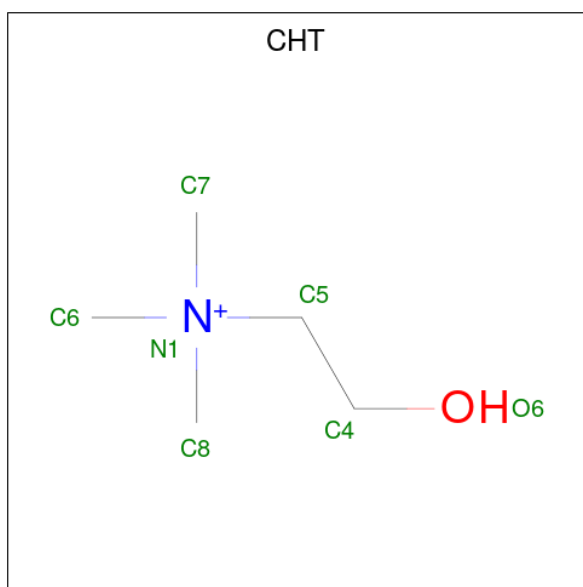
- Molecule 1 is a protein called Choline-sulfatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	508	Total	C	N	O	S	0	1	0
			4068	2571	712	764	21			
1	B	506	Total	C	N	O	S	0	1	0
			4009	2542	709	739	19			
1	C	505	Total	C	N	O	S	0	0	0
			4001	2537	700	744	20			
1	D	505	Total	C	N	O	S	0	0	0
			3941	2499	698	725	19			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	54	DDZ	CYS	modified residue	UNP O69787
A	105	LEU	PHE	variant	UNP O69787
B	54	DDZ	CYS	modified residue	UNP O69787
B	105	LEU	PHE	variant	UNP O69787
C	54	DDZ	CYS	modified residue	UNP O69787
C	105	LEU	PHE	variant	UNP O69787
D	54	DDZ	CYS	modified residue	UNP O69787
D	105	LEU	PHE	variant	UNP O69787

- Molecule 2 is CHOLINE ION (three-letter code: CHT) (formula: C₅H₁₄NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			7	5	1	1		
2	B	1	Total	C	N	O	0	0
			7	5	1	1		
2	C	1	Total	C	N	O	0	0
			7	5	1	1		
2	D	1	Total	C	N	O	0	0
			7	5	1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

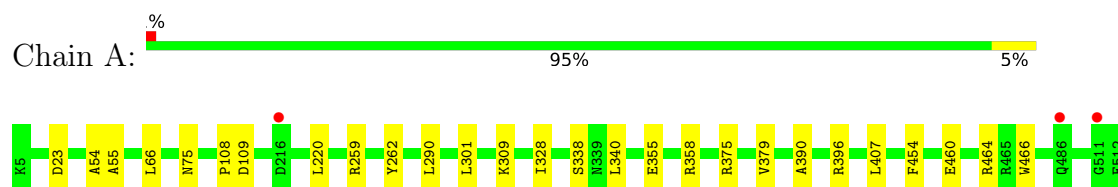
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	343	Total	O	0	0
			343	343		
5	B	375	Total	O	0	0
			375	375		
5	C	296	Total	O	0	0
			296	296		
5	D	204	Total	O	0	0
			204	204		

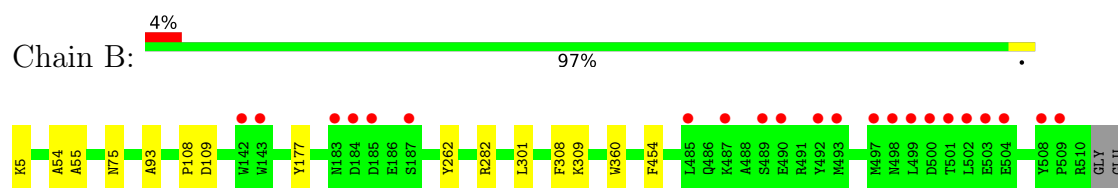
3 Residue-property plots [i](#)

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.

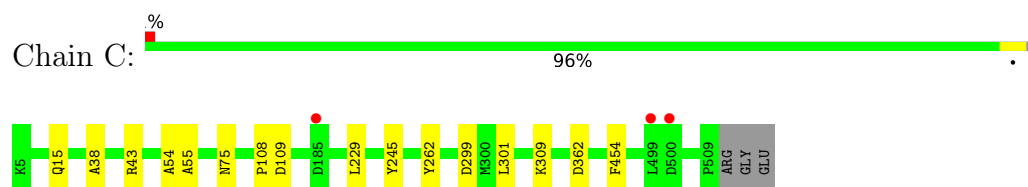
• Molecule 1: Choline-sulfatase



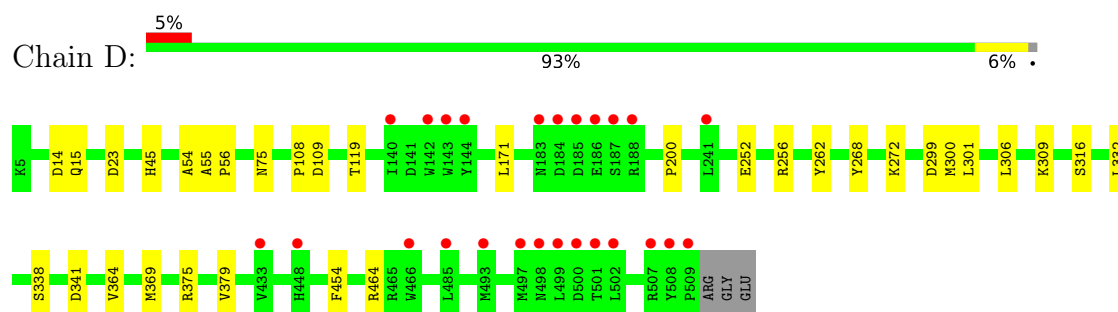
• Molecule 1: Choline-sulfatase



• Molecule 1: Choline-sulfatase



• Molecule 1: Choline-sulfatase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	128.54Å 206.90Å 116.60Å 90.00° 110.17° 90.00°	Depositor
Resolution (Å)	75.18 – 1.84 75.18 – 1.84	Depositor EDS
% Data completeness (in resolution range)	84.1 (75.18-1.84) 81.5 (75.18-1.84)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 1.84Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.169 , 0.199 0.170 , 0.171	Depositor DCC
R_{free} test set	12240 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	17304	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% 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: SO4, CHT, MG, DDZ

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	0.49	0/4174	0.64	0/5686
1	B	0.55	0/4115	0.66	0/5610
1	C	0.46	0/4107	0.60	0/5602
1	D	0.43	0/4046	0.58	0/5523
All	All	0.49	0/16442	0.62	0/22421

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	4068	0	3859	15	0
1	B	4009	0	3785	8	0
1	C	4001	0	3781	10	0
1	D	3941	0	3688	22	0
2	A	7	0	14	0	0
2	B	7	0	14	0	0
2	C	7	0	14	0	0
2	D	7	0	14	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	10	0	0	0	0
4	B	20	0	0	0	0
4	C	5	0	0	0	0
5	A	343	0	0	0	0
5	B	375	0	0	0	0
5	C	296	0	0	1	0
5	D	204	0	0	0	0
All	All	17304	0	15169	48	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 2.

All (48) 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:D:300:MET:HA	1:D:300:MET:CE	1.99	0.92
1:D:300:MET:HA	1:D:300:MET:HE3	1.70	0.73
1:A:290:LEU:CD2	1:A:328:ILE:HD11	2.24	0.67
1:D:300:MET:HA	1:D:300:MET:HE2	1.81	0.62
1:B:109:ASP:HB2	1:D:108:PRO:HG3	1.85	0.58
1:B:108:PRO:HG3	1:D:109:ASP:HB2	1.87	0.57
1:D:55:ALA:HB3	1:D:75:ASN:HA	1.87	0.57
1:A:338:SER:HB2	1:A:379:VAL:HG13	1.89	0.54
1:A:109:ASP:HB2	1:C:108:PRO:HG3	1.90	0.52
1:D:252:GLU:O	1:D:256:ARG:HG3	2.09	0.51
1:A:108:PRO:HG3	1:C:109:ASP:HB2	1.92	0.51
1:A:390:ALA:HB3	1:A:407:LEU:HD23	1.93	0.51
1:D:338:SER:HB2	1:D:379:VAL:HG13	1.92	0.51
1:D:300:MET:HG3	1:D:306:LEU:HB2	1.93	0.50
1:A:460:GLU:OE1	1:A:464:ARG:NE	2.42	0.50
1:D:14:ASP:O	1:D:200:PRO:HD2	2.11	0.50
1:D:300:MET:HE3	1:D:300:MET:CA	2.41	0.50
1:D:268:TYR:CZ	1:D:272:LYS:HE2	2.47	0.50
1:D:262:TYR:CE2	1:D:301:LEU:HD11	2.46	0.49
1:A:66:LEU:CD2	1:A:340:LEU:HD11	2.43	0.48
1:D:45:HIS:HB2	1:D:332:LEU:HD11	1.94	0.48
1:B:5:LYS:NZ	1:B:93:ALA:O	2.41	0.48
1:C:362:ASP:OD2	5:C:701:HOH:O	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:ALA:HB3	1:C:75:ASN:HA	1.95	0.48
1:B:360:TRP:CZ3	1:D:464:ARG:HG2	2.49	0.47
1:C:38:ALA:O	1:C:43:ARG:HD3	2.16	0.46
1:D:55:ALA:HB3	1:D:56:PRO:HD3	1.99	0.45
1:A:66:LEU:HD21	1:A:340:LEU:HD11	1.98	0.45
1:C:229:LEU:HD22	1:C:245:TYR:OH	2.18	0.44
1:D:15:GLN:HG2	1:D:299:ASP:HB2	2.00	0.44
1:A:262:TYR:CE1	1:A:301:LEU:HD11	2.53	0.43
1:A:466:TRP:CE3	1:A:466:TRP:HA	2.53	0.43
1:B:177:TYR:OH	1:B:282:ARG:NH2	2.44	0.43
1:C:15:GLN:HG2	1:C:299:ASP:HB2	2.01	0.43
1:D:119:THR:HG22	1:D:171:LEU:HD12	2.00	0.43
1:B:108:PRO:HG2	1:D:108:PRO:HG2	2.01	0.42
1:A:355:GLU:OE2	1:A:358:ARG:NE	2.41	0.42
1:B:262:TYR:CE1	1:B:301:LEU:HD11	2.55	0.42
1:C:262:TYR:CE1	1:C:301:LEU:HD11	2.55	0.42
1:A:108:PRO:HG2	1:C:108:PRO:HG2	2.03	0.41
1:B:55:ALA:HB3	1:B:75:ASN:HA	2.03	0.41
1:A:220:LEU:O	1:A:259:ARG:HD3	2.21	0.41
1:D:300:MET:HE1	1:D:316:SER:H	1.85	0.41
1:A:379:VAL:HB	1:A:396:ARG:HB3	2.03	0.41
1:D:341:ASP:HB3	1:D:364:VAL:O	2.21	0.41
1:A:55:ALA:HB3	1:A:75:ASN:HA	2.02	0.40
1:D:300:MET:HE1	1:D:316:SER:N	2.36	0.40
1:C:262:TYR:CD2	1:C:301:LEU:HD21	2.57	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	506/508 (100%)	494 (98%)	11 (2%)	1 (0%)	44 33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	504/508 (99%)	488 (97%)	15 (3%)	1 (0%)	44	33
1	C	502/508 (99%)	488 (97%)	14 (3%)	0	100	100
1	D	502/508 (99%)	489 (97%)	12 (2%)	1 (0%)	44	33
All	All	2014/2032 (99%)	1959 (97%)	52 (3%)	3 (0%)	48	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	ASP
1	D	23	ASP
1	B	308	PHE

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	424/432 (98%)	421 (99%)	3 (1%)	81	76
1	B	407/432 (94%)	405 (100%)	2 (0%)	86	83
1	C	411/432 (95%)	409 (100%)	2 (0%)	86	83
1	D	394/432 (91%)	390 (99%)	4 (1%)	73	64
All	All	1636/1728 (95%)	1625 (99%)	11 (1%)	81	76

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	309	LYS
1	A	375	ARG
1	A	454	PHE
1	B	309	LYS
1	B	454	PHE
1	C	309	LYS
1	C	454	PHE
1	D	309	LYS

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Mol	Chain	Res	Type
1	D	369	MET
1	D	375	ARG
1	D	454	PHE

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

Mol	Chain	Res	Type
1	A	265	ASN
1	D	297	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z > 2$
1	DDZ	D	54	3,1	4,6,7	0.91	0	3,7,9	2.13	1 (33%)
1	DDZ	B	54	3,1	4,6,7	1.02	0	3,7,9	3.65	1 (33%)
1	DDZ	A	54	3,1	4,6,7	1.25	1 (25%)	3,7,9	1.78	1 (33%)
1	DDZ	C	54	3,1	4,6,7	0.85	0	3,7,9	1.87	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
1	DDZ	D	54	3,1	-	0/2/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	DDZ	B	54	3,1	-	0/2/6/8	-
1	DDZ	A	54	3,1	-	0/2/6/8	-
1	DDZ	C	54	3,1	-	0/2/6/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	54	DDZ	OG2-CB	2.22	1.45	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	54	DDZ	OG2-CB-OG1	-6.21	100.34	111.27
1	D	54	DDZ	OG2-CB-OG1	-3.67	104.81	111.27
1	C	54	DDZ	OG2-CB-OG1	-3.09	105.83	111.27
1	A	54	DDZ	OG2-CB-OG1	-2.98	106.03	111.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 4 are monoatomic - leaving 11 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	CHT	D	1000	-	6,6,6	1.04	0	8,8,8	0.49	0
4	SO4	B	603	-	4,4,4	0.16	0	6,6,6	0.57	0
4	SO4	B	606	-	4,4,4	0.21	0	6,6,6	0.31	0
2	CHT	B	601	-	6,6,6	1.25	0	8,8,8	0.43	0
4	SO4	A	604	-	4,4,4	0.22	0	6,6,6	0.50	0
2	CHT	A	601	-	6,6,6	1.07	0	8,8,8	0.42	0
4	SO4	C	603	-	4,4,4	0.18	0	6,6,6	0.24	0
2	CHT	C	601	-	6,6,6	1.22	0	8,8,8	0.50	0
4	SO4	B	605	-	4,4,4	0.25	0	6,6,6	0.52	0
4	SO4	B	604	-	4,4,4	0.12	0	6,6,6	0.17	0
4	SO4	A	603	-	4,4,4	0.14	0	6,6,6	0.20	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
2	CHT	A	601	-	-	1/4/4/4	-
2	CHT	B	601	-	-	1/4/4/4	-
2	CHT	C	601	-	-	1/4/4/4	-
2	CHT	D	1000	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	CHT	O6-C4-C5-N1
2	C	601	CHT	O6-C4-C5-N1
2	A	601	CHT	O6-C4-C5-N1

There are no ring outliers.

No monomer is involved in short contacts.

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	507/508 (99%)	-0.27	3 (0%) 85 91	11, 28, 51, 71	1 (0%)
1	B	505/508 (99%)	-0.22	22 (4%) 39 42	15, 26, 52, 98	1 (0%)
1	C	504/508 (99%)	-0.20	3 (0%) 85 91	22, 32, 49, 74	0
1	D	504/508 (99%)	0.27	25 (4%) 35 37	25, 38, 63, 92	0
All	All	2020/2032 (99%)	-0.11	53 (2%) 57 62	11, 31, 56, 98	2 (0%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	501	THR	5.6
1	B	497	MET	4.8
1	D	499	LEU	4.8
1	B	499	LEU	4.6
1	A	486	GLN	3.8
1	B	508	TYR	3.7
1	B	509	PRO	3.7
1	D	500	ASP	3.6
1	B	502	LEU	3.5
1	D	509	PRO	3.2
1	D	140	ILE	3.0
1	D	497	MET	3.0
1	B	498	ASN	3.0
1	B	487	LYS	3.0
1	C	500	ASP	2.9
1	B	187	SER	2.9
1	D	187	SER	2.9
1	D	501	THR	2.9
1	D	183	ASN	2.9
1	D	241	LEU	2.8
1	B	504	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	500	ASP	2.7
1	D	144	TYR	2.7
1	B	503	GLU	2.7
1	D	466	TRP	2.6
1	A	511	GLY	2.6
1	D	184	ASP	2.6
1	C	499	LEU	2.5
1	D	186	GLU	2.5
1	D	433	VAL	2.5
1	D	498	ASN	2.5
1	B	492	TYR	2.5
1	D	143	TRP	2.5
1	D	185	ASP	2.4
1	D	448	HIS	2.4
1	A	216	ASP	2.4
1	B	185	ASP	2.4
1	D	485	LEU	2.4
1	B	183	ASN	2.4
1	C	185	ASP	2.4
1	B	142	TRP	2.3
1	D	508	TYR	2.3
1	D	142	TRP	2.3
1	B	489	SER	2.3
1	B	485	LEU	2.2
1	D	493	MET	2.2
1	B	143	TRP	2.2
1	B	490	GLU	2.2
1	D	507	ARG	2.2
1	D	188	ARG	2.1
1	B	493	MET	2.1
1	B	184	ASP	2.0
1	D	502	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	DDZ	D	54	7/8	0.91	0.10	28,30,48,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	DDZ	C	54	7/8	0.93	0.09	23,29,37,39	0
1	DDZ	B	54	7/8	0.95	0.08	15,18,31,33	0
1	DDZ	A	54	7/8	0.96	0.07	22,24,34,36	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
4	SO4	A	604	5/5	0.84	0.11	38,40,47,54	5
4	SO4	B	606	5/5	0.84	0.13	44,48,50,51	5
2	CHT	B	601	7/7	0.85	0.20	51,55,60,61	0
2	CHT	A	601	7/7	0.86	0.17	36,38,49,50	0
3	MG	C	602	1/1	0.86	0.25	34,34,34,34	0
3	MG	D	1001	1/1	0.87	0.12	48,48,48,48	0
2	CHT	C	601	7/7	0.88	0.18	48,49,56,57	0
4	SO4	B	603	5/5	0.90	0.08	45,53,55,56	0
2	CHT	D	1000	7/7	0.90	0.17	45,50,52,53	0
4	SO4	A	603	5/5	0.91	0.08	66,67,71,71	0
3	MG	B	602	1/1	0.93	0.22	31,31,31,31	0
4	SO4	C	603	5/5	0.93	0.10	60,61,63,65	0
3	MG	A	602	1/1	0.94	0.13	32,32,32,32	0
4	SO4	B	604	5/5	0.97	0.07	48,49,51,54	5
4	SO4	B	605	5/5	0.97	0.10	32,33,35,36	5

6.5 Other polymers [i](#)

There are no such residues in this entry.