



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 06:17 AM UTC

PDB ID : 3DPJ / pdb_00003dpj
Title : The crystal structure of a TetR transcription regulator from *Silicibacter pomeroyi* DSS
Authors : Tan, K.; Li, H.; Freeman, L.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2008-07-08
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

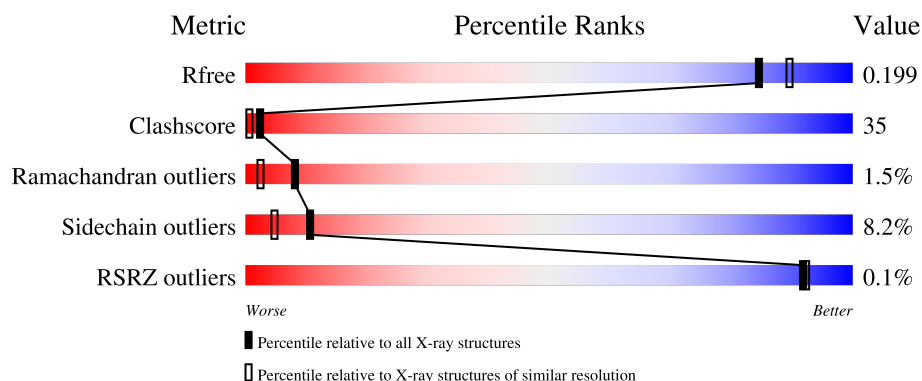
1 Overall quality at a glance

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}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (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 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	194	47% 47% 6%
1	B	194	48% 47% ...
1	C	194	% 51% 44% 5%
1	D	194	41% 47% 9% .
1	E	194	54% 41% 5% .

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Mol	Chain	Length	Quality of chain
1	F	194	 47% 43% 6% • •
1	G	194	 53% 42% 5% •
1	H	194	 48% 43% 6% • •

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MES	G	192	-	-	X	-
3	EDO	C	195	-	-	X	-
3	EDO	D	195	-	-	X	-
3	EDO	F	195	-	-	X	-
3	EDO	H	198	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12978 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 Transcription regulator, TetR family.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	Se	0	0	0
			1514	949	274	281	3	7			
1	B	190	Total	C	N	O	S	Se	0	0	0
			1487	934	269	275	3	6			
1	C	194	Total	C	N	O	S	Se	0	0	0
			1514	949	274	281	3	7			
1	D	190	Total	C	N	O	S	Se	0	0	0
			1487	934	269	275	3	6			
1	E	193	Total	C	N	O	S	Se	0	0	0
			1505	944	273	279	3	6			
1	F	188	Total	C	N	O	S	Se	0	0	0
			1473	925	267	272	3	6			
1	G	193	Total	C	N	O	S	Se	0	0	0
			1505	944	273	279	3	6			
1	H	188	Total	C	N	O	S	Se	0	0	0
			1473	925	267	272	3	6			

There are 24 discrepancies between the modelled and reference sequences:

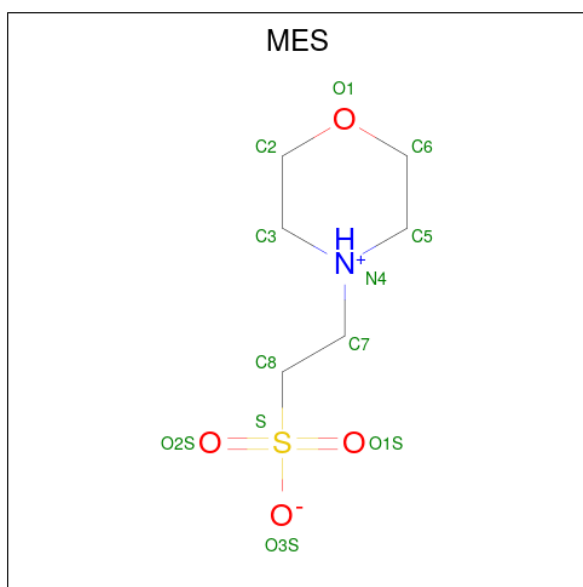
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q5LS67
A	-1	ASN	-	expression tag	UNP Q5LS67
A	0	ALA	-	expression tag	UNP Q5LS67
B	-2	SER	-	expression tag	UNP Q5LS67
B	-1	ASN	-	expression tag	UNP Q5LS67
B	0	ALA	-	expression tag	UNP Q5LS67
C	-2	SER	-	expression tag	UNP Q5LS67
C	-1	ASN	-	expression tag	UNP Q5LS67
C	0	ALA	-	expression tag	UNP Q5LS67
D	-2	SER	-	expression tag	UNP Q5LS67
D	-1	ASN	-	expression tag	UNP Q5LS67
D	0	ALA	-	expression tag	UNP Q5LS67
E	-2	SER	-	expression tag	UNP Q5LS67

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	ASN	-	expression tag	UNP Q5LS67
E	0	ALA	-	expression tag	UNP Q5LS67
F	-2	SER	-	expression tag	UNP Q5LS67
F	-1	ASN	-	expression tag	UNP Q5LS67
F	0	ALA	-	expression tag	UNP Q5LS67
G	-2	SER	-	expression tag	UNP Q5LS67
G	-1	ASN	-	expression tag	UNP Q5LS67
G	0	ALA	-	expression tag	UNP Q5LS67
H	-2	SER	-	expression tag	UNP Q5LS67
H	-1	ASN	-	expression tag	UNP Q5LS67
H	0	ALA	-	expression tag	UNP Q5LS67

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



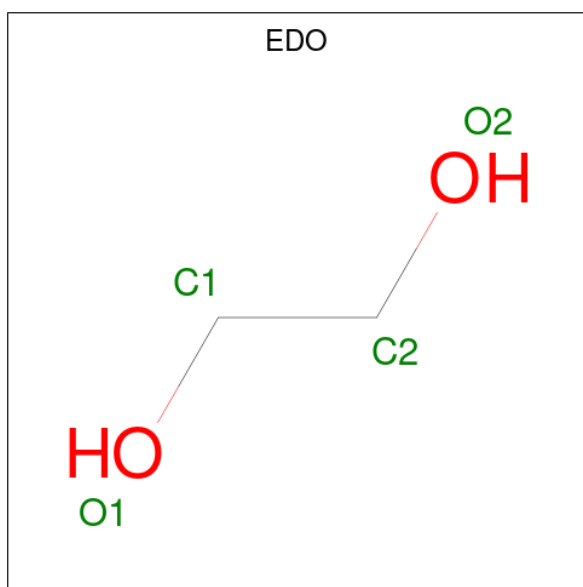
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	E	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	F	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	G	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	H	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	C	O	0	0
			4	2	2		

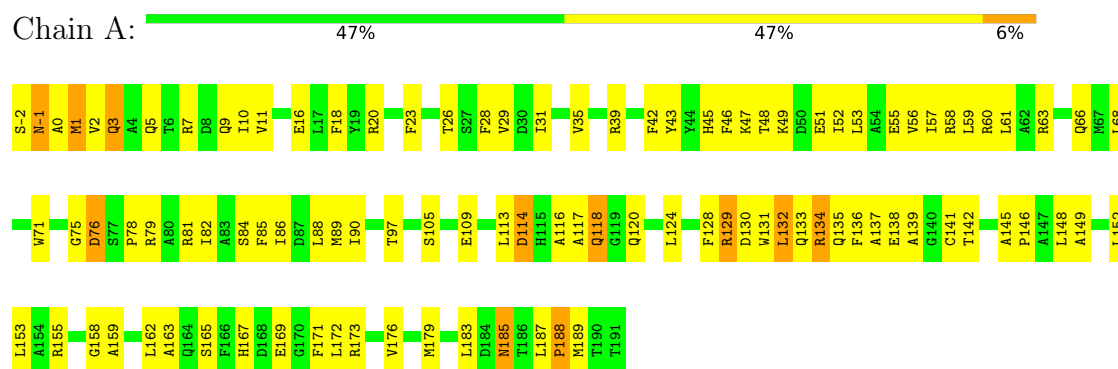
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	101	Total	O	0	0
			101	101		
4	B	100	Total	O	0	0
			100	100		
4	C	95	Total	O	0	0
			95	95		
4	D	107	Total	O	0	0
			107	107		
4	E	95	Total	O	0	0
			95	95		
4	F	107	Total	O	0	0
			107	107		
4	G	94	Total	O	0	0
			94	94		
4	H	105	Total	O	0	0
			105	105		

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.

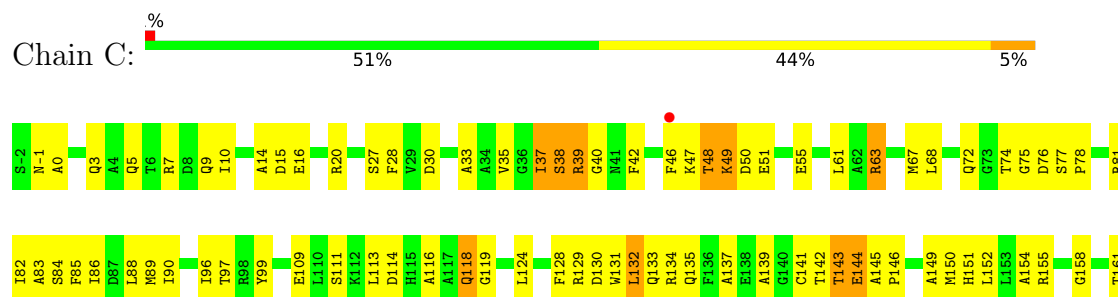
• Molecule 1: Transcription regulator, TetR family



• Molecule 1: Transcription regulator, TetR family



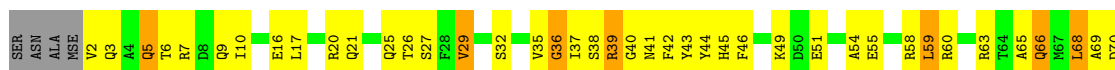
• Molecule 1: Transcription regulator, TetR family





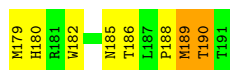
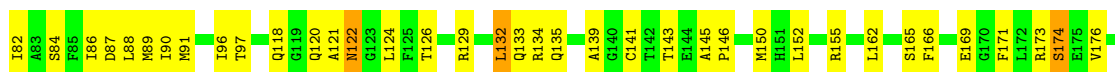
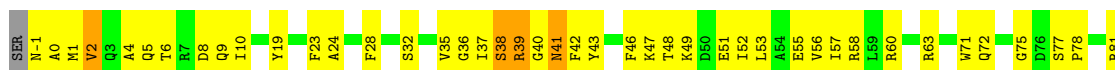
- Molecule 1: Transcription regulator, TetR family

Chain D: 41% 47% 9%



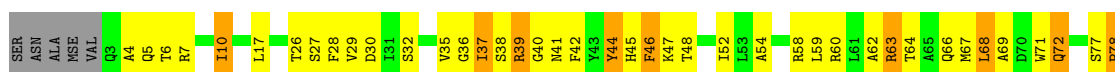
- Molecule 1: Transcription regulator, TetR family

Chain E: 54% 41% 5%



- Molecule 1: Transcription regulator, TetR family

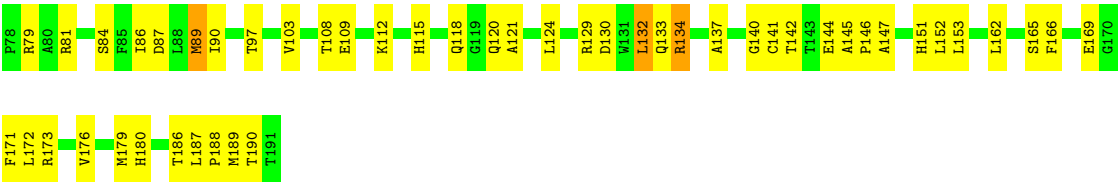
Chain F: 47% 43% 6%



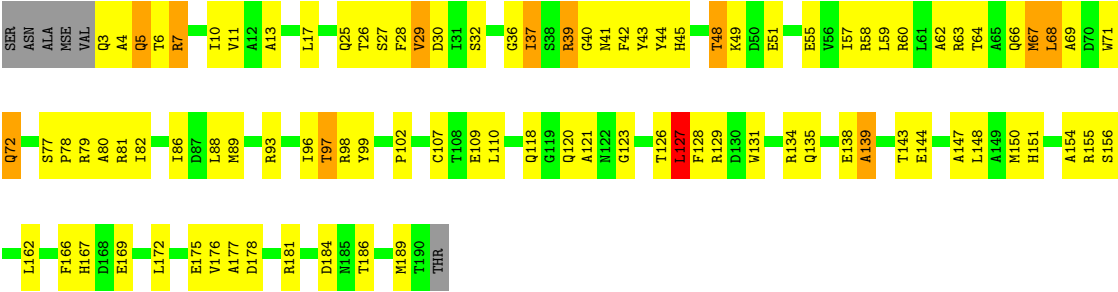
- Molecule 1: Transcription regulator, TetR family

Chain G: 53% 42% 5%





● Molecule 1: Transcription regulator, TetR family



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.52Å 93.07Å 93.40Å 89.35° 71.02° 71.04°	Depositor
Resolution (Å)	41.61 – 1.90 41.61 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.4 (41.61-1.90) 95.8 (41.61-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 1.89Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.193 , 0.243 0.177 , 0.199	Depositor DCC
R_{free} test set	6943 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	28.1	Xtriage
Anisotropy	0.575	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 66.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.469 for h,h-k,h-l 0.457 for -h,-h+l,-h+k 0.458 for -h,-l,-k	Xtriage
Reported twinning fraction	0.502 for h,h-k,h-l	Depositor
Outliers	0 of 138037 reflections	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	12978	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 94.80 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.2214e-09. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: EDO, MES

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	0/1536	0.88	0/2065
1	B	0.50	0/1510	0.88	0/2032
1	C	0.51	0/1536	0.81	1/2065 (0.0%)
1	D	0.50	0/1510	0.86	3/2032 (0.1%)
1	E	0.50	0/1527	0.86	1/2054 (0.0%)
1	F	0.50	0/1496	0.85	1/2012 (0.0%)
1	G	0.50	0/1527	0.91	5/2054 (0.2%)
1	H	0.48	0/1496	0.82	0/2012
All	All	0.50	0/12138	0.86	11/16326 (0.1%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	39	ARG	N-CA-C	-7.17	104.27	112.87
1	C	49	LYS	N-CA-C	-6.59	104.17	111.82
1	G	39	ARG	N-CA-C	-6.24	104.77	112.38
1	F	46	PHE	N-CA-C	6.21	118.86	109.23
1	D	190	THR	N-CA-C	5.93	116.11	108.34

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	1514	0	1485	127	0
1	B	1487	0	1457	107	0
1	C	1514	0	1485	102	0
1	D	1487	0	1457	118	0
1	E	1505	0	1473	79	0
1	F	1473	0	1441	123	0
1	G	1505	0	1473	99	0
1	H	1473	0	1441	116	0
2	A	12	0	12	3	0
2	B	12	0	12	4	0
2	C	12	0	12	5	0
2	D	12	0	12	2	0
2	E	12	0	12	4	0
2	F	12	0	12	5	0
2	G	12	0	12	7	0
2	H	12	0	12	3	0
3	A	4	0	6	2	0
3	B	12	0	18	2	0
3	C	28	0	42	13	0
3	D	20	0	30	7	0
3	E	12	0	18	1	0
3	F	16	0	24	7	0
3	H	28	0	42	14	0
4	A	101	0	0	14	0
4	B	100	0	0	13	0
4	C	95	0	0	17	0
4	D	107	0	0	16	0
4	E	95	0	0	8	0
4	F	107	0	0	8	0
4	G	94	0	0	12	0
4	H	105	0	0	13	0
All	All	12978	0	11988	852	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 35.

The worst 5 of 852 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:72:GLN:HA	1:D:81:ARG:HD3	1.19	1.15
1:E:6:THR:HA	1:E:9:GLN:HE21	1.19	1.04
1:B:144:GLU:HG3	1:B:148:LEU:HG	1.36	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:63:ARG:HD3	2:E:192:MES:H81	1.36	1.03
1:B:72:GLN:HA	1:B:81:ARG:HD3	1.41	1.02

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	192/194 (99%)	178 (93%)	9 (5%)	5 (3%)	4	1
1	B	188/194 (97%)	170 (90%)	14 (7%)	4 (2%)	5	1
1	C	192/194 (99%)	172 (90%)	19 (10%)	1 (0%)	24	16
1	D	188/194 (97%)	151 (80%)	30 (16%)	7 (4%)	2	0
1	E	191/194 (98%)	179 (94%)	11 (6%)	1 (0%)	24	16
1	F	186/194 (96%)	169 (91%)	14 (8%)	3 (2%)	7	2
1	G	191/194 (98%)	175 (92%)	16 (8%)	0	100	100
1	H	186/194 (96%)	166 (89%)	18 (10%)	2 (1%)	11	4
All	All	1514/1552 (98%)	1360 (90%)	131 (9%)	23 (2%)	8	2

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	74	THR
1	F	127	LEU
1	A	117	ALA
1	A	118	GLN
1	A	129	ARG

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	154/147 (105%)	145 (94%)	9 (6%)	18	10
1	B	151/147 (103%)	141 (93%)	10 (7%)	15	8
1	C	154/147 (105%)	140 (91%)	14 (9%)	9	3
1	D	151/147 (103%)	133 (88%)	18 (12%)	5	2
1	E	152/147 (103%)	137 (90%)	15 (10%)	7	3
1	F	149/147 (101%)	136 (91%)	13 (9%)	9	4
1	G	152/147 (103%)	144 (95%)	8 (5%)	20	12
1	H	149/147 (101%)	137 (92%)	12 (8%)	11	5
All	All	1212/1176 (103%)	1113 (92%)	99 (8%)	10	5

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	118	GLN
1	F	48	THR
1	E	132	LEU
1	E	190	THR
1	F	82	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	122	ASN
1	H	92	ASN
1	F	157	GLN
1	G	135	GLN
1	H	167	HIS

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

38 ligands 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$
3	EDO	C	196	-	3,3,3	0.49	0	2,2,2	0.27	0
3	EDO	D	196	-	3,3,3	0.50	0	2,2,2	0.29	0
3	EDO	E	195	-	3,3,3	0.44	0	2,2,2	0.33	0
2	MES	G	192	-	12,12,12	2.21	1 (8%)	15,16,16	2.82	8 (53%)
3	EDO	A	193	-	3,3,3	0.47	0	2,2,2	0.33	0
3	EDO	H	196	-	3,3,3	0.51	0	2,2,2	0.19	0
2	MES	F	192	-	12,12,12	2.14	1 (8%)	15,16,16	2.52	7 (46%)
3	EDO	B	195	-	3,3,3	0.47	0	2,2,2	0.34	0
3	EDO	F	195	-	3,3,3	0.42	0	2,2,2	0.37	0
3	EDO	H	194	-	3,3,3	0.54	0	2,2,2	0.17	0
3	EDO	D	195	-	3,3,3	0.66	0	2,2,2	0.02	0
3	EDO	C	194	-	3,3,3	0.45	0	2,2,2	0.32	0
3	EDO	D	197	-	3,3,3	0.46	0	2,2,2	0.36	0
3	EDO	H	193	-	3,3,3	0.53	0	2,2,2	0.17	0
2	MES	H	192	-	12,12,12	2.50	1 (8%)	15,16,16	2.73	8 (53%)
2	MES	C	192	-	12,12,12	2.12	1 (8%)	15,16,16	2.30	5 (33%)
3	EDO	F	196	-	3,3,3	0.48	0	2,2,2	0.29	0
2	MES	B	192	-	12,12,12	2.03	1 (8%)	15,16,16	2.51	7 (46%)
3	EDO	E	194	-	3,3,3	0.60	0	2,2,2	0.10	0
3	EDO	C	193	-	3,3,3	0.52	0	2,2,2	0.21	0
3	EDO	H	195	-	3,3,3	0.50	0	2,2,2	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	B	193	-	3,3,3	0.42	0	2,2,2	0.54	0
2	MES	A	192	-	12,12,12	2.20	1 (8%)	15,16,16	2.41	6 (40%)
3	EDO	H	198	-	3,3,3	0.54	0	2,2,2	0.43	0
3	EDO	B	194	-	3,3,3	0.49	0	2,2,2	0.31	0
3	EDO	F	194	-	3,3,3	0.31	0	2,2,2	0.79	0
2	MES	E	192	-	12,12,12	2.27	1 (8%)	15,16,16	2.35	7 (46%)
3	EDO	C	198	-	3,3,3	0.43	0	2,2,2	0.44	0
3	EDO	F	193	-	3,3,3	0.41	0	2,2,2	0.53	0
3	EDO	D	194	-	3,3,3	0.54	0	2,2,2	0.20	0
3	EDO	H	197	-	3,3,3	0.36	0	2,2,2	0.57	0
3	EDO	C	197	-	3,3,3	0.42	0	2,2,2	0.47	0
3	EDO	C	195	-	3,3,3	0.54	0	2,2,2	0.19	0
3	EDO	E	193	-	3,3,3	0.54	0	2,2,2	0.21	0
2	MES	D	192	-	12,12,12	1.86	1 (8%)	15,16,16	2.54	7 (46%)
3	EDO	H	199	-	3,3,3	0.40	0	2,2,2	0.55	0
3	EDO	C	199	-	3,3,3	0.50	0	2,2,2	0.25	0
3	EDO	D	193	-	3,3,3	0.44	0	2,2,2	0.33	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	C	196	-	-	1/1/1/1	-
3	EDO	D	196	-	-	1/1/1/1	-
3	EDO	E	195	-	-	0/1/1/1	-
2	MES	G	192	-	-	4/6/14/14	0/1/1/1
3	EDO	A	193	-	-	1/1/1/1	-
3	EDO	H	196	-	-	0/1/1/1	-
2	MES	F	192	-	-	1/6/14/14	0/1/1/1
3	EDO	B	195	-	-	0/1/1/1	-
3	EDO	F	195	-	-	1/1/1/1	-
3	EDO	H	194	-	-	0/1/1/1	-
3	EDO	D	195	-	-	1/1/1/1	-
3	EDO	C	194	-	-	0/1/1/1	-
3	EDO	D	197	-	-	0/1/1/1	-
3	EDO	H	193	-	-	1/1/1/1	-
2	MES	H	192	-	-	5/6/14/14	0/1/1/1
2	MES	C	192	-	-	6/6/14/14	0/1/1/1
3	EDO	F	196	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MES	B	192	-	-	5/6/14/14	0/1/1/1
3	EDO	E	194	-	-	0/1/1/1	-
3	EDO	C	193	-	-	0/1/1/1	-
3	EDO	H	195	-	-	0/1/1/1	-
3	EDO	B	193	-	-	0/1/1/1	-
2	MES	A	192	-	-	5/6/14/14	0/1/1/1
3	EDO	H	198	-	-	1/1/1/1	-
3	EDO	B	194	-	-	1/1/1/1	-
3	EDO	F	194	-	-	0/1/1/1	-
2	MES	E	192	-	-	4/6/14/14	0/1/1/1
3	EDO	C	198	-	-	1/1/1/1	-
3	EDO	F	193	-	-	1/1/1/1	-
3	EDO	D	194	-	-	0/1/1/1	-
3	EDO	H	197	-	-	1/1/1/1	-
3	EDO	C	197	-	-	1/1/1/1	-
3	EDO	C	195	-	-	0/1/1/1	-
3	EDO	E	193	-	-	1/1/1/1	-
2	MES	D	192	-	-	5/6/14/14	0/1/1/1
3	EDO	H	199	-	-	1/1/1/1	-
3	EDO	C	199	-	-	0/1/1/1	-
3	EDO	D	193	-	-	1/1/1/1	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	192	MES	C8-S	-8.27	1.66	1.77
2	E	192	MES	C8-S	-7.51	1.67	1.77
2	G	192	MES	C8-S	-7.35	1.67	1.77
2	A	192	MES	C8-S	-7.23	1.67	1.77
2	F	192	MES	C8-S	-6.99	1.67	1.77

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	192	MES	C5-N4-C3	7.26	124.47	108.84
2	C	192	MES	C5-N4-C3	5.70	121.12	108.84
2	H	192	MES	C5-N4-C3	5.64	120.99	108.84
2	A	192	MES	C5-N4-C3	5.36	120.38	108.84
2	G	192	MES	C5-N4-C3	5.28	120.21	108.84

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	192	MES	C8-C7-N4-C3
2	A	192	MES	N4-C7-C8-S
2	A	192	MES	C7-C8-S-O2S
2	A	192	MES	C7-C8-S-O3S
2	B	192	MES	C8-C7-N4-C3

There are no ring outliers.

29 monomers are involved in 79 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	192	MES	7	0
3	A	193	EDO	2	0
3	H	196	EDO	3	0
2	F	192	MES	5	0
3	B	195	EDO	1	0
3	F	195	EDO	5	0
3	H	194	EDO	3	0
3	D	195	EDO	4	0
3	C	194	EDO	2	0
3	H	193	EDO	1	0
2	H	192	MES	3	0
2	C	192	MES	5	0
3	F	196	EDO	1	0
2	B	192	MES	4	0
3	E	194	EDO	1	0
3	C	193	EDO	1	0
2	A	192	MES	3	0
3	H	198	EDO	6	0
3	B	194	EDO	1	0
2	E	192	MES	4	0
3	C	198	EDO	2	0
3	F	193	EDO	1	0
3	D	194	EDO	1	0
3	H	197	EDO	1	0
3	C	197	EDO	2	0
3	C	195	EDO	5	0
2	D	192	MES	2	0
3	C	199	EDO	2	0
3	D	193	EDO	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 [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	187/194 (96%)	-0.92	0 100 100	21, 46, 98, 134	0
1	B	184/194 (94%)	-1.10	0 100 100	25, 44, 77, 102	0
1	C	187/194 (96%)	-1.07	1 (0%) 87 89	24, 42, 87, 128	0
1	D	184/194 (94%)	-0.99	0 100 100	21, 43, 87, 101	0
1	E	186/194 (95%)	-1.11	0 100 100	22, 42, 87, 110	0
1	F	182/194 (93%)	-1.08	0 100 100	26, 44, 87, 152	0
1	G	186/194 (95%)	-0.94	0 100 100	22, 48, 94, 121	0
1	H	182/194 (93%)	-0.91	0 100 100	27, 49, 96, 140	0
All	All	1478/1552 (95%)	-1.02	1 (0%) 92 92	21, 45, 90, 152	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	46	PHE	2.3

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 oligosaccharides 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	EDO	E	195	4/4	0.92	0.06	73,74,76,77	0
3	EDO	C	197	4/4	0.96	0.05	75,75,79,82	0
3	EDO	H	195	4/4	0.96	0.05	46,50,51,53	0
3	EDO	D	197	4/4	0.97	0.05	54,59,66,70	0
3	EDO	B	193	4/4	0.97	0.06	47,58,64,70	0
2	MES	G	192	12/12	0.97	0.07	57,69,202,202	0
3	EDO	H	199	4/4	0.97	0.04	49,50,50,53	0
3	EDO	B	194	4/4	0.98	0.05	45,46,46,47	0
3	EDO	C	199	4/4	0.98	0.03	57,58,59,60	0
3	EDO	C	194	4/4	0.98	0.04	56,59,63,68	0
2	MES	C	192	12/12	0.99	0.03	24,41,62,68	0
3	EDO	B	195	4/4	0.99	0.02	31,32,43,47	0
3	EDO	C	193	4/4	0.99	0.04	36,41,48,53	0
2	MES	D	192	12/12	0.99	0.03	29,41,82,83	0
3	EDO	C	195	4/4	0.99	0.04	37,39,39,41	0
3	EDO	C	196	4/4	0.99	0.04	45,45,48,48	0
2	MES	E	192	12/12	0.99	0.05	40,51,194,195	0
3	EDO	C	198	4/4	0.99	0.04	55,56,56,58	0
2	MES	F	192	12/12	0.99	0.03	47,50,73,74	0
3	EDO	D	193	4/4	0.99	0.04	31,35,41,42	0
3	EDO	D	194	4/4	0.99	0.04	38,45,55,59	0
3	EDO	D	195	4/4	0.99	0.10	34,35,38,47	0
3	EDO	D	196	4/4	0.99	0.07	60,60,60,61	0
2	MES	A	192	12/12	0.99	0.02	35,45,64,65	0
3	EDO	E	193	4/4	0.99	0.04	39,42,44,45	0
3	EDO	E	194	4/4	0.99	0.06	25,33,36,43	0
2	MES	H	192	12/12	0.99	0.04	69,72,77,79	0
3	EDO	F	193	4/4	0.99	0.02	24,32,36,42	0
3	EDO	F	194	4/4	0.99	0.07	57,58,59,61	0
3	EDO	F	195	4/4	0.99	0.05	47,48,49,50	0
3	EDO	F	196	4/4	0.99	0.04	36,43,43,47	0
3	EDO	H	193	4/4	0.99	0.03	39,40,40,43	0
3	EDO	H	194	4/4	0.99	0.05	37,39,39,44	0
3	EDO	A	193	4/4	0.99	0.04	37,40,42,51	0
3	EDO	H	196	4/4	0.99	0.05	42,47,47,48	0
3	EDO	H	197	4/4	0.99	0.05	53,56,60,63	0
2	MES	B	192	12/12	0.99	0.03	37,43,63,71	0
3	EDO	H	198	4/4	1.00	0.08	33,37,43,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.