



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:52 AM UTC

PDB ID : 8T0U / pdb_00008t0u
Title : Crystal structure of dimethylsulfone monooxygenase SfnG from *Pseudomonas fluorescens*
Authors : Gonzalez, R.; Soule, J.; Dowling, D.P.
Deposited on : 2023-06-01
Resolution : 2.60 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	:	4-5-2 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

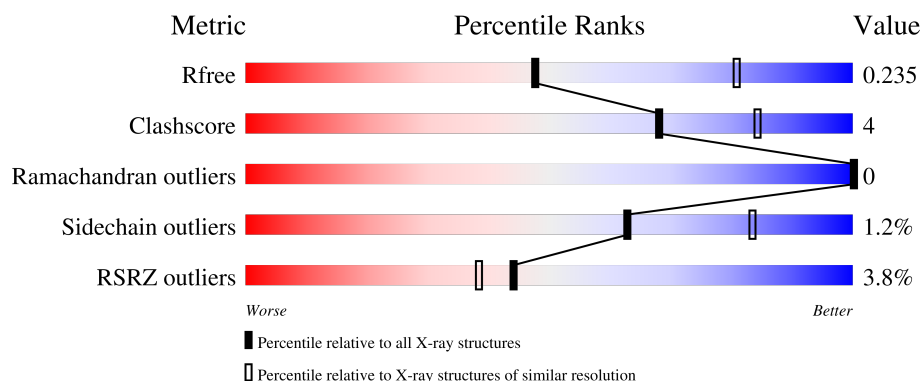
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	387	 2% 74% 9% 15%
1	B	387	 2% 73% 12% 15%
1	C	387	 3% 75% 7% 18%
1	D	387	 3% 70% 9% 21%
1	E	387	 2% 78% 7% 15%

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Mol	Chain	Length	Quality of chain
1	F	387	 4% 74% 9% 16%
1	G	387	 4% 69% 7% 24%
1	H	387	 4% 71% 9% 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19746 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 FMNH(2)-dependent dimethylsulfone monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2528	1615	449	463	1			
1	B	330	Total	C	N	O	S	0	2	0
			2581	1650	459	471	1			
1	C	319	Total	C	N	O	S	0	1	0
			2434	1563	432	438	1			
1	D	304	Total	C	N	O	S	0	1	0
			2327	1488	415	423	1			
1	E	329	Total	C	N	O	S	0	0	0
			2553	1630	455	467	1			
1	F	324	Total	C	N	O	S	0	1	0
			2519	1613	448	457	1			
1	G	295	Total	C	N	O	S	0	0	0
			2285	1464	407	413	1			
1	H	306	Total	C	N	O	S	0	1	0
			2350	1510	420	419	1			

There are 184 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	initiating methionine	UNP Q3KC85
A	-21	GLY	-	expression tag	UNP Q3KC85
A	-20	SER	-	expression tag	UNP Q3KC85
A	-19	SER	-	expression tag	UNP Q3KC85
A	-18	HIS	-	expression tag	UNP Q3KC85
A	-17	HIS	-	expression tag	UNP Q3KC85
A	-16	HIS	-	expression tag	UNP Q3KC85
A	-15	HIS	-	expression tag	UNP Q3KC85
A	-14	HIS	-	expression tag	UNP Q3KC85
A	-13	HIS	-	expression tag	UNP Q3KC85
A	-12	SER	-	expression tag	UNP Q3KC85
A	-11	SER	-	expression tag	UNP Q3KC85
A	-10	GLY	-	expression tag	UNP Q3KC85

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	LEU	-	expression tag	UNP Q3KC85
A	-8	VAL	-	expression tag	UNP Q3KC85
A	-7	PRO	-	expression tag	UNP Q3KC85
A	-6	ARG	-	expression tag	UNP Q3KC85
A	-5	GLY	-	expression tag	UNP Q3KC85
A	-4	SER	-	expression tag	UNP Q3KC85
A	-3	HIS	-	expression tag	UNP Q3KC85
A	-2	MET	-	expression tag	UNP Q3KC85
A	-1	ALA	-	expression tag	UNP Q3KC85
A	0	SER	-	expression tag	UNP Q3KC85
B	-22	MET	-	initiating methionine	UNP Q3KC85
B	-21	GLY	-	expression tag	UNP Q3KC85
B	-20	SER	-	expression tag	UNP Q3KC85
B	-19	SER	-	expression tag	UNP Q3KC85
B	-18	HIS	-	expression tag	UNP Q3KC85
B	-17	HIS	-	expression tag	UNP Q3KC85
B	-16	HIS	-	expression tag	UNP Q3KC85
B	-15	HIS	-	expression tag	UNP Q3KC85
B	-14	HIS	-	expression tag	UNP Q3KC85
B	-13	HIS	-	expression tag	UNP Q3KC85
B	-12	SER	-	expression tag	UNP Q3KC85
B	-11	SER	-	expression tag	UNP Q3KC85
B	-10	GLY	-	expression tag	UNP Q3KC85
B	-9	LEU	-	expression tag	UNP Q3KC85
B	-8	VAL	-	expression tag	UNP Q3KC85
B	-7	PRO	-	expression tag	UNP Q3KC85
B	-6	ARG	-	expression tag	UNP Q3KC85
B	-5	GLY	-	expression tag	UNP Q3KC85
B	-4	SER	-	expression tag	UNP Q3KC85
B	-3	HIS	-	expression tag	UNP Q3KC85
B	-2	MET	-	expression tag	UNP Q3KC85
B	-1	ALA	-	expression tag	UNP Q3KC85
B	0	SER	-	expression tag	UNP Q3KC85
C	-22	MET	-	initiating methionine	UNP Q3KC85
C	-21	GLY	-	expression tag	UNP Q3KC85
C	-20	SER	-	expression tag	UNP Q3KC85
C	-19	SER	-	expression tag	UNP Q3KC85
C	-18	HIS	-	expression tag	UNP Q3KC85
C	-17	HIS	-	expression tag	UNP Q3KC85
C	-16	HIS	-	expression tag	UNP Q3KC85
C	-15	HIS	-	expression tag	UNP Q3KC85
C	-14	HIS	-	expression tag	UNP Q3KC85

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-13	HIS	-	expression tag	UNP Q3KC85
C	-12	SER	-	expression tag	UNP Q3KC85
C	-11	SER	-	expression tag	UNP Q3KC85
C	-10	GLY	-	expression tag	UNP Q3KC85
C	-9	LEU	-	expression tag	UNP Q3KC85
C	-8	VAL	-	expression tag	UNP Q3KC85
C	-7	PRO	-	expression tag	UNP Q3KC85
C	-6	ARG	-	expression tag	UNP Q3KC85
C	-5	GLY	-	expression tag	UNP Q3KC85
C	-4	SER	-	expression tag	UNP Q3KC85
C	-3	HIS	-	expression tag	UNP Q3KC85
C	-2	MET	-	expression tag	UNP Q3KC85
C	-1	ALA	-	expression tag	UNP Q3KC85
C	0	SER	-	expression tag	UNP Q3KC85
D	-22	MET	-	initiating methionine	UNP Q3KC85
D	-21	GLY	-	expression tag	UNP Q3KC85
D	-20	SER	-	expression tag	UNP Q3KC85
D	-19	SER	-	expression tag	UNP Q3KC85
D	-18	HIS	-	expression tag	UNP Q3KC85
D	-17	HIS	-	expression tag	UNP Q3KC85
D	-16	HIS	-	expression tag	UNP Q3KC85
D	-15	HIS	-	expression tag	UNP Q3KC85
D	-14	HIS	-	expression tag	UNP Q3KC85
D	-13	HIS	-	expression tag	UNP Q3KC85
D	-12	SER	-	expression tag	UNP Q3KC85
D	-11	SER	-	expression tag	UNP Q3KC85
D	-10	GLY	-	expression tag	UNP Q3KC85
D	-9	LEU	-	expression tag	UNP Q3KC85
D	-8	VAL	-	expression tag	UNP Q3KC85
D	-7	PRO	-	expression tag	UNP Q3KC85
D	-6	ARG	-	expression tag	UNP Q3KC85
D	-5	GLY	-	expression tag	UNP Q3KC85
D	-4	SER	-	expression tag	UNP Q3KC85
D	-3	HIS	-	expression tag	UNP Q3KC85
D	-2	MET	-	expression tag	UNP Q3KC85
D	-1	ALA	-	expression tag	UNP Q3KC85
D	0	SER	-	expression tag	UNP Q3KC85
E	-22	MET	-	initiating methionine	UNP Q3KC85
E	-21	GLY	-	expression tag	UNP Q3KC85
E	-20	SER	-	expression tag	UNP Q3KC85
E	-19	SER	-	expression tag	UNP Q3KC85
E	-18	HIS	-	expression tag	UNP Q3KC85

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-17	HIS	-	expression tag	UNP Q3KC85
E	-16	HIS	-	expression tag	UNP Q3KC85
E	-15	HIS	-	expression tag	UNP Q3KC85
E	-14	HIS	-	expression tag	UNP Q3KC85
E	-13	HIS	-	expression tag	UNP Q3KC85
E	-12	SER	-	expression tag	UNP Q3KC85
E	-11	SER	-	expression tag	UNP Q3KC85
E	-10	GLY	-	expression tag	UNP Q3KC85
E	-9	LEU	-	expression tag	UNP Q3KC85
E	-8	VAL	-	expression tag	UNP Q3KC85
E	-7	PRO	-	expression tag	UNP Q3KC85
E	-6	ARG	-	expression tag	UNP Q3KC85
E	-5	GLY	-	expression tag	UNP Q3KC85
E	-4	SER	-	expression tag	UNP Q3KC85
E	-3	HIS	-	expression tag	UNP Q3KC85
E	-2	MET	-	expression tag	UNP Q3KC85
E	-1	ALA	-	expression tag	UNP Q3KC85
E	0	SER	-	expression tag	UNP Q3KC85
F	-22	MET	-	initiating methionine	UNP Q3KC85
F	-21	GLY	-	expression tag	UNP Q3KC85
F	-20	SER	-	expression tag	UNP Q3KC85
F	-19	SER	-	expression tag	UNP Q3KC85
F	-18	HIS	-	expression tag	UNP Q3KC85
F	-17	HIS	-	expression tag	UNP Q3KC85
F	-16	HIS	-	expression tag	UNP Q3KC85
F	-15	HIS	-	expression tag	UNP Q3KC85
F	-14	HIS	-	expression tag	UNP Q3KC85
F	-13	HIS	-	expression tag	UNP Q3KC85
F	-12	SER	-	expression tag	UNP Q3KC85
F	-11	SER	-	expression tag	UNP Q3KC85
F	-10	GLY	-	expression tag	UNP Q3KC85
F	-9	LEU	-	expression tag	UNP Q3KC85
F	-8	VAL	-	expression tag	UNP Q3KC85
F	-7	PRO	-	expression tag	UNP Q3KC85
F	-6	ARG	-	expression tag	UNP Q3KC85
F	-5	GLY	-	expression tag	UNP Q3KC85
F	-4	SER	-	expression tag	UNP Q3KC85
F	-3	HIS	-	expression tag	UNP Q3KC85
F	-2	MET	-	expression tag	UNP Q3KC85
F	-1	ALA	-	expression tag	UNP Q3KC85
F	0	SER	-	expression tag	UNP Q3KC85
G	-22	MET	-	initiating methionine	UNP Q3KC85

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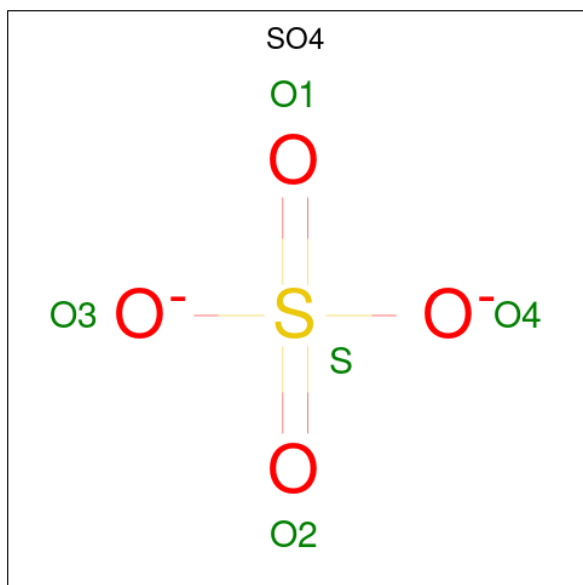
Chain	Residue	Modelled	Actual	Comment	Reference
G	-21	GLY	-	expression tag	UNP Q3KC85
G	-20	SER	-	expression tag	UNP Q3KC85
G	-19	SER	-	expression tag	UNP Q3KC85
G	-18	HIS	-	expression tag	UNP Q3KC85
G	-17	HIS	-	expression tag	UNP Q3KC85
G	-16	HIS	-	expression tag	UNP Q3KC85
G	-15	HIS	-	expression tag	UNP Q3KC85
G	-14	HIS	-	expression tag	UNP Q3KC85
G	-13	HIS	-	expression tag	UNP Q3KC85
G	-12	SER	-	expression tag	UNP Q3KC85
G	-11	SER	-	expression tag	UNP Q3KC85
G	-10	GLY	-	expression tag	UNP Q3KC85
G	-9	LEU	-	expression tag	UNP Q3KC85
G	-8	VAL	-	expression tag	UNP Q3KC85
G	-7	PRO	-	expression tag	UNP Q3KC85
G	-6	ARG	-	expression tag	UNP Q3KC85
G	-5	GLY	-	expression tag	UNP Q3KC85
G	-4	SER	-	expression tag	UNP Q3KC85
G	-3	HIS	-	expression tag	UNP Q3KC85
G	-2	MET	-	expression tag	UNP Q3KC85
G	-1	ALA	-	expression tag	UNP Q3KC85
G	0	SER	-	expression tag	UNP Q3KC85
H	-22	MET	-	initiating methionine	UNP Q3KC85
H	-21	GLY	-	expression tag	UNP Q3KC85
H	-20	SER	-	expression tag	UNP Q3KC85
H	-19	SER	-	expression tag	UNP Q3KC85
H	-18	HIS	-	expression tag	UNP Q3KC85
H	-17	HIS	-	expression tag	UNP Q3KC85
H	-16	HIS	-	expression tag	UNP Q3KC85
H	-15	HIS	-	expression tag	UNP Q3KC85
H	-14	HIS	-	expression tag	UNP Q3KC85
H	-13	HIS	-	expression tag	UNP Q3KC85
H	-12	SER	-	expression tag	UNP Q3KC85
H	-11	SER	-	expression tag	UNP Q3KC85
H	-10	GLY	-	expression tag	UNP Q3KC85
H	-9	LEU	-	expression tag	UNP Q3KC85
H	-8	VAL	-	expression tag	UNP Q3KC85
H	-7	PRO	-	expression tag	UNP Q3KC85
H	-6	ARG	-	expression tag	UNP Q3KC85
H	-5	GLY	-	expression tag	UNP Q3KC85
H	-4	SER	-	expression tag	UNP Q3KC85
H	-3	HIS	-	expression tag	UNP Q3KC85

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-2	MET	-	expression tag	UNP Q3KC85
H	-1	ALA	-	expression tag	UNP Q3KC85
H	0	SER	-	expression tag	UNP Q3KC85

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		

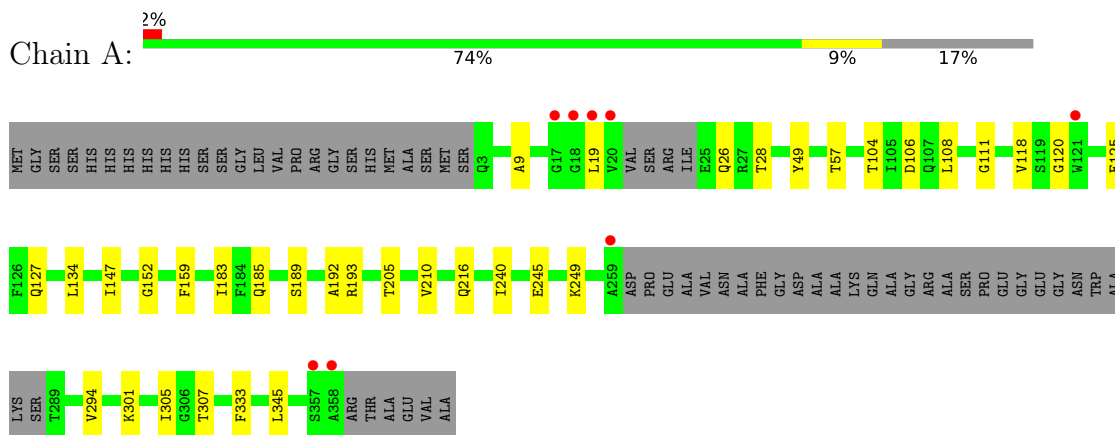
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total	O	0	0
			13	13		
3	B	16	Total	O	0	0
			16	16		
3	C	4	Total	O	0	0
			4	4		
3	D	6	Total	O	0	0
			6	6		
3	E	14	Total	O	0	0
			14	14		
3	F	8	Total	O	0	0
			8	8		
3	G	2	Total	O	0	0
			2	2		
3	H	6	Total	O	0	0
			6	6		

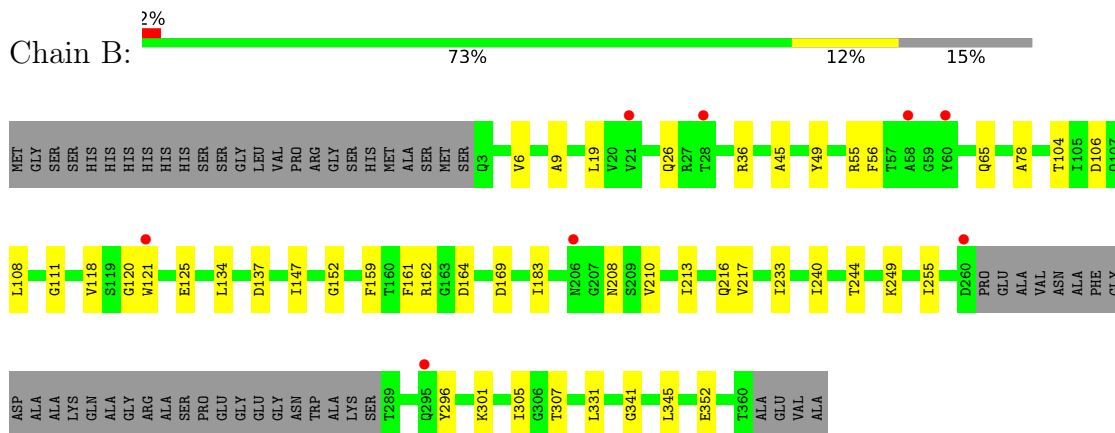
3 Residue-property plots [i](#)

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.

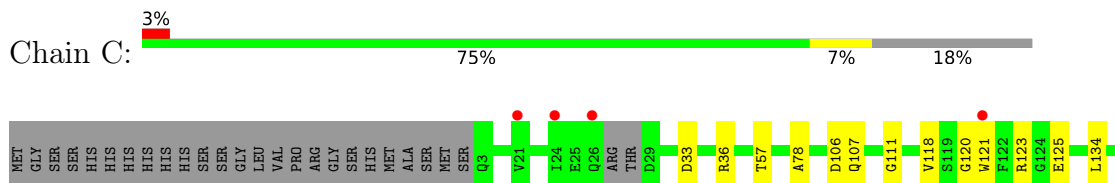
- Molecule 1: FMNH(2)-dependent dimethylsulfone monooxygenase

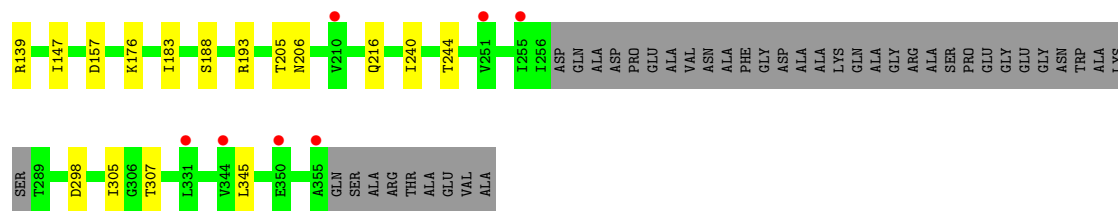


- Molecule 1: FMNH(2)-dependent dimethylsulfone monooxygenase

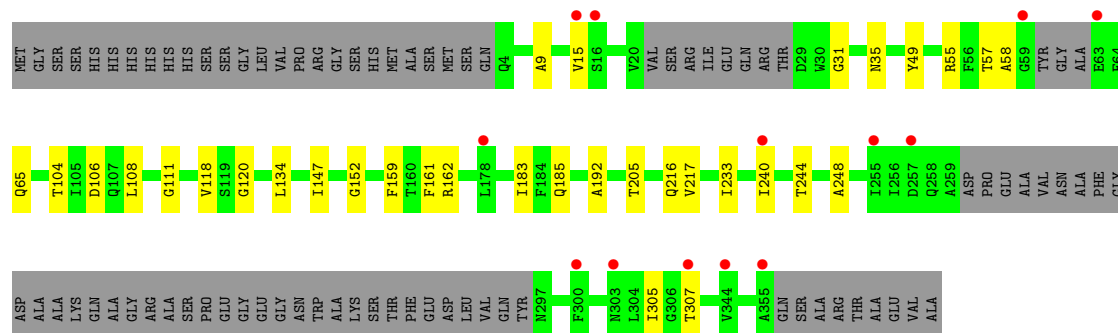


- Molecule 1: FMNH(2)-dependent dimethylsulfone monooxygenase

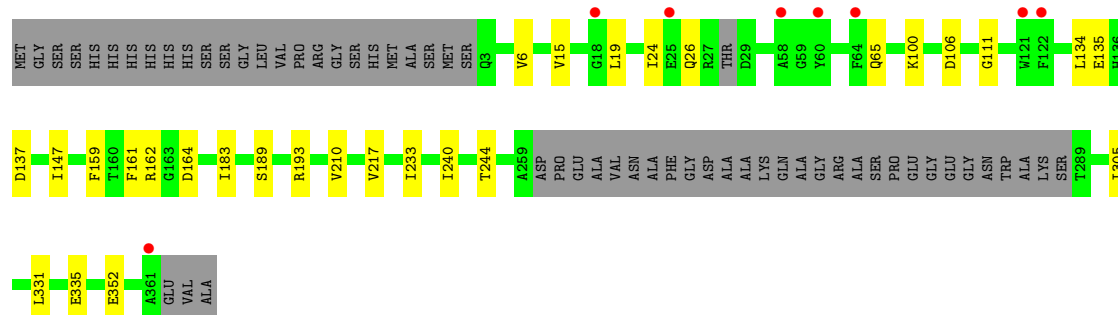
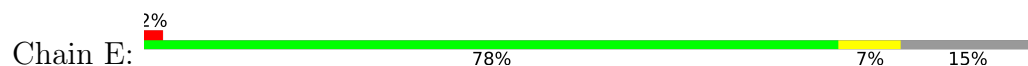




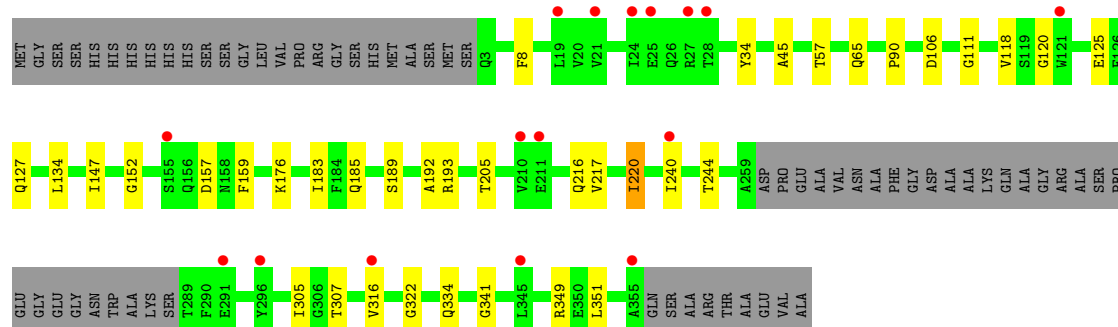
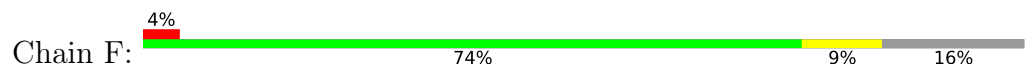
• Molecule 1: FMNH(2)-dependent dimethylsulfone monooxygenase



• Molecule 1: FMNH(2)-dependent dimethylsulfone monooxygenase



• Molecule 1: FMNH(2)-dependent dimethylsulfone monooxygenase



[illegible]

Chain H:

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	88.78Å 94.51Å 102.06Å 103.83° 100.58° 96.52°	Depositor
Resolution (Å)	72.66 – 2.60 72.66 – 2.60	Depositor EDS
% Data completeness (in resolution range)	95.8 (72.66-2.60) 95.8 (72.66-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.62Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.201 , 0.236 0.200 , 0.235	Depositor DCC
R_{free} test set	4601 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	64.9	Xtriage
Anisotropy	0.411	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19746	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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

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	0.10	0/2583	0.27	0/3499
1	B	0.11	0/2641	0.27	0/3582
1	C	0.09	0/2493	0.24	0/3387
1	D	0.09	0/2379	0.23	0/3229
1	E	0.10	0/2609	0.26	0/3540
1	F	0.09	0/2579	0.25	0/3500
1	G	0.09	0/2335	0.24	0/3167
1	H	0.08	0/2408	0.25	0/3271
All	All	0.09	0/20027	0.25	0/27175

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	2528	0	2459	18	0
1	B	2581	0	2502	27	0
1	C	2434	0	2313	15	0
1	D	2327	0	2242	19	0
1	E	2553	0	2460	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2519	0	2432	20	0
1	G	2285	0	2217	17	0
1	H	2350	0	2251	19	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
2	C	10	0	0	0	0
2	D	15	0	0	0	0
2	E	10	0	0	0	0
2	F	15	0	0	0	0
2	G	15	0	0	0	0
2	H	10	0	0	0	0
3	A	13	0	0	0	0
3	B	16	0	0	1	0
3	C	4	0	0	0	0
3	D	6	0	0	0	0
3	E	14	0	0	0	0
3	F	8	0	0	0	0
3	G	2	0	0	0	0
3	H	6	0	0	0	0
All	All	19746	0	18876	138	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 (138) 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:240:ILE:HB	1:D:305:ILE:HG23	1.67	0.75
1:F:240:ILE:HB	1:F:305:ILE:HG23	1.72	0.71
1:C:240:ILE:HB	1:C:305:ILE:HG23	1.74	0.70
1:B:240:ILE:HB	1:B:305:ILE:HG23	1.74	0.68
1:C:205:THR:OG1	1:C:216:GLN:NE2	2.28	0.67
1:A:240:ILE:HB	1:A:305:ILE:HG23	1.77	0.66
1:E:240:ILE:HB	1:E:305:ILE:HG23	1.78	0.66
1:F:205:THR:OG1	1:F:216:GLN:NE2	2.29	0.66
1:H:240:ILE:HB	1:H:305:ILE:HG23	1.78	0.64
1:B:137:ASP:HB2	1:C:123:ARG:HH12	1.64	0.62
1:C:57:THR:HG22	1:C:125:GLU:HG3	1.82	0.61
1:G:62:ALA:O	1:G:65:GLN:NE2	2.34	0.60
1:B:56:PHE:N	1:B:125:GLU:OE2	2.35	0.60
1:E:137:ASP:HB2	1:H:123[A]:ARG:HH12	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:36[B]:ARG:HH11	1:C:78:ALA:HB2	1.68	0.58
1:B:213:ILE:HA	1:B:216:GLN:HE21	1.69	0.57
1:G:147:ILE:HG23	1:G:183:ILE:HD13	1.86	0.57
1:H:147:ILE:HG23	1:H:183:ILE:HD13	1.86	0.57
1:G:58:ALA:HA	1:G:65:GLN:HE22	1.70	0.57
1:C:206:ASN:ND2	1:C:298:ASP:OD2	2.38	0.57
1:B:19:LEU:HB3	1:B:26:GLN:HE22	1.69	0.56
1:B:36[A]:ARG:HH11	1:B:78:ALA:HB2	1.70	0.56
1:D:147:ILE:HG23	1:D:183:ILE:HD13	1.87	0.56
1:H:205:THR:OG1	1:H:216:GLN:NE2	2.39	0.55
1:A:28:THR:HG22	1:A:333:PHE:H	1.72	0.55
1:E:147:ILE:HG23	1:E:183:ILE:HD13	1.86	0.55
1:F:147:ILE:HG23	1:F:183:ILE:HD13	1.88	0.55
1:D:205:THR:OG1	1:D:216:GLN:OE1	2.24	0.55
1:A:245:GLU:HG2	1:A:249:LYS:HE2	1.88	0.54
1:F:57:THR:HG22	1:F:125:GLU:HG3	1.88	0.54
1:A:134:LEU:HD23	1:D:134:LEU:HD23	1.89	0.54
1:A:205:THR:OG1	1:A:216:GLN:OE1	2.26	0.53
1:H:123[A]:ARG:HD3	1:H:133:TRP:CD1	2.43	0.53
1:C:33:ASP:OD1	1:C:36[A]:ARG:NH2	2.41	0.53
1:F:157:ASP:OD1	1:F:176:LYS:NZ	2.38	0.53
1:G:185:GLN:NE2	1:G:192:ALA:O	2.40	0.53
1:E:134:LEU:HD23	1:H:134:LEU:HD23	1.90	0.52
1:C:147:ILE:HG23	1:C:183:ILE:HD13	1.91	0.52
1:E:15:VAL:HG12	1:E:65:GLN:HB3	1.93	0.51
1:B:217:VAL:HG22	1:B:233:ILE:HD13	1.93	0.51
1:A:118:VAL:HG12	1:A:120:GLY:H	1.75	0.51
1:B:36[A]:ARG:NH2	3:B:602:HOH:O	2.43	0.51
1:G:106:ASP:CG	1:G:111:GLY:HA2	2.36	0.50
1:C:118:VAL:HG12	1:C:120:GLY:H	1.77	0.50
1:E:164:ASP:OD2	1:H:127:GLN:NE2	2.42	0.50
1:H:118:VAL:HG12	1:H:120:GLY:H	1.77	0.49
1:F:45:ALA:HB1	1:F:341:GLY:HA3	1.94	0.49
1:B:162:ARG:HB3	1:D:162:ARG:HB3	1.93	0.49
1:E:135:GLU:OE1	1:H:123[A]:ARG:NH1	2.45	0.49
1:B:106:ASP:CG	1:B:111:GLY:HA2	2.38	0.49
1:A:106:ASP:CG	1:A:111:GLY:HA2	2.38	0.49
1:A:152:GLY:HA3	1:A:159:PHE:CE1	2.49	0.48
1:E:217:VAL:HG22	1:E:233:ILE:HD13	1.96	0.48
1:B:134:LEU:HD23	1:C:134:LEU:HD23	1.96	0.48
1:D:55:ARG:NH2	1:D:57:THR:O	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:118:VAL:HG12	1:F:120:GLY:H	1.78	0.48
1:B:152:GLY:HA3	1:B:159:PHE:CE1	2.50	0.47
1:D:58:ALA:HA	1:D:65:GLN:HE22	1.79	0.47
1:C:157:ASP:OD1	1:C:176:LYS:NZ	2.43	0.47
1:E:162:ARG:HB3	1:G:162:ARG:HB3	1.95	0.47
1:B:208:ASN:HA	1:B:301:LYS:HE2	1.96	0.47
1:C:106:ASP:CG	1:C:111:GLY:HA2	2.39	0.47
1:B:6:VAL:HG23	1:B:352:GLU:OE2	2.14	0.47
1:B:164:ASP:OD1	1:D:162:ARG:NH2	2.42	0.47
1:B:255:ILE:HD11	1:B:331:LEU:HD11	1.95	0.47
1:C:107:GLN:NE2	1:C:176:LYS:O	2.42	0.47
1:E:106:ASP:CG	1:E:111:GLY:HA2	2.39	0.47
1:G:152:GLY:HA3	1:G:159:PHE:CE1	2.50	0.47
1:A:57:THR:HG22	1:A:125:GLU:HG3	1.96	0.47
1:D:217:VAL:HG22	1:D:233:ILE:HG21	1.96	0.47
1:G:307:THR:HG23	1:G:310:GLN:H	1.80	0.47
1:H:8:PHE:HE2	1:H:349:ARG:HH12	1.63	0.47
1:H:57:THR:HG22	1:H:125:GLU:HG3	1.96	0.47
1:A:294:VAL:HG11	1:A:301:LYS:HE3	1.96	0.46
1:B:9:ALA:HB2	1:B:49:TYR:HB2	1.96	0.46
1:A:127:GLN:NE2	1:B:169:ASP:OD2	2.36	0.46
1:B:147:ILE:HG23	1:B:183:ILE:HD13	1.96	0.46
1:D:9:ALA:HB2	1:D:49:TYR:HB2	1.96	0.46
1:G:9:ALA:HB2	1:G:49:TYR:HB2	1.97	0.46
1:F:134:LEU:HD23	1:G:134:LEU:HD23	1.98	0.46
1:H:9:ALA:HB2	1:H:49:TYR:HB2	1.98	0.46
1:E:6:VAL:HG23	1:E:352:GLU:OE2	2.16	0.46
1:G:118:VAL:HG12	1:G:120:GLY:H	1.80	0.46
1:D:118:VAL:HG12	1:D:120:GLY:H	1.80	0.46
1:C:188:SER:O	1:C:193:ARG:NH1	2.49	0.46
1:D:185:GLN:NE2	1:D:192:ALA:O	2.44	0.46
1:A:147:ILE:HG23	1:A:183:ILE:HD13	1.96	0.45
1:G:151:ARG:NH2	1:G:199:VAL:O	2.40	0.45
1:B:159:PHE:CZ	1:B:161:PHE:HB2	2.52	0.45
1:H:106:ASP:CG	1:H:111:GLY:HA2	2.42	0.45
1:F:217:VAL:HG11	1:F:322:GLY:HA3	1.98	0.45
1:A:9:ALA:HB2	1:A:49:TYR:HB2	1.99	0.45
1:D:152:GLY:HA3	1:D:159:PHE:CE1	2.51	0.45
1:E:24:ILE:HD13	1:E:331:LEU:HD21	1.99	0.45
1:A:19:LEU:H	1:A:26:GLN:HE22	1.65	0.45
1:A:28:THR:HG21	1:A:333:PHE:HD2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:SER:O	1:A:193:ARG:HG2	2.17	0.44
1:B:45:ALA:HB1	1:B:341:GLY:HA3	1.98	0.44
1:H:189:SER:O	1:H:193:ARG:HG2	2.18	0.44
1:B:249:LYS:HE3	1:B:249:LYS:HB2	1.86	0.44
1:E:100:LYS:NZ	1:F:65:GLN:O	2.43	0.44
1:F:189:SER:O	1:F:193:ARG:HG2	2.17	0.44
1:B:55:ARG:HB2	1:B:65:GLN:HG2	2.00	0.44
1:D:15:VAL:HG12	1:D:65:GLN:HB3	1.99	0.44
1:H:185:GLN:NE2	1:H:192:ALA:O	2.39	0.44
1:B:19:LEU:HD12	1:B:296:TYR:HE2	1.82	0.43
1:E:19:LEU:HB3	1:E:26:GLN:HE22	1.82	0.43
1:E:164:ASP:OD1	1:G:162:ARG:NH2	2.42	0.43
1:F:127:GLN:NE2	1:G:164:ASP:OD2	2.50	0.43
1:H:34:TYR:O	1:H:334:GLN:NE2	2.48	0.43
1:A:104:THR:O	1:A:108:LEU:HG	2.19	0.43
1:F:152:GLY:HA3	1:F:159:PHE:CE1	2.54	0.43
1:D:248:ALA:HB1	1:D:305:ILE:HG22	1.99	0.43
1:F:106:ASP:CG	1:F:111:GLY:HA2	2.44	0.43
1:E:189:SER:O	1:E:193:ARG:HG2	2.18	0.43
1:F:185:GLN:NE2	1:F:192:ALA:O	2.41	0.43
1:H:153:ILE:HD11	1:H:168:PHE:CZ	2.54	0.42
1:G:240:ILE:HB	1:G:305:ILE:HG22	2.01	0.42
1:H:217:VAL:HG22	1:H:233:ILE:HG21	2.01	0.42
1:D:159:PHE:CZ	1:D:161:PHE:HB2	2.55	0.42
1:F:34:TYR:CZ	1:F:334:GLN:HG3	2.55	0.42
1:G:28:THR:HG21	1:G:333:PHE:HD2	1.84	0.42
1:B:118:VAL:HG12	1:B:120:GLY:H	1.84	0.42
1:G:339:TYR:CE1	1:G:343:ARG:HG3	2.55	0.42
1:F:193:ARG:HB2	1:F:220:ILE:HD11	2.01	0.41
1:D:31:GLY:O	1:D:35:ASN:ND2	2.47	0.41
1:B:104:THR:O	1:B:108:LEU:HG	2.20	0.41
1:E:19:LEU:HB3	1:E:26:GLN:NE2	2.36	0.41
1:B:301:LYS:HE2	1:B:301:LYS:HB3	1.95	0.41
1:C:134:LEU:HB2	1:C:139:ARG:HG2	2.03	0.41
1:E:159:PHE:CZ	1:E:161:PHE:HB2	2.55	0.41
1:F:8:PHE:HE2	1:F:349:ARG:HH12	1.69	0.41
1:A:185:GLN:NE2	1:A:192:ALA:O	2.42	0.41
1:D:104:THR:O	1:D:108:LEU:HG	2.20	0.40
1:H:203:TYR:CD2	1:H:220:ILE:HD13	2.56	0.40
1:D:106:ASP:CG	1:D:111:GLY:HA2	2.47	0.40
1:F:90:PRO:HD2	1:F:118:VAL:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:316:VAL:HG21	1:F:351:LEU:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	317/387 (82%)	312 (98%)	5 (2%)	0	100	100
1	B	328/387 (85%)	326 (99%)	2 (1%)	0	100	100
1	C	314/387 (81%)	311 (99%)	3 (1%)	0	100	100
1	D	297/387 (77%)	295 (99%)	2 (1%)	0	100	100
1	E	323/387 (84%)	321 (99%)	2 (1%)	0	100	100
1	F	321/387 (83%)	317 (99%)	4 (1%)	0	100	100
1	G	287/387 (74%)	285 (99%)	2 (1%)	0	100	100
1	H	301/387 (78%)	298 (99%)	3 (1%)	0	100	100
All	All	2488/3096 (80%)	2465 (99%)	23 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	249/303 (82%)	246 (99%)	3 (1%)	63	83
1	B	252/303 (83%)	247 (98%)	5 (2%)	48	74
1	C	228/303 (75%)	224 (98%)	4 (2%)	51	76
1	D	223/303 (74%)	221 (99%)	2 (1%)	70	87
1	E	248/303 (82%)	245 (99%)	3 (1%)	63	83
1	F	244/303 (80%)	241 (99%)	3 (1%)	63	83
1	G	223/303 (74%)	222 (100%)	1 (0%)	84	93
1	H	221/303 (73%)	220 (100%)	1 (0%)	81	92
All	All	1888/2424 (78%)	1866 (99%)	22 (1%)	63	83

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	210	VAL
1	A	307	THR
1	A	345	LEU
1	B	121	TRP
1	B	210	VAL
1	B	244	THR
1	B	307	THR
1	B	345	LEU
1	C	121	TRP
1	C	244	THR
1	C	307	THR
1	C	345	LEU
1	D	244	THR
1	D	307	THR
1	E	210	VAL
1	E	244	THR
1	E	335	GLU
1	F	220	ILE
1	F	244	THR
1	F	307	THR
1	G	180	ARG
1	H	244	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	4	GLN
1	A	94	GLN
1	A	295	GLN
1	A	356	GLN
1	B	156	GLN
1	B	216	GLN
1	C	94	GLN
1	C	216	GLN
1	D	156	GLN
1	D	206	ASN
1	E	73	HIS
1	E	94	GLN
1	E	295	GLN
1	F	66	HIS
1	F	81	GLN
1	F	156	GLN
1	F	216	GLN
1	F	303	ASN
1	G	94	GLN
1	H	94	GLN
1	H	216	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

20 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	$\# Z > 2$
2	SO4	F	503	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	C	502	-	4,4,4	0.23	0	6,6,6	0.14	0
2	SO4	A	501	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	D	502	-	4,4,4	0.24	0	6,6,6	0.12	0
2	SO4	A	502	-	4,4,4	0.24	0	6,6,6	0.05	0
2	SO4	F	502	-	4,4,4	0.23	0	6,6,6	0.09	0
2	SO4	H	502	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	F	501	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	E	501	-	4,4,4	0.23	0	6,6,6	0.06	0
2	SO4	E	502	-	4,4,4	0.23	0	6,6,6	0.09	0
2	SO4	G	503	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	B	503	-	4,4,4	0.23	0	6,6,6	0.11	0
2	SO4	G	502	-	4,4,4	0.26	0	6,6,6	0.11	0
2	SO4	C	501	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	D	501	-	4,4,4	0.25	0	6,6,6	0.08	0
2	SO4	G	501	-	4,4,4	0.23	0	6,6,6	0.14	0
2	SO4	B	501	-	4,4,4	0.23	0	6,6,6	0.05	0
2	SO4	D	503	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	H	501	-	4,4,4	0.25	0	6,6,6	0.05	0
2	SO4	B	502	-	4,4,4	0.24	0	6,6,6	0.08	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	323/387 (83%)	0.15	8 (2%)	58	52	41, 64, 95, 120	0
1	B	330/387 (85%)	0.09	8 (2%)	59	54	32, 59, 103, 127	2 (0%)
1	C	319/387 (82%)	0.50	11 (3%)	48	42	46, 78, 115, 126	1 (0%)
1	D	304/387 (78%)	0.49	13 (4%)	40	34	30, 74, 109, 119	1 (0%)
1	E	329/387 (85%)	0.10	8 (2%)	59	54	43, 60, 109, 126	0
1	F	324/387 (83%)	0.42	16 (4%)	35	29	31, 74, 113, 129	1 (0%)
1	G	295/387 (76%)	0.56	17 (5%)	29	23	47, 74, 117, 125	0
1	H	306/387 (79%)	0.60	16 (5%)	33	27	38, 81, 119, 129	1 (0%)
All	All	2530/3096 (81%)	0.36	97 (3%)	44	38	30, 69, 113, 129	6 (0%)

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	60	TYR	5.4
1	B	260	ASP	4.0
1	H	24	ILE	4.0
1	E	121	TRP	4.0
1	C	210	VAL	3.8
1	H	121	TRP	3.8
1	B	58	ALA	3.7
1	A	358	ALA	3.7
1	H	206	ASN	3.7
1	E	361	ALA	3.6
1	F	121	TRP	3.5
1	H	256	ILE	3.5
1	A	19	LEU	3.4
1	A	20	VAL	3.3
1	E	122	PHE	3.3
1	G	59	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	F	24	ILE	3.2
1	C	121	TRP	3.1
1	G	121	TRP	3.0
1	F	27	ARG	2.9
1	D	59	GLY	2.9
1	A	17	GLY	2.9
1	H	123[A]	ARG	2.9
1	B	295	GLN	2.8
1	H	323	VAL	2.8
1	H	19	LEU	2.8
1	E	60	TYR	2.7
1	A	121	TRP	2.7
1	F	291	GLU	2.6
1	D	16	SER	2.6
1	F	316	VAL	2.6
1	G	5	ALA	2.6
1	A	259	ALA	2.6
1	D	344	VAL	2.6
1	D	300	PHE	2.6
1	D	355	ALA	2.6
1	E	58	ALA	2.6
1	F	28	THR	2.5
1	G	16	SER	2.5
1	D	178	LEU	2.5
1	F	211	GLU	2.5
1	D	303	ASN	2.5
1	D	257	ASP	2.5
1	E	18	GLY	2.4
1	F	345	LEU	2.4
1	B	121	TRP	2.4
1	C	21	VAL	2.4
1	C	344	VAL	2.4
1	C	26	GLN	2.4
1	D	240	ILE	2.4
1	H	338	GLU	2.4
1	F	21	VAL	2.4
1	F	355	ALA	2.4
1	A	18	GLY	2.3
1	G	58	ALA	2.3
1	H	5	ALA	2.3
1	C	331	LEU	2.3
1	G	210	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	355	ALA	2.2
1	G	255	ILE	2.2
1	C	350	GLU	2.2
1	C	24	ILE	2.2
1	E	64	PHE	2.2
1	F	240	ILE	2.2
1	G	30	TRP	2.2
1	E	25	GLU	2.2
1	H	350	GLU	2.2
1	H	23	ARG	2.2
1	F	19	LEU	2.2
1	G	242	ARG	2.1
1	C	251	VAL	2.1
1	H	22	SER	2.1
1	H	313	GLU	2.1
1	D	307	THR	2.1
1	G	28	THR	2.1
1	B	21	VAL	2.1
1	C	255	ILE	2.1
1	G	246	GLU	2.1
1	B	28	THR	2.1
1	G	342	GLN	2.1
1	H	254	GLN	2.1
1	D	255	ILE	2.1
1	F	210	VAL	2.1
1	G	344	VAL	2.1
1	D	63	GLU	2.0
1	F	25	GLU	2.0
1	A	357	SER	2.0
1	D	15	VAL	2.0
1	G	62	ALA	2.0
1	F	155	SER	2.0
1	G	252	LEU	2.0
1	G	345	LEU	2.0
1	G	351	LEU	2.0
1	B	206	ASN	2.0
1	H	208	ASN	2.0
1	H	21	VAL	2.0
1	F	296	TYR	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 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($\text{\AA}^2$)	Q<0.9
2	SO4	B	503	5/5	0.65	0.13	69,74,101,104	5
2	SO4	F	503	5/5	0.75	0.11	83,84,94,97	5
2	SO4	G	503	5/5	0.81	0.12	66,82,87,94	5
2	SO4	G	502	5/5	0.84	0.13	56,58,67,75	5
2	SO4	D	503	5/5	0.88	0.09	79,80,93,93	5
2	SO4	F	502	5/5	0.89	0.10	60,66,69,78	5
2	SO4	A	502	5/5	0.90	0.11	67,68,72,79	5
2	SO4	D	502	5/5	0.91	0.10	64,71,86,96	5
2	SO4	C	502	5/5	0.91	0.10	54,63,68,70	5
2	SO4	E	502	5/5	0.92	0.10	58,62,79,81	5
2	SO4	B	502	5/5	0.94	0.11	51,59,73,81	5
2	SO4	C	501	5/5	0.94	0.09	67,67,75,76	0
2	SO4	D	501	5/5	0.95	0.07	57,57,68,70	0
2	SO4	A	501	5/5	0.95	0.06	52,60,62,68	0
2	SO4	H	502	5/5	0.95	0.08	69,70,77,81	5
2	SO4	H	501	5/5	0.96	0.06	62,74,80,83	0
2	SO4	B	501	5/5	0.96	0.08	53,55,57,64	0
2	SO4	E	501	5/5	0.97	0.06	49,62,63,64	0
2	SO4	F	501	5/5	0.98	0.04	51,55,67,70	0
2	SO4	G	501	5/5	0.98	0.06	54,55,67,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.