



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 10:26 AM UTC

PDB ID : 5W79 / pdb_00005w79
Title : Crystal Structure of the Group II Chaperonin from Methanococcus Maripaludis, Cysteine-less mutant in the Apo State
Authors : Dalton, K.M.; Lopez, T.; Liu, C.; Ralston, C.Y.; Pereira, J.H.; Chartron, J.W.; McAndrew, R.P.; Douglas, N.R.; Adams, P.D.; Pande, V.S.; Frydman, J.
Deposited on : 2017-06-19
Resolution : 3.12 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

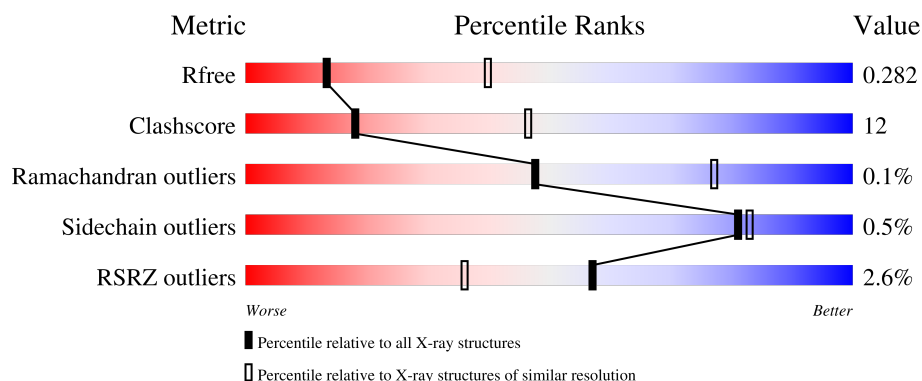
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.12 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	1816 (3.14-3.10)
Clashscore	190562	1906 (3.14-3.10)
Ramachandran outliers	187476	1802 (3.14-3.10)
Sidechain outliers	187428	1802 (3.14-3.10)
RSRZ outliers	180081	1816 (3.14-3.10)

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	543	2% 68% 27% 5%
1	B	543	3% 72% 22% 5%
1	C	543	2% 68% 27% 5%
1	D	543	2% 70% 25% 5%

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Mol	Chain	Length	Quality of chain		
1	E	543	 3%70%24%5%		
1	F	543	 2%69%26%5%		
1	G	543	 3%70%25%5%		
1	H	543	 2%70%25%5%		

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 31143 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 Chaperonin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	515	Total	C	N	O	S	0	0	0
			3887	2419	670	778	20			
1	B	515	Total	C	N	O	S	0	0	0
			3887	2419	670	778	20			
1	C	515	Total	C	N	O	S	0	0	0
			3887	2419	670	778	20			
1	D	515	Total	C	N	O	S	0	0	0
			3887	2419	670	778	20			
1	E	515	Total	C	N	O	S	0	0	0
			3887	2419	670	778	20			
1	F	515	Total	C	N	O	S	0	0	0
			3887	2419	670	778	20			
1	G	515	Total	C	N	O	S	0	0	0
			3887	2419	670	778	20			
1	H	515	Total	C	N	O	S	0	0	0
			3887	2419	670	778	20			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	140	MET	CYS	engineered mutation	UNP Q877G8
A	237	GLU	CYS	engineered mutation	UNP Q877G8
A	286	VAL	CYS	engineered mutation	UNP Q877G8
A	304	MET	VAL	engineered mutation	UNP Q877G8
A	359	VAL	CYS	engineered mutation	UNP Q877G8
A	393	SER	CYS	engineered mutation	UNP Q877G8
A	470	TYR	CYS	engineered mutation	UNP Q877G8
A	484	THR	CYS	engineered mutation	UNP Q877G8
B	140	MET	CYS	engineered mutation	UNP Q877G8
B	237	GLU	CYS	engineered mutation	UNP Q877G8
B	286	VAL	CYS	engineered mutation	UNP Q877G8
B	304	MET	VAL	engineered mutation	UNP Q877G8
B	359	VAL	CYS	engineered mutation	UNP Q877G8

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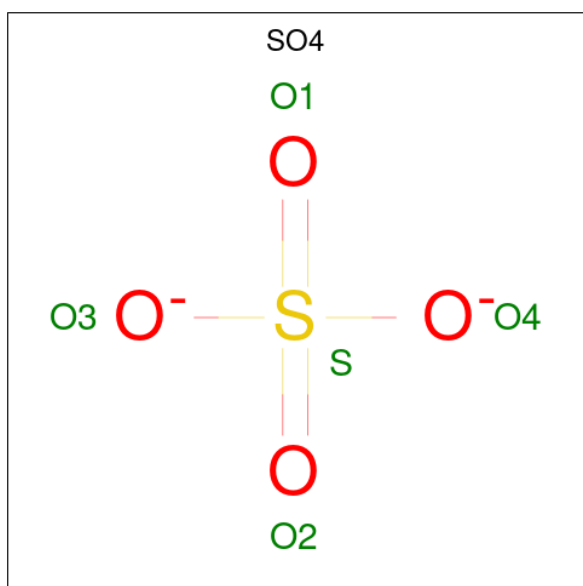
Chain	Residue	Modelled	Actual	Comment	Reference
B	393	SER	CYS	engineered mutation	UNP Q877G8
B	470	TYR	CYS	engineered mutation	UNP Q877G8
B	484	THR	CYS	engineered mutation	UNP Q877G8
C	140	MET	CYS	engineered mutation	UNP Q877G8
C	237	GLU	CYS	engineered mutation	UNP Q877G8
C	286	VAL	CYS	engineered mutation	UNP Q877G8
C	304	MET	VAL	engineered mutation	UNP Q877G8
C	359	VAL	CYS	engineered mutation	UNP Q877G8
C	393	SER	CYS	engineered mutation	UNP Q877G8
C	470	TYR	CYS	engineered mutation	UNP Q877G8
C	484	THR	CYS	engineered mutation	UNP Q877G8
D	140	MET	CYS	engineered mutation	UNP Q877G8
D	237	GLU	CYS	engineered mutation	UNP Q877G8
D	286	VAL	CYS	engineered mutation	UNP Q877G8
D	304	MET	VAL	engineered mutation	UNP Q877G8
D	359	VAL	CYS	engineered mutation	UNP Q877G8
D	393	SER	CYS	engineered mutation	UNP Q877G8
D	470	TYR	CYS	engineered mutation	UNP Q877G8
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E	237	GLU	CYS	engineered mutation	UNP Q877G8
E	286	VAL	CYS	engineered mutation	UNP Q877G8
E	304	MET	VAL	engineered mutation	UNP Q877G8
E	359	VAL	CYS	engineered mutation	UNP Q877G8
E	393	SER	CYS	engineered mutation	UNP Q877G8
E	470	TYR	CYS	engineered mutation	UNP Q877G8
E	484	THR	CYS	engineered mutation	UNP Q877G8
F	140	MET	CYS	engineered mutation	UNP Q877G8
F	237	GLU	CYS	engineered mutation	UNP Q877G8
F	286	VAL	CYS	engineered mutation	UNP Q877G8
F	304	MET	VAL	engineered mutation	UNP Q877G8
F	359	VAL	CYS	engineered mutation	UNP Q877G8
F	393	SER	CYS	engineered mutation	UNP Q877G8
F	470	TYR	CYS	engineered mutation	UNP Q877G8
F	484	THR	CYS	engineered mutation	UNP Q877G8
G	140	MET	CYS	engineered mutation	UNP Q877G8
G	237	GLU	CYS	engineered mutation	UNP Q877G8
G	286	VAL	CYS	engineered mutation	UNP Q877G8
G	304	MET	VAL	engineered mutation	UNP Q877G8
G	359	VAL	CYS	engineered mutation	UNP Q877G8
G	393	SER	CYS	engineered mutation	UNP Q877G8
G	470	TYR	CYS	engineered mutation	UNP Q877G8

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Chain	Residue	Modelled	Actual	Comment	Reference
G	484	THR	CYS	engineered mutation	UNP Q877G8
H	140	MET	CYS	engineered mutation	UNP Q877G8
H	237	GLU	CYS	engineered mutation	UNP Q877G8
H	286	VAL	CYS	engineered mutation	UNP Q877G8
H	304	MET	VAL	engineered mutation	UNP Q877G8
H	359	VAL	CYS	engineered mutation	UNP Q877G8
H	393	SER	CYS	engineered mutation	UNP Q877G8
H	470	TYR	CYS	engineered mutation	UNP Q877G8
H	484	THR	CYS	engineered mutation	UNP Q877G8

- 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	B	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	E	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		

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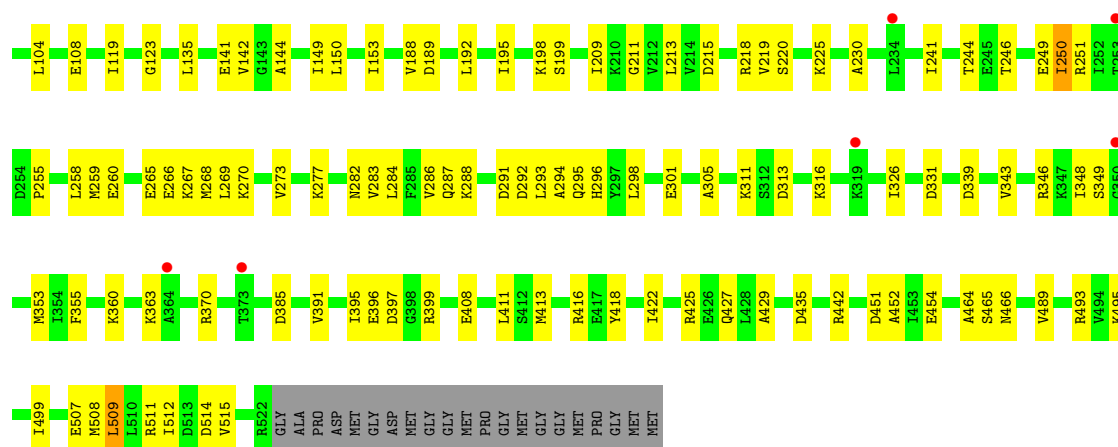
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

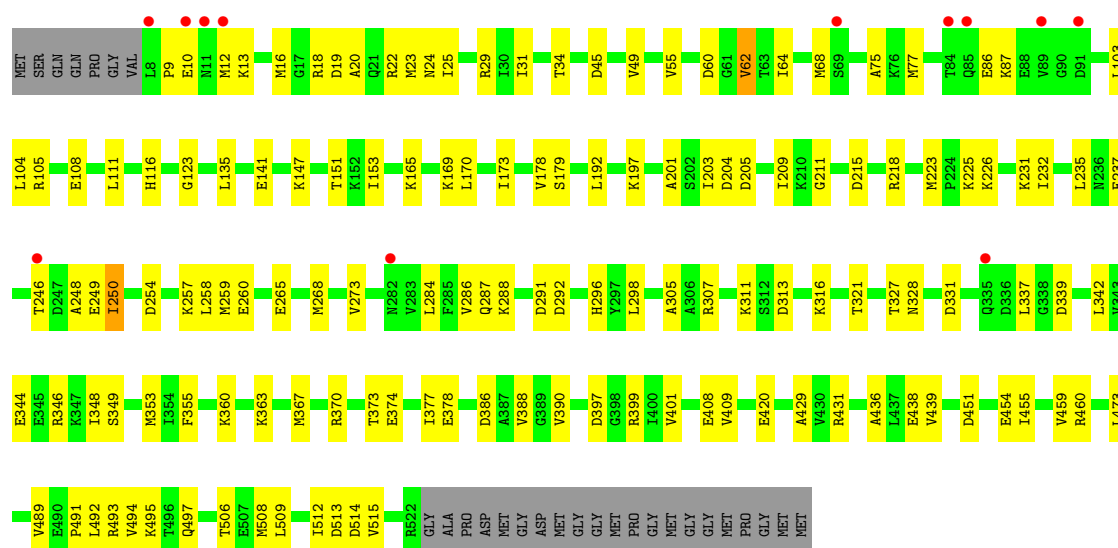
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O	0	0
			1	1		
3	C	1	Total	O	0	0
			1	1		
3	D	1	Total	O	0	0
			1	1		
3	E	1	Total	O	0	0
			1	1		
3	F	1	Total	O	0	0
			1	1		
3	G	1	Total	O	0	0
			1	1		
3	H	1	Total	O	0	0
			1	1		

Chain C: 2% 68% 27% 5%

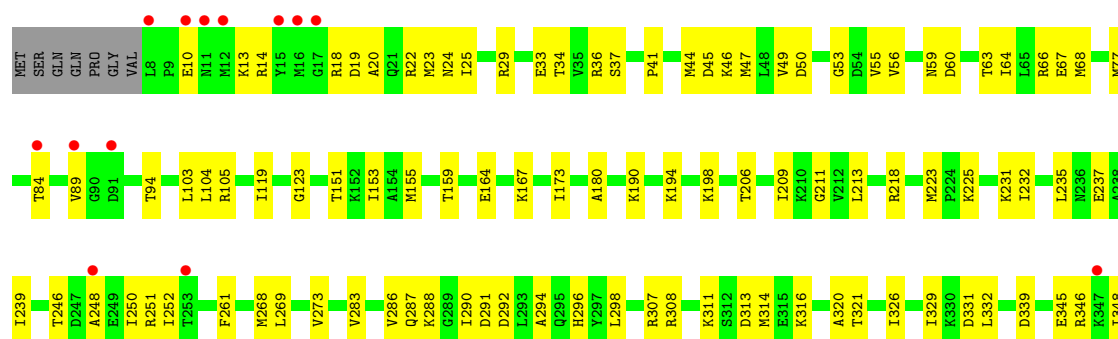


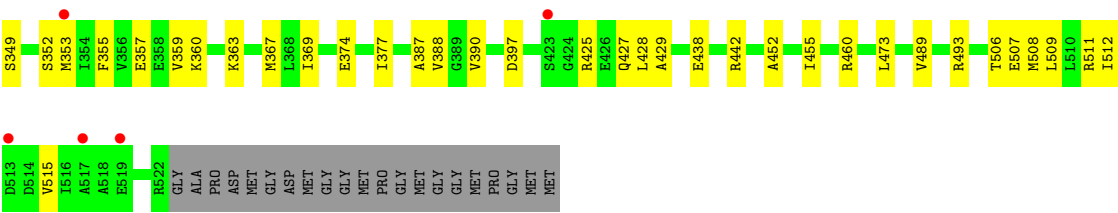


• Molecule 1: Chaperonin

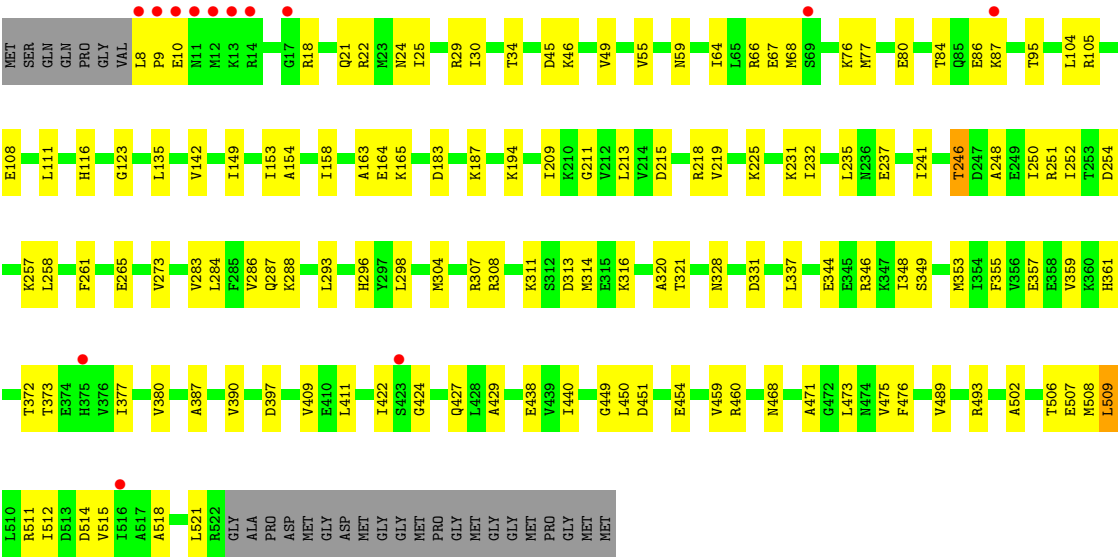


• Molecule 1: Chaperonin





● Molecule 1: Chaperonin



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	149.98Å 149.98Å 416.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	81.24 – 3.12 81.24 – 3.12	Depositor EDS
% Data completeness (in resolution range)	99.0 (81.24-3.12) 98.9 (81.24-3.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 3.13Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.249 , 0.281 0.250 , 0.282	Depositor DCC
R_{free} test set	4945 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	73.3	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	31143	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.06% 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	0.38	0/3911	0.59	0/5262
1	B	0.36	0/3911	0.57	1/5262 (0.0%)
1	C	0.37	0/3911	0.55	0/5262
1	D	0.39	0/3911	0.58	0/5262
1	E	0.43	1/3911 (0.0%)	0.57	0/5262
1	F	0.37	0/3911	0.56	0/5262
1	G	0.38	0/3911	0.56	1/5262 (0.0%)
1	H	0.39	0/3911	0.58	1/5262 (0.0%)
All	All	0.39	1/31288 (0.0%)	0.57	3/42096 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	92	GLY	C-O	12.55	1.33	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	497	GLN	CA-CB-CG	7.00	128.10	114.10
1	H	165	LYS	N-CA-C	-6.44	97.08	110.80
1	G	59	ASN	CB-CA-C	-6.31	97.60	109.72

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	3887	0	4039	117	0
1	B	3887	0	4040	99	0
1	C	3887	0	4040	107	0
1	D	3887	0	4040	105	0
1	E	3887	0	4040	112	0
1	F	3887	0	4040	104	0
1	G	3887	0	4040	111	0
1	H	3887	0	4040	124	0
2	A	5	0	0	0	0
2	B	5	0	0	1	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	1	0
2	F	5	0	0	0	0
2	G	5	0	0	1	0
2	H	5	0	0	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
All	All	31143	0	32319	773	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 12.

The worst 5 of 773 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:408:GLU:OE2	1:D:495:LYS:NZ	1.92	1.03
1:H:34:THR:O	1:H:46:LYS:NZ	1.94	1.00
1:H:218:ARG:HH22	1:H:225:LYS:HZ3	1.02	0.97
1:F:344:GLU:OE1	1:F:346:ARG:NH1	1.99	0.95
1:C:408:GLU:OE2	1:C:495:LYS:NZ	2.01	0.91

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	513/543 (94%)	501 (98%)	12 (2%)	0	100	100
1	B	513/543 (94%)	499 (97%)	13 (2%)	1 (0%)	43	71
1	C	513/543 (94%)	504 (98%)	9 (2%)	0	100	100
1	D	513/543 (94%)	502 (98%)	9 (2%)	2 (0%)	30	60
1	E	513/543 (94%)	503 (98%)	10 (2%)	0	100	100
1	F	513/543 (94%)	503 (98%)	10 (2%)	0	100	100
1	G	513/543 (94%)	500 (98%)	13 (2%)	0	100	100
1	H	513/543 (94%)	504 (98%)	9 (2%)	0	100	100
All	All	4104/4344 (94%)	4016 (98%)	85 (2%)	3 (0%)	48	77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	88	GLU
1	D	350	GLY
1	B	353	MET

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	416/434 (96%)	415 (100%)	1 (0%)	87	87
1	B	416/434 (96%)	414 (100%)	2 (0%)	81	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	416/434 (96%)	413 (99%)	3 (1%)	76	80
1	D	416/434 (96%)	412 (99%)	4 (1%)	68	77
1	E	416/434 (96%)	414 (100%)	2 (0%)	81	83
1	F	416/434 (96%)	414 (100%)	2 (0%)	81	83
1	G	416/434 (96%)	416 (100%)	0	100	100
1	H	416/434 (96%)	413 (99%)	3 (1%)	76	80
All	All	3328/3472 (96%)	3311 (100%)	17 (0%)	81	83

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	246	THR
1	H	509	LEU
1	D	241	ILE
1	D	390	VAL
1	D	509	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	375	HIS
1	G	375	HIS
1	G	324	ASN
1	G	500	GLN
1	B	324	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	E	601	-	4,4,4	0.21	0	6,6,6	0.16	0
2	SO4	C	601	-	4,4,4	0.27	0	6,6,6	0.17	0
2	SO4	G	601	-	4,4,4	0.22	0	6,6,6	0.11	0
2	SO4	D	601	-	4,4,4	0.22	0	6,6,6	0.05	0
2	SO4	F	601	-	4,4,4	0.22	0	6,6,6	0.14	0
2	SO4	B	601	-	4,4,4	0.23	0	6,6,6	0.13	0
2	SO4	A	601	-	4,4,4	0.22	0	6,6,6	0.12	0
2	SO4	H	601	-	4,4,4	0.25	0	6,6,6	0.06	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.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	601	SO4	1	0
2	G	601	SO4	1	0
2	B	601	SO4	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	515/543 (94%)	0.24	12 (2%) 61 39	39, 59, 93, 102	0
1	B	515/543 (94%)	0.29	17 (3%) 49 29	39, 66, 96, 108	0
1	C	515/543 (94%)	0.18	9 (1%) 69 48	39, 64, 85, 100	0
1	D	515/543 (94%)	0.17	11 (2%) 63 42	36, 61, 83, 94	0
1	E	515/543 (94%)	0.31	16 (3%) 51 31	39, 67, 94, 106	0
1	F	515/543 (94%)	0.15	12 (2%) 61 39	41, 64, 82, 99	0
1	G	515/543 (94%)	0.25	18 (3%) 47 27	43, 68, 87, 100	0
1	H	515/543 (94%)	0.23	13 (2%) 58 37	40, 63, 87, 101	0
All	All	4120/4344 (94%)	0.23	108 (2%) 57 36	36, 64, 91, 108	0

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	11	ASN	5.1
1	B	11	ASN	4.5
1	E	86	GLU	4.2
1	D	11	ASN	4.0
1	H	8	LEU	3.8

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	E	601	5/5	0.69	0.17	77,78,79,79	0
2	SO4	G	601	5/5	0.80	0.16	71,72,72,73	0
2	SO4	B	601	5/5	0.81	0.16	73,74,75,76	0
2	SO4	H	601	5/5	0.82	0.16	84,84,85,85	0
2	SO4	D	601	5/5	0.83	0.21	75,76,77,77	0
2	SO4	C	601	5/5	0.86	0.18	61,62,63,63	0
2	SO4	F	601	5/5	0.86	0.16	67,67,69,69	0
2	SO4	A	601	5/5	0.89	0.14	59,59,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.