



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 14, 2020 – 11:16 am BST

PDB ID : 2JD7
Title : Crystal Structure of the Fe-soaked Ferritin from the Hyperthermophilic Archaeal Anaerobe *Pyrococcus furiosus*
Authors : Tatur, J.; Hagen, W.R.; Matias, P.M.
Deposited on : 2007-01-05
Resolution : 2.80 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

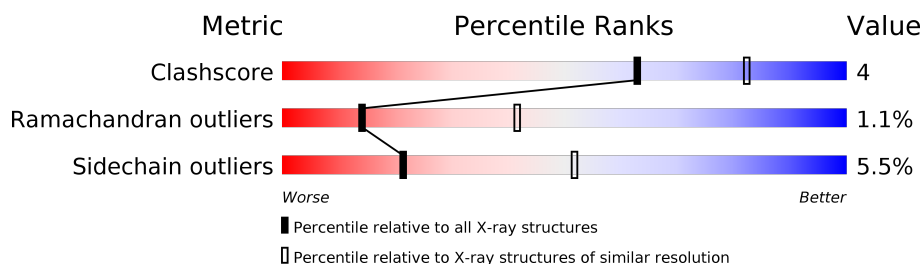
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)


























The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	0	174	79% 16% . .
1	1	174	79% 17% .
1	2	174	81% 12% . .
1	3	174	82% 12% . .
1	4	174	83% 12% . .
1	5	174	90% 6% . .
1	6	174	85% 10% . .
1	7	174	79% 13% . .




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Mol	Chain	Length	Quality of chain
1	8	174	 83% 11% . .
1	9	174	 80% 14% . .
1	A	174	 84% 10% . .
1	B	174	 82% 12% . .
1	C	174	 84% 11% . .
1	D	174	 84% 10% . .
1	E	174	 82% 12% . .
1	F	174	 81% 13% . .
1	G	174	 88% 7% . .
1	H	174	 76% 17% . .
1	I	174	 78% 15% . .
1	J	174	 90% 5% . .
1	K	174	 85% 10% . .
1	L	174	 87% 9% . .
1	M	174	 75% 21% . .
1	N	174	 83% 10% . .
1	O	174	 74% 20% . .
1	P	174	 76% 18% . .
1	Q	174	 82% 13% . .
1	R	174	 84% 10% . .
1	S	174	 84% 11% . .
1	T	174	 85% 10% . .
1	U	174	 88% 7% . .
1	V	174	 82% 11% . . .
1	W	174	 84% 10% . .

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Mol	Chain	Length	Quality of chain
1	X	174	 87% 9% . .
1	Y	174	 81% 14% . .
1	Z	174	 80% 16% . .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 50409 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 FERRITIN HOMOLOG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	1	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	2	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	3	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	4	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	5	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	6	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	7	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	8	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	9	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	A	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	B	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	C	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	D	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	E	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	F	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	167	Total	C	N	O	S	0	1	0
			1388	900	221	262	5			
1	H	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	I	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	J	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	K	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	L	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	M	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	N	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	O	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	P	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	Q	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	R	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	S	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	T	167	Total	C	N	O	S	0	1	0
			1388	900	221	262	5			
1	U	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	V	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	W	167	Total	C	N	O	S	0	1	0
			1388	900	221	262	5			
1	X	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	Y	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			
1	Z	167	Total	C	N	O	S	0	0	0
			1383	897	220	261	5			

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

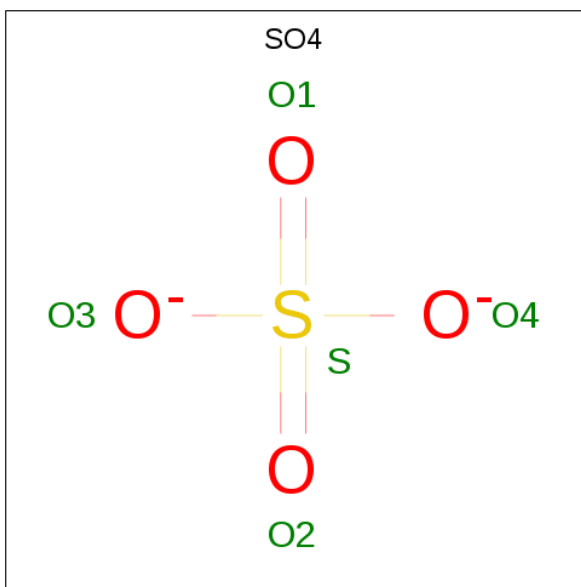
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	P	3	Total Fe 3 3	0	0
2	K	3	Total Fe 3 3	0	0
2	B	3	Total Fe 3 3	0	0
2	6	3	Total Fe 3 3	0	0
2	W	3	Total Fe 3 3	0	0
2	N	3	Total Fe 3 3	0	0
2	X	3	Total Fe 3 3	0	0
2	2	3	Total Fe 3 3	0	0
2	S	3	Total Fe 3 3	0	0
2	J	3	Total Fe 3 3	0	0
2	E	3	Total Fe 3 3	0	0
2	V	3	Total Fe 3 3	0	0
2	A	3	Total Fe 3 3	0	0
2	5	3	Total Fe 3 3	0	0
2	R	3	Total Fe 3 3	0	0
2	M	3	Total Fe 3 3	0	0
2	1	3	Total Fe 3 3	0	0
2	D	3	Total Fe 3 3	0	0
2	I	3	Total Fe 3 3	0	0
2	Z	3	Total Fe 3 3	0	0
2	4	3	Total Fe 3 3	0	0
2	U	3	Total Fe 3 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	9	3	Total 3	Fe 3	0	0
2	L	3	Total 3	Fe 3	0	0
2	0	3	Total 3	Fe 3	0	0
2	G	3	Total 3	Fe 3	0	0
2	Q	3	Total 3	Fe 3	0	0
2	H	3	Total 3	Fe 3	0	0
2	C	3	Total 3	Fe 3	0	0
2	7	3	Total 3	Fe 3	0	0
2	T	3	Total 3	Fe 3	0	0
2	8	3	Total 3	Fe 3	0	0
2	O	3	Total 3	Fe 3	0	0
2	Y	3	Total 3	Fe 3	0	0
2	3	3	Total 3	Fe 3	0	0
2	F	3	Total 3	Fe 3	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	1	1	Total	O	S	0	0
			5	4	1		
3	2	1	Total	O	S	0	0
			5	4	1		
3	3	1	Total	O	S	0	0
			5	4	1		
3	3	1	Total	O	S	0	0
			5	4	1		
3	8	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	I	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	O	1	Total	O	S	0	0
			5	4	1		
3	R	1	Total	O	S	0	0
			5	4	1		
3	S	1	Total	O	S	0	0
			5	4	1		
3	T	1	Total	O	S	0	0
			5	4	1		
3	V	1	Total	O	S	0	0
			5	4	1		
3	V	1	Total	O	S	0	0
			5	4	1		
3	W	1	Total	O	S	0	0
			5	4	1		
3	Y	1	Total	O	S	0	0
			5	4	1		
3	Y	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	0	7	Total	O	0	0
			7	7		
4	1	10	Total	O	0	0
			10	10		
4	2	7	Total	O	0	0
			7	7		
4	3	15	Total	O	0	0
			15	15		
4	4	8	Total	O	0	0
			8	8		
4	5	5	Total	O	0	0
			5	5		
4	6	8	Total	O	0	0
			8	8		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	7	11	Total O 11 11	0	0
4	8	9	Total O 9 9	0	0
4	9	7	Total O 7 7	0	0
4	A	13	Total O 13 13	0	0
4	B	17	Total O 17 17	0	0
4	C	8	Total O 8 8	0	0
4	D	16	Total O 16 16	0	0
4	E	18	Total O 18 18	0	0
4	F	21	Total O 21 21	0	0
4	G	14	Total O 14 14	0	0
4	H	2	Total O 2 2	0	0
4	I	5	Total O 5 5	0	0
4	J	16	Total O 16 16	0	0
4	K	4	Total O 4 4	0	0
4	L	9	Total O 9 9	0	0
4	M	11	Total O 11 11	0	0
4	N	3	Total O 3 3	0	0
4	O	5	Total O 5 5	0	0
4	P	5	Total O 5 5	0	0
4	Q	9	Total O 9 9	0	0
4	R	5	Total O 5 5	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	S	17	Total 17	O 17	0	0
4	T	13	Total 13	O 13	0	0
4	U	18	Total 18	O 18	0	0
4	V	13	Total 13	O 13	0	0
4	W	9	Total 9	O 9	0	0
4	X	14	Total 14	O 14	0	0
4	Y	11	Total 11	O 11	0	0
4	Z	5	Total 5	O 5	0	0

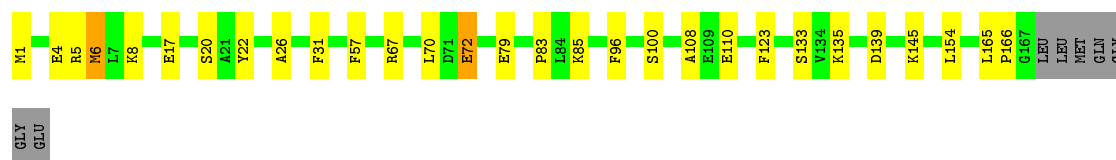
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.


Note EDS was not executed.

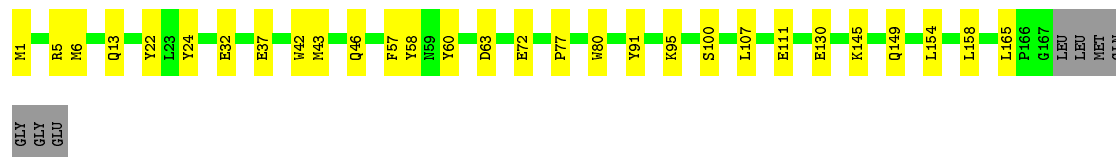
• Molecule 1: FERRITIN HOMOLOG

Chain 0: 




• Molecule 1: FERRITIN HOMOLOG

Chain 1: 




• Molecule 1: FERRITIN HOMOLOG

Chain 2: 




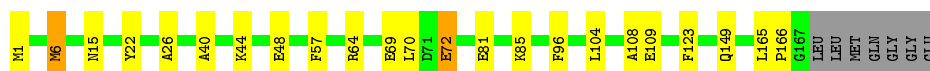
• Molecule 1: FERRITIN HOMOLOG

Chain 3: 



• Molecule 1: FERRITIN HOMOLOG

Chain 4: 



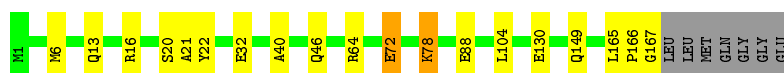
• Molecule 1: FERRITIN HOMOLOG

Chain 5: 90% 6% . .



• Molecule 1: FERRITIN HOMOLOG

Chain 6: 85% 10% . .



• Molecule 1: FERRITIN HOMOLOG

Chain 7: 79% 13% . .



• Molecule 1: FERRITIN HOMOLOG

Chain 8: 83% 11% . .



• Molecule 1: FERRITIN HOMOLOG

Chain 9: 80% 14% . .



• Molecule 1: FERRITIN HOMOLOG

Chain A: 84% 10% . .



• Molecule 1: FERRITIN HOMOLOG

Chain B: 82% 12% . .



• Molecule 1: FERRITIN HOMOLOG

Chain C: 84% 11% . .



• Molecule 1: FERRITIN HOMOLOG

Chain D: 84% 10% . .



• Molecule 1: FERRITIN HOMOLOG

Chain E: 82% 12% . .



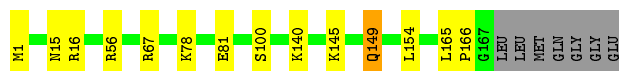
• Molecule 1: FERRITIN HOMOLOG

Chain F: 81% 13% . .



• Molecule 1: FERRITIN HOMOLOG

Chain G: 88% 7% . .



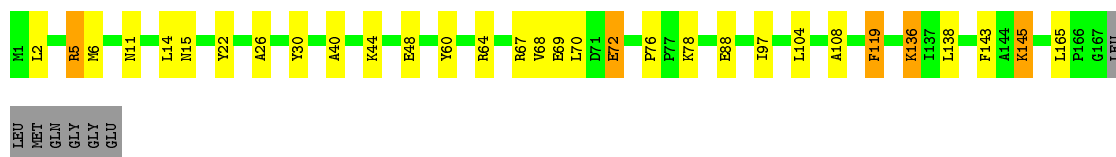
• Molecule 1: FERRITIN HOMOLOG

Chain H: 76% 17% . .



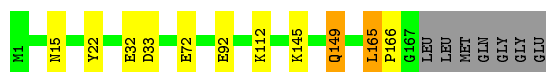
• Molecule 1: FERRITIN HOMOLOG

Chain I: 78% 15% . .



- Molecule 1: FERRITIN HOMOLOG

Chain J: 90% 5% . .



- Molecule 1: FERRITIN HOMOLOG

Chain K: 85% 10% . .



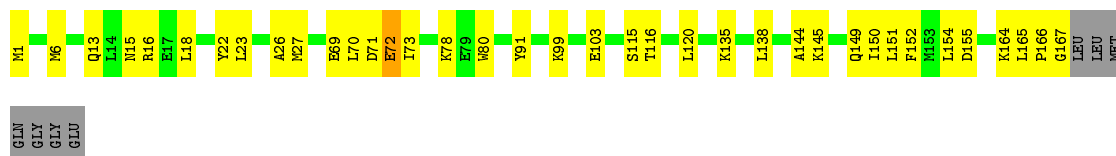
- Molecule 1: FERRITIN HOMOLOG

Chain L: 87% 9% . .



- Molecule 1: FERRITIN HOMOLOG

Chain M: 75% 21% . .



- Molecule 1: FERRITIN HOMOLOG

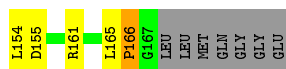
Chain N: 83% 10% . .



- Molecule 1: FERRITIN HOMOLOG

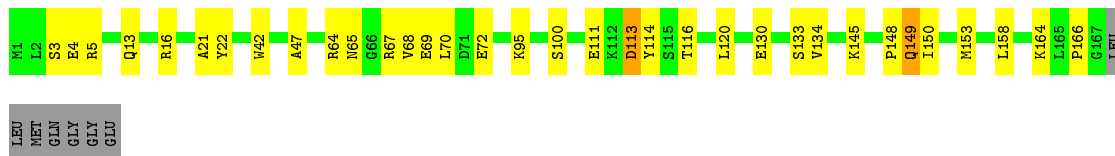
Chain O: 74% 20% . .





• Molecule 1: FERRITIN HOMOLOG

Chain P: 76% 18% . .



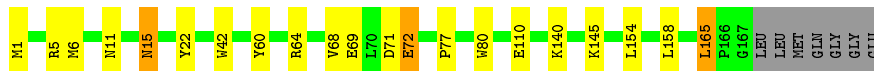
• Molecule 1: FERRITIN HOMOLOG

Chain Q: 82% 13% . .



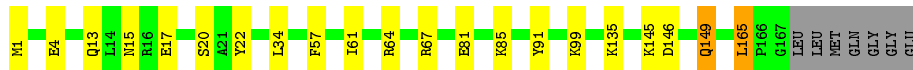
• Molecule 1: FERRITIN HOMOLOG

Chain R: 84% 10% . .



• Molecule 1: FERRITIN HOMOLOG

Chain S: 84% 11% . .



• Molecule 1: FERRITIN HOMOLOG

Chain T: 85% 10% . .



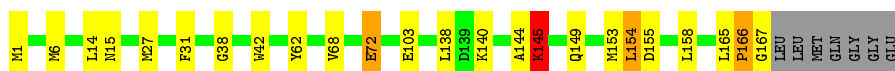
• Molecule 1: FERRITIN HOMOLOG

Chain U: 88% 7% . .



• Molecule 1: FERRITIN HOMOLOG

Chain V: 82% 11% . .



• Molecule 1: FERRITIN HOMOLOG

Chain W: 84% 10% • •



• Molecule 1: FERRITIN HOMOLOG

Chain X: 87% 9% • •



• Molecule 1: FERRITIN HOMOLOG

Chain Y: 81% 14% • •



• Molecule 1: FERRITIN HOMOLOG

Chain Z: 80% 16% • •



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	254.30 Å 342.88 Å 266.22 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	204.12 – 2.80	Depositor
% Data completeness (in resolution range)	99.1 (204.12-2.80)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.3.0021	Depositor
R, R_{free}	0.199 , 0.250	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	50409	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

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: FE, 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	0	0.69	0/1417	0.72	0/1908
1	1	0.70	0/1417	0.70	0/1908
1	2	0.68	0/1417	0.69	0/1908
1	3	0.74	0/1417	0.76	0/1908
1	4	0.73	0/1417	0.72	0/1908
1	5	0.68	0/1417	0.67	0/1908
1	6	0.67	0/1417	0.68	0/1908
1	7	0.71	0/1417	0.69	0/1908
1	8	0.74	0/1417	0.72	0/1908
1	9	0.68	0/1417	0.68	0/1908
1	A	0.77	0/1417	0.75	0/1908
1	B	0.82	1/1417 (0.1%)	0.80	2/1908 (0.1%)
1	C	0.78	0/1417	0.76	0/1908
1	D	0.76	0/1417	0.80	1/1908 (0.1%)
1	E	0.74	0/1417	0.74	0/1908
1	F	0.78	0/1417	0.73	0/1908
1	G	0.77	0/1425	0.76	1/1919 (0.1%)
1	H	0.68	0/1417	0.69	0/1908
1	I	0.75	1/1417 (0.1%)	0.75	0/1908
1	J	0.74	1/1417 (0.1%)	0.71	0/1908
1	K	0.67	0/1417	0.71	0/1908
1	L	0.71	0/1417	0.71	0/1908
1	M	0.71	0/1417	0.73	0/1908
1	N	0.69	0/1417	0.69	0/1908
1	O	0.72	0/1417	0.72	0/1908
1	P	0.72	0/1417	0.73	2/1908 (0.1%)
1	Q	0.75	1/1417 (0.1%)	0.71	0/1908
1	R	0.65	0/1417	0.65	0/1908
1	S	0.76	1/1417 (0.1%)	0.75	0/1908
1	T	0.79	0/1425	0.75	0/1919
1	U	0.80	0/1417	0.74	0/1908
1	V	0.78	0/1417	0.78	0/1908

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	W	0.84	0/1425	0.80	0/1919
1	X	0.73	0/1417	0.73	0/1908
1	Y	0.77	0/1417	0.78	1/1908 (0.1%)
1	Z	0.65	0/1417	0.69	0/1908
All	All	0.73	5/51036 (0.0%)	0.73	7/68721 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	E	0	1
1	U	0	1
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	92	GLU	CG-CD	6.07	1.61	1.51
1	J	92	GLU	CG-CD	5.89	1.60	1.51
1	S	4	GLU	CG-CD	5.54	1.60	1.51
1	B	81	GLU	CG-CD	5.49	1.60	1.51
1	I	15	ASN	CB-CG	5.38	1.63	1.51

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	64	ARG	NE-CZ-NH2	-7.66	116.47	120.30
1	B	64	ARG	NE-CZ-NH1	6.32	123.46	120.30
1	D	5	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	P	113	ASP	CB-CG-OD1	5.51	123.26	118.30
1	P	67	ARG	NE-CZ-NH1	5.27	122.93	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	78	LYS	Peptide
1	E	78	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	U	1	MET	Peptide

5.2 Too-close contacts ⓘ

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	0	1383	0	1352	14	0
1	1	1383	0	1352	12	0
1	2	1383	0	1352	15	0
1	3	1383	0	1352	14	0
1	4	1383	0	1352	14	0
1	5	1383	0	1352	7	0
1	6	1383	0	1352	13	0
1	7	1383	0	1352	18	0
1	8	1383	0	1352	8	0
1	9	1383	0	1352	14	0
1	A	1383	0	1352	8	0
1	B	1383	0	1352	16	0
1	C	1383	0	1352	12	0
1	D	1383	0	1352	9	0
1	E	1383	0	1352	13	0
1	F	1383	0	1352	13	0
1	G	1388	0	1358	9	0
1	H	1383	0	1352	24	0
1	I	1383	0	1352	22	0
1	J	1383	0	1352	5	0
1	K	1383	0	1352	8	0
1	L	1383	0	1352	8	0
1	M	1383	0	1352	20	0
1	N	1383	0	1352	19	0
1	O	1383	0	1352	29	0
1	P	1383	0	1352	22	0
1	Q	1383	0	1352	10	0
1	R	1383	0	1352	10	0
1	S	1383	0	1352	8	0
1	T	1388	0	1358	10	0
1	U	1383	0	1352	6	0
1	V	1383	0	1352	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	W	1388	0	1358	9	0
1	X	1383	0	1352	9	0
1	Y	1383	0	1352	18	0
1	Z	1383	0	1352	16	0
2	0	3	0	0	0	0
2	1	3	0	0	0	0
2	2	3	0	0	0	0
2	3	3	0	0	0	0
2	4	3	0	0	0	0
2	5	3	0	0	0	0
2	6	3	0	0	0	0
2	7	3	0	0	0	0
2	8	3	0	0	0	0
2	9	3	0	0	0	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	3	0	0	0	0
2	F	3	0	0	0	0
2	G	3	0	0	0	0
2	H	3	0	0	0	0
2	I	3	0	0	0	0
2	J	3	0	0	0	0
2	K	3	0	0	0	0
2	L	3	0	0	0	0
2	M	3	0	0	0	0
2	N	3	0	0	0	0
2	O	3	0	0	0	0
2	P	3	0	0	0	0
2	Q	3	0	0	0	0
2	R	3	0	0	0	0
2	S	3	0	0	0	0
2	T	3	0	0	0	0
2	U	3	0	0	0	0
2	V	3	0	0	0	0
2	W	3	0	0	0	0
2	X	3	0	0	0	0
2	Y	3	0	0	0	0
2	Z	3	0	0	0	0
3	1	5	0	0	0	0
3	2	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	3	10	0	0	0	0
3	8	5	0	0	0	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0
3	C	15	0	0	0	0
3	G	10	0	0	0	0
3	H	5	0	0	0	0
3	I	10	0	0	0	0
3	J	5	0	0	0	0
3	O	5	0	0	0	0
3	R	5	0	0	0	0
3	S	5	0	0	0	0
3	T	5	0	0	0	0
3	V	10	0	0	0	0
3	W	5	0	0	0	0
3	Y	10	0	0	1	0
4	0	7	0	0	0	0
4	1	10	0	0	0	0
4	2	7	0	0	1	0
4	3	15	0	0	2	0
4	4	8	0	0	0	0
4	5	5	0	0	0	0
4	6	8	0	0	0	0
4	7	11	0	0	0	0
4	8	9	0	0	0	0
4	9	7	0	0	0	0
4	A	13	0	0	1	0
4	B	17	0	0	2	0
4	C	8	0	0	1	0
4	D	16	0	0	1	0
4	E	18	0	0	2	0
4	F	21	0	0	1	0
4	G	14	0	0	1	0
4	H	2	0	0	2	0
4	I	5	0	0	0	0
4	J	16	0	0	1	0
4	K	4	0	0	1	0
4	L	9	0	0	1	0
4	M	11	0	0	0	0
4	N	3	0	0	0	0
4	O	5	0	0	1	0
4	P	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Q	9	0	0	0	0
4	R	5	0	0	0	0
4	S	17	0	0	1	0
4	T	13	0	0	0	0
4	U	18	0	0	1	0
4	V	13	0	0	2	0
4	W	9	0	0	0	0
4	X	14	0	0	1	0
4	Y	11	0	0	0	0
4	Z	5	0	0	0	0
All	All	50409	0	48690	417	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.

The worst 5 of 417 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:S:15:ASN:HB3	4:S:2004:HOH:O	1.48	1.11
1:A:2:LEU:O	1:A:3:SER:HB3	1.50	1.07
1:V:15:ASN:HB3	4:V:2002:HOH:O	1.51	1.06
1:5:69:GLU:HG3	1:N:78:LYS:HD2	1.36	1.05
1:B:15:ASN:HB3	4:B:2001:HOH:O	1.55	1.05

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	0	165/174 (95%)	161 (98%)	1 (1%)	3 (2%)	8 28
1	1	165/174 (95%)	159 (96%)	5 (3%)	1 (1%)	25 56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	165/174 (95%)	160 (97%)	2 (1%)	3 (2%)	8	28
1	3	165/174 (95%)	160 (97%)	2 (1%)	3 (2%)	8	28
1	4	165/174 (95%)	157 (95%)	8 (5%)	0	100	100
1	5	165/174 (95%)	161 (98%)	4 (2%)	0	100	100
1	6	165/174 (95%)	157 (95%)	7 (4%)	1 (1%)	25	56
1	7	165/174 (95%)	160 (97%)	3 (2%)	2 (1%)	13	39
1	8	165/174 (95%)	158 (96%)	5 (3%)	2 (1%)	13	39
1	9	165/174 (95%)	160 (97%)	3 (2%)	2 (1%)	13	39
1	A	165/174 (95%)	158 (96%)	2 (1%)	5 (3%)	4	15
1	B	165/174 (95%)	160 (97%)	4 (2%)	1 (1%)	25	56
1	C	165/174 (95%)	157 (95%)	7 (4%)	1 (1%)	25	56
1	D	165/174 (95%)	159 (96%)	3 (2%)	3 (2%)	8	28
1	E	165/174 (95%)	161 (98%)	2 (1%)	2 (1%)	13	39
1	F	165/174 (95%)	158 (96%)	5 (3%)	2 (1%)	13	39
1	G	166/174 (95%)	158 (95%)	7 (4%)	1 (1%)	25	56
1	H	165/174 (95%)	157 (95%)	6 (4%)	2 (1%)	13	39
1	I	165/174 (95%)	159 (96%)	5 (3%)	1 (1%)	25	56
1	J	165/174 (95%)	161 (98%)	2 (1%)	2 (1%)	13	39
1	K	165/174 (95%)	160 (97%)	4 (2%)	1 (1%)	25	56
1	L	165/174 (95%)	156 (94%)	9 (6%)	0	100	100
1	M	165/174 (95%)	153 (93%)	9 (6%)	3 (2%)	8	28
1	N	165/174 (95%)	163 (99%)	1 (1%)	1 (1%)	25	56
1	O	165/174 (95%)	155 (94%)	6 (4%)	4 (2%)	6	20
1	P	165/174 (95%)	158 (96%)	4 (2%)	3 (2%)	8	28
1	Q	165/174 (95%)	160 (97%)	3 (2%)	2 (1%)	13	39
1	R	165/174 (95%)	158 (96%)	5 (3%)	2 (1%)	13	39
1	S	165/174 (95%)	160 (97%)	3 (2%)	2 (1%)	13	39
1	T	166/174 (95%)	160 (96%)	5 (3%)	1 (1%)	25	56
1	U	165/174 (95%)	159 (96%)	4 (2%)	2 (1%)	13	39
1	V	165/174 (95%)	159 (96%)	4 (2%)	2 (1%)	13	39
1	W	166/174 (95%)	163 (98%)	2 (1%)	1 (1%)	25	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	X	165/174 (95%)	159 (96%)	4 (2%)	2 (1%)	13	39
1	Y	165/174 (95%)	158 (96%)	6 (4%)	1 (1%)	25	56
1	Z	165/174 (95%)	158 (96%)	6 (4%)	1 (1%)	25	56
All	All	5943/6264 (95%)	5720 (96%)	158 (3%)	65 (1%)	14	41

5 of 65 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	145	LYS
1	3	166	PRO
1	7	166	PRO
1	9	145	LYS
1	A	3	SER

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	0	142/147 (97%)	128 (90%)	14 (10%)	8	23
1	1	142/147 (97%)	133 (94%)	9 (6%)	18	46
1	2	142/147 (97%)	134 (94%)	8 (6%)	21	51
1	3	142/147 (97%)	132 (93%)	10 (7%)	15	40
1	4	142/147 (97%)	135 (95%)	7 (5%)	25	57
1	5	142/147 (97%)	138 (97%)	4 (3%)	43	77
1	6	142/147 (97%)	136 (96%)	6 (4%)	30	63
1	7	142/147 (97%)	128 (90%)	14 (10%)	8	23
1	8	142/147 (97%)	132 (93%)	10 (7%)	15	40
1	9	142/147 (97%)	133 (94%)	9 (6%)	18	46
1	A	142/147 (97%)	135 (95%)	7 (5%)	25	57
1	B	142/147 (97%)	134 (94%)	8 (6%)	21	51
1	C	142/147 (97%)	136 (96%)	6 (4%)	30	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	142/147 (97%)	134 (94%)	8 (6%)	21	51
1	E	142/147 (97%)	135 (95%)	7 (5%)	25	57
1	F	142/147 (97%)	132 (93%)	10 (7%)	15	40
1	G	143/147 (97%)	137 (96%)	6 (4%)	30	63
1	H	142/147 (97%)	134 (94%)	8 (6%)	21	51
1	I	142/147 (97%)	135 (95%)	7 (5%)	25	57
1	J	142/147 (97%)	136 (96%)	6 (4%)	30	63
1	K	142/147 (97%)	132 (93%)	10 (7%)	15	40
1	L	142/147 (97%)	135 (95%)	7 (5%)	25	57
1	M	142/147 (97%)	132 (93%)	10 (7%)	15	40
1	N	142/147 (97%)	137 (96%)	5 (4%)	36	70
1	O	142/147 (97%)	130 (92%)	12 (8%)	10	31
1	P	142/147 (97%)	135 (95%)	7 (5%)	25	57
1	Q	142/147 (97%)	133 (94%)	9 (6%)	18	46
1	R	142/147 (97%)	134 (94%)	8 (6%)	21	51
1	S	142/147 (97%)	134 (94%)	8 (6%)	21	51
1	T	143/147 (97%)	138 (96%)	5 (4%)	36	70
1	U	142/147 (97%)	137 (96%)	5 (4%)	36	70
1	V	142/147 (97%)	134 (94%)	8 (6%)	21	51
1	W	143/147 (97%)	137 (96%)	6 (4%)	30	63
1	X	142/147 (97%)	136 (96%)	6 (4%)	30	63
1	Y	142/147 (97%)	136 (96%)	6 (4%)	30	63
1	Z	142/147 (97%)	136 (96%)	6 (4%)	30	63
All	All	5115/5292 (97%)	4833 (94%)	282 (6%)	21	52

5 of 282 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	1	MET
1	I	145	LYS
1	W	119	PHE
1	F	72	GLU
1	H	1	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	149	GLN
1	J	149	GLN
1	U	149	GLN
1	I	149	GLN
1	K	149	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 134 ligands modelled in this entry, 108 are monoatomic - leaving 26 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	$\# Z > 2$
3	SO4	R	1168	-	4,4,4	0.18	0	6,6,6	0.25	0
3	SO4	C	1169	-	4,4,4	0.29	0	6,6,6	0.51	0
3	SO4	2	1668	-	4,4,4	0.16	0	6,6,6	0.25	0
3	SO4	O	1168	-	4,4,4	0.12	0	6,6,6	0.48	0
3	SO4	I	1168	-	4,4,4	0.38	0	6,6,6	0.51	0
3	SO4	G	1168	-	4,4,4	0.23	0	6,6,6	0.38	0
3	SO4	V	1669	-	4,4,4	0.14	0	6,6,6	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	1	1668	-	4,4,4	0.18	0	6,6,6	0.18	0
3	SO4	G	1169	-	4,4,4	0.18	0	6,6,6	0.27	0
3	SO4	B	1169	-	4,4,4	0.15	0	6,6,6	0.50	0
3	SO4	W	1668	-	4,4,4	0.20	0	6,6,6	0.40	0
3	SO4	B	1168	-	4,4,4	0.20	0	6,6,6	0.23	0
3	SO4	C	1170	-	4,4,4	0.15	0	6,6,6	0.30	0
3	SO4	Y	1669	-	4,4,4	0.24	0	6,6,6	0.29	0
3	SO4	H	1168	-	4,4,4	0.17	0	6,6,6	0.43	0
3	SO4	J	1168	-	4,4,4	0.20	0	6,6,6	0.27	0
3	SO4	Y	1668	-	4,4,4	0.19	0	6,6,6	0.30	0
3	SO4	V	1668	-	4,4,4	0.17	0	6,6,6	0.44	0
3	SO4	8	1668	-	4,4,4	0.16	0	6,6,6	0.36	0
3	SO4	3	1668	-	4,4,4	0.12	0	6,6,6	0.53	0
3	SO4	C	1168	-	4,4,4	0.13	0	6,6,6	0.26	0
3	SO4	A	1168	-	4,4,4	0.17	0	6,6,6	0.44	0
3	SO4	T	1668	-	4,4,4	0.21	0	6,6,6	0.37	0
3	SO4	I	1169	-	4,4,4	0.17	0	6,6,6	0.68	0
3	SO4	3	1669	-	4,4,4	0.23	0	6,6,6	0.53	0
3	SO4	S	1668	-	4,4,4	0.16	0	6,6,6	0.21	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	Y	1669	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.