W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 3, 2024 – 04:51 pm GMT

PDB ID	:	5JKL
Title	:	Binary crystal structure of positively and negatively supercharged variants Ftn(pos) and Ftn(neg) from human heavy chain ferritin (Mg formate condition)
Authors	:	Kuenzle, M.; Beck, T.
Deposited on	:	2016-04-26
Resolution	:	1.80 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

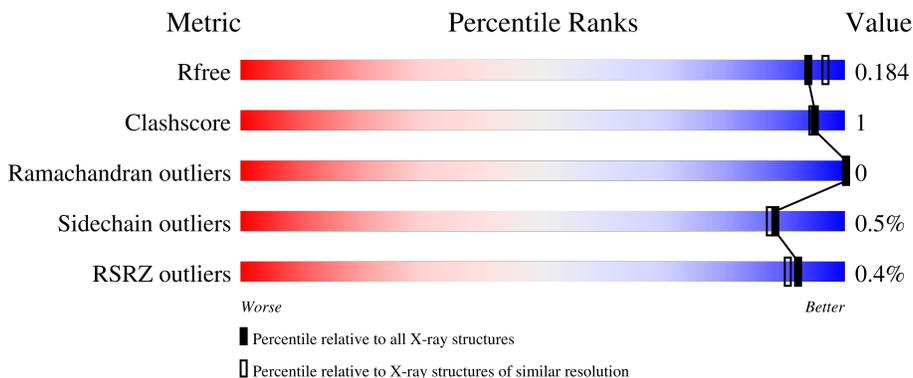|		
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.80 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	Percentile Ranks	Value
Rfree		0.184
Clashscore		1
Ramachandran outliers		0
Sidechain outliers		0.5%
RSRZ outliers		0.4%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 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 <=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	183	% 86% 8% 6%
1	B	183	% 91% · 6%
1	C	183	% 89% · · 6%
1	D	183	87% 7% 6%
1	E	183	% 87% 7% 6%

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Mol	Chain	Length	Quality of chain
1	F	183	87% 6% · 6%
2	G	183	89% 5% 6%
2	H	183	89% 5% 6%
2	I	183	90% · · 6%
2	J	183	92% · 6%
2	K	183	91% · · 6%
2	L	183	90% · 6%

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 18527 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 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	0	0
			1432	903	258	266	5			
1	B	172	Total	C	N	O	S	0	0	0
			1432	903	258	266	5			
1	C	172	Total	C	N	O	S	0	0	0
			1432	903	258	266	5			
1	D	172	Total	C	N	O	S	0	0	0
			1432	903	258	266	5			
1	E	172	Total	C	N	O	S	0	0	0
			1432	903	258	266	5			
1	F	172	Total	C	N	O	S	0	0	0
			1432	903	258	266	5			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	LYS	ALA	engineered mutation	UNP P02794
A	25	ARG	ASN	engineered mutation	UNP P02794
A	86	GLN	LYS	engineered mutation	UNP P02794
A	90	LYS	CYS	engineered mutation	UNP P02794
A	98	ARG	ASN	engineered mutation	UNP P02794
A	102	LYS	CYS	engineered mutation	UNP P02794
A	105	LYS	HIS	engineered mutation	UNP P02794
A	109	LYS	ASN	engineered mutation	UNP P02794
A	123	LYS	ASP	engineered mutation	UNP P02794
A	162	ARG	GLU	engineered mutation	UNP P02794
B	18	LYS	ALA	engineered mutation	UNP P02794
B	25	ARG	ASN	engineered mutation	UNP P02794
B	86	GLN	LYS	engineered mutation	UNP P02794
B	90	LYS	CYS	engineered mutation	UNP P02794
B	98	ARG	ASN	engineered mutation	UNP P02794
B	102	LYS	CYS	engineered mutation	UNP P02794
B	105	LYS	HIS	engineered mutation	UNP P02794

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PROTEIN DATA BANK

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Chain	Residue	Modelled	Actual	Comment	Reference
B	109	LYS	ASN	engineered mutation	UNP P02794
B	123	LYS	ASP	engineered mutation	UNP P02794
B	162	ARG	GLU	engineered mutation	UNP P02794
C	18	LYS	ALA	engineered mutation	UNP P02794
C	25	ARG	ASN	engineered mutation	UNP P02794
C	86	GLN	LYS	engineered mutation	UNP P02794
C	90	LYS	CYS	engineered mutation	UNP P02794
C	98	ARG	ASN	engineered mutation	UNP P02794
C	102	LYS	CYS	engineered mutation	UNP P02794
C	105	LYS	HIS	engineered mutation	UNP P02794
C	109	LYS	ASN	engineered mutation	UNP P02794
C	123	LYS	ASP	engineered mutation	UNP P02794
C	162	ARG	GLU	engineered mutation	UNP P02794
D	18	LYS	ALA	engineered mutation	UNP P02794
D	25	ARG	ASN	engineered mutation	UNP P02794
D	86	GLN	LYS	engineered mutation	UNP P02794
D	90	LYS	CYS	engineered mutation	UNP P02794
D	98	ARG	ASN	engineered mutation	UNP P02794
D	102	LYS	CYS	engineered mutation	UNP P02794
D	105	LYS	HIS	engineered mutation	UNP P02794
D	109	LYS	ASN	engineered mutation	UNP P02794
D	123	LYS	ASP	engineered mutation	UNP P02794
D	162	ARG	GLU	engineered mutation	UNP P02794
E	18	LYS	ALA	engineered mutation	UNP P02794
E	25	ARG	ASN	engineered mutation	UNP P02794
E	86	GLN	LYS	engineered mutation	UNP P02794
E	90	LYS	CYS	engineered mutation	UNP P02794
E	98	ARG	ASN	engineered mutation	UNP P02794
E	102	LYS	CYS	engineered mutation	UNP P02794
E	105	LYS	HIS	engineered mutation	UNP P02794
E	109	LYS	ASN	engineered mutation	UNP P02794
E	123	LYS	ASP	engineered mutation	UNP P02794
E	162	ARG	GLU	engineered mutation	UNP P02794
F	18	LYS	ALA	engineered mutation	UNP P02794
F	25	ARG	ASN	engineered mutation	UNP P02794
F	86	GLN	LYS	engineered mutation	UNP P02794
F	90	LYS	CYS	engineered mutation	UNP P02794
F	98	ARG	ASN	engineered mutation	UNP P02794
F	102	LYS	CYS	engineered mutation	UNP P02794
F	105	LYS	HIS	engineered mutation	UNP P02794
F	109	LYS	ASN	engineered mutation	UNP P02794
F	123	LYS	ASP	engineered mutation	UNP P02794

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Chain	Residue	Modelled	Actual	Comment	Reference
F	162	ARG	GLU	engineered mutation	UNP P02794

- Molecule 2 is a protein called Ferritin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	172	Total	C	N	O	S	0	0	0
			1422	890	246	281	5			
2	H	172	Total	C	N	O	S	0	0	0
			1422	890	246	281	5			
2	I	172	Total	C	N	O	S	0	0	0
			1422	890	246	281	5			
2	J	172	Total	C	N	O	S	0	0	0
			1422	890	246	281	5			
2	K	172	Total	C	N	O	S	0	0	0
			1422	890	246	281	5			
2	L	172	Total	C	N	O	S	0	0	0
			1422	890	246	281	5			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	18	GLU	ALA	engineered mutation	UNP P02794
G	86	GLN	LYS	engineered mutation	UNP P02794
G	90	GLU	CYS	engineered mutation	UNP P02794
G	102	GLU	CYS	engineered mutation	UNP P02794
G	105	GLU	HIS	engineered mutation	UNP P02794
H	18	GLU	ALA	engineered mutation	UNP P02794
H	86	GLN	LYS	engineered mutation	UNP P02794
H	90	GLU	CYS	engineered mutation	UNP P02794
H	102	GLU	CYS	engineered mutation	UNP P02794
H	105	GLU	HIS	engineered mutation	UNP P02794
I	18	GLU	ALA	engineered mutation	UNP P02794
I	86	GLN	LYS	engineered mutation	UNP P02794
I	90	GLU	CYS	engineered mutation	UNP P02794
I	102	GLU	CYS	engineered mutation	UNP P02794
I	105	GLU	HIS	engineered mutation	UNP P02794
J	18	GLU	ALA	engineered mutation	UNP P02794
J	86	GLN	LYS	engineered mutation	UNP P02794
J	90	GLU	CYS	engineered mutation	UNP P02794
J	102	GLU	CYS	engineered mutation	UNP P02794
J	105	GLU	HIS	engineered mutation	UNP P02794
K	18	GLU	ALA	engineered mutation	UNP P02794

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Chain	Residue	Modelled	Actual	Comment	Reference
K	86	GLN	LYS	engineered mutation	UNP P02794
K	90	GLU	CYS	engineered mutation	UNP P02794
K	102	GLU	CYS	engineered mutation	UNP P02794
K	105	GLU	HIS	engineered mutation	UNP P02794
L	18	GLU	ALA	engineered mutation	UNP P02794
L	86	GLN	LYS	engineered mutation	UNP P02794
L	90	GLU	CYS	engineered mutation	UNP P02794
L	102	GLU	CYS	engineered mutation	UNP P02794
L	105	GLU	HIS	engineered mutation	UNP P02794

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Fe 2	0	0
3	B	1	Total 1	Fe 1	0	0
3	C	1	Total 1	Fe 1	0	0
3	D	2	Total 2	Fe 2	0	0
3	E	1	Total 1	Fe 1	0	0
3	F	2	Total 2	Fe 2	0	0
3	G	2	Total 2	Fe 2	0	0
3	H	2	Total 2	Fe 2	0	0
3	I	1	Total 1	Fe 1	0	0
3	J	1	Total 1	Fe 1	0	0
3	K	1	Total 1	Fe 1	0	0
3	L	2	Total 2	Fe 2	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	Mg 2	0	0
4	B	1	Total 1	Mg 1	0	0
4	C	1	Total 1	Mg 1	0	0
4	D	2	Total 2	Mg 2	0	0
4	E	1	Total 1	Mg 1	0	0
4	F	1	Total 1	Mg 1	0	0
4	G	2	Total 2	Mg 2	0	0
4	H	1	Total 1	Mg 1	0	0
4	J	1	Total 1	Mg 1	0	0
4	K	1	Total 1	Mg 1	0	0
4	L	1	Total 1	Mg 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	Cl 1	0	0
5	D	1	Total 1	Cl 1	0	0
5	F	1	Total 1	Cl 1	0	0
5	G	1	Total 1	Cl 1	0	0
5	H	1	Total 1	Cl 1	0	0
5	L	1	Total 1	Cl 1	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

GOL
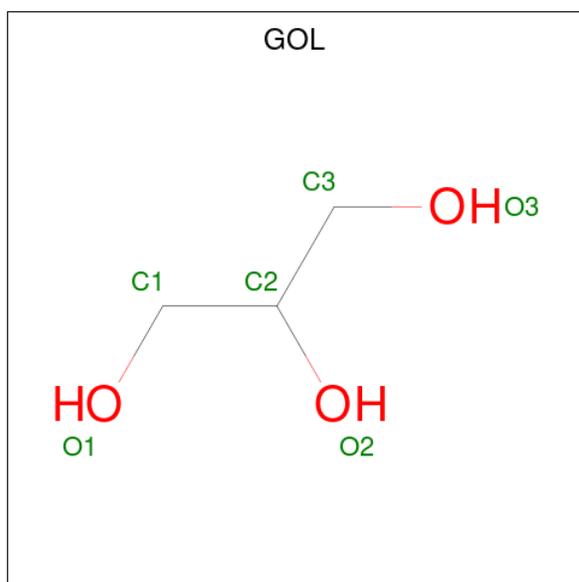
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total 6	C 3	O 3	0	0
6	C	1	Total 6	C 3	O 3	0	0
6	E	1	Total 6	C 3	O 3	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	112	Total 112	O 112	0	0
7	B	124	Total 124	O 124	0	0
7	C	135	Total 135	O 135	0	0
7	D	125	Total 125	O 125	0	0
7	E	113	Total 113	O 113	0	0
7	F	119	Total 119	O 119	0	0
7	G	116	Total 116	O 116	0	0
7	H	115	Total 115	O 115	0	0
7	I	103	Total 103	O 103	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	J	99	Total O 99　99		0	0
7	K	95	Total O 95　95		0	0
7	L	91	Total O 91　91		0	0

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: Ferritin heavy chain
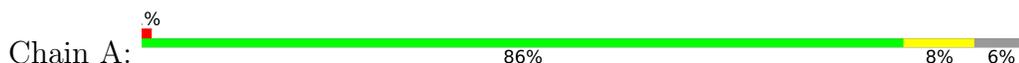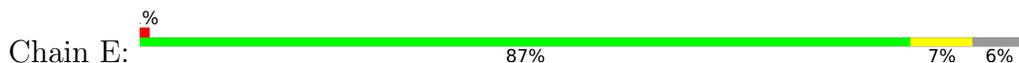
Chain A:

- Molecule 1: Ferritin heavy chain

Chain B:

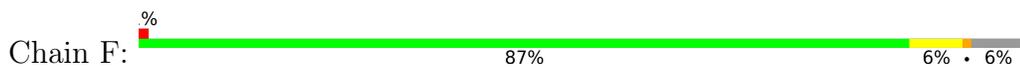- Molecule 1: Ferritin heavy chain

Chain C:

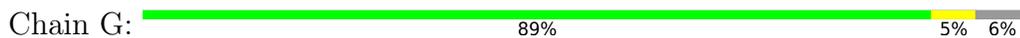- Molecule 1: Ferritin heavy chain

Chain D:

- Molecule 1: Ferritin heavy chain

Chain E:

- Molecule 1: Ferritin heavy chain

Chain F:

%

87%   6%   ·   6%

MET THR THR ALA SER T5 Y32 D44 R63 L72 R79 D84 K87 P88 D89 K90 W93 K102 R162 K172 G176 ASP SER ASP ASN GLU SER

• Molecule 2: Ferritin heavy chain

Chain G:

89%   5%   6%

MET THR THR ALA SER T5 K49 R63 E64 L72 R79 D84 D89 L97 P161 H173 G176 ASP SER ASP ASN GLU SER

• Molecule 2: Ferritin heavy chain

Chain H:

89%   5%   6%

MET THR THR ALA SER T5 A19 R22 Y32 R63 E64 D84 I85 Q86 L117 E167 G176 ASP SER ASP ASN GLU SER

• Molecule 2: Ferritin heavy chain

Chain I:

90%   · · 6%

MET THR THR ALA SER T5 R43 Y54 R63 E64 D84 K87 V110 R156 G176 ASP SER ASP ASN GLU SER

• Molecule 2: Ferritin heavy chain

Chain J:

92%   ·   6%

MET THR THR ALA SER T5 R63 E64 Q83 R156 G176 ASP SER ASP ASN GLU SER

• Molecule 2: Ferritin heavy chain

Chain K:

91%   · · 6%

MET THR THR ALA SER T5 R9 R22 D84 E105 D150 G176 ASP SER ASP ASN GLU SER

• Molecule 2: Ferritin heavy chain

Chain L:

%

90%   ·   6%

MET THR THR ALA SER T5 D15 I20 R63 R76 R79 D84 I85 Q86 L117 E162 G176 ASP SER ASP ASN GLU SER
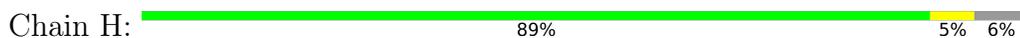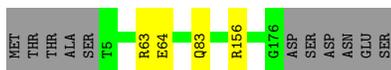
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α, β, γ	126.62Å 126.62Å 174.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.85 – 1.80 48.85 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.4 (48.85-1.80) 99.4 (48.85-1.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	4.32 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.147 , 0.176 0.159 , 0.184	Depositor DCC
R_{free} test set	12567 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	18.0	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 50.7	EDS
L-test for twinning[2]	$<\lvert L\rvert> = 0.44$, $<L^2> = 0.27$	Xtriage
Estimated twinning fraction	0.046 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	18527	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<\lvert L\rvert>$, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, FE, MG, CL

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	1.10	4/1460 (0.3%)	1.02	7/1957 (0.4%)
1	B	1.03	0/1460	1.02	4/1957 (0.2%)
1	C	1.04	1/1460 (0.1%)	0.98	5/1957 (0.3%)
1	D	1.01	1/1460 (0.1%)	0.96	5/1957 (0.3%)
1	E	1.05	1/1460 (0.1%)	0.94	3/1957 (0.2%)
1	F	1.01	0/1460	0.97	4/1957 (0.2%)
2	G	1.03	0/1450	1.00	4/1953 (0.2%)
2	H	1.07	2/1450 (0.1%)	1.01	5/1953 (0.3%)
2	I	1.06	3/1450 (0.2%)	0.96	5/1953 (0.3%)
2	J	1.04	2/1450 (0.1%)	0.95	3/1953 (0.2%)
2	K	1.05	1/1450 (0.1%)	0.98	4/1953 (0.2%)
2	L	0.96	0/1450	0.95	6/1953 (0.3%)
All	All	1.04	15/17460 (0.1%)	0.98	55/23460 (0.2%)

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	64	GLU	CD-OE2	6.96	1.33	1.25
1	C	61	GLU	CB-CG	-5.87	1.41	1.52
2	J	64	GLU	CG-CD	5.87	1.60	1.51
2	H	64	GLU	CD-OE1	5.60	1.31	1.25
1	E	27	GLU	CD-OE2	5.58	1.31	1.25

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	63	ARG	NE-CZ-NH2	-10.90	114.85	120.30
1	C	63	ARG	NE-CZ-NH1	-10.23	115.18	120.30
1	A	63	ARG	NE-CZ-NH1	-9.95	115.32	120.30
1	B	63	ARG	NE-CZ-NH1	-9.51	115.55	120.30
1	B	84	ASP	CB-CG-OD1	8.96	126.37	118.30

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	1432	0	1419	9	0
1	B	1432	0	1419	0	1
1	C	1432	0	1419	4	0
1	D	1432	0	1419	4	0
1	E	1432	0	1419	5	0
1	F	1432	0	1419	6	2
2	G	1422	0	1354	5	0
2	H	1422	0	1354	3	0
2	I	1422	0	1354	4	0
2	J	1422	0	1354	0	1
2	K	1422	0	1354	1	0
2	L	1422	0	1354	2	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	2	0	0	0	0
3	E	1	0	0	0	0
3	F	2	0	0	0	0
3	G	2	0	0	0	0
3	H	2	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	2	0	0	0	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	2	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	2	0	0	0	0
4	H	1	0	0	0	0
4	J	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	K	1	0	0	0	0
4	L	1	0	0	0	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	1	0
5	H	1	0	0	0	0
5	L	1	0	0	0	0
6	B	6	0	8	0	0
6	C	6	0	8	0	1
6	E	6	0	8	0	0
7	A	112	0	0	3	0
7	B	124	0	0	0	0
7	C	135	0	0	2	0
7	D	125	0	0	1	0
7	E	113	0	0	1	0
7	F	119	0	0	1	2
7	G	116	0	0	1	0
7	H	115	0	0	0	0
7	I	103	0	0	3	0
7	J	99	0	0	0	1
7	K	95	0	0	1	1
7	L	91	0	0	1	0
All	All	18527	0	16662	40	5

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 1.

The worst 5 of 40 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:A:86:GLN:NE2	2:H:86:GLN:OE1	2.08	0.87
2:I:63:ARG:NH1	7:I:301:HOH:O	2.16	0.78
2:K:105:GLU:HG3	7:K:312:HOH:O	1.90	0.71
1:A:162:ARG:CG	7:A:337:HOH:O	2.40	0.70
1:F:162:ARG:HG2	7:F:376:HOH:O	1.94	0.67

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:172:LYS:CE	7:F:380:HOH:O[3_755]	1.77	0.43
1:F:172:LYS:CD	7:F:380:HOH:O[3_755]	1.99	0.21
7:J:389:HOH:O	7:K:302:HOH:O[3_655]	2.13	0.07
2:J:83:GLN:OE1	2:J:83:GLN:OE1[2_675]	2.16	0.04
1:B:131:ASP:OD1	6:C:203:GOL:O1[4_575]	2.19	0.01

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	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
1	B	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
1	C	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
1	D	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
1	E	170/183 (93%)	166 (98%)	4 (2%)	0	100	100
1	F	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
2	G	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
2	H	170/183 (93%)	169 (99%)	1 (1%)	0	100	100
2	I	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
2	J	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
2	K	170/183 (93%)	167 (98%)	3 (2%)	0	100	100
2	L	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
All	All	2040/2196 (93%)	2014 (99%)	26 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	154/164 (94%)	154 (100%)	0	100	100
1	B	154/164 (94%)	153 (99%)	1 (1%)	86	84
1	C	154/164 (94%)	153 (99%)	1 (1%)	86	84
1	D	154/164 (94%)	153 (99%)	1 (1%)	86	84
1	E	154/164 (94%)	154 (100%)	0	100	100
1	F	154/164 (94%)	150 (97%)	4 (3%)	46	32
2	G	154/164 (94%)	153 (99%)	1 (1%)	86	84
2	H	154/164 (94%)	153 (99%)	1 (1%)	86	84
2	I	154/164 (94%)	154 (100%)	0	100	100
2	J	154/164 (94%)	154 (100%)	0	100	100
2	K	154/164 (94%)	154 (100%)	0	100	100
2	L	154/164 (94%)	154 (100%)	0	100	100
All	All	1848/1968 (94%)	1839 (100%)	9 (0%)	88	87

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	64	GLU
2	H	32	TYR
1	F	32	TYR
1	F	44	ASP
1	F	87	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 41 ligands modelled in this entry, 38 are monoatomic - leaving 3 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	#$|Z| > 2$
6	GOL	C	203	-	5,5,5	1.57	1 (20%)	5,5,5	1.74	1 (20%)
6	GOL	E	203	-	5,5,5	0.96	0	5,5,5	1.53	1 (20%)
6	GOL	B	203	-	5,5,5	0.43	0	5,5,5	0.50	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
6	GOL	C	203	-	-	2/4/4/4	-
6	GOL	E	203	-	-	4/4/4/4	-
6	GOL	B	203	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	203	GOL	O2-C2	3.25	1.53	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	C	203	GOL	O2-C2-C1	2.61	120.62	109.12
6	E	203	GOL	O3-C3-C2	2.23	120.90	110.20

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	E	203	GOL	C1-C2-C3-O3
6	E	203	GOL	O2-C2-C3-O3
6	C	203	GOL	C1-C2-C3-O3
6	E	203	GOL	O1-C1-C2-O2
6	C	203	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	203	GOL	0	1

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(Å²)	Q<0.9
1	A	172/183 (93%)	-0.55	2 (1%)	79	76	11, 15, 27, 47	0
1	B	172/183 (93%)	-0.64	1 (0%)	89	87	11, 15, 28, 50	0
1	C	172/183 (93%)	-0.59	2 (1%)	79	76	12, 15, 28, 55	0
1	D	172/183 (93%)	-0.60	0	100	100	12, 16, 29, 55	0
1	E	172/183 (93%)	-0.54	1 (0%)	89	87	12, 16, 29, 55	0
1	F	172/183 (93%)	-0.65	1 (0%)	89	87	12, 16, 28, 50	0
2	G	172/183 (93%)	-0.56	0	100	100	13, 17, 28, 41	0
2	H	172/183 (93%)	-0.56	0	100	100	13, 17, 29, 43	0
2	I	172/183 (93%)	-0.61	0	100	100	14, 18, 29, 40	0
2	J	172/183 (93%)	-0.57	0	100	100	13, 18, 30, 46	0
2	K	172/183 (93%)	-0.57	0	100	100	14, 19, 29, 46	0
2	L	172/183 (93%)	-0.53	1 (0%)	89	87	15, 19, 31, 49	0
All	All	2064/2196 (93%)	-0.58	8 (0%)	92	90	11, 17, 29, 55	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	161	PRO	4.4
2	L	162	GLU	3.6
1	C	162	ARG	3.1
1	F	162	ARG	2.7
1	E	162	ARG	2.3

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	MG	L	203	1/1	0.78	0.14	25,25,25,25	1
4	MG	D	204	1/1	0.79	0.14	26,26,26,26	1
4	MG	B	202	1/1	0.84	0.16	24,24,24,24	1
6	GOL	C	203	6/6	0.86	0.16	28,35,36,39	0
4	MG	A	204	1/1	0.87	0.14	20,20,20,20	1
4	MG	C	202	1/1	0.88	0.17	21,21,21,21	1
4	MG	K	202	1/1	0.89	0.09	24,24,24,24	1
4	MG	F	203	1/1	0.91	0.08	19,19,19,19	1
5	CL	A	205	1/1	0.92	0.13	28,28,28,28	1
6	GOL	E	203	6/6	0.92	0.10	25,29,32,33	0
4	MG	H	203	1/1	0.93	0.10	27,27,27,27	1
4	MG	E	202	1/1	0.94	0.07	33,33,33,33	0
4	MG	G	203	1/1	0.95	0.05	49,49,49,49	0
5	CL	L	204	1/1	0.97	0.13	32,32,32,32	1
6	GOL	B	203	6/6	0.97	0.10	24,25,28,28	0
4	MG	A	203	1/1	0.98	0.05	22,22,22,22	0
5	CL	D	205	1/1	0.98	0.10	28,28,28,28	0
5	CL	F	204	1/1	0.98	0.07	33,33,33,33	1
5	CL	H	204	1/1	0.98	0.06	30,30,30,30	0
3	FE	L	202	1/1	0.99	0.09	28,28,28,28	1
4	MG	J	202	1/1	0.99	0.04	24,24,24,24	0
3	FE	A	202	1/1	0.99	0.05	21,21,21,21	1
3	FE	B	201	1/1	0.99	0.03	23,23,23,23	0
3	FE	C	201	1/1	0.99	0.05	24,24,24,24	0
3	FE	D	201	1/1	0.99	0.02	25,25,25,25	0
4	MG	D	203	1/1	0.99	0.05	22,22,22,22	0
3	FE	E	201	1/1	0.99	0.03	25,25,25,25	0
3	FE	H	201	1/1	0.99	0.02	26,26,26,26	0
3	FE	I	201	1/1	0.99	0.04	29,29,29,29	0
3	FE	K	201	1/1	0.99	0.04	28,28,28,28	0
4	MG	G	204	1/1	0.99	0.05	21,21,21,21	0
3	FE	A	201	1/1	1.00	0.03	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	FE	J	201	1/1	1.00	0.04	29,29,29,29	0
3	FE	F	201	1/1	1.00	0.03	24,24,24,24	0
3	FE	L	201	1/1	1.00	0.02	28,28,28,28	0
5	CL	G	205	1/1	1.00	0.24	32,32,32,32	1
3	FE	F	202	1/1	1.00	0.07	22,22,22,22	1
3	FE	G	201	1/1	1.00	0.03	27,27,27,27	0
3	FE	G	202	1/1	1.00	0.07	23,23,23,23	1
3	FE	D	202	1/1	1.00	0.08	22,22,22,22	0
3	FE	H	202	1/1	1.00	0.08	25,25,25,25	0

6.5 Other polymers (i)

There are no such residues in this entry.