



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 11:05 am BST

PDB ID : 6H6T  
Title : Binary crystal structure of positively and negatively supercharged variants Ftn(pos) and Ftn(neg) from human heavy chain ferritin (propandiol condition, coordination number 8)  
Authors : Kuenzle, M.; Lach, M.; Beck, T.  
Deposited on : 2018-07-30  
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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) : 1.13  
EDS : 2.11  
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) : 2.11

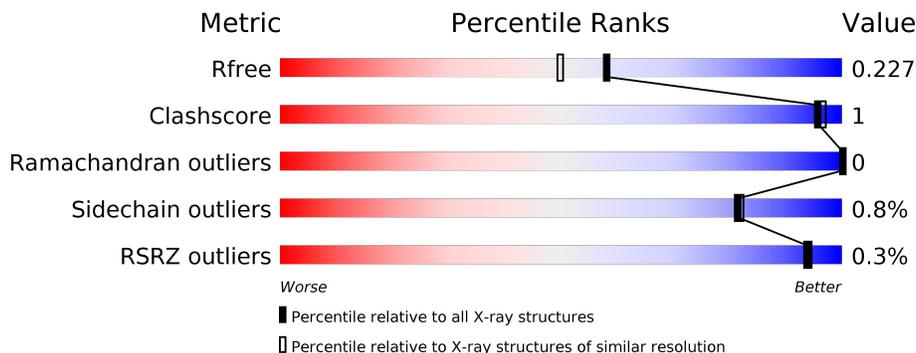
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	183	
1	B	183	
1	C	183	
1	D	183	
1	E	183	
1	F	183	

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Mol	Chain	Length	Quality of chain
2	G	183	 89% . . 6%
2	H	183	 91% . 6%
2	I	183	 86% 8% . 6%
2	J	183	 88% 6% . 5%
2	K	183	 90% . . 6%
2	L	183	 91% . 5%

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 17707 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
			Total	C	N	O	S			
1	A	172	1432	903	258	266	5	0	0	0
1	B	172	1432	903	258	266	5	0	0	0
1	C	172	1432	903	258	266	5	0	0	0
1	D	172	1432	903	258	266	5	0	0	0
1	E	173	1437	906	259	267	5	0	0	0
1	F	172	1432	903	258	266	5	0	0	0

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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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
			Total	C	N	O	S			
2	G	172	1422	890	246	281	5	0	0	0
2	H	172	1422	890	246	281	5	0	0	0
2	I	172	1422	890	246	281	5	0	0	0
2	J	173	1427	893	247	282	5	0	0	0
2	K	172	1422	890	246	281	5	0	0	0
2	L	173	1427	893	247	282	5	0	0	0

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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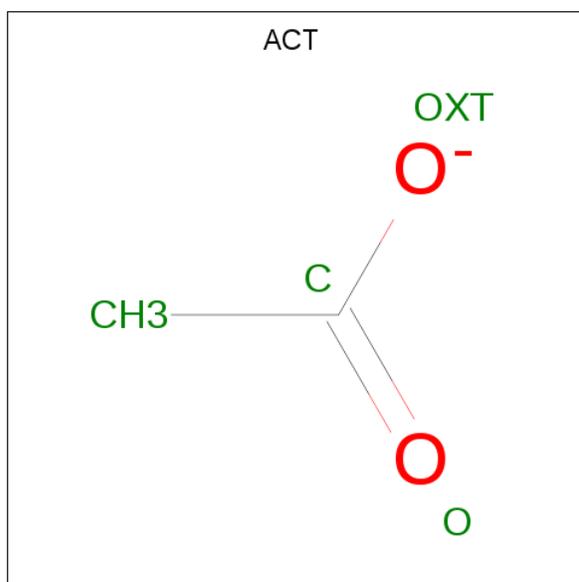
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Chain	Residue	Modelled	Actual	Comment	Reference
K	86	GLN	LYS	engineered mutation	UNP P02794
K	90	GLU	CYS	engineered mutation	UNP P02794
K	102	GLU	CYS	engineered mutation	UNP P02794
K	105	GLU	HIS	engineered mutation	UNP P02794
L	18	GLU	ALA	engineered 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	G	1	Total Fe 1 1	0	0
3	J	1	Total Fe 1 1	0	0
3	D	1	Total Fe 1 1	0	0
3	K	1	Total Fe 1 1	0	0
3	E	1	Total Fe 1 1	0	0
3	H	1	Total Fe 1 1	0	0
3	B	1	Total Fe 1 1	0	0
3	I	1	Total Fe 1 1	0	0
3	C	1	Total Fe 1 1	0	0
3	A	1	Total Fe 1 1	0	0
3	L	1	Total Fe 1 1	0	0
3	F	1	Total Fe 1 1	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



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

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Mg 1 1	0	0
5	A	1	Total Mg 1 1	0	0

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	J	1	Total Zn 1 1	0	0
6	K	1	Total Zn 1 1	0	0
6	E	1	Total Zn 1 1	0	0
6	C	1	Total Zn 1 1	0	0
6	L	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Zn	0	0
			1	1		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	G	1	Total	Cl	0	0
			1	1		
7	J	1	Total	Cl	0	0
			1	1		
7	E	1	Total	Cl	0	0
			1	1		
7	C	1	Total	Cl	0	0
			1	1		
7	L	1	Total	Cl	0	0
			1	1		
7	F	1	Total	Cl	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	49	Total	O	0	0
			49	49		
8	B	45	Total	O	0	0
			45	45		
8	C	38	Total	O	0	0
			38	38		
8	D	31	Total	O	0	0
			31	31		
8	E	52	Total	O	0	0
			52	52		
8	F	25	Total	O	0	0
			25	25		
8	G	54	Total	O	0	0
			54	54		
8	H	53	Total	O	0	0
			53	53		
8	I	41	Total	O	0	0
			41	41		
8	J	59	Total	O	0	0
			59	59		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
8	K	44	Total O 44 44	0	0
8	L	43	Total O 43 43	0	0

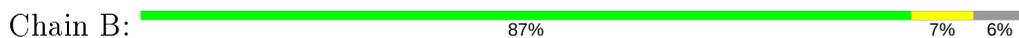
### 3 Residue-property plots [i](#)

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 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.

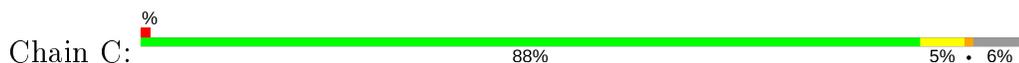
- Molecule 1: Ferritin heavy chain



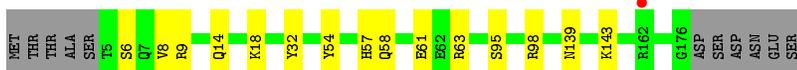
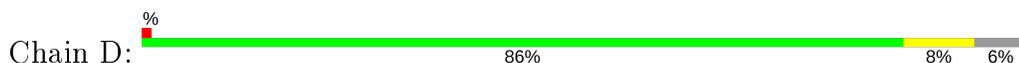
- Molecule 1: Ferritin heavy chain



- Molecule 1: Ferritin heavy chain



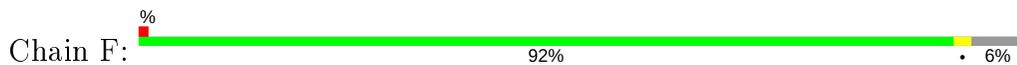
- Molecule 1: Ferritin heavy chain



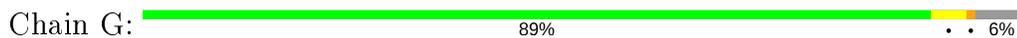
- Molecule 1: Ferritin heavy chain



- Molecule 1: Ferritin heavy chain



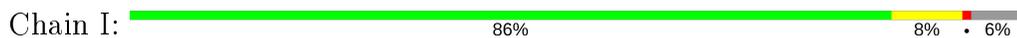
- Molecule 2: Ferritin heavy chain



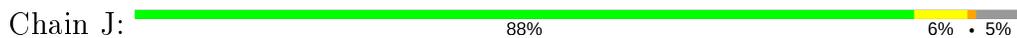
- Molecule 2: Ferritin heavy chain



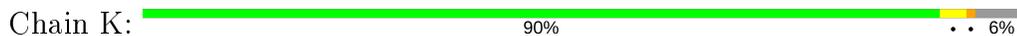
- Molecule 2: Ferritin heavy chain



- Molecule 2: Ferritin heavy chain



- Molecule 2: Ferritin heavy chain



- Molecule 2: Ferritin heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	153.23Å 153.23Å 135.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.46 – 1.90 48.46 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.46-1.90) 99.5 (48.46-1.90)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.86 (at 1.90Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.182 , 0.222 0.191 , 0.227	Depositor DCC
$R_{free}$ test set	12224 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.5	Xtrriage
Anisotropy	0.037	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 21.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.22$	Xtrriage
Estimated twinning fraction	0.144 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	17707	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MG, ACT, FE, ZN, 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	1.00	0/1460	1.01	10/1957 (0.5%)
1	B	0.98	0/1460	0.97	6/1957 (0.3%)
1	C	1.03	0/1460	1.02	7/1957 (0.4%)
1	D	0.90	0/1460	0.92	2/1957 (0.1%)
1	E	1.04	0/1465	0.99	2/1964 (0.1%)
1	F	0.89	0/1460	0.91	0/1957
2	G	1.03	1/1450 (0.1%)	1.03	6/1953 (0.3%)
2	H	1.00	0/1450	0.94	1/1953 (0.1%)
2	I	1.00	0/1450	1.01	7/1953 (0.4%)
2	J	1.05	1/1455 (0.1%)	1.01	7/1960 (0.4%)
2	K	0.97	1/1450 (0.1%)	0.95	6/1953 (0.3%)
2	L	0.97	0/1455	0.94	3/1960 (0.2%)
All	All	0.99	3/17475 (0.0%)	0.97	57/23481 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	93	TRP	CB-CG	-5.59	1.40	1.50
2	J	18	GLU	CD-OE1	5.57	1.31	1.25
2	K	39	TYR	CE1-CZ	-5.56	1.31	1.38

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	J	84	ASP	CB-CG-OD1	9.11	126.50	118.30
2	G	79	ARG	NE-CZ-NH1	8.83	124.71	120.30
2	G	84	ASP	CB-CG-OD1	8.71	126.14	118.30
2	I	131	ASP	CB-CG-OD2	-8.48	110.67	118.30
1	C	63	ARG	NE-CZ-NH2	-8.45	116.08	120.30

There are no chirality outliers.

There are no planarity outliers.

## 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	A	1432	0	1419	5	0
1	B	1432	0	1419	4	0
1	C	1432	0	1419	5	0
1	D	1432	0	1419	8	0
1	E	1437	0	1421	1	0
1	F	1432	0	1419	2	0
2	G	1422	0	1354	2	0
2	H	1422	0	1354	3	0
2	I	1422	0	1354	7	0
2	J	1427	0	1356	3	0
2	K	1422	0	1354	1	0
2	L	1427	0	1356	2	0
3	A	1	0	0	0	0
3	B	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
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
4	A	4	0	3	1	0
4	G	4	0	3	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	C	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
6	J	1	0	0	0	0
6	K	1	0	0	0	0
6	L	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	1	0	0	0	0
7	E	1	0	0	0	0
7	F	1	0	0	0	0
7	G	1	0	0	0	0
7	J	1	0	0	0	0
7	L	1	0	0	0	0
8	A	49	0	0	0	0
8	B	45	0	0	0	0
8	C	38	0	0	0	0
8	D	31	0	0	0	0
8	E	52	0	0	0	0
8	F	25	0	0	0	0
8	G	54	0	0	0	0
8	H	53	0	0	0	0
8	I	41	0	0	0	0
8	J	59	0	0	0	0
8	K	44	0	0	0	0
8	L	43	0	0	0	0
All	All	17707	0	16650	38	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 1.

The worst 5 of 38 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:63:ARG:NH1	1:C:63:ARG:HD3	1.98	0.78
2:H:63:ARG:NH2	2:I:63:ARG:HG2	2.10	0.65
2:G:72:LEU:HD22	2:G:132:PHE:CE2	2.35	0.62
1:D:6:SER:OG	1:D:8:VAL:HG22	2.08	0.54
2:G:72:LEU:HD22	2:G:132:PHE:CD2	2.42	0.54

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	170/183 (93%)	167 (98%)	3 (2%)	0	100	100
1	B	170/183 (93%)	166 (98%)	4 (2%)	0	100	100
1	C	170/183 (93%)	169 (99%)	1 (1%)	0	100	100
1	D	170/183 (93%)	167 (98%)	3 (2%)	0	100	100
1	E	171/183 (93%)	168 (98%)	3 (2%)	0	100	100
1	F	170/183 (93%)	166 (98%)	4 (2%)	0	100	100
2	G	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
2	H	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
2	I	170/183 (93%)	166 (98%)	4 (2%)	0	100	100
2	J	171/183 (93%)	169 (99%)	2 (1%)	0	100	100
2	K	170/183 (93%)	167 (98%)	3 (2%)	0	100	100
2	L	171/183 (93%)	169 (99%)	2 (1%)	0	100	100
All	All	2043/2196 (93%)	2010 (98%)	33 (2%)	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	154/164 (94%)	153 (99%)	1 (1%)	86	87
1	B	154/164 (94%)	154 (100%)	0	100	100
1	C	154/164 (94%)	152 (99%)	2 (1%)	69	68
1	D	154/164 (94%)	153 (99%)	1 (1%)	86	87
1	E	154/164 (94%)	154 (100%)	0	100	100
1	F	154/164 (94%)	153 (99%)	1 (1%)	86	87
2	G	154/164 (94%)	152 (99%)	2 (1%)	69	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	154/164 (94%)	153 (99%)	1 (1%)	86	87
2	I	154/164 (94%)	151 (98%)	3 (2%)	57	53
2	J	154/164 (94%)	153 (99%)	1 (1%)	86	87
2	K	154/164 (94%)	152 (99%)	2 (1%)	69	68
2	L	154/164 (94%)	153 (99%)	1 (1%)	86	87
All	All	1848/1968 (94%)	1833 (99%)	15 (1%)	81	82

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	44	ASP
2	H	64	GLU
2	K	32	TYR
2	G	32	TYR
2	J	32	TYR

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

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 26 are monoatomic - leaving 2 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
4	ACT	G	202	-	1,3,3	1.97	0	0,3,3	0.00	-
4	ACT	A	202	-	1,3,3	2.52	1 (100%)	0,3,3	0.00	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	202	ACT	CH3-C	2.52	1.52	1.48

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
4	A	202	ACT	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	172/183 (93%)	-0.26	1 (0%) 89   90	21, 26, 39, 68	0
1	B	172/183 (93%)	-0.28	0 100   100	19, 24, 37, 63	0
1	C	172/183 (93%)	-0.32	1 (0%) 89   90	20, 25, 36, 63	0
1	D	172/183 (93%)	-0.24	1 (0%) 89   90	22, 30, 42, 66	0
1	E	173/183 (94%)	-0.26	1 (0%) 89   90	17, 23, 36, 61	0
1	F	172/183 (93%)	-0.21	2 (1%) 79   81	24, 30, 44, 63	0
2	G	172/183 (93%)	-0.30	0 100   100	17, 22, 34, 43	0
2	H	172/183 (93%)	-0.28	0 100   100	18, 24, 36, 42	0
2	I	172/183 (93%)	-0.34	0 100   100	19, 25, 36, 44	0
2	J	173/183 (94%)	-0.25	0 100   100	17, 22, 34, 53	0
2	K	172/183 (93%)	-0.32	0 100   100	19, 25, 36, 46	0
2	L	173/183 (94%)	-0.32	0 100   100	19, 25, 37, 56	0
All	All	2067/2196 (94%)	-0.28	6 (0%) 94   94	17, 25, 38, 68	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	162	ARG	4.3
1	A	162	ARG	3.5
1	E	162	ARG	2.7
1	C	162	ARG	2.6
1	D	162	ARG	2.4

### 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 carbohydrates 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	MG	A	203	1/1	0.87	0.05	52,52,52,52	0
3	FE	A	201	1/1	0.88	0.13	76,76,76,76	0
3	FE	C	202	1/1	0.89	0.10	68,68,68,68	0
4	ACT	A	202	4/4	0.90	0.12	41,45,48,50	0
3	FE	B	201	1/1	0.91	0.06	70,70,70,70	0
4	ACT	G	202	4/4	0.91	0.13	33,34,42,47	0
3	FE	D	201	1/1	0.92	0.11	76,76,76,76	0
3	FE	F	202	1/1	0.93	0.15	78,78,78,78	0
3	FE	E	202	1/1	0.94	0.05	67,67,67,67	0
5	MG	B	202	1/1	0.94	0.05	43,43,43,43	0
3	FE	G	201	1/1	0.94	0.05	60,60,60,60	0
3	FE	L	202	1/1	0.96	0.06	62,62,62,62	0
3	FE	K	202	1/1	0.96	0.09	57,57,57,57	0
3	FE	J	202	1/1	0.98	0.04	48,48,48,48	0
3	FE	H	201	1/1	0.98	0.05	54,54,54,54	0
3	FE	I	201	1/1	0.98	0.04	55,55,55,55	0
7	CL	G	203	1/1	0.99	0.07	27,27,27,27	0
7	CL	E	203	1/1	0.99	0.06	24,24,24,24	1
6	ZN	K	201	1/1	0.99	0.03	34,34,34,34	0
6	ZN	F	201	1/1	1.00	0.03	39,39,39,39	1
6	ZN	J	201	1/1	1.00	0.07	35,35,35,35	1
6	ZN	E	201	1/1	1.00	0.07	31,31,31,31	1
7	CL	J	203	1/1	1.00	0.05	22,22,22,22	1
7	CL	C	203	1/1	1.00	0.07	30,30,30,30	0
6	ZN	C	201	1/1	1.00	0.03	34,34,34,34	0
7	CL	F	203	1/1	1.00	0.04	31,31,31,31	1
6	ZN	L	201	1/1	1.00	0.04	37,37,37,37	1
7	CL	L	203	1/1	1.00	0.09	19,19,19,19	1

### 6.5 Other polymers [i](#)

There are no such residues in this entry.