



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2017 – 10:25 PM EDT

PDB ID : 6BAL  
Title : 2.1 Angstrom Resolution Crystal Structure of Malate Dehydrogenase from Haemophilus influenzae in Complex with L-Malate  
Authors : Minasov, G.; Wawrzak, Z.; Skarina, T.; Grimshaw, S.; Satchell, K.J.F.; Savchenko, A.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : unknown  
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

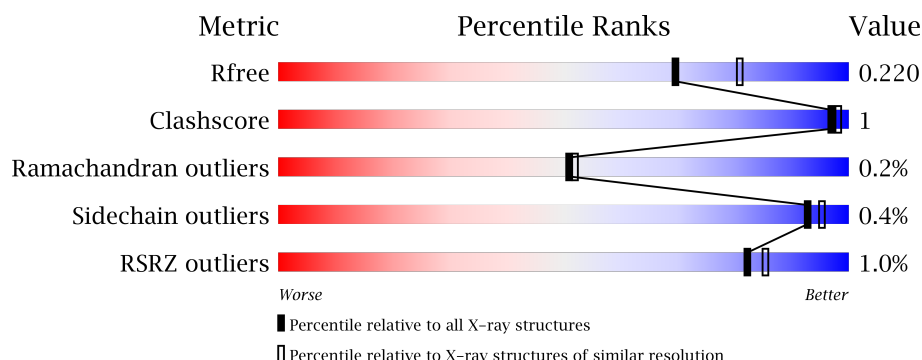
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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.



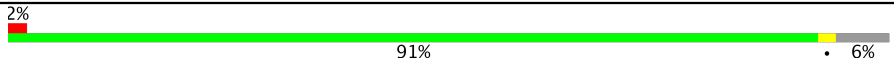


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	335	<div> <div>91%</div> <div>7%</div> </div>
1	B	335	<div> <div>91%</div> <div>7%</div> </div>
1	C	335	<div> <div>88%</div> <div>5%</div> <div>7%</div> </div>
1	D	335	<div> <div>90%</div> <div>7%</div> </div>
1	E	335	<div> <div>90%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	335	 2% 91% 6%
1	G	335	 % 88% 10%
1	H	335	 % 89% 7%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	A	402[A]	-	-	-	X
3	CL	A	402[B]	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19775 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 Malate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	S	0	1	0
			2301	1460	394	440	7			
1	B	313	Total	C	N	O	S	0	1	0
			2310	1465	395	443	7			
1	C	313	Total	C	N	O	S	0	6	0
			2351	1486	406	452	7			
1	D	312	Total	C	N	O	S	0	4	0
			2324	1472	398	447	7			
1	E	312	Total	C	N	O	S	0	1	0
			2304	1462	396	439	7			
1	F	314	Total	C	N	O	S	0	2	0
			2321	1473	397	444	7			
1	G	302	Total	C	N	O	S	0	1	0
			2225	1415	377	427	6			
1	H	313	Total	C	N	O	S	0	1	0
			2310	1465	396	442	7			

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	initiating methionine	UNP P44427
A	-22	HIS	-	expression tag	UNP P44427
A	-21	HIS	-	expression tag	UNP P44427
A	-20	HIS	-	expression tag	UNP P44427
A	-19	HIS	-	expression tag	UNP P44427
A	-18	HIS	-	expression tag	UNP P44427
A	-17	HIS	-	expression tag	UNP P44427
A	-16	SER	-	expression tag	UNP P44427
A	-15	SER	-	expression tag	UNP P44427
A	-14	GLY	-	expression tag	UNP P44427
A	-13	VAL	-	expression tag	UNP P44427
A	-12	ASP	-	expression tag	UNP P44427
A	-11	LEU	-	expression tag	UNP P44427

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	expression tag	UNP P44427
A	-9	THR	-	expression tag	UNP P44427
A	-8	GLU	-	expression tag	UNP P44427
A	-7	ASN	-	expression tag	UNP P44427
A	-6	LEU	-	expression tag	UNP P44427
A	-5	TYR	-	expression tag	UNP P44427
A	-4	PHE	-	expression tag	UNP P44427
A	-3	GLN	-	expression tag	UNP P44427
A	-2	SER	-	expression tag	UNP P44427
A	-1	ASN	-	expression tag	UNP P44427
A	0	ALA	-	expression tag	UNP P44427
B	-23	MET	-	initiating methionine	UNP P44427
B	-22	HIS	-	expression tag	UNP P44427
B	-21	HIS	-	expression tag	UNP P44427
B	-20	HIS	-	expression tag	UNP P44427
B	-19	HIS	-	expression tag	UNP P44427
B	-18	HIS	-	expression tag	UNP P44427
B	-17	HIS	-	expression tag	UNP P44427
B	-16	SER	-	expression tag	UNP P44427
B	-15	SER	-	expression tag	UNP P44427
B	-14	GLY	-	expression tag	UNP P44427
B	-13	VAL	-	expression tag	UNP P44427
B	-12	ASP	-	expression tag	UNP P44427
B	-11	LEU	-	expression tag	UNP P44427
B	-10	GLY	-	expression tag	UNP P44427
B	-9	THR	-	expression tag	UNP P44427
B	-8	GLU	-	expression tag	UNP P44427
B	-7	ASN	-	expression tag	UNP P44427
B	-6	LEU	-	expression tag	UNP P44427
B	-5	TYR	-	expression tag	UNP P44427
B	-4	PHE	-	expression tag	UNP P44427
B	-3	GLN	-	expression tag	UNP P44427
B	-2	SER	-	expression tag	UNP P44427
B	-1	ASN	-	expression tag	UNP P44427
B	0	ALA	-	expression tag	UNP P44427
C	-23	MET	-	initiating methionine	UNP P44427
C	-22	HIS	-	expression tag	UNP P44427
C	-21	HIS	-	expression tag	UNP P44427
C	-20	HIS	-	expression tag	UNP P44427
C	-19	HIS	-	expression tag	UNP P44427
C	-18	HIS	-	expression tag	UNP P44427
C	-17	HIS	-	expression tag	UNP P44427

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	SER	-	expression tag	UNP P44427
C	-15	SER	-	expression tag	UNP P44427
C	-14	GLY	-	expression tag	UNP P44427
C	-13	VAL	-	expression tag	UNP P44427
C	-12	ASP	-	expression tag	UNP P44427
C	-11	LEU	-	expression tag	UNP P44427
C	-10	GLY	-	expression tag	UNP P44427
C	-9	THR	-	expression tag	UNP P44427
C	-8	GLU	-	expression tag	UNP P44427
C	-7	ASN	-	expression tag	UNP P44427
C	-6	LEU	-	expression tag	UNP P44427
C	-5	TYR	-	expression tag	UNP P44427
C	-4	PHE	-	expression tag	UNP P44427
C	-3	GLN	-	expression tag	UNP P44427
C	-2	SER	-	expression tag	UNP P44427
C	-1	ASN	-	expression tag	UNP P44427
C	0	ALA	-	expression tag	UNP P44427
D	-23	MET	-	initiating methionine	UNP P44427
D	-22	HIS	-	expression tag	UNP P44427
D	-21	HIS	-	expression tag	UNP P44427
D	-20	HIS	-	expression tag	UNP P44427
D	-19	HIS	-	expression tag	UNP P44427
D	-18	HIS	-	expression tag	UNP P44427
D	-17	HIS	-	expression tag	UNP P44427
D	-16	SER	-	expression tag	UNP P44427
D	-15	SER	-	expression tag	UNP P44427
D	-14	GLY	-	expression tag	UNP P44427
D	-13	VAL	-	expression tag	UNP P44427
D	-12	ASP	-	expression tag	UNP P44427
D	-11	LEU	-	expression tag	UNP P44427
D	-10	GLY	-	expression tag	UNP P44427
D	-9	THR	-	expression tag	UNP P44427
D	-8	GLU	-	expression tag	UNP P44427
D	-7	ASN	-	expression tag	UNP P44427
D	-6	LEU	-	expression tag	UNP P44427
D	-5	TYR	-	expression tag	UNP P44427
D	-4	PHE	-	expression tag	UNP P44427
D	-3	GLN	-	expression tag	UNP P44427
D	-2	SER	-	expression tag	UNP P44427
D	-1	ASN	-	expression tag	UNP P44427
D	0	ALA	-	expression tag	UNP P44427
E	-23	MET	-	initiating methionine	UNP P44427

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-22	HIS	-	expression tag	UNP P44427
E	-21	HIS	-	expression tag	UNP P44427
E	-20	HIS	-	expression tag	UNP P44427
E	-19	HIS	-	expression tag	UNP P44427
E	-18	HIS	-	expression tag	UNP P44427
E	-17	HIS	-	expression tag	UNP P44427
E	-16	SER	-	expression tag	UNP P44427
E	-15	SER	-	expression tag	UNP P44427
E	-14	GLY	-	expression tag	UNP P44427
E	-13	VAL	-	expression tag	UNP P44427
E	-12	ASP	-	expression tag	UNP P44427
E	-11	LEU	-	expression tag	UNP P44427
E	-10	GLY	-	expression tag	UNP P44427
E	-9	THR	-	expression tag	UNP P44427
E	-8	GLU	-	expression tag	UNP P44427
E	-7	ASN	-	expression tag	UNP P44427
E	-6	LEU	-	expression tag	UNP P44427
E	-5	TYR	-	expression tag	UNP P44427
E	-4	PHE	-	expression tag	UNP P44427
E	-3	GLN	-	expression tag	UNP P44427
E	-2	SER	-	expression tag	UNP P44427
E	-1	ASN	-	expression tag	UNP P44427
E	0	ALA	-	expression tag	UNP P44427
F	-23	MET	-	initiating methionine	UNP P44427
F	-22	HIS	-	expression tag	UNP P44427
F	-21	HIS	-	expression tag	UNP P44427
F	-20	HIS	-	expression tag	UNP P44427
F	-19	HIS	-	expression tag	UNP P44427
F	-18	HIS	-	expression tag	UNP P44427
F	-17	HIS	-	expression tag	UNP P44427
F	-16	SER	-	expression tag	UNP P44427
F	-15	SER	-	expression tag	UNP P44427
F	-14	GLY	-	expression tag	UNP P44427
F	-13	VAL	-	expression tag	UNP P44427
F	-12	ASP	-	expression tag	UNP P44427
F	-11	LEU	-	expression tag	UNP P44427
F	-10	GLY	-	expression tag	UNP P44427
F	-9	THR	-	expression tag	UNP P44427
F	-8	GLU	-	expression tag	UNP P44427
F	-7	ASN	-	expression tag	UNP P44427
F	-6	LEU	-	expression tag	UNP P44427
F	-5	TYR	-	expression tag	UNP P44427

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-4	PHE	-	expression tag	UNP P44427
F	-3	GLN	-	expression tag	UNP P44427
F	-2	SER	-	expression tag	UNP P44427
F	-1	ASN	-	expression tag	UNP P44427
F	0	ALA	-	expression tag	UNP P44427
G	-23	MET	-	initiating methionine	UNP P44427
G	-22	HIS	-	expression tag	UNP P44427
G	-21	HIS	-	expression tag	UNP P44427
G	-20	HIS	-	expression tag	UNP P44427
G	-19	HIS	-	expression tag	UNP P44427
G	-18	HIS	-	expression tag	UNP P44427
G	-17	HIS	-	expression tag	UNP P44427
G	-16	SER	-	expression tag	UNP P44427
G	-15	SER	-	expression tag	UNP P44427
G	-14	GLY	-	expression tag	UNP P44427
G	-13	VAL	-	expression tag	UNP P44427
G	-12	ASP	-	expression tag	UNP P44427
G	-11	LEU	-	expression tag	UNP P44427
G	-10	GLY	-	expression tag	UNP P44427
G	-9	THR	-	expression tag	UNP P44427
G	-8	GLU	-	expression tag	UNP P44427
G	-7	ASN	-	expression tag	UNP P44427
G	-6	LEU	-	expression tag	UNP P44427
G	-5	TYR	-	expression tag	UNP P44427
G	-4	PHE	-	expression tag	UNP P44427
G	-3	GLN	-	expression tag	UNP P44427
G	-2	SER	-	expression tag	UNP P44427
G	-1	ASN	-	expression tag	UNP P44427
G	0	ALA	-	expression tag	UNP P44427
H	-23	MET	-	initiating methionine	UNP P44427
H	-22	HIS	-	expression tag	UNP P44427
H	-21	HIS	-	expression tag	UNP P44427
H	-20	HIS	-	expression tag	UNP P44427
H	-19	HIS	-	expression tag	UNP P44427
H	-18	HIS	-	expression tag	UNP P44427
H	-17	HIS	-	expression tag	UNP P44427
H	-16	SER	-	expression tag	UNP P44427
H	-15	SER	-	expression tag	UNP P44427
H	-14	GLY	-	expression tag	UNP P44427
H	-13	VAL	-	expression tag	UNP P44427
H	-12	ASP	-	expression tag	UNP P44427
H	-11	LEU	-	expression tag	UNP P44427

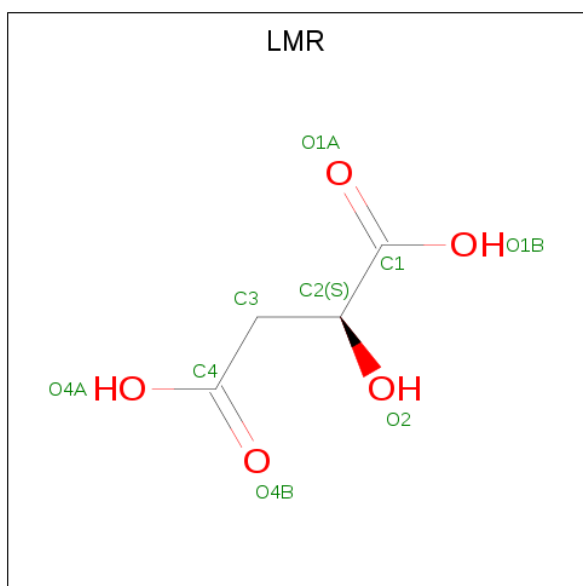
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Chain	Residue	Modelled	Actual	Comment	Reference
H	-10	GLY	-	expression tag	UNP P44427
H	-9	THR	-	expression tag	UNP P44427
H	-8	GLU	-	expression tag	UNP P44427
H	-7	ASN	-	expression tag	UNP P44427
H	-6	LEU	-	expression tag	UNP P44427
H	-5	TYR	-	expression tag	UNP P44427
H	-4	PHE	-	expression tag	UNP P44427
H	-3	GLN	-	expression tag	UNP P44427
H	-2	SER	-	expression tag	UNP P44427
H	-1	ASN	-	expression tag	UNP P44427
H	0	ALA	-	expression tag	UNP P44427

- Molecule 2 is (2S)-2-hydroxybutanedioic acid (three-letter code: LMR) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 9 4 5	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	2	Total Cl 3 3	0	1
3	D	2	Total Cl 2 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	3	Total 4	Cl 4	0	1
3	H	1	Total 1	Cl 1	0	0
3	B	2	Total 2	Cl 2	0	0
3	C	3	Total 4	Cl 4	0	1
3	A	2	Total 3	Cl 3	0	1
3	F	2	Total 2	Cl 2	0	0

- Molecule 4 is water.

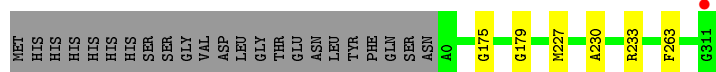
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	170	Total 174	O 174	0	4
4	B	163	Total 166	O 166	0	4
4	C	188	Total 192	O 192	0	4
4	D	195	Total 197	O 197	0	2
4	E	167	Total 170	O 170	0	4
4	F	138	Total 138	O 138	0	0
4	G	101	Total 101	O 101	0	0
4	H	158	Total 161	O 161	0	3

### 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.

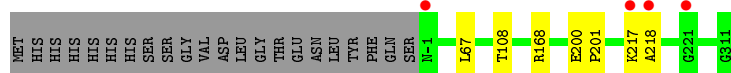
- Molecule 1: Malate dehydrogenase

Chain A: 




- Molecule 1: Malate dehydrogenase

Chain B: 

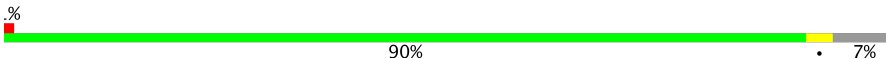


- Molecule 1: Malate dehydrogenase

Chain C: 




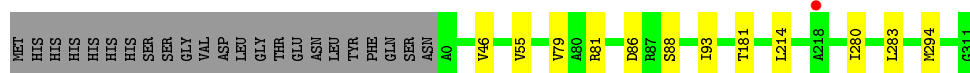
- Molecule 1: Malate dehydrogenase

Chain D: 

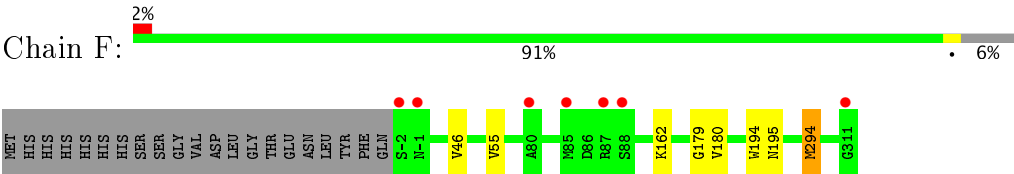


- Molecule 1: Malate dehydrogenase

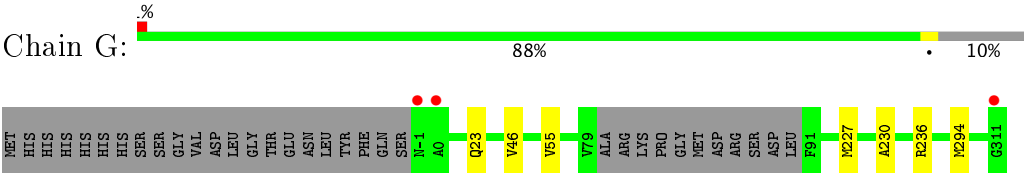
Chain E: 



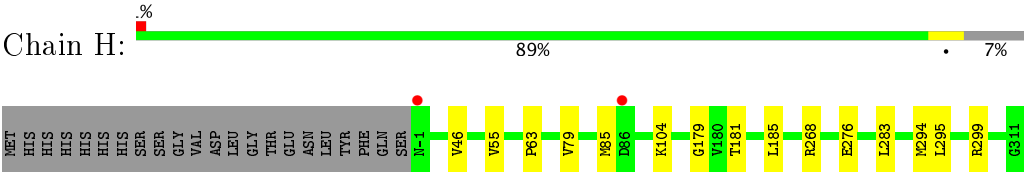
- Molecule 1: Malate dehydrogenase



• Molecule 1: Malate dehydrogenase



• Molecule 1: Malate dehydrogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.11Å 78.08Å 114.03Å 71.09° 75.44° 68.06°	Depositor
Resolution (Å)	29.75 – 2.10 29.75 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.8 (29.75-2.10) 89.2 (29.75-2.10)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.53 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.170 , 0.219 0.175 , 0.220	Depositor DCC
$R_{free}$ test set	6277 reflections (5.22%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.8	Xtriage
Anisotropy	0.120	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	19775	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.96 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.6345e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LMR, 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	0.43	0/2334	0.65	0/3169
1	B	0.42	0/2343	0.65	0/3181
1	C	0.43	0/2384	0.67	0/3236
1	D	0.43	0/2357	0.65	0/3200
1	E	0.42	0/2337	0.65	0/3172
1	F	0.40	0/2354	0.64	0/3197
1	G	0.40	0/2256	0.60	0/3064
1	H	0.41	0/2343	0.64	0/3181
All	All	0.42	0/18708	0.65	0/25400

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	2301	0	2387	2	0
1	B	2310	0	2393	3	0
1	C	2351	0	2424	14	0
1	D	2324	0	2401	4	0
1	E	2304	0	2394	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2321	0	2409	3	0
1	G	2225	0	2305	3	0
1	H	2310	0	2395	9	0
2	A	9	0	4	0	0
3	A	3	0	0	0	0
3	B	2	0	0	0	0
3	C	4	0	0	0	0
3	D	2	0	0	0	0
3	E	4	0	0	0	0
3	F	2	0	0	0	0
3	G	3	0	0	0	0
3	H	1	0	0	0	0
4	A	174	0	0	0	0
4	B	166	0	0	0	0
4	C	192	0	0	0	0
4	D	197	0	0	0	0
4	E	170	0	0	0	0
4	F	138	0	0	0	0
4	G	101	0	0	0	0
4	H	161	0	0	0	0
All	All	19775	0	19112	43	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.

All (43) 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:C:79:VAL:HG12	1:E:93:ILE:HD13	1.68	0.76
1:C:195[A]:ASN:HB2	1:C:197[A]:ASP:OD1	1.86	0.76
1:H:181:THR:HA	1:H:294:MET:HG3	1.67	0.75
1:C:79:VAL:HG11	1:E:79:VAL:HG11	1.71	0.72
1:H:181:THR:HA	1:H:294:MET:CG	2.25	0.67
1:C:79:VAL:HG11	1:E:79:VAL:CG1	2.25	0.67
1:E:81:ARG:HG2	1:E:214:LEU:HD11	1.84	0.59
1:C:195[A]:ASN:CB	1:C:197[A]:ASP:OD1	2.51	0.59
1:C:79:VAL:CG1	1:E:93:ILE:HD13	2.32	0.59
1:C:93:ILE:HD13	1:E:79:VAL:HG13	1.86	0.58
1:F:46[B]:VAL:HG23	1:F:55:VAL:HG11	1.89	0.55
1:E:181:THR:HA	1:E:294:MET:HG3	1.90	0.53
1:H:268:ARG:NH2	1:H:276:GLU:OE1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:295:LEU:O	1:C:299:ARG:HG2	2.11	0.51
1:E:86:ASP:C	1:E:88:SER:H	2.16	0.48
1:A:227:MET:HE3	1:A:230:ALA:HB3	1.96	0.46
1:D:227:MET:HE3	1:D:230:ALA:HB3	1.96	0.46
1:H:185:LEU:HD22	1:H:283:LEU:HD22	1.97	0.46
1:C:6:LEU:HD11	1:C:67:LEU:HD21	1.98	0.45
1:C:79:VAL:CG1	1:E:79:VAL:HG11	2.45	0.45
1:F:180:VAL:HG22	1:F:294:MET:HB3	1.99	0.44
1:H:295:LEU:HD13	1:H:299:ARG:NH2	2.33	0.44
1:H:46:VAL:HG23	1:H:55:VAL:HG11	2.00	0.44
1:E:46:VAL:HG23	1:E:55:VAL:HG11	2.00	0.43
1:C:23:GLN:HB3	1:C:236[A]:ARG:HD2	2.00	0.43
1:G:227:MET:HE3	1:G:230:ALA:HB3	2.01	0.42
1:H:63:PRO:CD	1:H:104:LYS:HD3	2.49	0.42
1:H:63:PRO:HD2	1:H:104:LYS:HD3	2.02	0.42
1:D:289:GLN:NE2	1:D:293:ASN:OD1	2.47	0.41
1:F:162:LYS:HD3	1:F:194:TRP:CZ3	2.56	0.41
1:C:1:MET:HG3	1:C:239:VAL:HG13	2.02	0.41
1:D:195[B]:ASN:OD1	1:D:196:GLU:N	2.53	0.41
1:G:23:GLN:HB3	1:G:236:ARG:HD2	2.03	0.41
1:D:30:LEU:O	1:D:55:VAL:HA	2.21	0.41
1:B:67:LEU:HB2	1:B:108:THR:HG21	2.01	0.41
1:B:217:LYS:O	1:B:218:ALA:HB3	2.20	0.41
1:C:295:LEU:HB2	1:C:296:PRO:HD3	2.03	0.41
1:G:46:VAL:HG23	1:G:55:VAL:HG11	2.02	0.41
1:C:237:SER:OG	1:C:249:GLU:OE2	2.31	0.41
1:H:79:VAL:HG11	1:H:85:MET:HE1	2.01	0.41
1:A:175:GLY:HA2	1:A:263:PHE:CE1	2.56	0.40
1:E:280:ILE:HD12	1:E:283:LEU:HD11	2.04	0.40
1:B:200:GLU:HB3	1:B:201:PRO:HD3	2.02	0.40

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	311/335 (93%)	305 (98%)	5 (2%)	1 (0%)	44	44
1	B	312/335 (93%)	304 (97%)	8 (3%)	0	100	100
1	C	317/335 (95%)	311 (98%)	6 (2%)	0	100	100
1	D	314/335 (94%)	309 (98%)	4 (1%)	1 (0%)	44	44
1	E	311/335 (93%)	307 (99%)	4 (1%)	0	100	100
1	F	314/335 (94%)	307 (98%)	6 (2%)	1 (0%)	44	44
1	G	299/335 (89%)	289 (97%)	10 (3%)	0	100	100
1	H	312/335 (93%)	304 (97%)	7 (2%)	1 (0%)	44	44
All	All	2490/2680 (93%)	2436 (98%)	50 (2%)	4 (0%)	51	52

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	179	GLY
1	F	179	GLY
1	H	179	GLY
1	A	179	GLY

### 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	245/265 (92%)	244 (100%)	1 (0%)	93	95
1	B	246/265 (93%)	245 (100%)	1 (0%)	93	95
1	C	251/265 (95%)	249 (99%)	2 (1%)	85	89
1	D	248/265 (94%)	247 (100%)	1 (0%)	93	95
1	E	245/265 (92%)	245 (100%)	0	100	100
1	F	248/265 (94%)	246 (99%)	2 (1%)	85	89
1	G	237/265 (89%)	236 (100%)	1 (0%)	93	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	246/265 (93%)	246 (100%)	0	100	100
All	All	1966/2120 (93%)	1958 (100%)	8 (0%)	93	95

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	233	ARG
1	B	168	ARG
1	C	87	ARG
1	C	294	MET
1	D	294	MET
1	F	195	ASN
1	F	294	MET
1	G	294	MET

Some 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 22 ligands modelled in this entry, 21 are monoatomic - leaving 1 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	$\# Z  > 2$
2	LMR	A	401	-	2,8,8	0.57	0	4,10,10	0.46	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
2	LMR	A	401	-	-	0/2/8/8	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [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 ⓘ

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	312/335 (93%)	-0.65	1 (0%) 93 94	22, 32, 53, 82	0
1	B	313/335 (93%)	-0.58	4 (1%) 77 81	22, 31, 64, 101	0
1	C	313/335 (93%)	-0.61	4 (1%) 77 81	19, 28, 55, 88	0
1	D	312/335 (93%)	-0.68	2 (0%) 89 91	20, 29, 48, 76	0
1	E	312/335 (93%)	-0.63	1 (0%) 93 94	21, 32, 57, 89	0
1	F	314/335 (93%)	-0.47	7 (2%) 62 67	23, 38, 68, 114	0
1	G	302/335 (90%)	-0.51	3 (0%) 82 85	27, 42, 63, 92	0
1	H	313/335 (93%)	-0.56	2 (0%) 89 91	24, 34, 63, 104	0
All	All	2491/2680 (92%)	-0.59	24 (0%) 82 85	19, 33, 60, 114	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	-2	SER	7.5
1	F	88	SER	6.3
1	B	-1	ASN	4.9
1	B	218	ALA	4.0
1	F	-1	ASN	3.7
1	H	-1	ASN	3.7
1	G	311	GLY	3.3
1	D	83	PRO	3.2
1	F	311	GLY	2.9
1	G	-1	ASN	2.9
1	C	-1	ASN	2.9
1	B	217	LYS	2.8
1	F	85	MET	2.7
1	H	86	ASP	2.6
1	B	221	GLY	2.5
1	A	311	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	G	0	ALA	2.3
1	E	218	ALA	2.3
1	F	87	ARG	2.3
1	C	84	GLY	2.3
1	D	311	GLY	2.2
1	C	85	MET	2.2
1	C	83	PRO	2.0
1	F	80	ALA	2.0

## 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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	CL	A	402[B]	1/1	0.98	0.11	2.83	35,35,35,35	1
3	CL	A	402[A]	1/1	0.98	0.11	2.83	29,29,29,29	1
2	LMR	A	401	9/9	0.96	0.14	1.85	47,50,55,56	0
3	CL	D	401	1/1	0.99	0.13	0.91	29,29,29,29	1
3	CL	C	402[B]	1/1	0.98	0.09	0.30	30,30,30,30	1
3	CL	C	402[A]	1/1	0.98	0.09	0.30	31,31,31,31	1
3	CL	G	401[A]	1/1	0.98	0.08	0.13	36,36,36,36	1
3	CL	G	401[B]	1/1	0.98	0.08	0.13	38,38,38,38	1
3	CL	E	402[A]	1/1	0.98	0.08	-0.48	29,29,29,29	1
3	CL	E	402[B]	1/1	0.98	0.08	-0.48	32,32,32,32	1
3	CL	F	401	1/1	0.96	0.06	-0.55	56,56,56,56	0
3	CL	H	401	1/1	0.99	0.08	-0.57	27,27,27,27	1
3	CL	C	401	1/1	0.99	0.06	-0.82	32,32,32,32	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CL	B	401	1/1	1.00	0.06	-0.85	32,32,32,32	0
3	CL	E	401	1/1	0.99	0.03	-2.93	39,39,39,39	0
3	CL	E	403	1/1	1.00	0.11	-	45,45,45,45	0
3	CL	A	403	1/1	0.98	0.10	-	46,46,46,46	0
3	CL	G	402	1/1	1.00	0.07	-	48,48,48,48	0
3	CL	D	402	1/1	0.98	0.10	-	49,49,49,49	0
3	CL	F	402	1/1	0.99	0.11	-	45,45,45,45	0
3	CL	C	403	1/1	1.00	0.06	-	44,44,44,44	0
3	CL	B	402	1/1	1.00	0.13	-	39,39,39,39	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.