



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 02:03 am BST

PDB ID : 2YVX
Title : Crystal structure of magnesium transporter MgtE
Authors : Hattori, M.; Tanaka, Y.; Fukai, S.; Ishitani, R.; Nureki, O.
Deposited on : 2007-04-18
Resolution : 3.50 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
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

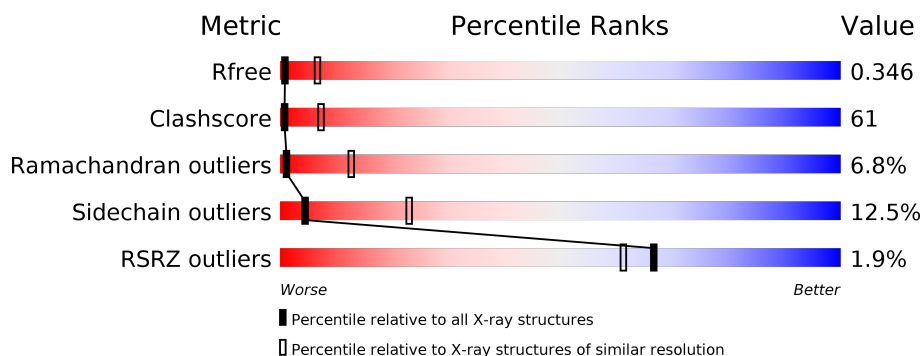
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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 $\leq 5\%$. 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	473	<div> <div>29%</div> <div>53%</div> <div>10%</div> <div>7%</div> </div>
1	B	473	<div> <div>26%</div> <div>55%</div> <div>12%</div> <div>7%</div> </div>
1	C	473	<div> <div>2%</div> <div>26%</div> <div>56%</div> <div>12%</div> <div>7%</div> </div>
1	D	473	<div> <div>5%</div> <div>26%</div> <div>55%</div> <div>11%</div> <div>7%</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MG	C	453	-	-	-	X

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13898 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 Mg2+ transporter MgtE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	442	Total	C	N	O	S	0	0	0
			3470	2238	577	648	7			
1	B	442	Total	C	N	O	S	0	0	0
			3470	2238	577	648	7			
1	C	442	Total	C	N	O	S	0	0	0
			3470	2238	577	648	7			
1	D	442	Total	C	N	O	S	0	0	0
			3470	2238	577	648	7			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	EXPRESSION TAG	UNP Q5SMG8
A	-21	GLY	-	EXPRESSION TAG	UNP Q5SMG8
A	-20	SER	-	EXPRESSION TAG	UNP Q5SMG8
A	-19	SER	-	EXPRESSION TAG	UNP Q5SMG8
A	-18	HIS	-	EXPRESSION TAG	UNP Q5SMG8
A	-17	HIS	-	EXPRESSION TAG	UNP Q5SMG8
A	-16	HIS	-	EXPRESSION TAG	UNP Q5SMG8
A	-15	HIS	-	EXPRESSION TAG	UNP Q5SMG8
A	-14	HIS	-	EXPRESSION TAG	UNP Q5SMG8
A	-13	HIS	-	EXPRESSION TAG	UNP Q5SMG8
A	-12	SER	-	EXPRESSION TAG	UNP Q5SMG8
A	-11	SER	-	EXPRESSION TAG	UNP Q5SMG8
A	-10	GLY	-	EXPRESSION TAG	UNP Q5SMG8
A	-9	LEU	-	EXPRESSION TAG	UNP Q5SMG8
A	-8	GLY	-	EXPRESSION TAG	UNP Q5SMG8
A	-7	VAL	-	EXPRESSION TAG	UNP Q5SMG8
A	-6	LEU	-	EXPRESSION TAG	UNP Q5SMG8
A	-5	PRO	-	EXPRESSION TAG	UNP Q5SMG8
A	-4	GLY	-	EXPRESSION TAG	UNP Q5SMG8
A	-3	GLY	-	EXPRESSION TAG	UNP Q5SMG8
A	-2	PRO	-	EXPRESSION TAG	UNP Q5SMG8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	LEU	-	EXPRESSION TAG	UNP Q5SMG8
A	0	HIS	-	EXPRESSION TAG	UNP Q5SMG8
B	-22	MET	-	EXPRESSION TAG	UNP Q5SMG8
B	-21	GLY	-	EXPRESSION TAG	UNP Q5SMG8
B	-20	SER	-	EXPRESSION TAG	UNP Q5SMG8
B	-19	SER	-	EXPRESSION TAG	UNP Q5SMG8
B	-18	HIS	-	EXPRESSION TAG	UNP Q5SMG8
B	-17	HIS	-	EXPRESSION TAG	UNP Q5SMG8
B	-16	HIS	-	EXPRESSION TAG	UNP Q5SMG8
B	-15	HIS	-	EXPRESSION TAG	UNP Q5SMG8
B	-14	HIS	-	EXPRESSION TAG	UNP Q5SMG8
B	-13	HIS	-	EXPRESSION TAG	UNP Q5SMG8
B	-12	SER	-	EXPRESSION TAG	UNP Q5SMG8
B	-11	SER	-	EXPRESSION TAG	UNP Q5SMG8
B	-10	GLY	-	EXPRESSION TAG	UNP Q5SMG8
B	-9	LEU	-	EXPRESSION TAG	UNP Q5SMG8
B	-8	GLY	-	EXPRESSION TAG	UNP Q5SMG8
B	-7	VAL	-	EXPRESSION TAG	UNP Q5SMG8
B	-6	LEU	-	EXPRESSION TAG	UNP Q5SMG8
B	-5	PRO	-	EXPRESSION TAG	UNP Q5SMG8
B	-4	GLY	-	EXPRESSION TAG	UNP Q5SMG8
B	-3	GLY	-	EXPRESSION TAG	UNP Q5SMG8
B	-2	PRO	-	EXPRESSION TAG	UNP Q5SMG8
B	-1	LEU	-	EXPRESSION TAG	UNP Q5SMG8
B	0	HIS	-	EXPRESSION TAG	UNP Q5SMG8
C	-22	MET	-	EXPRESSION TAG	UNP Q5SMG8
C	-21	GLY	-	EXPRESSION TAG	UNP Q5SMG8
C	-20	SER	-	EXPRESSION TAG	UNP Q5SMG8
C	-19	SER	-	EXPRESSION TAG	UNP Q5SMG8
C	-18	HIS	-	EXPRESSION TAG	UNP Q5SMG8
C	-17	HIS	-	EXPRESSION TAG	UNP Q5SMG8
C	-16	HIS	-	EXPRESSION TAG	UNP Q5SMG8
C	-15	HIS	-	EXPRESSION TAG	UNP Q5SMG8
C	-14	HIS	-	EXPRESSION TAG	UNP Q5SMG8
C	-13	HIS	-	EXPRESSION TAG	UNP Q5SMG8
C	-12	SER	-	EXPRESSION TAG	UNP Q5SMG8
C	-11	SER	-	EXPRESSION TAG	UNP Q5SMG8
C	-10	GLY	-	EXPRESSION TAG	UNP Q5SMG8
C	-9	LEU	-	EXPRESSION TAG	UNP Q5SMG8
C	-8	GLY	-	EXPRESSION TAG	UNP Q5SMG8
C	-7	VAL	-	EXPRESSION TAG	UNP Q5SMG8
C	-6	LEU	-	EXPRESSION TAG	UNP Q5SMG8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	PRO	-	EXPRESSION TAG	UNP Q5SMG8
C	-4	GLY	-	EXPRESSION TAG	UNP Q5SMG8
C	-3	GLY	-	EXPRESSION TAG	UNP Q5SMG8
C	-2	PRO	-	EXPRESSION TAG	UNP Q5SMG8
C	-1	LEU	-	EXPRESSION TAG	UNP Q5SMG8
C	0	HIS	-	EXPRESSION TAG	UNP Q5SMG8
D	-22	MET	-	EXPRESSION TAG	UNP Q5SMG8
D	-21	GLY	-	EXPRESSION TAG	UNP Q5SMG8
D	-20	SER	-	EXPRESSION TAG	UNP Q5SMG8
D	-19	SER	-	EXPRESSION TAG	UNP Q5SMG8
D	-18	HIS	-	EXPRESSION TAG	UNP Q5SMG8
D	-17	HIS	-	EXPRESSION TAG	UNP Q5SMG8
D	-16	HIS	-	EXPRESSION TAG	UNP Q5SMG8
D	-15	HIS	-	EXPRESSION TAG	UNP Q5SMG8
D	-14	HIS	-	EXPRESSION TAG	UNP Q5SMG8
D	-13	HIS	-	EXPRESSION TAG	UNP Q5SMG8
D	-12	SER	-	EXPRESSION TAG	UNP Q5SMG8
D	-11	SER	-	EXPRESSION TAG	UNP Q5SMG8
D	-10	GLY	-	EXPRESSION TAG	UNP Q5SMG8
D	-9	LEU	-	EXPRESSION TAG	UNP Q5SMG8
D	-8	GLY	-	EXPRESSION TAG	UNP Q5SMG8
D	-7	VAL	-	EXPRESSION TAG	UNP Q5SMG8
D	-6	LEU	-	EXPRESSION TAG	UNP Q5SMG8
D	-5	PRO	-	EXPRESSION TAG	UNP Q5SMG8
D	-4	GLY	-	EXPRESSION TAG	UNP Q5SMG8
D	-3	GLY	-	EXPRESSION TAG	UNP Q5SMG8
D	-2	PRO	-	EXPRESSION TAG	UNP Q5SMG8
D	-1	LEU	-	EXPRESSION TAG	UNP Q5SMG8
D	0	HIS	-	EXPRESSION TAG	UNP Q5SMG8

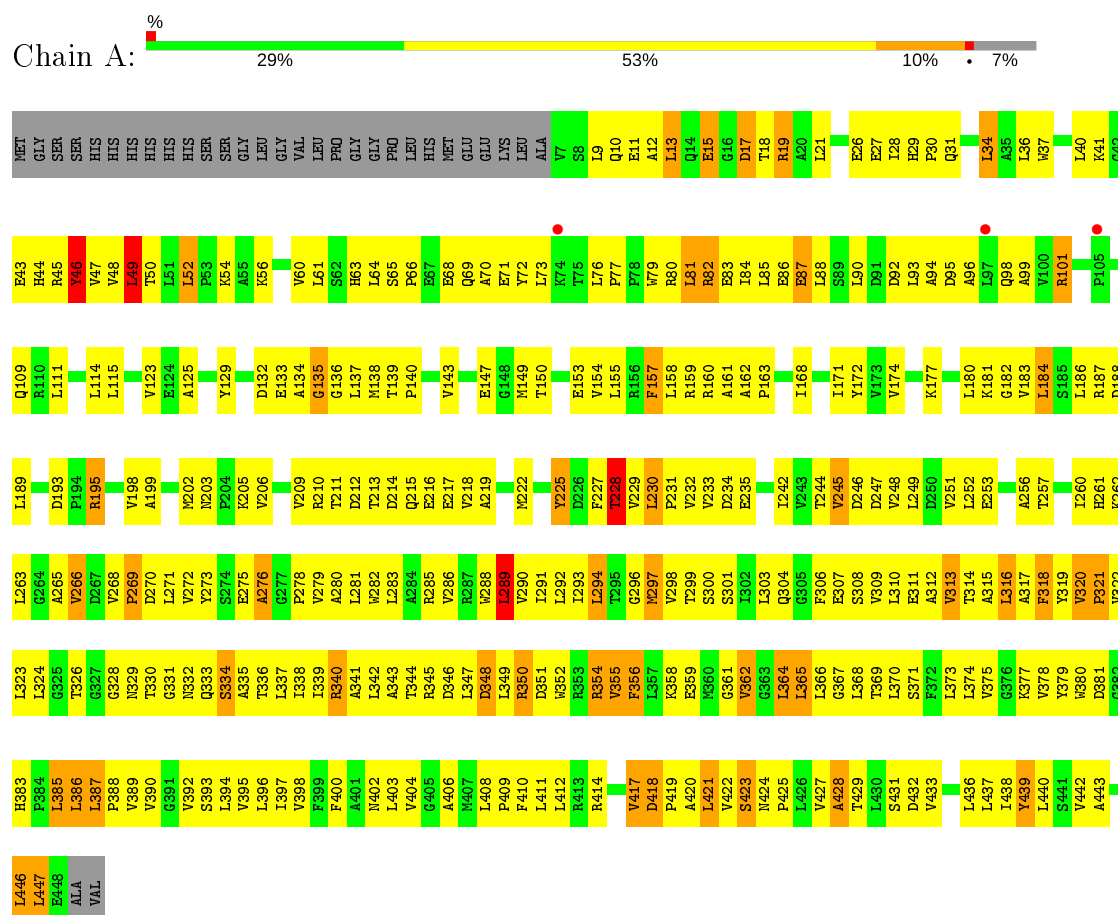
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	5	Total Mg 5 5	0	0
2	A	4	Total Mg 4 4	0	0
2	D	4	Total Mg 4 4	0	0
2	C	5	Total Mg 5 5	0	0

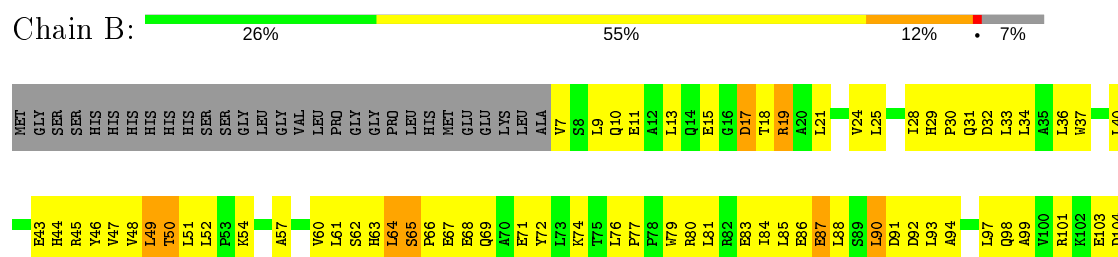
3 Residue-property plots

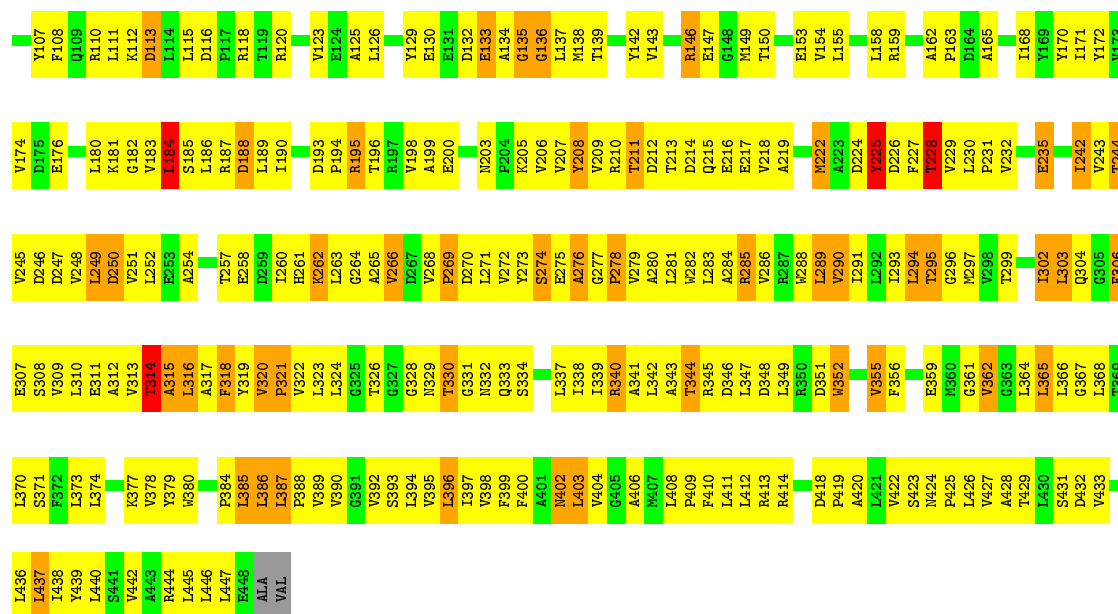
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Mg²⁺ transporter MgtE

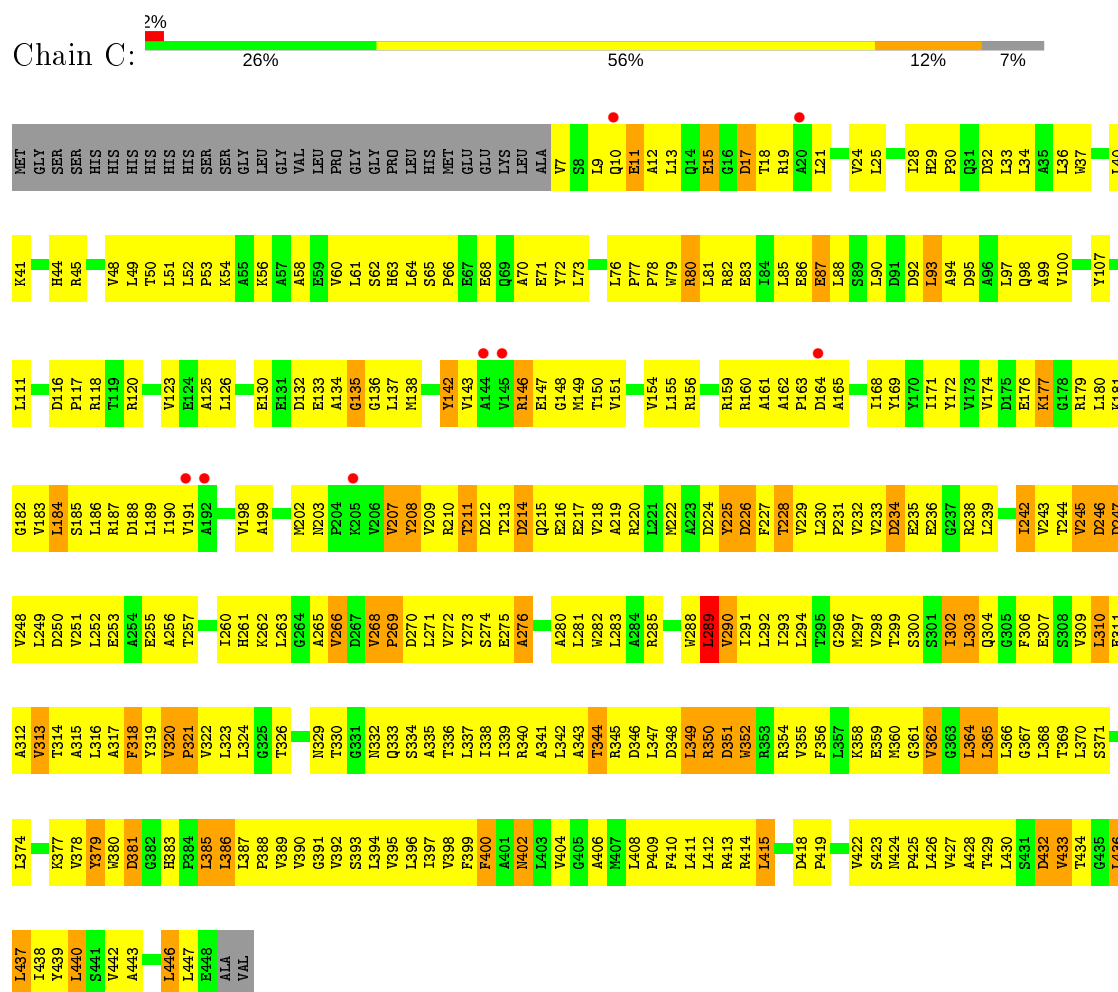


• Molecule 1: Mg²⁺ transporter MgtE





- Molecule 1: Mg²⁺ transporter MgtE



- Molecule 1: Mg²⁺ transporter MgtE



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	118.31Å 134.90Å 366.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.69 – 3.50 49.69 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.69-3.50) 98.3 (49.69-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 3.40Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.294 , 0.341 0.303 , 0.346	Depositor DCC
R_{free} test set	1854 reflections (4.63%)	wwPDB-VP
Wilson B-factor (Å ²)	97.1	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.35$, $\langle L^2 \rangle = 0.18$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	13898	wwPDB-VP
Average B, all atoms (Å ²)	115.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.64	0/3530	0.76	0/4815
1	B	0.65	0/3530	0.76	2/4815 (0.0%)
1	C	0.56	0/3530	0.70	0/4815
1	D	0.57	3/3530 (0.1%)	0.72	1/4815 (0.0%)
All	All	0.61	3/14120 (0.0%)	0.73	3/19260 (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	D	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	311	GLU	CB-CG	8.63	1.68	1.52
1	D	315	ALA	CA-CB	-7.63	1.36	1.52
1	D	314	THR	C-O	-6.37	1.11	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	311	GLU	N-CA-CB	6.01	121.42	110.60
1	B	314	THR	CB-CA-C	-5.83	95.85	111.60
1	B	264	GLY	N-CA-C	-5.27	99.93	113.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	439	TYR	Sidechain
1	D	439	TYR	Sidechain

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	3470	0	3576	445	0
1	B	3470	0	3577	460	0
1	C	3470	0	3577	514	0
1	D	3470	0	3577	524	1
2	A	4	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	4	0	0	0	0
All	All	13898	0	14307	1711	1

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 61.

The worst 5 of 1711 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:333:GLN:NE2	1:D:265:ALA:HB3	1.50	1.26
1:A:311:GLU:O	1:A:314:THR:OG1	1.56	1.23
1:C:340:ARG:HH12	1:D:260:ILE:HB	1.08	1.18
1:B:268:VAL:HB	1:B:271:LEU:HD11	1.28	1.15
1:A:378:VAL:HG11	1:A:390:VAL:HG21	1.28	1.15

All (1) 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:D:109:GLN:NE2	1:D:109:GLN:NE2[3_656]	1.97	0.23

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	440/473 (93%)	310 (70%)	100 (23%)	30 (7%)	1	13
1	B	440/473 (93%)	312 (71%)	96 (22%)	32 (7%)	1	11
1	C	440/473 (93%)	315 (72%)	98 (22%)	27 (6%)	1	15
1	D	440/473 (93%)	307 (70%)	103 (23%)	30 (7%)	1	13
All	All	1760/1892 (93%)	1244 (71%)	397 (23%)	119 (7%)	1	13

5 of 119 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	LEU
1	A	266	VAL
1	A	269	PRO
1	A	386	LEU
1	A	428	ALA

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	376/400 (94%)	329 (88%)	47 (12%)	4	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	376/400 (94%)	330 (88%)	46 (12%)	5	23
1	C	376/400 (94%)	326 (87%)	50 (13%)	4	21
1	D	376/400 (94%)	331 (88%)	45 (12%)	5	24
All	All	1504/1600 (94%)	1316 (88%)	188 (12%)	4	23

5 of 188 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	352	TRP
1	C	211	THR
1	D	349	LEU
1	B	362	VAL
1	C	71	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	31	GLN
1	C	215	GLN
1	D	332	ASN
1	C	10	GLN
1	D	333	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 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

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

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	442/473 (93%)	-0.51	3 (0%) 87 83	41, 99, 150, 167	0
1	B	442/473 (93%)	-0.52	0 100 100	51, 95, 135, 161	0
1	C	442/473 (93%)	-0.32	8 (1%) 68 62	61, 122, 167, 194	0
1	D	442/473 (93%)	-0.12	23 (5%) 27 24	63, 141, 188, 203	0
All	All	1768/1892 (93%)	-0.37	34 (1%) 66 61	41, 108, 174, 203	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	145	VAL	5.0
1	D	145	VAL	4.6
1	D	134	ALA	4.1
1	D	23	GLU	3.9
1	A	74	LYS	3.8

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no 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, 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(\AA^2)	Q<0.9
2	MG	D	452	1/1	0.76	0.28	61,61,61,61	0
2	MG	C	453	1/1	0.77	0.95	60,60,60,60	0
2	MG	D	454	1/1	0.81	0.54	78,78,78,78	0
2	MG	C	455	1/1	0.89	0.31	67,67,67,67	0
2	MG	C	454	1/1	0.90	0.34	53,53,53,53	0
2	MG	D	451	1/1	0.90	0.28	61,61,61,61	0
2	MG	A	451	1/1	0.92	0.29	46,46,46,46	0
2	MG	B	453	1/1	0.93	0.19	40,40,40,40	0
2	MG	B	455	1/1	0.94	0.58	60,60,60,60	0
2	MG	C	451	1/1	0.95	0.48	33,33,33,33	0
2	MG	A	452	1/1	0.95	0.26	36,36,36,36	0
2	MG	C	452	1/1	0.96	0.30	38,38,38,38	0
2	MG	B	451	1/1	0.96	0.55	34,34,34,34	0
2	MG	B	452	1/1	0.97	0.23	39,39,39,39	0
2	MG	D	453	1/1	0.97	0.33	40,40,40,40	0
2	MG	A	454	1/1	0.98	0.54	68,68,68,68	0
2	MG	A	453	1/1	0.98	0.35	40,40,40,40	0
2	MG	B	454	1/1	0.98	0.24	33,33,33,33	0

6.5 Other polymers ⓘ

There are no such residues in this entry.