



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 07:42 am BST

PDB ID : 5LK5
Title : Crystal structure of the globular domain of human calreticulin mutant D71K
Authors : Gaboriaud, C.; Cioci, G.
Deposited on : 2016-07-21
Resolution : 2.30 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

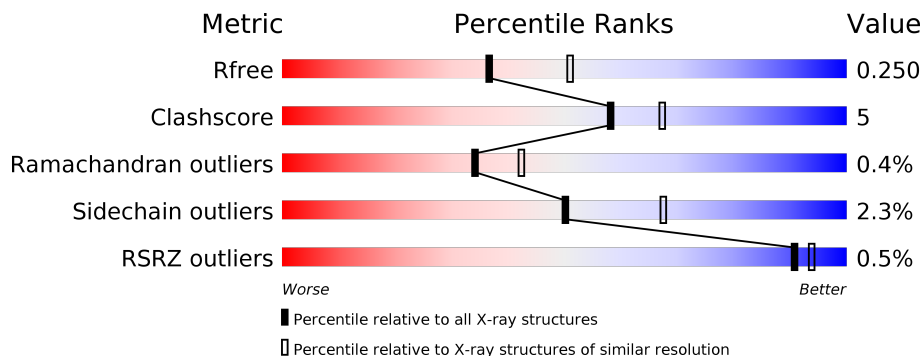
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	265	
1	B	265	
1	C	265	
1	D	265	
1	E	265	
1	F	265	

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Mol	Chain	Length	Quality of chain
1	G	265	 81% 14% . .
1	H	265	%  78% 15% . .
1	I	265	%  83% 11% 6%
1	J	265	%  80% 15% . .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 21334 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 Calreticulin, Calreticulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	256	2051	1305	330	410	6	0	0	0
1	B	251	2021	1288	325	402	6	0	0	0
1	C	255	2044	1301	329	408	6	0	1	0
1	D	256	2050	1304	330	410	6	0	0	0
1	E	249	2014	1283	327	398	6	0	0	0
1	F	255	2038	1297	328	407	6	0	0	0
1	G	255	2047	1302	332	407	6	0	0	0
1	H	254	2045	1299	332	408	6	0	1	0
1	I	250	2008	1280	323	399	6	0	0	0
1	J	255	2044	1300	331	407	6	0	0	0

There are 130 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	ASN	-	expression tag	UNP P27797
A	11	LYS	-	expression tag	UNP P27797
A	12	GLY	-	expression tag	UNP P27797
A	13	SER	-	expression tag	UNP P27797
A	14	ILE	-	expression tag	UNP P27797
A	15	GLU	-	expression tag	UNP P27797
A	16	GLY	-	expression tag	UNP P27797
A	17	ARG	-	expression tag	UNP P27797
A	71	LYS	ASP	engineered mutation	UNP P27797

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Chain	Residue	Modelled	Actual	Comment	Reference
A	205	GLY	-	linker	UNP P27797
A	206	SER	-	linker	UNP P27797
A	207	GLY	-	linker	UNP P27797
A	302	ASP	-	linker	UNP P27797
B	10	ASN	-	expression tag	UNP P27797
B	11	LYS	-	expression tag	UNP P27797
B	12	GLY	-	expression tag	UNP P27797
B	13	SER	-	expression tag	UNP P27797
B	14	ILE	-	expression tag	UNP P27797
B	15	GLU	-	expression tag	UNP P27797
B	16	GLY	-	expression tag	UNP P27797
B	17	ARG	-	expression tag	UNP P27797
B	71	LYS	ASP	engineered mutation	UNP P27797
B	299	GLY	-	linker	UNP P27797
B	300	SER	-	linker	UNP P27797
B	301	GLY	-	linker	UNP P27797
B	302	ASP	-	linker	UNP P27797
C	10	ASN	-	expression tag	UNP P27797
C	11	LYS	-	expression tag	UNP P27797
C	12	GLY	-	expression tag	UNP P27797
C	13	SER	-	expression tag	UNP P27797
C	14	ILE	-	expression tag	UNP P27797
C	15	GLU	-	expression tag	UNP P27797
C	16	GLY	-	expression tag	UNP P27797
C	17	ARG	-	expression tag	UNP P27797
C	71	LYS	ASP	engineered mutation	UNP P27797
C	205	GLY	-	linker	UNP P27797
C	206	SER	-	linker	UNP P27797
C	207	GLY	-	linker	UNP P27797
C	302	ASP	-	linker	UNP P27797
D	10	ASN	-	expression tag	UNP P27797
D	11	LYS	-	expression tag	UNP P27797
D	12	GLY	-	expression tag	UNP P27797
D	13	SER	-	expression tag	UNP P27797
D	14	ILE	-	expression tag	UNP P27797
D	15	GLU	-	expression tag	UNP P27797
D	16	GLY	-	expression tag	UNP P27797
D	17	ARG	-	expression tag	UNP P27797
D	71	LYS	ASP	engineered mutation	UNP P27797
D	205	GLY	-	linker	UNP P27797
D	206	SER	-	linker	UNP P27797
D	207	GLY	-	linker	UNP P27797

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Chain	Residue	Modelled	Actual	Comment	Reference
D	302	ASP	-	linker	UNP P27797
E	10	ASN	-	expression tag	UNP P27797
E	11	LYS	-	expression tag	UNP P27797
E	12	GLY	-	expression tag	UNP P27797
E	13	SER	-	expression tag	UNP P27797
E	14	ILE	-	expression tag	UNP P27797
E	15	GLU	-	expression tag	UNP P27797
E	16	GLY	-	expression tag	UNP P27797
E	17	ARG	-	expression tag	UNP P27797
E	71	LYS	ASP	engineered mutation	UNP P27797
E	299	GLY	-	linker	UNP P27797
E	300	SER	-	linker	UNP P27797
E	301	GLY	-	linker	UNP P27797
E	302	ASP	-	linker	UNP P27797
F	10	ASN	-	expression tag	UNP P27797
F	11	LYS	-	expression tag	UNP P27797
F	12	GLY	-	expression tag	UNP P27797
F	13	SER	-	expression tag	UNP P27797
F	14	ILE	-	expression tag	UNP P27797
F	15	GLU	-	expression tag	UNP P27797
F	16	GLY	-	expression tag	UNP P27797
F	17	ARG	-	expression tag	UNP P27797
F	71	LYS	ASP	engineered mutation	UNP P27797
F	205	GLY	-	linker	UNP P27797
F	206	SER	-	linker	UNP P27797
F	207	GLY	-	linker	UNP P27797
F	302	ASP	-	linker	UNP P27797
G	10	ASN	-	expression tag	UNP P27797
G	11	LYS	-	expression tag	UNP P27797
G	12	GLY	-	expression tag	UNP P27797
G	13	SER	-	expression tag	UNP P27797
G	14	ILE	-	expression tag	UNP P27797
G	15	GLU	-	expression tag	UNP P27797
G	16	GLY	-	expression tag	UNP P27797
G	17	ARG	-	expression tag	UNP P27797
G	71	LYS	ASP	engineered mutation	UNP P27797
G	205	GLY	-	linker	UNP P27797
G	206	SER	-	linker	UNP P27797
G	207	GLY	-	linker	UNP P27797
G	302	ASP	-	linker	UNP P27797
H	10	ASN	-	expression tag	UNP P27797
H	11	LYS	-	expression tag	UNP P27797

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Chain	Residue	Modelled	Actual	Comment	Reference
H	12	GLY	-	expression tag	UNP P27797
H	13	SER	-	expression tag	UNP P27797
H	14	ILE	-	expression tag	UNP P27797
H	15	GLU	-	expression tag	UNP P27797
H	16	GLY	-	expression tag	UNP P27797
H	17	ARG	-	expression tag	UNP P27797
H	71	LYS	ASP	engineered mutation	UNP P27797
H	205	GLY	-	linker	UNP P27797
H	206	SER	-	linker	UNP P27797
H	207	GLY	-	linker	UNP P27797
H	302	ASP	-	linker	UNP P27797
I	10	ASN	-	expression tag	UNP P27797
I	11	LYS	-	expression tag	UNP P27797
I	12	GLY	-	expression tag	UNP P27797
I	13	SER	-	expression tag	UNP P27797
I	14	ILE	-	expression tag	UNP P27797
I	15	GLU	-	expression tag	UNP P27797
I	16	GLY	-	expression tag	UNP P27797
I	17	ARG	-	expression tag	UNP P27797
I	71	LYS	ASP	engineered mutation	UNP P27797
I	299	GLY	-	linker	UNP P27797
I	300	SER	-	linker	UNP P27797
I	301	GLY	-	linker	UNP P27797
I	302	ASP	-	linker	UNP P27797
J	10	ASN	-	expression tag	UNP P27797
J	11	LYS	-	expression tag	UNP P27797
J	12	GLY	-	expression tag	UNP P27797
J	13	SER	-	expression tag	UNP P27797
J	14	ILE	-	expression tag	UNP P27797
J	15	GLU	-	expression tag	UNP P27797
J	16	GLY	-	expression tag	UNP P27797
J	17	ARG	-	expression tag	UNP P27797
J	71	LYS	ASP	engineered mutation	UNP P27797
J	205	GLY	-	linker	UNP P27797
J	206	SER	-	linker	UNP P27797
J	207	GLY	-	linker	UNP P27797
J	302	ASP	-	linker	UNP P27797

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	1	Total Cl 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	112	Total O 112 112	0	0
4	B	83	Total O 83 83	0	0
4	C	103	Total O 103 103	0	0
4	D	112	Total O 112 112	0	0
4	E	110	Total O 110 110	0	0

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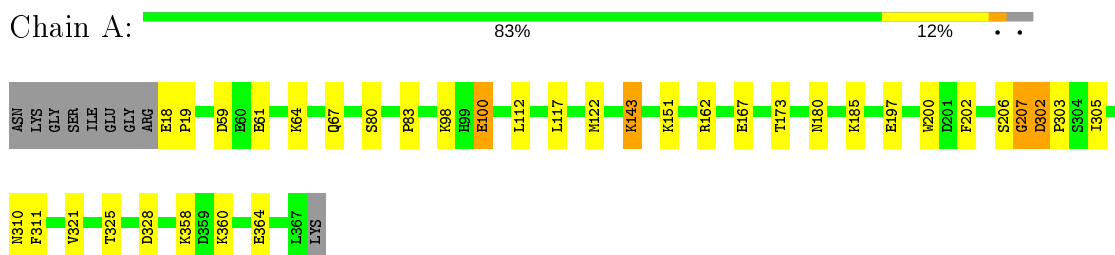
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	90	Total O 90 90	0	0
4	G	98	Total O 98 98	0	0
4	H	77	Total O 77 77	0	0
4	I	90	Total O 90 90	0	0
4	J	86	Total O 86 86	0	0

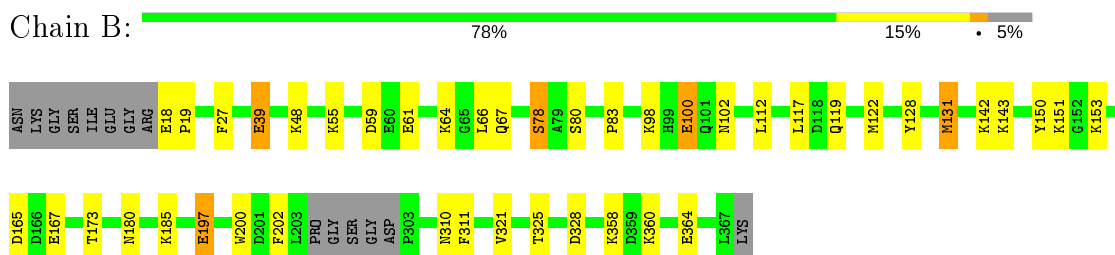
3 Residue-property plots [i](#)

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.

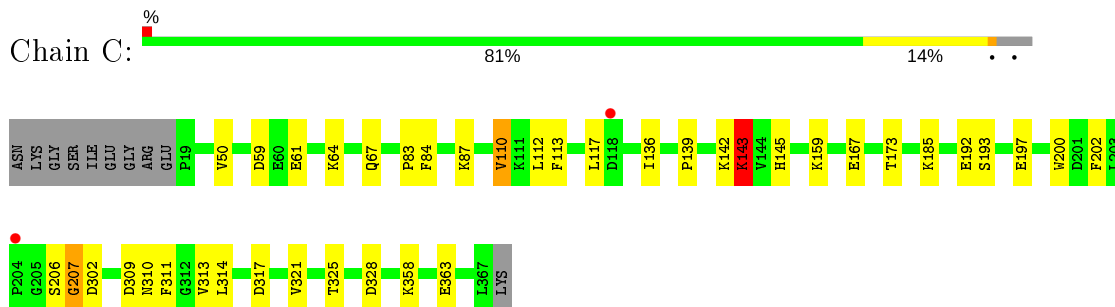
- Molecule 1: Calreticulin,Calreticulin



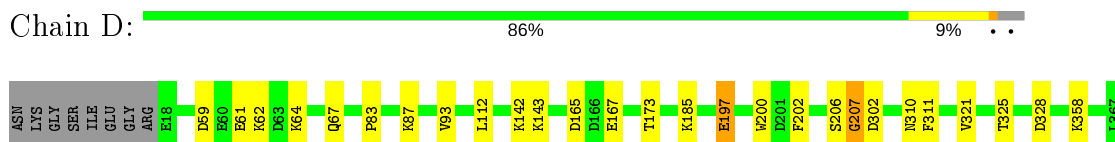
- Molecule 1: Calreticulin,Calreticulin



- Molecule 1: Calreticulin,Calreticulin

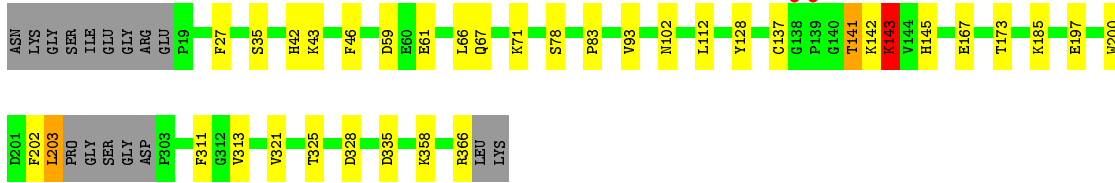
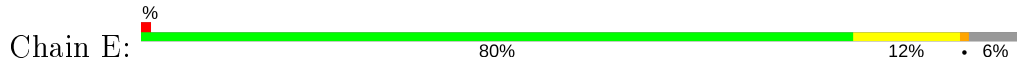


- Molecule 1: Calreticulin,Calreticulin

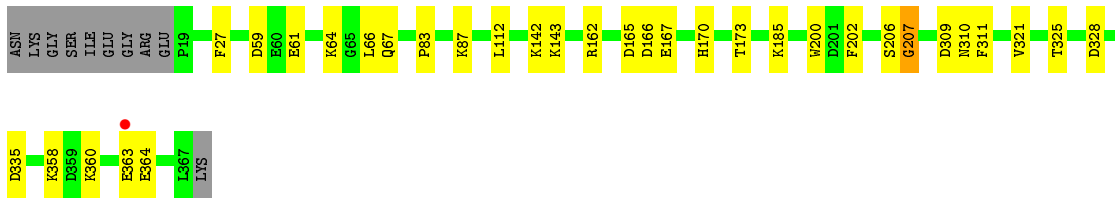
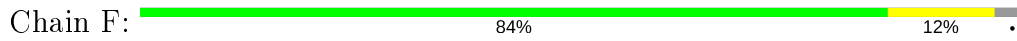


LYS

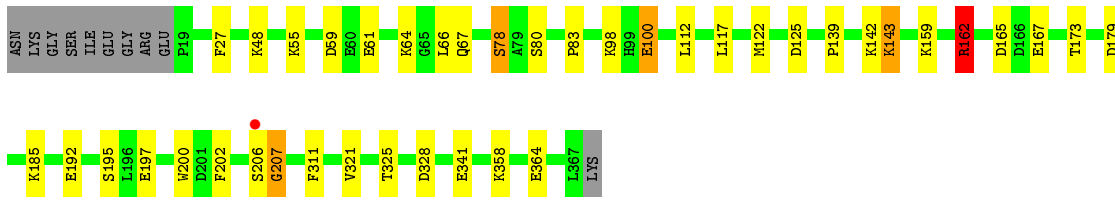
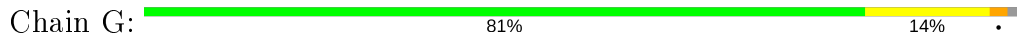
• Molecule 1: Calreticulin,Calreticulin



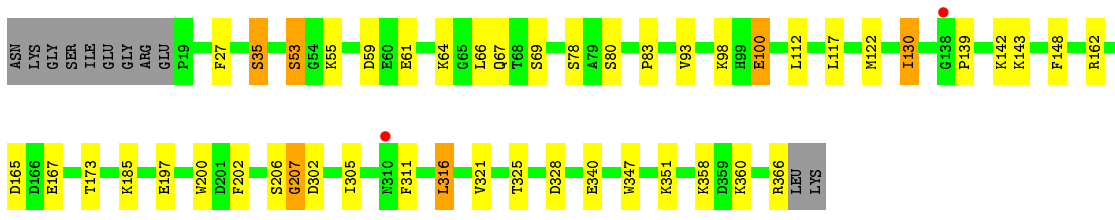
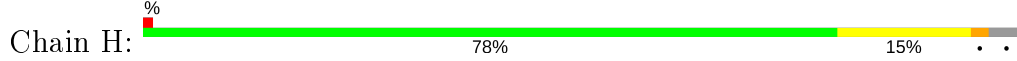
• Molecule 1: Calreticulin,Calreticulin



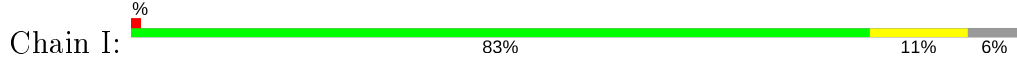
• Molecule 1: Calreticulin,Calreticulin

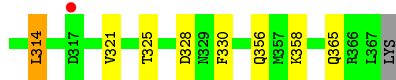


• Molecule 1: Calreticulin,Calreticulin

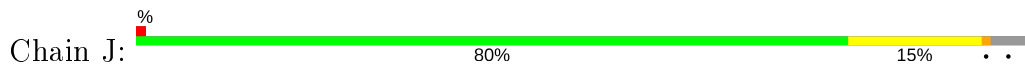


• Molecule 1: Calreticulin,Calreticulin





● Molecule 1: Calreticulin, Calreticulin



4 Data and refinement statistics

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α , β , γ	196.98Å 196.98Å 67.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.77 – 2.30 47.77 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.1 (47.77-2.30) 97.1 (47.77-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.210 , 0.247 0.215 , 0.250	Depositor DCC
R_{free} test set	5630 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	20.9	Xtrriage
Anisotropy	0.174	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtrriage
Estimated twinning fraction	0.000 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	21334	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 71.61 % 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 2.5480e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: CA, 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	0.80	2/2102 (0.1%)	0.94	10/2839 (0.4%)
1	B	0.83	3/2070 (0.1%)	0.90	9/2793 (0.3%)
1	C	0.83	3/2098 (0.1%)	1.08	10/2833 (0.4%)
1	D	0.80	1/2101 (0.0%)	0.95	6/2838 (0.2%)
1	E	0.82	3/2063 (0.1%)	0.93	8/2780 (0.3%)
1	F	0.82	2/2089 (0.1%)	0.96	8/2822 (0.3%)
1	G	0.85	5/2098 (0.2%)	1.01	13/2832 (0.5%)
1	H	0.82	5/2096 (0.2%)	1.00	8/2829 (0.3%)
1	I	0.80	1/2057 (0.0%)	0.88	4/2776 (0.1%)
1	J	0.83	2/2095 (0.1%)	0.99	6/2829 (0.2%)
All	All	0.82	27/20869 (0.1%)	0.97	82/28171 (0.3%)

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	2
1	C	0	1
1	D	0	2
1	F	0	2
1	G	0	1
1	H	0	1
All	All	0	9

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	207	GLY	C-N	13.94	1.66	1.34
1	F	207	GLY	C-N	10.94	1.59	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	207	GLY	C-N	9.19	1.55	1.34
1	G	207	GLY	C-N	8.51	1.53	1.34
1	G	80	SER	CB-OG	-7.62	1.32	1.42

The worst 5 of 82 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	207	GLY	O-C-N	-27.06	79.40	122.70
1	J	207	GLY	O-C-N	-20.90	89.25	122.70
1	H	207	GLY	O-C-N	-20.37	90.11	122.70
1	G	207	GLY	O-C-N	-17.49	94.72	122.70
1	D	207	GLY	O-C-N	-14.20	99.98	122.70

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	207	GLY	Mainchain,Peptide
1	C	207	GLY	Mainchain
1	D	207	GLY	Mainchain,Peptide
1	F	207	GLY	Mainchain,Peptide
1	G	207	GLY	Mainchain

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	2051	0	1917	19	0
1	B	2021	0	1893	25	0
1	C	2044	0	1915	23	0
1	D	2050	0	1915	11	0
1	E	2014	0	1899	19	0
1	F	2038	0	1901	13	0
1	G	2047	0	1921	21	0
1	H	2045	0	1914	25	0
1	I	2008	0	1877	12	0
1	J	2044	0	1912	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	E	1	0	0	0	0
4	A	112	0	0	2	1
4	B	83	0	0	3	0
4	C	103	0	0	8	0
4	D	112	0	0	3	1
4	E	110	0	0	4	1
4	F	90	0	0	1	1
4	G	98	0	0	3	0
4	H	77	0	0	3	0
4	I	90	0	0	3	0
4	J	86	0	0	7	0
All	All	21334	0	19064	190	2

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 5.

The worst 5 of 190 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:113:PHE:HB2	1:C:313:VAL:HG13	1.38	1.05
1:C:197:GLU:OE2	4:C:601:HOH:O	1.77	1.01
1:F:142:LYS:HE2	1:F:165:ASP:OD2	1.74	0.88
1:D:142:LYS:HE2	1:D:165:ASP:OD2	1.73	0.86
1:J:142:LYS:HE2	1:J:165:ASP:OD2	1.74	0.86

All (2) 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)
4:A:659:HOH:O	4:F:684:HOH:O[4_555]	1.97	0.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:709:HOH:O	4:E:601:HOH:O[3_564]	2.15	0.05

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	254/265 (96%)	245 (96%)	8 (3%)	1 (0%)	34	42
1	B	247/265 (93%)	237 (96%)	9 (4%)	1 (0%)	34	42
1	C	254/265 (96%)	245 (96%)	7 (3%)	2 (1%)	19	23
1	D	254/265 (96%)	244 (96%)	9 (4%)	1 (0%)	34	42
1	E	245/265 (92%)	236 (96%)	8 (3%)	1 (0%)	34	42
1	F	253/265 (96%)	242 (96%)	10 (4%)	1 (0%)	34	42
1	G	253/265 (96%)	246 (97%)	6 (2%)	1 (0%)	34	42
1	H	253/265 (96%)	244 (96%)	8 (3%)	1 (0%)	34	42
1	I	246/265 (93%)	238 (97%)	7 (3%)	1 (0%)	34	42
1	J	253/265 (96%)	244 (96%)	8 (3%)	1 (0%)	34	42
All	All	2512/2650 (95%)	2421 (96%)	80 (3%)	11 (0%)	34	42

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	302	ASP
1	B	321	VAL
1	D	321	VAL
1	E	321	VAL
1	F	321	VAL

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	222/231 (96%)	218 (98%)	4 (2%)	59	75
1	B	219/231 (95%)	215 (98%)	4 (2%)	59	75
1	C	222/231 (96%)	217 (98%)	5 (2%)	50	67
1	D	222/231 (96%)	218 (98%)	4 (2%)	59	75
1	E	219/231 (95%)	215 (98%)	4 (2%)	59	75
1	F	220/231 (95%)	215 (98%)	5 (2%)	50	67
1	G	222/231 (96%)	216 (97%)	6 (3%)	44	61
1	H	222/231 (96%)	214 (96%)	8 (4%)	35	49
1	I	217/231 (94%)	211 (97%)	6 (3%)	43	60
1	J	221/231 (96%)	217 (98%)	4 (2%)	59	75
All	All	2206/2310 (96%)	2156 (98%)	50 (2%)	50	67

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	162	ARG
1	G	55	LYS
1	J	35	SER
1	F	206	SER
1	F	363	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	70	GLN
1	I	115	ASN
1	F	170	HIS
1	B	365	GLN
1	D	154	ASN

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 11 ligands modelled in this entry, 11 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	J	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	207:GLY	C	302:ASP	N	1.66

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	256/265 (96%)	-0.13	0 100 100	10, 21, 39, 55	0
1	B	251/265 (94%)	-0.09	0 100 100	10, 22, 39, 57	0
1	C	255/265 (96%)	0.02	2 (0%) 86 89	11, 23, 40, 56	0
1	D	256/265 (96%)	-0.17	0 100 100	9, 20, 37, 53	0
1	E	249/265 (93%)	-0.07	2 (0%) 86 89	11, 21, 37, 53	0
1	F	255/265 (96%)	-0.18	1 (0%) 92 95	9, 20, 42, 52	0
1	G	255/265 (96%)	-0.01	1 (0%) 92 95	11, 22, 40, 58	0
1	H	254/265 (95%)	0.21	2 (0%) 86 89	14, 28, 42, 63	0
1	I	250/265 (94%)	0.03	2 (0%) 86 89	13, 23, 41, 61	0
1	J	255/265 (96%)	-0.07	2 (0%) 86 89	11, 22, 39, 56	0
All	All	2536/2650 (95%)	-0.05	12 (0%) 91 94	9, 22, 40, 63	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	204	PRO	3.1
1	H	138	GLY	2.7
1	I	203	LEU	2.6
1	G	206	SER	2.3
1	E	138	GLY	2.2

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(Å ²)	Q<0.9
2	CA	H	500	1/1	0.86	0.09	26,26,26,26	0
2	CA	I	500	1/1	0.87	0.07	20,20,20,20	0
2	CA	B	500	1/1	0.93	0.05	18,18,18,18	0
2	CA	E	401	1/1	0.93	0.05	18,18,18,18	0
2	CA	A	500	1/1	0.93	0.07	15,15,15,15	0
2	CA	G	401	1/1	0.94	0.08	14,14,14,14	0
2	CA	C	500	1/1	0.96	0.06	14,14,14,14	0
2	CA	J	500	1/1	0.97	0.06	18,18,18,18	0
2	CA	F	500	1/1	0.97	0.05	14,14,14,14	0
3	CL	E	402	1/1	0.98	0.12	31,31,31,31	0
2	CA	D	500	1/1	0.98	0.06	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.