



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:54 PM UTC

PDB ID : 5E7S / pdb_00005e7s
Title : Hexameric structure of a LonA protease domain in active state
Authors : Lin, C.-C.; Su, S.-C.; Chang, C.-I.
Deposited on : 2015-10-13
Resolution : 3.03 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

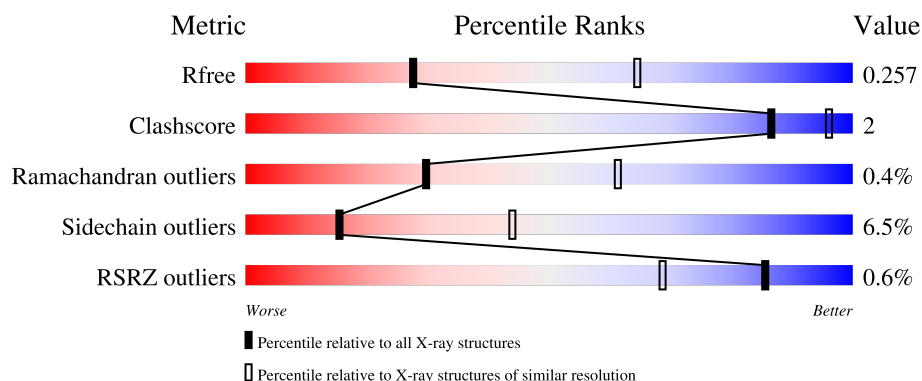
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.03 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}	180053	3685 (3.08-3.00)
Clashscore	190562	4007 (3.08-3.00)
Ramachandran outliers	187476	3834 (3.08-3.00)
Sidechain outliers	187428	3836 (3.08-3.00)
RSRZ outliers	180081	3684 (3.08-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	298	91% 5% .
1	B	298	90% 6% .
1	C	298	86% 9% . .
1	D	298	88% 7% . .
1	E	298	% 88% 8% . .

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Mol	Chain	Length	Quality of chain
1	F	298	90% 6% . .
1	G	298	% 87% 9% .
1	H	298	88% 7% . .
1	I	298	85% 10% . .
1	J	298	89% 8% .
1	K	298	87% 8% . .
1	L	298	3% 81% 10% . 7%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 26298 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 Lon protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	0	0
			2199	1393	380	418	8			
1	B	288	Total	C	N	O	S	0	0	0
			2199	1393	380	418	8			
1	C	287	Total	C	N	O	S	0	0	0
			2192	1388	379	417	8			
1	D	289	Total	C	N	O	S	0	0	0
			2206	1398	381	419	8			
1	E	288	Total	C	N	O	S	0	0	0
			2202	1396	380	418	8			
1	F	287	Total	C	N	O	S	0	0	0
			2192	1388	379	417	8			
1	G	289	Total	C	N	O	S	0	0	0
			2206	1398	381	419	8			
1	H	287	Total	C	N	O	S	0	1	0
			2198	1392	379	419	8			
1	I	287	Total	C	N	O	S	0	0	0
			2192	1388	379	417	8			
1	J	289	Total	C	N	O	S	0	0	0
			2206	1398	381	419	8			
1	K	288	Total	C	N	O	S	0	0	0
			2199	1393	380	418	8			
1	L	276	Total	C	N	O	S	0	0	0
			2107	1337	364	399	7			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	490	MET	-	expression tag	UNP A0A059VAZ3
A	782	HIS	-	expression tag	UNP A0A059VAZ3
A	783	HIS	-	expression tag	UNP A0A059VAZ3
A	784	HIS	-	expression tag	UNP A0A059VAZ3
A	785	HIS	-	expression tag	UNP A0A059VAZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	786	HIS	-	expression tag	UNP A0A059VAZ3
A	787	HIS	-	expression tag	UNP A0A059VAZ3
B	490	MET	-	expression tag	UNP A0A059VAZ3
B	782	HIS	-	expression tag	UNP A0A059VAZ3
B	783	HIS	-	expression tag	UNP A0A059VAZ3
B	784	HIS	-	expression tag	UNP A0A059VAZ3
B	785	HIS	-	expression tag	UNP A0A059VAZ3
B	786	HIS	-	expression tag	UNP A0A059VAZ3
B	787	HIS	-	expression tag	UNP A0A059VAZ3
C	490	MET	-	expression tag	UNP A0A059VAZ3
C	782	HIS	-	expression tag	UNP A0A059VAZ3
C	783	HIS	-	expression tag	UNP A0A059VAZ3
C	784	HIS	-	expression tag	UNP A0A059VAZ3
C	785	HIS	-	expression tag	UNP A0A059VAZ3
C	786	HIS	-	expression tag	UNP A0A059VAZ3
C	787	HIS	-	expression tag	UNP A0A059VAZ3
D	490	MET	-	expression tag	UNP A0A059VAZ3
D	782	HIS	-	expression tag	UNP A0A059VAZ3
D	783	HIS	-	expression tag	UNP A0A059VAZ3
D	784	HIS	-	expression tag	UNP A0A059VAZ3
D	785	HIS	-	expression tag	UNP A0A059VAZ3
D	786	HIS	-	expression tag	UNP A0A059VAZ3
D	787	HIS	-	expression tag	UNP A0A059VAZ3
E	490	MET	-	expression tag	UNP A0A059VAZ3
E	782	HIS	-	expression tag	UNP A0A059VAZ3
E	783	HIS	-	expression tag	UNP A0A059VAZ3
E	784	HIS	-	expression tag	UNP A0A059VAZ3
E	785	HIS	-	expression tag	UNP A0A059VAZ3
E	786	HIS	-	expression tag	UNP A0A059VAZ3
E	787	HIS	-	expression tag	UNP A0A059VAZ3
F	490	MET	-	expression tag	UNP A0A059VAZ3
F	782	HIS	-	expression tag	UNP A0A059VAZ3
F	783	HIS	-	expression tag	UNP A0A059VAZ3
F	784	HIS	-	expression tag	UNP A0A059VAZ3
F	785	HIS	-	expression tag	UNP A0A059VAZ3
F	786	HIS	-	expression tag	UNP A0A059VAZ3
F	787	HIS	-	expression tag	UNP A0A059VAZ3
G	490	MET	-	expression tag	UNP A0A059VAZ3
G	782	HIS	-	expression tag	UNP A0A059VAZ3
G	783	HIS	-	expression tag	UNP A0A059VAZ3
G	784	HIS	-	expression tag	UNP A0A059VAZ3
G	785	HIS	-	expression tag	UNP A0A059VAZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
G	786	HIS	-	expression tag	UNP A0A059VAZ3
G	787	HIS	-	expression tag	UNP A0A059VAZ3
H	490	MET	-	expression tag	UNP A0A059VAZ3
H	782	HIS	-	expression tag	UNP A0A059VAZ3
H	783	HIS	-	expression tag	UNP A0A059VAZ3
H	784	HIS	-	expression tag	UNP A0A059VAZ3
H	785	HIS	-	expression tag	UNP A0A059VAZ3
H	786	HIS	-	expression tag	UNP A0A059VAZ3
H	787	HIS	-	expression tag	UNP A0A059VAZ3
I	490	MET	-	expression tag	UNP A0A059VAZ3
I	782	HIS	-	expression tag	UNP A0A059VAZ3
I	783	HIS	-	expression tag	UNP A0A059VAZ3
I	784	HIS	-	expression tag	UNP A0A059VAZ3
I	785	HIS	-	expression tag	UNP A0A059VAZ3
I	786	HIS	-	expression tag	UNP A0A059VAZ3
I	787	HIS	-	expression tag	UNP A0A059VAZ3
J	490	MET	-	expression tag	UNP A0A059VAZ3
J	782	HIS	-	expression tag	UNP A0A059VAZ3
J	783	HIS	-	expression tag	UNP A0A059VAZ3
J	784	HIS	-	expression tag	UNP A0A059VAZ3
J	785	HIS	-	expression tag	UNP A0A059VAZ3
J	786	HIS	-	expression tag	UNP A0A059VAZ3
J	787	HIS	-	expression tag	UNP A0A059VAZ3
K	490	MET	-	expression tag	UNP A0A059VAZ3
K	782	HIS	-	expression tag	UNP A0A059VAZ3
K	783	HIS	-	expression tag	UNP A0A059VAZ3
K	784	HIS	-	expression tag	UNP A0A059VAZ3
K	785	HIS	-	expression tag	UNP A0A059VAZ3
K	786	HIS	-	expression tag	UNP A0A059VAZ3
K	787	HIS	-	expression tag	UNP A0A059VAZ3
L	490	MET	-	expression tag	UNP A0A059VAZ3
L	782	HIS	-	expression tag	UNP A0A059VAZ3
L	783	HIS	-	expression tag	UNP A0A059VAZ3
L	784	HIS	-	expression tag	UNP A0A059VAZ3
L	785	HIS	-	expression tag	UNP A0A059VAZ3
L	786	HIS	-	expression tag	UNP A0A059VAZ3
L	787	HIS	-	expression tag	UNP A0A059VAZ3

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Lon protease

Chain A:  91% 5% .



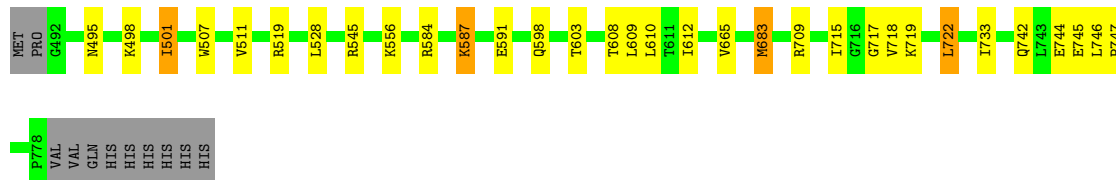
- Molecule 1: Lon protease

Chain B:  90% 6% .



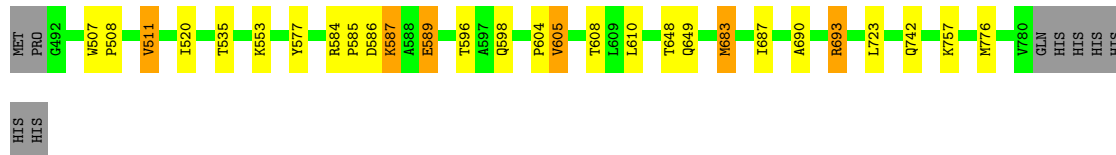
- Molecule 1: Lon protease

Chain C:  86% 9% . .



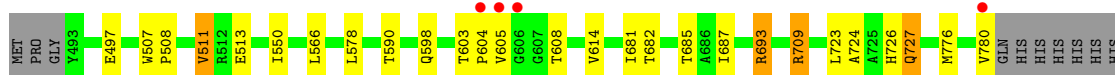
- Molecule 1: Lon protease

Chain D:  88% 7% . .

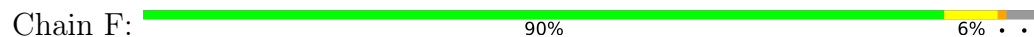


- Molecule 1: Lon protease

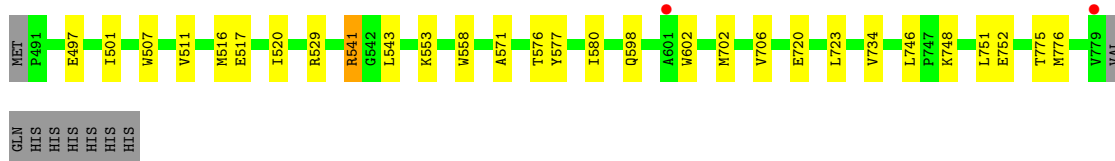
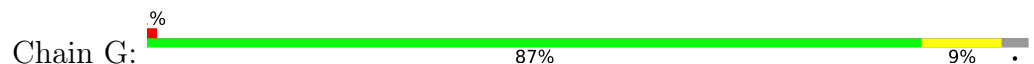
Chain E:  88% 8% . .



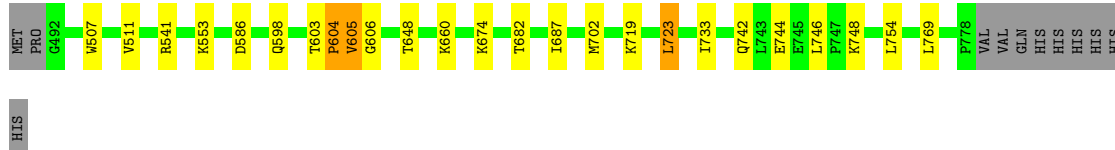
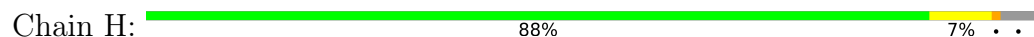
- Molecule 1: Lon protease



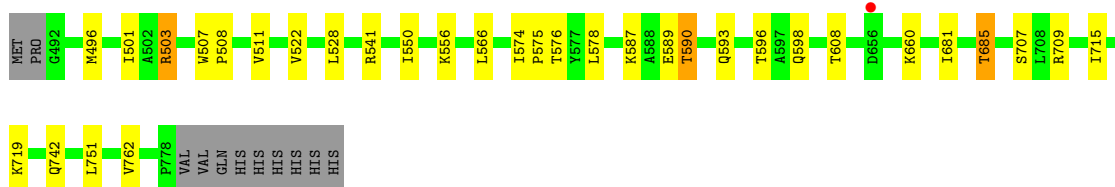
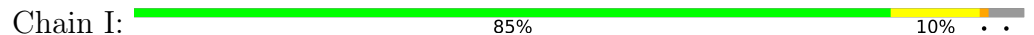
- Molecule 1: Lon protease



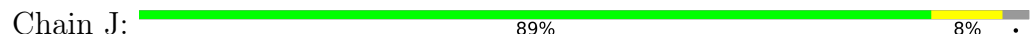
- Molecule 1: Lon protease



- Molecule 1: Lon protease



- Molecule 1: Lon protease



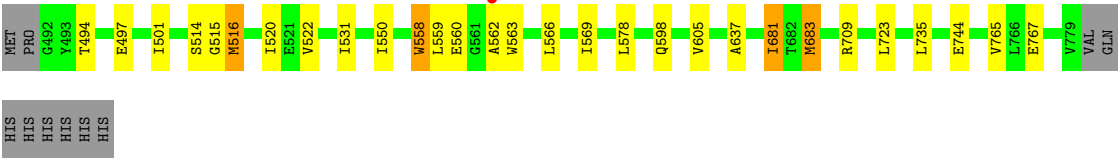
- Molecule 1: Lon protease

Chain K:

87%

8%

••



• Molecule 1: Lon protease

Chain L:

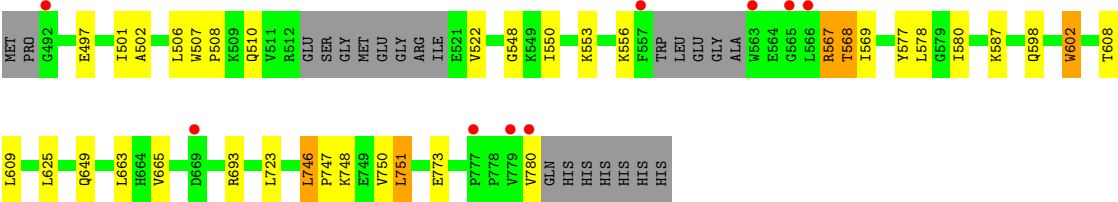
3%

81%

10%

•

7%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	116.31Å 212.79Å 178.92Å 90.00° 100.80° 90.00°	Depositor
Resolution (Å)	20.00 – 3.03 20.00 – 3.03	Depositor EDS
% Data completeness (in resolution range)	90.5 (20.00-3.03) 90.5 (20.00-3.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 3.04Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.227 , 0.279 (Not available) , 0.257	Depositor DCC
R_{free} test set	3798 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å ²)	63.1	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 12.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	26298	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.37% 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](#)

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	0/2241	0.72	0/3040
1	B	0.44	0/2241	0.74	0/3040
1	C	0.44	0/2234	0.76	0/3030
1	D	0.43	0/2248	0.73	0/3050
1	E	0.43	0/2244	0.74	0/3045
1	F	0.43	0/2234	0.70	0/3030
1	G	0.44	0/2249	0.74	0/3051
1	H	0.43	0/2243	0.71	0/3042
1	I	0.42	0/2234	0.73	0/3030
1	J	0.45	0/2248	0.73	0/3050
1	K	0.45	0/2241	0.72	0/3040
1	L	0.46	0/2145	0.77	0/2909
All	All	0.44	0/26802	0.73	0/36357

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 [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	2199	0	2240	5	0
1	B	2199	0	2240	14	0
1	C	2192	0	2231	14	0
1	D	2206	0	2249	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2202	0	2246	10	0
1	F	2192	0	2231	4	0
1	G	2206	0	2248	11	0
1	H	2198	0	2237	9	0
1	I	2192	0	2231	8	0
1	J	2206	0	2249	5	0
1	K	2199	0	2240	11	0
1	L	2107	0	2156	12	0
All	All	26298	0	26798	110	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 2.

The worst 5 of 110 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:665:VAL:HG11	1:C:683:MET:HE1	1.39	1.01
1:B:637:ALA:HB2	1:B:683:MET:CE	1.97	0.93
1:K:558:TRP:HZ3	1:K:562:ALA:HA	1.41	0.86
1:C:665:VAL:CG1	1:C:683:MET:HE1	2.11	0.79
1:K:637:ALA:HB2	1:K:683:MET:HE3	1.65	0.77

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	286/298 (96%)	277 (97%)	9 (3%)	0	100	100
1	B	286/298 (96%)	276 (96%)	10 (4%)	0	100	100
1	C	285/298 (96%)	272 (95%)	11 (4%)	2 (1%)	18	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	287/298 (96%)	278 (97%)	7 (2%)	2 (1%)	18	49
1	E	286/298 (96%)	277 (97%)	9 (3%)	0	100	100
1	F	285/298 (96%)	279 (98%)	6 (2%)	0	100	100
1	G	287/298 (96%)	274 (96%)	12 (4%)	1 (0%)	36	67
1	H	286/298 (96%)	275 (96%)	9 (3%)	2 (1%)	18	49
1	I	285/298 (96%)	275 (96%)	9 (3%)	1 (0%)	30	61
1	J	287/298 (96%)	279 (97%)	7 (2%)	1 (0%)	36	67
1	K	286/298 (96%)	274 (96%)	11 (4%)	1 (0%)	36	67
1	L	270/298 (91%)	258 (96%)	10 (4%)	2 (1%)	18	49
All	All	3416/3576 (96%)	3294 (96%)	110 (3%)	12 (0%)	30	61

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	718	VAL
1	D	605	VAL
1	G	602	TRP
1	H	605	VAL
1	K	515	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	229/239 (96%)	220 (96%)	9 (4%)	28	59
1	B	229/239 (96%)	220 (96%)	9 (4%)	28	59
1	C	228/239 (95%)	209 (92%)	19 (8%)	10	34
1	D	230/239 (96%)	215 (94%)	15 (6%)	15	44
1	E	230/239 (96%)	215 (94%)	15 (6%)	15	44
1	F	228/239 (95%)	214 (94%)	14 (6%)	17	46
1	G	230/239 (96%)	217 (94%)	13 (6%)	18	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	229/239 (96%)	216 (94%)	13 (6%)	18	49
1	I	228/239 (95%)	207 (91%)	21 (9%)	8	30
1	J	230/239 (96%)	214 (93%)	16 (7%)	14	41
1	K	229/239 (96%)	210 (92%)	19 (8%)	10	34
1	L	221/239 (92%)	205 (93%)	16 (7%)	13	40
All	All	2741/2868 (96%)	2562 (94%)	179 (6%)	15	44

5 of 179 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	587	LYS
1	J	756	ILE
1	I	660	LYS
1	J	516	MET
1	K	558	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	628	GLN
1	L	495	ASN
1	E	727	GLN
1	E	649	GLN
1	L	598	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 oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	288/298 (96%)	-0.25	1 (0%) 90 79	37, 62, 84, 101	0
1	B	288/298 (96%)	-0.22	1 (0%) 90 79	39, 68, 99, 117	0
1	C	287/298 (96%)	-0.09	0 100 100	40, 72, 103, 122	0
1	D	289/298 (96%)	-0.18	0 100 100	38, 63, 86, 108	0
1	E	288/298 (96%)	-0.13	4 (1%) 73 50	38, 69, 102, 121	0
1	F	287/298 (96%)	-0.07	1 (0%) 90 79	38, 68, 97, 116	0
1	G	289/298 (96%)	-0.15	2 (0%) 84 66	38, 69, 95, 108	0
1	H	287/298 (96%)	-0.09	0 100 100	40, 71, 92, 103	1 (0%)
1	I	287/298 (96%)	-0.03	1 (0%) 90 79	39, 80, 101, 110	0
1	J	289/298 (96%)	-0.04	1 (0%) 90 79	40, 81, 103, 115	0
1	K	288/298 (96%)	-0.02	1 (0%) 90 79	41, 83, 117, 134	0
1	L	276/298 (92%)	-0.03	9 (3%) 49 27	40, 71, 98, 119	0
All	All	3443/3576 (96%)	-0.11	21 (0%) 85 69	37, 70, 102, 134	1 (0%)

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	563	TRP	3.9
1	B	779	VAL	3.5
1	L	557	PHE	3.4
1	L	565	GLY	3.4
1	L	566	LEU	3.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.