



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 07:16 AM UTC

PDB ID : 2C8T / pdb_00002c8t
Title : The 3.0 Å Resolution Structure of Caseinolytic Clp Protease 1 from Mycobacterium tuberculosis
Authors : Ingvarsson, H.; Høgbom, M.; Jones, T.A.; Unge, T.
Deposited on : 2005-12-07
Resolution : 3.00 Å (reported)

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

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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

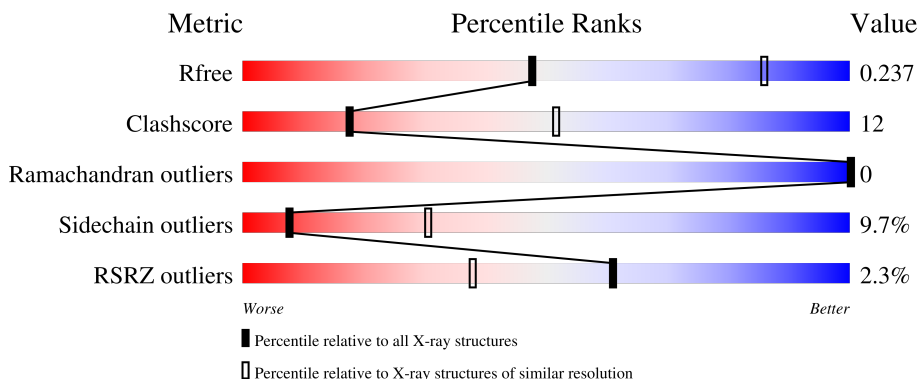
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	206	62% 17% 17%
1	B	206	64% 15% 17%
1	C	206	62% 18% 17%
1	D	206	62% 17% 5% 17%
1	E	206	61% 17% 5% 17%

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Mol	Chain	Length	Quality of chain
1	F	206	<p>3% 62% 18% • 17%</p>
1	G	206	<p>4% 63% 16% 5% 17%</p>
1	H	206	<p>3% 63% 17% • 17%</p>
1	I	206	<p>2% 62% 17% • 17%</p>
1	J	206	<p>61% 18% • 17%</p>
1	K	206	<p>64% 15% • 17%</p>
1	L	206	<p>2% 63% 17% • 17%</p>
1	M	206	<p>2% 61% 18% • 17%</p>
1	N	206	<p>3% 64% 16% • 17%</p>

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 18482 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 ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUB-UNIT 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	171	1322	839	224	250	9	0	0	0
1	B	171	1320	839	223	249	9	0	0	0
1	C	171	1320	839	223	249	9	0	0	0
1	D	171	1320	839	223	249	9	0	0	0
1	E	171	1320	839	223	249	9	0	0	0
1	F	171	1320	839	223	249	9	0	0	0
1	G	171	1320	839	223	249	9	0	0	0
1	H	171	1320	839	223	249	9	0	0	0
1	I	171	1320	839	223	249	9	0	0	0
1	J	171	1320	839	223	249	9	0	0	0
1	K	171	1320	839	223	249	9	0	0	0
1	L	171	1320	839	223	249	9	0	0	0
1	M	171	1320	839	223	249	9	0	0	0
1	N	171	1320	839	223	249	9	0	0	0

There are 98 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP P0A526
A	1	ALA	-	expression tag	UNP P0A526
A	201	GLY	-	expression tag	UNP P0A526
A	202	HIS	-	expression tag	UNP P0A526
A	203	HIS	-	expression tag	UNP P0A526
A	204	HIS	-	expression tag	UNP P0A526
A	205	HIS	-	expression tag	UNP P0A526
B	0	MET	-	expression tag	UNP P0A526
B	1	ALA	-	expression tag	UNP P0A526
B	201	GLY	-	expression tag	UNP P0A526
B	202	HIS	-	expression tag	UNP P0A526
B	203	HIS	-	expression tag	UNP P0A526
B	204	HIS	-	expression tag	UNP P0A526
B	205	HIS	-	expression tag	UNP P0A526
C	0	MET	-	expression tag	UNP P0A526
C	1	ALA	-	expression tag	UNP P0A526
C	201	GLY	-	expression tag	UNP P0A526
C	202	HIS	-	expression tag	UNP P0A526
C	203	HIS	-	expression tag	UNP P0A526
C	204	HIS	-	expression tag	UNP P0A526
C	205	HIS	-	expression tag	UNP P0A526
D	0	MET	-	expression tag	UNP P0A526
D	1	ALA	-	expression tag	UNP P0A526
D	201	GLY	-	expression tag	UNP P0A526
D	202	HIS	-	expression tag	UNP P0A526
D	203	HIS	-	expression tag	UNP P0A526
D	204	HIS	-	expression tag	UNP P0A526
D	205	HIS	-	expression tag	UNP P0A526
E	0	MET	-	expression tag	UNP P0A526
E	1	ALA	-	expression tag	UNP P0A526
E	201	GLY	-	expression tag	UNP P0A526
E	202	HIS	-	expression tag	UNP P0A526
E	203	HIS	-	expression tag	UNP P0A526
E	204	HIS	-	expression tag	UNP P0A526
E	205	HIS	-	expression tag	UNP P0A526
F	0	MET	-	expression tag	UNP P0A526
F	1	ALA	-	expression tag	UNP P0A526
F	201	GLY	-	expression tag	UNP P0A526
F	202	HIS	-	expression tag	UNP P0A526
F	203	HIS	-	expression tag	UNP P0A526
F	204	HIS	-	expression tag	UNP P0A526
F	205	HIS	-	expression tag	UNP P0A526
G	0	MET	-	expression tag	UNP P0A526

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1	ALA	-	expression tag	UNP P0A526
G	201	GLY	-	expression tag	UNP P0A526
G	202	HIS	-	expression tag	UNP P0A526
G	203	HIS	-	expression tag	UNP P0A526
G	204	HIS	-	expression tag	UNP P0A526
G	205	HIS	-	expression tag	UNP P0A526
H	0	MET	-	expression tag	UNP P0A526
H	1	ALA	-	expression tag	UNP P0A526
H	201	GLY	-	expression tag	UNP P0A526
H	202	HIS	-	expression tag	UNP P0A526
H	203	HIS	-	expression tag	UNP P0A526
H	204	HIS	-	expression tag	UNP P0A526
H	205	HIS	-	expression tag	UNP P0A526
I	0	MET	-	expression tag	UNP P0A526
I	1	ALA	-	expression tag	UNP P0A526
I	201	GLY	-	expression tag	UNP P0A526
I	202	HIS	-	expression tag	UNP P0A526
I	203	HIS	-	expression tag	UNP P0A526
I	204	HIS	-	expression tag	UNP P0A526
I	205	HIS	-	expression tag	UNP P0A526
J	0	MET	-	expression tag	UNP P0A526
J	1	ALA	-	expression tag	UNP P0A526
J	201	GLY	-	expression tag	UNP P0A526
J	202	HIS	-	expression tag	UNP P0A526
J	203	HIS	-	expression tag	UNP P0A526
J	204	HIS	-	expression tag	UNP P0A526
J	205	HIS	-	expression tag	UNP P0A526
K	0	MET	-	expression tag	UNP P0A526
K	1	ALA	-	expression tag	UNP P0A526
K	201	GLY	-	expression tag	UNP P0A526
K	202	HIS	-	expression tag	UNP P0A526
K	203	HIS	-	expression tag	UNP P0A526
K	204	HIS	-	expression tag	UNP P0A526
K	205	HIS	-	expression tag	UNP P0A526
L	0	MET	-	expression tag	UNP P0A526
L	1	ALA	-	expression tag	UNP P0A526
L	201	GLY	-	expression tag	UNP P0A526
L	202	HIS	-	expression tag	UNP P0A526
L	203	HIS	-	expression tag	UNP P0A526
L	204	HIS	-	expression tag	UNP P0A526
L	205	HIS	-	expression tag	UNP P0A526
M	0	MET	-	expression tag	UNP P0A526

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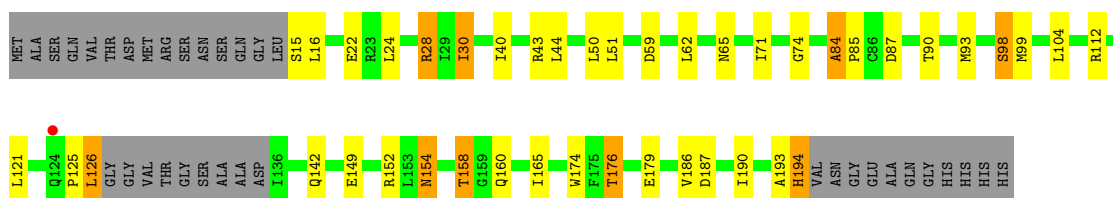
Chain	Residue	Modelled	Actual	Comment	Reference
M	1	ALA	-	expression tag	UNP P0A526
M	201	GLY	-	expression tag	UNP P0A526
M	202	HIS	-	expression tag	UNP P0A526
M	203	HIS	-	expression tag	UNP P0A526
M	204	HIS	-	expression tag	UNP P0A526
M	205	HIS	-	expression tag	UNP P0A526
N	0	MET	-	expression tag	UNP P0A526
N	1	ALA	-	expression tag	UNP P0A526
N	201	GLY	-	expression tag	UNP P0A526
N	202	HIS	-	expression tag	UNP P0A526
N	203	HIS	-	expression tag	UNP P0A526
N	204	HIS	-	expression tag	UNP P0A526
N	205	HIS	-	expression tag	UNP P0A526

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.

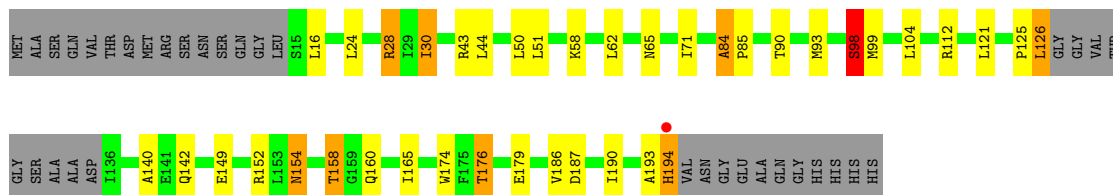
- Molecule 1: ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1

Chain A: 



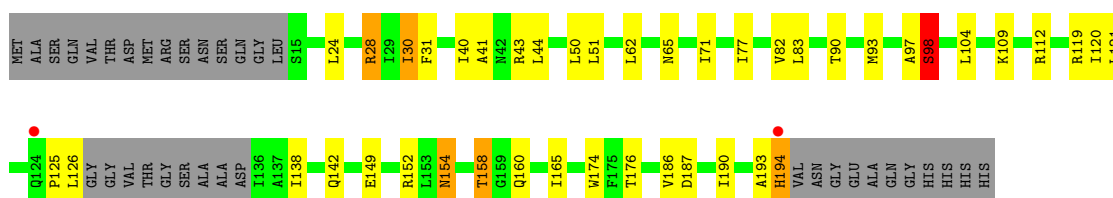
- Molecule 1: ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1

Chain B: 



- Molecule 1: ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1

Chain C: 



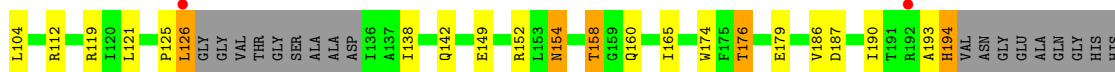
- Molecule 1: ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1

Chain D: 



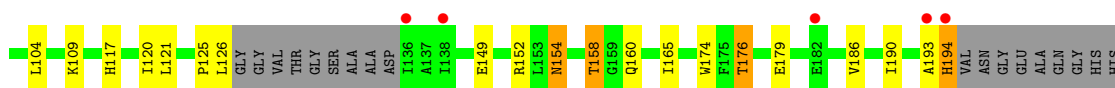


● Molecule 1: ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1



HIS
HIS

● Molecule 1: ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1

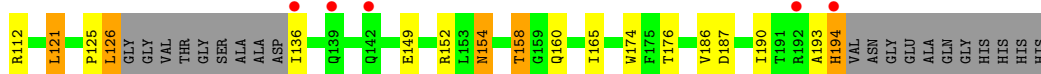


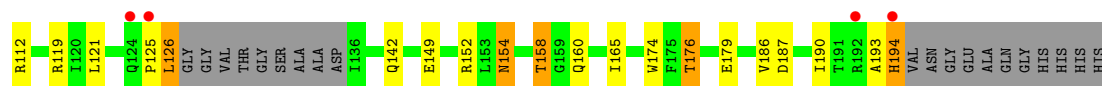
HIS
HIS

● Molecule 1: ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1

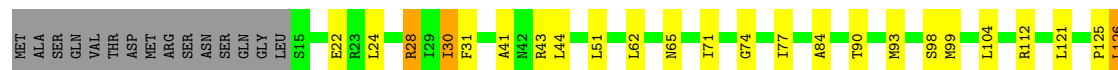


● Molecule 1: ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1





● Molecule 1: ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	96.72Å 168.22Å 103.76Å 90.00° 114.60° 90.00°	Depositor
Resolution (Å)	19.87 – 3.00 19.87 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.87-3.00) 99.6 (19.87-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.98Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.213 , 0.238 0.215 , 0.237	Depositor DCC
R_{free} test set	3036 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	53.2	Xtrriage
Anisotropy	0.116	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	18482	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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	0.70	0/1344	0.96	2/1815 (0.1%)
1	B	0.78	0/1342	1.00	3/1812 (0.2%)
1	C	0.88	0/1342	1.04	2/1812 (0.1%)
1	D	0.91	0/1342	1.05	3/1812 (0.2%)
1	E	0.84	0/1342	1.03	3/1812 (0.2%)
1	F	0.96	0/1342	1.06	0/1812
1	G	0.87	0/1342	1.01	2/1812 (0.1%)
1	H	0.88	0/1342	1.03	3/1812 (0.2%)
1	I	0.94	0/1342	1.08	4/1812 (0.2%)
1	J	0.82	0/1342	1.02	3/1812 (0.2%)
1	K	0.76	0/1342	1.00	1/1812 (0.1%)
1	L	0.91	0/1342	1.06	3/1812 (0.2%)
1	M	0.77	0/1342	0.97	0/1812
1	N	0.75	0/1342	0.99	3/1812 (0.2%)
All	All	0.84	0/18790	1.02	32/25371 (0.1%)

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	31	PHE	N-CA-C	6.79	119.98	108.90
1	K	31	PHE	N-CA-C	6.16	118.94	108.90
1	B	98	SER	CB-CA-C	-6.14	109.48	116.54
1	G	84	ALA	CA-C-N	5.85	125.72	119.28
1	G	84	ALA	C-N-CA	5.85	125.72	119.28

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	1322	0	1316	41	0
1	B	1320	0	1315	38	0
1	C	1320	0	1315	34	0
1	D	1320	0	1315	38	0
1	E	1320	0	1315	39	0
1	F	1320	0	1315	40	0
1	G	1320	0	1315	44	0
1	H	1320	0	1315	31	0
1	I	1320	0	1315	34	0
1	J	1320	0	1315	41	0
1	K	1320	0	1315	35	0
1	L	1320	0	1315	37	0
1	M	1320	0	1315	38	0
1	N	1320	0	1315	35	0
All	All	18482	0	18411	456	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 12.

The worst 5 of 456 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:M:121:LEU:HD11	1:N:142:GLN:HE22	1.18	1.09
1:D:142:GLN:HE22	1:E:121:LEU:HD11	1.13	1.07
1:E:90:THR:HG22	1:E:104:LEU:HD12	1.36	1.06
1:L:90:THR:HG22	1:L:104:LEU:HD12	1.34	1.06
1:J:90:THR:HG22	1:J:104:LEU:HD12	1.40	1.04

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	167/206 (81%)	161 (96%)	6 (4%)	0	100	100
1	B	167/206 (81%)	161 (96%)	6 (4%)	0	100	100
1	C	167/206 (81%)	161 (96%)	6 (4%)	0	100	100
1	D	167/206 (81%)	161 (96%)	6 (4%)	0	100	100
1	E	167/206 (81%)	161 (96%)	6 (4%)	0	100	100
1	F	167/206 (81%)	161 (96%)	6 (4%)	0	100	100
1	G	167/206 (81%)	160 (96%)	7 (4%)	0	100	100
1	H	167/206 (81%)	161 (96%)	6 (4%)	0	100	100
1	I	167/206 (81%)	162 (97%)	5 (3%)	0	100	100
1	J	167/206 (81%)	160 (96%)	7 (4%)	0	100	100
1	K	167/206 (81%)	161 (96%)	6 (4%)	0	100	100
1	L	167/206 (81%)	160 (96%)	7 (4%)	0	100	100
1	M	167/206 (81%)	159 (95%)	8 (5%)	0	100	100
1	N	167/206 (81%)	160 (96%)	7 (4%)	0	100	100
All	All	2338/2884 (81%)	2249 (96%)	89 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	136/161 (84%)	122 (90%)	14 (10%)	7	28
1	B	135/161 (84%)	123 (91%)	12 (9%)	9	34
1	C	135/161 (84%)	121 (90%)	14 (10%)	7	28
1	D	135/161 (84%)	122 (90%)	13 (10%)	8	31
1	E	135/161 (84%)	122 (90%)	13 (10%)	8	31
1	F	135/161 (84%)	122 (90%)	13 (10%)	8	31
1	G	135/161 (84%)	122 (90%)	13 (10%)	8	31
1	H	135/161 (84%)	122 (90%)	13 (10%)	8	31
1	I	135/161 (84%)	121 (90%)	14 (10%)	7	28
1	J	135/161 (84%)	122 (90%)	13 (10%)	8	31
1	K	135/161 (84%)	121 (90%)	14 (10%)	7	28
1	L	135/161 (84%)	123 (91%)	12 (9%)	9	34
1	M	135/161 (84%)	121 (90%)	14 (10%)	7	28
1	N	135/161 (84%)	123 (91%)	12 (9%)	9	34
All	All	1891/2254 (84%)	1707 (90%)	184 (10%)	8	30

5 of 184 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	176	THR
1	K	186	VAL
1	J	28	ARG
1	J	190	ILE
1	L	44	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	47	GLN
1	L	142	GLN
1	M	154	ASN
1	E	47	GLN
1	D	154	ASN

5.3.3 RNA

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	171/206 (83%)	-0.19	1 (0%) 85 69	12, 14, 20, 23	0
1	B	171/206 (83%)	-0.31	1 (0%) 85 69	12, 14, 20, 23	0
1	C	171/206 (83%)	-0.29	2 (1%) 76 55	12, 14, 20, 23	0
1	D	171/206 (83%)	-0.12	8 (4%) 36 19	12, 14, 20, 23	0
1	E	171/206 (83%)	-0.19	2 (1%) 76 55	12, 14, 20, 23	0
1	F	171/206 (83%)	-0.07	7 (4%) 41 23	12, 14, 20, 23	0
1	G	171/206 (83%)	-0.06	9 (5%) 32 16	12, 14, 20, 23	0
1	H	171/206 (83%)	-0.21	6 (3%) 47 27	12, 14, 20, 23	0
1	I	171/206 (83%)	-0.16	4 (2%) 61 38	12, 14, 20, 23	0
1	J	171/206 (83%)	-0.34	1 (0%) 85 69	12, 14, 20, 23	0
1	K	171/206 (83%)	-0.32	0 100 100	12, 14, 20, 23	0
1	L	171/206 (83%)	-0.19	4 (2%) 61 38	12, 14, 20, 23	0
1	M	171/206 (83%)	-0.19	4 (2%) 61 38	12, 14, 20, 23	0
1	N	171/206 (83%)	-0.09	6 (3%) 47 27	12, 14, 20, 23	0
All	All	2394/2884 (83%)	-0.19	55 (2%) 61 38	12, 14, 20, 23	0

The worst 5 of 55 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	138	ILE	5.5
1	G	194	HIS	5.5
1	F	136	ILE	4.3
1	D	194	HIS	4.3
1	N	138	ILE	4.2

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 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.