



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:15 PM UTC

PDB ID : 3QWD / pdb_00003qwd
Title : Crystal structure of ClpP from Staphylococcus aureus
Authors : Geiger, S.R.; Boettcher, T.; Sieber, S.A.; Cramer, P.
Deposited on : 2011-02-28
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

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

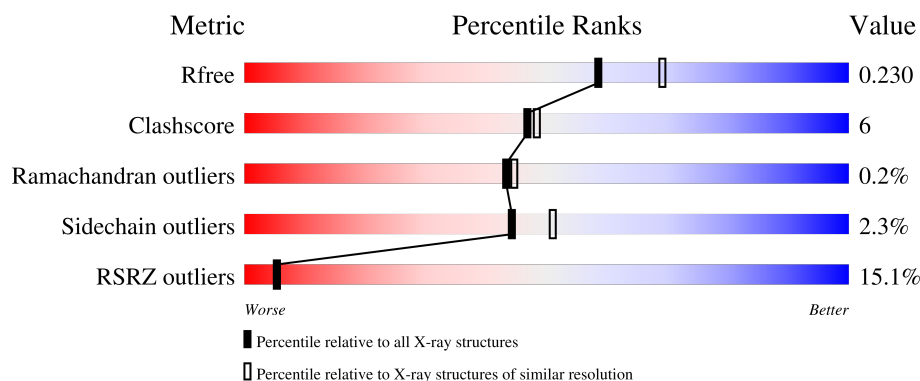
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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 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	203	 12% 78% 12% • 8%
1	B	203	 17% 79% 12% • 8%
1	C	203	 17% 76% 12% • 8%
1	D	203	 14% 76% 12% • 10%
1	E	203	 10% 82% 10% • 7%

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Mol	Chain	Length	Quality of chain
1	F	203	
1	G	203	
1	H	203	
1	I	203	
1	J	203	
1	K	203	
1	L	203	
1	M	203	
1	N	203	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20404 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 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	187	Total	C	N	O	S	0	3	0
			1455	920	244	283	8			
1	B	187	Total	C	N	O	S	0	3	0
			1454	919	244	284	7			
1	C	186	Total	C	N	O	S	0	2	0
			1444	914	243	280	7			
1	D	182	Total	C	N	O	S	0	2	0
			1413	895	238	273	7			
1	E	188	Total	C	N	O	S	0	3	0
			1459	921	247	284	7			
1	F	182	Total	C	N	O	S	0	2	0
			1418	896	239	276	7			
1	G	185	Total	C	N	O	S	0	1	0
			1424	899	240	278	7			
1	H	192	Total	C	N	O	S	0	2	0
			1489	941	253	288	7			
1	I	186	Total	C	N	O	S	0	2	0
			1442	912	242	281	7			
1	J	186	Total	C	N	O	S	0	2	0
			1437	909	242	279	7			
1	K	179	Total	C	N	O	S	0	4	0
			1411	895	236	273	7			
1	L	180	Total	C	N	O	S	0	3	0
			1413	895	237	274	7			
1	M	186	Total	C	N	O	S	0	1	0
			1436	907	241	281	7			
1	N	183	Total	C	N	O	S	0	1	0
			1409	891	236	275	7			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	196	TRP	-	expression tag	UNP Q2G036

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Chain	Residue	Modelled	Actual	Comment	Reference
A	197	SER	-	expression tag	UNP Q2G036
A	198	HIS	-	expression tag	UNP Q2G036
A	199	PRO	-	expression tag	UNP Q2G036
A	200	GLN	-	expression tag	UNP Q2G036
A	201	PHE	-	expression tag	UNP Q2G036
A	202	GLU	-	expression tag	UNP Q2G036
A	203	LYS	-	expression tag	UNP Q2G036
B	196	TRP	-	expression tag	UNP Q2G036
B	197	SER	-	expression tag	UNP Q2G036
B	198	HIS	-	expression tag	UNP Q2G036
B	199	PRO	-	expression tag	UNP Q2G036
B	200	GLN	-	expression tag	UNP Q2G036
B	201	PHE	-	expression tag	UNP Q2G036
B	202	GLU	-	expression tag	UNP Q2G036
B	203	LYS	-	expression tag	UNP Q2G036
C	196	TRP	-	expression tag	UNP Q2G036
C	197	SER	-	expression tag	UNP Q2G036
C	198	HIS	-	expression tag	UNP Q2G036
C	199	PRO	-	expression tag	UNP Q2G036
C	200	GLN	-	expression tag	UNP Q2G036
C	201	PHE	-	expression tag	UNP Q2G036
C	202	GLU	-	expression tag	UNP Q2G036
C	203	LYS	-	expression tag	UNP Q2G036
D	196	TRP	-	expression tag	UNP Q2G036
D	197	SER	-	expression tag	UNP Q2G036
D	198	HIS	-	expression tag	UNP Q2G036
D	199	PRO	-	expression tag	UNP Q2G036
D	200	GLN	-	expression tag	UNP Q2G036
D	201	PHE	-	expression tag	UNP Q2G036
D	202	GLU	-	expression tag	UNP Q2G036
D	203	LYS	-	expression tag	UNP Q2G036
E	196	TRP	-	expression tag	UNP Q2G036
E	197	SER	-	expression tag	UNP Q2G036
E	198	HIS	-	expression tag	UNP Q2G036
E	199	PRO	-	expression tag	UNP Q2G036
E	200	GLN	-	expression tag	UNP Q2G036
E	201	PHE	-	expression tag	UNP Q2G036
E	202	GLU	-	expression tag	UNP Q2G036
E	203	LYS	-	expression tag	UNP Q2G036
F	196	TRP	-	expression tag	UNP Q2G036
F	197	SER	-	expression tag	UNP Q2G036
F	198	HIS	-	expression tag	UNP Q2G036

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Chain	Residue	Modelled	Actual	Comment	Reference
F	199	PRO	-	expression tag	UNP Q2G036
F	200	GLN	-	expression tag	UNP Q2G036
F	201	PHE	-	expression tag	UNP Q2G036
F	202	GLU	-	expression tag	UNP Q2G036
F	203	LYS	-	expression tag	UNP Q2G036
G	196	TRP	-	expression tag	UNP Q2G036
G	197	SER	-	expression tag	UNP Q2G036
G	198	HIS	-	expression tag	UNP Q2G036
G	199	PRO	-	expression tag	UNP Q2G036
G	200	GLN	-	expression tag	UNP Q2G036
G	201	PHE	-	expression tag	UNP Q2G036
G	202	GLU	-	expression tag	UNP Q2G036
G	203	LYS	-	expression tag	UNP Q2G036
H	196	TRP	-	expression tag	UNP Q2G036
H	197	SER	-	expression tag	UNP Q2G036
H	198	HIS	-	expression tag	UNP Q2G036
H	199	PRO	-	expression tag	UNP Q2G036
H	200	GLN	-	expression tag	UNP Q2G036
H	201	PHE	-	expression tag	UNP Q2G036
H	202	GLU	-	expression tag	UNP Q2G036
H	203	LYS	-	expression tag	UNP Q2G036
I	196	TRP	-	expression tag	UNP Q2G036
I	197	SER	-	expression tag	UNP Q2G036
I	198	HIS	-	expression tag	UNP Q2G036
I	199	PRO	-	expression tag	UNP Q2G036
I	200	GLN	-	expression tag	UNP Q2G036
I	201	PHE	-	expression tag	UNP Q2G036
I	202	GLU	-	expression tag	UNP Q2G036
I	203	LYS	-	expression tag	UNP Q2G036
J	196	TRP	-	expression tag	UNP Q2G036
J	197	SER	-	expression tag	UNP Q2G036
J	198	HIS	-	expression tag	UNP Q2G036
J	199	PRO	-	expression tag	UNP Q2G036
J	200	GLN	-	expression tag	UNP Q2G036
J	201	PHE	-	expression tag	UNP Q2G036
J	202	GLU	-	expression tag	UNP Q2G036
J	203	LYS	-	expression tag	UNP Q2G036
K	196	TRP	-	expression tag	UNP Q2G036
K	197	SER	-	expression tag	UNP Q2G036
K	198	HIS	-	expression tag	UNP Q2G036
K	199	PRO	-	expression tag	UNP Q2G036
K	200	GLN	-	expression tag	UNP Q2G036

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Chain	Residue	Modelled	Actual	Comment	Reference
K	201	PHE	-	expression tag	UNP Q2G036
K	202	GLU	-	expression tag	UNP Q2G036
K	203	LYS	-	expression tag	UNP Q2G036
L	196	TRP	-	expression tag	UNP Q2G036
L	197	SER	-	expression tag	UNP Q2G036
L	198	HIS	-	expression tag	UNP Q2G036
L	199	PRO	-	expression tag	UNP Q2G036
L	200	GLN	-	expression tag	UNP Q2G036
L	201	PHE	-	expression tag	UNP Q2G036
L	202	GLU	-	expression tag	UNP Q2G036
L	203	LYS	-	expression tag	UNP Q2G036
M	196	TRP	-	expression tag	UNP Q2G036
M	197	SER	-	expression tag	UNP Q2G036
M	198	HIS	-	expression tag	UNP Q2G036
M	199	PRO	-	expression tag	UNP Q2G036
M	200	GLN	-	expression tag	UNP Q2G036
M	201	PHE	-	expression tag	UNP Q2G036
M	202	GLU	-	expression tag	UNP Q2G036
M	203	LYS	-	expression tag	UNP Q2G036
N	196	TRP	-	expression tag	UNP Q2G036
N	197	SER	-	expression tag	UNP Q2G036
N	198	HIS	-	expression tag	UNP Q2G036
N	199	PRO	-	expression tag	UNP Q2G036
N	200	GLN	-	expression tag	UNP Q2G036
N	201	PHE	-	expression tag	UNP Q2G036
N	202	GLU	-	expression tag	UNP Q2G036
N	203	LYS	-	expression tag	UNP Q2G036

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	B	1	Total Cl 1 1	0	0
2	C	1	Total Cl 1 1	0	0
2	D	1	Total Cl 1 1	0	0
2	L	2	Total Cl 2 2	0	0
2	M	1	Total Cl 1 1	0	0

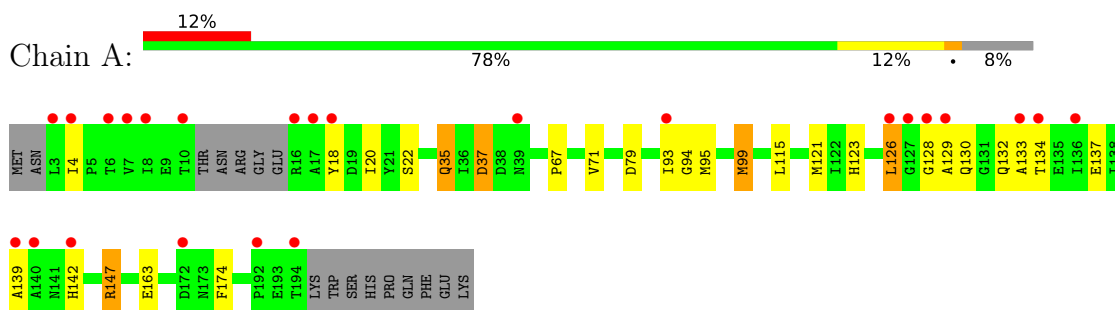
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	39	Total 39	O 39	0	0
3	B	28	Total 28	O 28	0	0
3	C	19	Total 19	O 19	0	0
3	D	16	Total 16	O 16	0	0
3	E	25	Total 25	O 25	0	0
3	F	10	Total 10	O 10	0	0
3	G	27	Total 27	O 27	0	0
3	H	22	Total 22	O 22	0	0
3	I	23	Total 23	O 23	0	0
3	J	16	Total 16	O 16	0	0
3	K	17	Total 17	O 17	0	0
3	L	22	Total 22	O 22	0	0
3	M	9	Total 9	O 9	0	0
3	N	20	Total 20	O 20	0	0

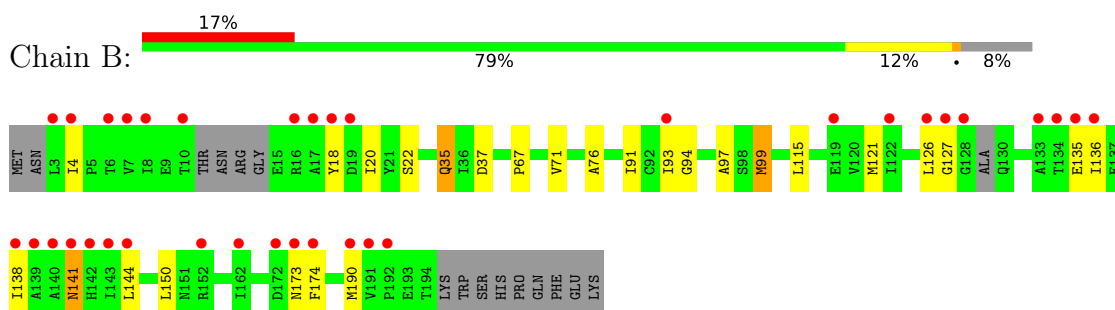
3 Residue-property plots [i](#)

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.

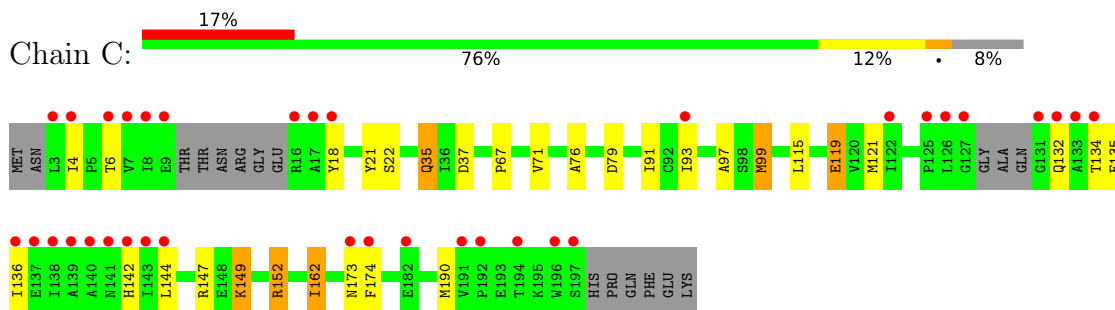
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



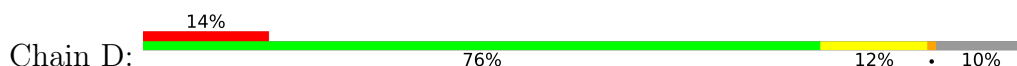
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

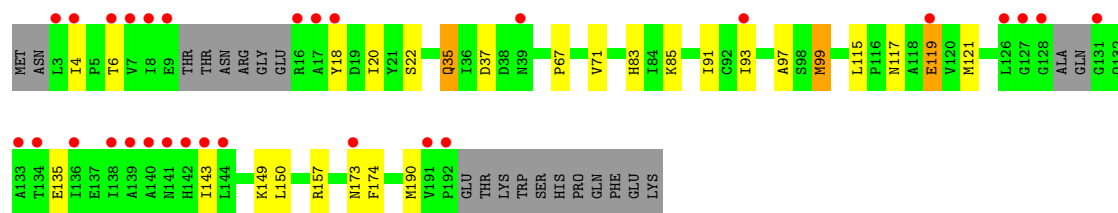


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

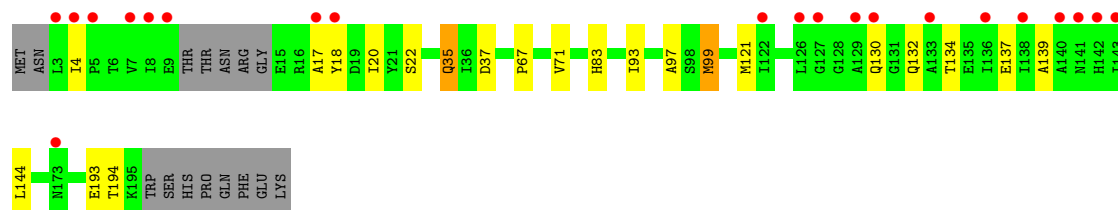
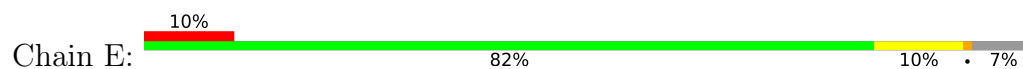


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

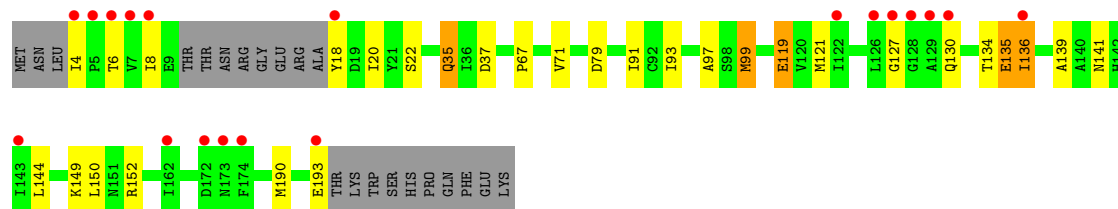
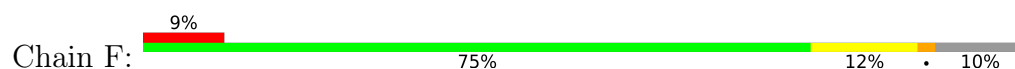




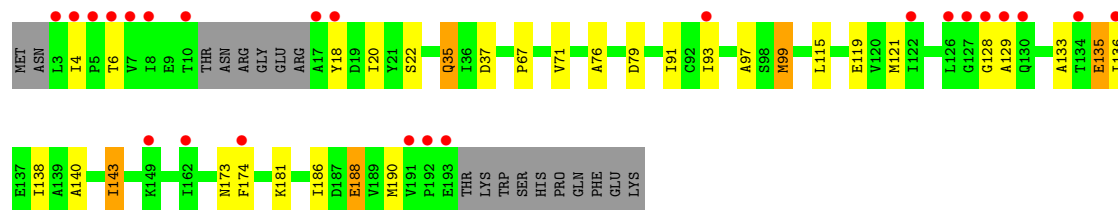
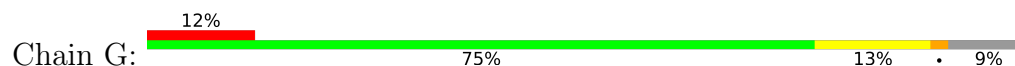
• Molecule 1: ATP-dependent Clp protease proteolytic subunit



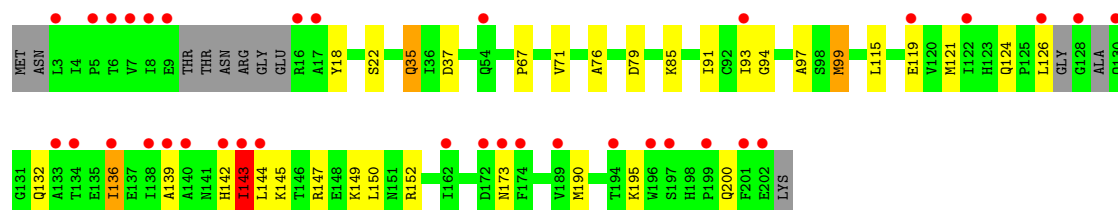
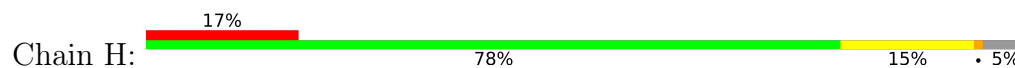
• Molecule 1: ATP-dependent Clp protease proteolytic subunit



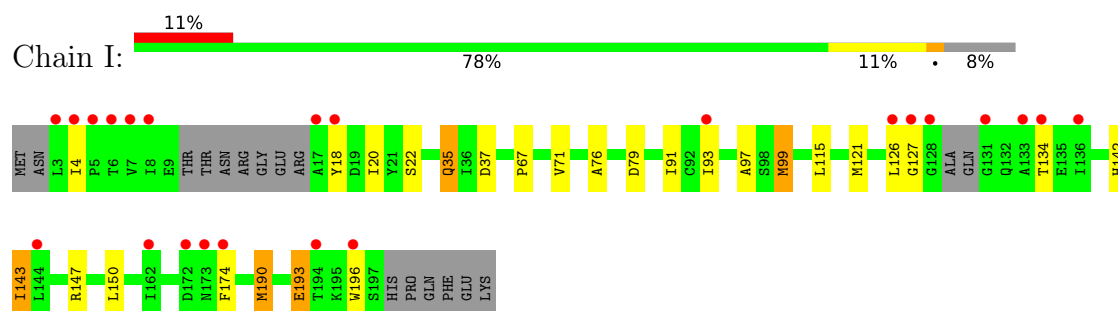
• Molecule 1: ATP-dependent Clp protease proteolytic subunit



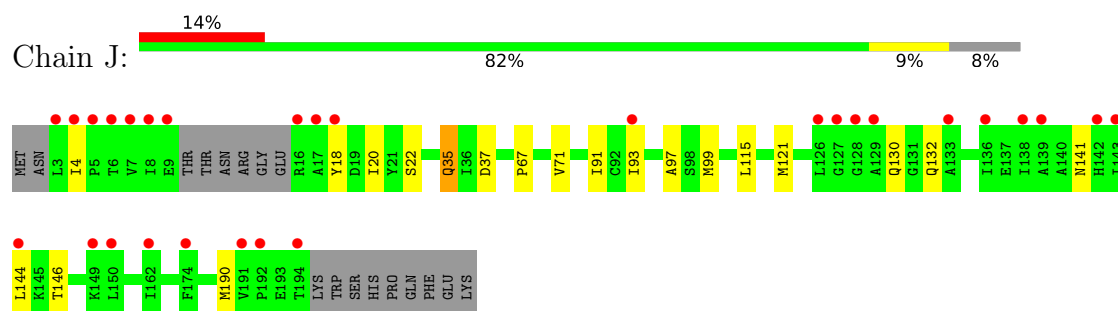
• Molecule 1: ATP-dependent Clp protease proteolytic subunit



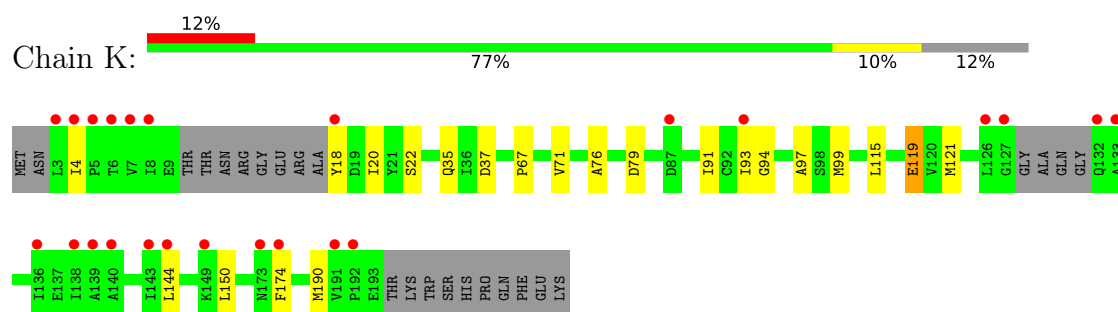
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



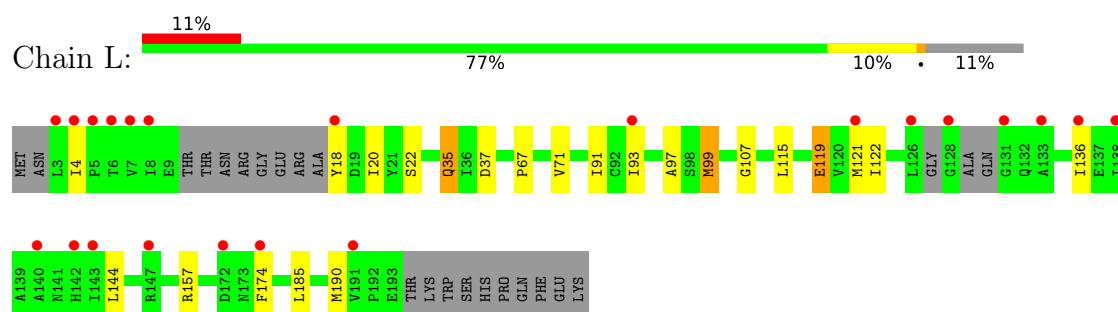
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



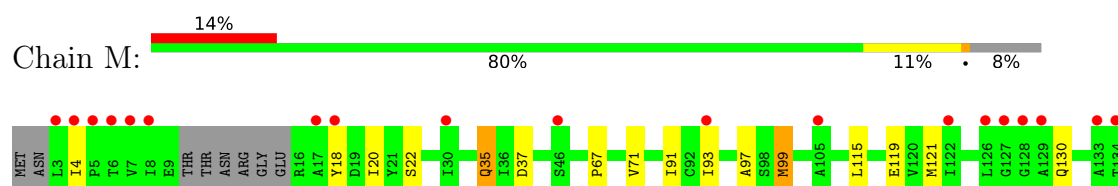
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

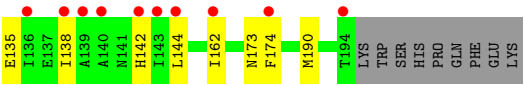


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

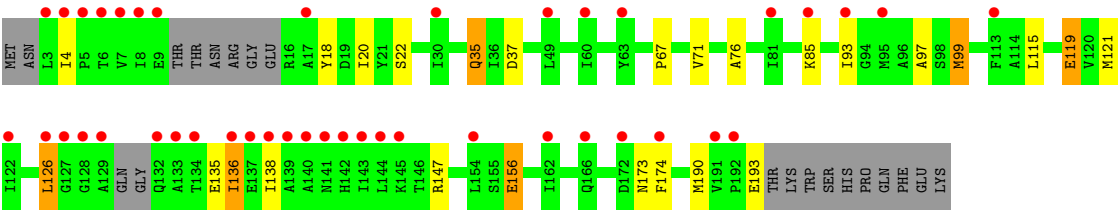
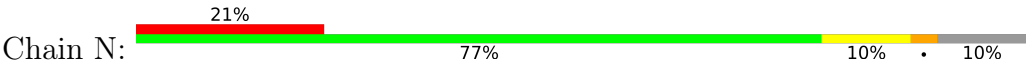


- Molecule 1: ATP-dependent Clp protease proteolytic subunit





● Molecule 1: ATP-dependent Clp protease proteolytic subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	172.05Å 177.97Å 100.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.99 – 2.10 88.99 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (88.99-2.10) 99.8 (88.99-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.10Å)	Xtriage
Refinement program	BUSTER 2.9.2	Depositor
R, R_{free}	0.208 , 0.226 0.226 , 0.230	Depositor DCC
R_{free} test set	8969 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	46.0	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 67.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.013 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20404	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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:
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	0.89	1/1483 (0.1%)	1.32	4/2002 (0.2%)
1	B	0.84	1/1481 (0.1%)	1.31	3/1998 (0.2%)
1	C	0.92	2/1468 (0.1%)	1.30	5/1980 (0.3%)
1	D	0.90	1/1437 (0.1%)	1.34	3/1938 (0.2%)
1	E	0.94	1/1487 (0.1%)	1.36	3/2007 (0.1%)
1	F	0.86	1/1443 (0.1%)	1.32	6/1947 (0.3%)
1	G	0.86	1/1445 (0.1%)	1.33	1/1951 (0.1%)
1	H	0.86	1/1516 (0.1%)	1.34	7/2046 (0.3%)
1	I	0.87	2/1467 (0.1%)	1.29	2/1980 (0.1%)
1	J	0.83	0/1462	1.35	1/1974 (0.1%)
1	K	0.79	0/1441	1.30	1/1944 (0.1%)
1	L	0.84	1/1439 (0.1%)	1.31	1/1939 (0.1%)
1	M	0.80	1/1457 (0.1%)	1.30	3/1967 (0.2%)
1	N	0.83	1/1429 (0.1%)	1.37	5/1928 (0.3%)
All	All	0.86	14/20455 (0.1%)	1.32	45/27601 (0.2%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	99	MET	SD-CE	-7.59	1.60	1.79
1	L	99	MET	SD-CE	-7.06	1.61	1.79
1	M	99	MET	SD-CE	-6.48	1.63	1.79
1	G	99	MET	SD-CE	-6.44	1.63	1.79
1	B	99	MET	SD-CE	-6.25	1.64	1.79
1	E	99	MET	SD-CE	-6.11	1.64	1.79
1	N	99	MET	SD-CE	-6.09	1.64	1.79
1	C	162	ILE	CG1-CD1	6.04	1.75	1.51
1	C	99	MET	SD-CE	-5.89	1.64	1.79
1	I	99	MET	SD-CE	-5.33	1.66	1.79
1	H	99	MET	SD-CE	-5.30	1.66	1.79
1	D	99	MET	SD-CE	-5.23	1.66	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	99	MET	SD-CE	-5.22	1.66	1.79
1	I	190	MET	SD-CE	-5.16	1.66	1.79

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	156	GLU	CB-CG-CD	9.22	128.28	112.60
1	H	143	ILE	N-CA-CB	7.84	119.73	110.95
1	B	126	LEU	N-CA-C	7.42	119.06	110.97
1	D	143	ILE	N-CA-C	-6.77	98.53	108.54
1	N	135	GLU	CA-C-N	6.12	128.85	120.46
1	N	135	GLU	C-N-CA	6.12	128.85	120.46
1	C	37	ASP	CA-CB-CG	6.02	118.62	112.60
1	F	139	ALA	CA-C-N	5.98	128.61	120.54
1	F	139	ALA	C-N-CA	5.98	128.61	120.54
1	N	126	LEU	N-CA-C	5.93	117.42	111.07
1	A	37	ASP	CA-CB-CG	5.78	118.38	112.60
1	K	37	ASP	CA-CB-CG	5.76	118.36	112.60
1	I	37	ASP	CA-CB-CG	5.72	118.32	112.60
1	H	37	ASP	CA-CB-CG	5.65	118.25	112.60
1	E	37	ASP	CA-CB-CG	5.63	118.23	112.60
1	G	37	ASP	CA-CB-CG	5.62	118.22	112.60
1	B	37	ASP	CA-CB-CG	5.61	118.21	112.60
1	N	37	ASP	CA-CB-CG	5.60	118.20	112.60
1	F	134	THR	CA-C-N	5.59	130.08	121.19
1	F	134	THR	C-N-CA	5.59	130.08	121.19
1	M	37	ASP	CA-CB-CG	5.58	118.19	112.60
1	I	143	ILE	N-CA-CB	5.58	117.01	110.82
1	L	37	ASP	CA-CB-CG	5.54	118.14	112.60
1	H	143	ILE	CB-CA-C	5.53	117.55	111.08
1	C	134	THR	CA-C-N	5.51	127.98	120.54
1	C	134	THR	C-N-CA	5.51	127.98	120.54
1	D	37	ASP	CA-CB-CG	5.51	118.11	112.60
1	A	126	LEU	N-CA-C	5.48	117.69	111.11
1	J	37	ASP	CA-CB-CG	5.48	118.08	112.60
1	C	135	GLU	CA-C-N	5.44	128.14	120.42
1	C	135	GLU	C-N-CA	5.44	128.14	120.42
1	H	143	ILE	CA-C-N	5.34	128.18	120.38
1	H	143	ILE	C-N-CA	5.34	128.18	120.38
1	D	143	ILE	N-CA-CB	5.27	116.85	110.95
1	B	141	ASN	CA-CB-CG	5.27	117.87	112.60
1	E	139	ALA	CA-C-N	5.23	127.60	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	139	ALA	C-N-CA	5.23	127.60	120.54
1	F	141	ASN	CA-CB-CG	5.20	117.80	112.60
1	A	139	ALA	CA-C-N	5.19	127.19	120.44
1	A	139	ALA	C-N-CA	5.19	127.19	120.44
1	M	135	GLU	CA-C-N	5.03	127.35	120.46
1	M	135	GLU	C-N-CA	5.03	127.35	120.46
1	H	139	ALA	CA-C-N	5.02	127.01	120.28
1	H	139	ALA	C-N-CA	5.02	127.01	120.28
1	F	37	ASP	CA-CB-CG	5.01	117.61	112.60

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	1455	0	1476	20	0
1	B	1454	0	1464	19	0
1	C	1444	0	1460	26	0
1	D	1413	0	1433	21	0
1	E	1459	0	1472	15	0
1	F	1418	0	1435	22	0
1	G	1424	0	1438	24	0
1	H	1489	0	1480	23	0
1	I	1442	0	1446	22	0
1	J	1437	0	1449	15	0
1	K	1411	0	1434	17	0
1	L	1413	0	1434	17	0
1	M	1436	0	1453	14	0
1	N	1409	0	1419	16	0
2	A	1	0	0	1	0
2	B	1	0	0	0	0
2	C	1	0	0	1	0
2	D	1	0	0	0	0
2	L	2	0	0	0	0
2	M	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	39	0	0	0	0
3	B	28	0	0	1	0
3	C	19	0	0	1	0
3	D	16	0	0	0	0
3	E	25	0	0	0	0
3	F	10	0	0	0	0
3	G	27	0	0	1	0
3	H	22	0	0	0	0
3	I	23	0	0	0	0
3	J	16	0	0	0	0
3	K	17	0	0	1	0
3	L	22	0	0	0	0
3	M	9	0	0	0	0
3	N	20	0	0	1	0
All	All	20404	0	20293	229	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 6.

All (229) 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:162:ILE:CD1	1:C:162:ILE:CG1	1.75	1.57
1:N:93:ILE:HG23	1:N:115:LEU:HD12	1.73	0.69
1:A:71:VAL:HG22	1:A:99:MET:HE3	1.76	0.67
1:F:144:LEU:HD12	1:G:119:GLU:HG2	1.77	0.67
1:B:91:ILE:HG23	1:B:190:MET:HE1	1.77	0.66
1:C:91:ILE:HG23	1:C:190:MET:HE1	1.78	0.66
1:A:142[A]:HIS:CE1	2:A:204:CL:CL	2.88	0.64
1:K:91:ILE:HG23	1:K:190:MET:HE1	1.80	0.63
1:F:35:GLN:HG3	1:F:67:PRO:HG2	1.82	0.62
1:G:35:GLN:HG3	1:G:67:PRO:HG2	1.82	0.61
1:E:35:GLN:HG3	1:E:67:PRO:HG2	1.82	0.61
1:E:144:LEU:HD12	1:F:119:GLU:HG2	1.81	0.61
1:H:124:GLN:O	1:H:147:ARG:NH2	2.34	0.61
1:C:152:ARG:NH1	1:C:162:ILE:HD11	2.15	0.61
1:J:91:ILE:HG23	1:J:190:MET:HE1	1.83	0.60
1:A:35:GLN:HG3	1:A:67:PRO:HG2	1.83	0.60
1:D:35:GLN:HG3	1:D:67:PRO:HG2	1.83	0.60
1:J:35:GLN:HG3	1:J:67:PRO:HG2	1.83	0.60
1:C:4:ILE:HD12	1:C:21:TYR:HE1	1.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:71:VAL:HG22	1:M:99:MET:HE3	1.84	0.60
1:B:35:GLN:HG3	1:B:67:PRO:HG2	1.83	0.60
1:C:35:GLN:HG3	1:C:67:PRO:HG2	1.83	0.60
1:H:35:GLN:HG3	1:H:67:PRO:HG2	1.85	0.59
1:M:35:GLN:HG3	1:M:67:PRO:HG2	1.82	0.59
1:I:91:ILE:HG23	1:I:190:MET:HE1	1.85	0.59
1:L:35:GLN:HG3	1:L:67:PRO:HG2	1.85	0.59
1:A:128:GLY:HA3	1:A:133:ALA:HB3	1.83	0.59
1:K:35[A]:GLN:HG2	1:K:67:PRO:HG2	1.85	0.58
1:H:71:VAL:HG22	1:H:99:MET:HE3	1.86	0.58
1:D:91:ILE:HG23	1:D:190:MET:HE1	1.84	0.58
1:B:91:ILE:CG2	1:B:190:MET:HE1	2.33	0.58
1:E:71:VAL:HG22	1:E:99:MET:HE3	1.85	0.58
1:K:71:VAL:HG22	1:K:99:MET:HE3	1.85	0.58
1:N:35:GLN:HG3	1:N:67:PRO:HG2	1.85	0.58
1:M:91:ILE:HG23	1:M:190:MET:HE1	1.85	0.57
1:A:93:ILE:HG23	1:A:115:LEU:HD12	1.86	0.57
1:F:136:ILE:HG22	1:G:174:PHE:HZ	1.69	0.57
1:E:97:ALA:HB1	1:E:121:MET:HE2	1.87	0.57
1:D:71:VAL:HG22	1:D:99:MET:HE3	1.87	0.57
1:I:35:GLN:HG3	1:I:67:PRO:HG2	1.87	0.56
1:I:71:VAL:HG22	1:I:99:MET:HE3	1.87	0.56
1:B:71:VAL:HG22	1:B:99:MET:HE3	1.87	0.56
1:C:91:ILE:CG2	1:C:190:MET:HE1	2.35	0.56
1:H:91:ILE:HG23	1:H:190:MET:HE1	1.86	0.56
1:G:128:GLY:HA3	1:G:133:ALA:HB3	1.86	0.56
1:C:93:ILE:HG23	1:C:115:LEU:HD12	1.88	0.56
1:F:4:ILE:HG23	1:F:20:ILE:HG22	1.88	0.56
1:I:97:ALA:HB1	1:I:121:MET:HE2	1.87	0.56
1:F:91:ILE:HG23	1:F:190:MET:HE1	1.88	0.56
1:C:97:ALA:HB1	1:C:121:MET:HE2	1.87	0.56
1:F:71:VAL:HG22	1:F:99:MET:HE3	1.87	0.55
1:K:91:ILE:CG2	1:K:190:MET:HE1	2.36	0.55
1:C:71:VAL:HG22	1:C:99:MET:HE3	1.88	0.55
1:M:4:ILE:HG23	1:M:20:ILE:HG22	1.87	0.55
1:A:121[A]:MET:HE3	1:A:123:HIS:HB3	1.89	0.55
1:N:4:ILE:HG23	1:N:20:ILE:HG22	1.87	0.55
1:B:4:ILE:HG23	1:B:20:ILE:HG22	1.87	0.55
1:L:4:ILE:HG23	1:L:20:ILE:HG22	1.89	0.55
1:L:97:ALA:HB1	1:L:121:MET:HE2	1.87	0.55
1:J:4:ILE:HG23	1:J:20:ILE:HG22	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:142[B]:HIS:CE1	2:C:204:CL:CL	2.96	0.55
1:M:97:ALA:HB1	1:M:121:MET:HE2	1.88	0.55
1:K:4:ILE:HG23	1:K:20:ILE:HG22	1.90	0.54
1:J:97:ALA:HB1	1:J:121:MET:HE2	1.90	0.54
1:B:93:ILE:HG23	1:B:115:LEU:HD12	1.89	0.54
1:A:4:ILE:HG23	1:A:20:ILE:HG22	1.89	0.54
1:G:71:VAL:HG22	1:G:99:MET:HE3	1.90	0.54
1:F:97:ALA:HB1	1:F:121:MET:HE2	1.90	0.53
1:J:71:VAL:HG22	1:J:99:MET:HE3	1.89	0.53
1:N:71:VAL:HG22	1:N:99:MET:HE3	1.90	0.53
1:H:143:ILE:HG12	1:H:145:LYS:HD3	1.91	0.53
1:H:195:LYS:HA	1:N:85:LYS:HE2	1.90	0.53
1:I:4:ILE:HG23	1:I:20:ILE:HG22	1.90	0.53
1:H:76:ALA:HB1	1:I:93:ILE:HG22	1.91	0.52
1:I:79:ASP:HB3	1:J:115:LEU:HD13	1.91	0.52
1:M:91:ILE:CG2	1:M:190:MET:HE1	2.40	0.52
1:N:97:ALA:HB1	1:N:121:MET:HE2	1.91	0.52
1:N:115:LEU:HD23	1:N:190:MET:HB2	1.91	0.52
1:L:71:VAL:HG22	1:L:99:MET:HE3	1.91	0.52
1:G:135:GLU:HA	1:G:138:ILE:HD12	1.92	0.52
1:J:91:ILE:CG2	1:J:190:MET:HE1	2.40	0.52
1:A:79:ASP:HB3	1:B:115:LEU:HD13	1.91	0.52
1:H:136:ILE:HG23	1:I:174:PHE:HZ	1.74	0.52
1:C:144:LEU:HD12	1:D:119:GLU:HG2	1.91	0.52
1:G:93:ILE:HG23	1:G:115:LEU:HD12	1.93	0.51
1:D:4:ILE:HG23	1:D:20:ILE:HG22	1.91	0.51
1:H:93:ILE:HG22	1:N:76:ALA:HB1	1.92	0.51
1:H:79:ASP:HB3	1:I:115:LEU:HD13	1.93	0.50
1:F:93:ILE:O	1:F:93:ILE:HG13	2.10	0.50
1:E:4:ILE:HG23	1:E:20:ILE:HG22	1.93	0.50
1:A:126:LEU:HD23	1:A:147:ARG:HH21	1.77	0.50
1:M:121:MET:HG3	1:M:173:ASN:O	2.12	0.50
1:J:144:LEU:HD12	1:K:119:GLU:HG2	1.94	0.50
1:B:18:TYR:HB3	1:B:22:SER:HB2	1.94	0.50
1:F:135:GLU:CD	1:F:135:GLU:H	2.20	0.50
1:H:85:LYS:HG2	1:I:193:GLU:HG2	1.94	0.50
1:I:126:LEU:O	1:I:142:HIS:CE1	2.64	0.50
1:C:147:ARG:NH1	3:C:217:HOH:O	2.45	0.49
1:G:4:ILE:HG23	1:G:20:ILE:HG22	1.94	0.49
1:M:144:LEU:HD12	1:N:119:GLU:HG2	1.95	0.49
1:A:174:PHE:CE2	1:G:143:ILE:HD13	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:ALA:HB1	1:C:93:ILE:HG22	1.95	0.49
1:M:93:ILE:HG23	1:M:115:LEU:HD12	1.95	0.49
1:M:18:TYR:HB3	1:M:22:SER:HB2	1.95	0.49
1:M:121:MET:HB2	1:M:174:PHE:CE1	2.48	0.48
1:N:18:TYR:HB3	1:N:22:SER:HB2	1.95	0.48
1:E:18:TYR:HB3	1:E:22:SER:HB2	1.95	0.48
1:H:91:ILE:CG2	1:H:190:MET:HE1	2.42	0.48
1:J:141:ASN:HA	1:J:146:THR:HG23	1.95	0.48
1:N:136:ILE:H	1:N:136:ILE:HD12	1.78	0.48
1:A:37:ASP:HB3	1:A:132:GLN:HG3	1.95	0.48
1:J:93:ILE:HG23	1:J:115:LEU:HD12	1.95	0.48
1:K:18:TYR:HB3	1:K:22:SER:HB2	1.95	0.48
1:K:93:ILE:HG23	1:K:115:LEU:HD12	1.96	0.48
1:B:97:ALA:HB1	1:B:121:MET:HE2	1.95	0.48
1:D:91:ILE:CG2	1:D:190:MET:HE1	2.43	0.48
1:H:93:ILE:HG23	1:H:115:LEU:HD12	1.95	0.48
1:I:18:TYR:HB3	1:I:22:SER:HB2	1.96	0.48
1:I:91:ILE:CG2	1:I:190:MET:HE1	2.44	0.48
1:K:97:ALA:HB1	1:K:121:MET:HE2	1.96	0.48
1:L:18:TYR:HB3	1:L:22:SER:HB2	1.96	0.47
1:C:18:TYR:HB3	1:C:22:SER:HB2	1.96	0.47
1:E:134:THR:HG22	1:E:137:GLU:OE1	2.14	0.47
1:D:83:HIS:O	1:E:193:GLU:HG2	2.15	0.47
1:L:93:ILE:HG23	1:L:115:LEU:HD12	1.97	0.47
1:L:107:GLY:O	1:L:157:ARG:NH2	2.48	0.47
1:H:97:ALA:HB1	1:H:121:MET:HE2	1.97	0.47
1:B:91:ILE:HG23	1:B:190:MET:CE	2.43	0.47
1:D:93:ILE:HG23	1:D:115:LEU:HD12	1.97	0.47
1:I:193:GLU:HA	1:I:196:TRP:CD1	2.50	0.47
1:B:22:SER:HB3	1:C:6:THR:O	2.15	0.47
1:B:94:GLY:HA2	3:B:215:HOH:O	2.15	0.46
1:F:18:TYR:HB3	1:F:22:SER:HB2	1.97	0.46
1:K:144:LEU:HD12	1:L:119:GLU:HG2	1.96	0.46
1:L:91:ILE:HG23	1:L:190:MET:HE1	1.96	0.46
1:J:18:TYR:HB3	1:J:22:SER:HB2	1.97	0.46
1:G:91:ILE:HG23	1:G:190:MET:HE1	1.97	0.46
1:K:91:ILE:HG23	1:K:190:MET:CE	2.45	0.46
1:A:121[B]:MET:HE1	1:G:140:ALA:HB2	1.98	0.46
1:C:91:ILE:HG23	1:C:190:MET:CE	2.43	0.46
1:I:193:GLU:HA	1:I:196:TRP:HD1	1.80	0.46
1:A:93:ILE:HG22	1:G:76:ALA:HB1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:97:ALA:HB1	1:G:121:MET:HE2	1.98	0.46
1:H:18:TYR:HB3	1:H:22:SER:HB2	1.97	0.45
1:D:18:TYR:HB3	1:D:22:SER:HB2	1.97	0.45
1:E:17:ALA:O	1:F:8:ILE:HD11	2.17	0.45
1:F:91:ILE:CG2	1:F:190:MET:HE1	2.45	0.45
1:L:91:ILE:CG2	1:L:190:MET:HE1	2.47	0.45
1:N:126:LEU:HA	1:N:147:ARG:NH2	2.31	0.45
1:A:94:GLY:HA2	3:G:211:HOH:O	2.16	0.45
1:K:99:MET:HE1	1:K:150:LEU:CD2	2.47	0.45
1:G:18:TYR:HB3	1:G:22:SER:HB2	1.97	0.45
1:A:18:TYR:HB3	1:A:22:SER:HB2	1.99	0.45
1:C:22:SER:HB3	1:D:6:THR:O	2.17	0.45
1:J:91:ILE:HG23	1:J:190:MET:CE	2.47	0.45
1:E:22:SER:HB3	1:F:6:THR:O	2.16	0.45
1:H:91:ILE:HG23	1:H:190:MET:CE	2.47	0.45
1:E:93:ILE:O	1:E:93:ILE:HG13	2.16	0.44
1:L:144:LEU:HD12	1:M:119:GLU:HG2	2.00	0.44
1:N:121:MET:HG3	1:N:173:ASN:O	2.16	0.44
1:H:121:MET:HG3	1:H:173:ASN:O	2.17	0.44
1:M:91:ILE:HG23	1:M:190:MET:CE	2.47	0.44
1:B:121:MET:HB2	1:B:174:PHE:CE1	2.52	0.43
1:G:136:ILE:H	1:G:136:ILE:HD12	1.83	0.43
1:C:35:GLN:HB3	1:C:132:GLN:NE2	2.33	0.43
1:H:94:GLY:HA2	3:N:206:HOH:O	2.18	0.43
1:A:128:GLY:CA	1:A:133:ALA:HB3	2.49	0.43
1:K:121:MET:HB2	1:K:174:PHE:CE1	2.52	0.43
1:F:99:MET:HE1	1:F:150:LEU:CD2	2.47	0.43
1:G:121:MET:HG3	1:G:173:ASN:O	2.19	0.43
1:H:195:LYS:HG2	1:N:85:LYS:HG2	2.00	0.43
1:F:22:SER:HB3	1:G:6:THR:O	2.19	0.43
1:D:97:ALA:HB1	1:D:121:MET:HE2	2.00	0.43
1:B:138:ILE:O	1:B:141:ASN:HB2	2.18	0.43
1:C:162:ILE:CD1	1:C:162:ILE:CB	2.84	0.43
1:D:135:GLU:HB2	1:E:130:GLN:NE2	2.34	0.43
1:I:76:ALA:HB1	1:J:93:ILE:HG22	2.01	0.43
1:B:121:MET:HG3	1:B:173:ASN:O	2.19	0.42
1:C:76:ALA:HB1	1:D:93:ILE:HG22	2.00	0.42
1:G:190:MET:HE3	1:G:190:MET:HB2	1.89	0.42
1:C:79:ASP:HB3	1:D:115:LEU:HD13	2.02	0.42
1:I:126:LEU:HG	1:I:147:ARG:HH21	1.84	0.42
1:D:121:MET:HG3	1:D:173:ASN:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:67:PRO:HB2	1:F:130:GLN:HE22	1.84	0.42
1:H:190:MET:HE3	1:H:190:MET:HB2	1.82	0.42
1:K:76:ALA:HB1	1:L:93:ILE:HG22	2.00	0.42
1:C:121:MET:HG3	1:C:173:ASN:O	2.19	0.42
1:C:149:LYS:HE3	1:D:117:ASN:OD1	2.19	0.42
1:I:93:ILE:HG23	1:I:115:LEU:HD12	2.01	0.42
1:D:190:MET:HE3	1:D:190:MET:HB2	1.89	0.42
1:H:99:MET:HE1	1:H:150:LEU:CD2	2.50	0.42
1:A:134:THR:HG22	1:A:137:GLU:HG3	2.02	0.42
1:B:144:LEU:HD12	1:C:119:GLU:HG2	2.00	0.42
1:I:190:MET:HE3	1:I:190:MET:HB2	1.86	0.42
1:B:99:MET:HE1	1:B:150:LEU:CD2	2.49	0.42
1:H:149:LYS:HD2	1:H:152:ARG:HH22	1.85	0.42
1:N:126:LEU:HA	1:N:147:ARG:HH22	1.84	0.42
1:A:115:LEU:HD13	1:G:79:ASP:HB3	2.01	0.42
1:F:79:ASP:HB3	1:G:115:LEU:HD13	2.02	0.41
1:G:121:MET:HB2	1:G:174:PHE:CE1	2.55	0.41
1:J:190:MET:HE3	1:J:190:MET:HB2	1.87	0.41
1:L:122:ILE:HG21	1:L:185:LEU:HD11	2.01	0.41
1:C:121:MET:HB2	1:C:174:PHE:CE1	2.55	0.41
1:K:79:ASP:HB3	1:L:115:LEU:HD13	2.03	0.41
1:A:130:GLN:HE21	1:G:136:ILE:HD13	1.84	0.41
1:D:85:LYS:HE3	1:E:194:THR:O	2.21	0.41
1:D:99:MET:HE1	1:D:150:LEU:CD2	2.51	0.41
1:D:121:MET:HB2	1:D:174:PHE:CE1	2.55	0.41
1:E:83:HIS:O	1:F:193:GLU:HG2	2.20	0.41
1:F:149:LYS:HE2	1:F:152:ARG:HH12	1.86	0.41
1:G:181:LYS:HA	1:G:186:ILE:HG13	2.02	0.41
1:L:121:MET:HB2	1:L:174:PHE:CE1	2.56	0.41
1:F:190:MET:HE3	1:F:190:MET:HB2	1.85	0.41
1:B:136:ILE:HG22	1:C:174:PHE:HZ	1.86	0.40
1:D:91:ILE:HG23	1:D:190:MET:CE	2.50	0.40
1:F:91:ILE:HG23	1:F:190:MET:CE	2.51	0.40
1:N:121:MET:HB2	1:N:174:PHE:CE1	2.56	0.40
1:J:35:GLN:HB3	1:J:132:GLN:NE2	2.36	0.40
1:K:94:GLY:HA2	3:K:208:HOH:O	2.21	0.40
1:A:95:MET:SD	1:A:121[B]:MET:HE2	2.60	0.40
1:H:126:LEU:HD22	1:H:142[A]:HIS:HE1	1.86	0.40
1:L:136:ILE:HG22	1:M:174:PHE:HZ	1.86	0.40
1:I:91:ILE:HG23	1:I:190:MET:CE	2.51	0.40
1:I:99:MET:HE1	1:I:150:LEU:CD2	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:181:LYS:HD3	1:G:188:GLU:HA	2.03	0.40

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	186/203 (92%)	182 (98%)	3 (2%)	1 (0%)	24	22
1	B	184/203 (91%)	180 (98%)	3 (2%)	1 (0%)	24	22
1	C	182/203 (90%)	178 (98%)	4 (2%)	0	100	100
1	D	178/203 (88%)	173 (97%)	5 (3%)	0	100	100
1	E	187/203 (92%)	180 (96%)	7 (4%)	0	100	100
1	F	180/203 (89%)	174 (97%)	5 (3%)	1 (1%)	21	18
1	G	182/203 (90%)	177 (97%)	4 (2%)	1 (0%)	24	22
1	H	187/203 (92%)	181 (97%)	6 (3%)	0	100	100
1	I	182/203 (90%)	179 (98%)	2 (1%)	1 (0%)	24	22
1	J	184/203 (91%)	178 (97%)	5 (3%)	1 (0%)	24	22
1	K	177/203 (87%)	173 (98%)	4 (2%)	0	100	100
1	L	176/203 (87%)	174 (99%)	2 (1%)	0	100	100
1	M	183/203 (90%)	180 (98%)	3 (2%)	0	100	100
1	N	178/203 (88%)	173 (97%)	5 (3%)	0	100	100
All	All	2546/2842 (90%)	2482 (98%)	58 (2%)	6 (0%)	43	44

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	129	ALA

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Mol	Chain	Res	Type
1	G	129	ALA
1	J	130	GLN
1	B	127	GLY
1	F	127	GLY
1	I	127	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	158/171 (92%)	155 (98%)	3 (2%)	50	58
1	B	157/171 (92%)	155 (99%)	2 (1%)	61	69
1	C	156/171 (91%)	151 (97%)	5 (3%)	34	38
1	D	153/171 (90%)	149 (97%)	4 (3%)	40	46
1	E	157/171 (92%)	155 (99%)	2 (1%)	61	69
1	F	154/171 (90%)	150 (97%)	4 (3%)	40	46
1	G	153/171 (90%)	149 (97%)	4 (3%)	40	46
1	H	159/171 (93%)	152 (96%)	7 (4%)	25	26
1	I	155/171 (91%)	151 (97%)	4 (3%)	40	46
1	J	154/171 (90%)	153 (99%)	1 (1%)	78	86
1	K	155/171 (91%)	154 (99%)	1 (1%)	78	86
1	L	155/171 (91%)	153 (99%)	2 (1%)	61	69
1	M	155/171 (91%)	150 (97%)	5 (3%)	34	38
1	N	151/171 (88%)	145 (96%)	6 (4%)	28	29
All	All	2172/2394 (91%)	2122 (98%)	50 (2%)	44	51

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	147	ARG

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Mol	Chain	Res	Type
1	A	163	GLU
1	B	35	GLN
1	B	135	GLU
1	C	35	GLN
1	C	119	GLU
1	C	136	ILE
1	C	149	LYS
1	C	152	ARG
1	D	35	GLN
1	D	119	GLU
1	D	149	LYS
1	D	157	ARG
1	E	35	GLN
1	E	132	GLN
1	F	35	GLN
1	F	119	GLU
1	F	135	GLU
1	F	136	ILE
1	G	35	GLN
1	G	135	GLU
1	G	143	ILE
1	G	188	GLU
1	H	35	GLN
1	H	119	GLU
1	H	132	GLN
1	H	136	ILE
1	H	143	ILE
1	H	144	LEU
1	H	200	GLN
1	I	35	GLN
1	I	134	THR
1	I	143	ILE
1	I	193	GLU
1	J	35	GLN
1	K	119	GLU
1	L	35	GLN
1	L	119	GLU
1	M	35	GLN
1	M	130	GLN
1	M	138	ILE
1	M	142	HIS
1	M	162	ILE

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Mol	Chain	Res	Type
1	N	35	GLN
1	N	119	GLU
1	N	136	ILE
1	N	138	ILE
1	N	156	GLU
1	N	193	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	GLN
1	A	117	ASN
1	A	130	GLN
1	A	132	GLN
1	A	141	ASN
1	B	82	GLN
1	B	117	ASN
1	B	132	GLN
1	B	141	ASN
1	C	82	GLN
1	C	117	ASN
1	C	132	GLN
1	D	82	GLN
1	D	83	HIS
1	D	132	GLN
1	E	82	GLN
1	E	83	HIS
1	F	82	GLN
1	F	130	GLN
1	F	141	ASN
1	G	82	GLN
1	H	82	GLN
1	H	141	ASN
1	H	200	GLN
1	I	42	ASN
1	I	82	GLN
1	I	142	HIS
1	J	65	ASN
1	J	82	GLN
1	J	83	HIS
1	J	132	GLN
1	J	141	ASN

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Mol	Chain	Res	Type
1	J	173	ASN
1	K	82	GLN
1	L	82	GLN
1	M	82	GLN
1	M	117	ASN
1	N	82	GLN
1	N	117	ASN

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 ⓘ

Of 7 ligands modelled in this entry, 7 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

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	187/203 (92%)	0.69	24 (12%) 7 8	31, 56, 108, 157	3 (1%)
1	B	187/203 (92%)	1.05	35 (18%) 3 3	37, 69, 118, 151	3 (1%)
1	C	186/203 (91%)	0.86	35 (18%) 3 3	34, 61, 114, 142	2 (1%)
1	D	182/203 (89%)	0.75	29 (15%) 5 5	33, 56, 101, 145	2 (1%)
1	E	188/203 (92%)	0.58	21 (11%) 10 10	27, 50, 100, 132	3 (1%)
1	F	182/203 (89%)	0.71	19 (10%) 11 12	30, 62, 99, 163	2 (1%)
1	G	185/203 (91%)	0.74	24 (12%) 7 7	35, 61, 106, 175	1 (0%)
1	H	192/203 (94%)	1.01	35 (18%) 3 3	34, 66, 114, 146	2 (1%)
1	I	186/203 (91%)	0.73	23 (12%) 8 8	31, 55, 104, 157	2 (1%)
1	J	186/203 (91%)	1.01	29 (15%) 5 5	36, 70, 114, 149	2 (1%)
1	K	179/203 (88%)	0.96	24 (13%) 7 7	37, 68, 110, 158	4 (2%)
1	L	180/203 (88%)	0.84	22 (12%) 8 8	37, 63, 109, 166	3 (1%)
1	M	186/203 (91%)	1.21	29 (15%) 5 5	41, 75, 114, 148	1 (0%)
1	N	183/203 (90%)	1.35	42 (22%) 2 2	40, 79, 117, 175	1 (0%)
All	All	2589/2842 (91%)	0.89	391 (15%) 5 5	27, 65, 113, 175	31 (1%)

All (391) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	17	ALA	6.9
1	F	7	VAL	6.2
1	L	128	GLY	6.0
1	A	3	LEU	5.9
1	K	3	LEU	5.9
1	N	133	ALA	5.8
1	C	3	LEU	5.6
1	A	129	ALA	5.6

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Mol	Chain	Res	Type	RSRZ
1	J	194	THR	5.6
1	M	144	LEU	5.5
1	D	7	VAL	5.5
1	H	128	GLY	5.4
1	B	7	VAL	5.4
1	D	3	LEU	5.4
1	N	132	GLN	5.2
1	I	17	ALA	5.2
1	J	136	ILE	5.1
1	C	7	VAL	5.1
1	J	7	VAL	5.1
1	G	17	ALA	5.1
1	K	8	ILE	5.0
1	G	7	VAL	5.0
1	C	197	SER	4.9
1	H	7	VAL	4.9
1	B	139	ALA	4.9
1	N	143	ILE	4.9
1	A	136	ILE	4.9
1	F	126	LEU	4.9
1	G	126	LEU	4.9
1	C	127	GLY	4.9
1	G	3	LEU	4.8
1	M	133	ALA	4.8
1	M	136	ILE	4.8
1	H	17	ALA	4.8
1	N	144	LEU	4.8
1	E	17	ALA	4.8
1	B	3	LEU	4.7
1	H	143	ILE	4.7
1	C	133	ALA	4.7
1	K	127	GLY	4.7
1	E	129	ALA	4.6
1	G	129	ALA	4.6
1	B	128	GLY	4.6
1	I	126	LEU	4.6
1	B	136	ILE	4.6
1	H	133	ALA	4.6
1	J	3	LEU	4.6
1	J	129	ALA	4.5
1	H	3	LEU	4.5
1	M	3	LEU	4.5

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Mol	Chain	Res	Type	RSRZ
1	N	126	LEU	4.5
1	H	126	LEU	4.5
1	F	128	GLY	4.5
1	I	3	LEU	4.5
1	N	138	ILE	4.4
1	L	7	VAL	4.4
1	E	3	LEU	4.4
1	N	3	LEU	4.4
1	I	4	ILE	4.4
1	E	7	VAL	4.3
1	I	172	ASP	4.3
1	L	136	ILE	4.3
1	D	128	GLY	4.3
1	M	129	ALA	4.3
1	B	17	ALA	4.3
1	E	142[A]	HIS	4.3
1	L	3	LEU	4.2
1	L	143	ILE	4.2
1	I	7	VAL	4.2
1	K	18	TYR	4.2
1	C	196	TRP	4.2
1	C	8	ILE	4.1
1	M	143	ILE	4.1
1	J	126	LEU	4.1
1	L	126	LEU	4.1
1	B	143	ILE	4.1
1	D	4	ILE	4.1
1	C	17	ALA	4.1
1	C	6	THR	4.0
1	I	136	ILE	4.0
1	F	6	THR	4.0
1	H	196	TRP	4.0
1	N	129	ALA	4.0
1	K	136	ILE	4.0
1	N	136	ILE	4.0
1	A	126	LEU	3.9
1	K	7	VAL	3.9
1	K	132	GLN	3.9
1	G	191	VAL	3.9
1	B	4	ILE	3.9
1	M	138	ILE	3.9
1	A	7	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	D	142[A]	HIS	3.9
1	H	8	ILE	3.9
1	D	126	LEU	3.9
1	D	144	LEU	3.9
1	B	18	TYR	3.8
1	M	4	ILE	3.8
1	H	140	ALA	3.8
1	E	4	ILE	3.8
1	E	18	TYR	3.8
1	A	17	ALA	3.8
1	D	17	ALA	3.8
1	M	139	ALA	3.8
1	C	4	ILE	3.7
1	H	93	ILE	3.7
1	M	194	THR	3.7
1	B	144	LEU	3.7
1	D	133	ALA	3.7
1	L	6	THR	3.7
1	B	93	ILE	3.7
1	G	4	ILE	3.7
1	H	6	THR	3.7
1	B	10	THR	3.6
1	E	133	ALA	3.6
1	K	143	ILE	3.6
1	G	6	THR	3.6
1	N	17	ALA	3.6
1	B	126	LEU	3.6
1	F	127	GLY	3.6
1	M	128	GLY	3.6
1	C	136	ILE	3.6
1	E	173[A]	ASN	3.6
1	F	18	TYR	3.6
1	I	18	TYR	3.6
1	B	134	THR	3.5
1	N	4	ILE	3.5
1	B	138	ILE	3.5
1	I	8	ILE	3.5
1	J	93	ILE	3.5
1	F	129	ALA	3.5
1	E	126	LEU	3.5
1	D	143	ILE	3.5
1	E	122	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	F	8	ILE	3.5
1	F	136	ILE	3.5
1	H	144	LEU	3.5
1	D	6	THR	3.5
1	G	136	ILE	3.4
1	H	136	ILE	3.4
1	K	4	ILE	3.4
1	H	142[A]	HIS	3.4
1	H	138	ILE	3.4
1	M	126	LEU	3.4
1	M	134	THR	3.4
1	A	16	ARG	3.4
1	C	138	ILE	3.4
1	E	8	ILE	3.4
1	L	133	ALA	3.4
1	N	93	ILE	3.4
1	G	174	PHE	3.4
1	N	191	VAL	3.4
1	K	174	PHE	3.4
1	N	134	THR	3.3
1	C	18	TYR	3.3
1	J	18	TYR	3.3
1	N	5	PRO	3.3
1	G	130	GLN	3.3
1	A	4	ILE	3.3
1	N	139	ALA	3.3
1	K	149	LYS	3.3
1	F	5	PRO	3.3
1	J	127	GLY	3.3
1	N	8	ILE	3.3
1	C	132	GLN	3.3
1	H	134	THR	3.3
1	G	192	PRO	3.3
1	I	93	ILE	3.3
1	M	174	PHE	3.3
1	C	142[A]	HIS	3.2
1	C	16	ARG	3.2
1	A	6	THR	3.2
1	A	127	GLY	3.2
1	C	191	VAL	3.2
1	N	145	LYS	3.2
1	G	18	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	H	201	PHE	3.2
1	M	7	VAL	3.2
1	M	17	ALA	3.2
1	G	8	ILE	3.2
1	J	4	ILE	3.2
1	D	141	ASN	3.2
1	F	173	ASN	3.2
1	C	140	ALA	3.1
1	M	140	ALA	3.1
1	A	8	ILE	3.1
1	M	142	HIS	3.1
1	B	133	ALA	3.1
1	E	136	ILE	3.1
1	L	18	TYR	3.1
1	H	194	THR	3.1
1	J	6	THR	3.1
1	B	191	VAL	3.1
1	B	162	ILE	3.1
1	C	122	ILE	3.1
1	B	140	ALA	3.0
1	J	8	ILE	3.0
1	H	119	GLU	3.0
1	N	85	LYS	3.0
1	N	142	HIS	3.0
1	K	192	PRO	3.0
1	I	133	ALA	2.9
1	I	144	LEU	2.9
1	K	126	LEU	2.9
1	N	7	VAL	2.9
1	I	6	THR	2.9
1	B	8	ILE	2.9
1	M	122	ILE	2.9
1	B	174	PHE	2.9
1	K	140	ALA	2.9
1	N	6	THR	2.9
1	A	133	ALA	2.9
1	A	140	ALA	2.9
1	D	127	GLY	2.9
1	H	199	PRO	2.8
1	H	202	GLU	2.8
1	H	197	SER	2.8
1	A	142[A]	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
1	H	16	ARG	2.8
1	I	127	GLY	2.8
1	K	6	THR	2.8
1	L	4	ILE	2.8
1	L	174	PHE	2.8
1	A	128	GLY	2.8
1	D	18	TYR	2.8
1	C	134	THR	2.8
1	B	122	ILE	2.8
1	D	173	ASN	2.8
1	B	16	ARG	2.8
1	J	128	GLY	2.8
1	H	139	ALA	2.8
1	E	5	PRO	2.8
1	E	138	ILE	2.8
1	F	162	ILE	2.8
1	L	8	ILE	2.8
1	N	127	GLY	2.7
1	C	174	PHE	2.7
1	N	174	PHE	2.7
1	L	140	ALA	2.7
1	J	192	PRO	2.7
1	C	141	ASN	2.7
1	C	173	ASN	2.7
1	L	191	VAL	2.7
1	B	127	GLY	2.7
1	A	194	THR	2.6
1	M	46	SER	2.6
1	H	162	ILE	2.6
1	K	138	ILE	2.6
1	N	60	ILE	2.6
1	I	128	GLY	2.6
1	G	193	GLU	2.6
1	B	190	MET	2.6
1	D	139	ALA	2.6
1	E	141	ASN	2.6
1	N	140	ALA	2.6
1	N	192	PRO	2.6
1	F	143	ILE	2.6
1	J	138	ILE	2.6
1	I	196	TRP	2.6
1	B	192	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	126	LEU	2.6
1	C	144	LEU	2.6
1	F	122	ILE	2.6
1	M	127	GLY	2.6
1	A	134	THR	2.6
1	H	172	ASP	2.6
1	I	5	PRO	2.6
1	N	137	GLU	2.5
1	F	4	ILE	2.5
1	G	162	ILE	2.5
1	J	149	LYS	2.5
1	J	16	ARG	2.5
1	I	174	PHE	2.5
1	C	182	GLU	2.5
1	E	140	ALA	2.5
1	D	131	GLY	2.5
1	L	142[A]	HIS	2.5
1	N	128	GLY	2.5
1	B	135	GLU	2.5
1	E	130	GLN	2.5
1	G	127	GLY	2.5
1	D	93	ILE	2.5
1	D	191	VAL	2.4
1	E	143	ILE	2.5
1	G	93	ILE	2.5
1	G	134	THR	2.4
1	J	133	ALA	2.4
1	G	128	GLY	2.4
1	H	174	PHE	2.4
1	H	173	ASN	2.4
1	C	93	ILE	2.4
1	D	192	PRO	2.4
1	H	5	PRO	2.4
1	J	142[A]	HIS	2.4
1	A	93	ILE	2.4
1	C	143	ILE	2.4
1	C	9	GLU	2.4
1	M	8	ILE	2.4
1	M	93	ILE	2.4
1	N	162	ILE	2.4
1	I	194	THR	2.4
1	M	6	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	192	PRO	2.4
1	K	5	PRO	2.4
1	N	63	TYR	2.3
1	F	193	GLU	2.3
1	J	144	LEU	2.3
1	B	172	ASP	2.3
1	B	141	ASN	2.3
1	B	173	ASN	2.3
1	I	131	GLY	2.3
1	B	119[A]	GLU	2.3
1	J	5	PRO	2.3
1	E	127	GLY	2.3
1	K	144	LEU	2.3
1	N	49	LEU	2.3
1	B	142[A]	HIS	2.3
1	A	10	THR	2.3
1	I	134	THR	2.3
1	I	173[A]	ASN	2.3
1	N	141	ASN	2.3
1	D	9	GLU	2.2
1	K	133	ALA	2.2
1	J	9	GLU	2.2
1	H	54	GLN	2.2
1	A	192	PRO	2.2
1	D	8	ILE	2.2
1	N	81	ILE	2.2
1	B	19	ASP	2.2
1	C	131	GLY	2.2
1	L	131	GLY	2.2
1	F	130	GLN	2.2
1	A	39	ASN	2.2
1	C	194	THR	2.2
1	D	136	ILE	2.2
1	G	5	PRO	2.2
1	L	5	PRO	2.2
1	L	93	ILE	2.2
1	L	172	ASP	2.2
1	K	191	VAL	2.2
1	C	137	GLU	2.2
1	D	119	GLU	2.2
1	N	9	GLU	2.2
1	A	139	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	L	147	ARG	2.2
1	A	18	TYR	2.2
1	A	172	ASP	2.2
1	C	125	PRO	2.1
1	F	172	ASP	2.2
1	D	138	ILE	2.1
1	J	162	ILE	2.1
1	M	162	ILE	2.1
1	C	139	ALA	2.1
1	D	140	ALA	2.1
1	D	16	ARG	2.1
1	K	173[A]	ASN	2.1
1	D	134	THR	2.1
1	H	122	ILE	2.1
1	K	93	ILE	2.1
1	J	150	LEU	2.1
1	L	121	MET	2.1
1	K	87	ASP	2.1
1	M	18	TYR	2.1
1	I	162	ILE	2.1
1	M	30	ILE	2.1
1	J	191	VAL	2.1
1	K	139	ALA	2.1
1	H	9	GLU	2.1
1	N	95	MET	2.1
1	D	39	ASN	2.1
1	G	149	LYS	2.1
1	J	143	ILE	2.1
1	L	138	ILE	2.1
1	H	189	VAL	2.1
1	J	174	PHE	2.1
1	J	139	ALA	2.1
1	H	130	GLN	2.0
1	N	166	GLN	2.0
1	N	172	ASP	2.0
1	B	152	ARG	2.0
1	G	10	THR	2.0
1	M	5	PRO	2.0
1	G	122	ILE	2.0
1	N	30	ILE	2.0
1	N	122	ILE	2.0
1	E	9	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	F	174	PHE	2.0
1	N	113	PHE	2.0
1	M	105	ALA	2.0
1	N	154	LEU	2.0
1	B	6	THR	2.0

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](#)

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($\text{\AA}^2$)	Q<0.9
2	CL	M	204	1/1	0.81	0.14	93,93,93,93	0
2	CL	L	204	1/1	0.88	0.12	98,98,98,98	0
2	CL	C	204	1/1	0.92	0.15	82,82,82,82	0
2	CL	B	204	1/1	0.93	0.15	99,99,99,99	0
2	CL	D	204	1/1	0.94	0.12	78,78,78,78	0
2	CL	L	205	1/1	0.96	0.07	81,81,81,81	0
2	CL	A	204	1/1	0.96	0.14	81,81,81,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.