



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2024 – 08:22 PM EST

PDB ID : 3QWD
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 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

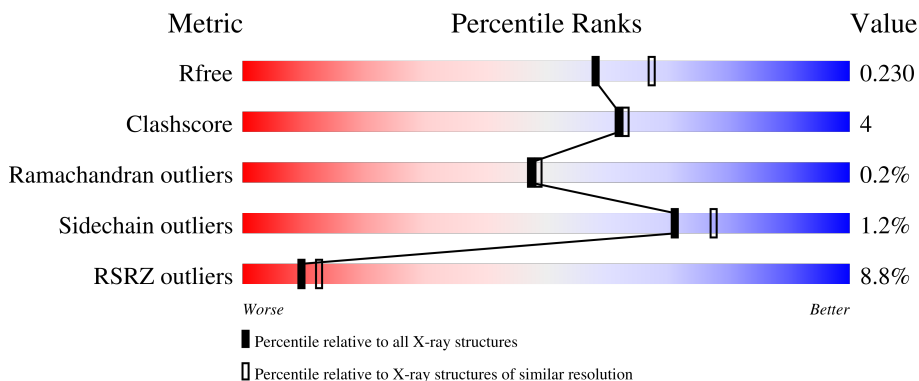
1 Overall quality at a glance

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.



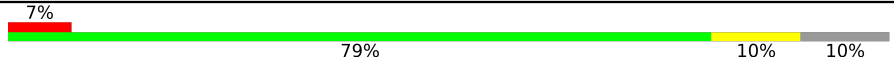
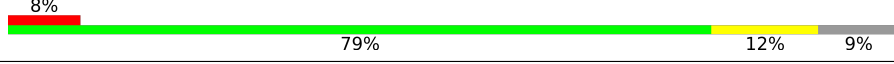



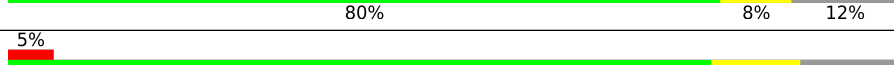
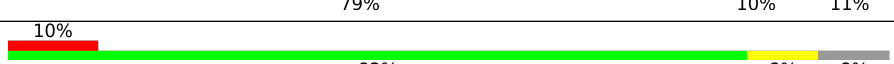
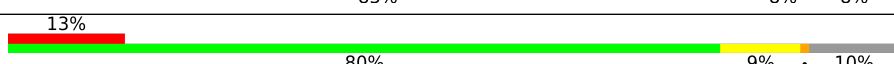

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	 7% 80% 12% 8%
1	B	203	 11% 81% 11% 8%
1	C	203	 10% 80% 10% 8%
1	D	203	 7% 79% 11% 10%
1	E	203	 6% 85% 8% 7%

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Mol	Chain	Length	Quality of chain
1	F	203	 <p>7% 79% 10% 10%</p>
1	G	203	 <p>8% 79% 12% 9%</p>
1	H	203	 <p>8% 81% 13% 5%</p>
1	I	203	 <p>6% 81% 9% 8%</p>
1	J	203	 <p>8% 84% 8% 8%</p>
1	K	203	 <p>5% 80% 8% 12%</p>
1	L	203	 <p>5% 79% 10% 11%</p>
1	M	203	 <p>10% 83% 8% 8%</p>
1	N	203	 <p>13% 80% 9% 10%</p>

2 Entry composition [i](#)

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

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 (three-letter code: 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

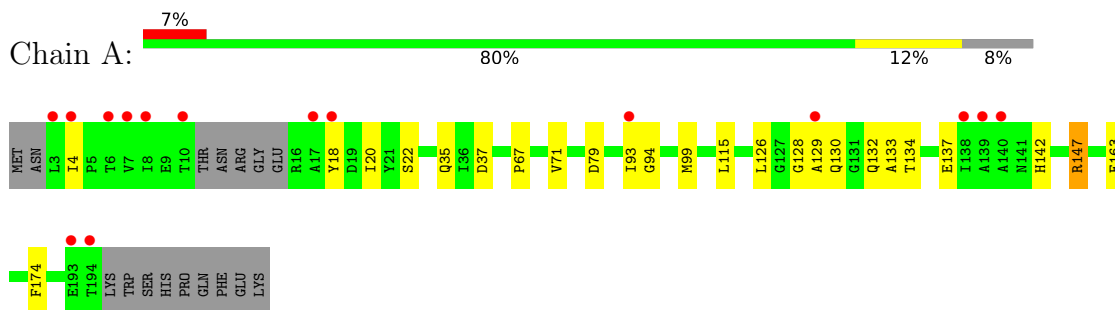
- Molecule 3 is water.

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

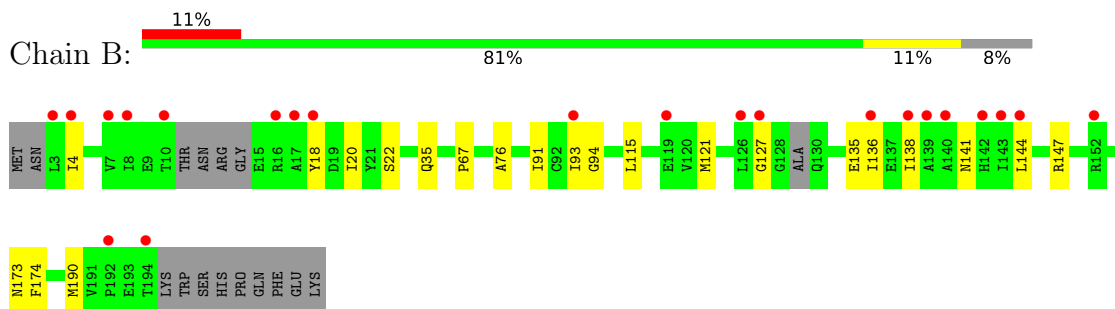
3 Residue-property plots [i](#)

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.

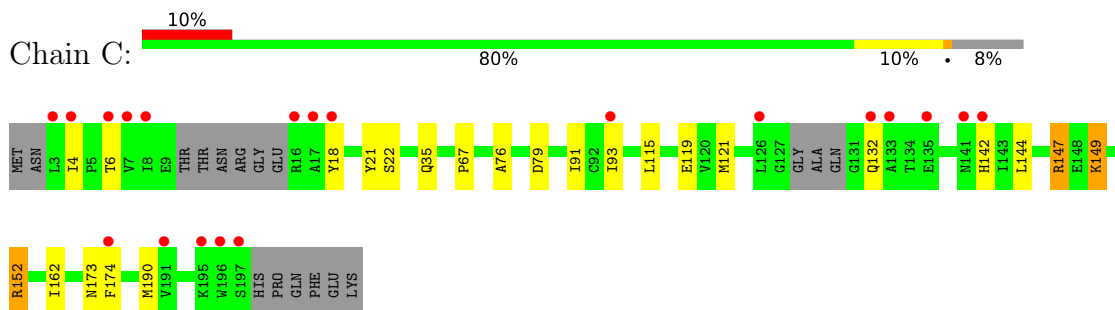
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



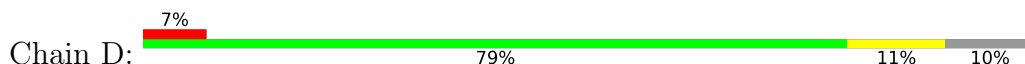
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

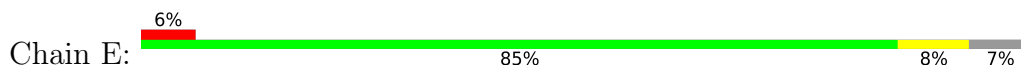


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

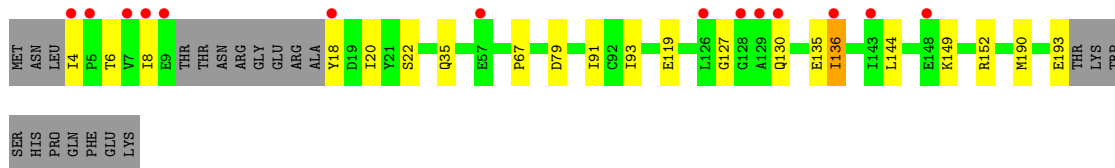
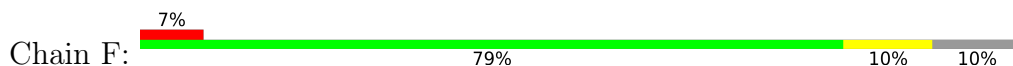




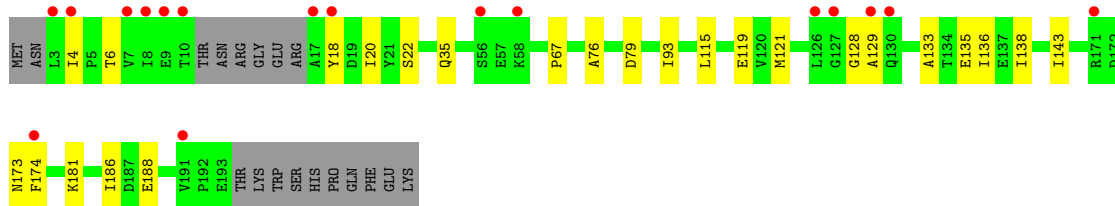
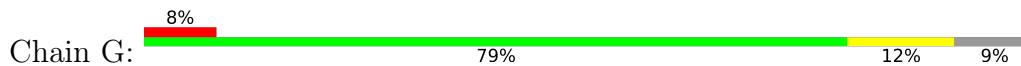
● Molecule 1: ATP-dependent Clp protease proteolytic subunit



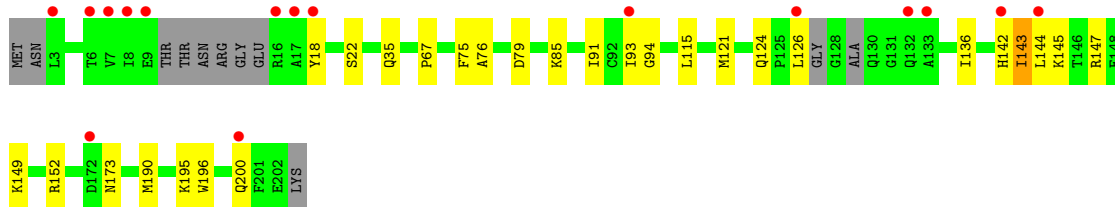
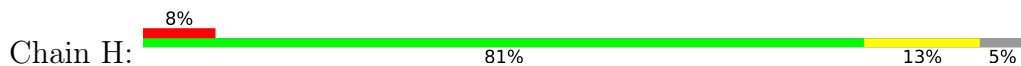
● Molecule 1: ATP-dependent Clp protease proteolytic subunit



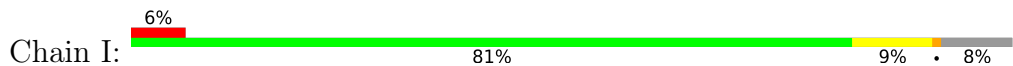
● Molecule 1: ATP-dependent Clp protease proteolytic subunit

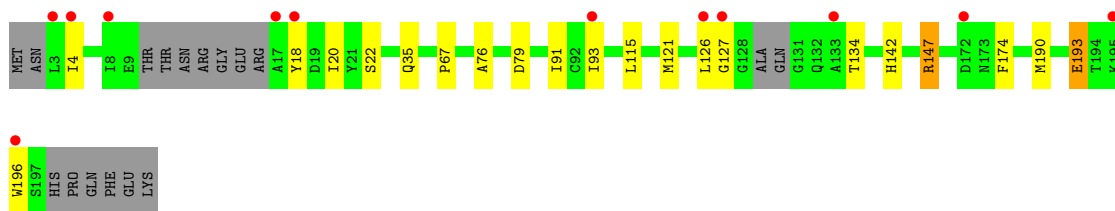


● Molecule 1: ATP-dependent Clp protease proteolytic subunit

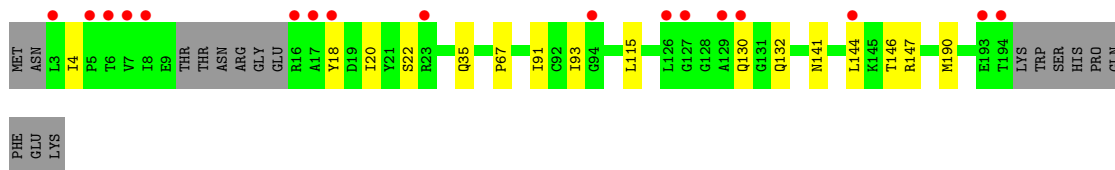
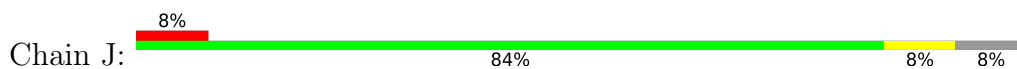


● Molecule 1: ATP-dependent Clp protease proteolytic subunit

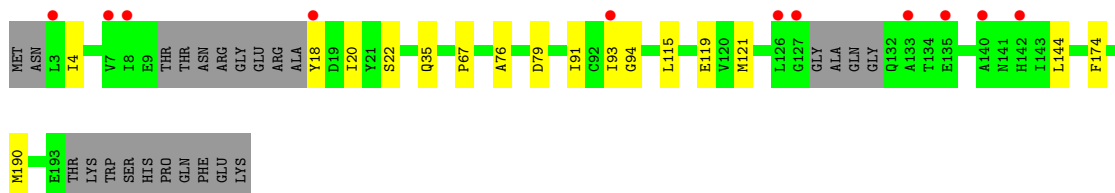
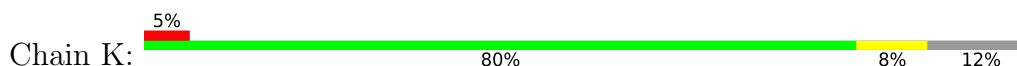




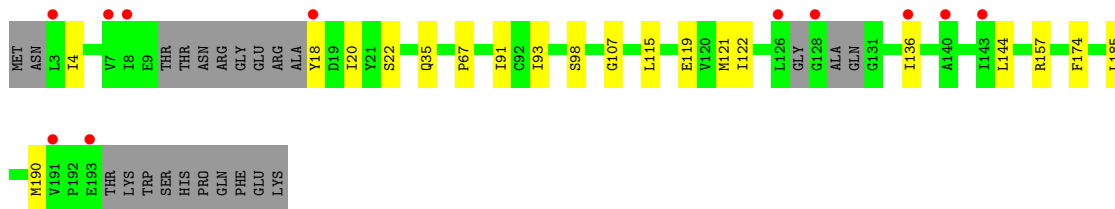
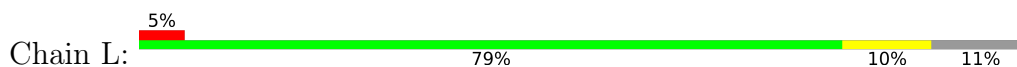
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



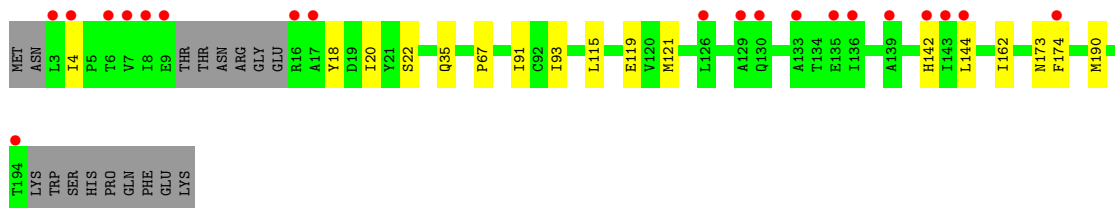
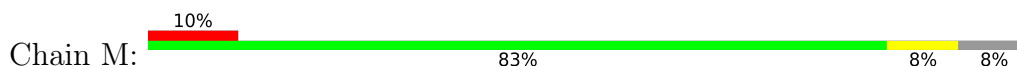
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



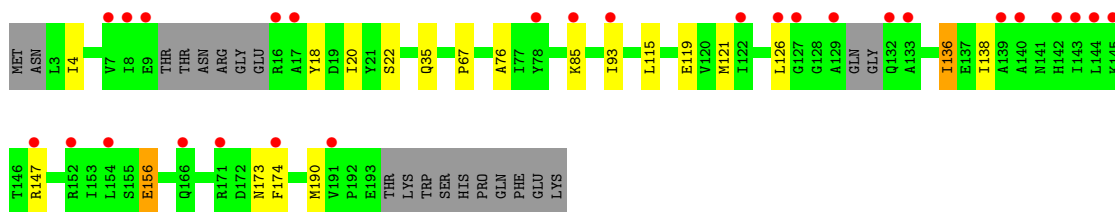
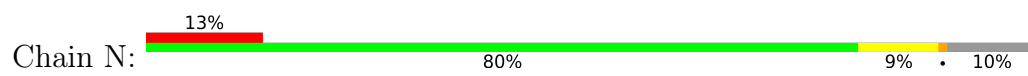
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



- Molecule 1: ATP-dependent Clp protease proteolytic subunit



- Molecule 1: ATP-dependent Clp protease proteolytic subunit



4 Data and refinement statistics i

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) 99.5 (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)	Xtrriage
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	Xtrriage
Anisotropy	0.389	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 58.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.013 for k,h,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20404	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtrriage'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	0.51	0/1483	0.67	0/2002
1	B	0.48	0/1481	0.65	0/1998
1	C	0.53	0/1468	0.67	0/1980
1	D	0.52	0/1437	0.69	0/1938
1	E	0.56	0/1487	0.70	0/2007
1	F	0.49	0/1443	0.66	0/1947
1	G	0.50	0/1445	0.67	0/1951
1	H	0.48	0/1516	0.67	0/2046
1	I	0.51	0/1467	0.65	0/1980
1	J	0.47	0/1462	0.68	0/1974
1	K	0.45	0/1441	0.64	0/1944
1	L	0.48	0/1439	0.66	0/1939
1	M	0.45	0/1457	0.65	0/1967
1	N	0.47	0/1429	0.69	1/1928 (0.1%)
All	All	0.49	0/20455	0.67	1/27601 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	156	GLU	CB-CG-CD	5.21	128.28	114.20

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	1455	0	1476	17	0
1	B	1454	0	1464	16	0
1	C	1444	0	1460	23	0
1	D	1413	0	1433	16	0
1	E	1459	0	1472	13	0
1	F	1418	0	1435	16	0
1	G	1424	0	1438	19	0
1	H	1489	0	1480	17	0
1	I	1442	0	1446	17	0
1	J	1437	0	1449	11	0
1	K	1411	0	1434	14	0
1	L	1413	0	1434	15	0
1	M	1436	0	1453	11	0
1	N	1409	0	1419	14	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
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	178	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 4.

The worst 5 of 178 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:F:144:LEU:HD12	1:G:119:GLU:HG2	1.77	0.67
1:A:142[A]:HIS:CE1	2:A:204:CL:CL	2.88	0.64
1:F:35:GLN:HG3	1:F:67:PRO:HG2	1.82	0.62

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%)	29 26
1	B	184/203 (91%)	180 (98%)	3 (2%)	1 (0%)	29 26
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%)	25 21
1	G	182/203 (90%)	177 (97%)	4 (2%)	1 (0%)	29 26
1	H	187/203 (92%)	181 (97%)	6 (3%)	0	100 100
1	I	182/203 (90%)	179 (98%)	2 (1%)	1 (0%)	29 26
1	J	184/203 (91%)	178 (97%)	5 (3%)	1 (0%)	29 26
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%)	47 49

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	129	ALA
1	G	129	ALA
1	J	130	GLN
1	B	127	GLY
1	F	127	GLY

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	158/171 (92%)	156 (99%)	2 (1%)	69	75
1	B	157/171 (92%)	155 (99%)	2 (1%)	69	75
1	C	156/171 (91%)	153 (98%)	3 (2%)	57	63
1	D	153/171 (90%)	150 (98%)	3 (2%)	55	60
1	E	157/171 (92%)	157 (100%)	0	100	100
1	F	154/171 (90%)	153 (99%)	1 (1%)	86	90
1	G	153/171 (90%)	153 (100%)	0	100	100
1	H	159/171 (93%)	154 (97%)	5 (3%)	40	43
1	I	155/171 (91%)	152 (98%)	3 (2%)	57	63
1	J	154/171 (90%)	153 (99%)	1 (1%)	86	90
1	K	155/171 (91%)	155 (100%)	0	100	100
1	L	155/171 (91%)	154 (99%)	1 (1%)	86	90
1	M	155/171 (91%)	153 (99%)	2 (1%)	69	75
1	N	151/171 (88%)	148 (98%)	3 (2%)	55	60
All	All	2172/2394 (91%)	2146 (99%)	26 (1%)	71	77

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	196	TRP
1	I	147	ARG
1	N	138	ILE

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Mol	Chain	Res	Type
1	I	134	THR
1	I	193	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	132	GLN
1	H	200	GLN
1	I	142	HIS
1	J	132	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [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	187/203 (92%)	0.51	15 (8%) 12 16	35, 57, 108, 157	0
1	B	187/203 (92%)	0.70	22 (11%) 4 5	51, 69, 118, 151	0
1	C	186/203 (91%)	0.58	20 (10%) 5 7	43, 61, 114, 142	0
1	D	182/203 (89%)	0.58	14 (7%) 13 17	42, 56, 101, 145	0
1	E	188/203 (92%)	0.41	13 (6%) 16 21	32, 50, 100, 132	0
1	F	182/203 (89%)	0.40	14 (7%) 13 17	40, 62, 99, 163	0
1	G	185/203 (91%)	0.60	17 (9%) 9 11	40, 61, 106, 175	0
1	H	192/203 (94%)	0.50	16 (8%) 11 14	45, 66, 114, 146	0
1	I	186/203 (91%)	0.48	12 (6%) 18 23	41, 56, 104, 157	0
1	J	186/203 (91%)	0.67	17 (9%) 9 12	50, 70, 114, 149	0
1	K	179/203 (88%)	0.46	11 (6%) 21 26	49, 69, 110, 158	0
1	L	180/203 (88%)	0.43	11 (6%) 21 26	44, 63, 109, 166	0
1	M	186/203 (91%)	0.72	20 (10%) 5 7	50, 75, 114, 148	0
1	N	183/203 (90%)	0.95	27 (14%) 2 3	55, 79, 117, 175	0
All	All	2589/2842 (91%)	0.57	229 (8%) 10 12	32, 65, 113, 175	0

The worst 5 of 229 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	17	ALA	12.9
1	K	8	ILE	9.4
1	C	3	LEU	8.3
1	G	126	LEU	7.8
1	B	3	LEU	7.7

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 monosaccharides 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	CL	B	204	1/1	0.74	0.17	99,99,99,99	0
2	CL	M	204	1/1	0.78	0.11	93,93,93,93	0
2	CL	L	204	1/1	0.87	0.12	98,98,98,98	0
2	CL	C	204	1/1	0.88	0.19	82,82,82,82	0
2	CL	L	205	1/1	0.92	0.15	81,81,81,81	0
2	CL	D	204	1/1	0.94	0.26	78,78,78,78	0
2	CL	A	204	1/1	0.97	0.21	81,81,81,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.