wwPDB X-ray Structure Validation Summary Report (i)

Nov 6, 2023 – 12:57 PM EST

PDB ID	:	5W18
Title	:	Staphylococcus aureus ClpP in complex with (S)-N-((2R,6S,8aS,14aS,20S,23aS)-2,6-dimethyl-5,8,14,19,23-pentaoxooctadecahydro-1H,5H,14H,19H-pyrido[2,1-i]dipyrrolo[2,1-c:2',1'-l][1]oxa[4,7,10,13]tetraazacyclohexadecin-20-yl)-3-phenyl-2-(3-phenylureido)propanamide
Authors	:	Lee, R.E.; Griffith, E.C.
Deposited on	:	2017-06-02
Resolution	:	2.44 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 (i) 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 (i)) were used in the production of this report:

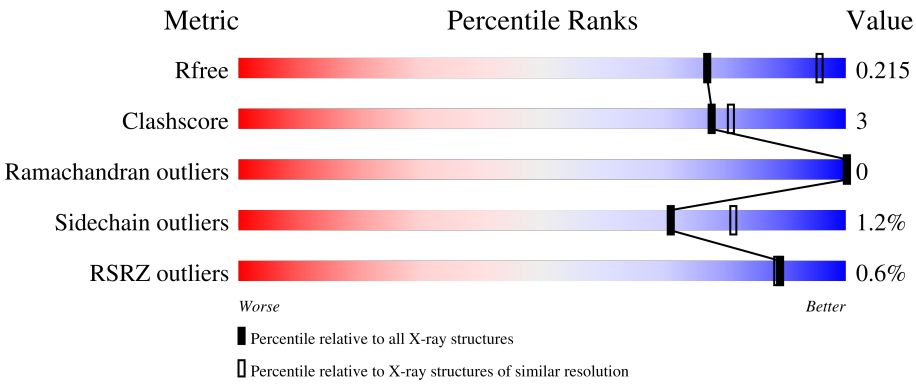
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.44 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	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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 <=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	78% 9% 12%
1	B	203	80% 9% 11%
1	C	203	78% 10% 12%
1	D	203	76% 11% • 11%

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Mol	Chain	Length	Quality of chain
1	E	203	%, 76%, 10%, 12%
1	F	203	82%, 6%, 12%
1	G	203	77%, 12%, 11%
1	I	203	76%, 12%, 12%
1	K	203	77%, 11%, 11%
1	L	203	76%, 12%, 11%
1	M	203	%, 77%, 9%, 12%
1	N	203	%, 78%, 9%, 12%
1	S	203	2%, 78%, 9%, 12%
1	T	203	79%, 8%, 12%
2	H	7	43%, 43%, 14%
2	J	7	57%, 29%, 14%
2	O	7	29%, 57%, 14%
2	P	7	71%, 14%, 14%
2	Q	7	43%, 29%, 29%
2	R	7	71%, 29%
2	U	7	43%, 43%, 14%
2	V	7	14%, 57%, 29%, 14%
2	X	7	43%, 43%, 14%
2	Y	7	43%, 43%, 14%
2	Z	7	43%, 57%
2	a	7	57%, 43%
2	b	7	86%, 14%
2	c	7	57%, 43%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 20484 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	179	1366	860	233	267	6	0	0	0
1	B	180	1356	854	229	267	6	0	0	0
1	C	179	1363	857	232	268	6	0	0	0
1	D	180	1381	871	234	270	6	0	0	0
1	E	178	1364	860	232	266	6	0	0	0
1	F	179	1354	851	231	266	6	0	0	0
1	G	180	1361	856	230	269	6	0	0	0
1	I	179	1350	849	229	266	6	0	0	0
1	K	180	1371	862	234	269	6	0	0	0
1	L	180	1373	865	232	270	6	0	0	0
1	M	179	1376	868	233	269	6	0	0	0
1	N	179	1359	856	229	268	6	0	0	0
1	S	178	1351	850	228	267	6	0	0	0
1	T	178	1351	850	231	264	6	0	0	0

There are 112 discrepancies between the modelled and reference sequences:

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

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Chain	Residue	Modelled	Actual	Comment	Reference
A	197	GLU	-	expression tag	UNP Q2G036
A	198	HIS	-	expression tag	UNP Q2G036
A	199	HIS	-	expression tag	UNP Q2G036
A	200	HIS	-	expression tag	UNP Q2G036
A	201	HIS	-	expression tag	UNP Q2G036
A	202	HIS	-	expression tag	UNP Q2G036
A	203	HIS	-	expression tag	UNP Q2G036
B	196	LEU	-	expression tag	UNP Q2G036
B	197	GLU	-	expression tag	UNP Q2G036
B	198	HIS	-	expression tag	UNP Q2G036
B	199	HIS	-	expression tag	UNP Q2G036
B	200	HIS	-	expression tag	UNP Q2G036
B	201	HIS	-	expression tag	UNP Q2G036
B	202	HIS	-	expression tag	UNP Q2G036
B	203	HIS	-	expression tag	UNP Q2G036
C	196	LEU	-	expression tag	UNP Q2G036
C	197	GLU	-	expression tag	UNP Q2G036
C	198	HIS	-	expression tag	UNP Q2G036
C	199	HIS	-	expression tag	UNP Q2G036
C	200	HIS	-	expression tag	UNP Q2G036
C	201	HIS	-	expression tag	UNP Q2G036
C	202	HIS	-	expression tag	UNP Q2G036
C	203	HIS	-	expression tag	UNP Q2G036
D	196	LEU	-	expression tag	UNP Q2G036
D	197	GLU	-	expression tag	UNP Q2G036
D	198	HIS	-	expression tag	UNP Q2G036
D	199	HIS	-	expression tag	UNP Q2G036
D	200	HIS	-	expression tag	UNP Q2G036
D	201	HIS	-	expression tag	UNP Q2G036
D	202	HIS	-	expression tag	UNP Q2G036
D	203	HIS	-	expression tag	UNP Q2G036
E	196	LEU	-	expression tag	UNP Q2G036
E	197	GLU	-	expression tag	UNP Q2G036
E	198	HIS	-	expression tag	UNP Q2G036
E	199	HIS	-	expression tag	UNP Q2G036
E	200	HIS	-	expression tag	UNP Q2G036
E	201	HIS	-	expression tag	UNP Q2G036
E	202	HIS	-	expression tag	UNP Q2G036
E	203	HIS	-	expression tag	UNP Q2G036
F	196	LEU	-	expression tag	UNP Q2G036
F	197	GLU	-	expression tag	UNP Q2G036
F	198	HIS	-	expression tag	UNP Q2G036

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Chain	Residue	Modelled	Actual	Comment	Reference
F	199	HIS	-	expression tag	UNP Q2G036
F	200	HIS	-	expression tag	UNP Q2G036
F	201	HIS	-	expression tag	UNP Q2G036
F	202	HIS	-	expression tag	UNP Q2G036
F	203	HIS	-	expression tag	UNP Q2G036
G	196	LEU	-	expression tag	UNP Q2G036
G	197	GLU	-	expression tag	UNP Q2G036
G	198	HIS	-	expression tag	UNP Q2G036
G	199	HIS	-	expression tag	UNP Q2G036
G	200	HIS	-	expression tag	UNP Q2G036
G	201	HIS	-	expression tag	UNP Q2G036
G	202	HIS	-	expression tag	UNP Q2G036
G	203	HIS	-	expression tag	UNP Q2G036
I	196	LEU	-	expression tag	UNP Q2G036
I	197	GLU	-	expression tag	UNP Q2G036
I	198	HIS	-	expression tag	UNP Q2G036
I	199	HIS	-	expression tag	UNP Q2G036
I	200	HIS	-	expression tag	UNP Q2G036
I	201	HIS	-	expression tag	UNP Q2G036
I	202	HIS	-	expression tag	UNP Q2G036
I	203	HIS	-	expression tag	UNP Q2G036
K	196	LEU	-	expression tag	UNP Q2G036
K	197	GLU	-	expression tag	UNP Q2G036
K	198	HIS	-	expression tag	UNP Q2G036
K	199	HIS	-	expression tag	UNP Q2G036
K	200	HIS	-	expression tag	UNP Q2G036
K	201	HIS	-	expression tag	UNP Q2G036
K	202	HIS	-	expression tag	UNP Q2G036
K	203	HIS	-	expression tag	UNP Q2G036
L	196	LEU	-	expression tag	UNP Q2G036
L	197	GLU	-	expression tag	UNP Q2G036
L	198	HIS	-	expression tag	UNP Q2G036
L	199	HIS	-	expression tag	UNP Q2G036
L	200	HIS	-	expression tag	UNP Q2G036
L	201	HIS	-	expression tag	UNP Q2G036
L	202	HIS	-	expression tag	UNP Q2G036
L	203	HIS	-	expression tag	UNP Q2G036
M	196	LEU	-	expression tag	UNP Q2G036
M	197	GLU	-	expression tag	UNP Q2G036
M	198	HIS	-	expression tag	UNP Q2G036
M	199	HIS	-	expression tag	UNP Q2G036
M	200	HIS	-	expression tag	UNP Q2G036

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Chain	Residue	Modelled	Actual	Comment	Reference
M	201	HIS	-	expression tag	UNP Q2G036
M	202	HIS	-	expression tag	UNP Q2G036
M	203	HIS	-	expression tag	UNP Q2G036
N	196	LEU	-	expression tag	UNP Q2G036
N	197	GLU	-	expression tag	UNP Q2G036
N	198	HIS	-	expression tag	UNP Q2G036
N	199	HIS	-	expression tag	UNP Q2G036
N	200	HIS	-	expression tag	UNP Q2G036
N	201	HIS	-	expression tag	UNP Q2G036
N	202	HIS	-	expression tag	UNP Q2G036
N	203	HIS	-	expression tag	UNP Q2G036
S	196	LEU	-	expression tag	UNP Q2G036
S	197	GLU	-	expression tag	UNP Q2G036
S	198	HIS	-	expression tag	UNP Q2G036
S	199	HIS	-	expression tag	UNP Q2G036
S	200	HIS	-	expression tag	UNP Q2G036
S	201	HIS	-	expression tag	UNP Q2G036
S	202	HIS	-	expression tag	UNP Q2G036
S	203	HIS	-	expression tag	UNP Q2G036
T	196	LEU	-	expression tag	UNP Q2G036
T	197	GLU	-	expression tag	UNP Q2G036
T	198	HIS	-	expression tag	UNP Q2G036
T	199	HIS	-	expression tag	UNP Q2G036
T	200	HIS	-	expression tag	UNP Q2G036
T	201	HIS	-	expression tag	UNP Q2G036
T	202	HIS	-	expression tag	UNP Q2G036
T	203	HIS	-	expression tag	UNP Q2G036

- Molecule 2 is a protein called 9V7-PHE-SER-PRO-YCP-ALA-MP8.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	H	7	54	39	7	8	0	0	0
2	J	7	54	39	7	8	0	0	0
2	O	7	54	39	7	8	0	0	0
2	P	7	54	39	7	8	0	0	0
2	Q	7	54	39	7	8	0	0	0
2	R	7	54	39	7	8	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	U	7	54	39	7	8	0	0	0
2	V	7	54	39	7	8	0	0	0
2	X	7	54	39	7	8	0	0	0
2	Y	7	54	39	7	8	0	0	0
2	Z	7	54	39	7	8	0	0	0
2	a	7	54	39	7	8	0	0	0
2	b	7	54	39	7	8	0	0	0
2	c	7	54	39	7	8	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	33	33	33	0	0
3	B	40	40	40	0	0
3	C	56	56	56	0	0
3	D	45	45	45	0	0
3	E	65	65	65	0	0
3	F	54	54	54	0	0
3	G	45	45	45	0	0
3	I	26	26	26	0	0
3	K	41	41	41	0	0
3	L	62	62	62	0	0
3	M	57	57	57	0	0

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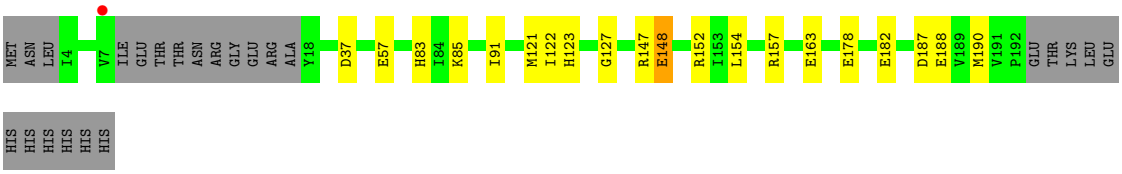
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	N	62	62	62	0	0
			Total	O		
3	S	33	33	33	0	0
			Total	O		
3	T	30	30	30	0	0
			Total	O		
3	Y	1	1	1	0	0
			Total	O		
3	Z	1	1	1	0	0
			Total	O		
3	a	1	1	1	0	0

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.

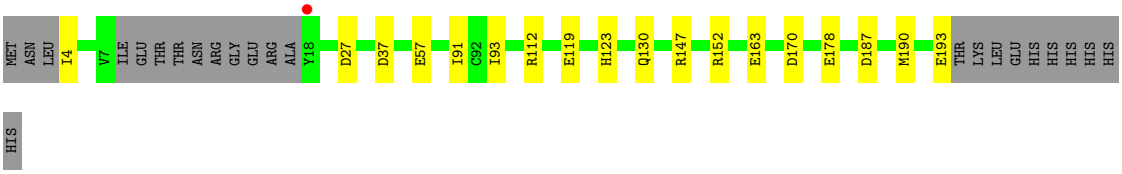
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain A:



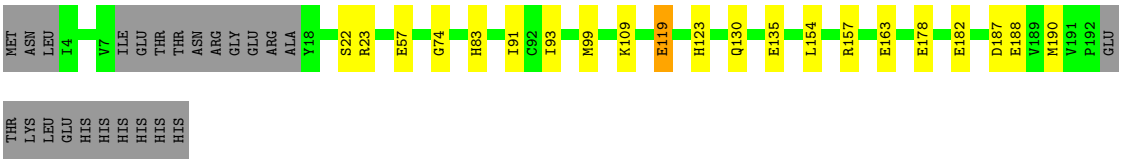
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain B:



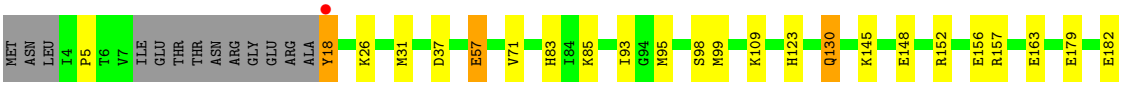
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain C:



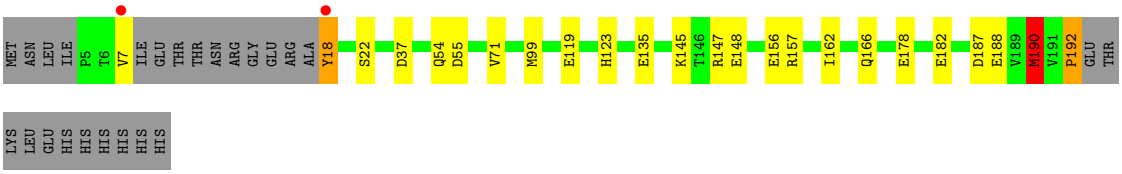
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain D:



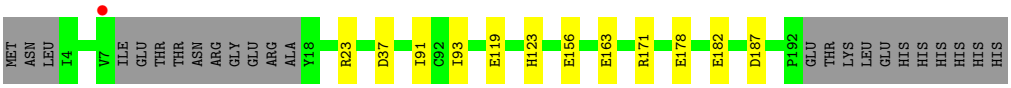
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain E:



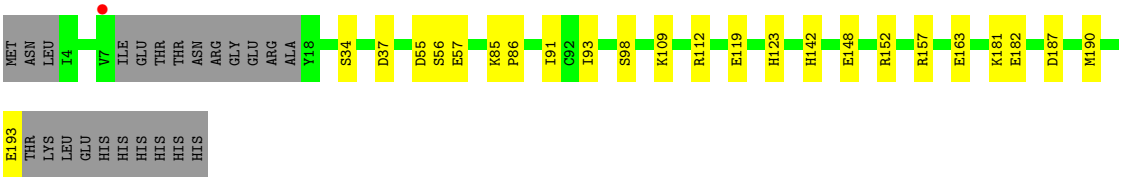
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain F:



• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain G:

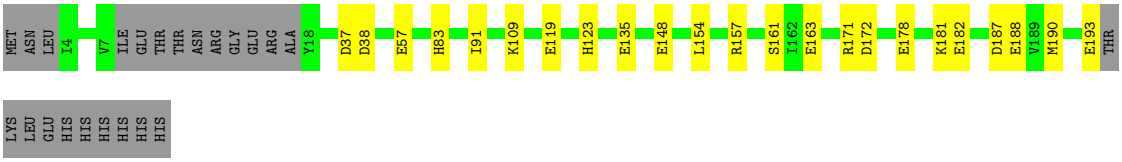


• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain I:

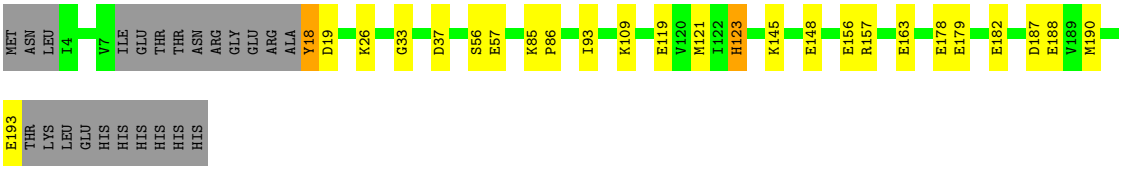
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain K:



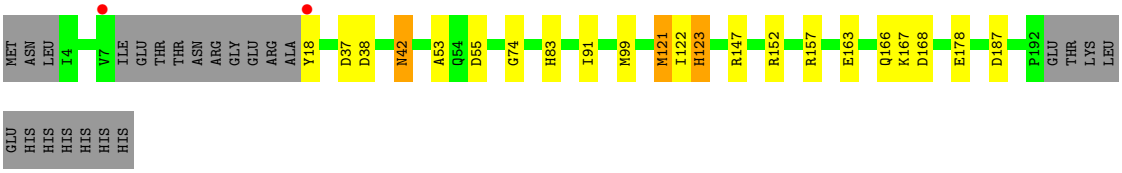
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain L:



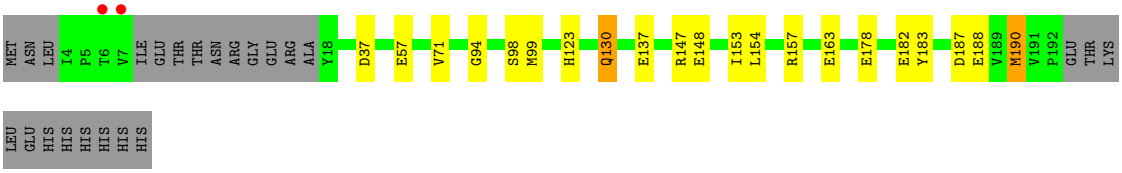
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain M:



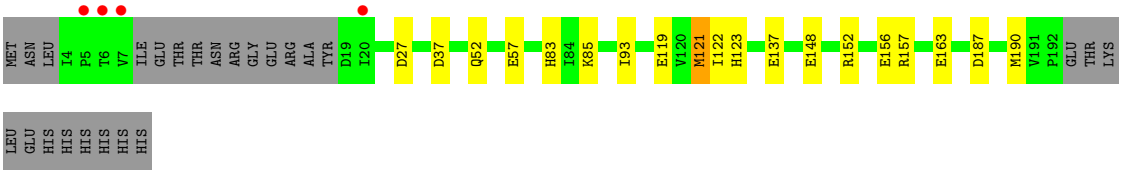
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain N:



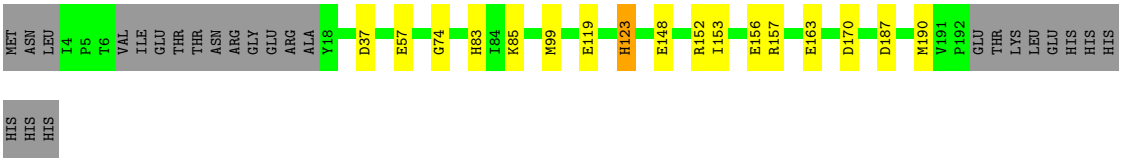
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain S:

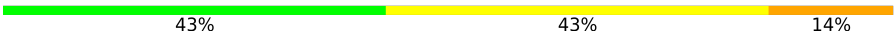


• Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain T:

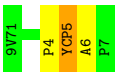


• Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain H: 

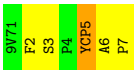
• Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain J:



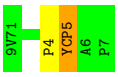
• Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain O:



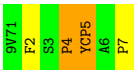
• Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain P:



• Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

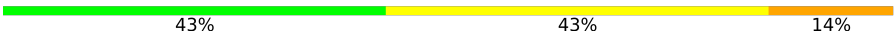
Chain Q:

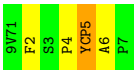


• Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain R:

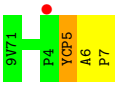
• Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain U: 



• Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain V:

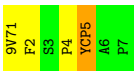


- Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain X: 43% 43% 14%

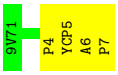
- Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain Y: 43% 43% 14%



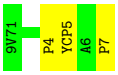
- Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain Z: 43% 57%



- Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain a: 57% 43%



- Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain b: 86% 14%

- Molecule 2: 9V7-PHE-SER-PRO-YCP-ALA-MP8

Chain c: 57% 43%

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	94.92Å 126.38Å 146.06Å 90.00° 93.42° 90.00°	Depositor
Resolution (Å)	50.00 – 2.44 48.94 – 2.44	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.00-2.44) 99.6 (48.94-2.44)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.26 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.189 , 0.210 0.193 , 0.215	Depositor DCC
R_{free} test set	6556 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	33.6	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 31.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	20484	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: YCP, MP8, 9V7

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	1.22	7/1383 (0.5%)	1.04	7/1867 (0.4%)
1	B	1.19	9/1373 (0.7%)	1.00	9/1859 (0.5%)
1	C	1.31	13/1380 (0.9%)	1.02	5/1865 (0.3%)
1	D	1.38	15/1399 (1.1%)	1.03	6/1890 (0.3%)
1	E	1.33	11/1382 (0.8%)	1.08	9/1866 (0.5%)
1	F	1.26	7/1371 (0.5%)	1.00	5/1855 (0.3%)
1	G	1.29	13/1378 (0.9%)	0.99	7/1864 (0.4%)
1	I	1.22	13/1367 (1.0%)	1.01	9/1849 (0.5%)
1	K	1.34	14/1388 (1.0%)	1.06	10/1875 (0.5%)
1	L	1.43	21/1391 (1.5%)	1.01	4/1882 (0.2%)
1	M	1.25	7/1394 (0.5%)	1.05	7/1883 (0.4%)
1	N	1.29	13/1376 (0.9%)	1.01	6/1861 (0.3%)
1	S	1.22	9/1368 (0.7%)	1.00	5/1850 (0.3%)
1	T	1.21	8/1368 (0.6%)	1.01	5/1848 (0.3%)
2	H	1.35	1/29 (3.4%)	0.77	0/37
2	J	1.27	0/29	0.90	0/37
2	O	1.29	1/29 (3.4%)	0.97	0/37
2	P	1.28	0/29	1.12	0/37
2	Q	1.72	1/29 (3.4%)	1.15	0/37
2	R	1.47	0/29	0.82	0/37
2	U	0.96	0/29	0.87	0/37
2	V	1.27	0/29	0.84	0/37
2	X	1.40	0/29	0.87	0/37
2	Y	1.22	0/29	0.94	0/37
2	Z	1.43	1/29 (3.4%)	1.08	0/37
2	a	1.60	1/29 (3.4%)	0.69	0/37
2	b	1.16	0/29	0.70	0/37
2	c	1.56	1/29 (3.4%)	0.83	0/37
All	All	1.29	166/19724 (0.8%)	1.02	94/26632 (0.4%)

The worst 5 of 166 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	182	GLU	CD-OE1	13.86	1.41	1.25
1	C	119	GLU	CD-OE1	12.62	1.39	1.25
1	D	57	GLU	CD-OE2	12.53	1.39	1.25
1	G	57	GLU	CD-OE2	12.35	1.39	1.25
1	T	163	GLU	CD-OE1	11.61	1.38	1.25

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	55	ASP	CB-CG-OD2	-13.87	105.82	118.30
1	L	157	ARG	NE-CZ-NH2	-9.25	115.67	120.30
1	D	157	ARG	NE-CZ-NH2	-9.08	115.76	120.30
1	K	157	ARG	NE-CZ-NH2	-8.89	115.86	120.30
1	S	157	ARG	NE-CZ-NH2	-8.53	116.04	120.30

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	1366	0	1374	9	0
1	B	1356	0	1343	5	0
1	C	1363	0	1360	10	0
1	D	1381	0	1387	12	0
1	E	1364	0	1371	6	0
1	F	1354	0	1343	2	0
1	G	1361	0	1349	11	0
1	I	1350	0	1336	11	0
1	K	1371	0	1371	6	0
1	L	1373	0	1365	10	0
1	M	1376	0	1385	10	0
1	N	1359	0	1356	7	0
1	S	1351	0	1345	10	0
1	T	1351	0	1350	7	0
2	H	54	0	43	2	0
2	J	54	0	43	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	O	54	0	43	3	0
2	P	54	0	43	1	0
2	Q	54	0	43	3	0
2	R	54	0	43	1	0
2	U	54	0	43	3	0
2	V	54	0	43	2	0
2	X	54	0	43	3	0
2	Y	54	0	43	4	0
2	Z	54	0	43	1	0
2	a	54	0	43	0	0
2	b	54	0	43	0	0
2	c	54	0	43	0	0
3	A	33	0	0	1	0
3	B	40	0	0	0	0
3	C	56	0	0	1	0
3	D	45	0	0	2	0
3	E	65	0	0	2	0
3	F	54	0	0	0	0
3	G	45	0	0	2	0
3	I	26	0	0	1	0
3	K	41	0	0	0	0
3	L	62	0	0	0	0
3	M	57	0	0	0	0
3	N	62	0	0	3	0
3	S	33	0	0	0	0
3	T	30	0	0	0	0
3	Y	1	0	0	0	0
3	Z	1	0	0	0	0
3	a	1	0	0	0	0
All	All	20484	0	19637	105	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 3.

The worst 5 of 105 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:D:95:MET:HG3	3:D:301:HOH:O	1.59	1.00
1:S:190:MET:CE	1:T:83:HIS:CE1	2.55	0.89
1:B:190:MET:HE2	1:C:83:HIS:CE1	2.11	0.84
1:A:148:GLU:OE1	1:A:152:ARG:NH2	2.09	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:HIS:CE1	1:G:190:MET:CE	2.62	0.82

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	175/203 (86%)	172 (98%)	3 (2%)	0	100	100
1	B	176/203 (87%)	172 (98%)	4 (2%)	0	100	100
1	C	175/203 (86%)	172 (98%)	3 (2%)	0	100	100
1	D	176/203 (87%)	171 (97%)	5 (3%)	0	100	100
1	E	174/203 (86%)	170 (98%)	4 (2%)	0	100	100
1	F	175/203 (86%)	171 (98%)	4 (2%)	0	100	100
1	G	176/203 (87%)	172 (98%)	4 (2%)	0	100	100
1	I	175/203 (86%)	171 (98%)	4 (2%)	0	100	100
1	K	176/203 (87%)	171 (97%)	5 (3%)	0	100	100
1	L	176/203 (87%)	171 (97%)	5 (3%)	0	100	100
1	M	175/203 (86%)	170 (97%)	5 (3%)	0	100	100
1	N	175/203 (86%)	172 (98%)	3 (2%)	0	100	100
1	S	174/203 (86%)	170 (98%)	4 (2%)	0	100	100
1	T	174/203 (86%)	170 (98%)	4 (2%)	0	100	100
2	H	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	J	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	O	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	P	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	Q	4/7 (57%)	3 (75%)	1 (25%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	R	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	U	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	V	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	X	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	Y	4/7 (57%)	2 (50%)	2 (50%)	0	100	100
2	Z	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	a	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	b	4/7 (57%)	3 (75%)	1 (25%)	0	100	100
2	c	4/7 (57%)	2 (50%)	2 (50%)	0	100	100
All	All	2508/2940 (85%)	2435 (97%)	73 (3%)	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	146/171 (85%)	145 (99%)	1 (1%)	84	90
1	B	143/171 (84%)	142 (99%)	1 (1%)	84	90
1	C	145/171 (85%)	143 (99%)	2 (1%)	67	78
1	D	148/171 (86%)	145 (98%)	3 (2%)	55	67
1	E	146/171 (85%)	142 (97%)	4 (3%)	44	57
1	F	143/171 (84%)	142 (99%)	1 (1%)	84	90
1	G	144/171 (84%)	143 (99%)	1 (1%)	84	90
1	I	142/171 (83%)	141 (99%)	1 (1%)	84	90
1	K	146/171 (85%)	145 (99%)	1 (1%)	84	90
1	L	146/171 (85%)	144 (99%)	2 (1%)	67	78
1	M	148/171 (86%)	146 (99%)	2 (1%)	67	78
1	N	145/171 (85%)	143 (99%)	2 (1%)	67	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	144/171 (84%)	142 (99%)	2 (1%)	67	78
1	T	143/171 (84%)	142 (99%)	1 (1%)	84	90
2	H	3/3 (100%)	3 (100%)	0	100	100
2	J	3/3 (100%)	3 (100%)	0	100	100
2	O	3/3 (100%)	3 (100%)	0	100	100
2	P	3/3 (100%)	3 (100%)	0	100	100
2	Q	3/3 (100%)	3 (100%)	0	100	100
2	R	3/3 (100%)	3 (100%)	0	100	100
2	U	3/3 (100%)	3 (100%)	0	100	100
2	V	3/3 (100%)	3 (100%)	0	100	100
2	X	3/3 (100%)	3 (100%)	0	100	100
2	Y	3/3 (100%)	3 (100%)	0	100	100
2	Z	3/3 (100%)	3 (100%)	0	100	100
2	a	3/3 (100%)	3 (100%)	0	100	100
2	b	3/3 (100%)	3 (100%)	0	100	100
2	c	3/3 (100%)	3 (100%)	0	100	100
All	All	2071/2436 (85%)	2047 (99%)	24 (1%)	71	81

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	123	HIS
1	M	121	MET
1	L	123	HIS
1	M	123	HIS
1	D	130	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	47	GLN
1	L	151	ASN
1	T	39	ASN
1	S	52	GLN
1	G	151	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

28 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	YCP	H	5	2	6,8,9	1.34	1 (16%)	5,9,11	1.20	1 (20%)
2	YCP	Z	5	2	6,8,9	1.16	1 (16%)	5,9,11	1.51	1 (20%)
2	YCP	Y	5	2	6,8,9	1.16	1 (16%)	5,9,11	1.78	1 (20%)
2	YCP	U	5	2	6,8,9	1.61	2 (33%)	5,9,11	1.37	1 (20%)
2	YCP	X	5	2	6,8,9	1.27	1 (16%)	5,9,11	1.76	1 (20%)
2	MP8	a	7	2	5,8,9	1.30	1 (20%)	3,10,12	0.87	0
2	YCP	V	5	2	6,8,9	0.73	0	5,9,11	1.61	1 (20%)
2	YCP	Q	5	2	6,8,9	1.19	1 (16%)	5,9,11	1.67	1 (20%)
2	MP8	O	7	2	5,8,9	0.45	0	3,10,12	0.81	0
2	YCP	a	5	2	6,8,9	1.41	1 (16%)	5,9,11	1.32	1 (20%)
2	YCP	J	5	2	6,8,9	1.56	1 (16%)	5,9,11	1.82	1 (20%)
2	MP8	H	7	2	5,8,9	0.61	0	3,10,12	0.83	0
2	YCP	P	5	2	6,8,9	1.42	1 (16%)	5,9,11	1.37	1 (20%)
2	MP8	X	7	2	5,8,9	0.79	0	3,10,12	1.00	0
2	YCP	R	5	2	6,8,9	1.25	1 (16%)	5,9,11	1.34	1 (20%)
2	MP8	Y	7	2	5,8,9	0.69	0	3,10,12	0.99	0
2	MP8	V	7	2	5,8,9	1.24	1 (20%)	3,10,12	0.64	0
2	MP8	c	7	2	5,8,9	1.03	1 (20%)	3,10,12	0.70	0
2	MP8	J	7	2	5,8,9	0.76	0	3,10,12	0.88	0
2	YCP	c	5	2	6,8,9	1.37	1 (16%)	5,9,11	1.51	1 (20%)
2	MP8	Z	7	2	5,8,9	1.30	1 (20%)	3,10,12	0.73	0
2	MP8	U	7	2	5,8,9	0.75	0	3,10,12	0.43	0
2	MP8	b	7	2	5,8,9	0.92	0	3,10,12	0.97	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	YCP	b	5	2	6,8,9	1.60	1 (16%)	5,9,11	1.47	1 (20%)
2	MP8	R	7	2	5,8,9	0.82	0	3,10,12	0.80	0
2	MP8	Q	7	2	5,8,9	1.61	1 (20%)	3,10,12	0.67	0
2	MP8	P	7	2	5,8,9	0.91	0	3,10,12	1.16	0
2	YCP	O	5	2	6,8,9	1.47	1 (16%)	5,9,11	1.63	1 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	YCP	H	5	2	-	0/1/10/12	0/1/1/1
2	YCP	Z	5	2	-	0/1/10/12	0/1/1/1
2	YCP	Y	5	2	-	0/1/10/12	0/1/1/1
2	YCP	U	5	2	-	0/1/10/12	0/1/1/1
2	YCP	X	5	2	-	0/1/10/12	0/1/1/1
2	MP8	a	7	2	-	0/0/11/13	0/1/1/1
2	YCP	V	5	2	-	0/1/10/12	0/1/1/1
2	YCP	Q	5	2	-	0/1/10/12	0/1/1/1
2	MP8	O	7	2	-	0/0/11/13	0/1/1/1
2	YCP	a	5	2	-	0/1/10/12	0/1/1/1
2	YCP	J	5	2	-	0/1/10/12	0/1/1/1
2	MP8	H	7	2	-	0/0/11/13	0/1/1/1
2	YCP	P	5	2	-	0/1/10/12	0/1/1/1
2	MP8	X	7	2	-	0/0/11/13	0/1/1/1
2	YCP	R	5	2	-	0/1/10/12	0/1/1/1
2	MP8	Y	7	2	-	0/0/11/13	0/1/1/1
2	MP8	V	7	2	-	0/0/11/13	0/1/1/1
2	MP8	c	7	2	-	0/0/11/13	0/1/1/1
2	MP8	J	7	2	-	0/0/11/13	0/1/1/1
2	YCP	c	5	2	-	0/1/10/12	0/1/1/1
2	MP8	Z	7	2	-	0/0/11/13	0/1/1/1
2	MP8	U	7	2	-	0/0/11/13	0/1/1/1
2	MP8	b	7	2	-	0/0/11/13	0/1/1/1
2	YCP	b	5	2	-	0/1/10/12	0/1/1/1
2	MP8	R	7	2	-	0/0/11/13	0/1/1/1
2	MP8	Q	7	2	-	0/0/11/13	0/1/1/1
2	MP8	P	7	2	-	0/0/11/13	0/1/1/1
2	YCP	O	5	2	-	0/1/10/12	0/1/1/1

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	5	YCP	CG-CD	3.33	1.64	1.51
2	Q	7	MP8	CB-CA	-3.24	1.47	1.54
2	H	5	YCP	CD-CE	3.00	1.63	1.49
2	b	5	YCP	CG-CD	2.92	1.63	1.51
2	O	5	YCP	CG-CD	2.78	1.62	1.51

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	J	5	YCP	O-C-CA	-3.99	114.33	124.78
2	X	5	YCP	O-C-CA	-3.90	114.56	124.78
2	Q	5	YCP	O-C-CA	-3.69	115.11	124.78
2	Y	5	YCP	O-C-CA	-3.60	115.34	124.78
2	V	5	YCP	O-C-CA	-3.55	115.48	124.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	5	YCP	1	0
2	Y	5	YCP	1	0
2	U	5	YCP	1	0
2	X	5	YCP	1	0
2	V	5	YCP	1	0
2	Q	5	YCP	1	0
2	O	7	MP8	1	0
2	J	5	YCP	1	0
2	P	5	YCP	1	0
2	O	5	YCP	1	0

5.5 Carbohydrates (i)

There are no monosaccharides 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	179/203 (88%)	-0.36	1 (0%)	89	89	30, 35, 44, 53	0
1	B	180/203 (88%)	-0.30	1 (0%)	89	89	30, 35, 43, 52	0
1	C	179/203 (88%)	-0.32	0	100	100	26, 32, 41, 48	0
1	D	180/203 (88%)	-0.37	1 (0%)	89	89	24, 30, 39, 46	0
1	E	178/203 (87%)	-0.33	2 (1%)	80	79	24, 30, 38, 49	0
1	F	179/203 (88%)	-0.33	1 (0%)	89	89	24, 31, 42, 50	0
1	G	180/203 (88%)	-0.42	1 (0%)	89	89	30, 35, 43, 51	0
1	I	179/203 (88%)	-0.32	0	100	100	32, 37, 44, 52	0
1	K	180/203 (88%)	-0.36	0	100	100	28, 33, 42, 50	0
1	L	180/203 (88%)	-0.36	0	100	100	25, 31, 38, 47	0
1	M	179/203 (88%)	-0.25	2 (1%)	80	79	26, 31, 41, 48	0
1	N	179/203 (88%)	-0.46	2 (1%)	80	79	26, 32, 40, 51	0
1	S	178/203 (87%)	-0.20	4 (2%)	62	58	30, 37, 45, 51	0
1	T	178/203 (87%)	-0.17	0	100	100	33, 38, 46, 50	0
2	H	4/7 (57%)	-0.69	0	100	100	37, 38, 41, 44	0
2	J	4/7 (57%)	-0.31	0	100	100	36, 39, 40, 43	0
2	O	4/7 (57%)	-0.50	0	100	100	33, 36, 38, 41	0
2	P	4/7 (57%)	-0.71	0	100	100	30, 32, 34, 37	0
2	Q	4/7 (57%)	-0.27	0	100	100	32, 33, 35, 39	0
2	R	4/7 (57%)	-0.75	0	100	100	35, 37, 38, 40	0
2	U	4/7 (57%)	0.10	0	100	100	38, 40, 41, 44	0
2	V	4/7 (57%)	0.54	1 (25%)	0	0	40, 42, 44, 48	0
2	X	4/7 (57%)	-0.38	0	100	100	35, 35, 38, 41	0
2	Y	4/7 (57%)	-0.86	0	100	100	34, 36, 36, 41	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
2	Z	4/7 (57%)	-0.05	0	100	100	32, 35, 38, 41	0
2	a	4/7 (57%)	-0.44	0	100	100	36, 37, 40, 41	0
2	b	4/7 (57%)	0.12	0	100	100	40, 43, 43, 44	0
2	c	4/7 (57%)	-0.01	0	100	100	41, 43, 44, 46	0
All	All	2564/2940 (87%)	-0.33	16 (0%)	89	89	24, 34, 43, 53	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	S	7	VAL	6.5
1	S	6	THR	4.9
1	N	7	VAL	4.7
1	D	18	TYR	4.1
1	G	7	VAL	3.5

6.2 Non-standard residues in protein, DNA, RNA chains (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	MP8	O	7	8/9	0.94	0.14	35,36,37,39	0
2	MP8	Y	7	8/9	0.94	0.12	35,36,36,38	0
2	MP8	Z	7	8/9	0.94	0.10	34,35,37,38	0
2	MP8	b	7	8/9	0.94	0.14	40,42,44,45	0
2	MP8	R	7	8/9	0.95	0.12	37,38,39,41	0
2	MP8	U	7	8/9	0.95	0.15	39,40,41,42	0
2	MP8	V	7	8/9	0.95	0.09	39,40,42,46	0
2	YCP	R	5	8/9	0.95	0.13	37,39,40,40	0
2	YCP	b	5	8/9	0.95	0.20	43,43,44,44	0
2	YCP	O	5	8/9	0.95	0.15	38,38,39,40	0
2	MP8	c	7	8/9	0.95	0.15	42,43,43,44	0
2	YCP	X	5	8/9	0.96	0.09	37,38,39,40	0
2	YCP	Z	5	8/9	0.96	0.18	37,38,38,38	0
2	YCP	a	5	8/9	0.96	0.12	37,37,38,38	0
2	YCP	P	5	8/9	0.96	0.13	34,35,36,36	0
2	MP8	J	7	8/9	0.96	0.12	38,39,40,40	0
2	MP8	a	7	8/9	0.96	0.11	36,37,38,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	YCP	V	5	8/9	0.96	0.14	43,44,45,45	0
2	MP8	Q	7	8/9	0.96	0.13	33,34,34,37	0
2	MP8	H	7	8/9	0.97	0.11	37,38,39,41	0
2	MP8	X	7	8/9	0.97	0.14	35,36,37,39	0
2	YCP	Q	5	8/9	0.97	0.12	33,35,36,36	0
2	YCP	H	5	8/9	0.97	0.10	39,40,41,41	0
2	YCP	U	5	8/9	0.97	0.20	41,42,43,44	0
2	YCP	J	5	8/9	0.97	0.19	40,41,41,42	0
2	YCP	c	5	8/9	0.97	0.15	43,44,44,44	0
2	YCP	Y	5	8/9	0.98	0.10	37,38,39,40	0
2	MP8	P	7	8/9	0.98	0.13	31,32,34,34	0

6.3 Carbohydrates (i)

There are no monosaccharides 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.