



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 04:33 PM GMT

PDB ID : 2FHG  
Title : Crystal Structure of Mycobacterial Tuberculosis Proteasome  
Authors : Hu, G.; Lin, G.; Wang, M.; Dick, L.; Xu, R.M.; Nathan, C.; Li, H.  
Deposited on : 2005-12-23  
Resolution : 3.23 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

---

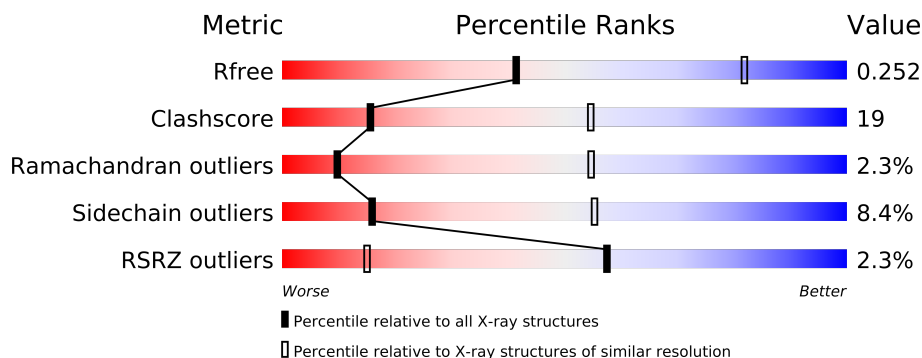
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.23 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.









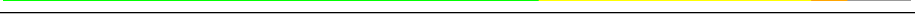


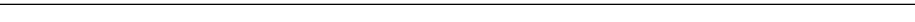



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1080 (3.30-3.18)
Clashscore	79885	1369 (3.30-3.18)
Ramachandran outliers	78287	1342 (3.30-3.18)
Sidechain outliers	78261	1340 (3.30-3.18)
RSRZ outliers	66119	1081 (3.30-3.18)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	1	250	
1	A	250	
1	B	250	
1	D	250	
1	F	250	
1	I	250	
1	K	250	
1	M	250	
1	O	250	
1	Q	250	
1	S	250	
1	U	250	
1	W	250	
1	Y	250	

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	2	240	
2	C	240	
2	E	240	
2	G	240	
2	H	240	
2	J	240	
2	L	240	
2	N	240	
2	P	240	
2	R	240	
2	T	240	
2	V	240	
2	X	240	
2	Z	240	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 46846 atoms, of which 0 are hydrogen and 0 are deuterium.

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 20S proteasome, alpha and beta subunits.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	B	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	D	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	F	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	I	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	K	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	M	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	O	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	Q	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	S	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	U	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	W	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	Y	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			
1	1	220	Total	C	N	O	S	0	0	0
			1692	1058	309	322	3			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	INITIATING METHIONINE	GB 13881852

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ASN	-	CLONING ARTIFACT	GB 13881852
A	1	SER	-	CLONING ARTIFACT	GB 13881852
B	-1	MET	-	INITIATING METHIONINE	GB 13881852
B	0	ASN	-	CLONING ARTIFACT	GB 13881852
B	1	SER	-	CLONING ARTIFACT	GB 13881852
D	-1	MET	-	INITIATING METHIONINE	GB 13881852
D	0	ASN	-	CLONING ARTIFACT	GB 13881852
D	1	SER	-	CLONING ARTIFACT	GB 13881852
F	-1	MET	-	INITIATING METHIONINE	GB 13881852
F	0	ASN	-	CLONING ARTIFACT	GB 13881852
F	1	SER	-	CLONING ARTIFACT	GB 13881852
I	-1	MET	-	INITIATING METHIONINE	GB 13881852
I	0	ASN	-	CLONING ARTIFACT	GB 13881852
I	1	SER	-	CLONING ARTIFACT	GB 13881852
K	-1	MET	-	INITIATING METHIONINE	GB 13881852
K	0	ASN	-	CLONING ARTIFACT	GB 13881852
K	1	SER	-	CLONING ARTIFACT	GB 13881852
M	-1	MET	-	INITIATING METHIONINE	GB 13881852
M	0	ASN	-	CLONING ARTIFACT	GB 13881852
M	1	SER	-	CLONING ARTIFACT	GB 13881852
O	-1	MET	-	INITIATING METHIONINE	GB 13881852
O	0	ASN	-	CLONING ARTIFACT	GB 13881852
O	1	SER	-	CLONING ARTIFACT	GB 13881852
Q	-1	MET	-	INITIATING METHIONINE	GB 13881852
Q	0	ASN	-	CLONING ARTIFACT	GB 13881852
Q	1	SER	-	CLONING ARTIFACT	GB 13881852
S	-1	MET	-	INITIATING METHIONINE	GB 13881852
S	0	ASN	-	CLONING ARTIFACT	GB 13881852
S	1	SER	-	CLONING ARTIFACT	GB 13881852
U	-1	MET	-	INITIATING METHIONINE	GB 13881852
U	0	ASN	-	CLONING ARTIFACT	GB 13881852
U	1	SER	-	CLONING ARTIFACT	GB 13881852
W	-1	MET	-	INITIATING METHIONINE	GB 13881852
W	0	ASN	-	CLONING ARTIFACT	GB 13881852
W	1	SER	-	CLONING ARTIFACT	GB 13881852
Y	-1	MET	-	INITIATING METHIONINE	GB 13881852
Y	0	ASN	-	CLONING ARTIFACT	GB 13881852
Y	1	SER	-	CLONING ARTIFACT	GB 13881852
1	-1	MET	-	INITIATING METHIONINE	GB 13881852
1	0	ASN	-	CLONING ARTIFACT	GB 13881852
1	1	SER	-	CLONING ARTIFACT	GB 13881852

- Molecule 2 is a protein called proteasome, beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	C	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	E	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	G	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	J	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	L	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	N	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	P	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	R	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	T	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	V	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	X	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	Z	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0
2	2	222	Total 1638	C 1027	N 282	O 324	S 5	0	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	535	HIS	-	EXPRESSION TAG	GB 13881852
H	536	HIS	-	EXPRESSION TAG	GB 13881852
H	537	HIS	-	EXPRESSION TAG	GB 13881852
H	538	HIS	-	EXPRESSION TAG	GB 13881852
H	539	HIS	-	EXPRESSION TAG	GB 13881852
H	540	HIS	-	EXPRESSION TAG	GB 13881852
C	535	HIS	-	EXPRESSION TAG	GB 13881852
C	536	HIS	-	EXPRESSION TAG	GB 13881852
C	537	HIS	-	EXPRESSION TAG	GB 13881852
C	538	HIS	-	EXPRESSION TAG	GB 13881852
C	539	HIS	-	EXPRESSION TAG	GB 13881852
C	540	HIS	-	EXPRESSION TAG	GB 13881852

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
E	535	HIS	-	EXPRESSION TAG	GB 13881852
E	536	HIS	-	EXPRESSION TAG	GB 13881852
E	537	HIS	-	EXPRESSION TAG	GB 13881852
E	538	HIS	-	EXPRESSION TAG	GB 13881852
E	539	HIS	-	EXPRESSION TAG	GB 13881852
E	540	HIS	-	EXPRESSION TAG	GB 13881852
G	535	HIS	-	EXPRESSION TAG	GB 13881852
G	536	HIS	-	EXPRESSION TAG	GB 13881852
G	537	HIS	-	EXPRESSION TAG	GB 13881852
G	538	HIS	-	EXPRESSION TAG	GB 13881852
G	539	HIS	-	EXPRESSION TAG	GB 13881852
G	540	HIS	-	EXPRESSION TAG	GB 13881852
J	535	HIS	-	EXPRESSION TAG	GB 13881852
J	536	HIS	-	EXPRESSION TAG	GB 13881852
J	537	HIS	-	EXPRESSION TAG	GB 13881852
J	538	HIS	-	EXPRESSION TAG	GB 13881852
J	539	HIS	-	EXPRESSION TAG	GB 13881852
J	540	HIS	-	EXPRESSION TAG	GB 13881852
L	535	HIS	-	EXPRESSION TAG	GB 13881852
L	536	HIS	-	EXPRESSION TAG	GB 13881852
L	537	HIS	-	EXPRESSION TAG	GB 13881852
L	538	HIS	-	EXPRESSION TAG	GB 13881852
L	539	HIS	-	EXPRESSION TAG	GB 13881852
L	540	HIS	-	EXPRESSION TAG	GB 13881852
N	535	HIS	-	EXPRESSION TAG	GB 13881852
N	536	HIS	-	EXPRESSION TAG	GB 13881852
N	537	HIS	-	EXPRESSION TAG	GB 13881852
N	538	HIS	-	EXPRESSION TAG	GB 13881852
N	539	HIS	-	EXPRESSION TAG	GB 13881852
N	540	HIS	-	EXPRESSION TAG	GB 13881852
P	535	HIS	-	EXPRESSION TAG	GB 13881852
P	536	HIS	-	EXPRESSION TAG	GB 13881852
P	537	HIS	-	EXPRESSION TAG	GB 13881852
P	538	HIS	-	EXPRESSION TAG	GB 13881852
P	539	HIS	-	EXPRESSION TAG	GB 13881852
P	540	HIS	-	EXPRESSION TAG	GB 13881852
R	535	HIS	-	EXPRESSION TAG	GB 13881852
R	536	HIS	-	EXPRESSION TAG	GB 13881852
R	537	HIS	-	EXPRESSION TAG	GB 13881852
R	538	HIS	-	EXPRESSION TAG	GB 13881852
R	539	HIS	-	EXPRESSION TAG	GB 13881852
R	540	HIS	-	EXPRESSION TAG	GB 13881852

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
T	535	HIS	-	EXPRESSION TAG	GB 13881852
T	536	HIS	-	EXPRESSION TAG	GB 13881852
T	537	HIS	-	EXPRESSION TAG	GB 13881852
T	538	HIS	-	EXPRESSION TAG	GB 13881852
T	539	HIS	-	EXPRESSION TAG	GB 13881852
T	540	HIS	-	EXPRESSION TAG	GB 13881852
V	535	HIS	-	EXPRESSION TAG	GB 13881852
V	536	HIS	-	EXPRESSION TAG	GB 13881852
V	537	HIS	-	EXPRESSION TAG	GB 13881852
V	538	HIS	-	EXPRESSION TAG	GB 13881852
V	539	HIS	-	EXPRESSION TAG	GB 13881852
V	540	HIS	-	EXPRESSION TAG	GB 13881852
X	535	HIS	-	EXPRESSION TAG	GB 13881852
X	536	HIS	-	EXPRESSION TAG	GB 13881852
X	537	HIS	-	EXPRESSION TAG	GB 13881852
X	538	HIS	-	EXPRESSION TAG	GB 13881852
X	539	HIS	-	EXPRESSION TAG	GB 13881852
X	540	HIS	-	EXPRESSION TAG	GB 13881852
Z	535	HIS	-	EXPRESSION TAG	GB 13881852
Z	536	HIS	-	EXPRESSION TAG	GB 13881852
Z	537	HIS	-	EXPRESSION TAG	GB 13881852
Z	538	HIS	-	EXPRESSION TAG	GB 13881852
Z	539	HIS	-	EXPRESSION TAG	GB 13881852
Z	540	HIS	-	EXPRESSION TAG	GB 13881852
2	535	HIS	-	EXPRESSION TAG	GB 13881852
2	536	HIS	-	EXPRESSION TAG	GB 13881852
2	537	HIS	-	EXPRESSION TAG	GB 13881852
2	538	HIS	-	EXPRESSION TAG	GB 13881852
2	539	HIS	-	EXPRESSION TAG	GB 13881852
2	540	HIS	-	EXPRESSION TAG	GB 13881852

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	1	13	Total O 13 13	0	0
3	2	19	Total O 19 19	0	0
3	A	2	Total O 2 2	0	0
3	B	7	Total O 7 7	0	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	6	Total O 6 6	0	0
3	D	11	Total O 11 11	0	0
3	E	9	Total O 9 9	0	0
3	F	10	Total O 10 10	0	0
3	G	9	Total O 9 9	0	0
3	H	1	Total O 1 1	0	0
3	I	7	Total O 7 7	0	0
3	J	5	Total O 5 5	0	0
3	K	15	Total O 15 15	0	0
3	L	4	Total O 4 4	0	0
3	M	11	Total O 11 11	0	0
3	N	7	Total O 7 7	0	0
3	O	8	Total O 8 8	0	0
3	P	4	Total O 4 4	0	0
3	Q	6	Total O 6 6	0	0
3	R	5	Total O 5 5	0	0
3	S	13	Total O 13 13	0	0
3	T	6	Total O 6 6	0	0
3	U	7	Total O 7 7	0	0
3	V	10	Total O 10 10	0	0
3	W	8	Total O 8 8	0	0

*Continued on next page...*

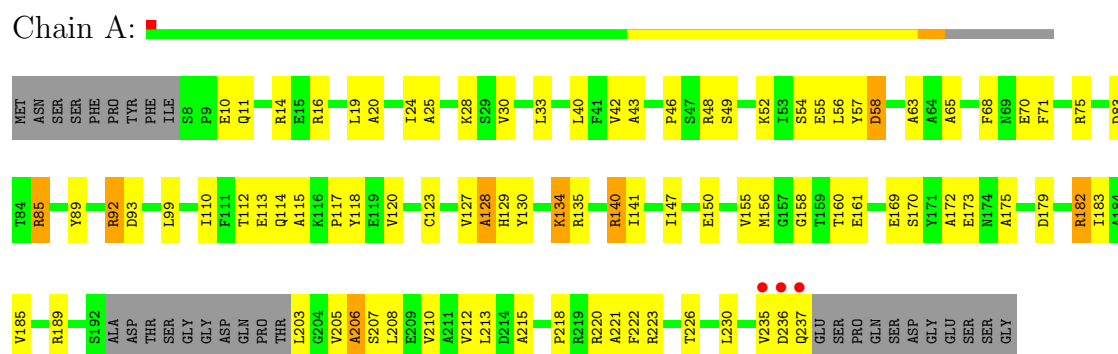
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	X	4	Total 4	O 4	0	0
3	Y	12	Total 12	O 12	0	0
3	Z	7	Total 7	O 7	0	0

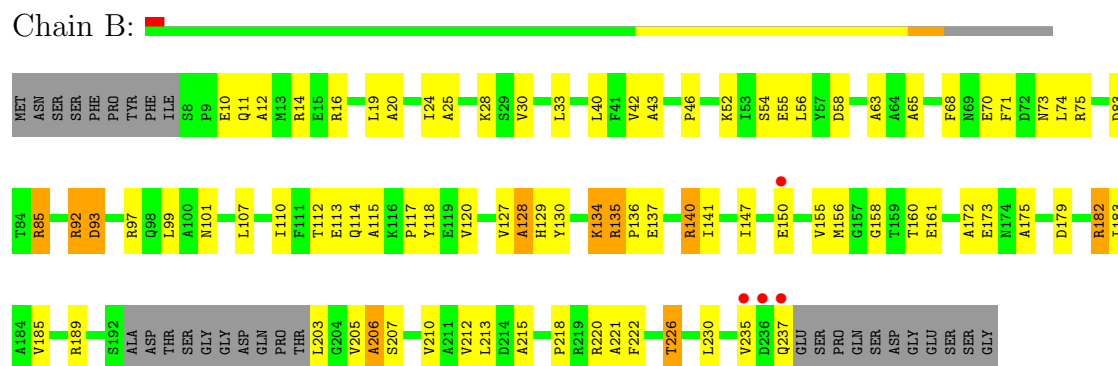
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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.

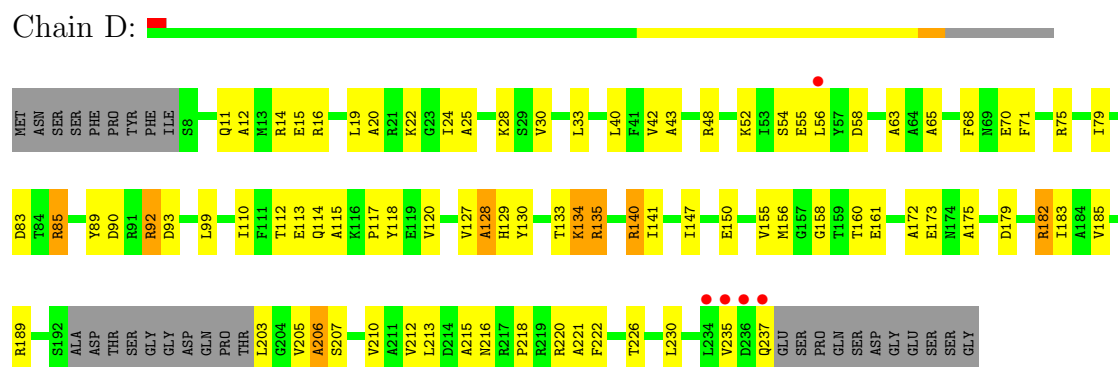
- Molecule 1: 20S proteasome, alpha and beta subunits



- Molecule 1: 20S proteasome, alpha and beta subunits

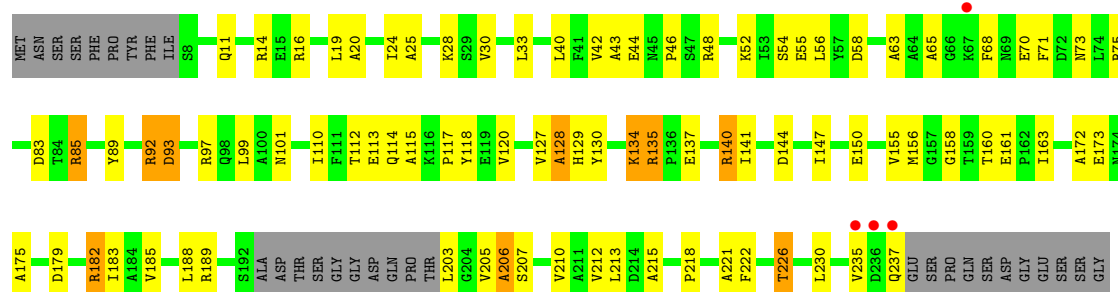


- Molecule 1: 20S proteasome, alpha and beta subunits



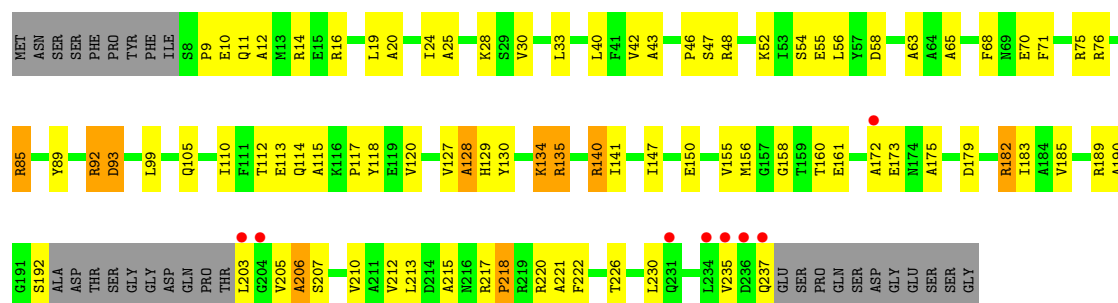
- Molecule 1: 20S proteasome, alpha and beta subunits

## Chain F:



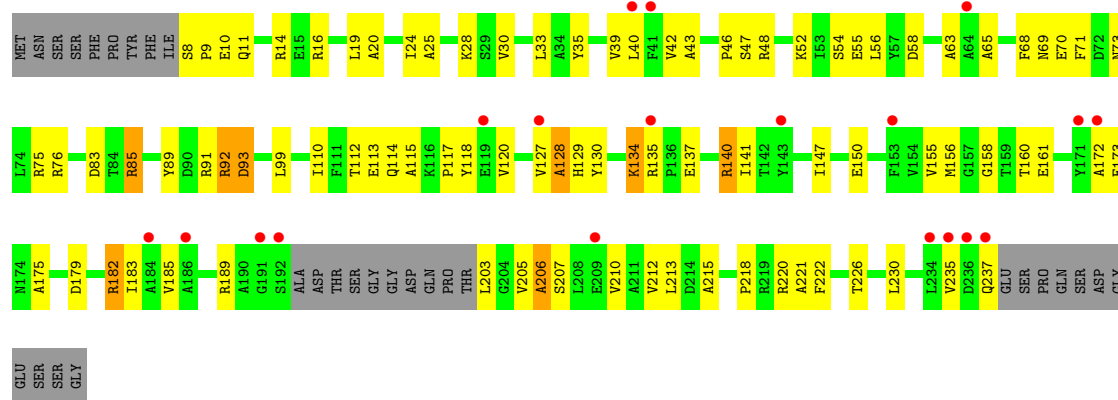
- Molecule 1: 20S proteasome, alpha and beta subunits

## Chain I:



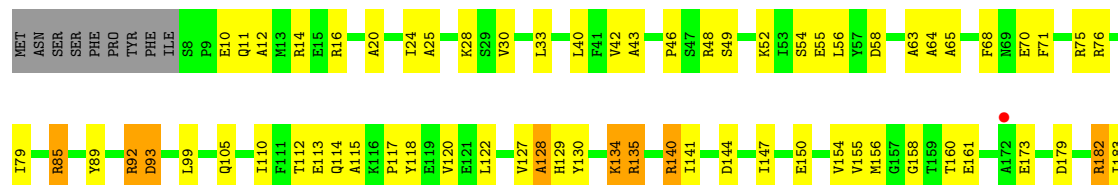
- Molecule 1: 20S proteasome, alpha and beta subunits

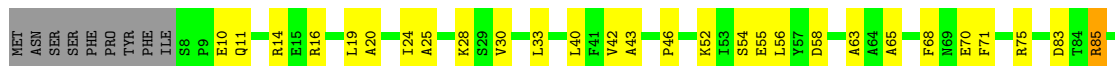
## Chain K:

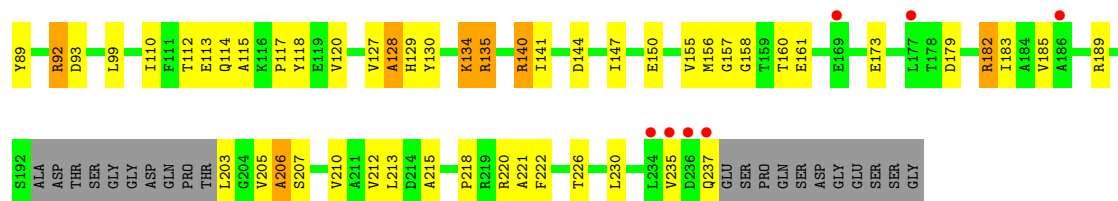


- Molecule 1: 20S proteasome, alpha and beta subunits

## Chain M:

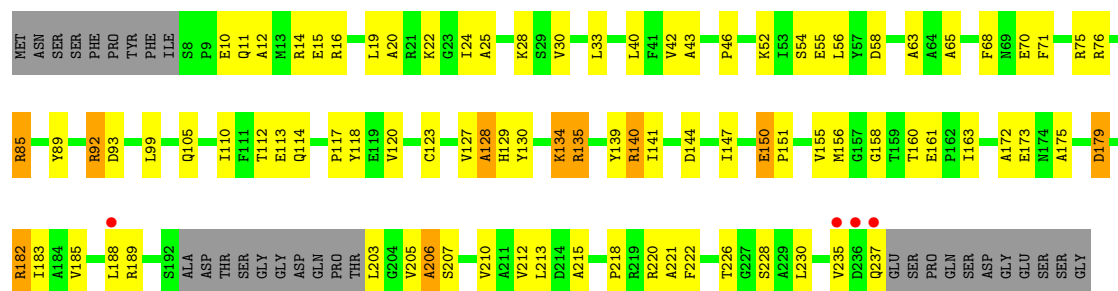






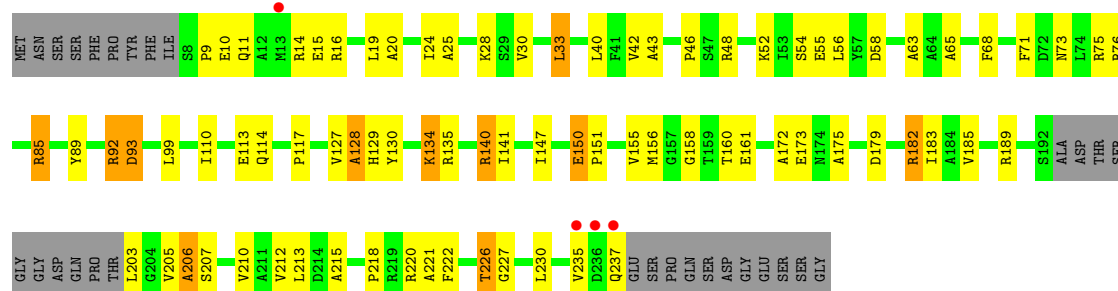
- Molecule 1: 20S proteasome, alpha and beta subunits

Chain W:



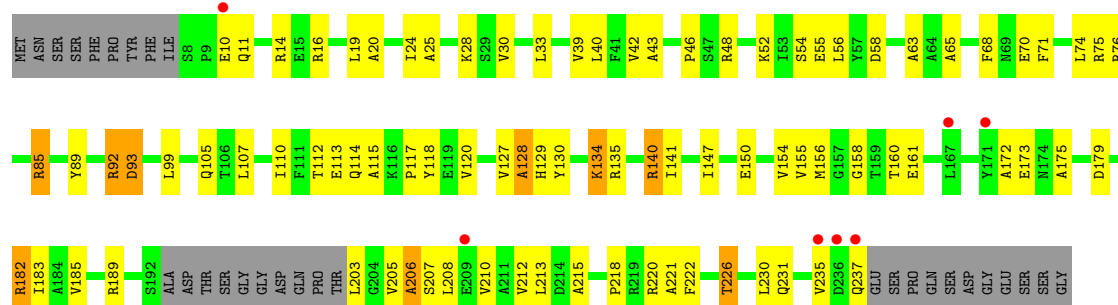
- Molecule 1: 20S proteasome, alpha and beta subunits

Chain Y:



- Molecule 1: 20S proteasome, alpha and beta subunits

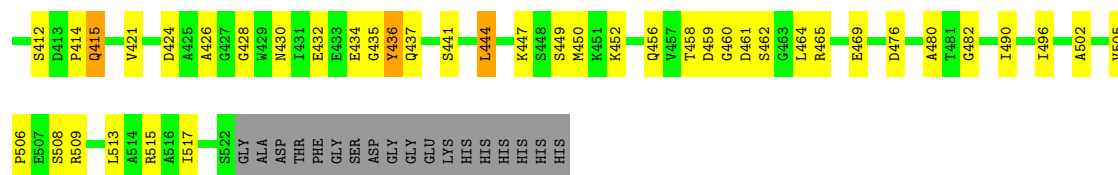
Chain 1:



- Molecule 2: proteasome, beta subunit

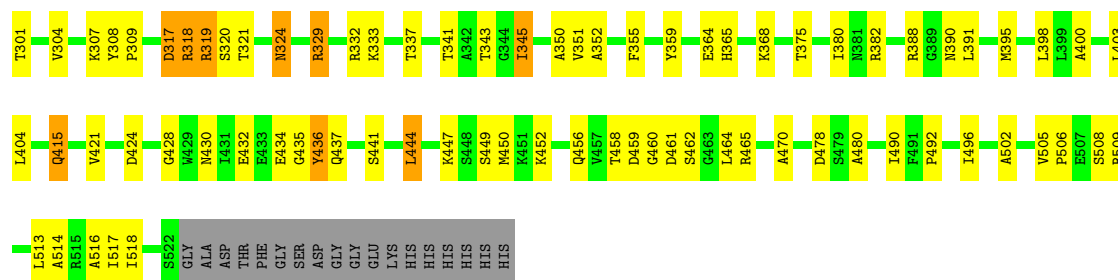
Chain H:





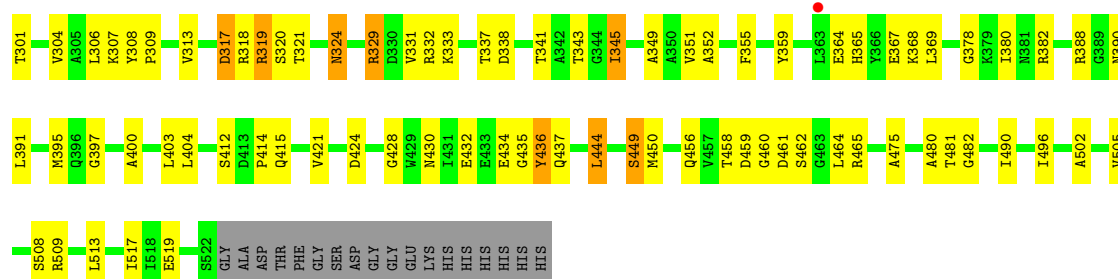
- Molecule 2: proteasome, beta subunit

Chain C:



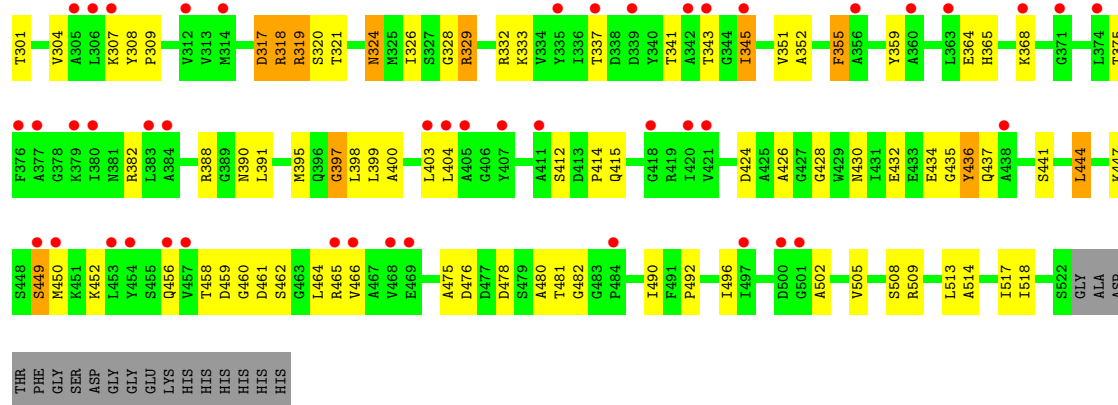
- Molecule 2: proteasome, beta subunit

Chain E:



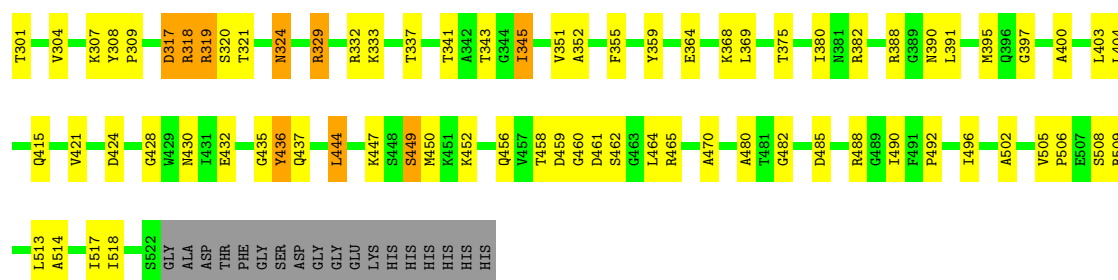
- Molecule 2: proteasome, beta subunit

Chain G:



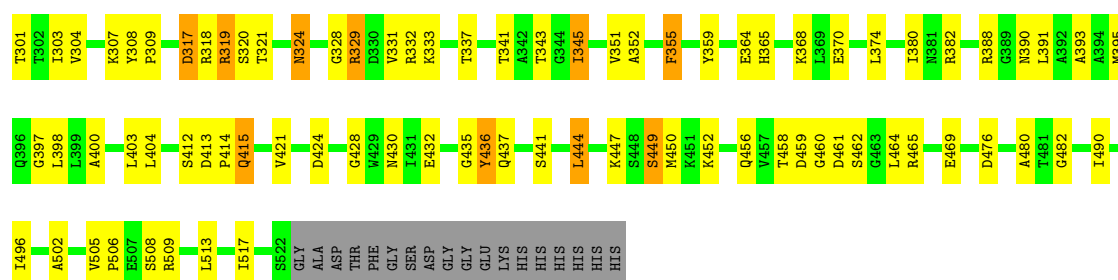
- Molecule 2: proteasome, beta subunit

Chain J:



- Molecule 2: proteasome, beta subunit

Chain L:



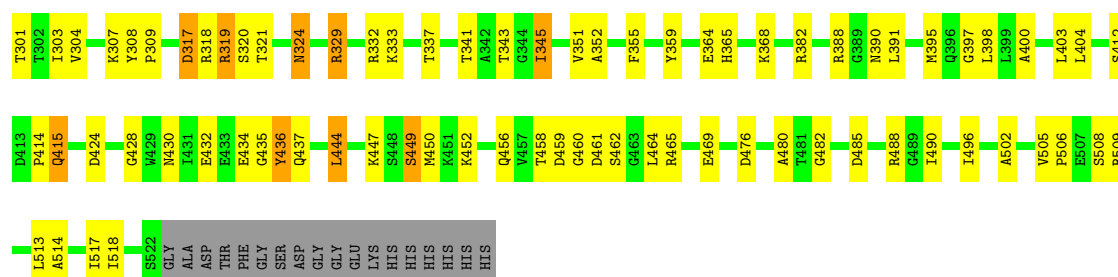
- Molecule 2: proteasome, beta subunit

Chain N:



- Molecule 2: proteasome, beta subunit

Chain P:

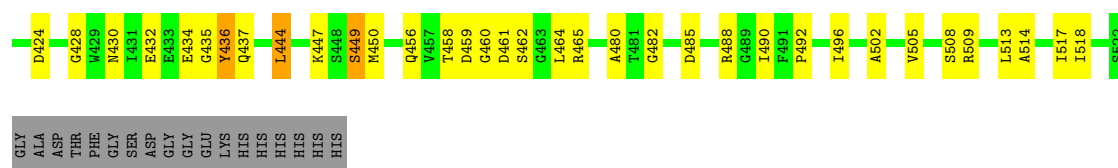


- Molecule 2: proteasome, beta subunit

Chain R:

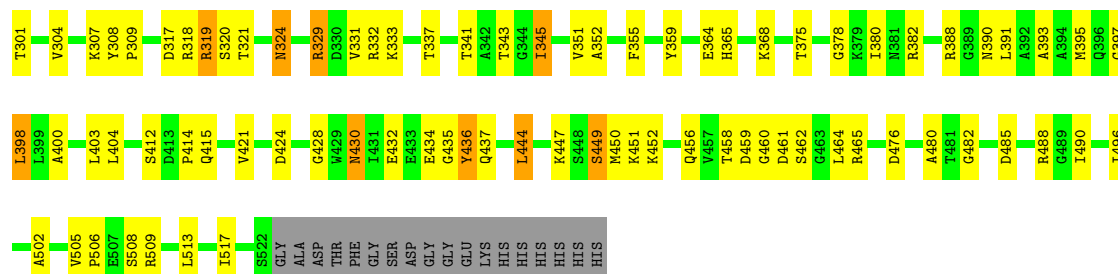






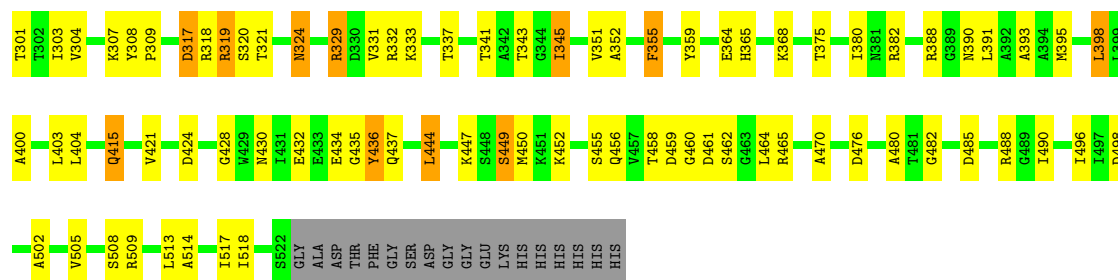
- Molecule 2: proteasome, beta subunit

Chain T:



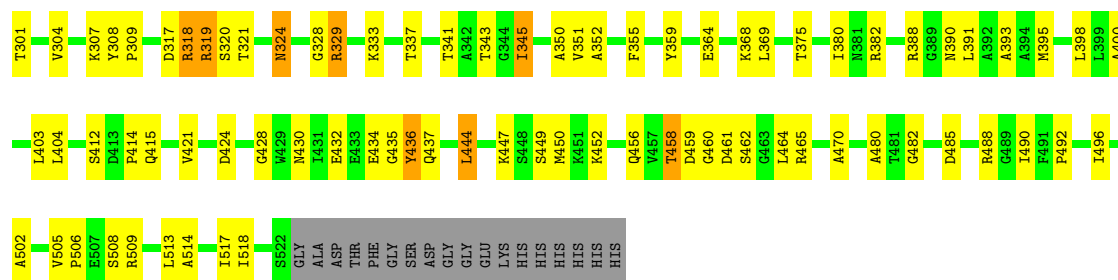
- Molecule 2: proteasome, beta subunit

Chain V:



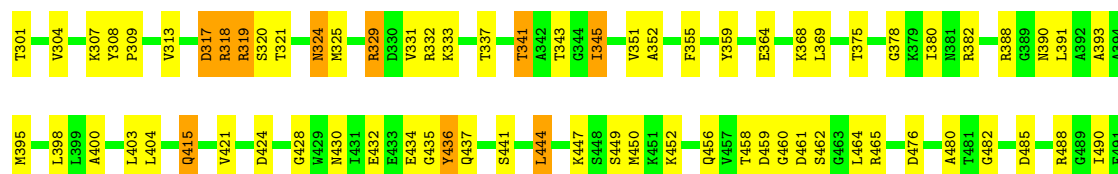
- Molecule 2: proteasome, beta subunit

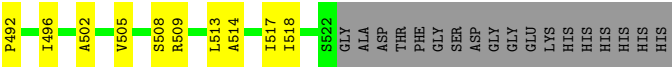
Chain X:



- Molecule 2: proteasome, beta subunit

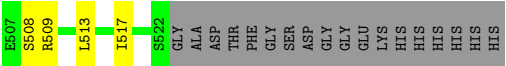
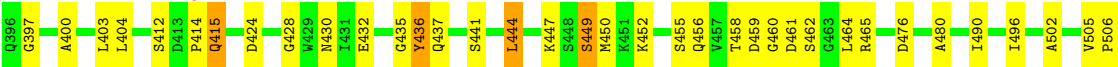
Chain Z:





● Molecule 2: proteasome, beta subunit

Chain 2:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	173.33Å 113.80Å 200.13Å 90.00° 113.93° 90.00°	Depositor
Resolution (Å)	50.00 – 3.23 49.63 – 3.23	Depositor EDS
% Data completeness (in resolution range)	79.6 (50.00-3.23) 79.6 (49.63-3.23)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.49 (at 3.25Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.243 , 0.266 0.248 , 0.252	Depositor DCC
$R_{free}$ test set	2776 reflections (3.13%)	DCC
Wilson B-factor (Å <sup>2</sup> )	82.0	Xtriage
Anisotropy	0.332	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 100.0	EDS
Estimated twinning fraction	0.046 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	1 of 91405 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	46846	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

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	1	0.43	0/1717	0.59	0/2320
1	A	0.54	1/1717 (0.1%)	0.63	0/2320
1	B	0.49	0/1717	0.62	0/2320
1	D	0.47	0/1717	0.61	0/2320
1	F	0.45	0/1717	0.60	0/2320
1	I	0.44	0/1717	0.60	0/2320
1	K	0.43	0/1717	0.59	0/2320
1	M	0.45	0/1717	0.60	0/2320
1	O	0.45	0/1717	0.60	0/2320
1	Q	0.44	0/1717	0.59	0/2320
1	S	0.43	0/1717	0.59	0/2320
1	U	0.43	0/1717	0.60	0/2320
1	W	0.47	0/1717	0.61	0/2320
1	Y	0.43	0/1717	0.59	0/2320
2	2	0.42	0/1662	0.61	0/2254
2	C	0.52	0/1662	0.65	0/2254
2	E	0.54	0/1662	0.66	0/2254
2	G	0.48	0/1662	0.65	0/2254
2	H	0.55	0/1662	0.66	0/2254
2	J	0.49	0/1662	0.63	0/2254
2	L	0.51	0/1662	0.65	0/2254
2	N	0.49	0/1662	0.64	0/2254
2	P	0.49	0/1662	0.64	0/2254
2	R	0.50	0/1662	0.65	0/2254
2	T	0.46	0/1662	0.63	0/2254
2	V	0.47	0/1662	0.65	0/2254
2	X	0.49	0/1662	0.64	0/2254
2	Z	0.48	0/1662	0.64	0/2254
All	All	0.47	1/47306 (0.0%)	0.62	0/64036

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	123	CYS	CB-SG	-5.45	1.73	1.81

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1692	0	1688	75	0
1	A	1692	0	1688	77	4
1	B	1692	0	1688	75	0
1	D	1692	0	1688	72	4
1	F	1692	0	1688	80	0
1	I	1692	0	1688	72	2
1	K	1692	0	1688	84	0
1	M	1692	0	1688	88	0
1	O	1692	0	1688	77	0
1	Q	1692	0	1688	68	0
1	S	1692	0	1688	77	0
1	U	1692	0	1688	69	2
1	W	1692	0	1688	77	1
1	Y	1692	0	1688	72	0
2	2	1638	0	1630	67	1
2	C	1638	0	1630	58	0
2	E	1638	0	1630	60	1
2	G	1638	0	1630	67	3
2	H	1638	0	1630	62	0
2	J	1638	0	1630	56	2
2	L	1638	0	1630	68	0
2	N	1638	0	1630	62	1
2	P	1638	0	1630	61	1
2	R	1638	0	1630	54	0
2	T	1638	0	1630	60	0
2	V	1638	0	1630	64	2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	X	1638	0	1630	59	3
2	Z	1638	0	1630	62	1
3	1	13	0	0	10	0
3	2	19	0	0	8	0
3	A	2	0	0	2	0
3	B	7	0	0	2	0
3	C	6	0	0	0	0
3	D	11	0	0	3	0
3	E	9	0	0	3	0
3	F	10	0	0	1	0
3	G	9	0	0	3	0
3	H	1	0	0	3	0
3	I	7	0	0	3	0
3	J	5	0	0	0	0
3	K	15	0	0	8	0
3	L	4	0	0	3	0
3	M	11	0	0	5	0
3	N	7	0	0	5	0
3	O	8	0	0	8	0
3	P	4	0	0	0	0
3	Q	6	0	0	2	0
3	R	5	0	0	2	0
3	S	13	0	0	3	0
3	T	6	0	0	4	0
3	U	7	0	0	1	0
3	V	10	0	0	4	0
3	W	8	0	0	3	0
3	X	4	0	0	1	0
3	Y	12	0	0	8	0
3	Z	7	0	0	4	0
All	All	46846	0	46452	1730	14

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 19.

The worst 5 of 1730 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:J:444:LEU:HD12	2:Z:444:LEU:HD12	1.27	1.15
2:L:444:LEU:HD12	2:P:444:LEU:HD12	1.30	1.13
2:J:452:LYS:HG3	3:Z:190:HOH:O	1.47	1.12
1:K:14:ARG:HG2	3:K:260:HOH:O	1.56	1.06
2:N:444:LEU:HD12	2:V:444:LEU:HD12	1.35	1.04

The worst 5 of 14 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:G:465:ARG:NE	2:X:458:THR:CG2[2_554]	1.40	0.80
1:A:236:ASP:O	1:D:133:THR:OG1[2_655]	1.59	0.61
2:N:456:GLN:NE2	2:Z:415:GLN:OE1[1_565]	1.83	0.37
1:W:228:SER:O	2:2:414:PRO:CB[2_544]	1.97	0.23
2:J:456:GLN:NE2	2:V:415:GLN:OE1[1_545]	2.00	0.20

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	1	216/250 (86%)	188 (87%)	22 (10%)	6 (3%)	8	48
1	A	216/250 (86%)	192 (89%)	19 (9%)	5 (2%)	10	55
1	B	216/250 (86%)	189 (88%)	21 (10%)	6 (3%)	8	48
1	D	216/250 (86%)	193 (89%)	18 (8%)	5 (2%)	10	55
1	F	216/250 (86%)	190 (88%)	20 (9%)	6 (3%)	8	48
1	I	216/250 (86%)	189 (88%)	22 (10%)	5 (2%)	10	55
1	K	216/250 (86%)	191 (88%)	20 (9%)	5 (2%)	10	55
1	M	216/250 (86%)	187 (87%)	24 (11%)	5 (2%)	10	55
1	O	216/250 (86%)	188 (87%)	23 (11%)	5 (2%)	10	55
1	Q	216/250 (86%)	188 (87%)	23 (11%)	5 (2%)	10	55
1	S	216/250 (86%)	189 (88%)	22 (10%)	5 (2%)	10	55
1	U	216/250 (86%)	189 (88%)	22 (10%)	5 (2%)	10	55
1	W	216/250 (86%)	192 (89%)	19 (9%)	5 (2%)	10	55
1	Y	216/250 (86%)	187 (87%)	23 (11%)	6 (3%)	8	48
2	2	220/240 (92%)	195 (89%)	22 (10%)	3 (1%)	16	68
2	C	220/240 (92%)	195 (89%)	22 (10%)	3 (1%)	16	68
2	E	220/240 (92%)	196 (89%)	19 (9%)	5 (2%)	10	55
2	G	220/240 (92%)	196 (89%)	18 (8%)	6 (3%)	8	49

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	220/240 (92%)	193 (88%)	22 (10%)	5 (2%)	10	55
2	J	220/240 (92%)	194 (88%)	22 (10%)	4 (2%)	13	63
2	L	220/240 (92%)	194 (88%)	21 (10%)	5 (2%)	10	55
2	N	220/240 (92%)	198 (90%)	16 (7%)	6 (3%)	8	49
2	P	220/240 (92%)	195 (89%)	19 (9%)	6 (3%)	8	49
2	R	220/240 (92%)	193 (88%)	22 (10%)	5 (2%)	10	55
2	T	220/240 (92%)	195 (89%)	19 (9%)	6 (3%)	8	49
2	V	220/240 (92%)	194 (88%)	21 (10%)	5 (2%)	10	55
2	X	220/240 (92%)	193 (88%)	23 (10%)	4 (2%)	13	63
2	Z	220/240 (92%)	192 (87%)	24 (11%)	4 (2%)	13	63
All	All	6104/6860 (89%)	5375 (88%)	588 (10%)	141 (2%)	10	55

5 of 141 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	128	ALA
1	B	128	ALA
1	D	128	ALA
1	F	128	ALA
1	I	128	ALA

### 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	1	169/194 (87%)	156 (92%)	13 (8%)	18	61
1	A	169/194 (87%)	156 (92%)	13 (8%)	18	61
1	B	169/194 (87%)	156 (92%)	13 (8%)	18	61
1	D	169/194 (87%)	156 (92%)	13 (8%)	18	61
1	F	169/194 (87%)	155 (92%)	14 (8%)	16	56
1	I	169/194 (87%)	156 (92%)	13 (8%)	18	61
1	K	169/194 (87%)	156 (92%)	13 (8%)	18	61

Continued on next page...



*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	169/194 (87%)	155 (92%)	14 (8%)	16	56
1	O	169/194 (87%)	156 (92%)	13 (8%)	18	61
1	Q	169/194 (87%)	155 (92%)	14 (8%)	16	56
1	S	169/194 (87%)	156 (92%)	13 (8%)	18	61
1	U	169/194 (87%)	156 (92%)	13 (8%)	18	61
1	W	169/194 (87%)	155 (92%)	14 (8%)	16	56
1	Y	169/194 (87%)	156 (92%)	13 (8%)	18	61
2	2	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	C	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	E	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	G	165/178 (93%)	151 (92%)	14 (8%)	15	54
2	H	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	J	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	L	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	N	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	P	165/178 (93%)	151 (92%)	14 (8%)	15	54
2	R	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	T	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	V	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	X	165/178 (93%)	150 (91%)	15 (9%)	14	49
2	Z	165/178 (93%)	149 (90%)	16 (10%)	12	46
All	All	4676/5208 (90%)	4281 (92%)	395 (8%)	16	55

5 of 395 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	150	GLU
2	P	444	LEU
2	Z	449	SER
2	N	319	ARG
1	O	113	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 154 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	98	GLN
2	P	415	GLN
1	1	51	GLN
1	M	165	ASN
1	O	73	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	1	220/250 (88%)	0.43	7 (3%) 45 10	100, 100, 100, 100	0
1	A	220/250 (88%)	0.38	3 (1%) 72 24	100, 100, 100, 100	0
1	B	220/250 (88%)	0.38	4 (1%) 65 20	100, 100, 100, 100	0
1	D	220/250 (88%)	0.50	5 (2%) 57 15	100, 100, 100, 100	0
1	F	220/250 (88%)	0.43	4 (1%) 65 20	100, 100, 100, 100	0
1	I	220/250 (88%)	0.51	8 (3%) 41 9	100, 100, 100, 100	0
1	K	220/250 (88%)	0.76	19 (8%) 11 3	100, 100, 100, 100	0
1	M	220/250 (88%)	0.45	4 (1%) 65 20	100, 100, 100, 100	0
1	O	220/250 (88%)	0.56	11 (5%) 28 6	100, 100, 100, 100	0
1	Q	220/250 (88%)	0.64	7 (3%) 45 10	100, 100, 100, 100	0
1	S	220/250 (88%)	0.54	10 (4%) 32 7	100, 100, 100, 100	0
1	U	220/250 (88%)	0.57	7 (3%) 45 10	100, 100, 100, 100	0
1	W	220/250 (88%)	0.42	4 (1%) 65 20	100, 100, 100, 100	0
1	Y	220/250 (88%)	0.54	4 (1%) 65 20	100, 100, 100, 100	0
2	2	222/240 (92%)	0.35	1 (0%) 88 48	100, 100, 100, 100	0
2	C	222/240 (92%)	0.45	0 100 100	100, 100, 100, 100	0
2	E	222/240 (92%)	0.41	1 (0%) 88 48	100, 100, 100, 100	0
2	G	222/240 (92%)	1.49	46 (20%) 1 1	100, 100, 100, 100	0
2	H	222/240 (92%)	0.46	0 100 100	100, 100, 100, 100	0
2	J	222/240 (92%)	0.29	0 100 100	100, 100, 100, 100	0
2	L	222/240 (92%)	0.31	0 100 100	100, 100, 100, 100	0
2	N	222/240 (92%)	0.28	0 100 100	100, 100, 100, 100	0
2	P	222/240 (92%)	0.35	0 100 100	100, 100, 100, 100	0
2	R	222/240 (92%)	0.35	0 100 100	100, 100, 100, 100	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
2	T	222/240 (92%)	0.28	0	100	100	100, 100, 100, 100	0
2	V	222/240 (92%)	0.32	0	100	100	100, 100, 100, 100	0
2	X	222/240 (92%)	0.24	0	100	100	100, 100, 100, 100	0
2	Z	222/240 (92%)	0.33	0	100	100	100, 100, 100, 100	0
All	All	6188/6860 (90%)	0.46	145 (2%)	57	15	100, 100, 100, 100	0

The worst 5 of 145 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	235	VAL	9.3
1	U	237	GLN	8.1
1	S	236	ASP	7.8
1	S	235	VAL	7.0
1	A	235	VAL	6.8

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.