



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 5, 2021 – 10:16 AM EDT

PDB ID : 3IPM
Title : Crystal Structure of Archaeal 20S Proteasome in Complex with the C-terminus of PAN
Authors : Yu, Y.; Cheng, Y.
Deposited on : 2009-08-17
Resolution : 4.00 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 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	:	2.23.2
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)	:	2.23.2

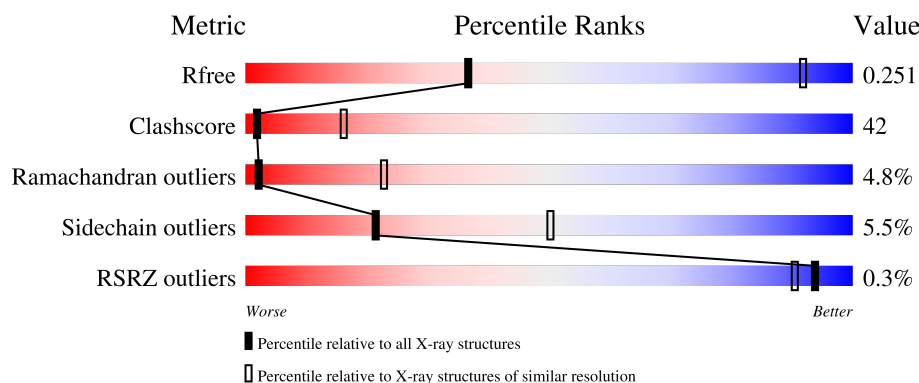
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1087 (4.30-3.70)
Clashscore	141614	1148 (4.30-3.70)
Ramachandran outliers	138981	1108 (4.30-3.70)
Sidechain outliers	138945	1099 (4.30-3.70)
RSRZ outliers	127900	1028 (4.34-3.66)

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	233	
1	B	233	
1	C	233	
1	D	233	
1	E	233	

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Mol	Chain	Length	Quality of chain
1	F	233	 32% 58% 8% .
1	G	233	 34% 55% 8% .
2	H	217	 % 42% 45% 6% 6%
2	I	217	 42% 44% 7% 6%
2	J	217	 45% 41% 7% 6%
2	K	217	 % 45% 42% 7% 6%
2	L	217	 43% 43% 7% 6%
2	M	217	 2% 41% 45% 7% 6%
2	N	217	 41% 44% 8% 6%
3	O	239	 42% 46% . 8%
3	P	239	 39% 49% . 8%
3	Q	239	 41% 46% 5% 8%
3	R	239	 40% 48% . 8%
3	S	239	 41% 48% . 8%
3	T	239	 40% 48% . 8%
3	U	239	 42% 46% . 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 35133 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 Proteasome subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	0	0
			1769	1123	299	344	3			
1	B	227	Total	C	N	O	S	0	0	0
			1769	1123	299	344	3			
1	C	227	Total	C	N	O	S	0	0	0
			1769	1123	299	344	3			
1	D	227	Total	C	N	O	S	0	0	0
			1769	1123	299	344	3			
1	E	227	Total	C	N	O	S	0	0	0
			1769	1123	299	344	3			
1	F	227	Total	C	N	O	S	0	0	0
			1769	1123	299	344	3			
1	G	227	Total	C	N	O	S	0	0	0
			1769	1123	299	344	3			

- Molecule 2 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	203	Total	C	N	O	S	0	0	0
			1557	985	264	297	11			
2	I	203	Total	C	N	O	S	0	0	0
			1557	985	264	297	11			
2	J	203	Total	C	N	O	S	0	0	0
			1557	985	264	297	11			
2	K	203	Total	C	N	O	S	0	0	0
			1557	985	264	297	11			
2	L	203	Total	C	N	O	S	0	0	0
			1557	985	264	297	11			
2	M	203	Total	C	N	O	S	0	0	0
			1557	985	264	297	11			
2	N	203	Total	C	N	O	S	0	0	0
			1557	985	264	297	11			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	204	HIS	-	expression tag	UNP P28061
H	205	HIS	-	expression tag	UNP P28061
H	206	HIS	-	expression tag	UNP P28061
H	207	HIS	-	expression tag	UNP P28061
H	208	HIS	-	expression tag	UNP P28061
H	209	HIS	-	expression tag	UNP P28061
I	204	HIS	-	expression tag	UNP P28061
I	205	HIS	-	expression tag	UNP P28061
I	206	HIS	-	expression tag	UNP P28061
I	207	HIS	-	expression tag	UNP P28061
I	208	HIS	-	expression tag	UNP P28061
I	209	HIS	-	expression tag	UNP P28061
J	204	HIS	-	expression tag	UNP P28061
J	205	HIS	-	expression tag	UNP P28061
J	206	HIS	-	expression tag	UNP P28061
J	207	HIS	-	expression tag	UNP P28061
J	208	HIS	-	expression tag	UNP P28061
J	209	HIS	-	expression tag	UNP P28061
K	204	HIS	-	expression tag	UNP P28061
K	205	HIS	-	expression tag	UNP P28061
K	206	HIS	-	expression tag	UNP P28061
K	207	HIS	-	expression tag	UNP P28061
K	208	HIS	-	expression tag	UNP P28061
K	209	HIS	-	expression tag	UNP P28061
L	204	HIS	-	expression tag	UNP P28061
L	205	HIS	-	expression tag	UNP P28061
L	206	HIS	-	expression tag	UNP P28061
L	207	HIS	-	expression tag	UNP P28061
L	208	HIS	-	expression tag	UNP P28061
L	209	HIS	-	expression tag	UNP P28061
M	204	HIS	-	expression tag	UNP P28061
M	205	HIS	-	expression tag	UNP P28061
M	206	HIS	-	expression tag	UNP P28061
M	207	HIS	-	expression tag	UNP P28061
M	208	HIS	-	expression tag	UNP P28061
M	209	HIS	-	expression tag	UNP P28061
N	204	HIS	-	expression tag	UNP P28061
N	205	HIS	-	expression tag	UNP P28061
N	206	HIS	-	expression tag	UNP P28061
N	207	HIS	-	expression tag	UNP P28061
N	208	HIS	-	expression tag	UNP P28061
N	209	HIS	-	expression tag	UNP P28061

- Molecule 3 is a protein called Proteasome activator PA26, Proteasome-activating nucleotidase fusion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	O	219	Total	C	N	O	S	0	0	0
			1693	1064	300	324	5			
3	P	219	Total	C	N	O	S	0	0	0
			1693	1064	300	324	5			
3	Q	219	Total	C	N	O	S	0	0	0
			1693	1064	300	324	5			
3	R	219	Total	C	N	O	S	0	0	0
			1693	1064	300	324	5			
3	S	219	Total	C	N	O	S	0	0	0
			1693	1064	300	324	5			
3	T	219	Total	C	N	O	S	0	0	0
			1693	1064	300	324	5			
3	U	219	Total	C	N	O	S	0	0	0
			1693	1064	300	324	5			

There are 77 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	-6	MET	-	initiating methionine	UNP Q38BM8
O	-5	ALA	-	expression tag	UNP Q38BM8
O	-4	HIS	-	expression tag	UNP Q38BM8
O	-3	HIS	-	expression tag	UNP Q38BM8
O	-2	HIS	-	expression tag	UNP Q38BM8
O	-1	HIS	-	expression tag	UNP Q38BM8
O	0	HIS	-	expression tag	UNP Q38BM8
O	1	HIS	-	expression tag	UNP Q38BM8
O	102	ALA	GLU	engineered mutation	UNP Q38BM8
O	224	GLY	-	linker	UNP Q38BM8
O	225	GLY	-	linker	UNP Q38BM8
P	-6	MET	-	initiating methionine	UNP Q38BM8
P	-5	ALA	-	expression tag	UNP Q38BM8
P	-4	HIS	-	expression tag	UNP Q38BM8
P	-3	HIS	-	expression tag	UNP Q38BM8
P	-2	HIS	-	expression tag	UNP Q38BM8
P	-1	HIS	-	expression tag	UNP Q38BM8
P	0	HIS	-	expression tag	UNP Q38BM8
P	1	HIS	-	expression tag	UNP Q38BM8
P	102	ALA	GLU	engineered mutation	UNP Q38BM8
P	224	GLY	-	linker	UNP Q38BM8
P	225	GLY	-	linker	UNP Q38BM8
Q	-6	MET	-	initiating methionine	UNP Q38BM8

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	-5	ALA	-	expression tag	UNP Q38BM8
Q	-4	HIS	-	expression tag	UNP Q38BM8
Q	-3	HIS	-	expression tag	UNP Q38BM8
Q	-2	HIS	-	expression tag	UNP Q38BM8
Q	-1	HIS	-	expression tag	UNP Q38BM8
Q	0	HIS	-	expression tag	UNP Q38BM8
Q	1	HIS	-	expression tag	UNP Q38BM8
Q	102	ALA	GLU	engineered mutation	UNP Q38BM8
Q	224	GLY	-	linker	UNP Q38BM8
Q	225	GLY	-	linker	UNP Q38BM8
R	-6	MET	-	initiating methionine	UNP Q38BM8
R	-5	ALA	-	expression tag	UNP Q38BM8
R	-4	HIS	-	expression tag	UNP Q38BM8
R	-3	HIS	-	expression tag	UNP Q38BM8
R	-2	HIS	-	expression tag	UNP Q38BM8
R	-1	HIS	-	expression tag	UNP Q38BM8
R	0	HIS	-	expression tag	UNP Q38BM8
R	1	HIS	-	expression tag	UNP Q38BM8
R	102	ALA	GLU	engineered mutation	UNP Q38BM8
R	224	GLY	-	linker	UNP Q38BM8
R	225	GLY	-	linker	UNP Q38BM8
S	-6	MET	-	initiating methionine	UNP Q38BM8
S	-5	ALA	-	expression tag	UNP Q38BM8
S	-4	HIS	-	expression tag	UNP Q38BM8
S	-3	HIS	-	expression tag	UNP Q38BM8
S	-2	HIS	-	expression tag	UNP Q38BM8
S	-1	HIS	-	expression tag	UNP Q38BM8
S	0	HIS	-	expression tag	UNP Q38BM8
S	1	HIS	-	expression tag	UNP Q38BM8
S	102	ALA	GLU	engineered mutation	UNP Q38BM8
S	224	GLY	-	linker	UNP Q38BM8
S	225	GLY	-	linker	UNP Q38BM8
T	-6	MET	-	initiating methionine	UNP Q38BM8
T	-5	ALA	-	expression tag	UNP Q38BM8
T	-4	HIS	-	expression tag	UNP Q38BM8
T	-3	HIS	-	expression tag	UNP Q38BM8
T	-2	HIS	-	expression tag	UNP Q38BM8
T	-1	HIS	-	expression tag	UNP Q38BM8
T	0	HIS	-	expression tag	UNP Q38BM8
T	1	HIS	-	expression tag	UNP Q38BM8
T	102	ALA	GLU	engineered mutation	UNP Q38BM8
T	224	GLY	-	linker	UNP Q38BM8

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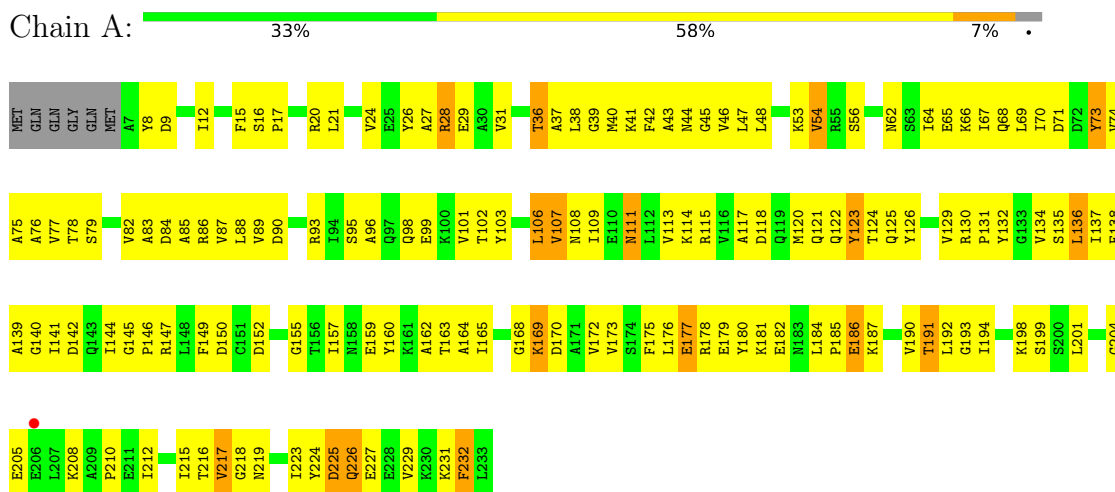
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Chain	Residue	Modelled	Actual	Comment	Reference
T	225	GLY	-	linker	UNP Q38BM8
U	-6	MET	-	initiating methionine	UNP Q38BM8
U	-5	ALA	-	expression tag	UNP Q38BM8
U	-4	HIS	-	expression tag	UNP Q38BM8
U	-3	HIS	-	expression tag	UNP Q38BM8
U	-2	HIS	-	expression tag	UNP Q38BM8
U	-1	HIS	-	expression tag	UNP Q38BM8
U	0	HIS	-	expression tag	UNP Q38BM8
U	1	HIS	-	expression tag	UNP Q38BM8
U	102	ALA	GLU	engineered mutation	UNP Q38BM8
U	224	GLY	-	linker	UNP Q38BM8
U	225	GLY	-	linker	UNP Q38BM8

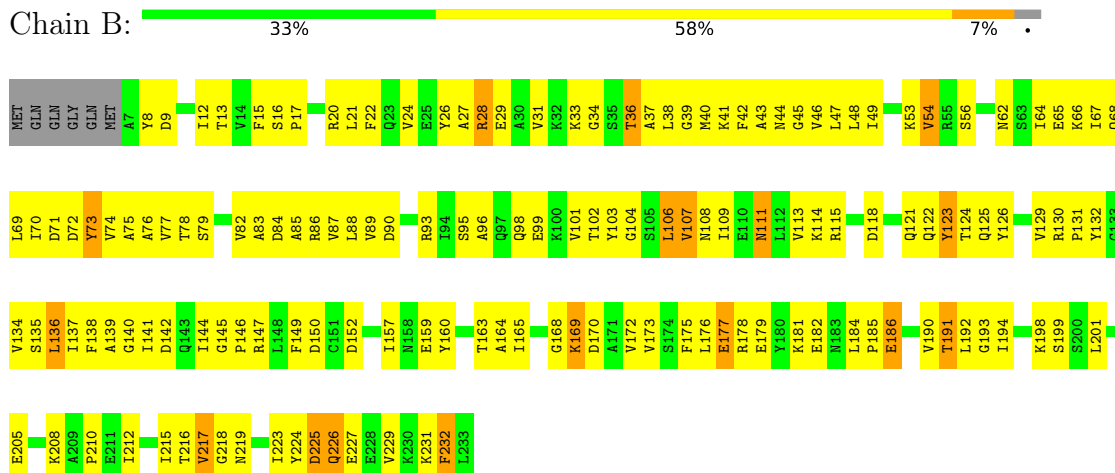
3 Residue-property plots

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: Proteasome subunit alpha

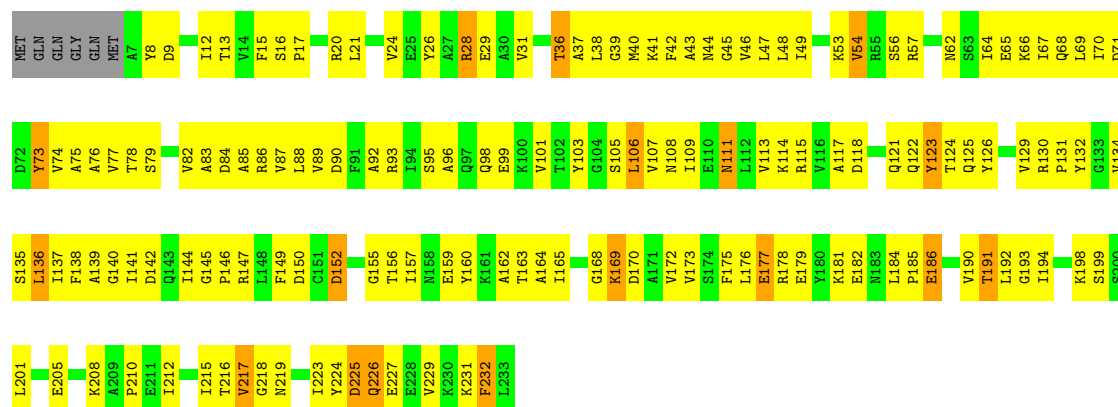


• Molecule 1: Proteasome subunit alpha

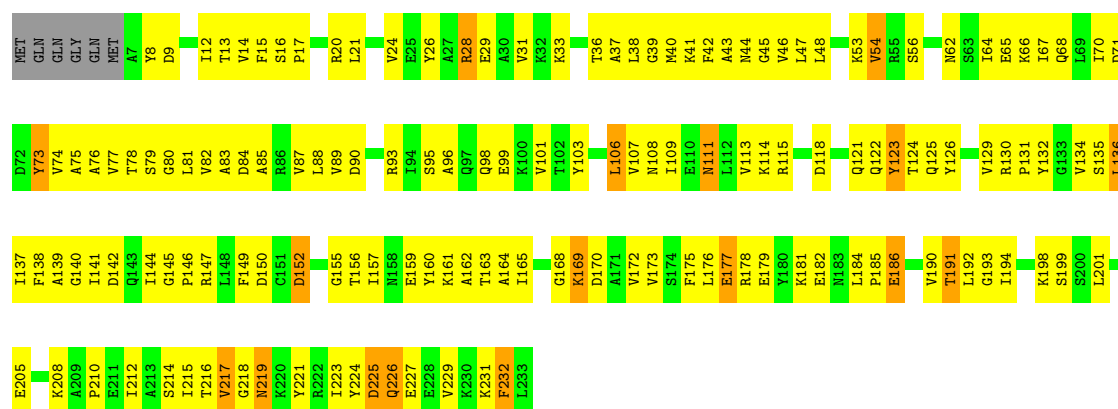


• Molecule 1: Proteasome subunit alpha

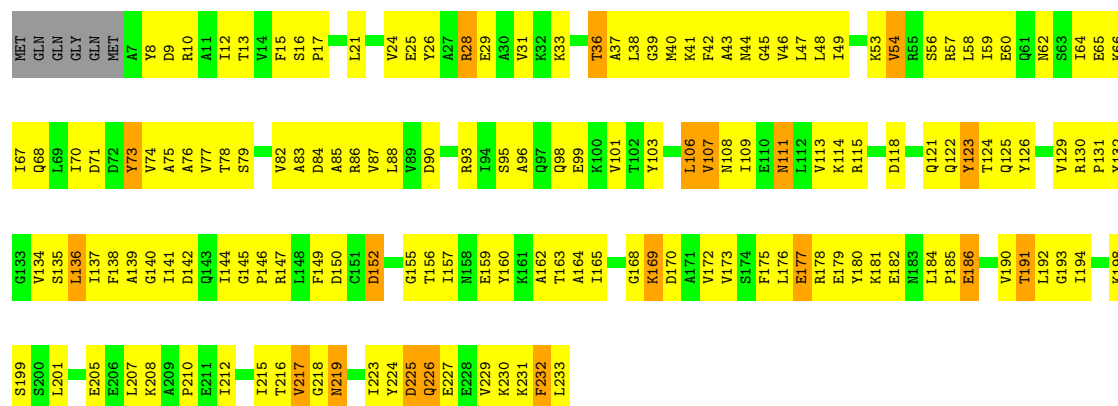




• Molecule 1: Proteasome subunit alpha

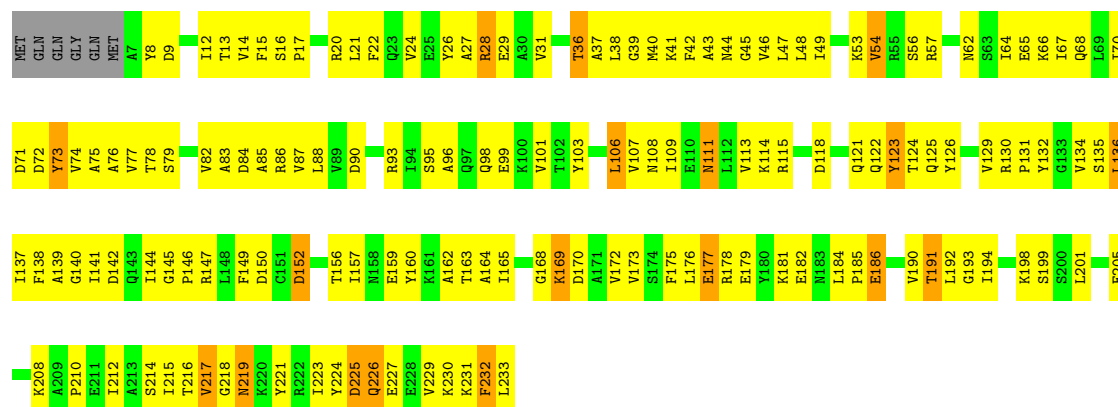


• Molecule 1: Proteasome subunit alpha

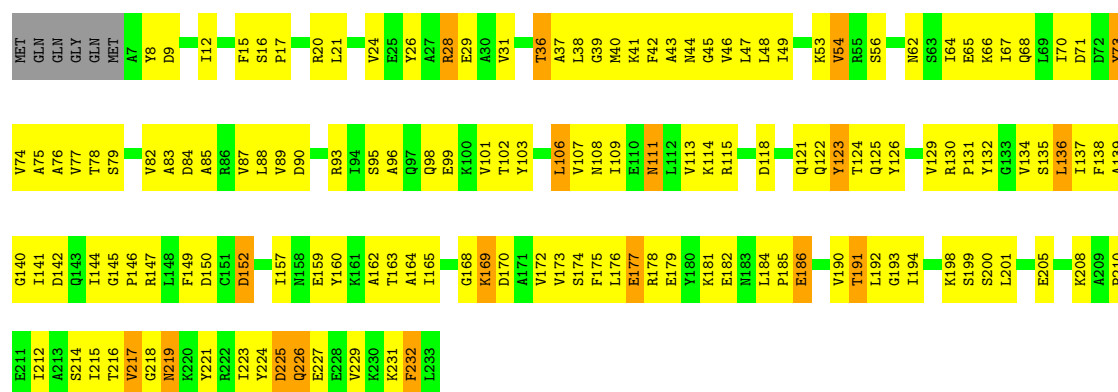


• Molecule 1: Proteasome subunit alpha

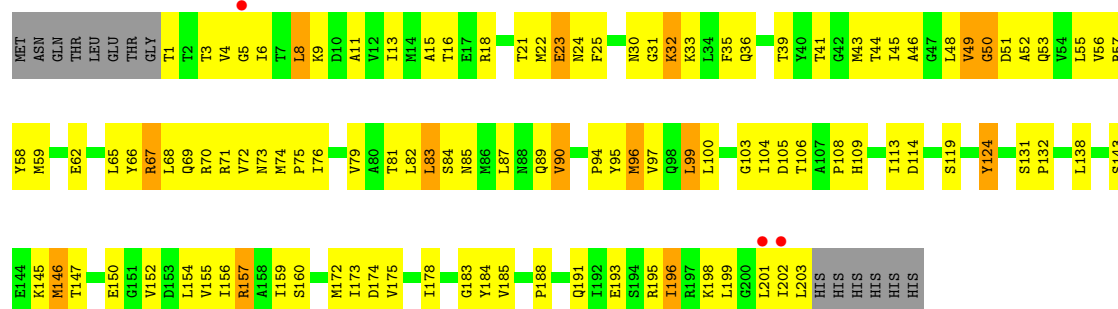




• Molecule 1: Proteasome subunit alpha

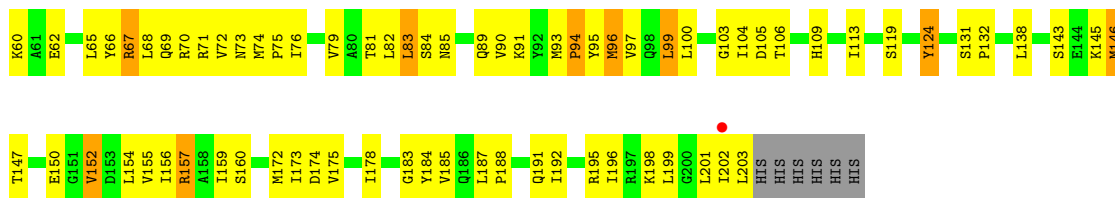


• Molecule 2: Proteasome subunit beta



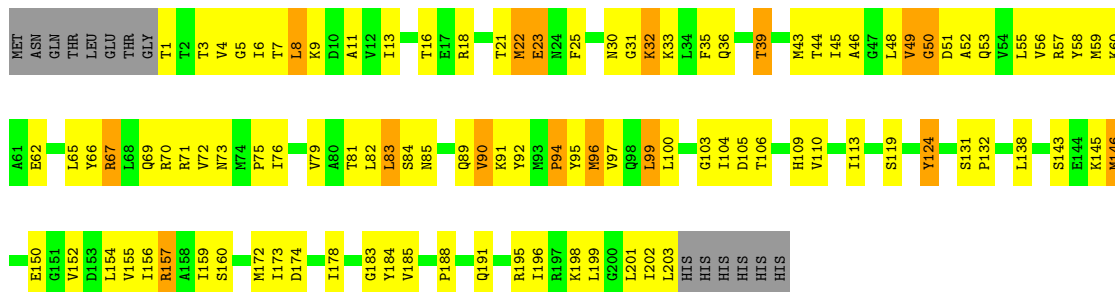
• Molecule 2: Proteasome subunit beta





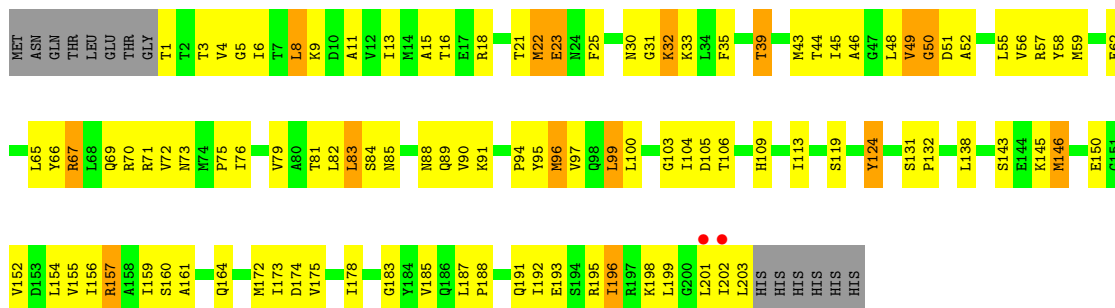
• Molecule 2: Proteasome subunit beta

Chain J: 45% 41% 7% 6%



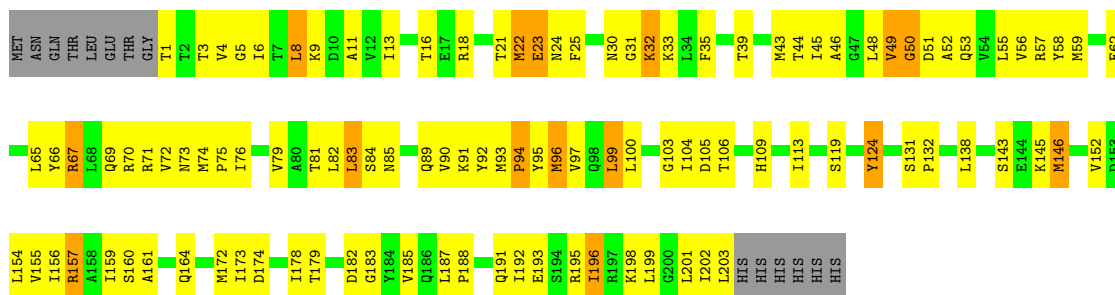
• Molecule 2: Proteasome subunit beta

Chain K: 45% 42% 7% 6%



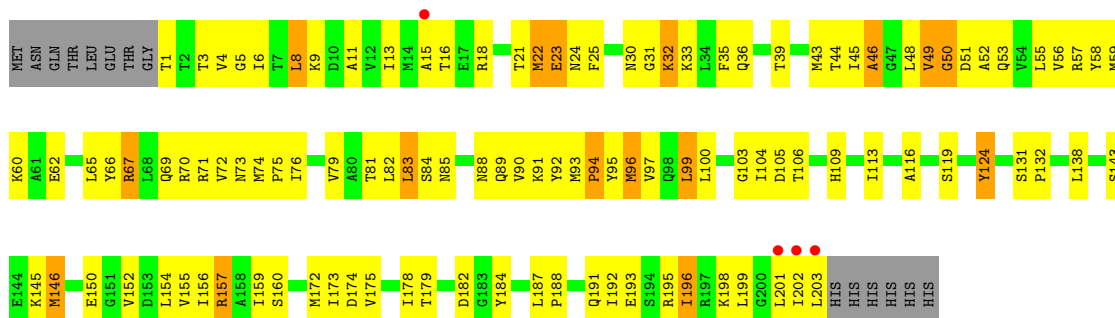
• Molecule 2: Proteasome subunit beta

Chain L: 43% 43% 7% 6%

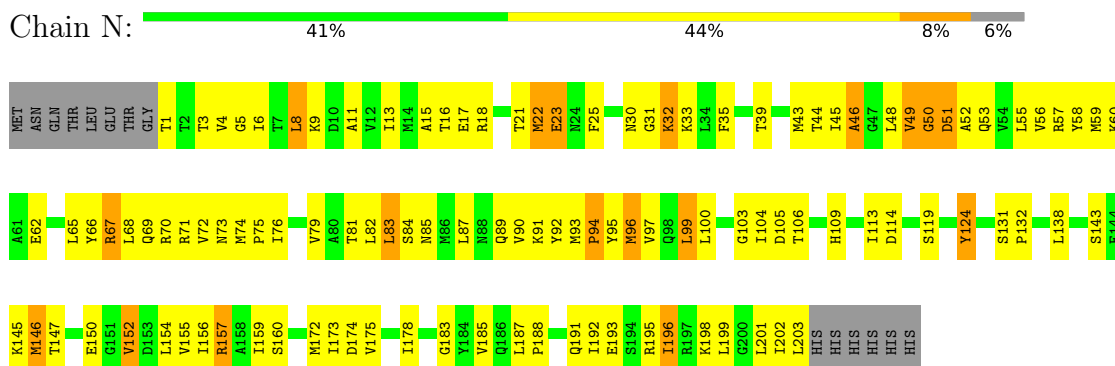


• Molecule 2: Proteasome subunit beta

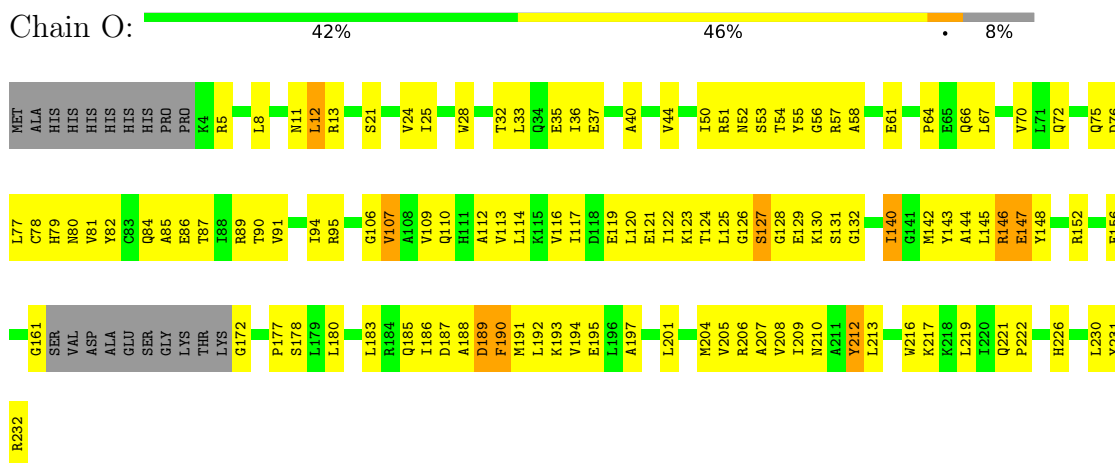
Chain M: 2% 41% 45% 7% 6%



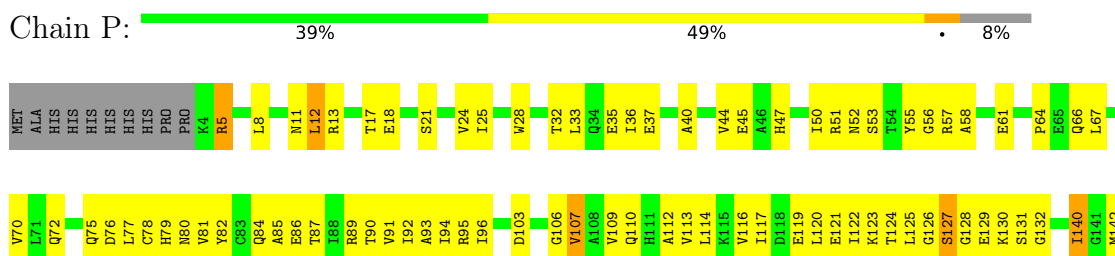
• Molecule 2: Proteasome subunit beta

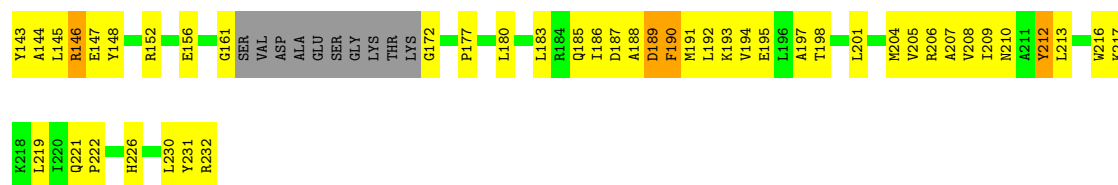


• Molecule 3: Proteasome activator PA26, Proteasome-activating nucleotidase fusion protein



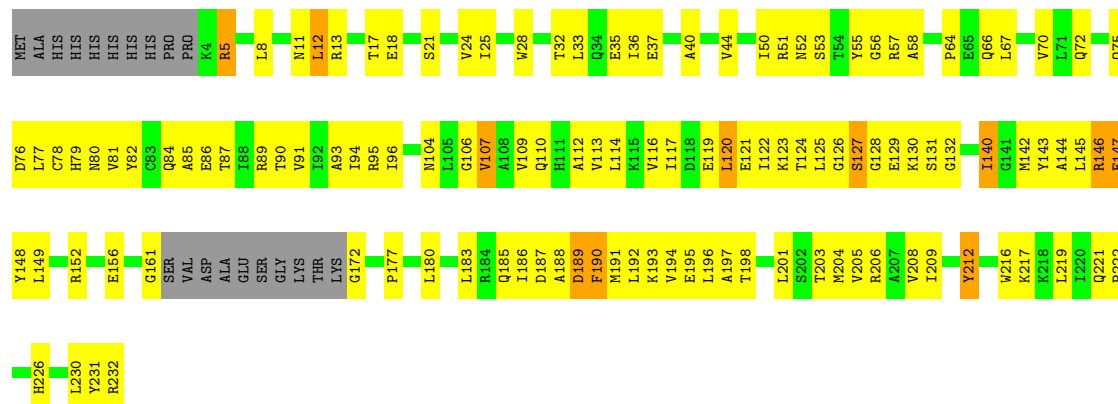
• Molecule 3: Proteasome activator PA26, Proteasome-activating nucleotidase fusion protein





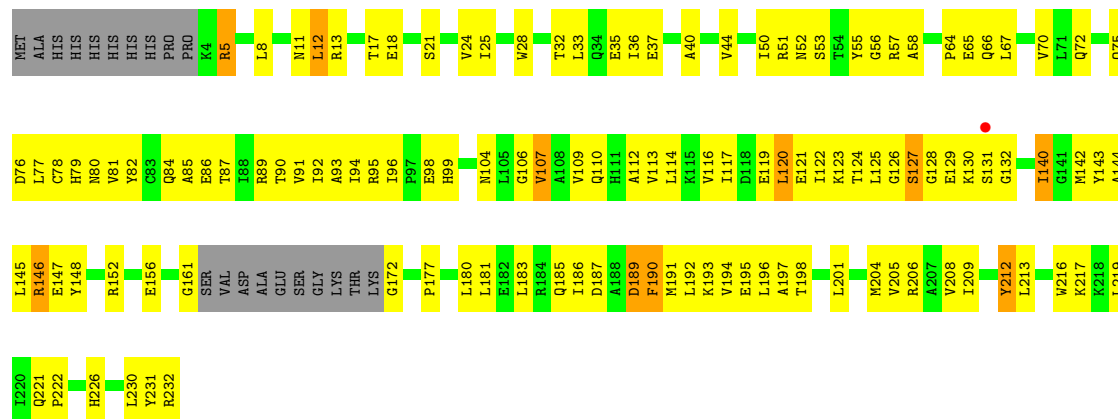
- Molecule 3: Proteasome activator PA26, Proteasome-activating nucleotidase fusion protein

Chain Q: 41% 46% 5% 8%



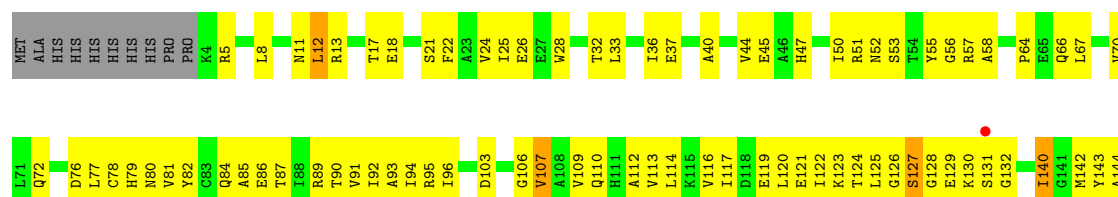
- Molecule 3: Proteasome activator PA26, Proteasome-activating nucleotidase fusion protein

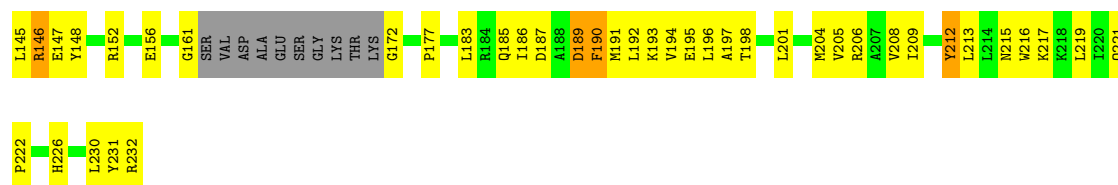
Chain R: 40% 48% 8%



- Molecule 3: Proteasome activator PA26, Proteasome-activating nucleotidase fusion protein

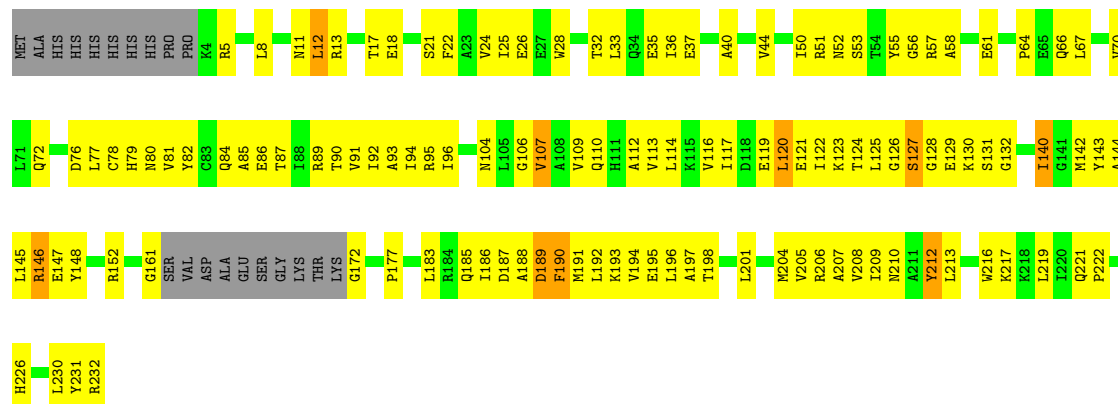
Chain S: 41% 48% 8%





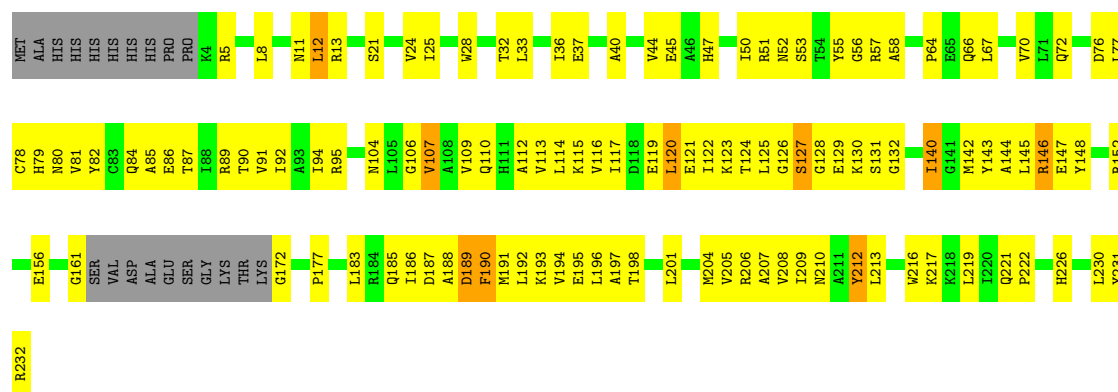
- Molecule 3: Proteasome activator PA26, Proteasome-activating nucleotidase fusion protein

Chain T: 40% 48% 8%



- Molecule 3: Proteasome activator PA26, Proteasome-activating nucleotidase fusion protein

Chain U: 42% 46% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 2 2	Depositor
Cell constants a, b, c, α , β , γ	166.89Å 166.89Å 412.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	89.51 – 4.00 89.51 – 4.00	Depositor EDS
% Data completeness (in resolution range)	98.4 (89.51-4.00) 97.4 (89.51-4.00)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 4.01Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.249 , 0.284 0.253 , 0.251	Depositor DCC
R_{free} test set	2470 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	97.4	Xtriage
Anisotropy	0.132	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 69.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	35133	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.44	0/1793	0.64	0/2416
1	B	0.45	0/1793	0.64	0/2416
1	C	0.44	0/1793	0.63	0/2416
1	D	0.43	0/1793	0.64	0/2416
1	E	0.43	0/1793	0.64	0/2416
1	F	0.43	0/1793	0.63	0/2416
1	G	0.44	0/1793	0.64	0/2416
2	H	0.45	0/1576	0.66	0/2129
2	I	0.44	0/1576	0.65	0/2129
2	J	0.44	0/1576	0.65	0/2129
2	K	0.43	0/1576	0.66	0/2129
2	L	0.44	0/1576	0.66	0/2129
2	M	0.43	0/1576	0.65	0/2129
2	N	0.44	0/1576	0.66	1/2129 (0.0%)
3	O	0.39	0/1717	0.58	0/2321
3	P	0.38	0/1717	0.57	0/2321
3	Q	0.39	0/1717	0.58	0/2321
3	R	0.40	0/1717	0.58	0/2321
3	S	0.41	0/1717	0.58	0/2321
3	T	0.41	0/1717	0.58	0/2321
3	U	0.38	0/1717	0.57	0/2321
All	All	0.42	0/35602	0.62	1/48062 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	17	GLU	N-CA-C	-5.04	97.39	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1769	0	1800	186	1
1	B	1769	0	1800	189	0
1	C	1769	0	1800	187	0
1	D	1769	0	1800	200	1
1	E	1769	0	1800	203	0
1	F	1769	0	1800	187	0
1	G	1769	0	1800	182	0
2	H	1557	0	1609	129	0
2	I	1557	0	1609	126	0
2	J	1557	0	1609	115	0
2	K	1557	0	1609	121	0
2	L	1557	0	1609	122	0
2	M	1557	0	1609	126	0
2	N	1557	0	1609	121	0
3	O	1693	0	1722	130	1
3	P	1693	0	1722	140	0
3	Q	1693	0	1722	138	0
3	R	1693	0	1722	152	1
3	S	1693	0	1722	146	0
3	T	1693	0	1722	154	0
3	U	1693	0	1722	141	0
All	All	35133	0	35917	2973	2

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 42.

The worst 5 of 2973 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)
2:N:39:THR:HB	2:N:73:ASN:HD21	1.11	1.15
2:M:39:THR:HB	2:M:73:ASN:HD21	1.08	1.14
2:K:39:THR:HB	2:K:73:ASN:HD21	1.10	1.13
2:I:39:THR:HB	2:I:73:ASN:HD21	1.11	1.13
2:L:39:THR:HB	2:L:73:ASN:HD21	1.12	1.10

All (2) 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	Interatomic distance (Å)	Clash overlap (Å)
1:D:178:ARG:NH2	3:O:54:THR:O[6_566]	2.07	0.13
1:A:204:GLY:O	3:R:65:GLU:OE1[6_556]	2.19	0.01

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	225/233 (97%)	168 (75%)	45 (20%)	12 (5%)	2	21
1	B	225/233 (97%)	169 (75%)	44 (20%)	12 (5%)	2	21
1	C	225/233 (97%)	169 (75%)	45 (20%)	11 (5%)	2	22
1	D	225/233 (97%)	171 (76%)	44 (20%)	10 (4%)	2	24
1	E	225/233 (97%)	169 (75%)	44 (20%)	12 (5%)	2	21
1	F	225/233 (97%)	169 (75%)	45 (20%)	11 (5%)	2	22
1	G	225/233 (97%)	169 (75%)	45 (20%)	11 (5%)	2	22
2	H	201/217 (93%)	154 (77%)	38 (19%)	9 (4%)	2	24
2	I	201/217 (93%)	153 (76%)	38 (19%)	10 (5%)	2	22
2	J	201/217 (93%)	153 (76%)	36 (18%)	12 (6%)	1	19
2	K	201/217 (93%)	154 (77%)	37 (18%)	10 (5%)	2	22
2	L	201/217 (93%)	154 (77%)	38 (19%)	9 (4%)	2	24
2	M	201/217 (93%)	155 (77%)	36 (18%)	10 (5%)	2	22
2	N	201/217 (93%)	153 (76%)	38 (19%)	10 (5%)	2	22
3	O	215/239 (90%)	168 (78%)	38 (18%)	9 (4%)	3	25
3	P	215/239 (90%)	167 (78%)	38 (18%)	10 (5%)	2	23
3	Q	215/239 (90%)	168 (78%)	37 (17%)	10 (5%)	2	23
3	R	215/239 (90%)	167 (78%)	38 (18%)	10 (5%)	2	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	S	215/239 (90%)	166 (77%)	40 (19%)	9 (4%)	3	25
3	T	215/239 (90%)	169 (79%)	37 (17%)	9 (4%)	3	25
3	U	215/239 (90%)	169 (79%)	36 (17%)	10 (5%)	2	23
All	All	4487/4823 (93%)	3434 (76%)	837 (19%)	216 (5%)	2	23

5 of 216 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	169	LYS
1	A	186	GLU
1	A	217	VAL
1	B	169	LYS
1	B	186	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	188/193 (97%)	176 (94%)	12 (6%)	17	45
1	B	188/193 (97%)	176 (94%)	12 (6%)	17	45
1	C	188/193 (97%)	176 (94%)	12 (6%)	17	45
1	D	188/193 (97%)	175 (93%)	13 (7%)	15	43
1	E	188/193 (97%)	175 (93%)	13 (7%)	15	43
1	F	188/193 (97%)	175 (93%)	13 (7%)	15	43
1	G	188/193 (97%)	175 (93%)	13 (7%)	15	43
2	H	170/183 (93%)	160 (94%)	10 (6%)	19	48
2	I	170/183 (93%)	160 (94%)	10 (6%)	19	48
2	J	170/183 (93%)	160 (94%)	10 (6%)	19	48
2	K	170/183 (93%)	160 (94%)	10 (6%)	19	48
2	L	170/183 (93%)	160 (94%)	10 (6%)	19	48
2	M	170/183 (93%)	160 (94%)	10 (6%)	19	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	N	170/183 (93%)	159 (94%)	11 (6%)	17	45
3	O	179/196 (91%)	173 (97%)	6 (3%)	37	61
3	P	179/196 (91%)	173 (97%)	6 (3%)	37	61
3	Q	179/196 (91%)	172 (96%)	7 (4%)	32	58
3	R	179/196 (91%)	172 (96%)	7 (4%)	32	58
3	S	179/196 (91%)	173 (97%)	6 (3%)	37	61
3	T	179/196 (91%)	172 (96%)	7 (4%)	32	58
3	U	179/196 (91%)	172 (96%)	7 (4%)	32	58
All	All	3759/4004 (94%)	3554 (94%)	205 (6%)	21	50

5 of 205 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	J	152	VAL
2	M	99	LEU
3	U	12	LEU
2	K	32	LYS
2	L	58	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
3	P	80	ASN
3	S	72	GLN
3	P	185	GLN
3	Q	200	HIS
3	S	111	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [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	227/233 (97%)	-0.23	1 (0%) 92 87	51, 89, 125, 148	2 (0%)
1	B	227/233 (97%)	-0.32	0 100 100	53, 88, 123, 148	2 (0%)
1	C	227/233 (97%)	-0.30	0 100 100	52, 88, 124, 146	2 (0%)
1	D	227/233 (97%)	-0.22	0 100 100	51, 87, 125, 147	2 (0%)
1	E	227/233 (97%)	-0.31	0 100 100	50, 88, 123, 147	2 (0%)
1	F	227/233 (97%)	-0.21	0 100 100	52, 87, 124, 146	1 (0%)
1	G	227/233 (97%)	-0.32	0 100 100	51, 88, 124, 146	1 (0%)
2	H	203/217 (93%)	-0.11	3 (1%) 73 64	48, 87, 111, 172	4 (1%)
2	I	203/217 (93%)	-0.27	1 (0%) 91 85	48, 87, 112, 171	3 (1%)
2	J	203/217 (93%)	-0.22	0 100 100	47, 87, 111, 172	4 (1%)
2	K	203/217 (93%)	-0.16	2 (0%) 82 74	49, 86, 111, 172	4 (1%)
2	L	203/217 (93%)	-0.25	0 100 100	48, 87, 112, 171	4 (1%)
2	M	203/217 (93%)	-0.14	4 (1%) 65 56	49, 87, 111, 172	3 (1%)
2	N	203/217 (93%)	-0.25	0 100 100	47, 87, 112, 172	4 (1%)
3	O	219/239 (91%)	-0.30	0 100 100	66, 97, 136, 174	0
3	P	219/239 (91%)	-0.34	0 100 100	65, 97, 135, 173	0
3	Q	219/239 (91%)	-0.33	0 100 100	65, 97, 135, 174	0
3	R	219/239 (91%)	-0.29	1 (0%) 91 85	66, 97, 136, 174	0
3	S	219/239 (91%)	-0.30	1 (0%) 91 85	65, 98, 137, 175	0
3	T	219/239 (91%)	-0.29	0 100 100	66, 98, 137, 174	0
3	U	219/239 (91%)	-0.37	0 100 100	64, 98, 137, 173	0
All	All	4543/4823 (94%)	-0.26	13 (0%) 94 90	47, 91, 128, 175	38 (0%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	M	202	ILE	3.1
1	A	206	GLU	2.9
2	M	201	LEU	2.8
2	H	5	GLY	2.7
2	H	201	LEU	2.6

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.