



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 23, 2017 – 11:53 PM EDT

PDB ID : 5LZP
EMDB ID: : EMD-4128
Title : Binding of the C-terminal GQYL motif of the bacterial proteasome activator
Bpa to the 20S proteasome
Authors : Bolten, M.; Delley, C.L.; Leibundgut, M.; Boehringer, D.; Ban, N.; Weber-
Ban, E.
Deposited on : unknown
Resolution : 3.45 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

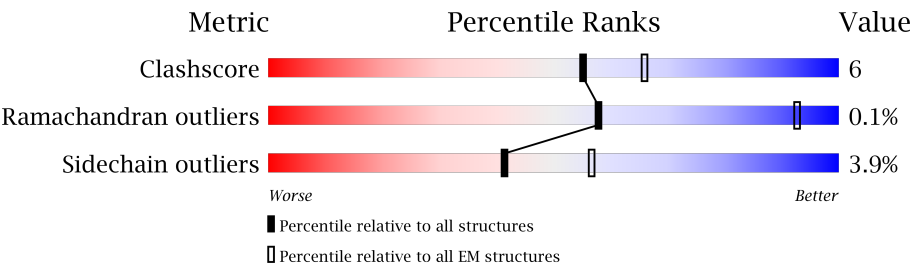
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.45 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.








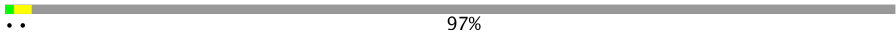
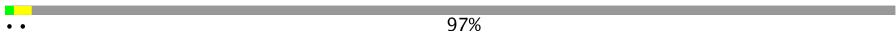
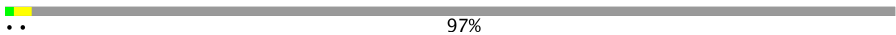
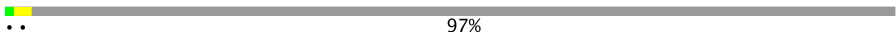
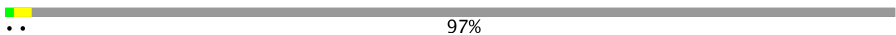
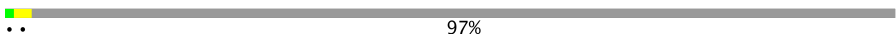
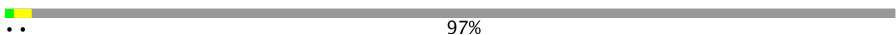













Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	0	241	<div><div>71%16%•11%</div></div>
1	2	241	<div><div>71%16%•11%</div></div>
1	4	241	<div><div>71%16%•11%</div></div>
1	6	241	<div><div>72%15%•11%</div></div>
1	8	241	<div><div>71%15%•11%</div></div>
1	B	241	<div><div>65%21%•11%</div></div>
1	D	241	<div><div>69%19%•10%</div></div>
1	H	241	<div><div>71%17%•11%</div></div>
1	J	241	<div><div>69%17%•11%</div></div>


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Mol	Chain	Length	Quality of chain
1	M	241	
1	Q	241	
1	S	241	
1	W	241	
1	Y	241	
2	1	180	
2	3	180	
2	5	180	
2	7	180	
2	V	180	
2	X	180	
2	Z	180	
3	A	242	
3	C	242	
3	E	242	
3	F	242	
3	G	242	
3	I	242	
3	K	242	
3	L	242	
3	N	242	
3	O	242	
3	P	242	
3	R	242	
3	T	242	

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Mol	Chain	Length	Quality of chain
3	U	242	 86%5% • 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 46557 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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					AltConf	Trace
1	0	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	2	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	4	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	6	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	8	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	B	214	Total	C	N	O	S	0	0
			1650	1033	302	312	3		
1	D	217	Total	C	N	O	S	0	0
			1668	1044	305	316	3		
1	H	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	J	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	M	214	Total	C	N	O	S	0	0
			1650	1033	302	312	3		
1	Q	214	Total	C	N	O	S	0	0
			1650	1033	302	312	3		
1	S	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	W	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	Y	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		

- Molecule 2 is a protein called Bacterial proteasome activator.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	5	Total	C	N	O	0	0
			39	25	6	8		

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	5	Total	C	N	O	0	0
			39	25	6	8		
2	5	5	Total	C	N	O	0	0
			39	25	6	8		
2	7	5	Total	C	N	O	0	0
			39	25	6	8		
2	V	5	Total	C	N	O	0	0
			39	25	6	8		
2	X	5	Total	C	N	O	0	0
			39	25	6	8		
2	Z	5	Total	C	N	O	0	0
			39	25	6	8		

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	-5	MET	-	initiating methionine	UNP P9WKX3
1	-4	HIS	-	expression tag	UNP P9WKX3
1	-3	HIS	-	expression tag	UNP P9WKX3
1	-2	HIS	-	expression tag	UNP P9WKX3
1	-1	HIS	-	expression tag	UNP P9WKX3
1	0	HIS	-	expression tag	UNP P9WKX3
1	1	HIS	-	expression tag	UNP P9WKX3
3	-5	MET	-	initiating methionine	UNP P9WKX3
3	-4	HIS	-	expression tag	UNP P9WKX3
3	-3	HIS	-	expression tag	UNP P9WKX3
3	-2	HIS	-	expression tag	UNP P9WKX3
3	-1	HIS	-	expression tag	UNP P9WKX3
3	0	HIS	-	expression tag	UNP P9WKX3
3	1	HIS	-	expression tag	UNP P9WKX3
5	-5	MET	-	initiating methionine	UNP P9WKX3
5	-4	HIS	-	expression tag	UNP P9WKX3
5	-3	HIS	-	expression tag	UNP P9WKX3
5	-2	HIS	-	expression tag	UNP P9WKX3
5	-1	HIS	-	expression tag	UNP P9WKX3
5	0	HIS	-	expression tag	UNP P9WKX3
5	1	HIS	-	expression tag	UNP P9WKX3
7	-5	MET	-	initiating methionine	UNP P9WKX3
7	-4	HIS	-	expression tag	UNP P9WKX3
7	-3	HIS	-	expression tag	UNP P9WKX3
7	-2	HIS	-	expression tag	UNP P9WKX3
7	-1	HIS	-	expression tag	UNP P9WKX3
7	0	HIS	-	expression tag	UNP P9WKX3

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Chain	Residue	Modelled	Actual	Comment	Reference
7	1	HIS	-	expression tag	UNP P9WKX3
V	-5	MET	-	initiating methionine	UNP P9WKX3
V	-4	HIS	-	expression tag	UNP P9WKX3
V	-3	HIS	-	expression tag	UNP P9WKX3
V	-2	HIS	-	expression tag	UNP P9WKX3
V	-1	HIS	-	expression tag	UNP P9WKX3
V	0	HIS	-	expression tag	UNP P9WKX3
V	1	HIS	-	expression tag	UNP P9WKX3
X	-5	MET	-	initiating methionine	UNP P9WKX3
X	-4	HIS	-	expression tag	UNP P9WKX3
X	-3	HIS	-	expression tag	UNP P9WKX3
X	-2	HIS	-	expression tag	UNP P9WKX3
X	-1	HIS	-	expression tag	UNP P9WKX3
X	0	HIS	-	expression tag	UNP P9WKX3
X	1	HIS	-	expression tag	UNP P9WKX3
Z	-5	MET	-	initiating methionine	UNP P9WKX3
Z	-4	HIS	-	expression tag	UNP P9WKX3
Z	-3	HIS	-	expression tag	UNP P9WKX3
Z	-2	HIS	-	expression tag	UNP P9WKX3
Z	-1	HIS	-	expression tag	UNP P9WKX3
Z	0	HIS	-	expression tag	UNP P9WKX3
Z	1	HIS	-	expression tag	UNP P9WKX3

- Molecule 3 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	222	Total	C	N	O	S	0	0
			1636	1026	282	323	5		
3	C	223	Total	C	N	O	S	0	0
			1640	1028	283	324	5		
3	E	222	Total	C	N	O	S	0	0
			1636	1026	282	323	5		
3	F	222	Total	C	N	O	S	0	0
			1636	1026	282	323	5		
3	G	222	Total	C	N	O	S	0	0
			1636	1026	282	323	5		
3	I	223	Total	C	N	O	S	0	0
			1640	1028	283	324	5		
3	K	222	Total	C	N	O	S	0	0
			1636	1026	282	323	5		
3	L	222	Total	C	N	O	S	0	0
			1636	1026	282	323	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	234	Total	C	N	O	S	0	0
			1715	1072	295	343	5		
3	O	223	Total	C	N	O	S	0	0
			1640	1028	283	324	5		
3	P	234	Total	C	N	O	S	0	0
			1715	1072	295	343	5		
3	R	223	Total	C	N	O	S	0	0
			1640	1028	283	324	5		
3	T	223	Total	C	N	O	S	0	0
			1640	1028	283	324	5		
3	U	223	Total	C	N	O	S	0	0
			1640	1028	283	324	5		

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	301	ALA	-	expression tag	UNP P9WHT9
A	535	TRP	-	expression tag	UNP P9WHT9
A	536	SER	-	expression tag	UNP P9WHT9
A	537	HIS	-	expression tag	UNP P9WHT9
A	538	PRO	-	expression tag	UNP P9WHT9
A	539	GLN	-	expression tag	UNP P9WHT9
A	540	PHE	-	expression tag	UNP P9WHT9
A	541	GLU	-	expression tag	UNP P9WHT9
A	542	LYS	-	expression tag	UNP P9WHT9
C	301	ALA	-	expression tag	UNP P9WHT9
C	535	TRP	-	expression tag	UNP P9WHT9
C	536	SER	-	expression tag	UNP P9WHT9
C	537	HIS	-	expression tag	UNP P9WHT9
C	538	PRO	-	expression tag	UNP P9WHT9
C	539	GLN	-	expression tag	UNP P9WHT9
C	540	PHE	-	expression tag	UNP P9WHT9
C	541	GLU	-	expression tag	UNP P9WHT9
C	542	LYS	-	expression tag	UNP P9WHT9
E	301	ALA	-	expression tag	UNP P9WHT9
E	535	TRP	-	expression tag	UNP P9WHT9
E	536	SER	-	expression tag	UNP P9WHT9
E	537	HIS	-	expression tag	UNP P9WHT9
E	538	PRO	-	expression tag	UNP P9WHT9
E	539	GLN	-	expression tag	UNP P9WHT9
E	540	PHE	-	expression tag	UNP P9WHT9
E	541	GLU	-	expression tag	UNP P9WHT9
E	542	LYS	-	expression tag	UNP P9WHT9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	301	ALA	-	expression tag	UNP P9WHT9
F	535	TRP	-	expression tag	UNP P9WHT9
F	536	SER	-	expression tag	UNP P9WHT9
F	537	HIS	-	expression tag	UNP P9WHT9
F	538	PRO	-	expression tag	UNP P9WHT9
F	539	GLN	-	expression tag	UNP P9WHT9
F	540	PHE	-	expression tag	UNP P9WHT9
F	541	GLU	-	expression tag	UNP P9WHT9
F	542	LYS	-	expression tag	UNP P9WHT9
G	301	ALA	-	expression tag	UNP P9WHT9
G	535	TRP	-	expression tag	UNP P9WHT9
G	536	SER	-	expression tag	UNP P9WHT9
G	537	HIS	-	expression tag	UNP P9WHT9
G	538	PRO	-	expression tag	UNP P9WHT9
G	539	GLN	-	expression tag	UNP P9WHT9
G	540	PHE	-	expression tag	UNP P9WHT9
G	541	GLU	-	expression tag	UNP P9WHT9
G	542	LYS	-	expression tag	UNP P9WHT9
I	301	ALA	-	expression tag	UNP P9WHT9
I	535	TRP	-	expression tag	UNP P9WHT9
I	536	SER	-	expression tag	UNP P9WHT9
I	537	HIS	-	expression tag	UNP P9WHT9
I	538	PRO	-	expression tag	UNP P9WHT9
I	539	GLN	-	expression tag	UNP P9WHT9
I	540	PHE	-	expression tag	UNP P9WHT9
I	541	GLU	-	expression tag	UNP P9WHT9
I	542	LYS	-	expression tag	UNP P9WHT9
K	301	ALA	-	expression tag	UNP P9WHT9
K	535	TRP	-	expression tag	UNP P9WHT9
K	536	SER	-	expression tag	UNP P9WHT9
K	537	HIS	-	expression tag	UNP P9WHT9
K	538	PRO	-	expression tag	UNP P9WHT9
K	539	GLN	-	expression tag	UNP P9WHT9
K	540	PHE	-	expression tag	UNP P9WHT9
K	541	GLU	-	expression tag	UNP P9WHT9
K	542	LYS	-	expression tag	UNP P9WHT9
L	301	ALA	-	expression tag	UNP P9WHT9
L	535	TRP	-	expression tag	UNP P9WHT9
L	536	SER	-	expression tag	UNP P9WHT9
L	537	HIS	-	expression tag	UNP P9WHT9
L	538	PRO	-	expression tag	UNP P9WHT9
L	539	GLN	-	expression tag	UNP P9WHT9

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Chain	Residue	Modelled	Actual	Comment	Reference
L	540	PHE	-	expression tag	UNP P9WHT9
L	541	GLU	-	expression tag	UNP P9WHT9
L	542	LYS	-	expression tag	UNP P9WHT9
N	301	ALA	-	expression tag	UNP P9WHT9
N	535	TRP	-	expression tag	UNP P9WHT9
N	536	SER	-	expression tag	UNP P9WHT9
N	537	HIS	-	expression tag	UNP P9WHT9
N	538	PRO	-	expression tag	UNP P9WHT9
N	539	GLN	-	expression tag	UNP P9WHT9
N	540	PHE	-	expression tag	UNP P9WHT9
N	541	GLU	-	expression tag	UNP P9WHT9
N	542	LYS	-	expression tag	UNP P9WHT9
O	301	ALA	-	expression tag	UNP P9WHT9
O	535	TRP	-	expression tag	UNP P9WHT9
O	536	SER	-	expression tag	UNP P9WHT9
O	537	HIS	-	expression tag	UNP P9WHT9
O	538	PRO	-	expression tag	UNP P9WHT9
O	539	GLN	-	expression tag	UNP P9WHT9
O	540	PHE	-	expression tag	UNP P9WHT9
O	541	GLU	-	expression tag	UNP P9WHT9
O	542	LYS	-	expression tag	UNP P9WHT9
P	301	ALA	-	expression tag	UNP P9WHT9
P	535	TRP	-	expression tag	UNP P9WHT9
P	536	SER	-	expression tag	UNP P9WHT9
P	537	HIS	-	expression tag	UNP P9WHT9
P	538	PRO	-	expression tag	UNP P9WHT9
P	539	GLN	-	expression tag	UNP P9WHT9
P	540	PHE	-	expression tag	UNP P9WHT9
P	541	GLU	-	expression tag	UNP P9WHT9
P	542	LYS	-	expression tag	UNP P9WHT9
R	301	ALA	-	expression tag	UNP P9WHT9
R	535	TRP	-	expression tag	UNP P9WHT9
R	536	SER	-	expression tag	UNP P9WHT9
R	537	HIS	-	expression tag	UNP P9WHT9
R	538	PRO	-	expression tag	UNP P9WHT9
R	539	GLN	-	expression tag	UNP P9WHT9
R	540	PHE	-	expression tag	UNP P9WHT9
R	541	GLU	-	expression tag	UNP P9WHT9
R	542	LYS	-	expression tag	UNP P9WHT9
T	301	ALA	-	expression tag	UNP P9WHT9
T	535	TRP	-	expression tag	UNP P9WHT9
T	536	SER	-	expression tag	UNP P9WHT9

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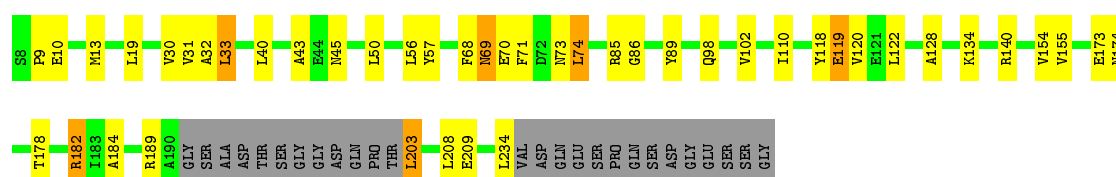
Chain	Residue	Modelled	Actual	Comment	Reference
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T	538	PRO	-	expression tag	UNP P9WHT9
T	539	GLN	-	expression tag	UNP P9WHT9
T	540	PHE	-	expression tag	UNP P9WHT9
T	541	GLU	-	expression tag	UNP P9WHT9
T	542	LYS	-	expression tag	UNP P9WHT9
U	301	ALA	-	expression tag	UNP P9WHT9
U	535	TRP	-	expression tag	UNP P9WHT9
U	536	SER	-	expression tag	UNP P9WHT9
U	537	HIS	-	expression tag	UNP P9WHT9
U	538	PRO	-	expression tag	UNP P9WHT9
U	539	GLN	-	expression tag	UNP P9WHT9
U	540	PHE	-	expression tag	UNP P9WHT9
U	541	GLU	-	expression tag	UNP P9WHT9
U	542	LYS	-	expression tag	UNP P9WHT9

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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

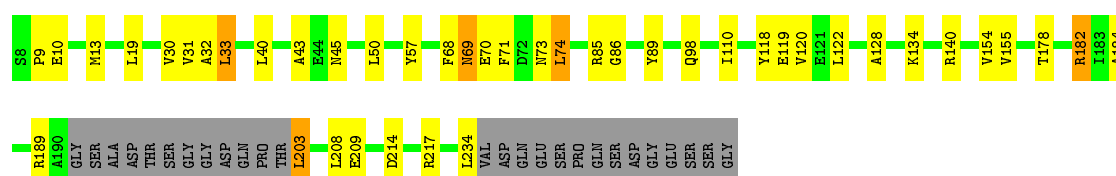
- Molecule 1: Proteasome subunit alpha

Chain 0: 



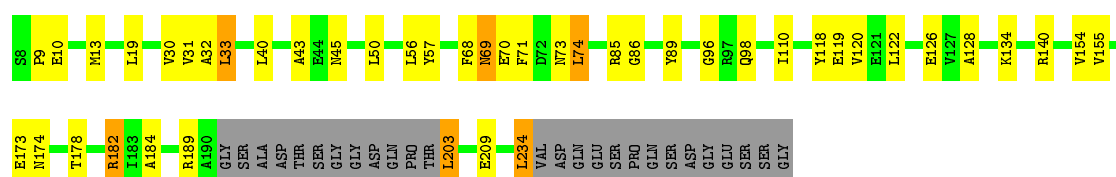
- Molecule 1: Proteasome subunit alpha

Chain 2: 



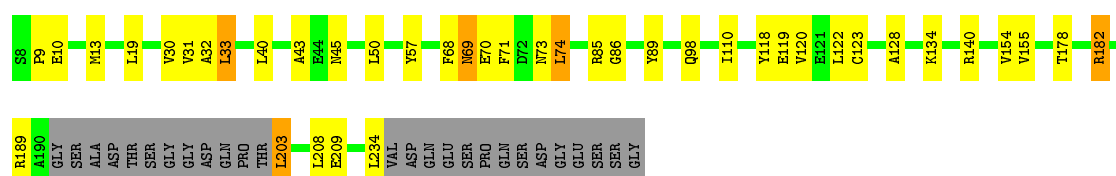
- Molecule 1: Proteasome subunit alpha

Chain 4: 



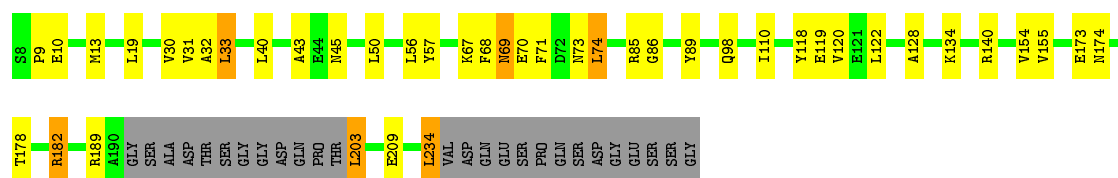
- Molecule 1: Proteasome subunit alpha

Chain 6: 



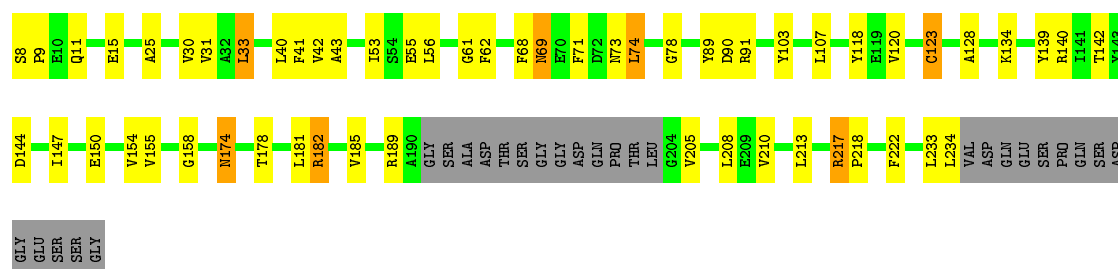
- Molecule 1: Proteasome subunit alpha

Chain 8:  71% 15% 11%



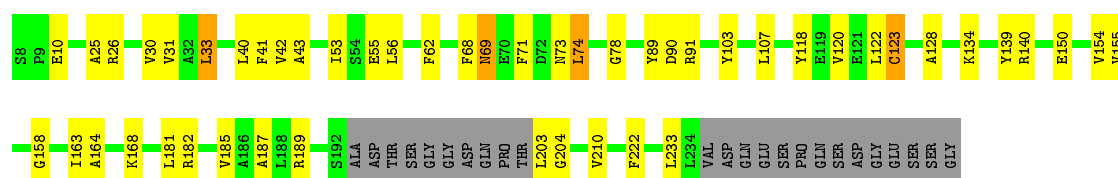
• Molecule 1: Proteasome subunit alpha

Chain B:  65% 21% 11%



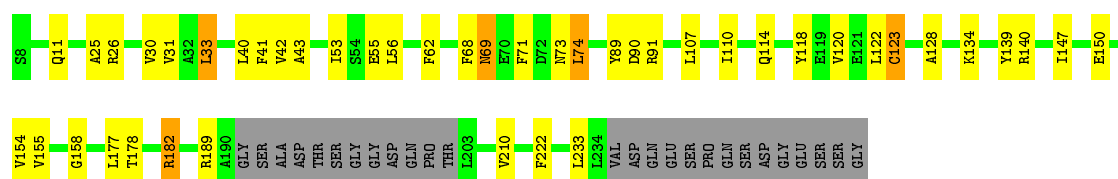
• Molecule 1: Proteasome subunit alpha

Chain D:  69% 19% 10%



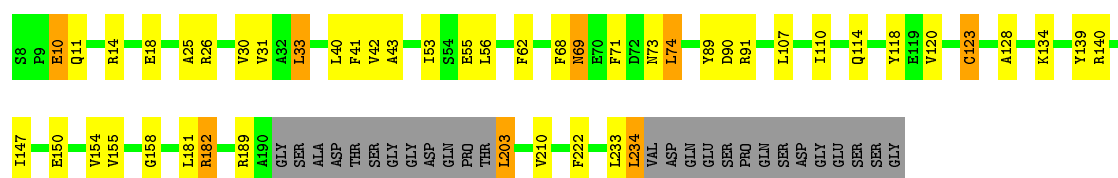
• Molecule 1: Proteasome subunit alpha

Chain H:  71% 17% 11%

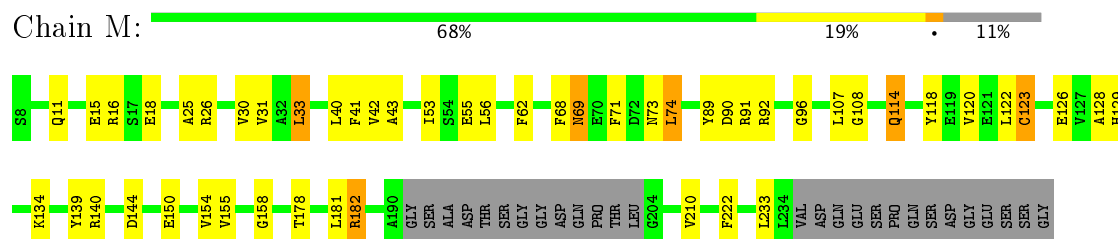


• Molecule 1: Proteasome subunit alpha

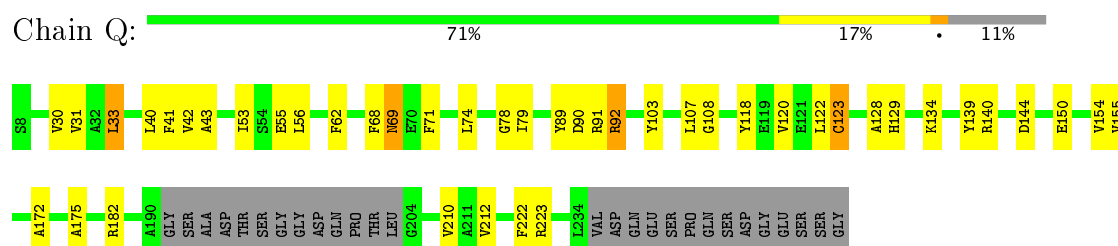
Chain J:  69% 17% 11%



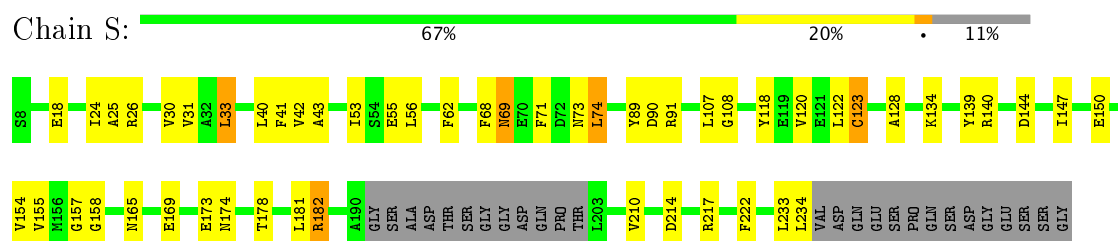
- Molecule 1: Proteasome subunit alpha



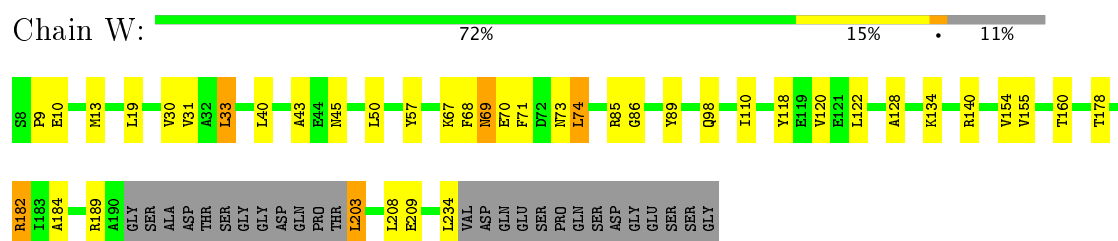
- Molecule 1: Proteasome subunit alpha



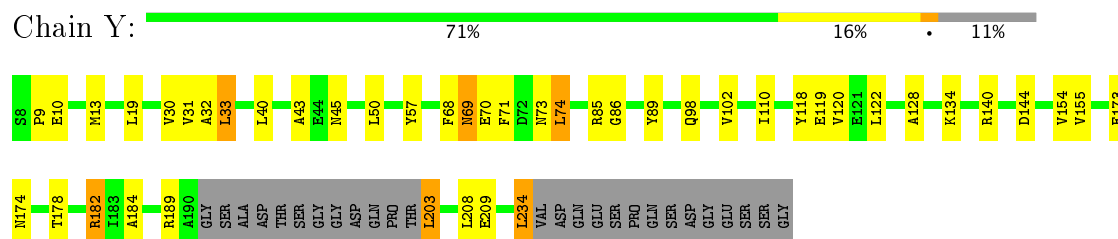
- Molecule 1: Proteasome subunit alpha



- Molecule 1: Proteasome subunit alpha



- Molecule 1: Proteasome subunit alpha



- Molecule 2: Bacterial proteasome activator

Chain 1: ..

97%

[illegible]


- Molecule 2: Bacterial proteasome activator

Chain 3: ..

97%

[illegible]

- Molecule 2: Bacterial proteasome activator

Chain 5: 

97%

[illegible]


- Molecule 2: Bacterial proteasome activator

Chain 7:

97%

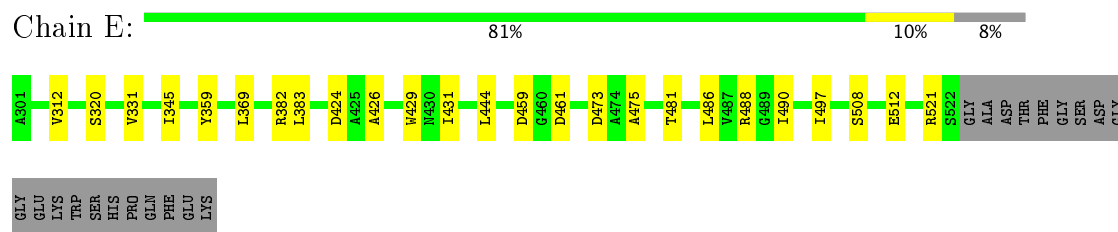
[illegible]

- Molecule 2: Bacterial proteasome activator

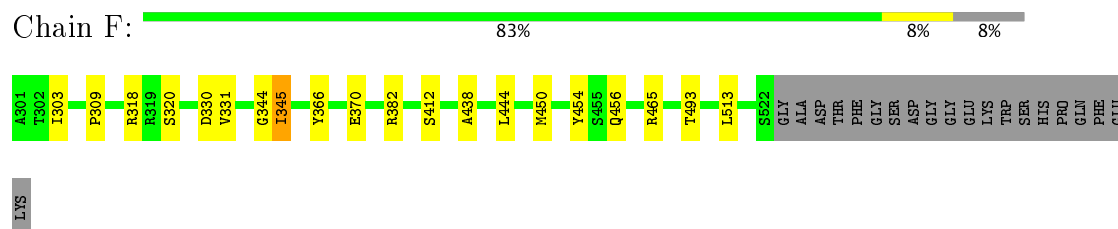
Chain V: 

97%

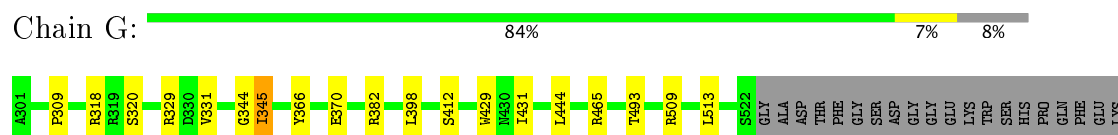


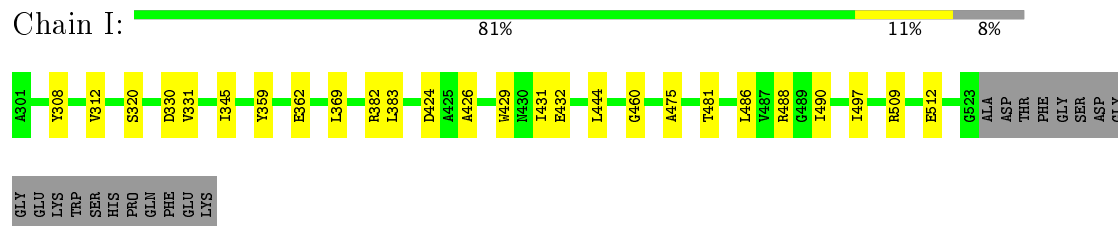
- Molecule 3: Proteasome subunit beta



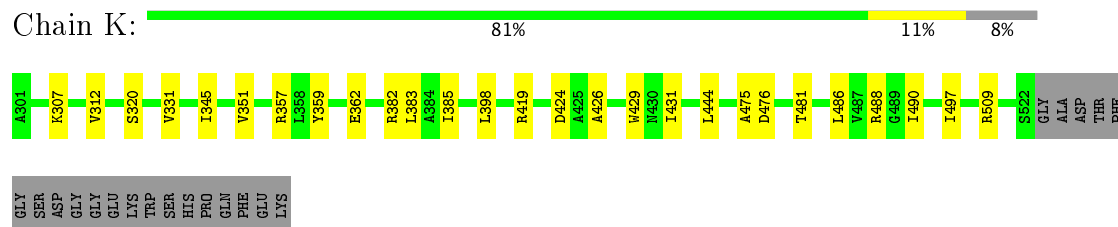
- Molecule 3: Proteasome subunit beta



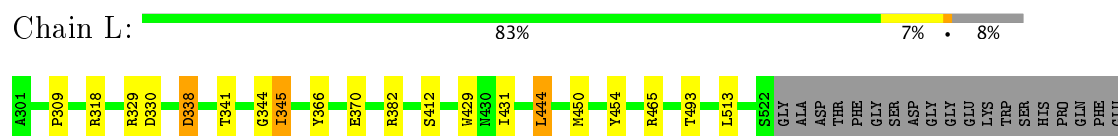
- Molecule 3: Proteasome subunit beta



- Molecule 3: Proteasome subunit beta




- Molecule 3: Proteasome subunit beta


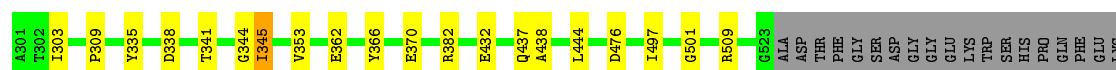


LYS

- Molecule 3: Proteasome subunit beta

Chain N:  84% 12%GLN
PHE
GLU
LYS


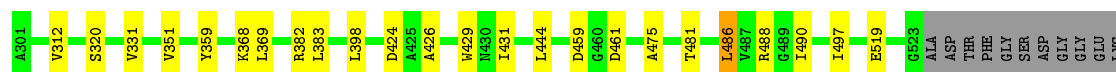
- Molecule 3: Proteasome subunit beta

Chain O:  84% 8% 8%


- Molecule 3: Proteasome subunit beta

Chain P:  90% 7%


- Molecule 3: Proteasome subunit beta

Chain R:  82% 10% 8%TRP
SER
HIS
PRO
GLN
PHE
GLU
LYS

- Molecule 3: Proteasome subunit beta

Chain T:  81% 11% 8%ASP
GLY
GLY
GLU
LYS
TRP
SER
HIS
PRO
GLN
PHE
GLU
LYS

- Molecule 3: Proteasome subunit beta

Chain U:  86% 5% 8%

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C7	Depositor
Number of particles used	48799	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3600	Depositor
Magnification	100000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

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 >2	RMSZ	# Z >2
1	0	0.39	0/1683	0.57	0/2274
1	2	0.39	0/1683	0.57	0/2274
1	4	0.39	0/1683	0.57	0/2274
1	6	0.39	0/1683	0.56	0/2274
1	8	0.39	0/1683	0.57	0/2274
1	B	0.36	0/1675	0.53	0/2263
1	D	0.35	0/1693	0.51	0/2287
1	H	0.35	0/1683	0.53	0/2274
1	J	0.37	0/1683	0.53	0/2274
1	M	0.36	0/1675	0.52	0/2263
1	Q	0.35	0/1675	0.52	0/2263
1	S	0.38	0/1683	0.54	0/2274
1	W	0.39	0/1683	0.57	0/2274
1	Y	0.41	0/1683	0.57	0/2274
2	1	0.78	0/39	1.18	0/50
2	3	0.74	0/39	1.07	0/50
2	5	0.62	0/39	0.99	0/50
2	7	0.65	0/39	1.00	0/50
2	V	0.68	0/39	1.14	0/50
2	X	0.70	0/39	1.13	0/50
2	Z	0.77	0/39	1.17	0/50
3	A	0.38	0/1660	0.58	0/2251
3	C	0.39	0/1664	0.58	0/2256
3	E	0.40	0/1660	0.58	0/2251
3	F	0.38	0/1660	0.57	0/2251
3	G	0.39	0/1660	0.58	0/2251
3	I	0.39	0/1664	0.59	0/2256
3	K	0.39	0/1660	0.58	0/2251
3	L	0.38	0/1660	0.58	0/2251
3	N	0.40	0/1740	0.58	0/2357
3	O	0.39	0/1664	0.58	0/2256
3	P	0.38	0/1740	0.56	0/2357
3	R	0.39	0/1664	0.60	0/2256
3	T	0.40	0/1664	0.59	0/2256

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
3	U	0.38	0/1664	0.57	0/2256
All	All	0.39	0/47245	0.57	0/63922

There are no bond length outliers.

There are no bond angle outliers.

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	0	1658	0	1659	33	0
1	2	1658	0	1659	31	0
1	4	1658	0	1659	33	0
1	6	1658	0	1659	28	0
1	8	1658	0	1659	33	0
1	B	1650	0	1648	35	0
1	D	1668	0	1667	27	0
1	H	1658	0	1659	24	0
1	J	1658	0	1659	27	0
1	M	1650	0	1648	31	0
1	Q	1650	0	1648	26	0
1	S	1658	0	1659	30	0
1	W	1658	0	1659	33	0
1	Y	1658	0	1659	34	0
2	1	39	0	32	5	0
2	3	39	0	32	5	0
2	5	39	0	32	5	0
2	7	39	0	32	5	0
2	V	39	0	32	7	0
2	X	39	0	32	5	0
2	Z	39	0	32	5	0
3	A	1636	0	1628	10	0
3	C	1640	0	1631	16	0
3	E	1636	0	1628	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	1636	0	1628	11	0
3	G	1636	0	1628	9	0
3	I	1640	0	1631	13	0
3	K	1636	0	1628	15	0
3	L	1636	0	1628	11	0
3	N	1715	0	1693	18	0
3	O	1640	0	1631	12	0
3	P	1715	0	1693	7	0
3	R	1640	0	1631	13	0
3	T	1640	0	1631	17	0
3	U	1640	0	1631	6	0
All	All	46557	0	46365	565	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 565 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)
2:5:170:THR:N	1:8:13:MET:SD	2.46	0.89
2:3:170:THR:N	1:6:13:MET:SD	2.47	0.87
2:V:170:THR:N	1:Y:13:MET:SD	2.48	0.86
2:1:170:THR:N	1:4:13:MET:SD	2.48	0.86
2:7:170:THR:N	1:W:13:MET:SD	2.51	0.84

There are no symmetry-related clashes.

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 PDB entries followed by that with respect to all EM entries.

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	0	211/241 (88%)	202 (96%)	9 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	211/241 (88%)	203 (96%)	8 (4%)	0	100	100
1	4	211/241 (88%)	203 (96%)	8 (4%)	0	100	100
1	6	211/241 (88%)	203 (96%)	8 (4%)	0	100	100
1	8	211/241 (88%)	202 (96%)	9 (4%)	0	100	100
1	B	210/241 (87%)	203 (97%)	7 (3%)	0	100	100
1	D	213/241 (88%)	205 (96%)	8 (4%)	0	100	100
1	H	211/241 (88%)	205 (97%)	6 (3%)	0	100	100
1	J	211/241 (88%)	204 (97%)	7 (3%)	0	100	100
1	M	210/241 (87%)	202 (96%)	8 (4%)	0	100	100
1	Q	210/241 (87%)	204 (97%)	6 (3%)	0	100	100
1	S	211/241 (88%)	204 (97%)	7 (3%)	0	100	100
1	W	211/241 (88%)	201 (95%)	10 (5%)	0	100	100
1	Y	211/241 (88%)	201 (95%)	10 (5%)	0	100	100
2	1	3/180 (2%)	3 (100%)	0	0	100	100
2	3	3/180 (2%)	3 (100%)	0	0	100	100
2	5	3/180 (2%)	3 (100%)	0	0	100	100
2	7	3/180 (2%)	2 (67%)	1 (33%)	0	100	100
2	V	3/180 (2%)	3 (100%)	0	0	100	100
2	X	3/180 (2%)	3 (100%)	0	0	100	100
2	Z	3/180 (2%)	3 (100%)	0	0	100	100
3	A	220/242 (91%)	211 (96%)	8 (4%)	1 (0%)	32	73
3	C	221/242 (91%)	211 (96%)	10 (4%)	0	100	100
3	E	220/242 (91%)	209 (95%)	11 (5%)	0	100	100
3	F	220/242 (91%)	211 (96%)	8 (4%)	1 (0%)	32	73
3	G	220/242 (91%)	212 (96%)	7 (3%)	1 (0%)	32	73
3	I	221/242 (91%)	210 (95%)	11 (5%)	0	100	100
3	K	220/242 (91%)	210 (96%)	10 (4%)	0	100	100
3	L	220/242 (91%)	213 (97%)	6 (3%)	1 (0%)	32	73
3	N	232/242 (96%)	221 (95%)	11 (5%)	0	100	100
3	O	221/242 (91%)	214 (97%)	6 (3%)	1 (0%)	32	73
3	P	232/242 (96%)	225 (97%)	6 (3%)	1 (0%)	38	77

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	R	221/242 (91%)	210 (95%)	11 (5%)	0	100	100
3	T	221/242 (91%)	210 (95%)	11 (5%)	0	100	100
3	U	221/242 (91%)	214 (97%)	6 (3%)	1 (0%)	32	73
All	All	6084/8022 (76%)	5843 (96%)	234 (4%)	7 (0%)	58	88

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	P	309	PRO
3	U	309	PRO
3	F	309	PRO
3	G	309	PRO
3	L	309	PRO

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 PDB entries followed by that with respect to all EM entries.

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	0	165/185 (89%)	156 (94%)	9 (6%)	25	62
1	2	165/185 (89%)	156 (94%)	9 (6%)	25	62
1	4	165/185 (89%)	156 (94%)	9 (6%)	25	62
1	6	165/185 (89%)	155 (94%)	10 (6%)	22	59
1	8	165/185 (89%)	156 (94%)	9 (6%)	25	62
1	B	164/185 (89%)	154 (94%)	10 (6%)	22	59
1	D	166/185 (90%)	158 (95%)	8 (5%)	30	66
1	H	165/185 (89%)	155 (94%)	10 (6%)	22	59
1	J	165/185 (89%)	154 (93%)	11 (7%)	19	57
1	M	164/185 (89%)	156 (95%)	8 (5%)	29	65
1	Q	164/185 (89%)	159 (97%)	5 (3%)	46	78
1	S	165/185 (89%)	156 (94%)	9 (6%)	25	62
1	W	165/185 (89%)	157 (95%)	8 (5%)	30	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Y	165/185 (89%)	156 (94%)	9 (6%)	25	62
2	1	3/147 (2%)	3 (100%)	0	100	100
2	3	3/147 (2%)	3 (100%)	0	100	100
2	5	3/147 (2%)	3 (100%)	0	100	100
2	7	3/147 (2%)	3 (100%)	0	100	100
2	V	3/147 (2%)	3 (100%)	0	100	100
2	X	3/147 (2%)	3 (100%)	0	100	100
2	Z	3/147 (2%)	3 (100%)	0	100	100
3	A	164/179 (92%)	161 (98%)	3 (2%)	64	86
3	C	164/179 (92%)	158 (96%)	6 (4%)	39	73
3	E	164/179 (92%)	161 (98%)	3 (2%)	64	86
3	F	164/179 (92%)	160 (98%)	4 (2%)	54	82
3	G	164/179 (92%)	160 (98%)	4 (2%)	54	82
3	I	164/179 (92%)	159 (97%)	5 (3%)	46	78
3	K	164/179 (92%)	160 (98%)	4 (2%)	54	82
3	L	164/179 (92%)	159 (97%)	5 (3%)	46	78
3	N	171/179 (96%)	166 (97%)	5 (3%)	48	79
3	O	164/179 (92%)	161 (98%)	3 (2%)	64	86
3	P	171/179 (96%)	167 (98%)	4 (2%)	56	82
3	R	164/179 (92%)	161 (98%)	3 (2%)	64	86
3	T	164/179 (92%)	161 (98%)	3 (2%)	64	86
3	U	164/179 (92%)	158 (96%)	6 (4%)	39	73
All	All	4639/6125 (76%)	4457 (96%)	182 (4%)	41	72

5 of 182 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	444	LEU
1	J	33	LEU
1	W	73	ASN
1	H	11	GLN
1	H	182	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	114	GLN
3	I	456	GLN
1	W	80	GLN
3	E	456	GLN
1	H	80	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates 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.