



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 09:28 PM UTC

PDB ID : 8CVT / pdb_00008cvt
EMDB ID : EMD-27018
Title : Human 19S-20S proteasome, state SD2
Authors : Zhao, J.
Deposited on : 2022-05-18
Resolution : 3.00 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

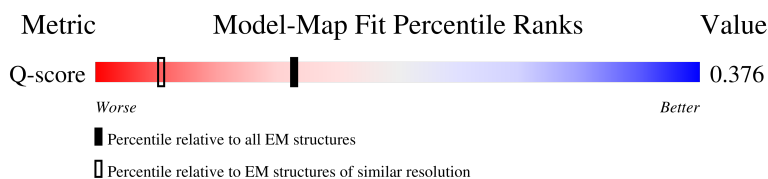
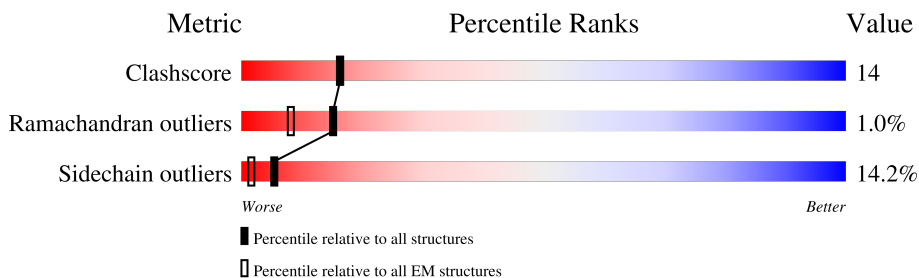
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 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.



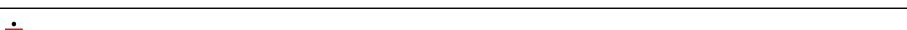
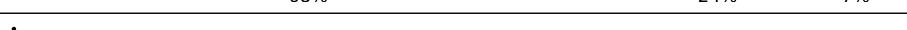
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	433	
2	B	440	
3	C	406	
4	D	418	

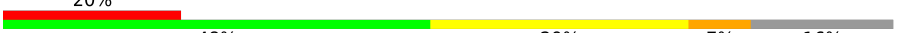
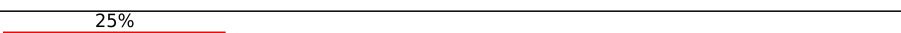
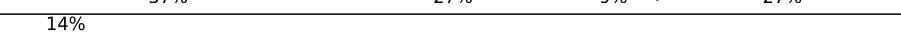
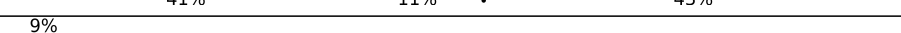
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Mol	Chain	Length	Quality of chain
5	E	389	
6	F	439	
7	G	246	
7	g	246	
8	H	234	
8	h	234	
9	I	261	
9	i	261	
10	J	248	
10	j	248	
11	K	241	
11	k	241	
12	L	263	
12	l	263	
13	M	255	
13	m	255	
14	N	239	
14	n	239	
15	O	277	
15	o	277	
16	P	205	
16	p	205	
17	Q	201	
17	q	201	
18	R	263	

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Mol	Chain	Length	Quality of chain
18	r	263	
19	S	241	
19	s	241	
20	T	264	
20	t	264	
21	U	953	
22	V	534	
23	W	456	
24	X	422	
25	Y	389	
26	Z	324	
27	a	376	
28	b	377	
29	c	310	
30	d	350	
31	e	70	
32	f	908	

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 101640 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 26S proteasome regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	380	Total	C	N	O	S	0	0
			2893	1817	515	543	18		

- Molecule 2 is a protein called 26S proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	370	Total	C	N	O	S	0	0
			2806	1763	478	553	12		

- Molecule 3 is a protein called 26S protease regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	363	Total	C	N	O	S	0	0
			2859	1804	513	525	17		

- Molecule 4 is a protein called 26S proteasome regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	380	Total	C	N	O	S	0	0
			3040	1923	524	580	13		

- Molecule 5 is a protein called 26S protease regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	375	Total	C	N	O	S	0	0
			2860	1796	512	536	16		

- Molecule 6 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	376	Total	C	N	O	S	0	0
			2855	1799	495	546	15		

- Molecule 7 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	239	Total	C	N	O	S	0	0
			1820	1157	304	346	13		
7	g	240	Total	C	N	O	S	0	0
			1826	1160	305	348	13		

- Molecule 8 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	230	Total	C	N	O	S	0	0
			1702	1082	285	330	5		
8	h	234	Total	C	N	O	S	0	0
			1721	1089	291	335	6		

- Molecule 9 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	248	Total	C	N	O	S	0	0
			1895	1195	324	368	8		
9	i	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		

- Molecule 10 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	239	Total	C	N	O	S	0	0
			1708	1059	309	335	5		
10	j	239	Total	C	N	O	S	0	0
			1704	1056	308	335	5		

- Molecule 11 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	237	Total	C	N	O	S	0	0
			1792	1122	296	363	11		
11	k	234	Total	C	N	O	S	0	0
			1759	1102	290	356	11		

- Molecule 12 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	238	Total	C	N	O	S	0	0
			1850	1159	334	346	11		
12	l	238	Total	C	N	O	S	0	0
			1850	1159	334	346	11		

- Molecule 13 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	240	Total	C	N	O	S	0	0
			1856	1178	314	353	11		
13	m	240	Total	C	N	O	S	0	0
			1856	1178	314	353	11		

- Molecule 14 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	195	Total	C	N	O	S	0	0
			1462	913	250	287	12		
14	n	205	Total	C	N	O	S	0	0
			1533	962	261	298	12		

- Molecule 15 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	222	Total	C	N	O	S	0	0
			1660	1044	282	322	12		
15	o	220	Total	C	N	O	S	0	0
			1643	1033	280	318	12		

- Molecule 16 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	205	Total	C	N	O	S	0	0
			1593	1015	263	295	20		
16	p	204	Total	C	N	O	S	0	0
			1585	1010	262	294	19		

- Molecule 17 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		

- Molecule 18 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	201	Total	C	N	O	S	0	0
			1548	974	273	292	9		
18	r	201	Total	C	N	O	S	0	0
			1548	974	273	292	9		

- Molecule 19 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	213	Total	C	N	O	S	0	0
			1644	1039	282	313	10		
19	s	213	Total	C	N	O	S	0	0
			1641	1036	282	313	10		

- Molecule 20 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	215	Total	C	N	O	S	0	0
			1673	1055	288	318	12		
20	t	215	Total	C	N	O	S	0	0
			1673	1055	288	318	12		

- Molecule 21 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	806	Total	C	N	O	S	0	0
			6287	3990	1075	1178	44		

- Molecule 22 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	447	Total	C	N	O	S	0	0
			3600	2287	639	660	14		

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	456	Total	C	N	O	S	0	0
			3703	2339	635	704	25		

- Molecule 24 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	380	Total	C	N	O	S	0	0
			3009	1918	509	570	12		

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	378	Total	C	N	O	S	0	0
			3115	1987	533	578	17		

- Molecule 26 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	286	Total	C	N	O	S	0	0
			2281	1457	392	427	5		

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	373	Total	C	N	O	S	0	0
			2995	1911	510	559	15		

- Molecule 28 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	191	Total	C	N	O	S	0	0
			1458	910	261	279	8		

- Molecule 29 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	278	Total	C	N	O	S	0	0
			2187	1389	374	406	18		

- Molecule 30 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	257	Total	C	N	O	S	0	0
			2116	1371	346	390	9		

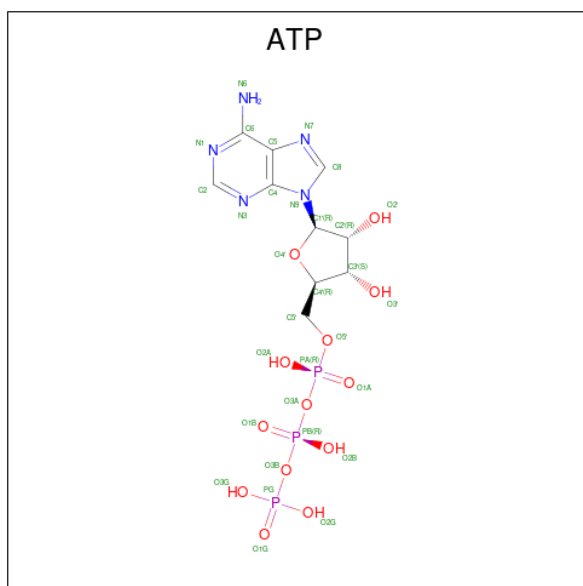
- Molecule 31 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	40	Total	C	N	O	S	0	0
			334	200	55	77	2		

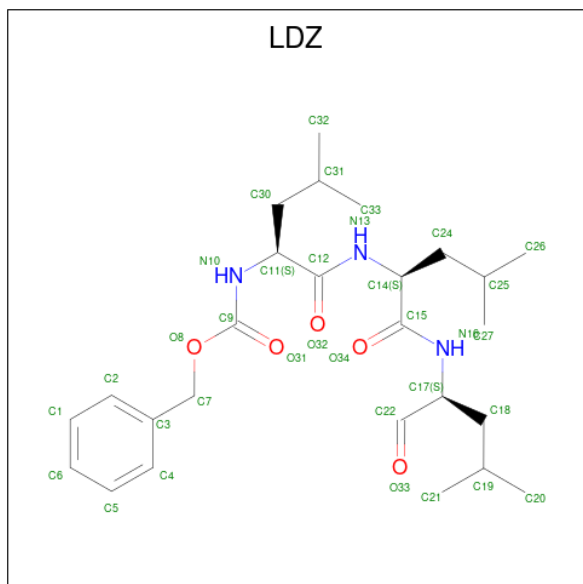
- Molecule 32 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	689	Total	C	N	O	S	0	0
			5319	3343	904	1037	35		

- Molecule 33 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



- Molecule 34 is N-[(benzyloxy)carbonyl]-L-leucyl-N-[(2S)-4-methyl-1-oxopentan-2-yl]-L-leucinamide (CCD ID: LDZ) (formula: $C_{26}H_{41}N_3O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
34	N	1	Total	C	N	O	0
			34	26	3	5	
34	O	1	Total	C	N	O	0
			34	26	3	5	
34	R	1	Total	C	N	O	0
			34	26	3	5	
34	n	1	Total	C	N	O	0
			34	26	3	5	
34	o	1	Total	C	N	O	0
			34	26	3	5	
34	r	1	Total	C	N	O	0
			34	26	3	5	

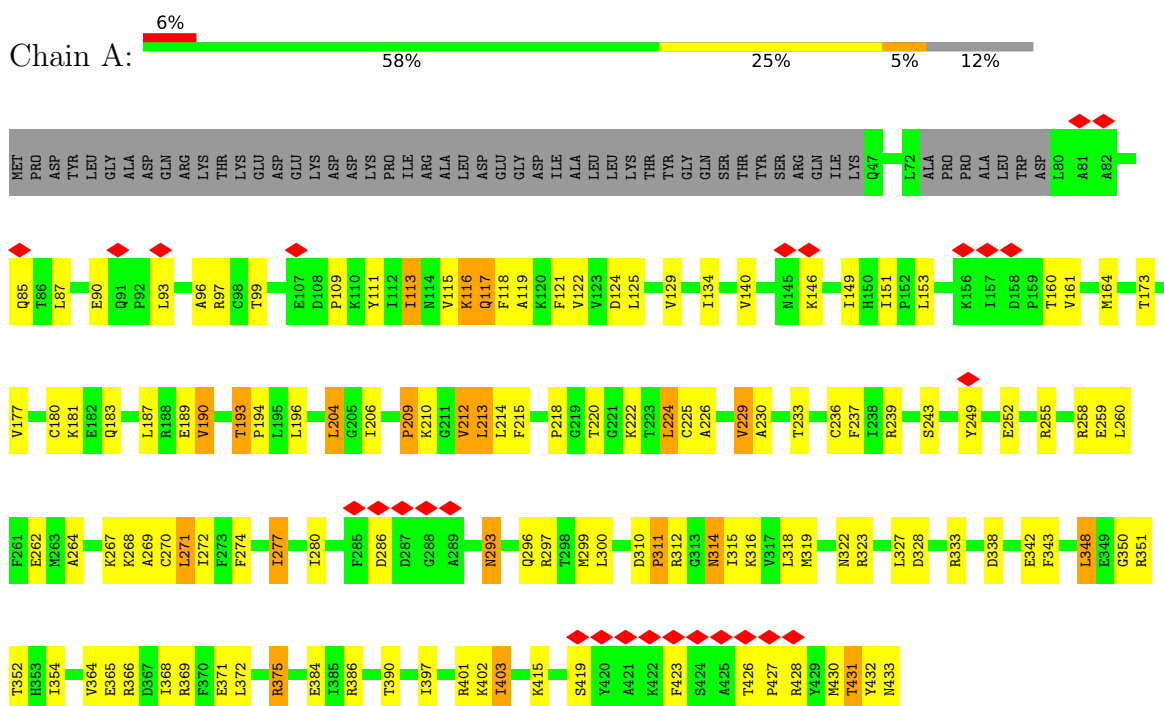
- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
35	c	1	Total	Zn	0
			1	1	

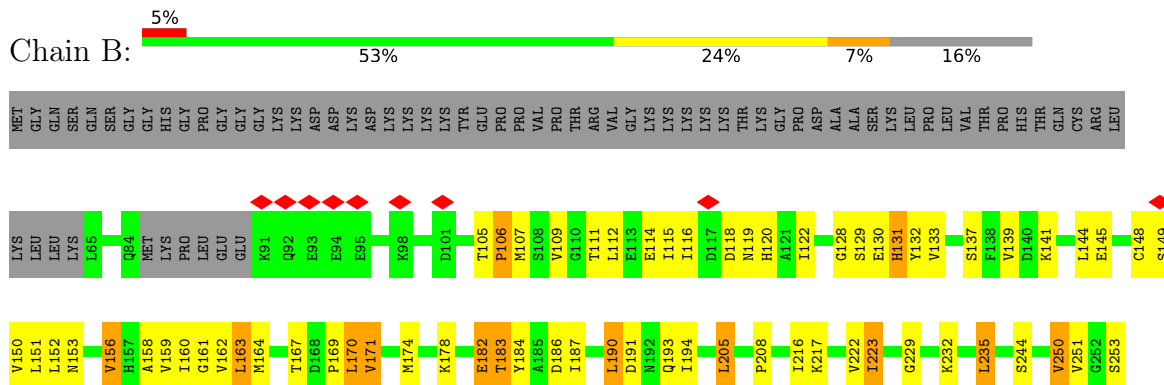
3 Residue-property plots

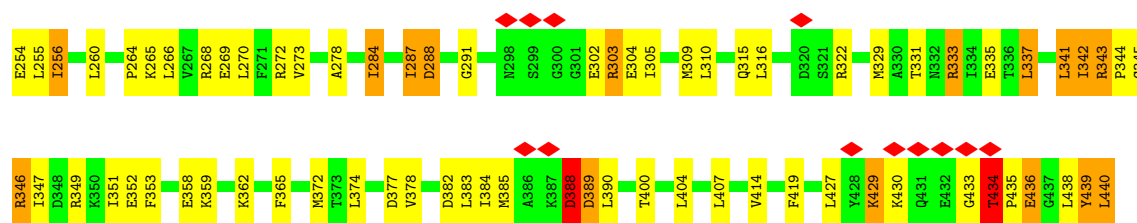
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: 26S proteasome regulatory subunit 7

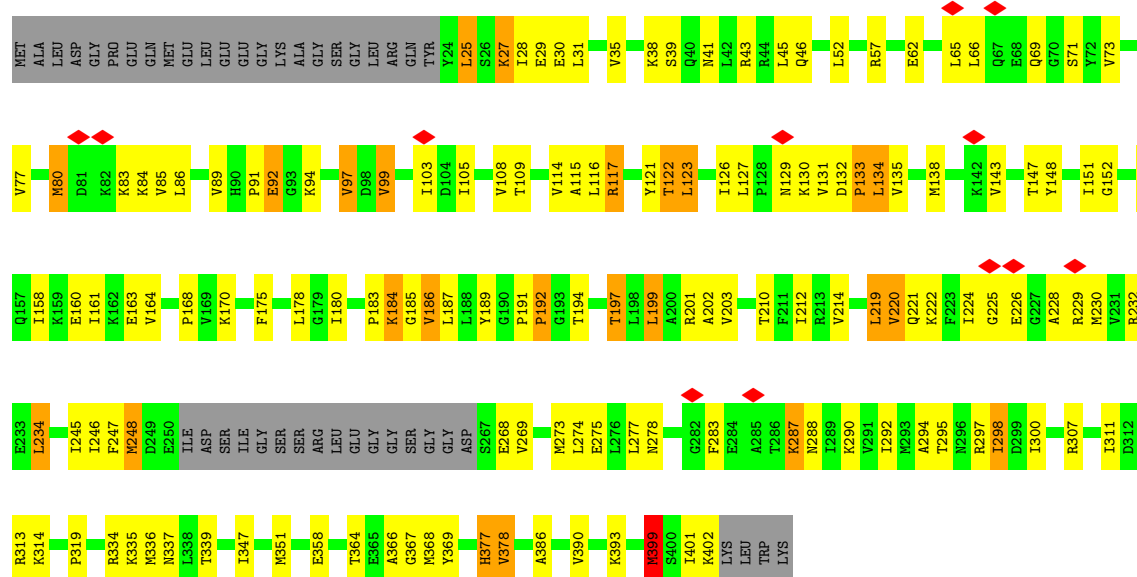


- Molecule 2: 26S proteasome regulatory subunit 4

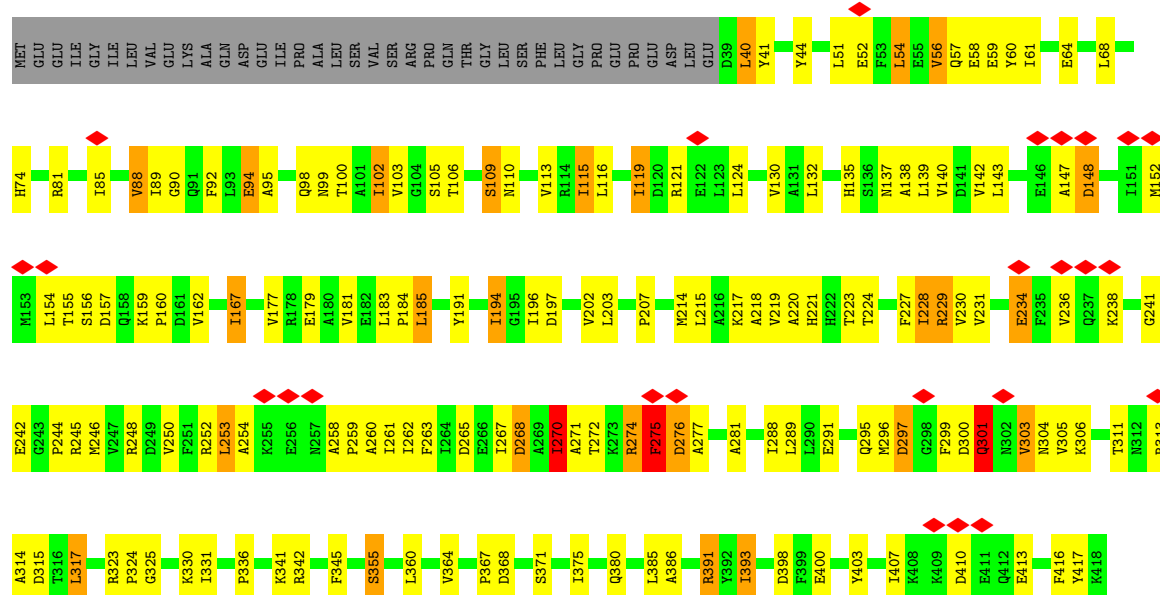




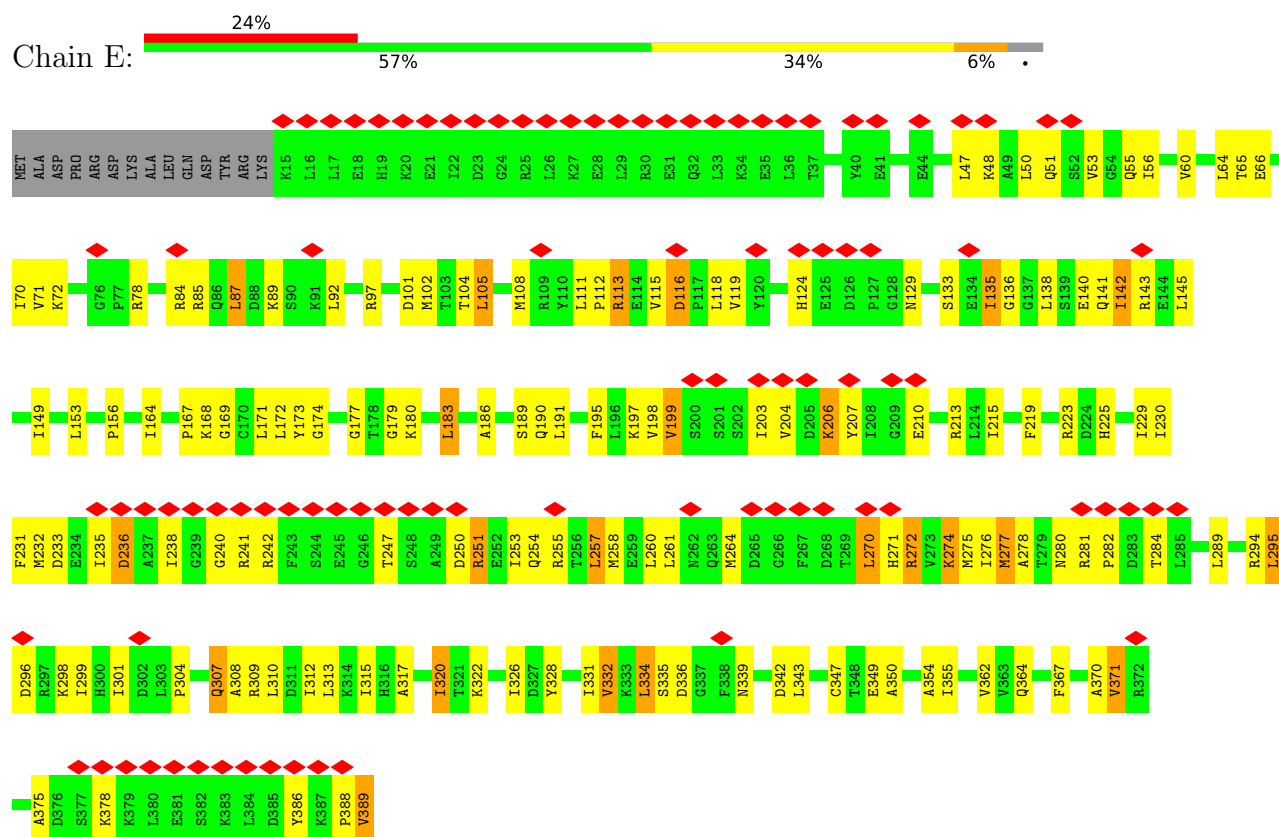
• Molecule 3: 26S protease regulatory subunit 8



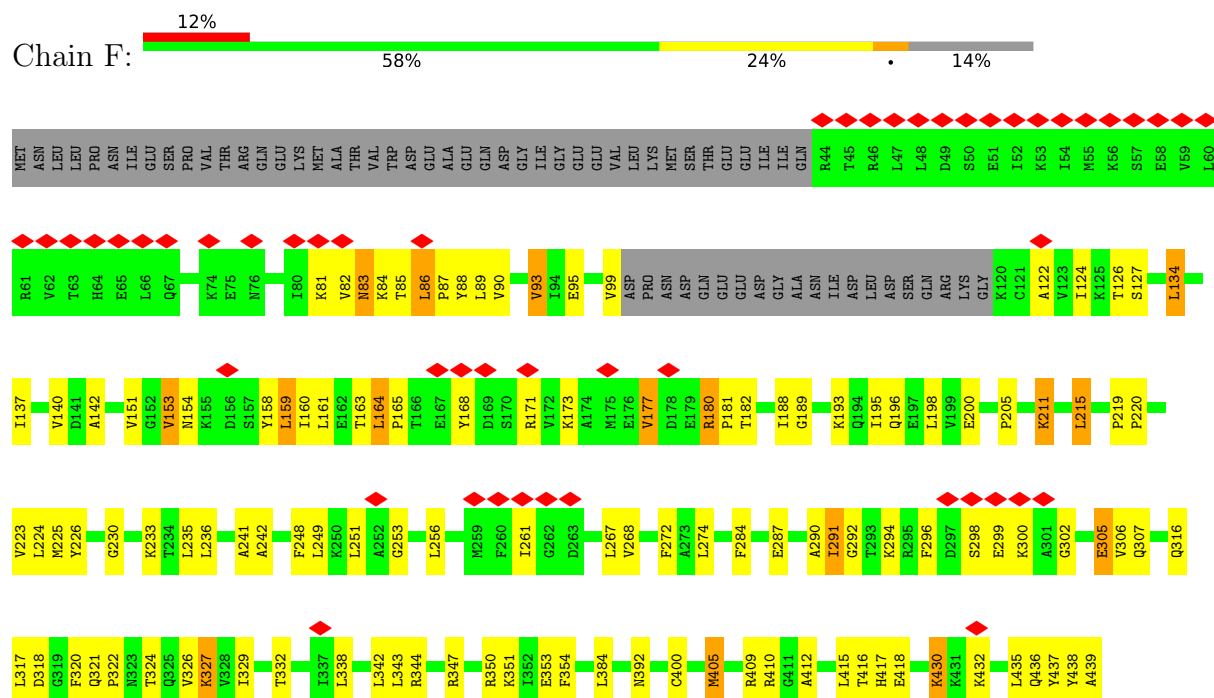
• Molecule 4: 26S proteasome regulatory subunit 6B



- Molecule 5: 26S protease regulatory subunit 10B

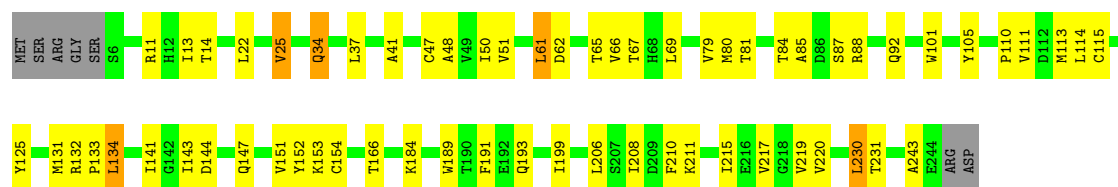


- Molecule 6: 26S proteasome regulatory subunit 6A



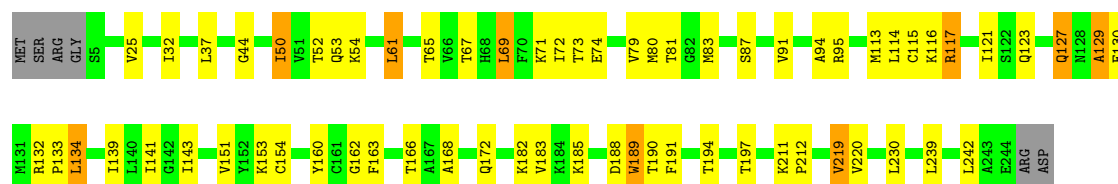
- Molecule 7: Proteasome subunit alpha type-6

Chain G:  72% 24% . .



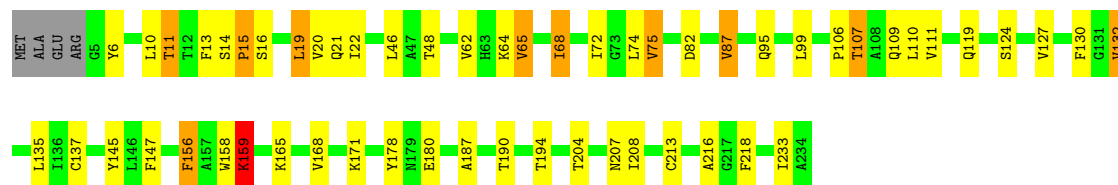
• Molecule 7: Proteasome subunit alpha type-6

Chain g:  71% 23% . .



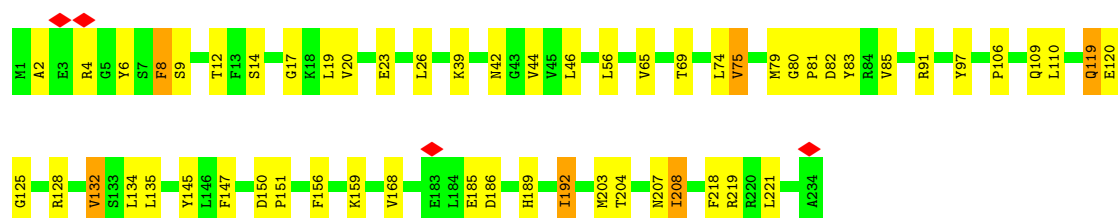
• Molecule 8: Proteasome subunit alpha type-2

Chain H:  74% 19% . .



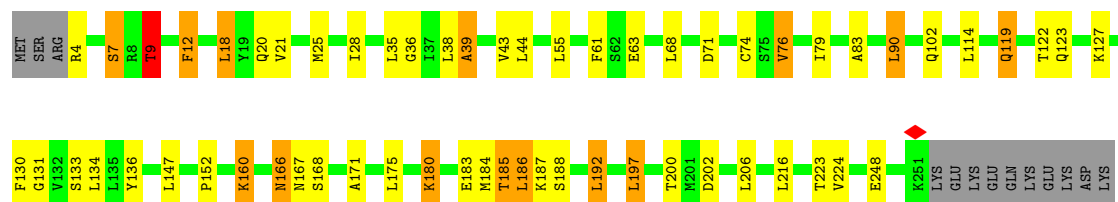
• Molecule 8: Proteasome subunit alpha type-2

Chain h:  76% 22% .



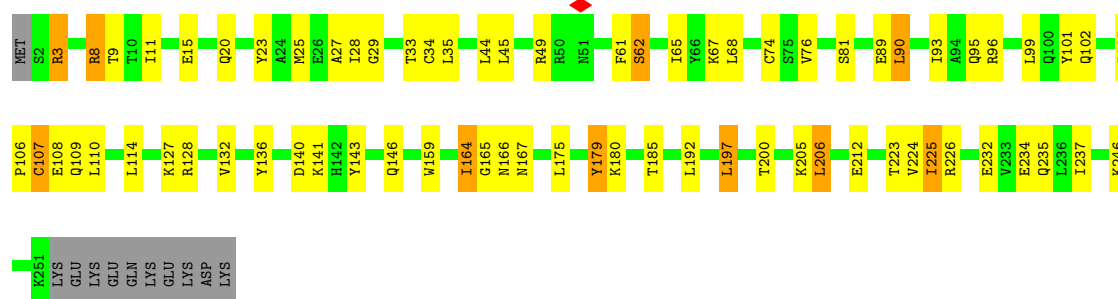
• Molecule 9: Proteasome subunit alpha type-4

Chain I:  72% 17% 5% 5%



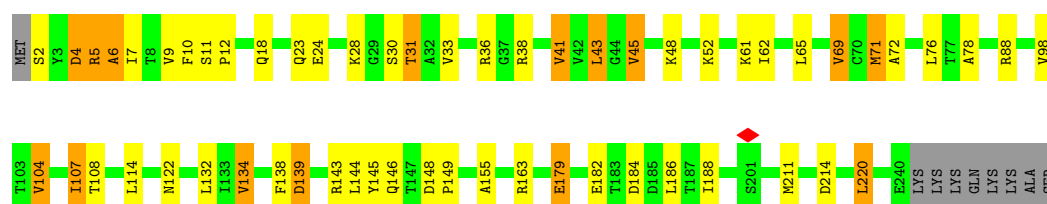
- Molecule 9: Proteasome subunit alpha type-4

Chain i: 



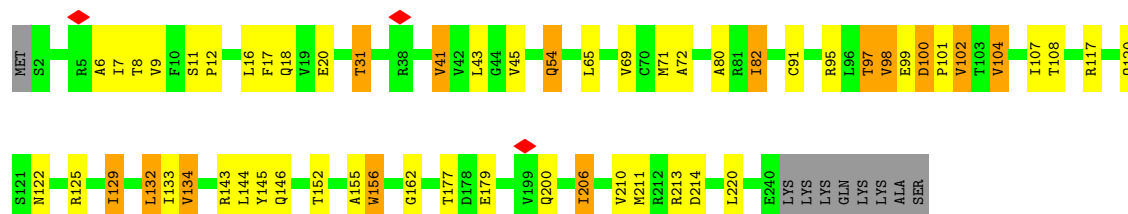
- Molecule 10: Proteasome subunit alpha type-7

Chain J: 



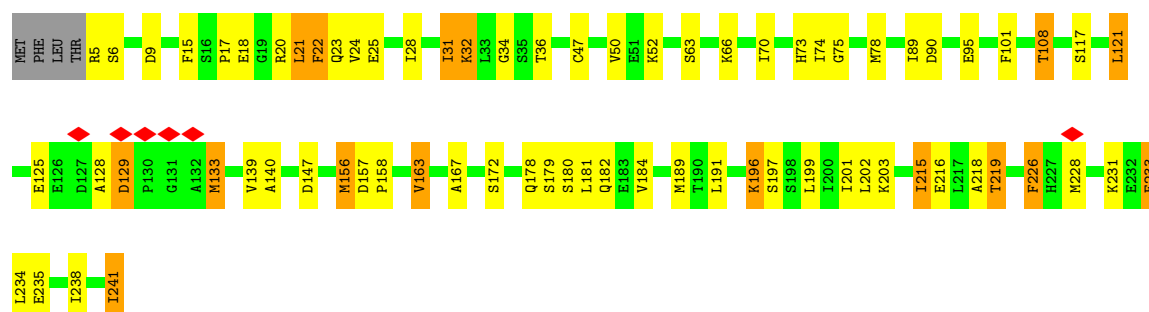
- Molecule 10: Proteasome subunit alpha type-7

Chain j: 

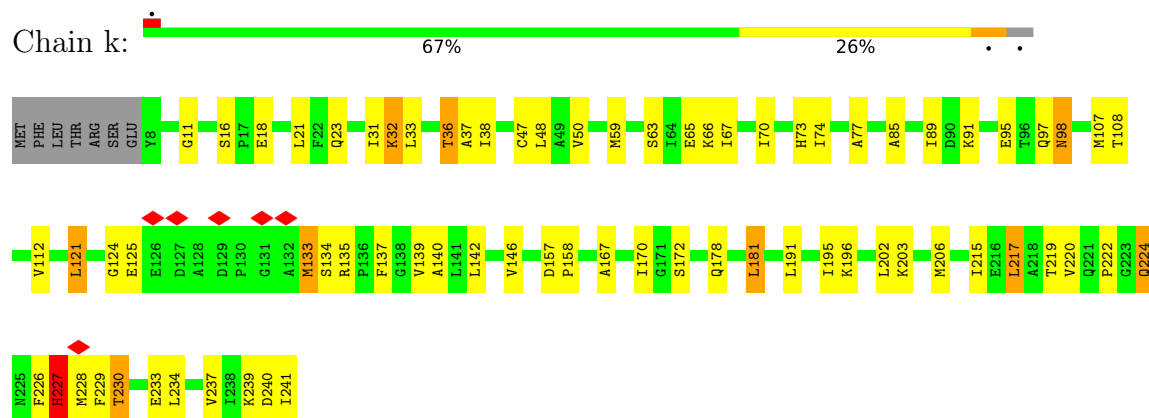


- Molecule 11: Proteasome subunit alpha type-5

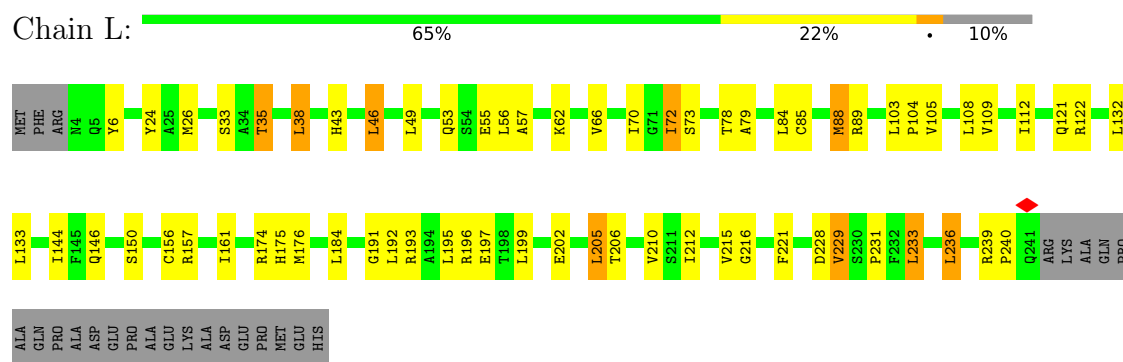
Chain K: 



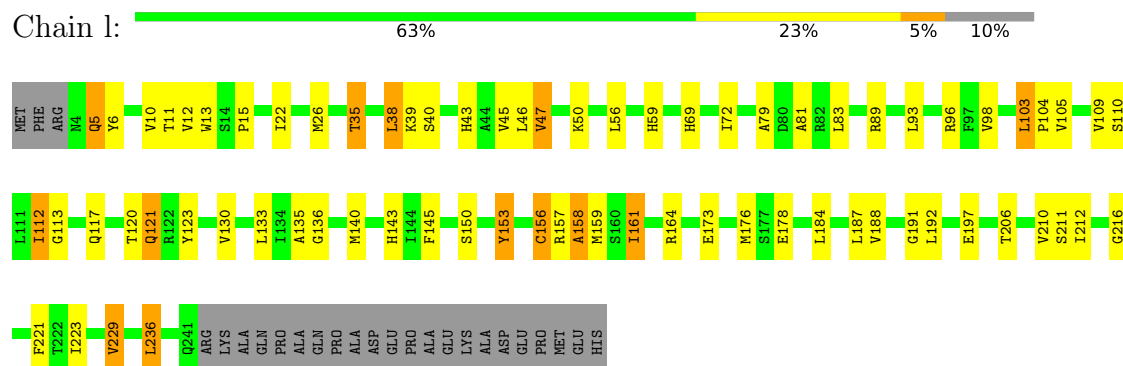
- Molecule 11: Proteasome subunit alpha type-5



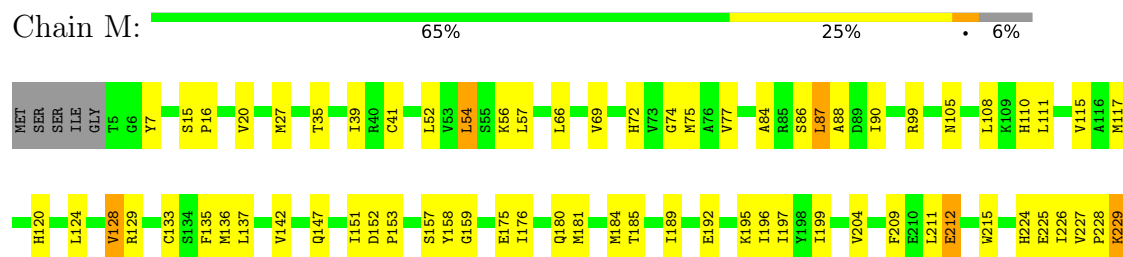
- Molecule 12: Proteasome subunit alpha type-1



- Molecule 12: Proteasome subunit alpha type-1



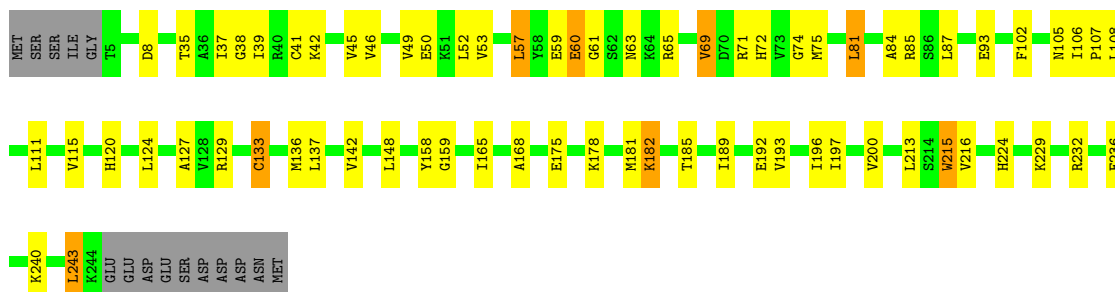
- Molecule 13: Proteasome subunit alpha type-3





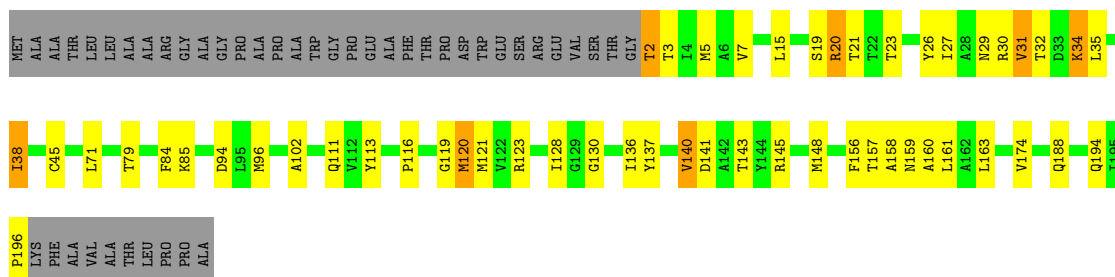
• Molecule 13: Proteasome subunit alpha type-3

Chain m: 67% 24% 6%



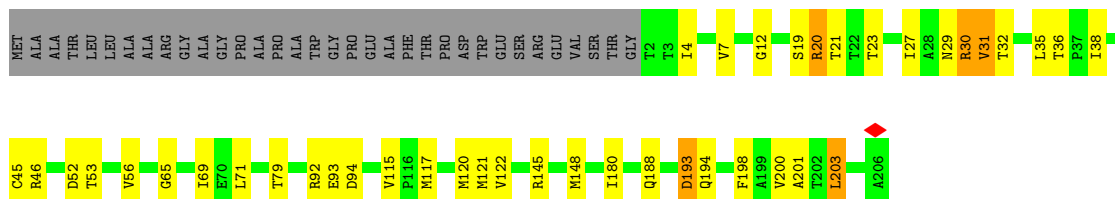
• Molecule 14: Proteasome subunit beta type-6

Chain N: 59% 19% 18%



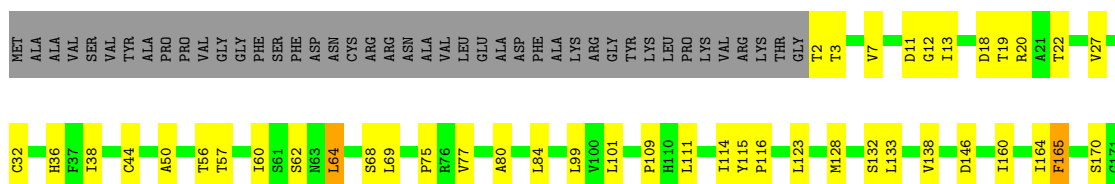
• Molecule 14: Proteasome subunit beta type-6

Chain n: 68% 15% 14%



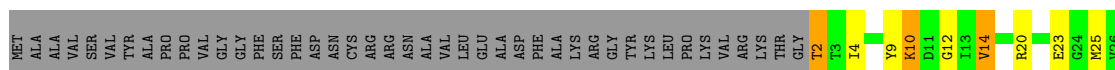
• Molecule 15: Proteasome subunit beta type-7

Chain O: 57% 20% 20%





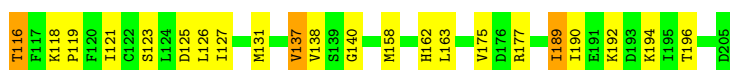
• Molecule 15: Proteasome subunit beta type-7



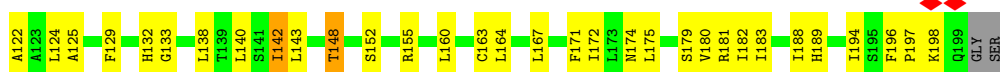
• Molecule 16: Proteasome subunit beta type-3



• Molecule 16: Proteasome subunit beta type-3

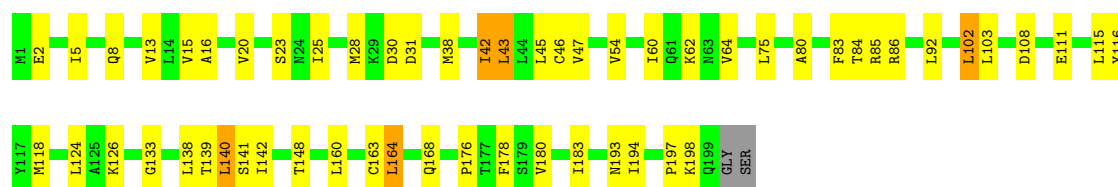


• Molecule 17: Proteasome subunit beta type-2



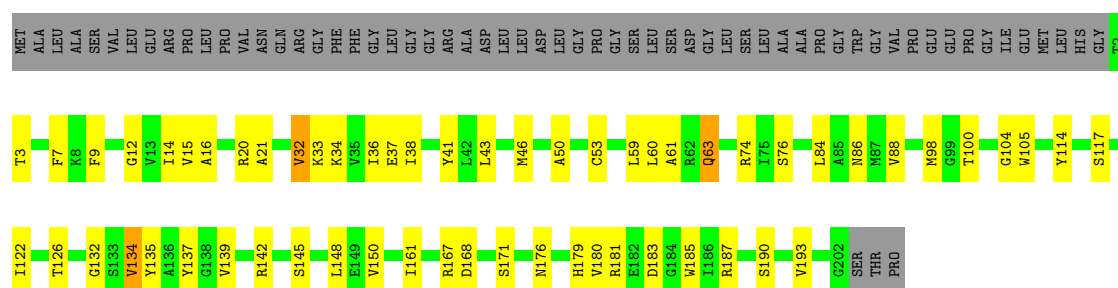
- Molecule 17: Proteasome subunit beta type-2

Chain q:  71% 26% ..



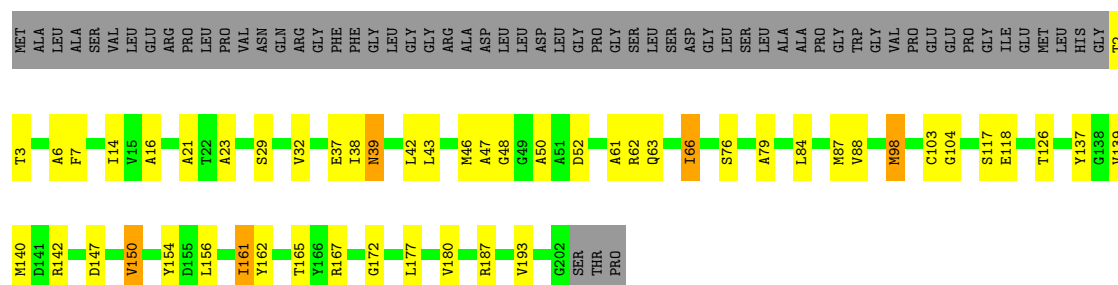
- Molecule 18: Proteasome subunit beta type-5

Chain R:  54% 21% • 24%



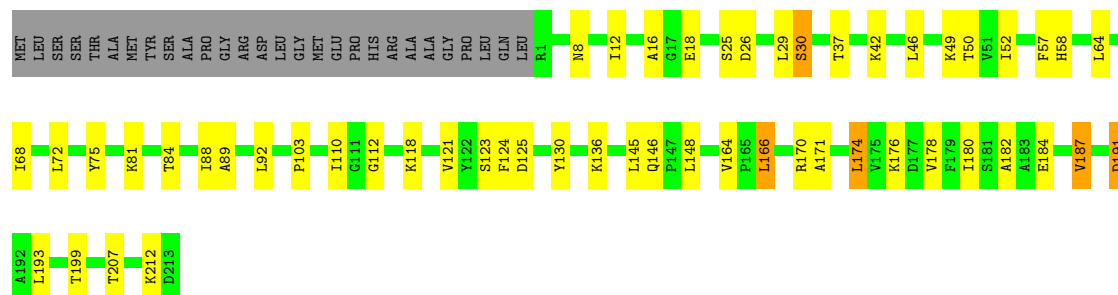
- Molecule 18: Proteasome subunit beta type-5

Chain r:  57% 18% • 24%



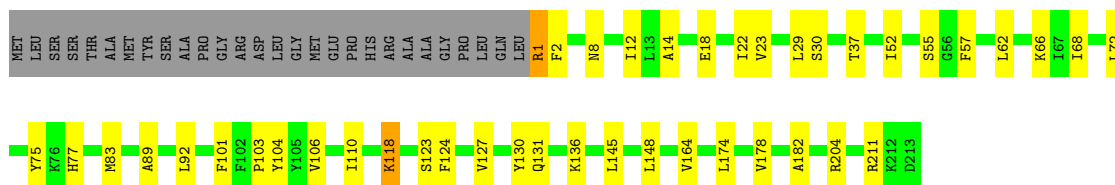
- Molecule 19: Proteasome subunit beta type-1

Chain S:  66% 20% • 12%



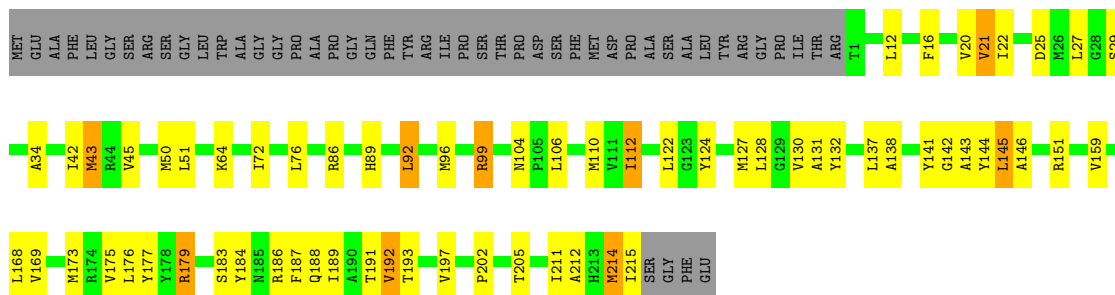
- Molecule 19: Proteasome subunit beta type-1

Chain s: 



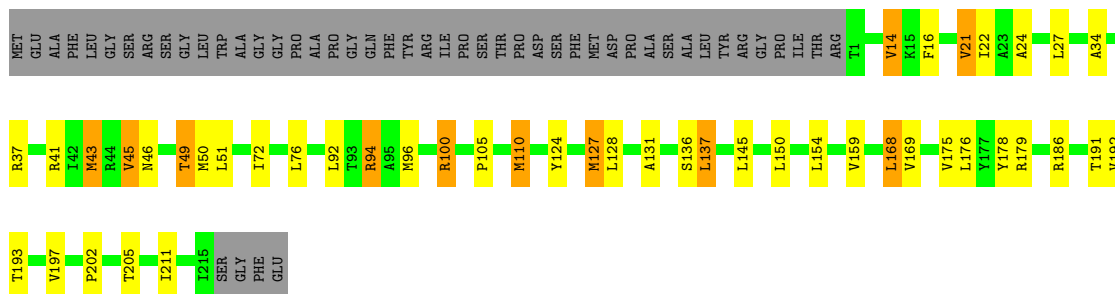
• Molecule 20: Proteasome subunit beta type-4

Chain T: 



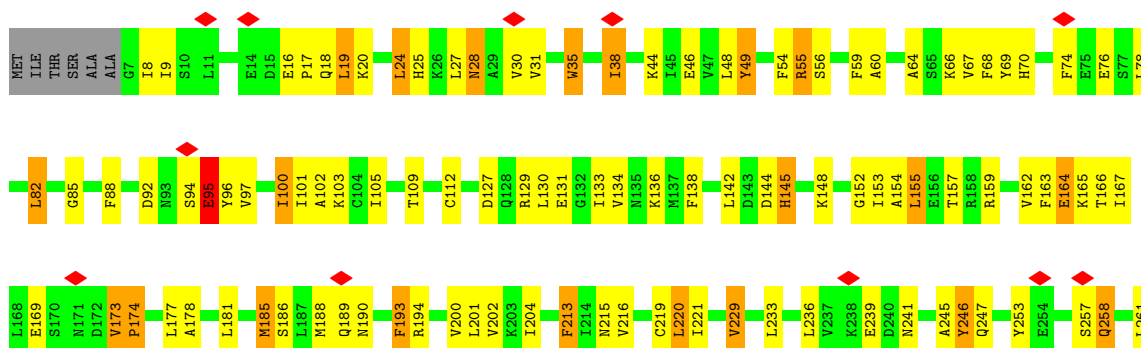
• Molecule 20: Proteasome subunit beta type-4

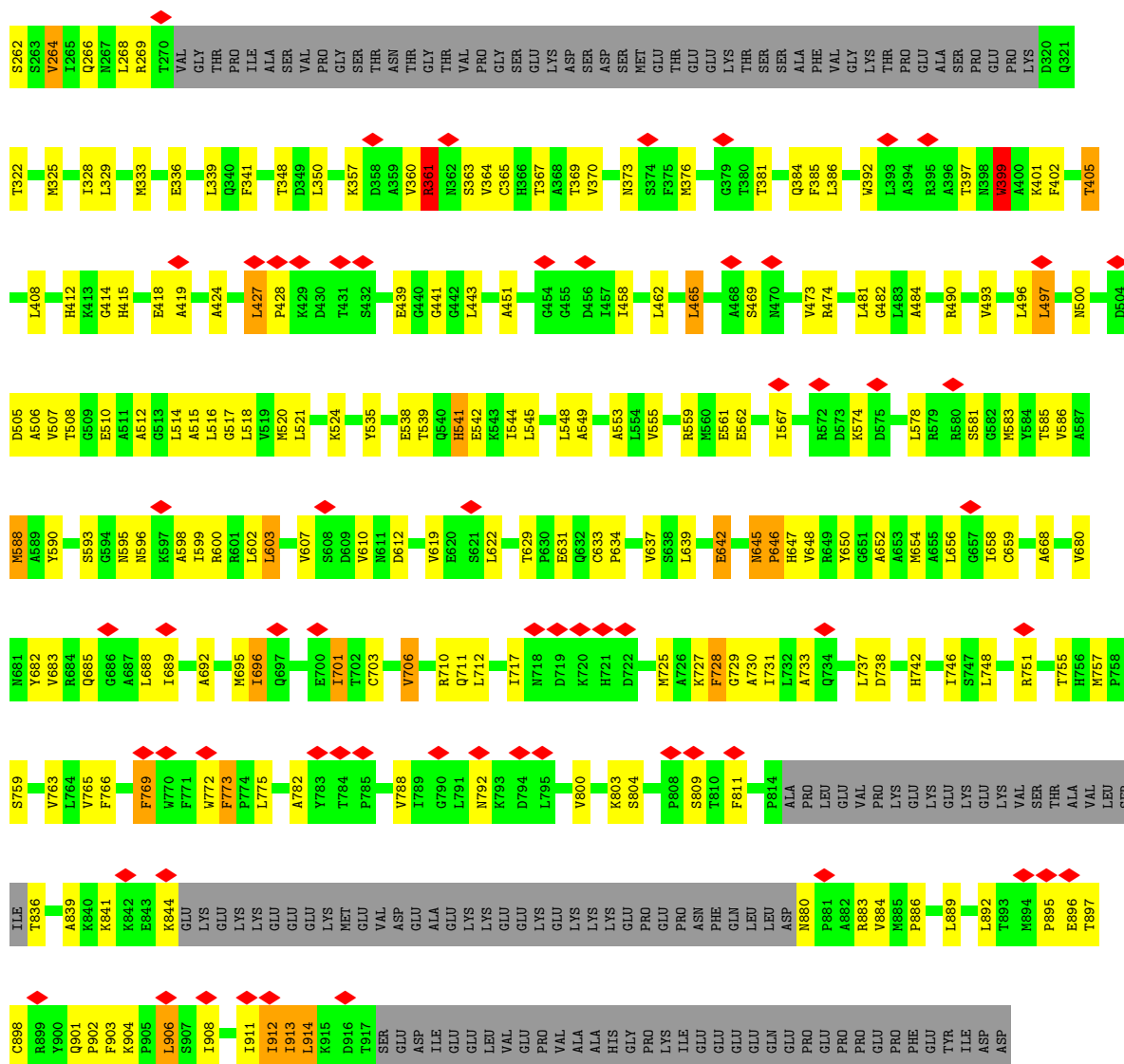
Chain t: 



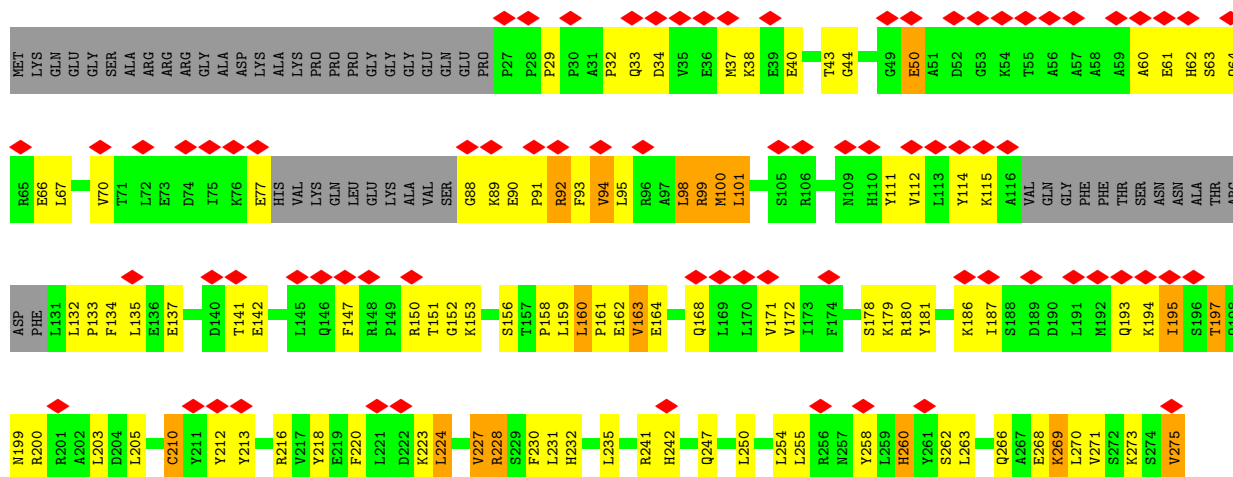
• Molecule 21: 26S proteasome non-ATPase regulatory subunit 1

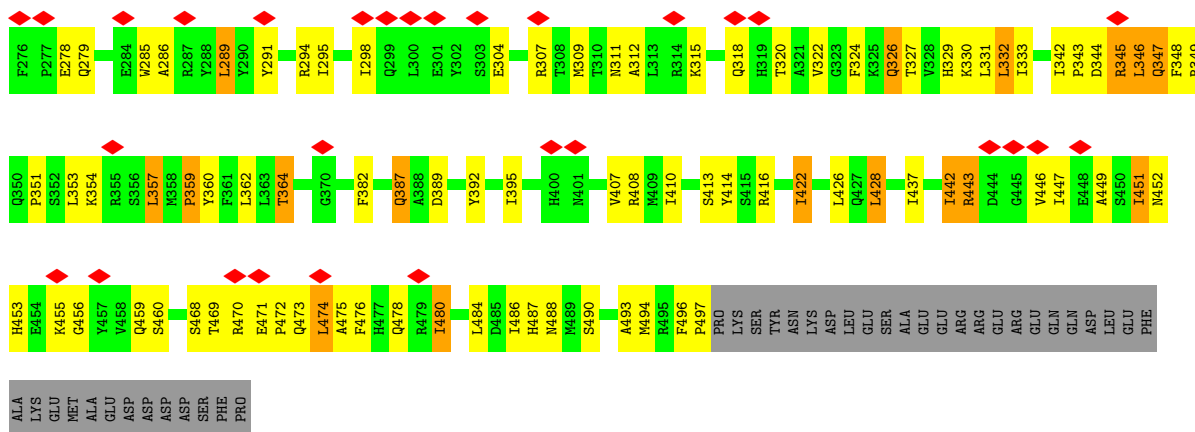
Chain U: 



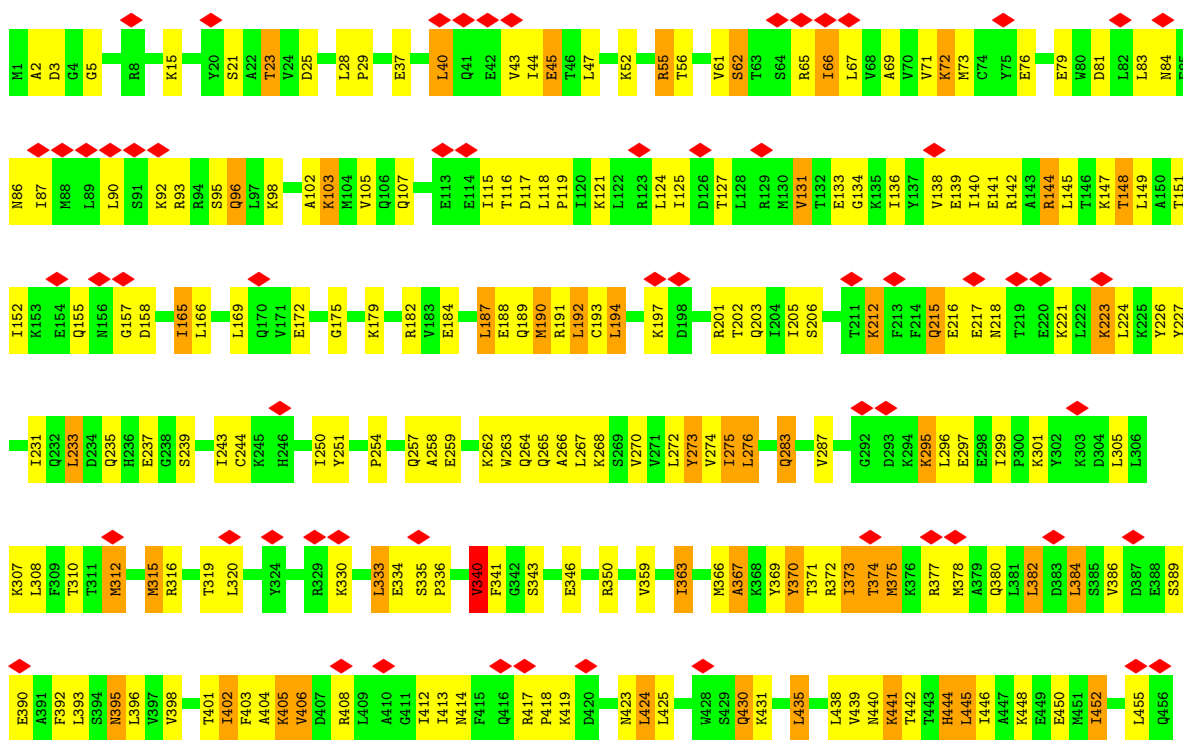


• Molecule 22: 26S proteasome non-ATPase regulatory subunit 3

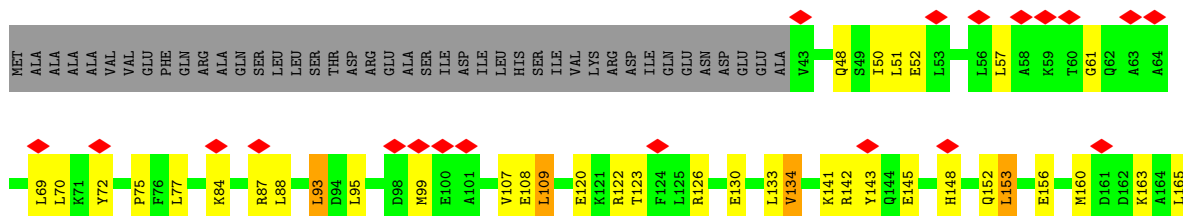


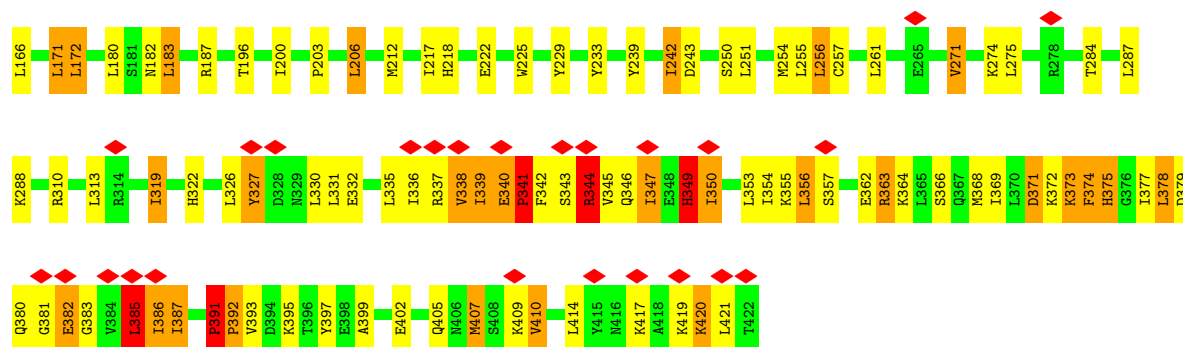


• Molecule 23: 26S proteasome non-ATPase regulatory subunit 12

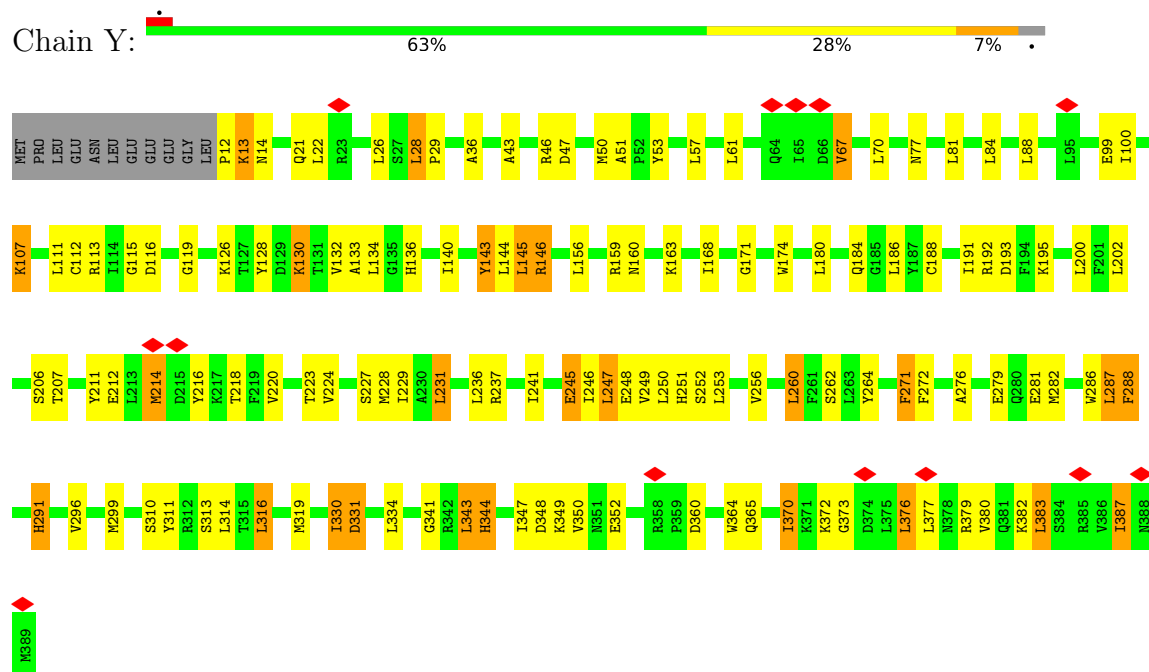


• Molecule 24: 26S proteasome non-ATPase regulatory subunit 11



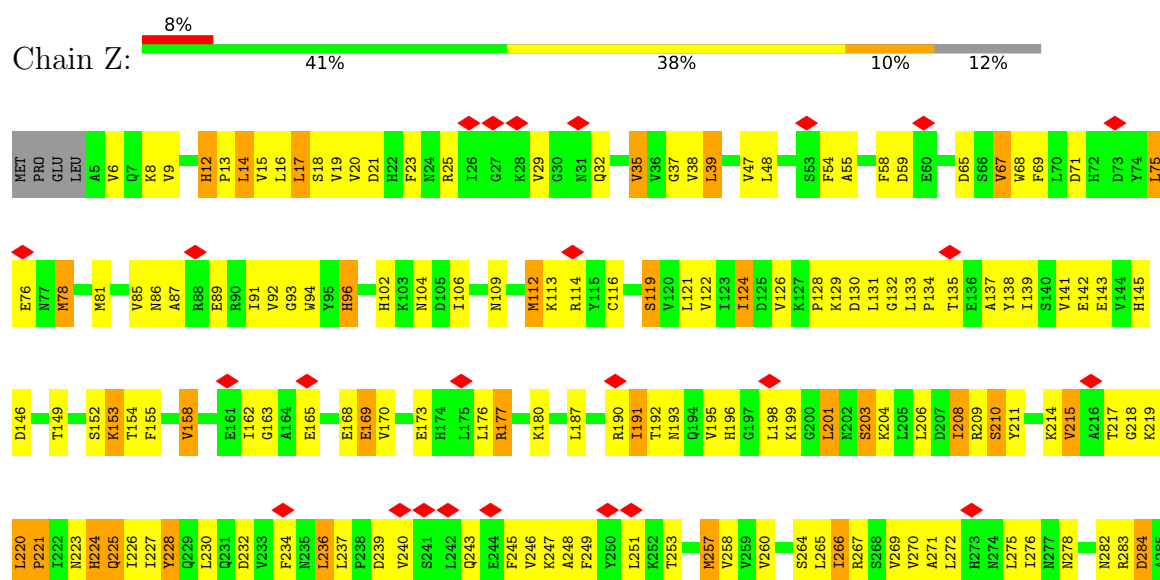


• Molecule 25: 26S proteasome non-ATPase regulatory subunit 6

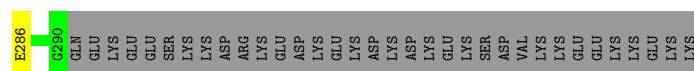


Chain Y: 63% 28% 7%

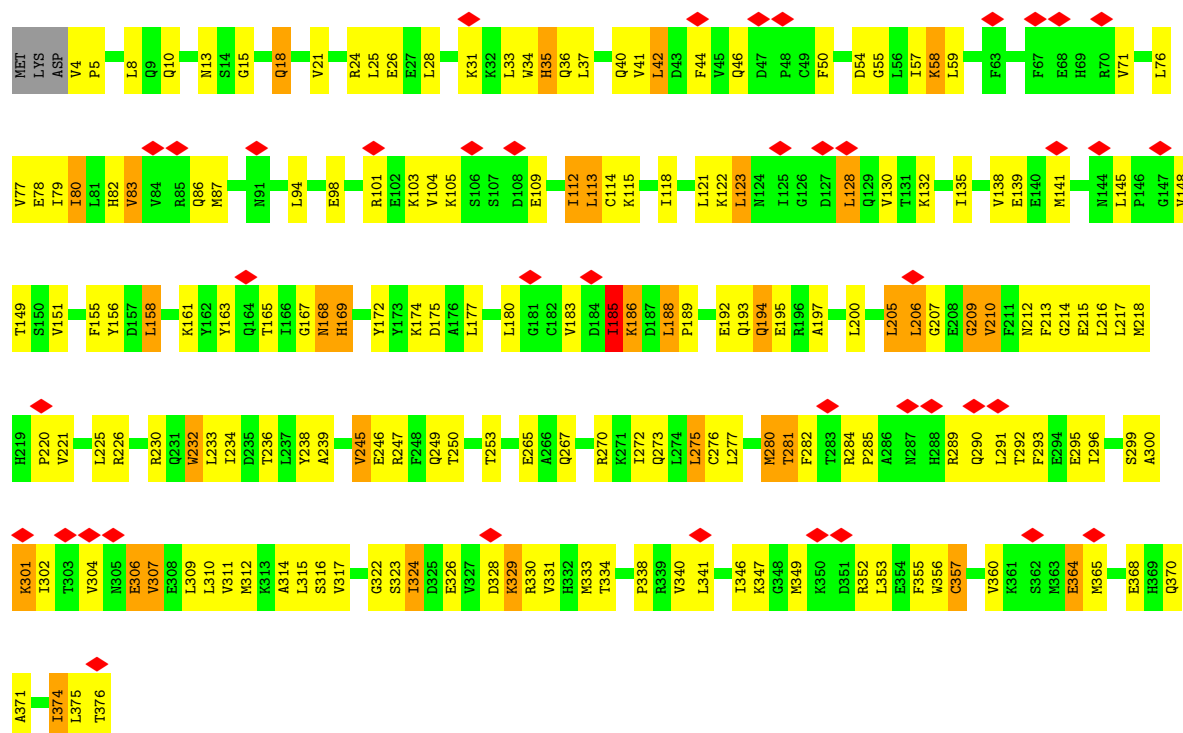
• Molecule 26: 26S proteasome non-ATPase regulatory subunit 7



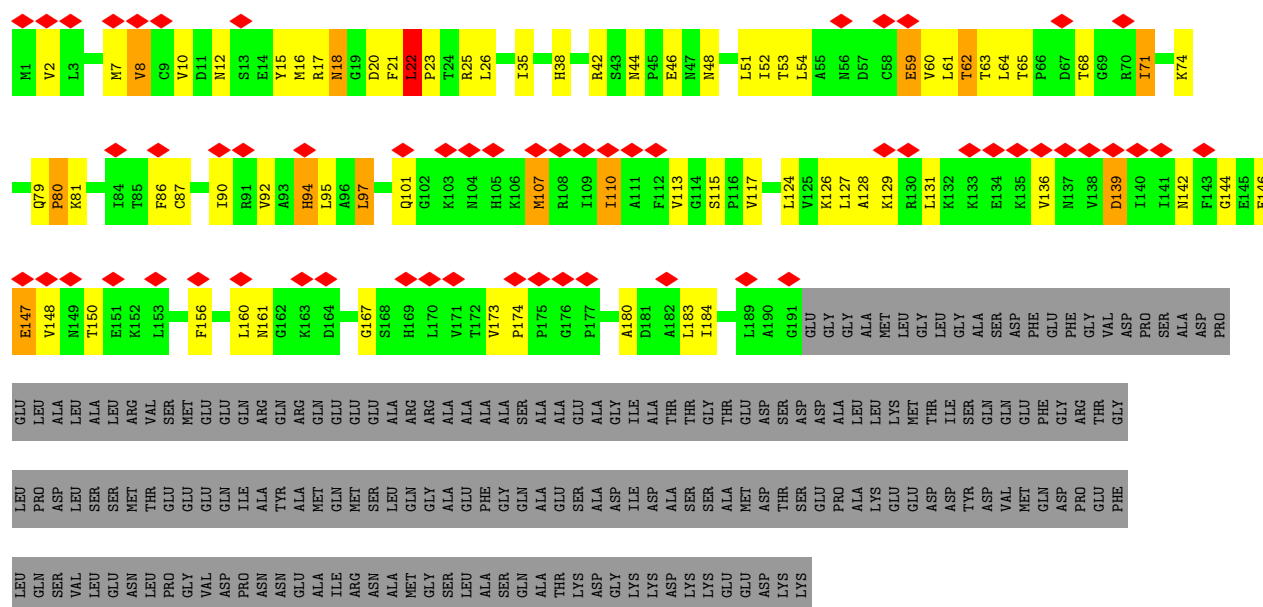
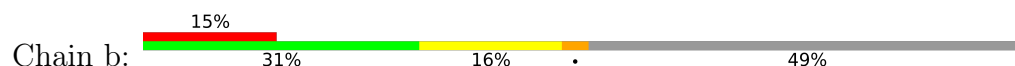
Chain Z: 8% 41% 38% 10% 12%



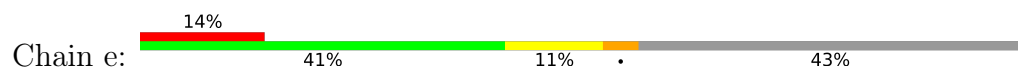
• Molecule 27: 26S proteasome non-ATPase regulatory subunit 13

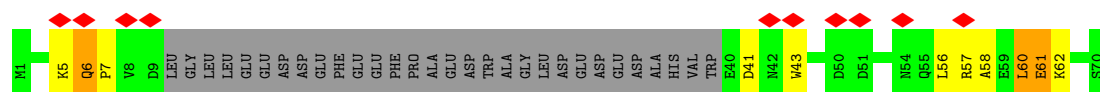


• Molecule 28: 26S proteasome non-ATPase regulatory subunit 4

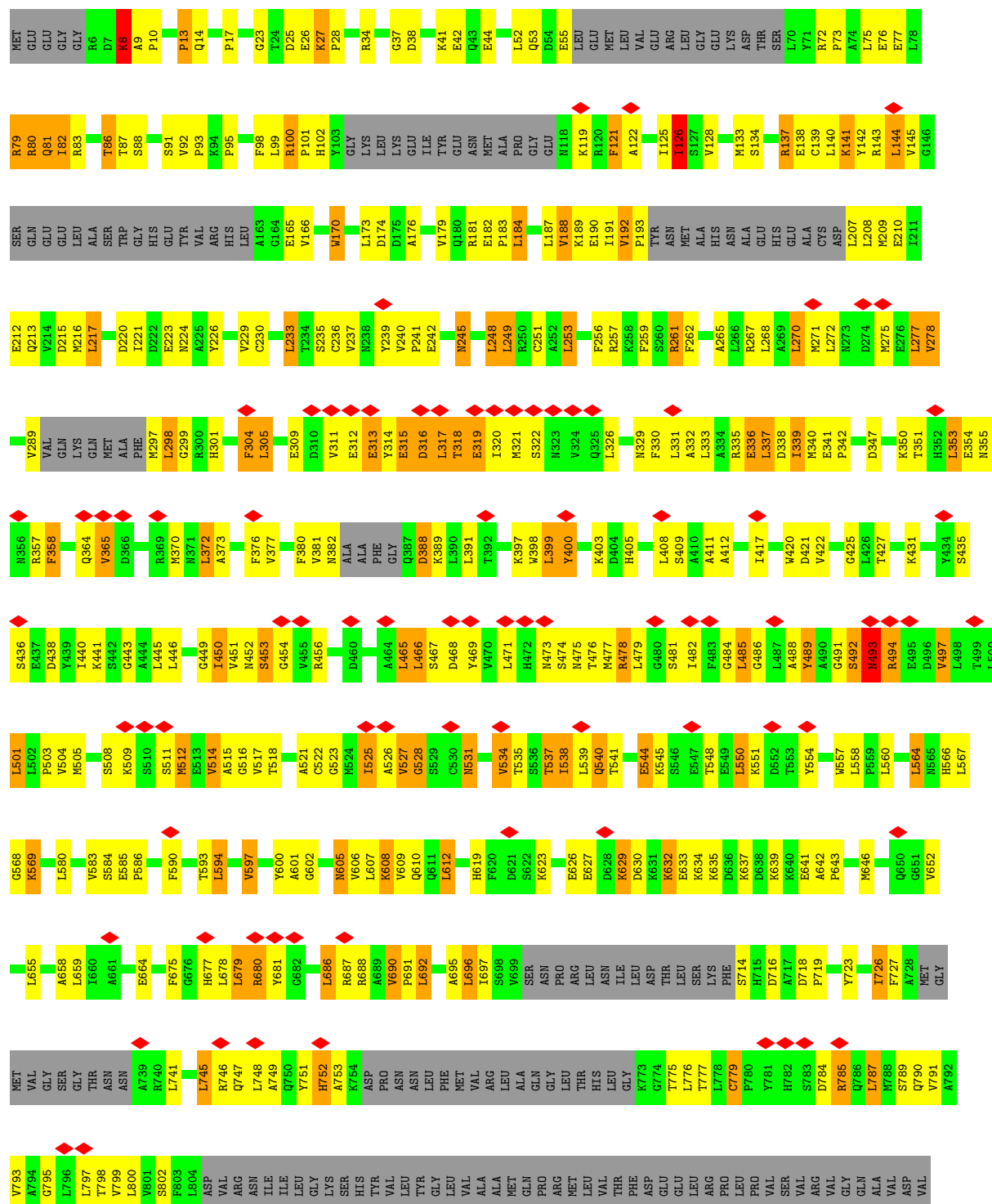


Chain c:





• Molecule 32: 26S proteasome non-ATPase regulatory subunit 2



VAL	GLY	GLN	ALA	GLY	LYS	PRO	LYS	THR	ILE	THR	GLY	PHE	GLN	THR	HIS	THR	THR	PRO	VAL	LEU	LEU	ALA	ALA	HIS	GLY	GLU	ARG	ALA	GLU	LEU	ALA	THR	GLU	GLU	PHE	LEU	PRO	VAL	THR	PRO	PRO	ILE	LEU	GLU	GLY	PHE	VAL	ILE	LEU	ARG	LYS	ASN	PRO	ASN	TYR	ASP	LEU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	147696	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.235	Depositor
Minimum map value	-0.680	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	360.4, 360.4, 360.4	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: LDZ, ZN, ATP

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	0.92	0/2939	1.30	3/3970 (0.1%)
2	B	0.93	0/2844	1.30	5/3846 (0.1%)
3	C	0.92	0/2896	1.27	7/3895 (0.2%)
4	D	0.91	0/3090	1.34	11/4168 (0.3%)
5	E	0.95	0/2904	1.28	4/3924 (0.1%)
6	F	0.93	0/2893	1.27	2/3908 (0.1%)
7	G	0.90	0/1853	1.31	0/2515
7	g	0.90	0/1859	1.29	2/2523 (0.1%)
8	H	0.91	0/1738	1.30	3/2365 (0.1%)
8	h	0.91	0/1756	1.27	2/2389 (0.1%)
9	I	0.90	0/1925	1.29	4/2606 (0.2%)
9	i	0.91	0/1942	1.27	0/2628
10	J	0.93	0/1732	1.36	6/2362 (0.3%)
10	j	0.95	0/1728	1.31	2/2358 (0.1%)
11	K	0.93	0/1820	1.32	4/2464 (0.2%)
11	k	0.91	0/1786	1.32	3/2419 (0.1%)
12	L	0.92	0/1885	1.25	0/2552
12	l	0.91	0/1885	1.26	4/2552 (0.2%)
13	M	0.90	0/1891	1.29	2/2552 (0.1%)
13	m	0.90	0/1891	1.28	1/2552 (0.0%)
14	N	0.89	0/1487	1.29	1/2013 (0.0%)
14	n	0.90	0/1561	1.33	2/2116 (0.1%)
15	O	0.93	0/1687	1.33	2/2288 (0.1%)
15	o	0.91	0/1670	1.26	0/2265
16	P	0.88	0/1622	1.32	3/2187 (0.1%)
16	p	0.87	0/1614	1.31	3/2177 (0.1%)
17	Q	0.88	0/1603	1.28	5/2174 (0.2%)
17	q	0.86	0/1603	1.26	2/2174 (0.1%)
18	R	0.88	0/1579	1.24	0/2134
18	r	0.88	0/1579	1.26	1/2134 (0.0%)
19	S	0.90	0/1674	1.32	1/2257 (0.0%)
19	s	0.89	0/1671	1.26	2/2253 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	T	0.88	0/1706	1.29	0/2312
20	t	0.88	0/1706	1.28	0/2312
21	U	0.92	0/6396	1.27	6/8646 (0.1%)
22	V	0.91	0/3668	1.30	4/4952 (0.1%)
23	W	0.89	0/3751	1.30	0/5042
24	X	0.90	0/3053	1.31	9/4115 (0.2%)
25	Y	0.85	0/3173	1.31	7/4273 (0.2%)
26	Z	0.92	0/2324	1.33	3/3150 (0.1%)
27	a	0.90	0/3053	1.30	4/4133 (0.1%)
28	b	0.97	0/1478	1.28	0/2001
29	c	0.93	0/2226	1.28	1/3007 (0.0%)
30	d	0.92	0/2162	1.30	3/2919 (0.1%)
31	e	0.86	0/338	1.27	0/450
32	f	0.94	1/5393 (0.0%)	1.33	11/7271 (0.2%)
All	All	0.91	1/103034 (0.0%)	1.30	135/139303 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	f	550	LEU	N-CA	5.07	1.49	1.46

The worst 5 of 135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	X	391	PRO	N-CA-C	8.94	121.61	110.70
3	C	192	PRO	N-CA-C	-8.59	101.89	113.40
11	K	233	GLU	N-CA-C	-8.30	103.15	113.28
26	Z	236	LEU	N-CA-C	-8.29	102.24	111.28
8	h	186	ASP	N-CA-C	-8.12	103.09	113.16

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	2893	0	2843	75	0
2	B	2806	0	2770	89	0
3	C	2859	0	2971	102	0
4	D	3040	0	3076	117	0
5	E	2860	0	2828	90	0
6	F	2855	0	2842	89	0
7	G	1820	0	1791	38	0
7	g	1826	0	1796	41	0
8	H	1702	0	1600	28	0
8	h	1721	0	1611	28	0
9	I	1895	0	1833	38	0
9	i	1912	0	1851	41	0
10	J	1708	0	1528	34	0
10	j	1704	0	1517	32	0
11	K	1792	0	1738	55	0
11	k	1759	0	1707	42	0
12	L	1850	0	1822	46	0
12	l	1850	0	1822	53	0
13	M	1856	0	1814	46	0
13	m	1856	0	1814	39	0
14	N	1462	0	1425	35	0
14	n	1533	0	1503	28	0
15	O	1660	0	1658	42	0
15	o	1643	0	1641	41	0
16	P	1593	0	1610	42	0
16	p	1585	0	1598	26	0
17	Q	1570	0	1547	39	0
17	q	1570	0	1547	28	0
18	R	1548	0	1496	43	0
18	r	1548	0	1496	30	0
19	S	1644	0	1627	29	0
19	s	1641	0	1618	23	0
20	T	1673	0	1639	45	0
20	t	1673	0	1639	28	0
21	U	6287	0	6336	188	0
22	V	3600	0	3655	186	0
23	W	3703	0	3822	177	0
24	X	3009	0	3113	126	0
25	Y	3115	0	3120	97	0
26	Z	2281	0	2312	134	0
27	a	2995	0	3012	131	0
28	b	1458	0	1505	51	0
29	c	2187	0	2215	90	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	d	2116	0	2146	94	0
31	e	334	0	294	13	0
32	f	5319	0	5329	345	0
33	A	31	0	12	0	0
33	C	31	0	12	1	0
33	D	31	0	12	0	0
33	F	31	0	12	2	0
34	N	34	0	41	2	0
34	O	34	0	41	3	0
34	R	34	0	41	3	0
34	n	34	0	41	1	0
34	o	34	0	41	7	0
34	r	34	0	41	5	0
35	c	1	0	0	0	0
All	All	101640	0	100771	2883	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 14.

The worst 5 of 2883 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)
32:f:488:ALA:HB1	32:f:489:TYR:CE1	1.73	1.23
32:f:597:VAL:CG1	32:f:630:ASP:HB2	1.72	1.18
32:f:184:LEU:CD2	32:f:224:ASN:HA	1.74	1.17
32:f:184:LEU:HD22	32:f:224:ASN:O	1.46	1.15
32:f:184:LEU:HD22	32:f:224:ASN:CA	1.76	1.14

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	A	376/433 (87%)	355 (94%)	14 (4%)	7 (2%)	6	30
2	B	366/440 (83%)	335 (92%)	25 (7%)	6 (2%)	7	34
3	C	359/406 (88%)	341 (95%)	14 (4%)	4 (1%)	11	43
4	D	378/418 (90%)	343 (91%)	26 (7%)	9 (2%)	4	24
5	E	373/389 (96%)	354 (95%)	18 (5%)	1 (0%)	36	70
6	F	372/439 (85%)	356 (96%)	14 (4%)	2 (0%)	24	60
7	G	237/246 (96%)	233 (98%)	3 (1%)	1 (0%)	30	65
7	g	238/246 (97%)	233 (98%)	3 (1%)	2 (1%)	16	50
8	H	228/234 (97%)	219 (96%)	5 (2%)	4 (2%)	6	31
8	h	232/234 (99%)	225 (97%)	7 (3%)	0	100	100
9	I	246/261 (94%)	236 (96%)	6 (2%)	4 (2%)	7	34
9	i	248/261 (95%)	238 (96%)	6 (2%)	4 (2%)	7	34
10	J	237/248 (96%)	225 (95%)	10 (4%)	2 (1%)	16	50
10	j	237/248 (96%)	225 (95%)	10 (4%)	2 (1%)	16	50
11	K	235/241 (98%)	226 (96%)	9 (4%)	0	100	100
11	k	232/241 (96%)	225 (97%)	7 (3%)	0	100	100
12	L	236/263 (90%)	232 (98%)	4 (2%)	0	100	100
12	l	236/263 (90%)	228 (97%)	7 (3%)	1 (0%)	30	65
13	M	238/255 (93%)	233 (98%)	4 (2%)	1 (0%)	30	65
13	m	238/255 (93%)	231 (97%)	6 (2%)	1 (0%)	30	65
14	N	193/239 (81%)	187 (97%)	6 (3%)	0	100	100
14	n	203/239 (85%)	193 (95%)	9 (4%)	1 (0%)	24	60
15	O	220/277 (79%)	210 (96%)	8 (4%)	2 (1%)	14	48
15	o	218/277 (79%)	210 (96%)	5 (2%)	3 (1%)	9	36
16	P	203/205 (99%)	189 (93%)	13 (6%)	1 (0%)	24	60
16	p	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
17	Q	197/201 (98%)	191 (97%)	6 (3%)	0	100	100
17	q	197/201 (98%)	192 (98%)	4 (2%)	1 (0%)	24	60
18	R	199/263 (76%)	199 (100%)	0	0	100	100
18	r	199/263 (76%)	197 (99%)	2 (1%)	0	100	100
19	S	211/241 (88%)	206 (98%)	4 (2%)	1 (0%)	24	60
19	s	211/241 (88%)	207 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	213/264 (81%)	207 (97%)	6 (3%)	0	100	100
20	t	213/264 (81%)	209 (98%)	4 (2%)	0	100	100
21	U	798/953 (84%)	769 (96%)	21 (3%)	8 (1%)	12	45
22	V	441/534 (83%)	414 (94%)	24 (5%)	3 (1%)	18	53
23	W	454/456 (100%)	426 (94%)	17 (4%)	11 (2%)	4	24
24	X	378/422 (90%)	355 (94%)	14 (4%)	9 (2%)	4	24
25	Y	376/389 (97%)	351 (93%)	21 (6%)	4 (1%)	11	43
26	Z	284/324 (88%)	256 (90%)	24 (8%)	4 (1%)	9	36
27	a	371/376 (99%)	345 (93%)	23 (6%)	3 (1%)	16	50
28	b	189/377 (50%)	179 (95%)	6 (3%)	4 (2%)	5	27
29	c	274/310 (88%)	256 (93%)	17 (6%)	1 (0%)	30	65
30	d	255/350 (73%)	232 (91%)	13 (5%)	10 (4%)	2	14
31	e	36/70 (51%)	29 (81%)	6 (17%)	1 (3%)	4	21
32	f	669/908 (74%)	612 (92%)	46 (7%)	11 (2%)	7	34
All	All	12946/14870 (87%)	12308 (95%)	509 (4%)	129 (1%)	15	45

5 of 129 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	116	LYS
1	A	117	GLN
1	A	431	THR
2	B	278	ALA
2	B	389	ASP

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	A	297/372 (80%)	251 (84%)	46 (16%)	2	13
2	B	300/385 (78%)	245 (82%)	55 (18%)	2	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	315/352 (90%)	272 (86%)	43 (14%)	3	17
4	D	333/366 (91%)	284 (85%)	49 (15%)	3	15
5	E	298/341 (87%)	258 (87%)	40 (13%)	4	18
6	F	295/379 (78%)	259 (88%)	36 (12%)	5	21
7	G	192/210 (91%)	173 (90%)	19 (10%)	7	30
7	g	193/210 (92%)	171 (89%)	22 (11%)	5	24
8	H	165/191 (86%)	143 (87%)	22 (13%)	4	18
8	h	165/191 (86%)	146 (88%)	19 (12%)	5	24
9	I	191/221 (86%)	170 (89%)	21 (11%)	6	25
9	i	193/221 (87%)	163 (84%)	30 (16%)	2	13
10	J	153/211 (72%)	129 (84%)	24 (16%)	2	13
10	j	152/211 (72%)	126 (83%)	26 (17%)	2	11
11	K	193/203 (95%)	163 (84%)	30 (16%)	2	13
11	k	189/203 (93%)	160 (85%)	29 (15%)	3	14
12	L	198/224 (88%)	178 (90%)	20 (10%)	7	29
12	l	198/224 (88%)	178 (90%)	20 (10%)	7	29
13	M	192/212 (91%)	175 (91%)	17 (9%)	9	34
13	m	192/212 (91%)	170 (88%)	22 (12%)	5	24
14	N	152/181 (84%)	131 (86%)	21 (14%)	3	17
14	n	159/181 (88%)	147 (92%)	12 (8%)	12	41
15	O	179/228 (78%)	160 (89%)	19 (11%)	6	27
15	o	177/228 (78%)	162 (92%)	15 (8%)	10	36
16	P	173/174 (99%)	150 (87%)	23 (13%)	4	18
16	p	172/174 (99%)	155 (90%)	17 (10%)	7	30
17	Q	164/171 (96%)	146 (89%)	18 (11%)	6	25
17	q	164/171 (96%)	142 (87%)	22 (13%)	4	18
18	R	153/202 (76%)	140 (92%)	13 (8%)	10	36
18	r	153/202 (76%)	137 (90%)	16 (10%)	6	27
19	S	175/199 (88%)	164 (94%)	11 (6%)	16	48
19	s	174/199 (87%)	164 (94%)	10 (6%)	18	52
20	T	176/215 (82%)	155 (88%)	21 (12%)	5	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	t	176/215 (82%)	159 (90%)	17 (10%)	8	30
21	U	685/816 (84%)	585 (85%)	100 (15%)	3	15
22	V	387/460 (84%)	331 (86%)	56 (14%)	3	15
23	W	416/416 (100%)	338 (81%)	78 (19%)	1	9
24	X	327/362 (90%)	272 (83%)	55 (17%)	2	11
25	Y	334/344 (97%)	288 (86%)	46 (14%)	3	17
26	Z	257/295 (87%)	199 (77%)	58 (23%)	1	5
27	a	333/336 (99%)	274 (82%)	59 (18%)	2	10
28	b	167/312 (54%)	141 (84%)	26 (16%)	2	13
29	c	243/268 (91%)	193 (79%)	50 (21%)	1	7
30	d	231/294 (79%)	189 (82%)	42 (18%)	2	9
31	e	38/63 (60%)	34 (90%)	4 (10%)	6	27
32	f	580/763 (76%)	453 (78%)	127 (22%)	1	5
All	All	10749/12608 (85%)	9223 (86%)	1526 (14%)	5	16

5 of 1526 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	Z	208	ILE
32	f	174	ASP
27	a	105	LYS
26	Z	206	LEU
29	c	106	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 288 such sidechains are listed below:

Mol	Chain	Res	Type
7	g	193	GLN
20	t	147	GLN
8	h	169	ASN
12	l	59	HIS
17	Q	71	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
34	LDZ	O	301	-	33,34,34	1.82	7 (21%)	42,44,44	1.55	7 (16%)
33	ATP	A	501	-	32,33,33	0.54	0	48,52,52	0.68	0
34	LDZ	R	301	-	33,34,34	1.81	7 (21%)	42,44,44	1.68	7 (16%)
34	LDZ	n	301	-	33,34,34	1.84	7 (21%)	42,44,44	1.63	6 (14%)
34	LDZ	N	301	-	33,34,34	1.76	7 (21%)	42,44,44	1.30	5 (11%)
34	LDZ	o	301	-	33,34,34	1.79	7 (21%)	42,44,44	1.36	6 (14%)
34	LDZ	r	301	-	33,34,34	1.86	7 (21%)	42,44,44	1.60	9 (21%)
33	ATP	D	501	-	32,33,33	0.53	0	48,52,52	0.56	0
33	ATP	F	501	-	32,33,33	0.57	0	48,52,52	0.62	0
33	ATP	C	501	-	32,33,33	0.53	0	48,52,52	0.55	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	LDZ	O	301	-	-	16/38/39/39	0/1/1/1
33	ATP	A	501	-	-	2/22/38/38	0/3/3/3
34	LDZ	R	301	-	-	15/38/39/39	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	LDZ	n	301	-	-	14/38/39/39	0/1/1/1
34	LDZ	N	301	-	-	17/38/39/39	0/1/1/1
34	LDZ	o	301	-	-	9/38/39/39	0/1/1/1
34	LDZ	r	301	-	-	12/38/39/39	0/1/1/1
33	ATP	D	501	-	-	4/22/38/38	0/3/3/3
33	ATP	F	501	-	-	8/22/38/38	0/3/3/3
33	ATP	C	501	-	-	5/22/38/38	0/3/3/3

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	r	301	LDZ	C12-N13	5.75	1.46	1.34
34	O	301	LDZ	C12-N13	5.65	1.46	1.34
34	n	301	LDZ	C15-N16	5.64	1.46	1.34
34	R	301	LDZ	C15-N16	5.52	1.45	1.34
34	R	301	LDZ	C12-N13	5.33	1.45	1.34

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	O	301	LDZ	O8-C9-N10	5.17	121.51	110.45
34	n	301	LDZ	C14-C15-N16	4.99	127.27	116.63
34	r	301	LDZ	O8-C9-N10	4.92	120.97	110.45
34	r	301	LDZ	C11-C12-N13	4.65	126.56	116.63
34	R	301	LDZ	O8-C9-N10	4.57	120.23	110.45

There are no chirality outliers.

5 of 102 torsion outliers are listed below:

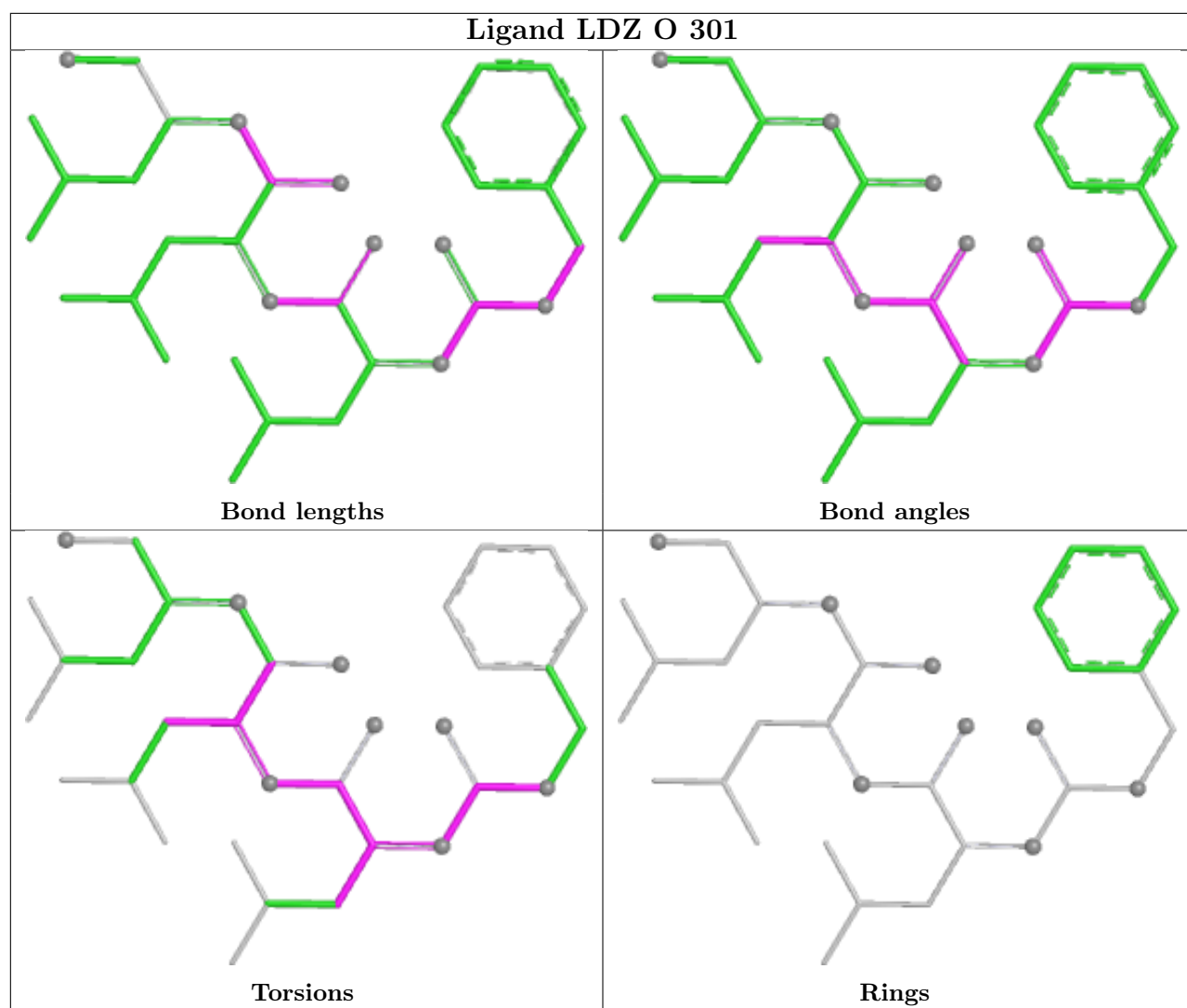
Mol	Chain	Res	Type	Atoms
33	C	501	ATP	C5'-O5'-PA-O2A
33	C	501	ATP	C5'-O5'-PA-O3A
33	F	501	ATP	C3'-C4'-C5'-O5'
34	N	301	LDZ	O31-C9-O8-C7
34	N	301	LDZ	N10-C9-O8-C7

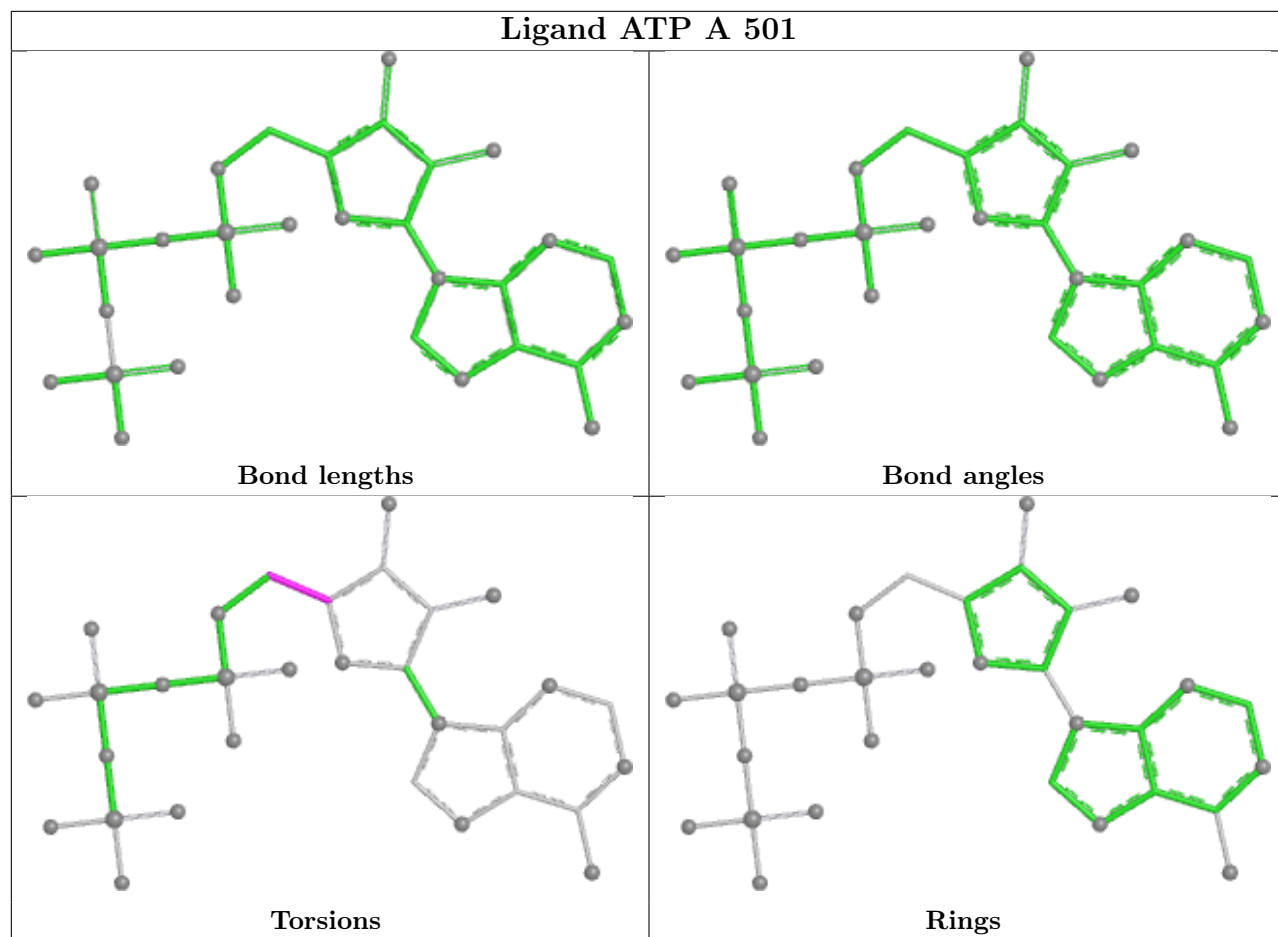
There are no ring outliers.

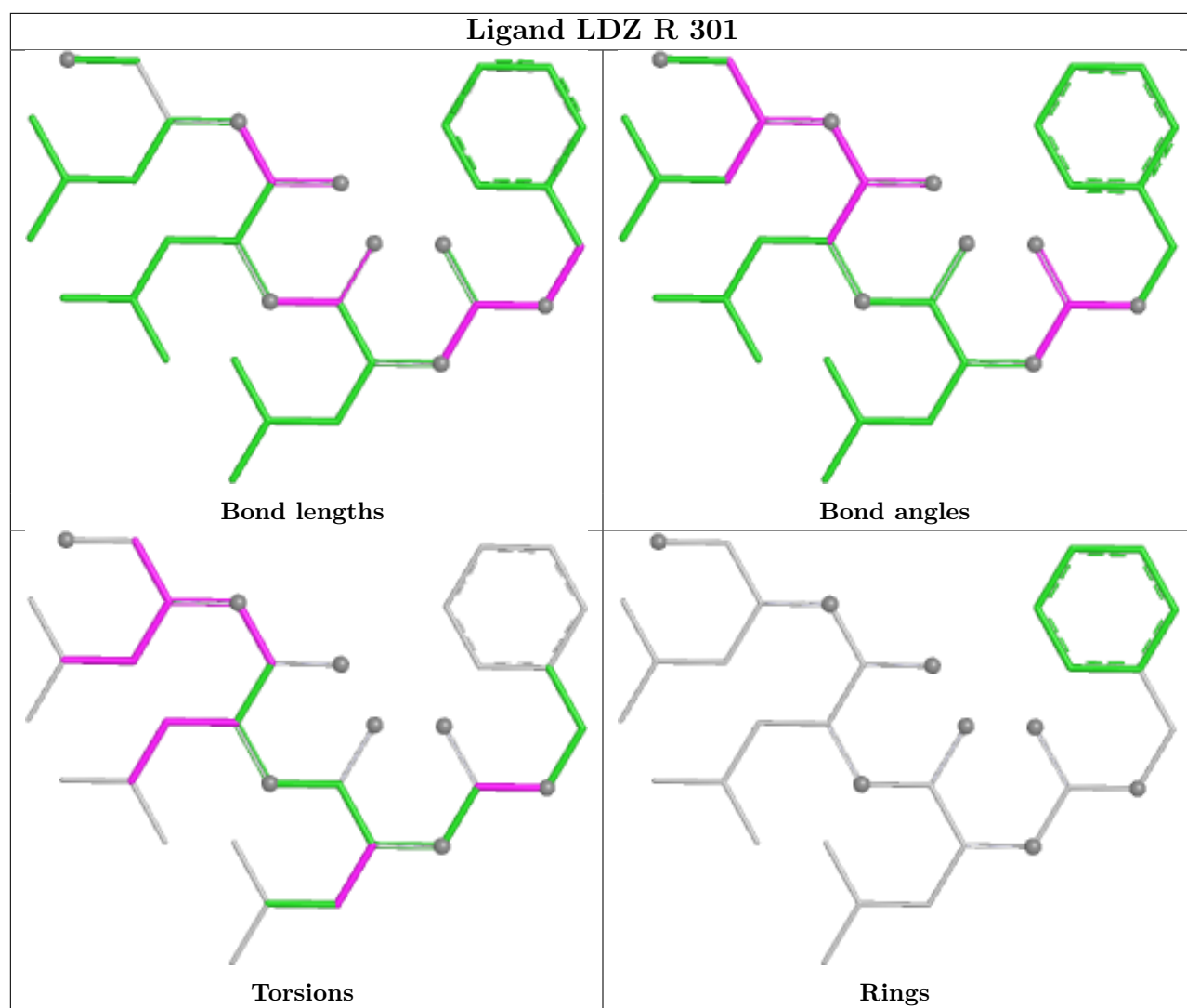
8 monomers are involved in 24 short contacts:

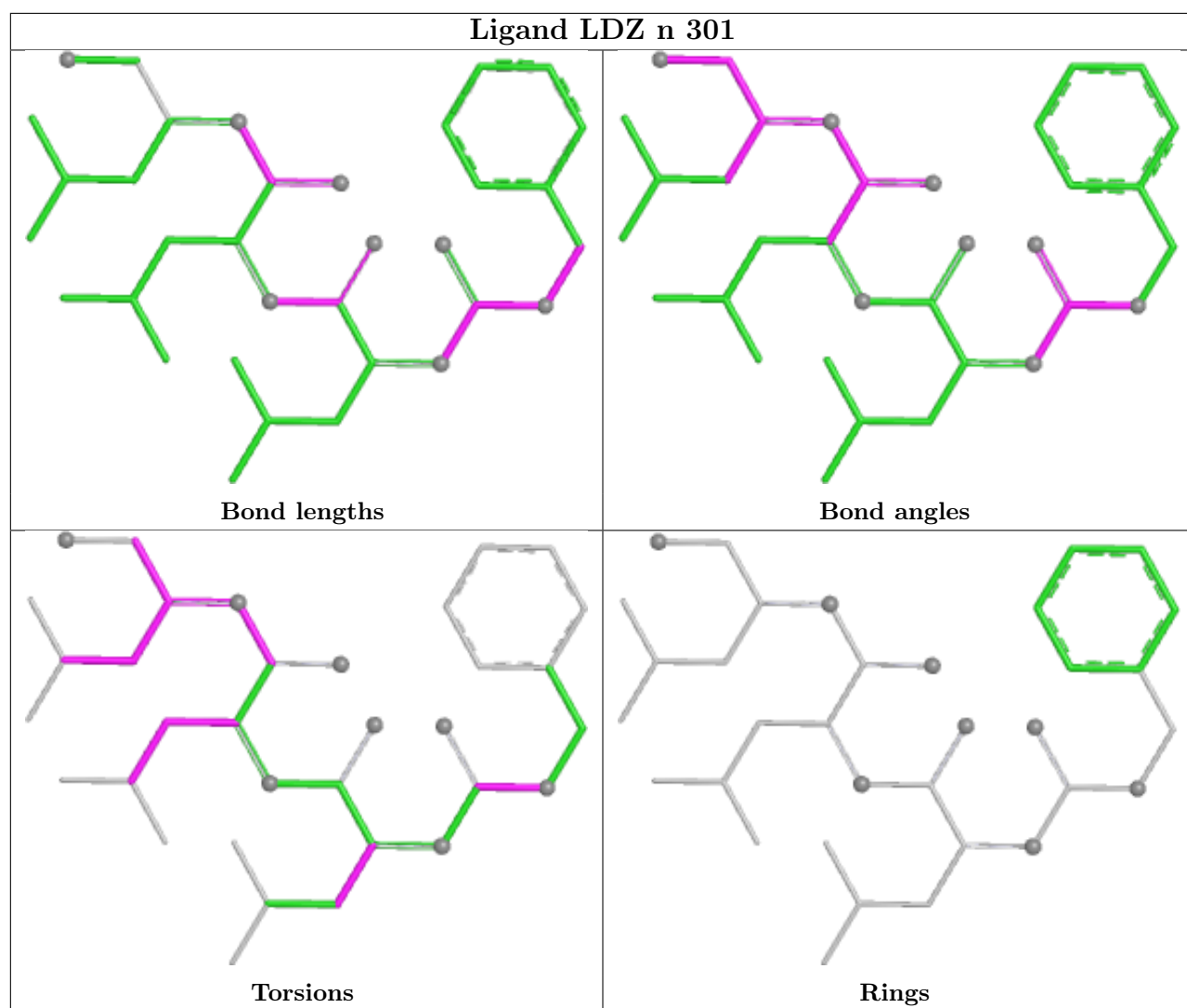
Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	O	301	LDZ	3	0
34	R	301	LDZ	3	0
34	n	301	LDZ	1	0
34	N	301	LDZ	2	0
34	o	301	LDZ	7	0
34	r	301	LDZ	5	0
33	F	501	ATP	2	0
33	C	501	ATP	1	0

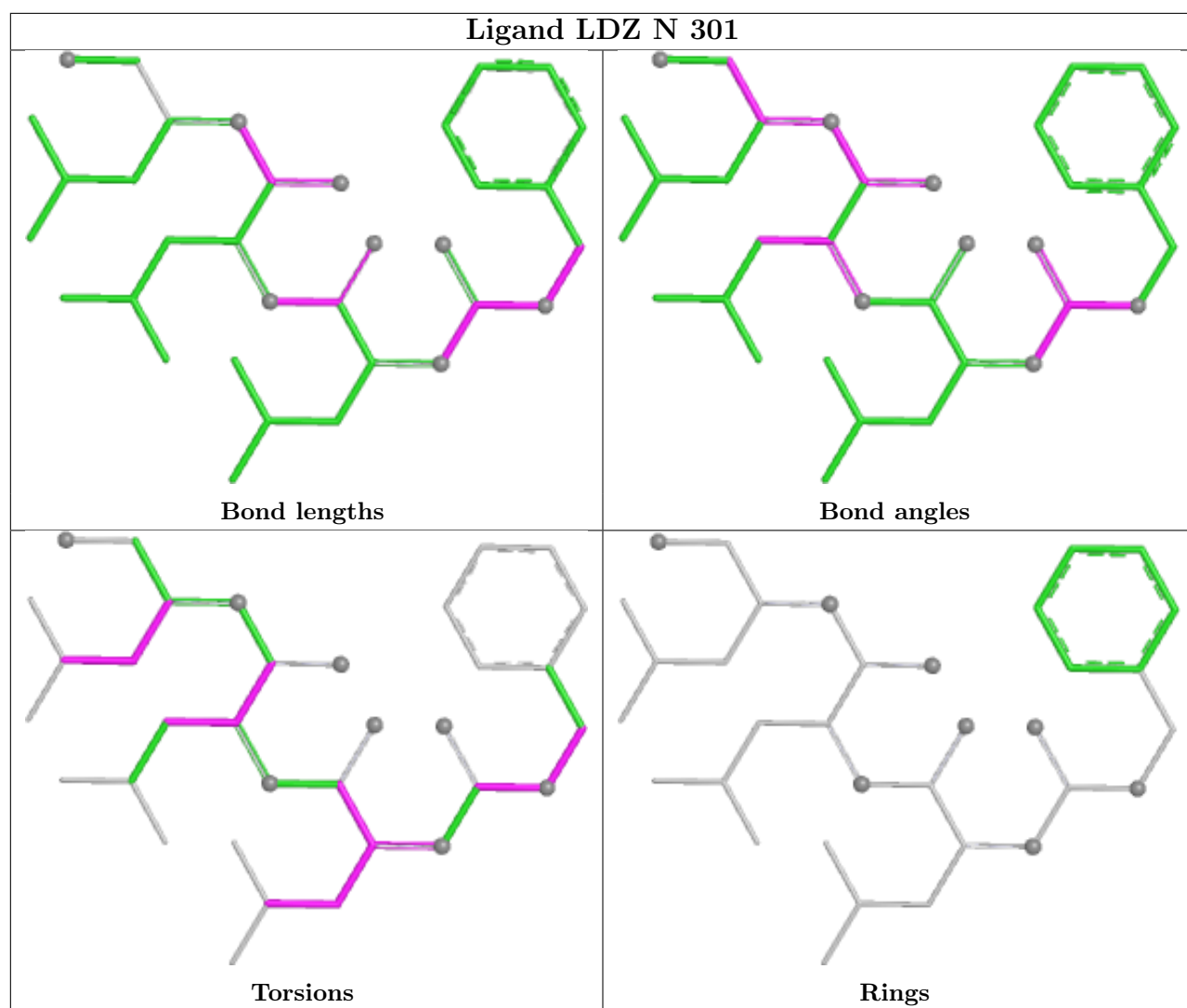
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

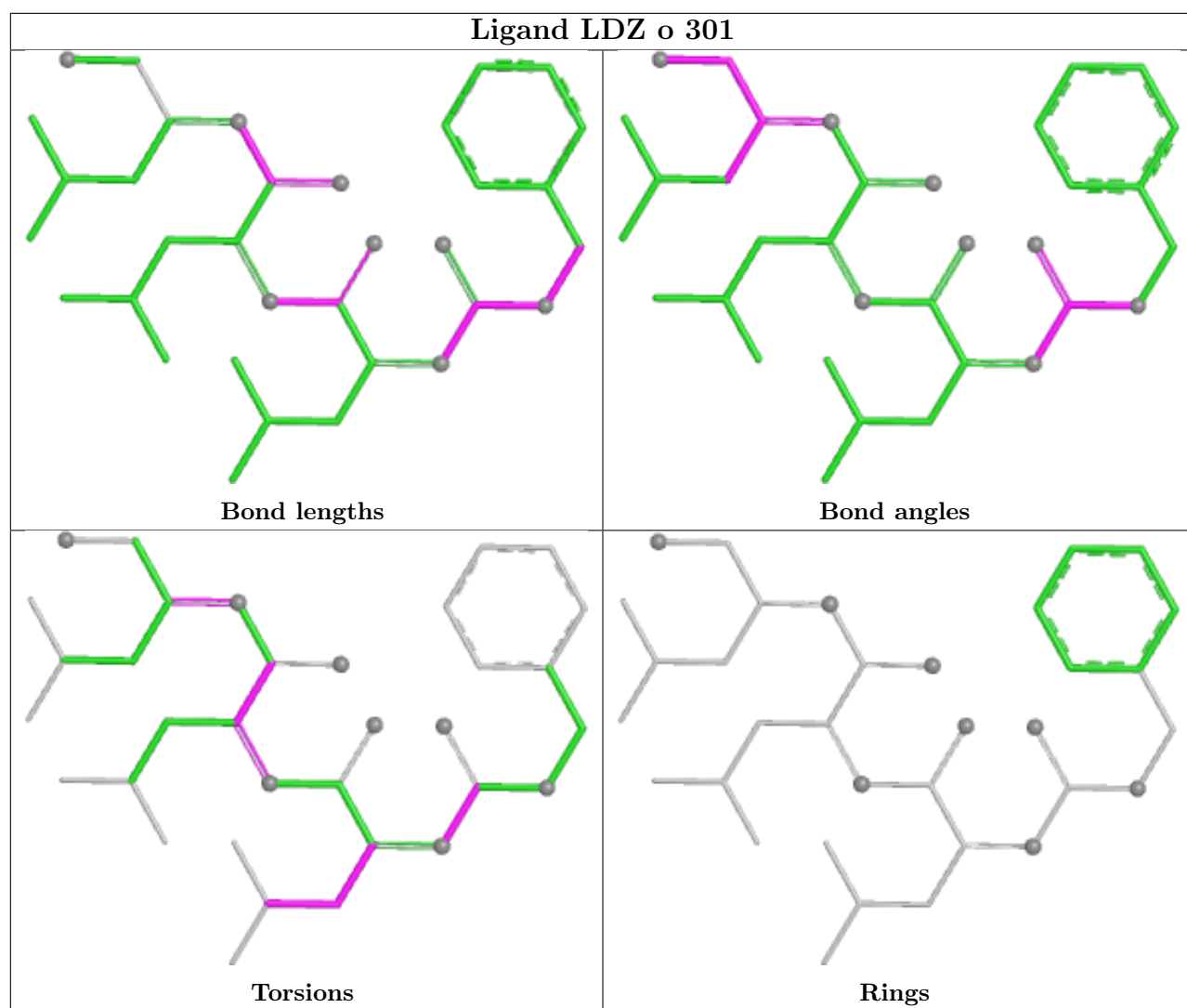


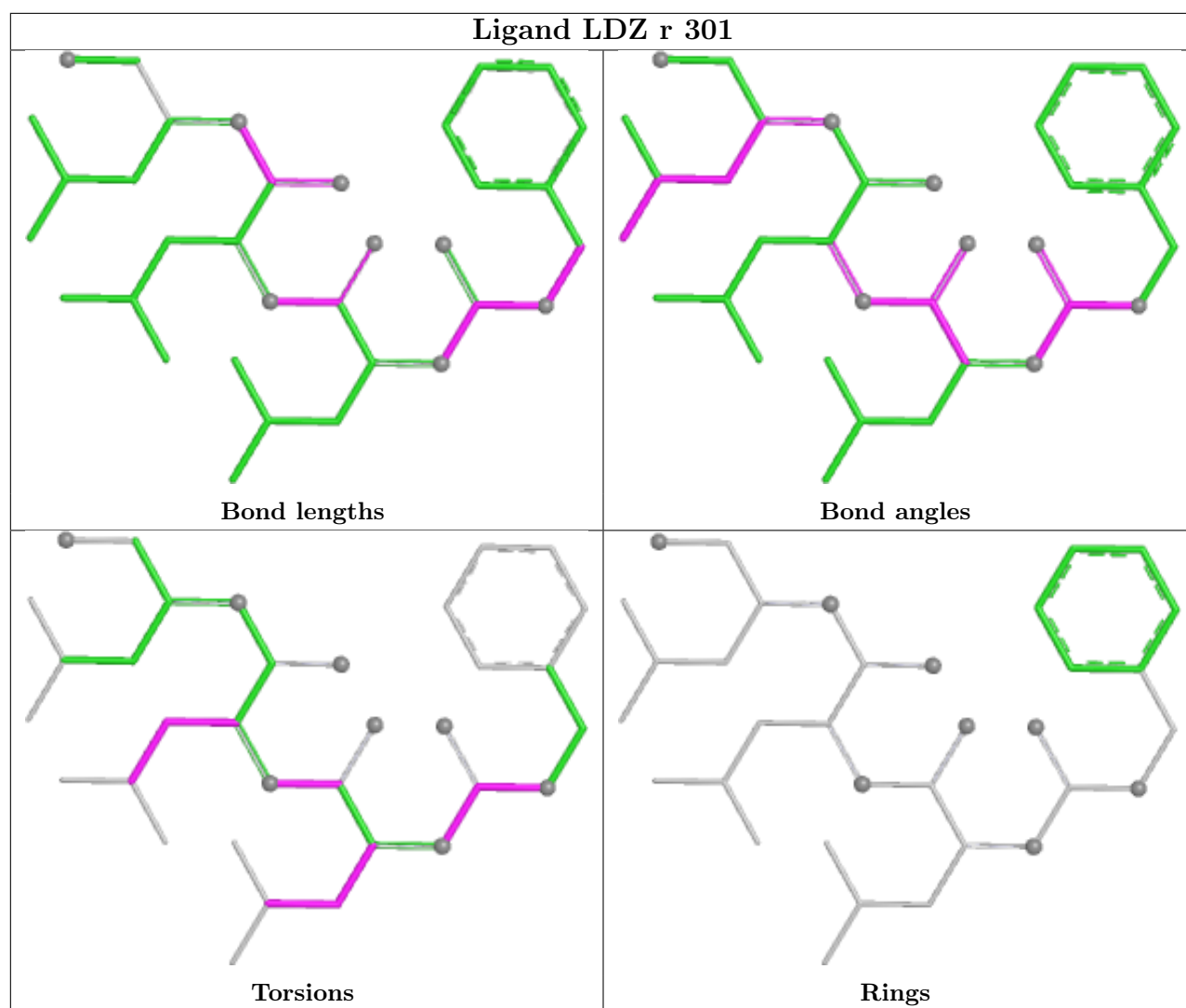


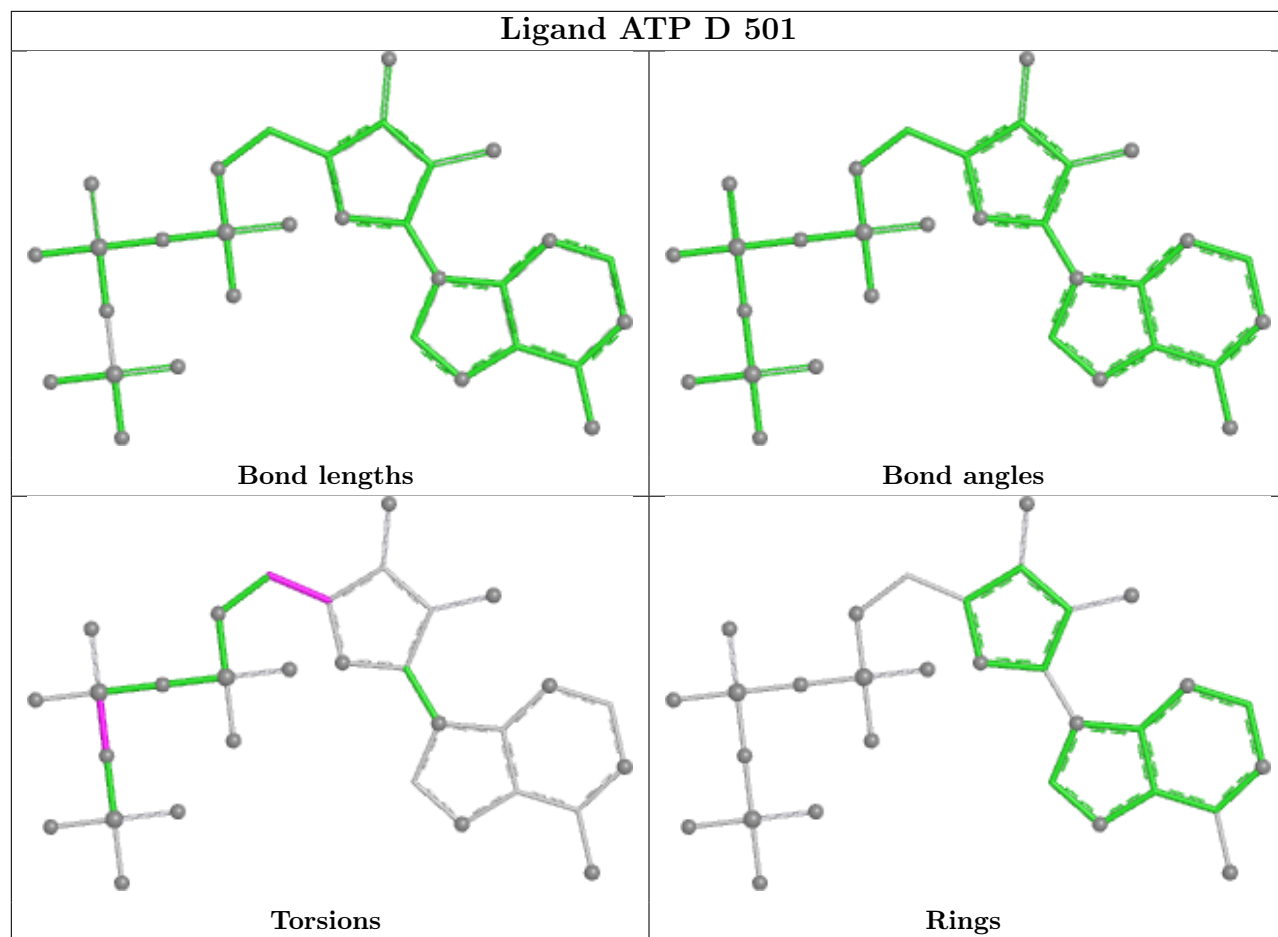


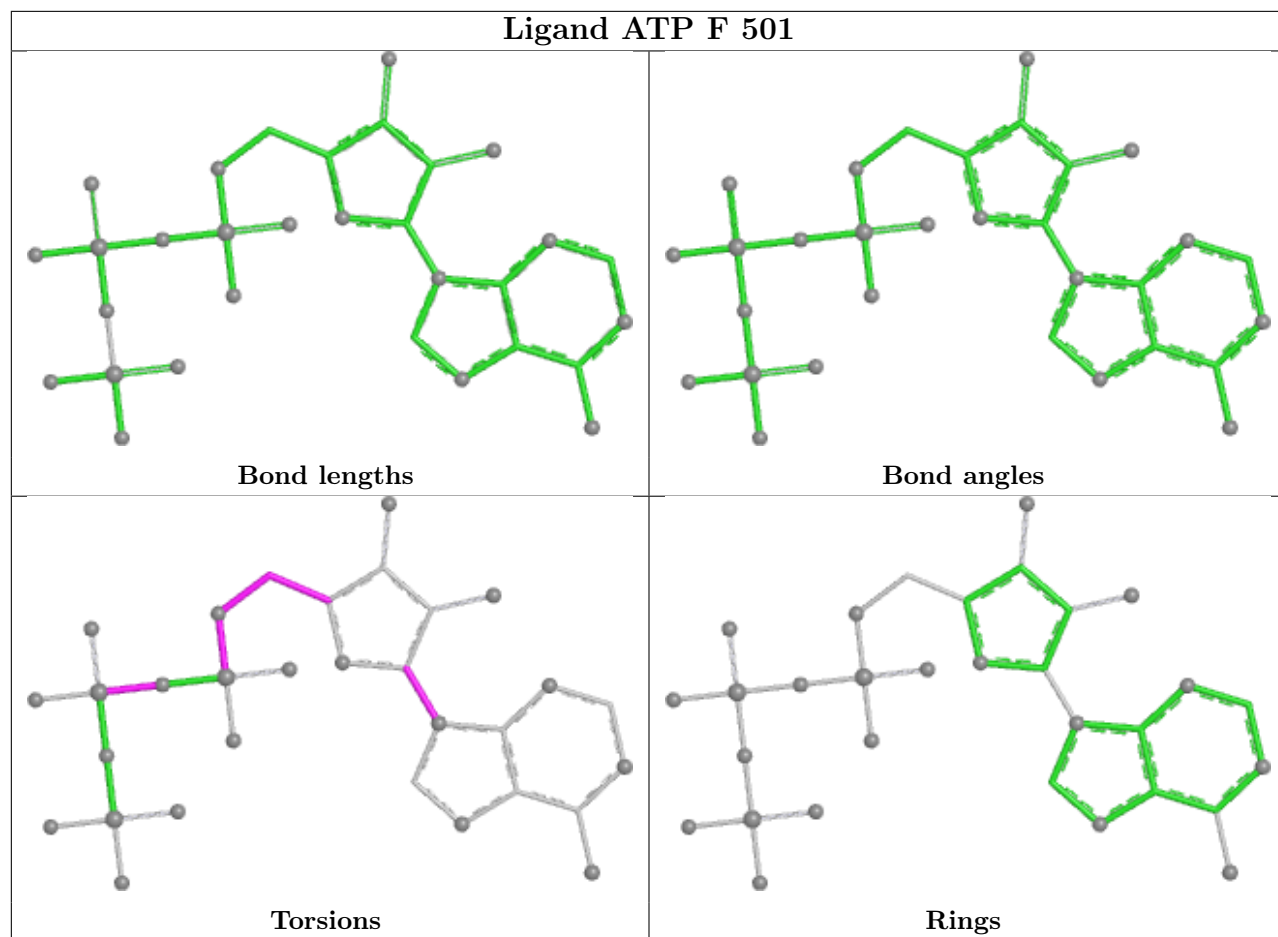


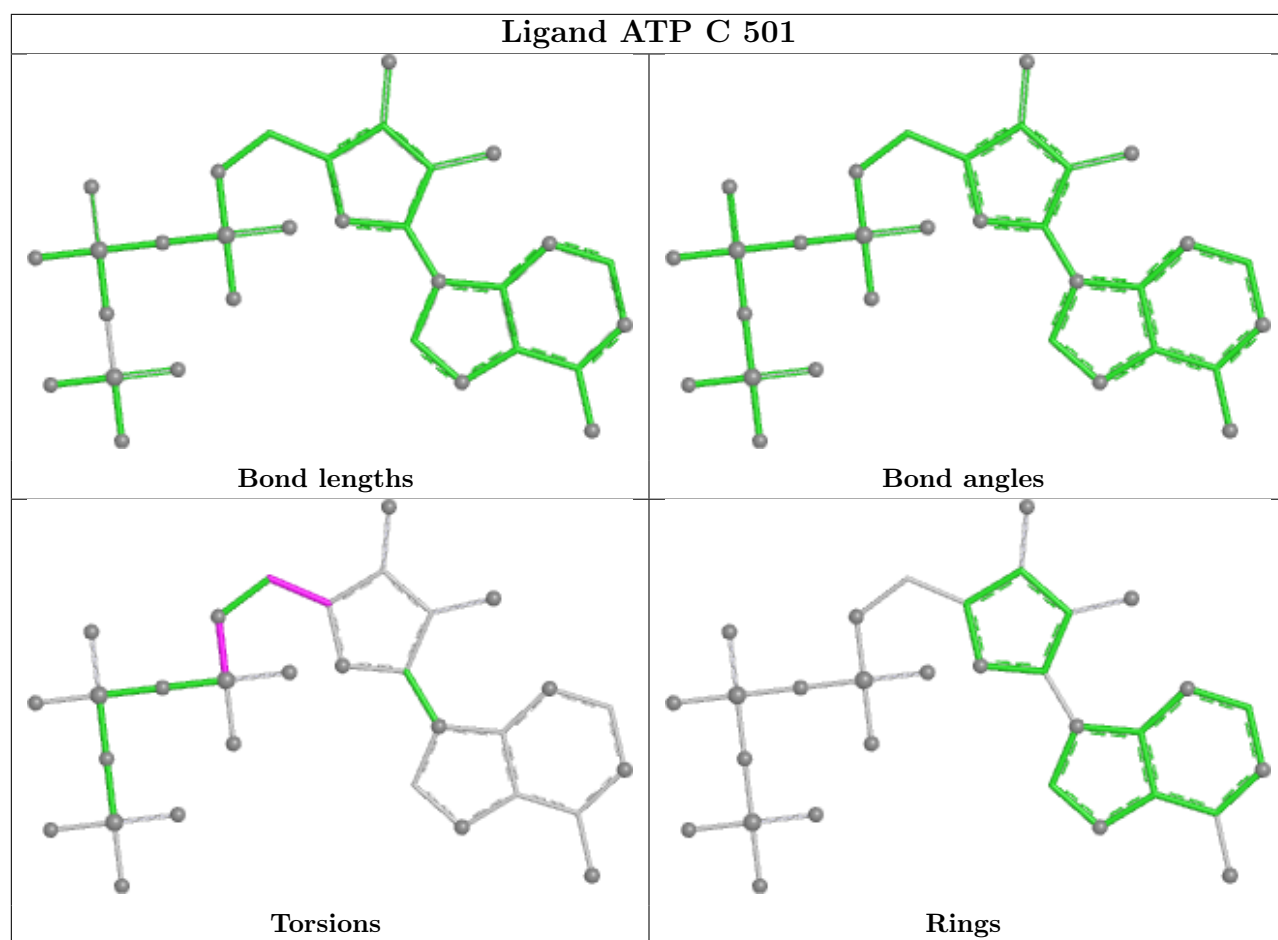












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

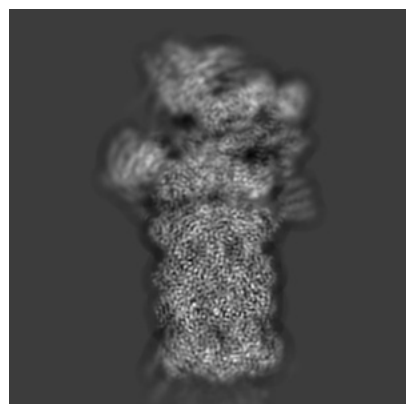
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27018. These allow visual inspection of the internal detail of the map and identification of artifacts.

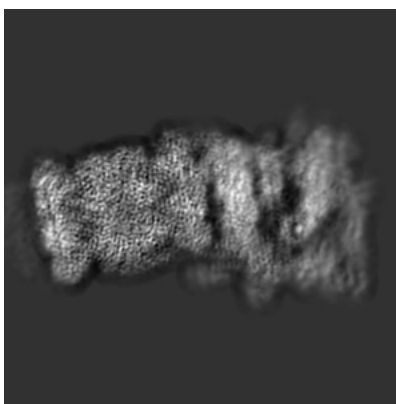
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

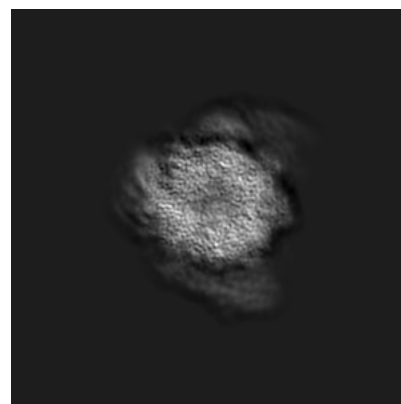
6.1.1 Primary map



X

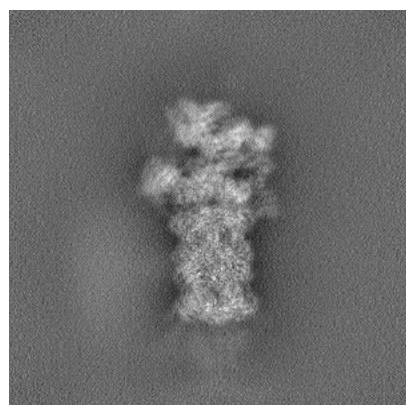


Y

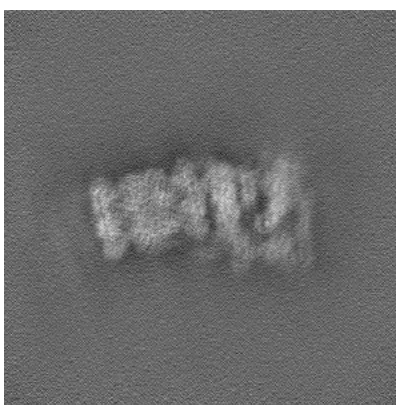


Z

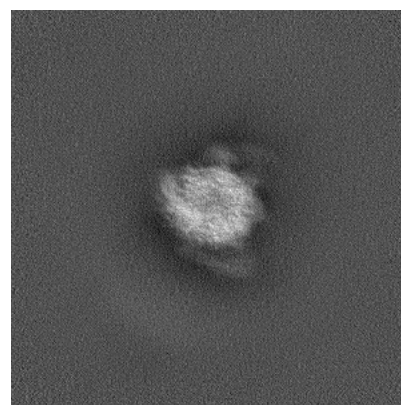
6.1.2 Raw map



X



Y

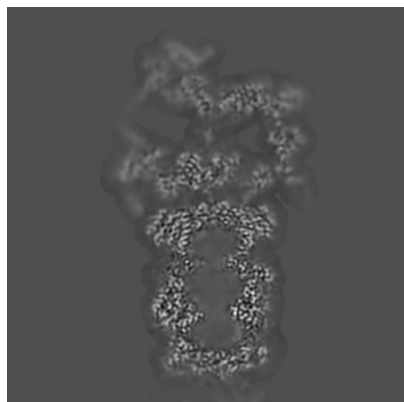


Z

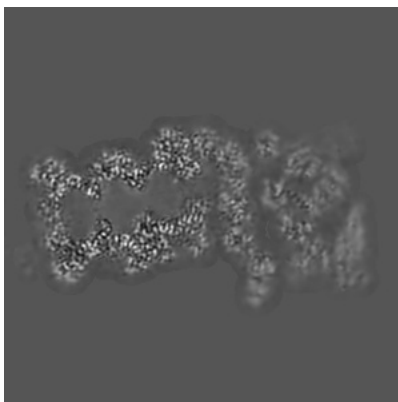
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

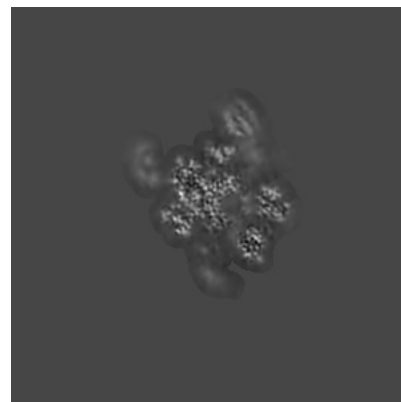
6.2.1 Primary map



X Index: 170

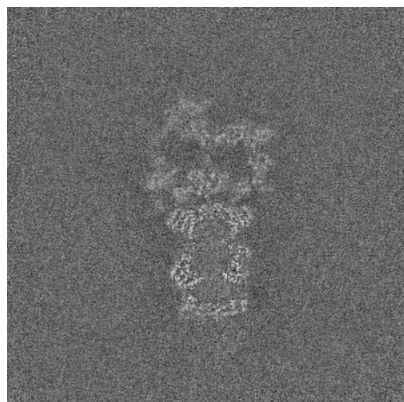


Y Index: 170

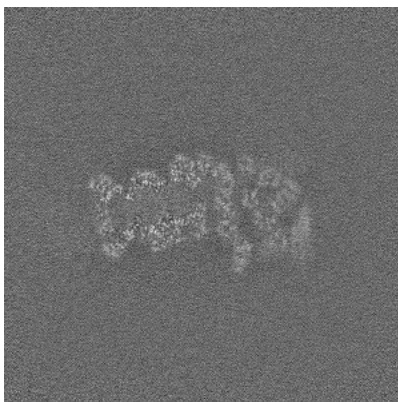


Z Index: 170

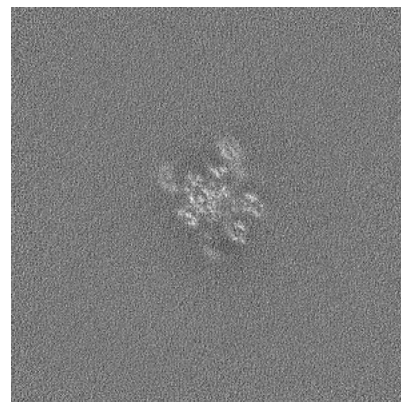
6.2.2 Raw map



X Index: 256



Y Index: 256

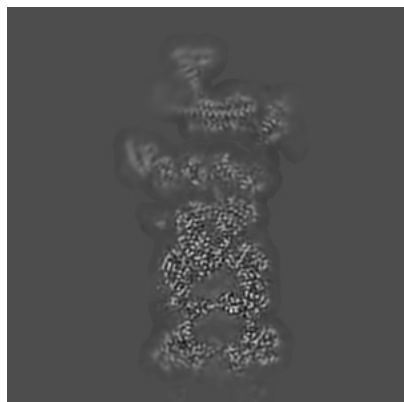


Z Index: 256

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

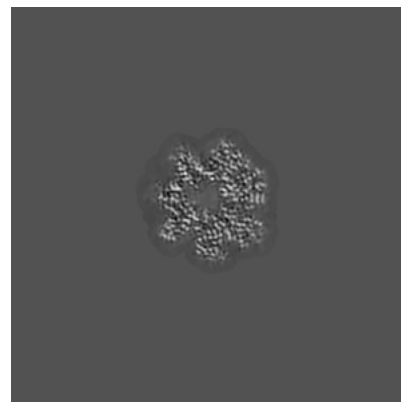
6.3.1 Primary map



X Index: 153

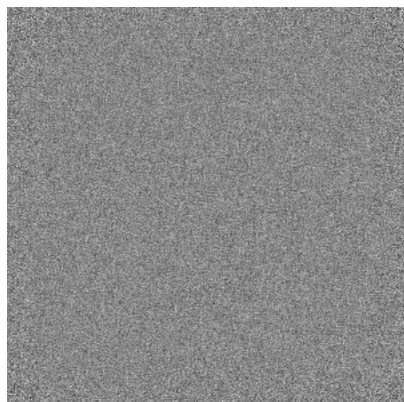


Y Index: 193

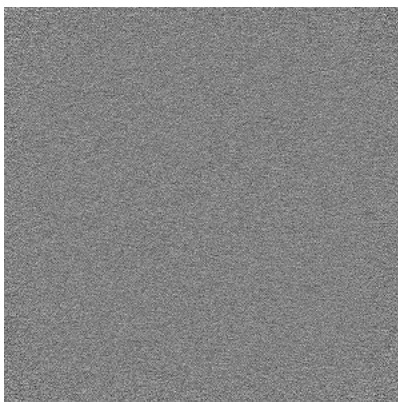


Z Index: 80

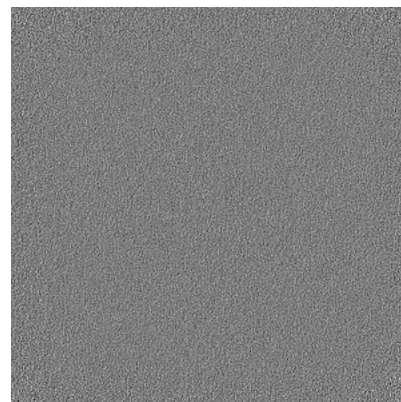
6.3.2 Raw map



X Index: 0



Y Index: 0

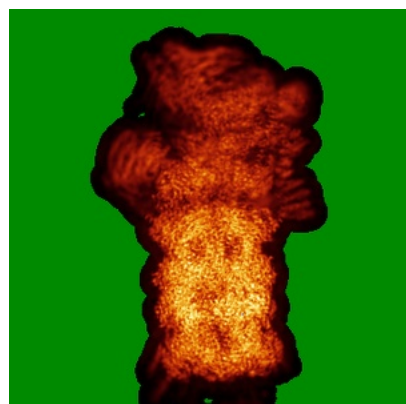


Z Index: 511

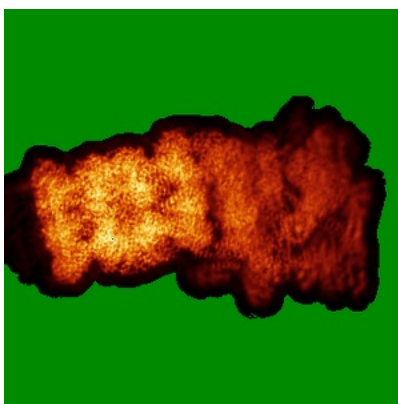
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

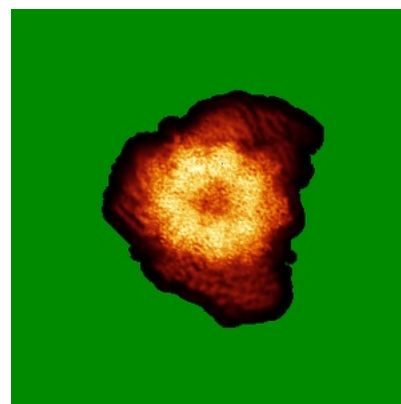
6.4.1 Primary map



X

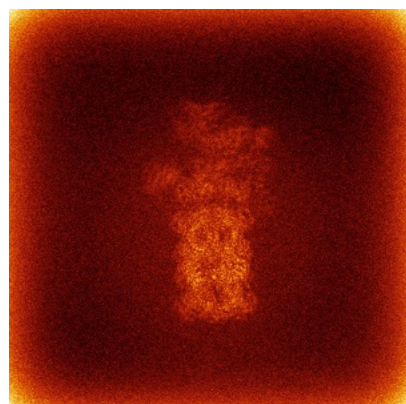


Y

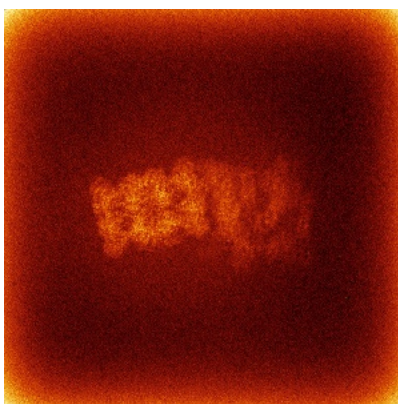


Z

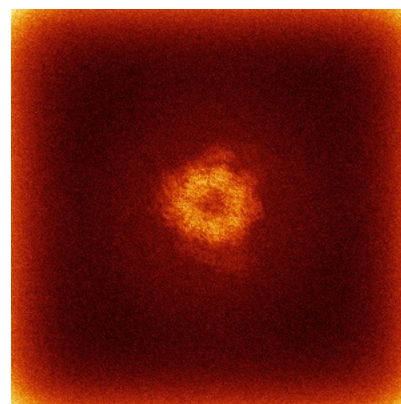
6.4.2 Raw map



X



Y

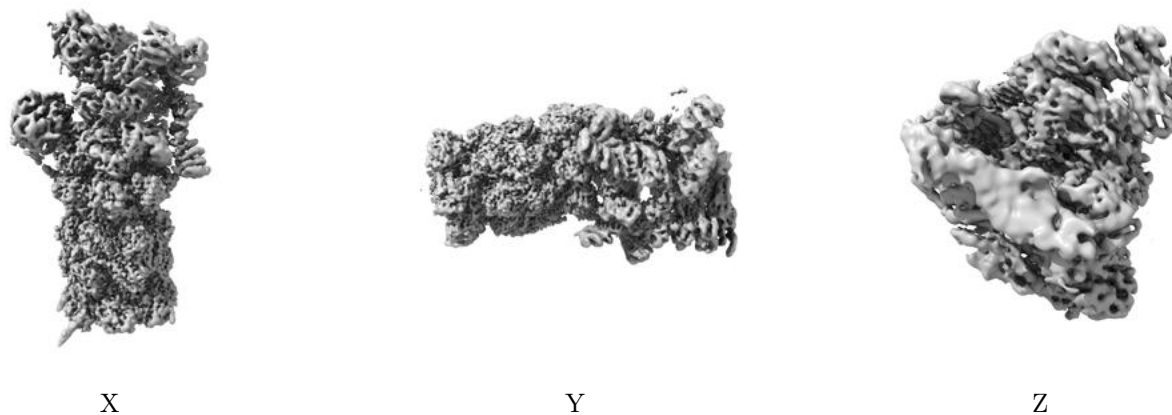


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

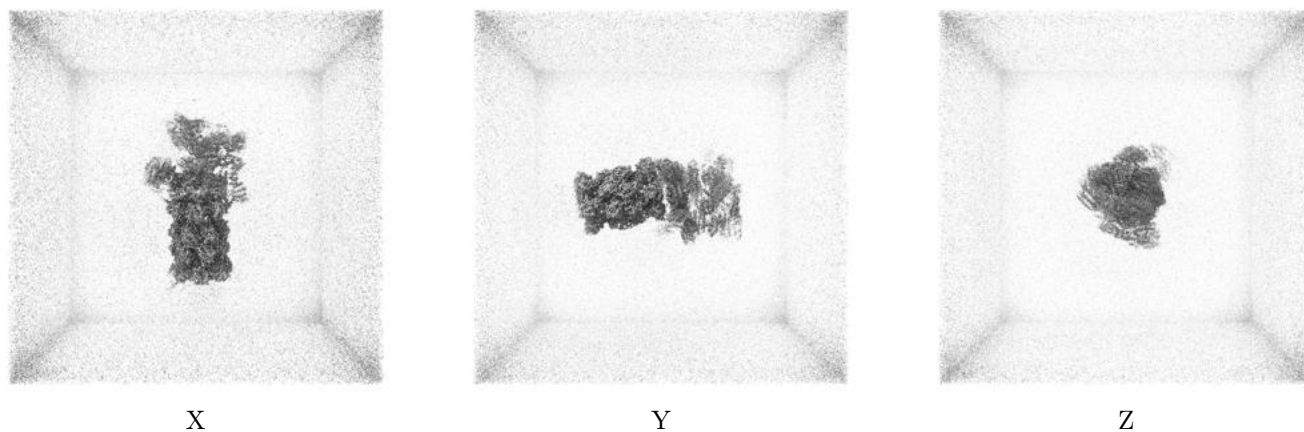
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

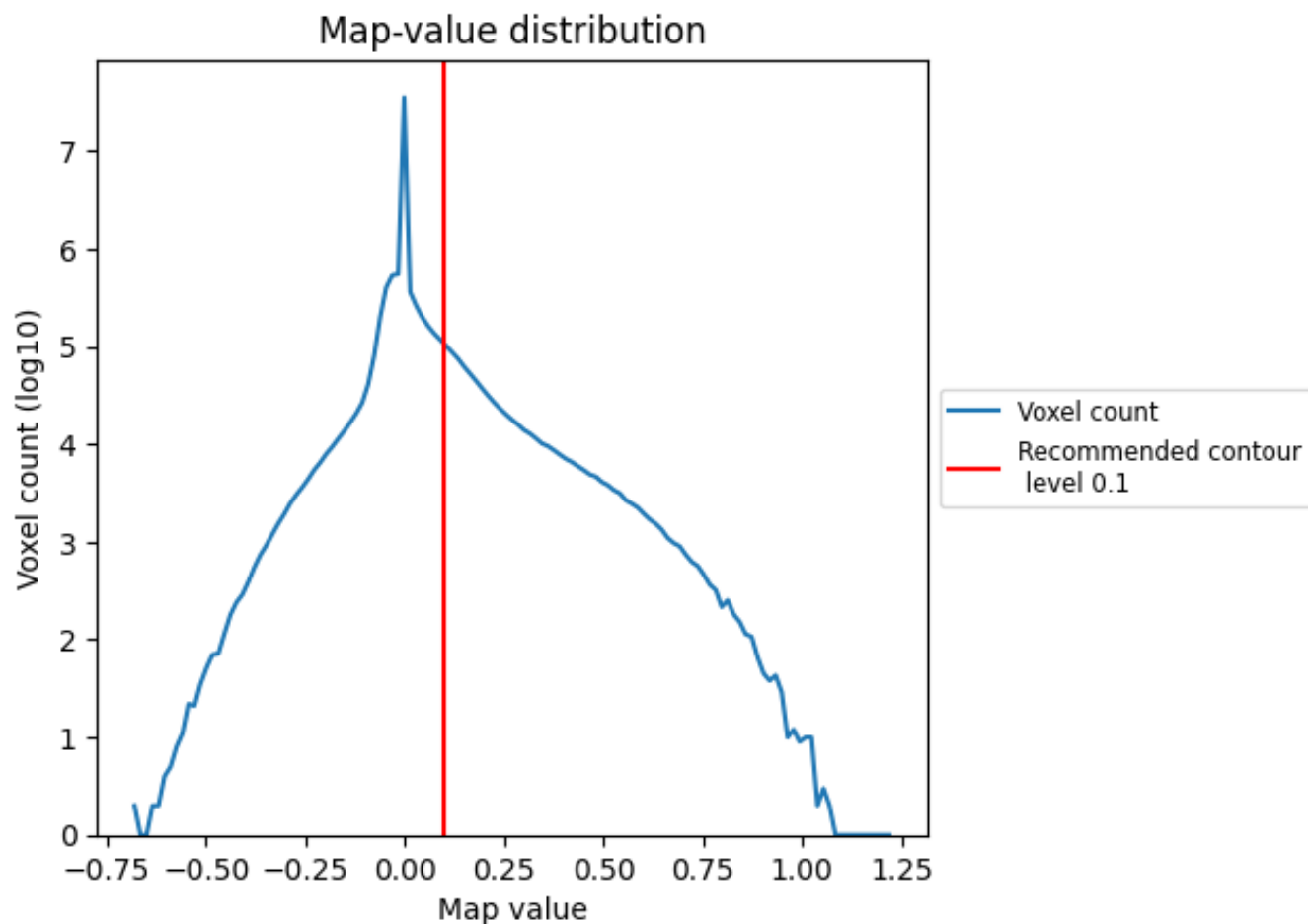
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

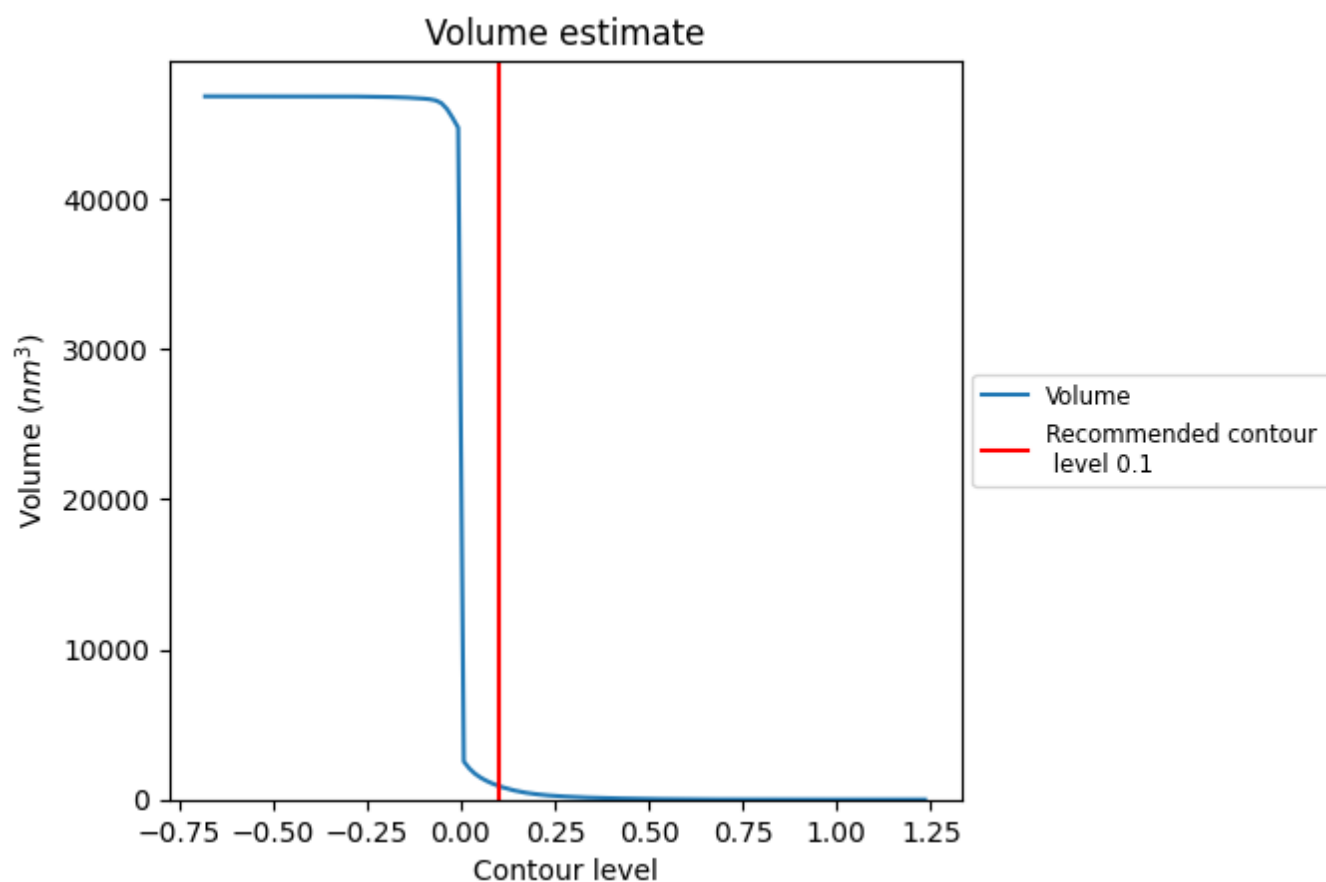
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

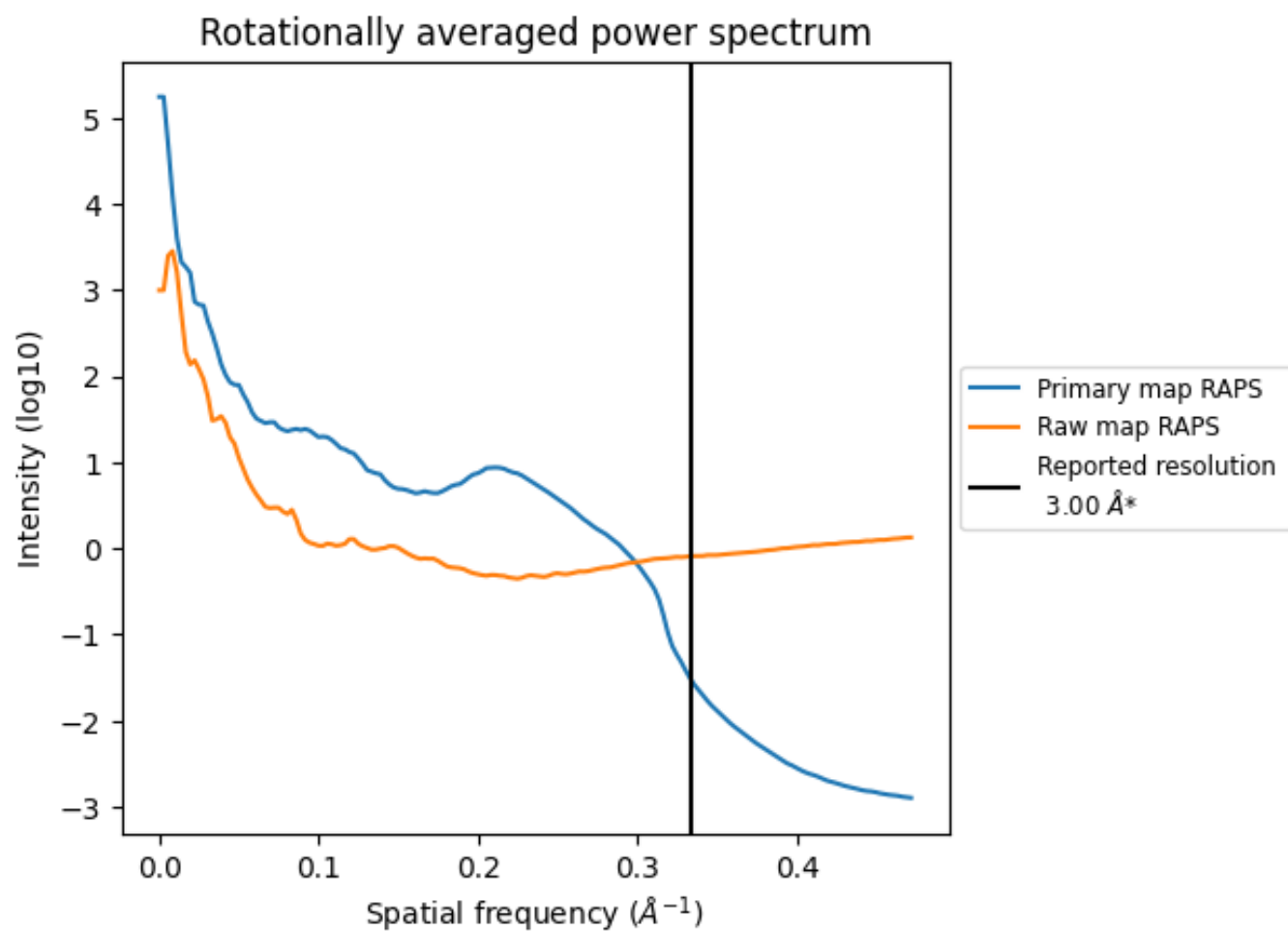
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 915 nm^3 ; this corresponds to an approximate mass of 827 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

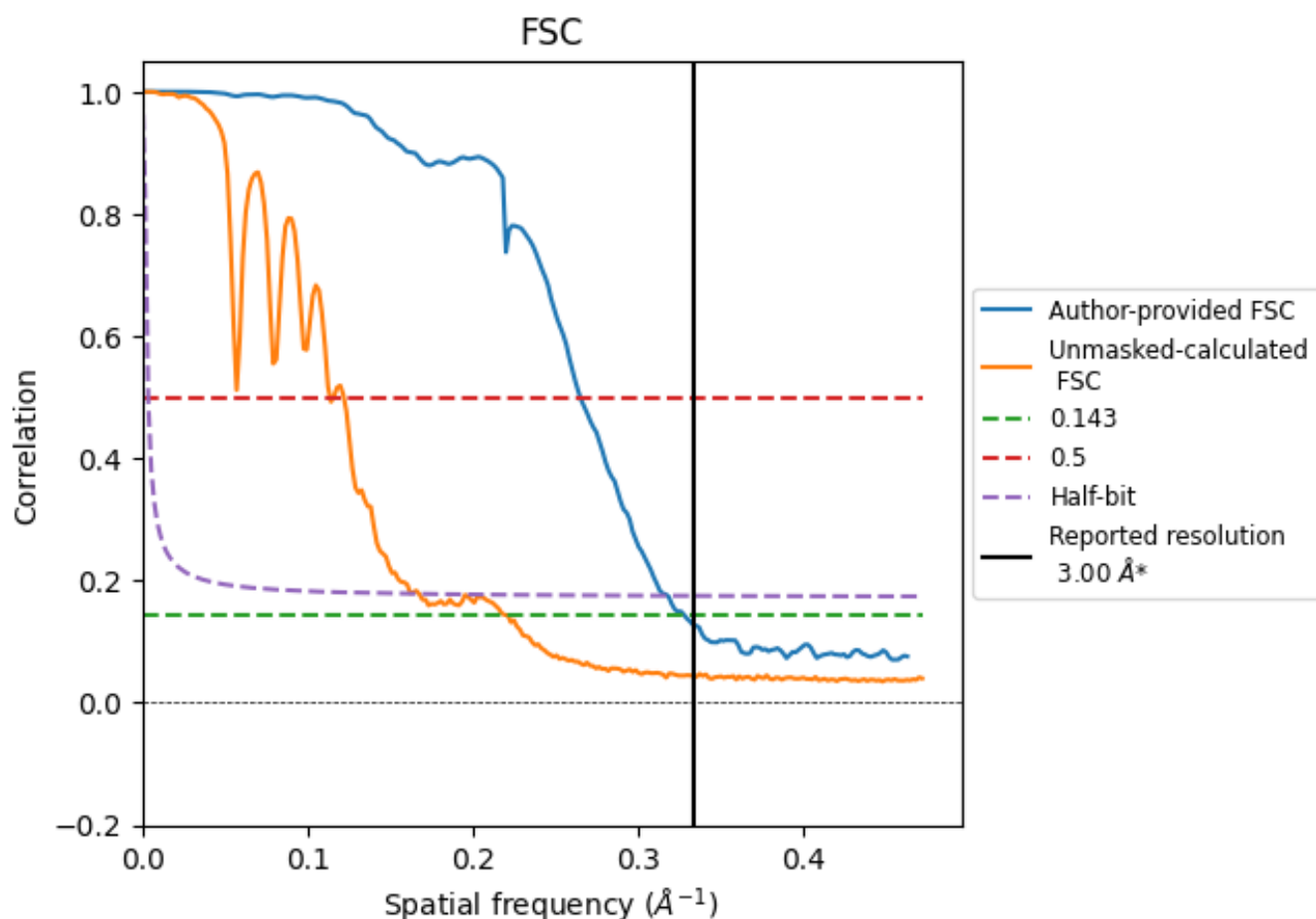


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

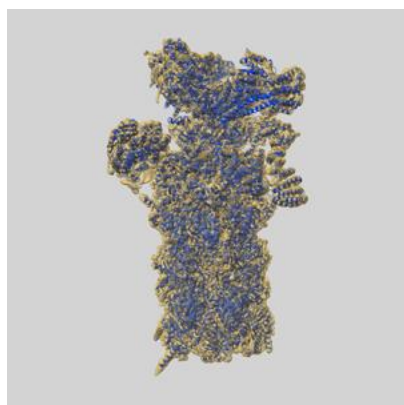
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.05	3.78	3.15
Unmasked-calculated*	4.52	8.80	5.97

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.52 differs from the reported value 3.0 by more than 10 %

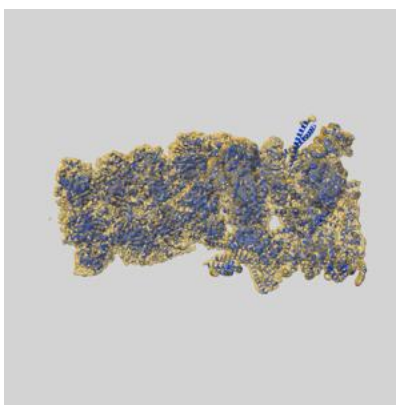
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27018 and PDB model 8CVT. Per-residue inclusion information can be found in section [3](#) on page [12](#).

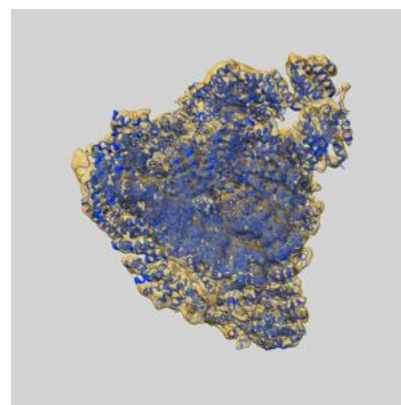
9.1 Map-model overlay [i](#)



X



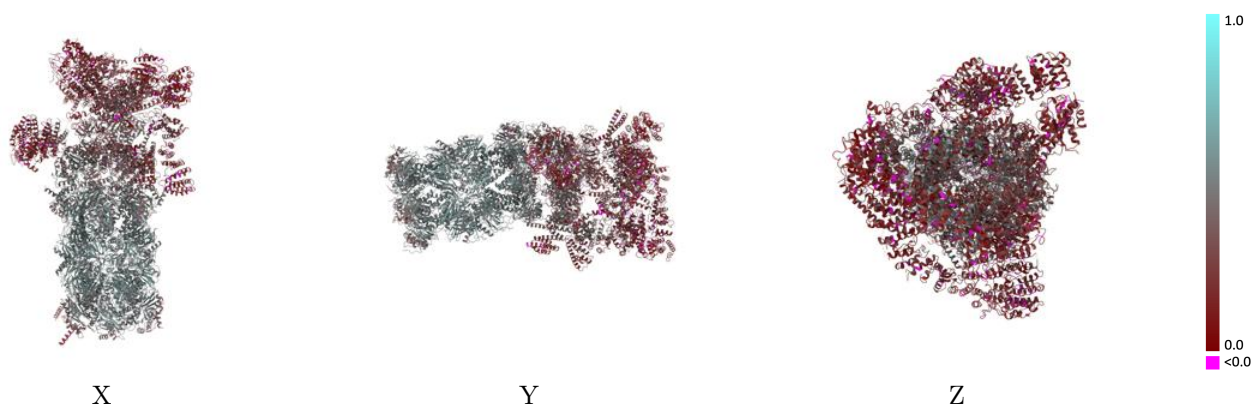
Y



Z

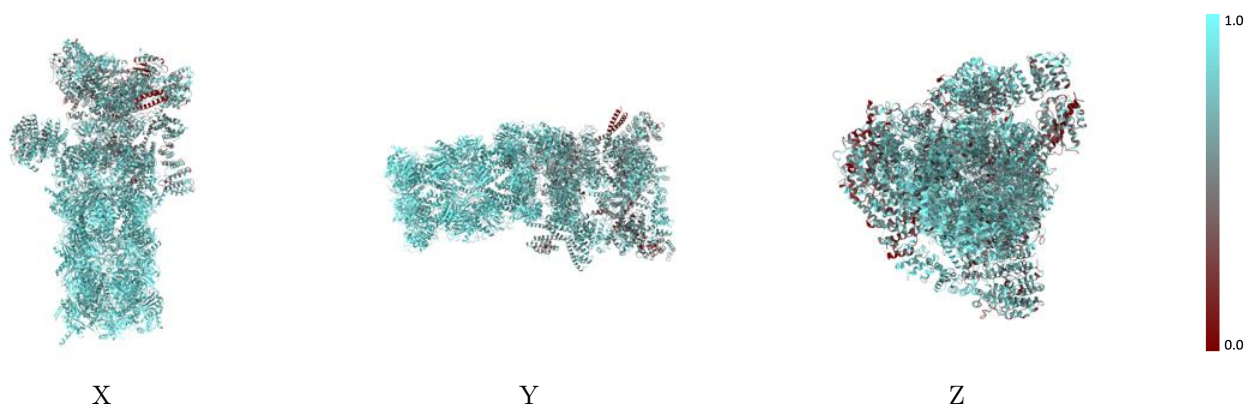
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



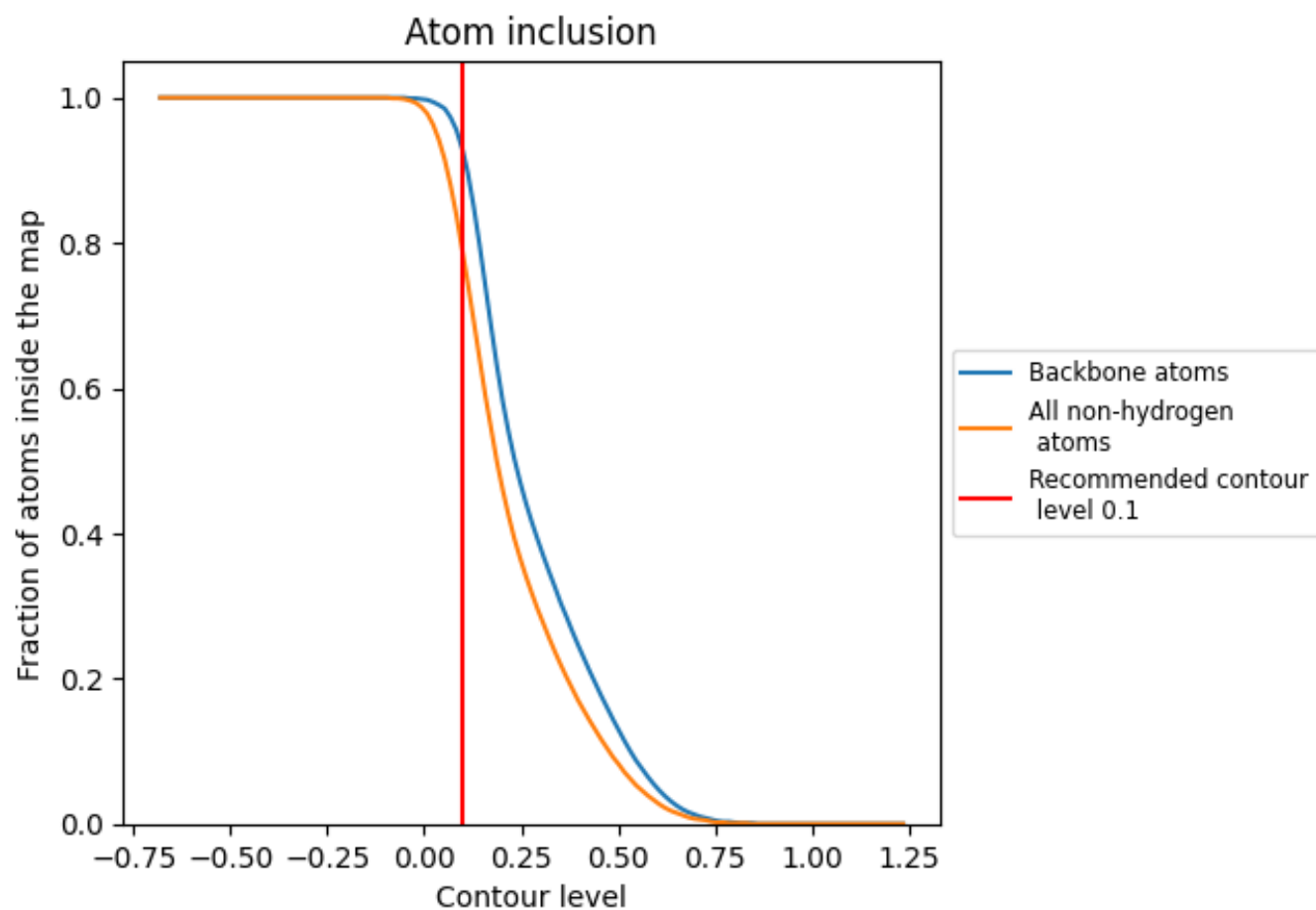
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7850	 0.3760
A	 0.7510	 0.3770
B	 0.7520	 0.3790
C	 0.8000	 0.3780
D	 0.7300	 0.3490
E	 0.5960	 0.2150
F	 0.7010	 0.3270
G	 0.8900	 0.4870
H	 0.9250	 0.4980
I	 0.8830	 0.4860
J	 0.8980	 0.4890
K	 0.8720	 0.4810
L	 0.9080	 0.4940
M	 0.8760	 0.4730
N	 0.9270	 0.5340
O	 0.9190	 0.5220
P	 0.9290	 0.5310
Q	 0.9210	 0.5350
R	 0.9220	 0.5360
S	 0.9390	 0.5350
T	 0.9330	 0.5310
U	 0.7050	 0.2050
V	 0.5590	 0.1920
W	 0.6350	 0.2210
X	 0.6590	 0.3040
Y	 0.7390	 0.3020
Z	 0.6780	 0.2770
a	 0.6720	 0.1950
b	 0.4950	 0.1800
c	 0.6340	 0.2680
d	 0.4930	 0.1770
e	 0.6000	 0.2260
f	 0.6920	 0.1850
g	 0.9000	 0.4780
h	 0.9140	 0.4860



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Chain	Atom inclusion	Q-score
i	 0.8790	 0.4450
j	 0.8790	 0.4460
k	 0.8690	 0.4680
l	 0.9110	 0.4880
m	 0.8920	 0.4850
n	 0.9170	 0.5270
o	 0.9270	 0.5350
p	 0.9330	 0.5320
q	 0.9350	 0.5350
r	 0.9450	 0.5430
s	 0.9400	 0.5500
t	 0.9450	 0.5480