



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 03:51 AM UTC

PDB ID : 7UNF / pdb_00007unf
EMDB ID : EMD-26623
Title : CryoEM structure of a mEAK7 bound human V-ATPase complex
Authors : Wang, R.; Li, X.
Deposited on : 2022-04-10
Resolution : 4.08 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

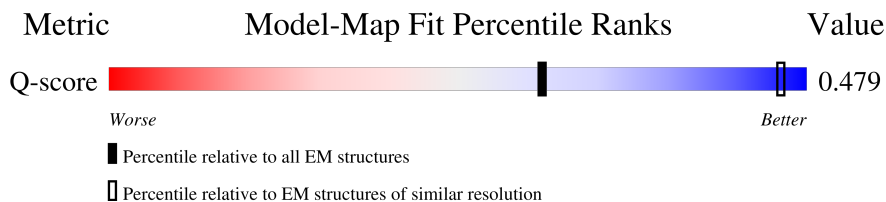
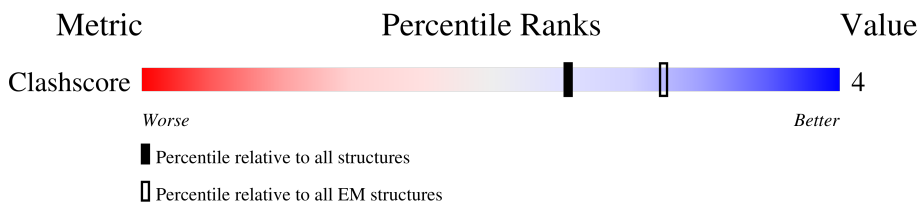
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

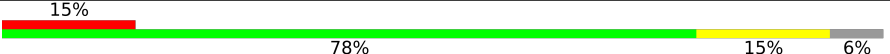
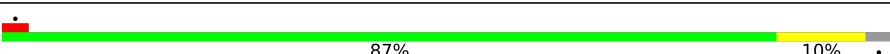
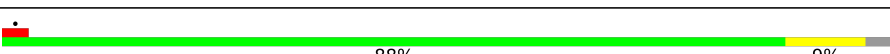
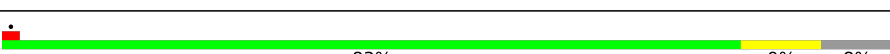
The reported resolution of this entry is 4.08 Å.

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.



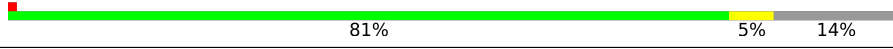
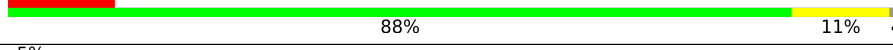
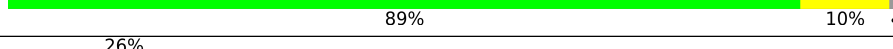
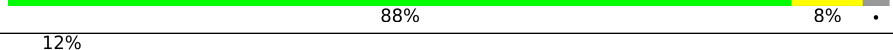
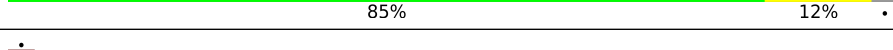
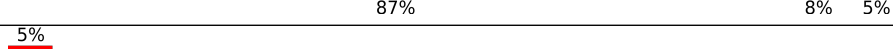
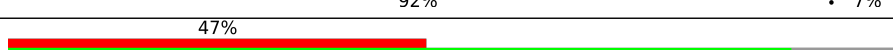
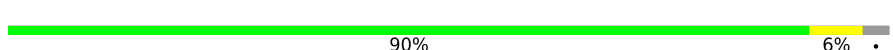
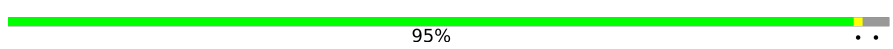
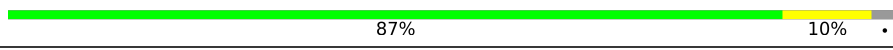
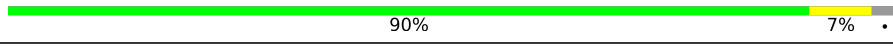
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	6428 (3.58 - 4.58)

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	856	
2	U	456	
3	L	617	
3	M	617	
3	N	617	
4	O	511	

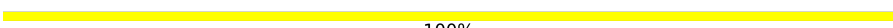
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Mol	Chain	Length	Quality of chain
4	P	511	
4	Q	511	
5	D	247	
6	b	226	
6	c	226	
6	d	226	
7	e	118	
7	f	118	
7	g	118	
8	F	119	
9	C	382	
10	H	483	
11	k	351	
12	m	81	
13	n	137	
14	s	470	
15	r	345	
16	0	155	
16	2	155	
16	3	155	
16	4	155	
16	5	155	
16	6	155	
16	7	155	
16	8	155	

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Mol	Chain	Length	Quality of chain
16	9	155	 88% 9%
17	1	205	 92% 8%
18	t	8	 25% 75%
19	w	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
20	ADP	M	701	-	-	X	-

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 66971 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 V-type proton ATPase 116 kDa subunit a 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	752	Total	C	N	O	S	0	0
			6127	4000	1016	1066	45		

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	252	ARG	PRO	conflict	UNP Q9HBG4
a	841	ASP	-	expression tag	UNP Q9HBG4
a	842	TYR	-	expression tag	UNP Q9HBG4
a	843	LYS	-	expression tag	UNP Q9HBG4
a	844	ASP	-	expression tag	UNP Q9HBG4
a	845	ASP	-	expression tag	UNP Q9HBG4
a	846	ASP	-	expression tag	UNP Q9HBG4
a	847	ASP	-	expression tag	UNP Q9HBG4
a	848	LYS	-	expression tag	UNP Q9HBG4
a	849	ASP	-	expression tag	UNP Q9HBG4
a	850	TYR	-	expression tag	UNP Q9HBG4
a	851	LYS	-	expression tag	UNP Q9HBG4
a	852	ASP	-	expression tag	UNP Q9HBG4
a	853	ASP	-	expression tag	UNP Q9HBG4
a	854	ASP	-	expression tag	UNP Q9HBG4
a	855	ASP	-	expression tag	UNP Q9HBG4
a	856	LYS	-	expression tag	UNP Q9HBG4

- Molecule 2 is a protein called KIAA1609 protein, isoform CRA_a.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	U	427	Total	C	N	O	S	0	0
			3365	2119	594	631	21		

- Molecule 3 is a protein called V-type proton ATPase catalytic subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	600	Total	C	N	O	S	0	0
			4656	2952	786	890	28		
3	M	600	Total	C	N	O	S	0	0
			4656	2952	786	890	28		
3	N	600	Total	C	N	O	S	0	0
			4656	2952	786	890	28		

- Molecule 4 is a protein called V-type proton ATPase subunit B, brain isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	468	Total	C	N	O	S	0	0
			3666	2325	625	696	20		
4	P	468	Total	C	N	O	S	0	0
			3666	2325	625	696	20		
4	Q	468	Total	C	N	O	S	0	0
			3666	2325	625	696	20		

- Molecule 5 is a protein called V-type proton ATPase subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	213	Total	C	N	O	S	0	0
			1717	1090	310	312	5		

- Molecule 6 is a protein called V-type proton ATPase subunit E 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	223	Total	C	N	O	S	0	0
			1809	1134	320	345	10		
6	c	219	Total	C	N	O	S	0	0
			1782	1120	316	336	10		
6	d	224	Total	C	N	O	S	0	0
			1817	1140	321	346	10		

- Molecule 7 is a protein called V-type proton ATPase subunit G 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	e	114	Total	C	N	O	S	0	0
			938	573	179	183	3		
7	f	114	Total	C	N	O	S	0	0
			938	573	179	183	3		
7	g	112	Total	C	N	O	S	0	0
			923	565	176	179	3		

- Molecule 8 is a protein called V-type proton ATPase subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	108	Total	C	N	O	S	0	0
			856	538	155	162	1		

- Molecule 9 is a protein called V-type proton ATPase subunit C 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	C	356	Total	C	N	O	0	0
			1770	1058	356	356		

- Molecule 10 is a protein called V-type proton ATPase subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	H	425	Total	C	N	O	0	0
			2111	1261	425	425		

- Molecule 11 is a protein called V-type proton ATPase subunit d 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	350	Total	C	N	O	S	0	0
			2836	1829	462	531	14		

- Molecule 12 is a protein called V-type proton ATPase subunit e 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	76	Total	C	N	O	S	0	0
			621	430	94	92	5		

- Molecule 13 is a protein called Ribonuclease kappa.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	85	Total	C	N	O	S	0	0
			658	434	102	115	7		

- Molecule 14 is a protein called V-type proton ATPase subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	s	204	Total	C	N	O	S	0	0
			1662	1086	267	299	10		

- Molecule 15 is a protein called ATPase H(+)-transporting lysosomal accessory protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	r	45	Total	C	N	O	S	0	0
			377	256	53	65	3		

- Molecule 16 is a protein called V-type proton ATPase 16 kDa proteolipid subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	8	150	Total	C	N	O	S	0	0
			1065	698	169	191	7		
16	9	150	Total	C	N	O	S	0	0
			1065	698	169	191	7		
16	2	150	Total	C	N	O	S	0	0
			1065	698	169	191	7		
16	3	150	Total	C	N	O	S	0	0
			1065	698	169	191	7		
16	4	150	Total	C	N	O	S	0	0
			1065	698	169	191	7		
16	5	150	Total	C	N	O	S	0	0
			1065	698	169	191	7		
16	6	150	Total	C	N	O	S	0	0
			1065	698	169	191	7		
16	7	150	Total	C	N	O	S	0	0
			1065	698	169	191	7		
16	0	150	Total	C	N	O	S	0	0
			1065	698	169	191	7		

- Molecule 17 is a protein called V-type proton ATPase 21 kDa proteolipid subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	1	204	Total	C	N	O	S	0	0
			1498	990	238	259	11		

- Molecule 18 is an oligosaccharide called alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose-(1-3)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



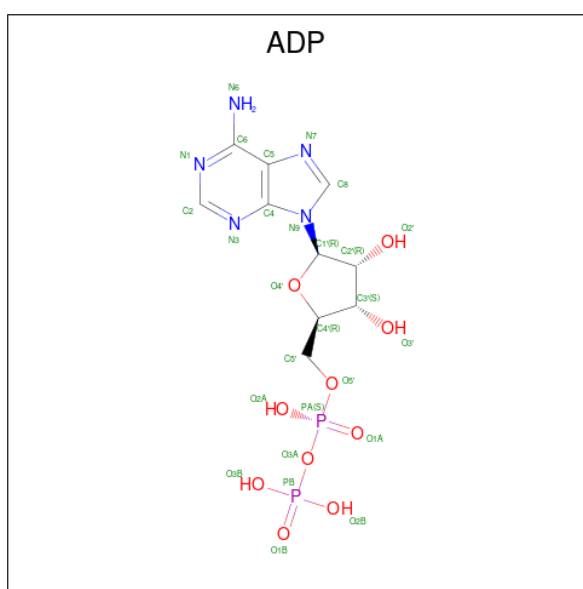
Mol	Chain	Residues	Atoms				AltConf	Trace
18	t	8	Total	C	N	O	0	0
			94	52	2	40		

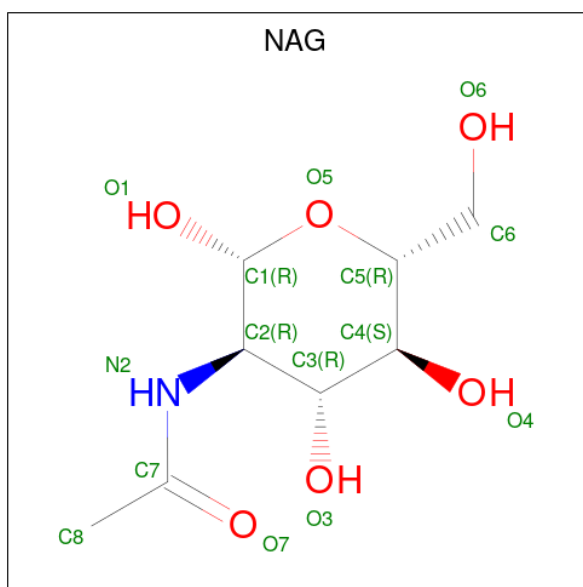
- Molecule 19 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose.



Mol	Chain	Residues	Atoms			AltConf	Trace
19	w	2	Total	C	O	0	0
			22	12	10		

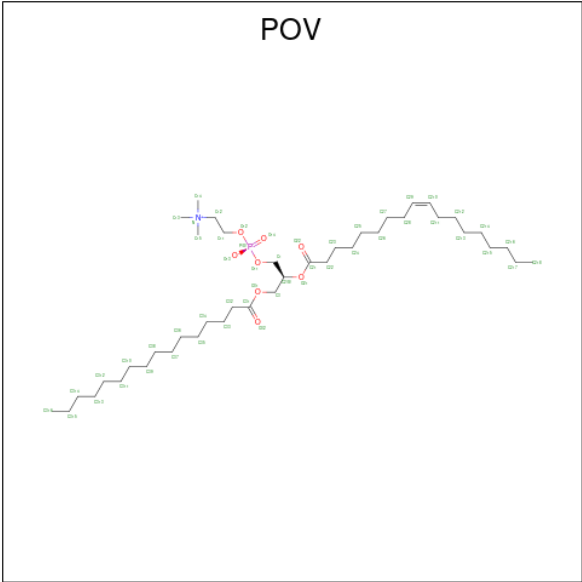
- Molecule 20 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



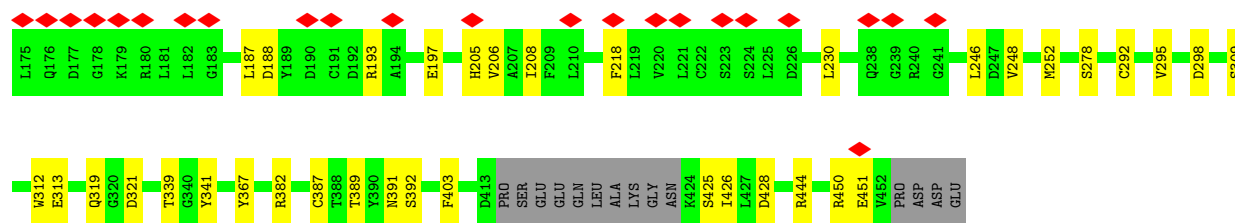


Mol	Chain	Residues	Atoms				AltConf
21	s	1	Total	C	N	O	0
			14	8	1	5	
21	s	1	Total	C	N	O	0
			14	8	1	5	
21	s	1	Total	C	N	O	0
			14	8	1	5	
21	s	1	Total	C	N	O	0
			14	8	1	5	
21	s	1	Total	C	N	O	0
			14	8	1	5	
21	s	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 22 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylammonio)ethyl phosphate (CCD ID: POV) (formula: C₄₂H₈₂NO₈P).

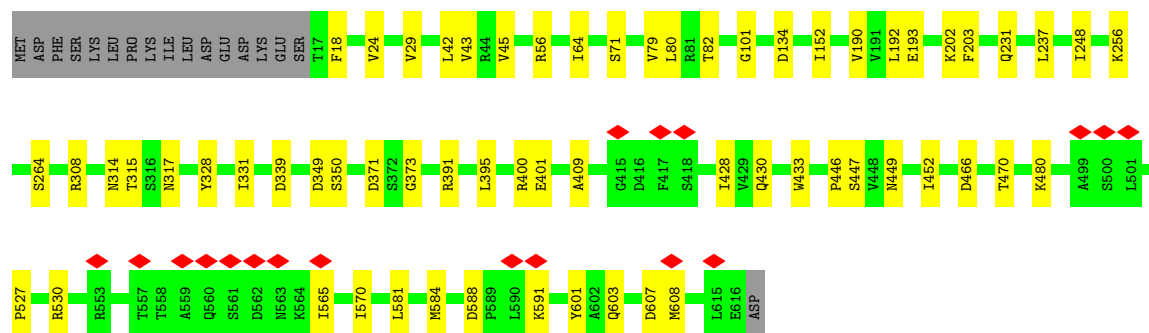


Mol	Chain	Residues	Atoms					AltConf
22	s	1	Total	C	N	O	P	0
			43	33	1	8	1	
22	s	1	Total	C	N	O	P	0
			46	36	1	8	1	
22	r	1	Total	C	N	O	P	0
			49	39	1	8	1	
22	r	1	Total	C	N	O	P	0
			44	34	1	8	1	
22	r	1	Total	C	N	O	P	0
			49	39	1	8	1	
22	8	1	Total	C	N	O	P	0
			34	24	1	8	1	
22	1	1	Total	C	N	O	P	0
			45	35	1	8	1	
22	1	1	Total	C	N	O	P	0
			38	28	1	8	1	
22	1	1	Total	C	N	O	P	0
			40	30	1	8	1	



• Molecule 3: V-type proton ATPase catalytic subunit A

Chain L: 87% 10% .



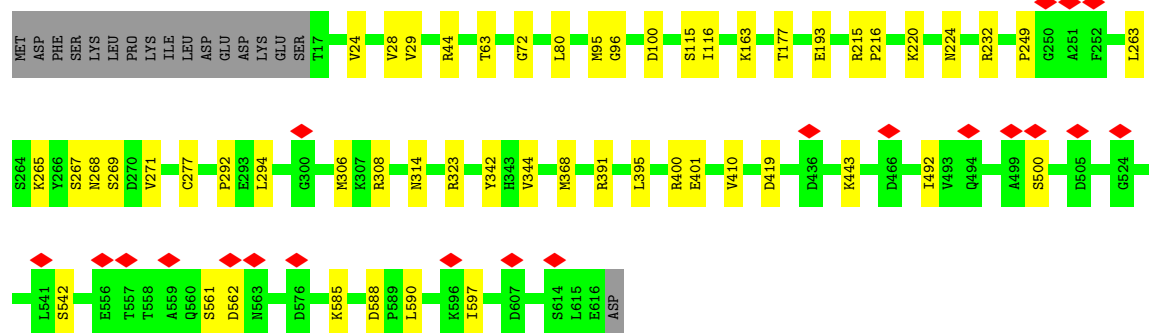
• Molecule 3: V-type proton ATPase catalytic subunit A

Chain M: 83% 14% .

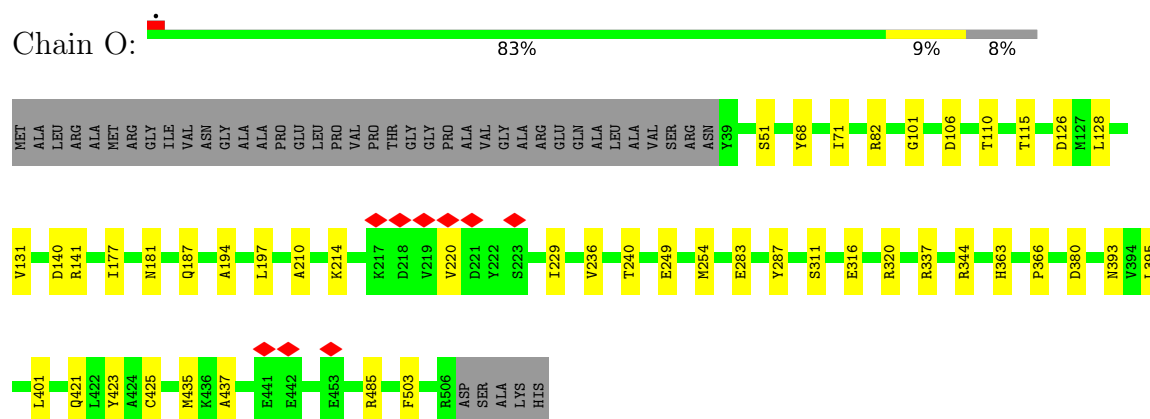


• Molecule 3: V-type proton ATPase catalytic subunit A

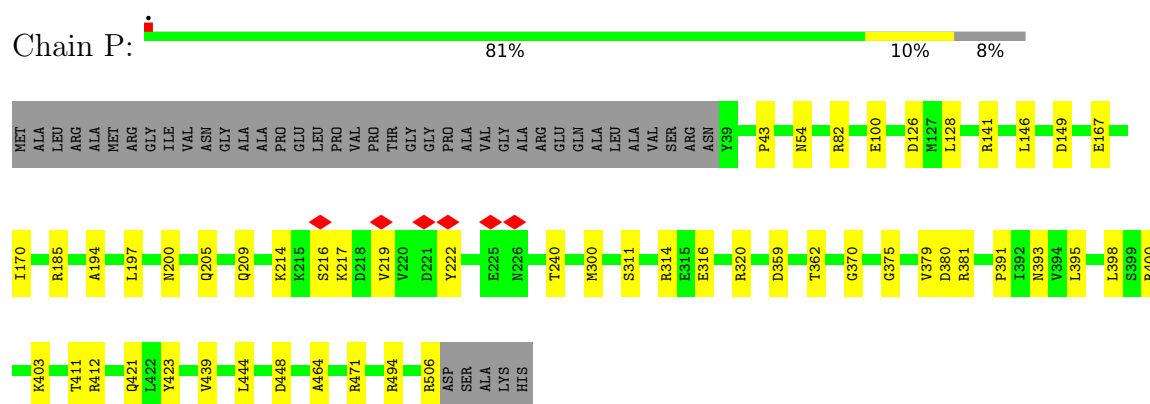
Chain N: 88% 9% .



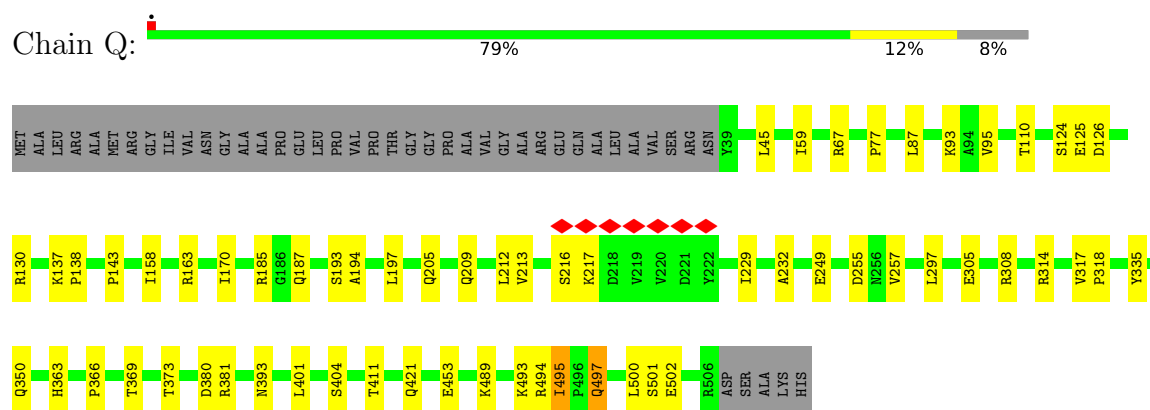
• Molecule 4: V-type proton ATPase subunit B, brain isoform



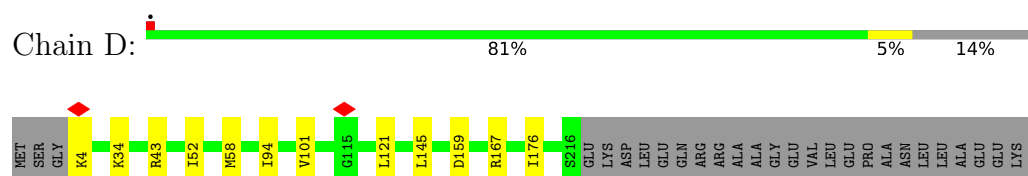
• Molecule 4: V-type proton ATPase subunit B, brain isoform



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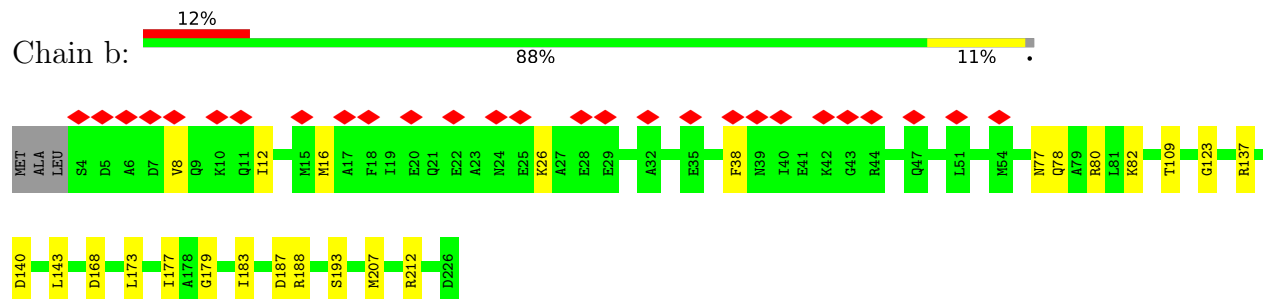


• Molecule 5: V-type proton ATPase subunit D

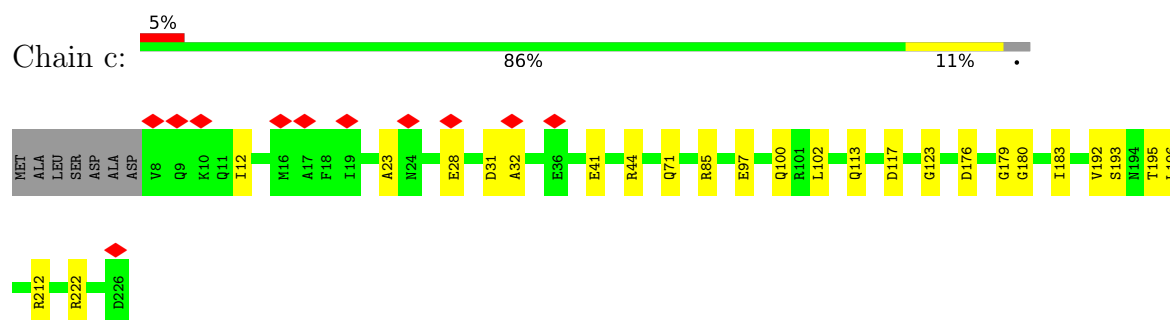


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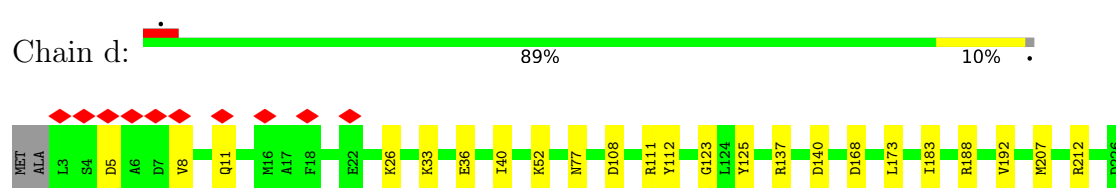
- Molecule 6: V-type proton ATPase subunit E 1



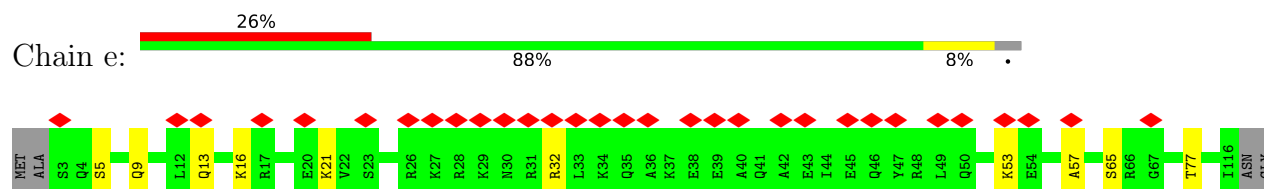
- Molecule 6: V-type proton ATPase subunit E 1



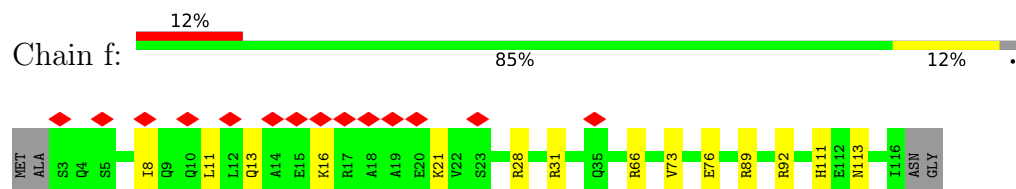
- Molecule 6: V-type proton ATPase subunit E 1



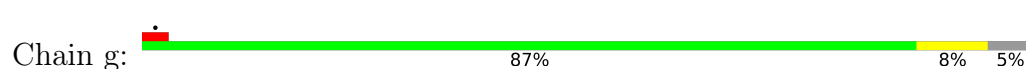
- Molecule 7: V-type proton ATPase subunit G 1

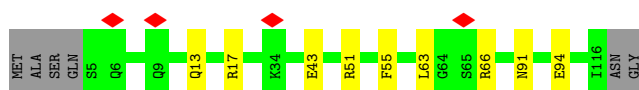


- Molecule 7: V-type proton ATPase subunit G 1

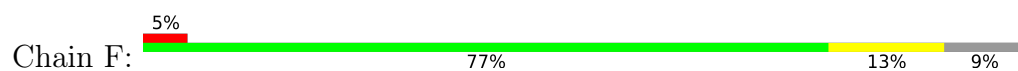


- Molecule 7: V-type proton ATPase subunit G 1

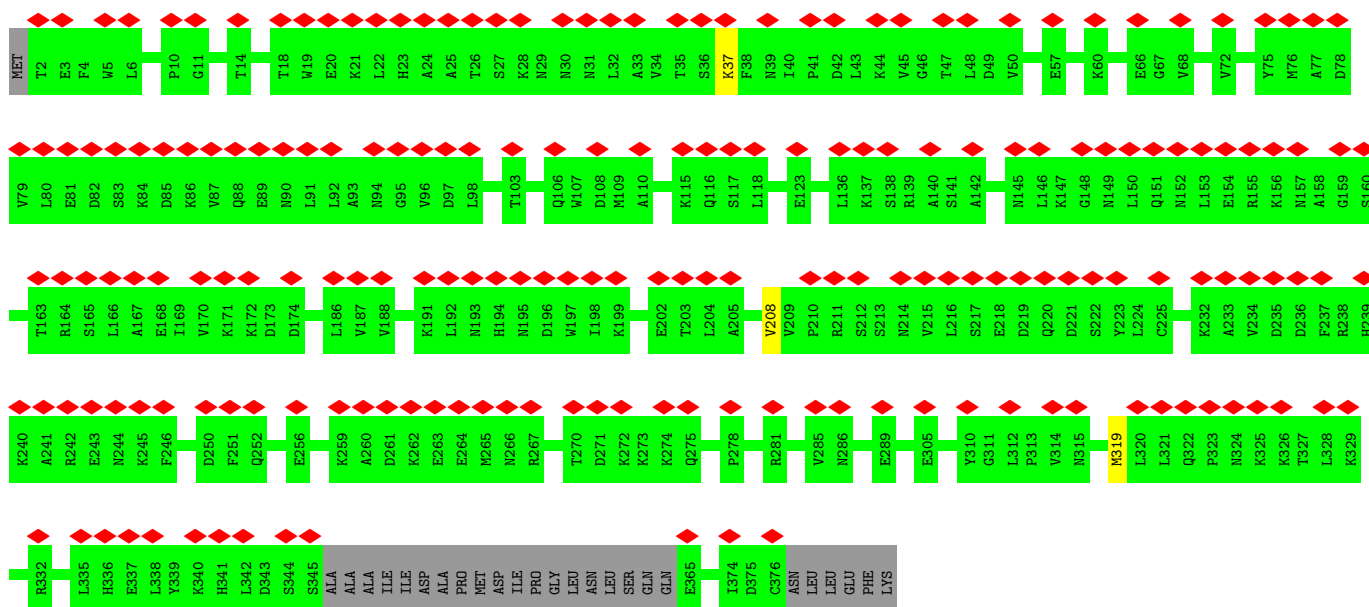




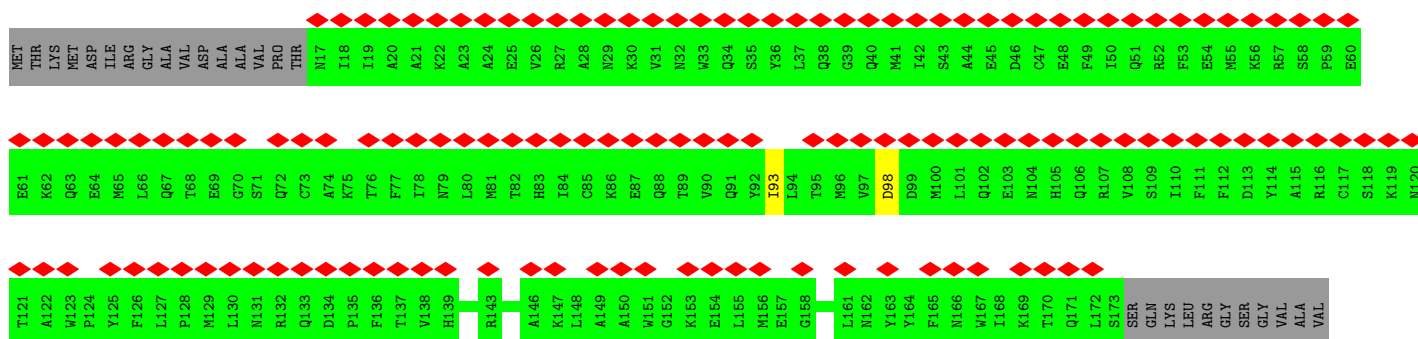
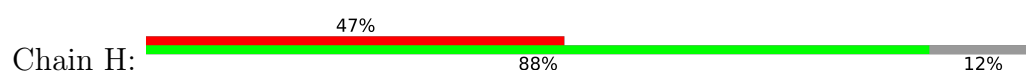
• Molecule 8: V-type proton ATPase subunit F

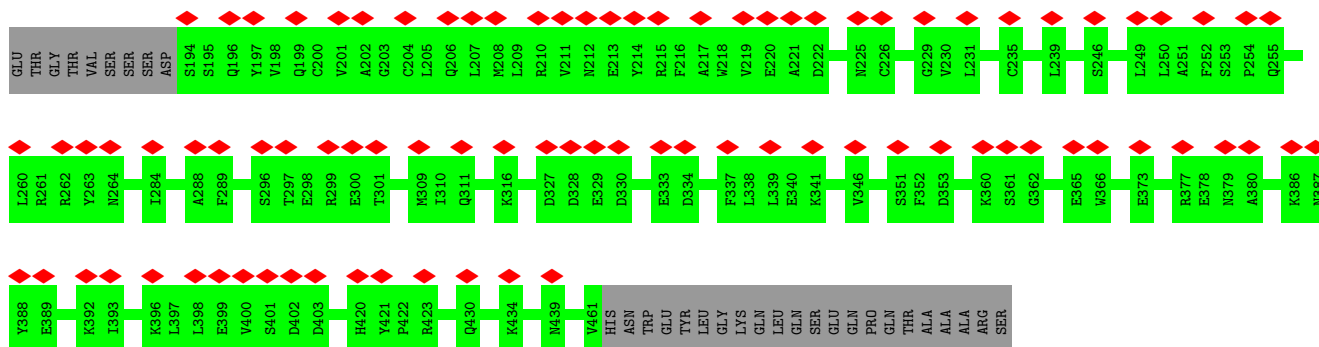


• Molecule 9: V-type proton ATPase subunit C 1

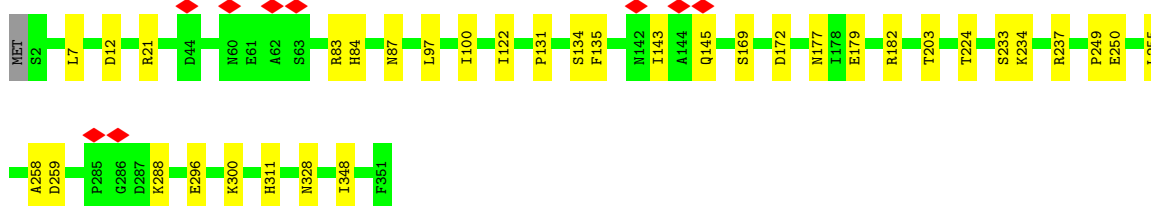


• Molecule 10: V-type proton ATPase subunit H





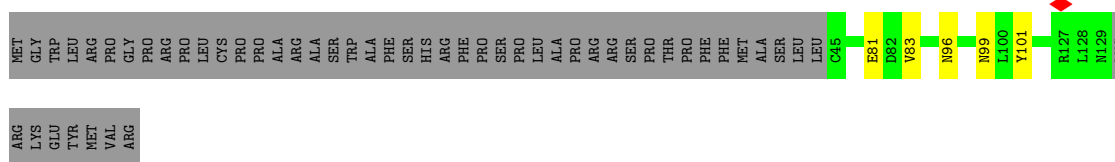
- Molecule 11: V-type proton ATPase subunit d 1



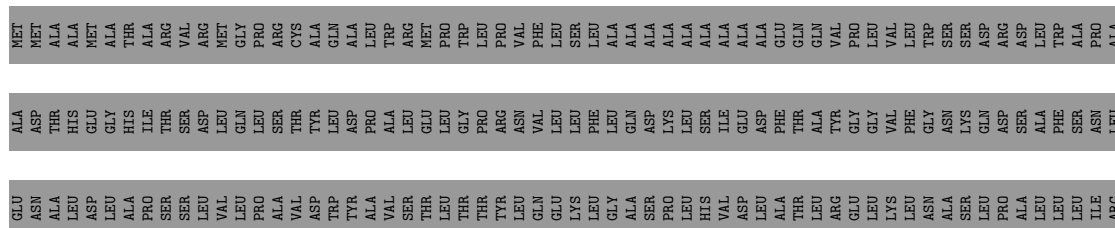
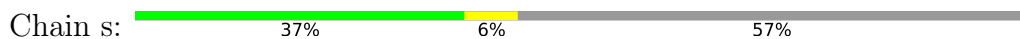
- Molecule 12: V-type proton ATPase subunit e 1



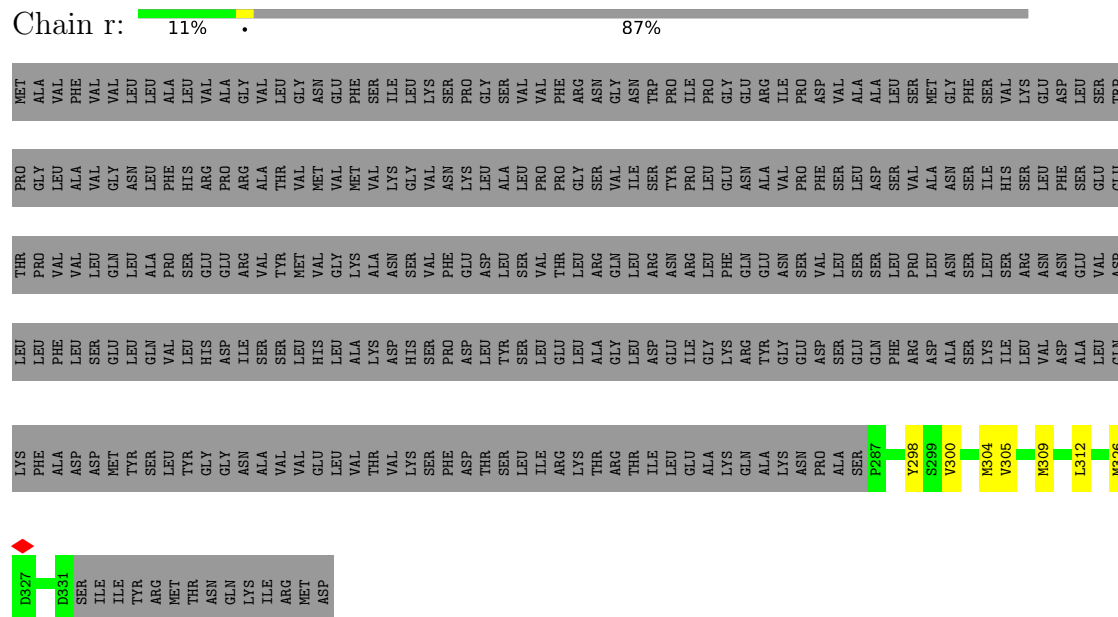
- Molecule 13: Ribonuclease kappa



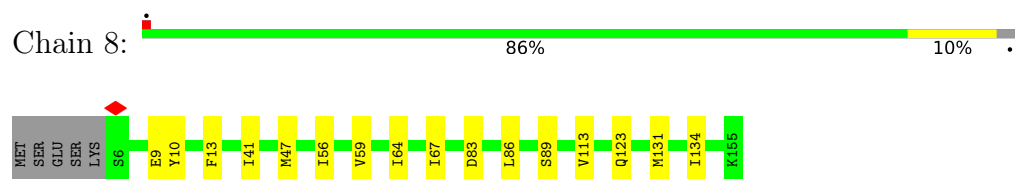
- Molecule 14: V-type proton ATPase subunit S1



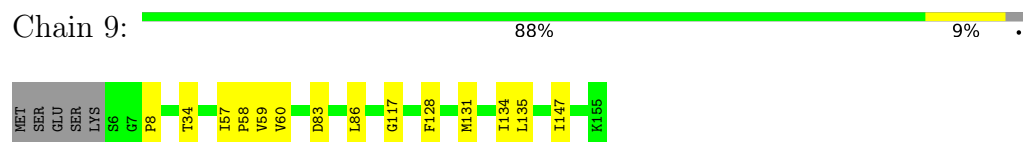
- Molecule 15: ATPase H(+)-transporting lysosomal accessory protein 2



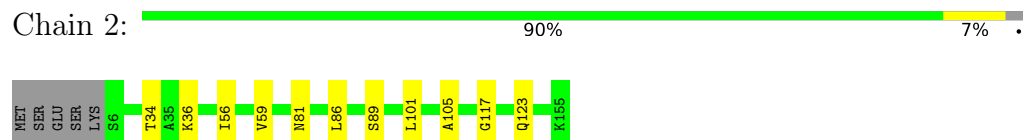
- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit



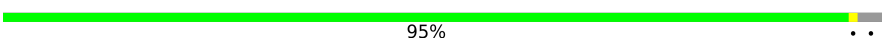
- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

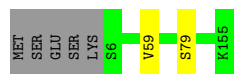


- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit



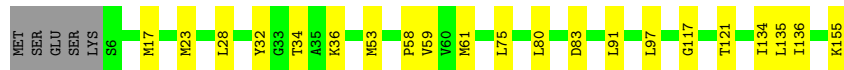
- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain 3:  95% ..



- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain 4:  83% 14% .



- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain 5:  87% 10% .



- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain 6:  90% 7% .



- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain 7:  88% 8% .

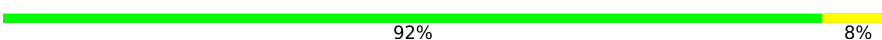


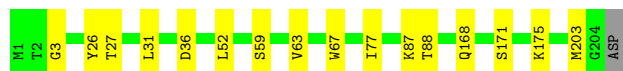
- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain 0:  90% 6% .



- Molecule 17: V-type proton ATPase 21 kDa proteolipid subunit

Chain 1:  92% 8%



- Molecule 18: α -D-glucopyranose-(1-3)- α -D-glucopyranose-(1-3)- α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-3)- β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain t:  25% 75%

MAN1	MAN2	MAN3	MAN4	MAN5	MAN6	GLC7	GLC8
------	------	------	------	------	------	------	------

- Molecule 19: α -D-mannopyranose-(1-6)- α -D-mannopyranose

Chain w:  100%

MAN1	MAN2
------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24984	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	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	23.543	Depositor
Minimum map value	-13.098	Depositor
Average map value	0.004	Depositor
Map value standard deviation	1.021	Depositor
Recommended contour level	2.95	Depositor
Map size ($\text{\AA}$)	404.16, 404.16, 404.16	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.842, 0.842, 0.842	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, GLC, MAN, POV, BMA, ADP

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	0.26	0/6278	0.56	3/8497 (0.0%)
2	U	0.36	1/3445 (0.0%)	0.53	0/4660
3	L	0.28	0/4752	0.53	0/6435
3	M	0.32	0/4752	0.53	0/6435
3	N	0.27	0/4752	0.53	0/6435
4	O	0.32	0/3739	0.51	0/5067
4	P	0.34	0/3739	0.53	0/5067
4	Q	0.43	2/3739 (0.1%)	0.60	4/5067 (0.1%)
5	D	0.22	0/1735	0.50	0/2320
6	b	0.24	0/1826	0.53	0/2444
6	c	0.27	0/1799	0.57	0/2407
6	d	0.25	0/1834	0.54	0/2455
7	e	0.20	0/945	0.53	0/1258
7	f	0.23	0/945	0.47	0/1258
7	g	0.20	0/930	0.49	0/1238
8	F	0.23	0/869	0.51	0/1174
9	C	0.15	0/1768	0.44	0/2466
10	H	0.16	0/2109	0.50	0/2941
11	k	0.27	0/2902	0.54	0/3930
12	m	0.28	0/646	0.57	0/887
13	n	0.25	0/674	0.64	0/915
14	s	0.60	6/1716 (0.3%)	0.69	2/2333 (0.1%)
15	r	0.27	0/390	0.51	0/534
16	0	0.31	0/1080	0.56	2/1461 (0.1%)
16	2	0.31	0/1080	0.58	2/1461 (0.1%)
16	3	0.30	0/1080	0.52	0/1461
16	4	0.30	0/1080	0.49	0/1461
16	5	0.31	0/1080	0.53	0/1461
16	6	0.29	0/1080	0.51	0/1461
16	7	0.32	0/1080	0.56	2/1461 (0.1%)
16	8	0.33	0/1080	0.56	0/1461
16	9	0.31	0/1080	0.53	0/1461

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	1	0.31	0/1532	0.49	0/2082
All	All	0.31	9/67536 (0.0%)	0.54	15/91454 (0.0%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	502	GLU	C-N	7.89	1.45	1.33
14	s	416	SER	C-O	-7.84	1.15	1.23
4	Q	497	GLN	CA-C	-6.58	1.44	1.52
14	s	422	PHE	C-O	-6.56	1.16	1.24
2	U	389	THR	C-N	-6.50	1.24	1.33

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	178	ASN	N-CA-C	10.76	122.97	111.03
14	s	417	ASP	N-CA-C	7.83	120.03	110.41
4	Q	501	SER	N-CA-C	7.77	121.64	112.93
4	Q	497	GLN	N-CA-C	7.55	119.52	111.28
4	Q	495	ILE	CA-C-N	6.79	126.82	119.90

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	6127	0	6155	56	0
2	U	3365	0	3271	52	0
3	L	4656	0	4642	38	0
3	M	4656	0	4642	74	0
3	N	4656	0	4642	39	0
4	O	3666	0	3665	29	0
4	P	3666	0	3665	50	0
4	Q	3666	0	3665	43	0
5	D	1717	0	1829	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	b	1809	0	1870	17	0
6	c	1782	0	1852	21	0
6	d	1817	0	1881	24	0
7	e	938	0	947	8	0
7	f	938	0	947	9	0
7	g	923	0	934	5	0
8	F	856	0	860	10	0
9	C	1770	0	780	2	0
10	H	2111	0	937	1	0
11	k	2836	0	2770	24	0
12	m	621	0	640	2	0
13	n	658	0	652	4	0
14	s	1662	0	1582	17	0
15	r	377	0	365	13	0
16	0	1065	0	1131	6	0
16	2	1065	0	1131	10	0
16	3	1065	0	1131	2	0
16	4	1065	0	1131	19	0
16	5	1065	0	1131	13	0
16	6	1065	0	1131	8	0
16	7	1065	0	1131	8	0
16	8	1065	0	1131	15	0
16	9	1065	0	1131	10	0
17	1	1498	0	1544	17	0
18	t	94	0	79	0	0
19	w	22	0	19	0	0
20	M	27	0	12	12	0
21	s	84	0	78	0	0
22	1	123	0	162	6	0
22	8	34	0	42	8	0
22	r	142	0	207	13	0
22	s	89	0	125	10	0
All	All	66971	0	65640	580	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 4.

The worst 5 of 580 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)
15:r:300:VAL:CG1	15:r:304:MET:HE2	1.66	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:234:LEU:HD21	3:M:433:TRP:CZ2	1.84	1.13
2:U:367:TYR:HE1	2:U:382:ARG:O	1.34	1.09
22:8:201:POV:H22	17:1:27:THR:HG22	1.33	1.07
3:M:234:LEU:HD21	3:M:433:TRP:CE2	1.90	1.05

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	NAG	t	1	18	14,14,15	0.25	0	17,19,21	0.66	1 (5%)
18	NAG	t	2	18	14,14,15	0.28	0	17,19,21	0.55	0
18	BMA	t	3	18	11,11,12	0.63	0	15,15,17	0.82	0
18	MAN	t	4	18	11,11,12	0.73	0	15,15,17	1.18	2 (13%)
18	MAN	t	5	18	11,11,12	0.72	0	15,15,17	1.37	2 (13%)
18	MAN	t	6	18	11,11,12	1.00	1 (9%)	15,15,17	0.88	1 (6%)
18	GLC	t	7	18	11,11,12	0.60	0	15,15,17	0.85	1 (6%)
18	GLC	t	8	18	11,11,12	0.56	0	15,15,17	0.90	1 (6%)
19	MAN	w	1	19	11,11,12	0.82	0	15,15,17	1.30	2 (13%)
19	MAN	w	2	19	11,11,12	1.14	1 (9%)	15,15,17	1.64	2 (13%)

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
18	NAG	t	1	18	-	2/6/23/26	0/1/1/1
18	NAG	t	2	18	-	0/6/23/26	0/1/1/1
18	BMA	t	3	18	-	2/2/19/22	0/1/1/1
18	MAN	t	4	18	-	2/2/19/22	0/1/1/1
18	MAN	t	5	18	-	2/2/19/22	0/1/1/1
18	MAN	t	6	18	-	0/2/19/22	0/1/1/1
18	GLC	t	7	18	-	2/2/19/22	0/1/1/1
18	GLC	t	8	18	-	0/2/19/22	0/1/1/1
19	MAN	w	1	19	-	1/2/19/22	0/1/1/1
19	MAN	w	2	19	-	0/2/19/22	1/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	w	2	MAN	O5-C5	2.90	1.49	1.43
18	t	6	MAN	O5-C1	-2.28	1.39	1.43

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	w	2	MAN	C1-O5-C5	5.18	119.13	112.19
18	t	5	MAN	O2-C2-C3	-3.65	102.60	110.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	w	1	MAN	C1-O5-C5	3.31	116.63	112.19
18	t	5	MAN	C1-O5-C5	3.27	116.57	112.19
18	t	4	MAN	C1-O5-C5	2.89	116.06	112.19

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

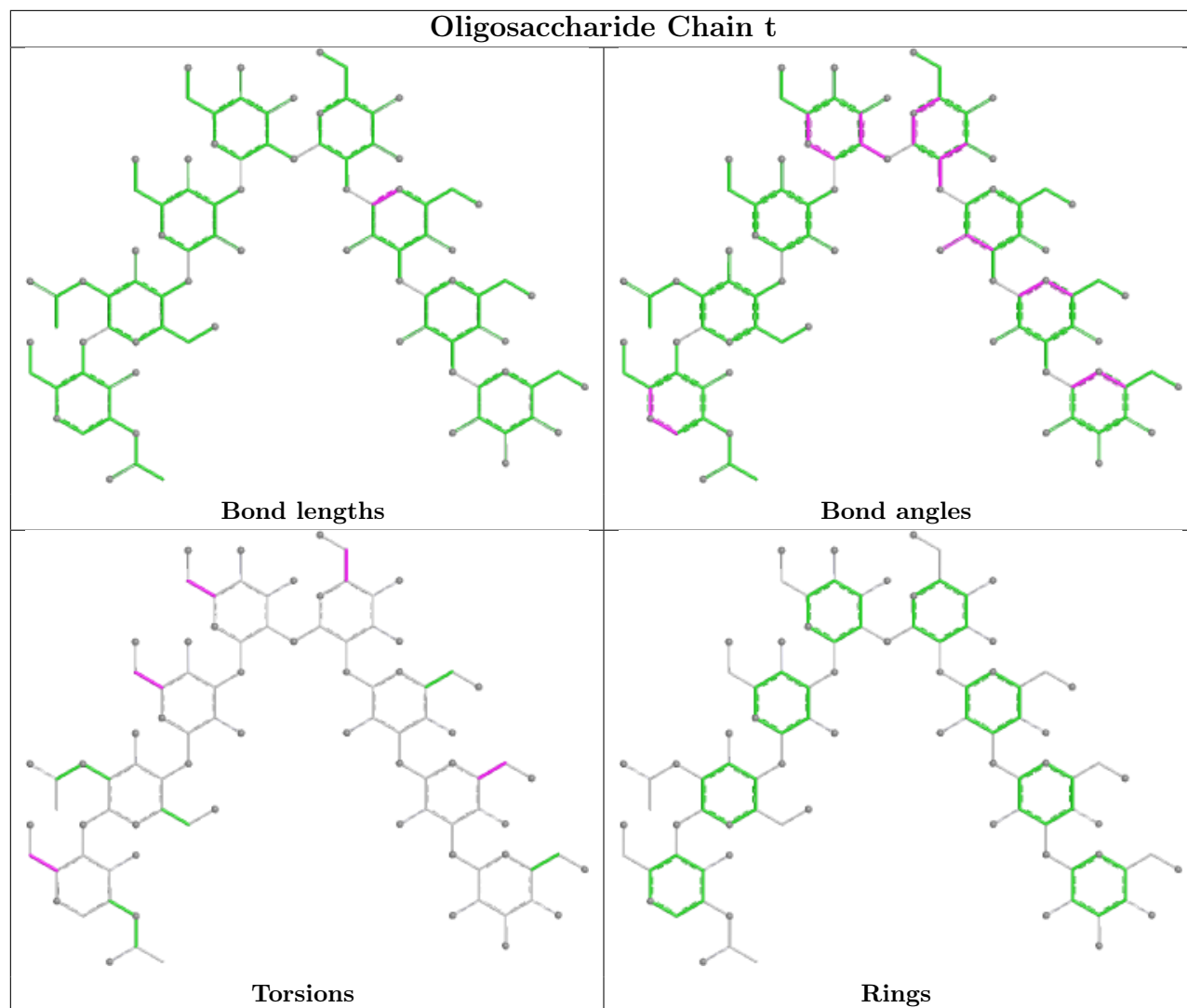
Mol	Chain	Res	Type	Atoms
18	t	5	MAN	O5-C5-C6-O6
18	t	5	MAN	C4-C5-C6-O6
18	t	3	BMA	O5-C5-C6-O6
18	t	4	MAN	O5-C5-C6-O6
18	t	1	NAG	O5-C5-C6-O6

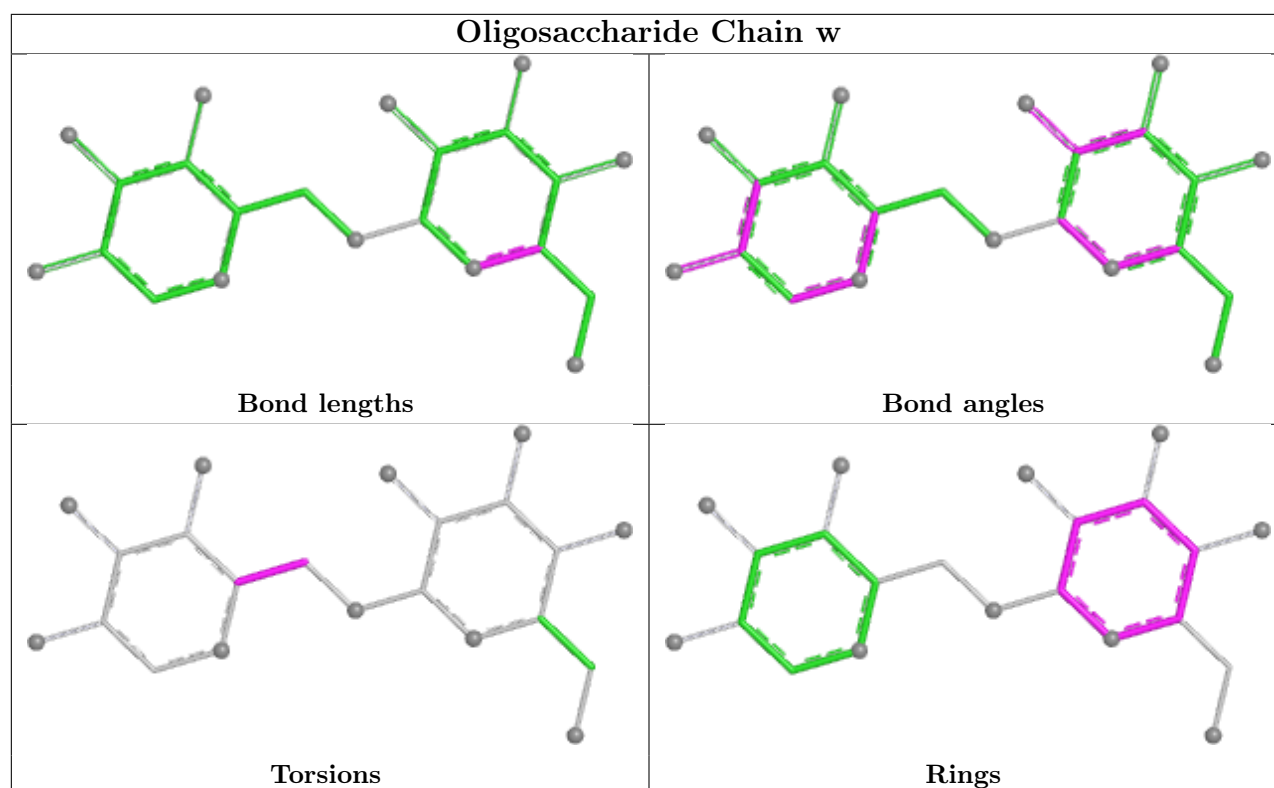
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	w	2	MAN	C1-C2-C3-C4-C5-O5

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

16 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	POV	8	201	-	33,33,51	1.44	8 (24%)	39,41,59	1.51	7 (17%)
22	POV	1	301	-	44,44,51	1.24	5 (11%)	50,52,59	1.21	4 (8%)
21	NAG	s	505	14	14,14,15	0.34	0	17,19,21	0.50	0
21	NAG	s	504	-	14,14,15	0.50	0	17,19,21	0.48	0
22	POV	1	303	-	39,39,51	1.31	5 (12%)	45,47,59	1.23	4 (8%)
22	POV	r	401	-	48,48,51	1.18	5 (10%)	54,56,59	1.13	3 (5%)
21	NAG	s	506	14	14,14,15	0.38	0	17,19,21	0.45	0
22	POV	s	507	-	42,42,51	1.71	11 (26%)	48,50,59	1.50	8 (16%)
21	NAG	s	501	14	14,14,15	0.39	0	17,19,21	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	POV	s	508	-	45,45,51	1.21	5 (11%)	51,53,59	1.22	4 (7%)
21	NAG	s	503	14	14,14,15	0.20	0	17,19,21	0.47	0
20	ADP	M	701	-	28,29,29	0.92	0	43,45,45	1.84	8 (18%)
22	POV	r	402	-	43,43,51	1.22	5 (11%)	49,51,59	1.17	3 (6%)
22	POV	r	403	-	48,48,51	1.11	7 (14%)	54,56,59	1.12	4 (7%)
21	NAG	s	502	14	14,14,15	0.52	0	17,19,21	0.82	1 (5%)
22	POV	1	302	-	37,37,51	1.37	6 (16%)	43,45,59	1.29	4 (9%)

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
22	POV	8	201	-	-	10/37/37/55	-
22	POV	1	301	-	-	18/48/48/55	-
21	NAG	s	505	14	-	2/6/23/26	0/1/1/1
21	NAG	s	504	-	-	0/6/23/26	0/1/1/1
22	POV	1	303	-	-	28/43/43/55	-
22	POV	r	401	-	-	19/52/52/55	-
21	NAG	s	506	14	-	2/6/23/26	0/1/1/1
22	POV	s	507	-	-	26/46/46/55	-
21	NAG	s	501	14	-	2/6/23/26	0/1/1/1
22	POV	s	508	-	-	28/49/49/55	-
21	NAG	s	503	14	-	2/6/23/26	0/1/1/1
20	ADP	M	701	-	-	2/16/32/32	0/3/3/3
22	POV	r	402	-	-	24/47/47/55	-
22	POV	r	403	-	-	27/52/52/55	-
21	NAG	s	502	14	-	3/6/23/26	0/1/1/1
22	POV	1	302	-	-	20/41/41/55	-

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	s	507	POV	O21-C2	-4.61	1.35	1.46
22	1	301	POV	C29-C210	3.86	1.53	1.31
22	1	303	POV	C29-C210	3.83	1.53	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	r	401	POV	C29-C210	3.79	1.53	1.31
22	1	302	POV	C29-C210	3.78	1.53	1.31

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	M	701	ADP	C5-C4-N3	-5.48	119.17	126.72
22	r	403	POV	O21-C21-C22	5.24	122.82	111.48
22	8	201	POV	O21-C21-C22	4.92	122.12	111.48
22	s	507	POV	O21-C21-C22	4.85	121.97	111.48
20	M	701	ADP	N3-C4-N9	4.76	135.26	127.17

There are no chirality outliers.

5 of 213 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
20	M	701	ADP	C5'-O5'-PA-O2A
22	s	507	POV	C1-O11-P-O12
22	s	507	POV	C1-O11-P-O13
22	s	507	POV	C1-O11-P-O14
22	s	507	POV	C11-O12-P-O11

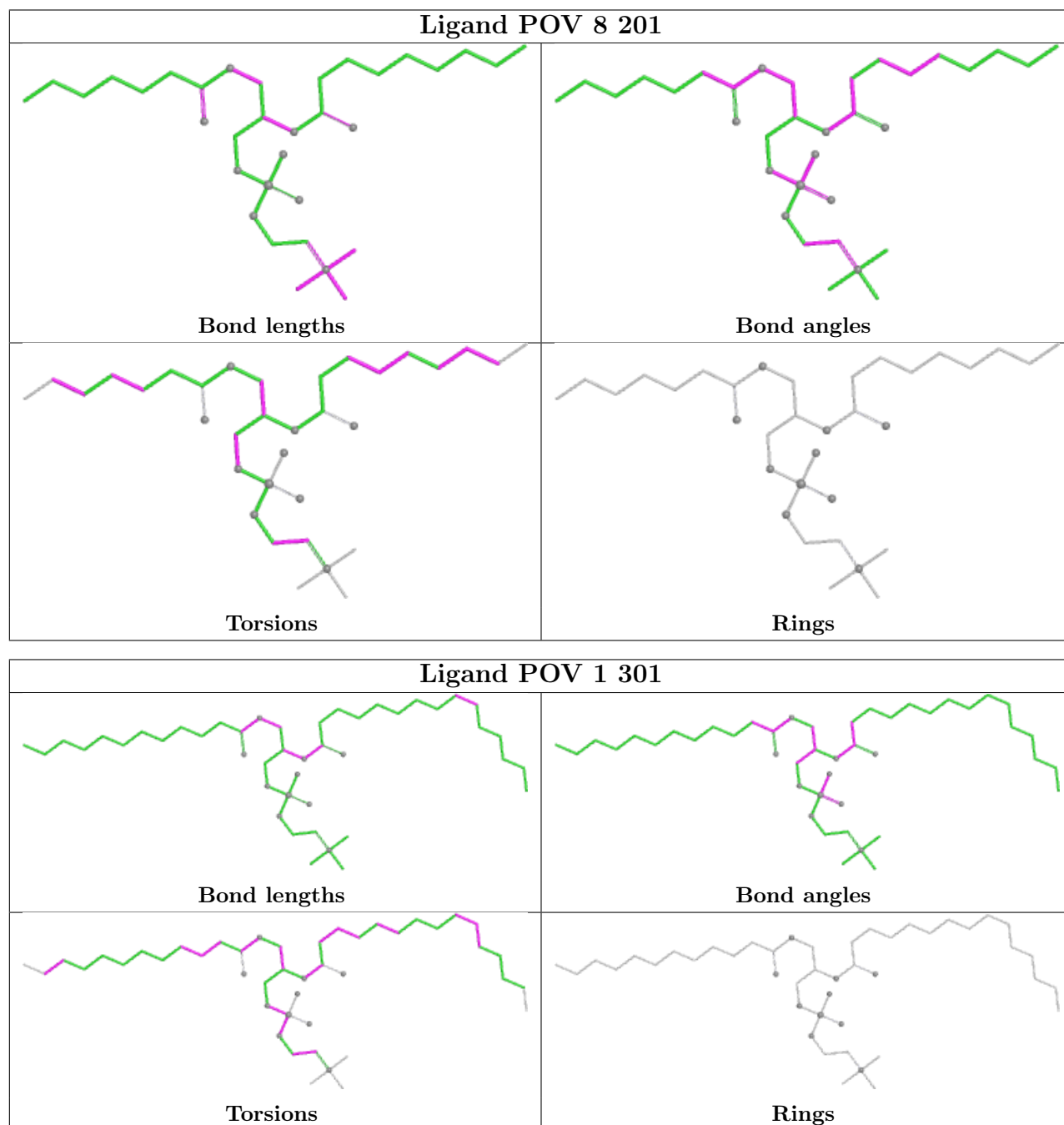
There are no ring outliers.

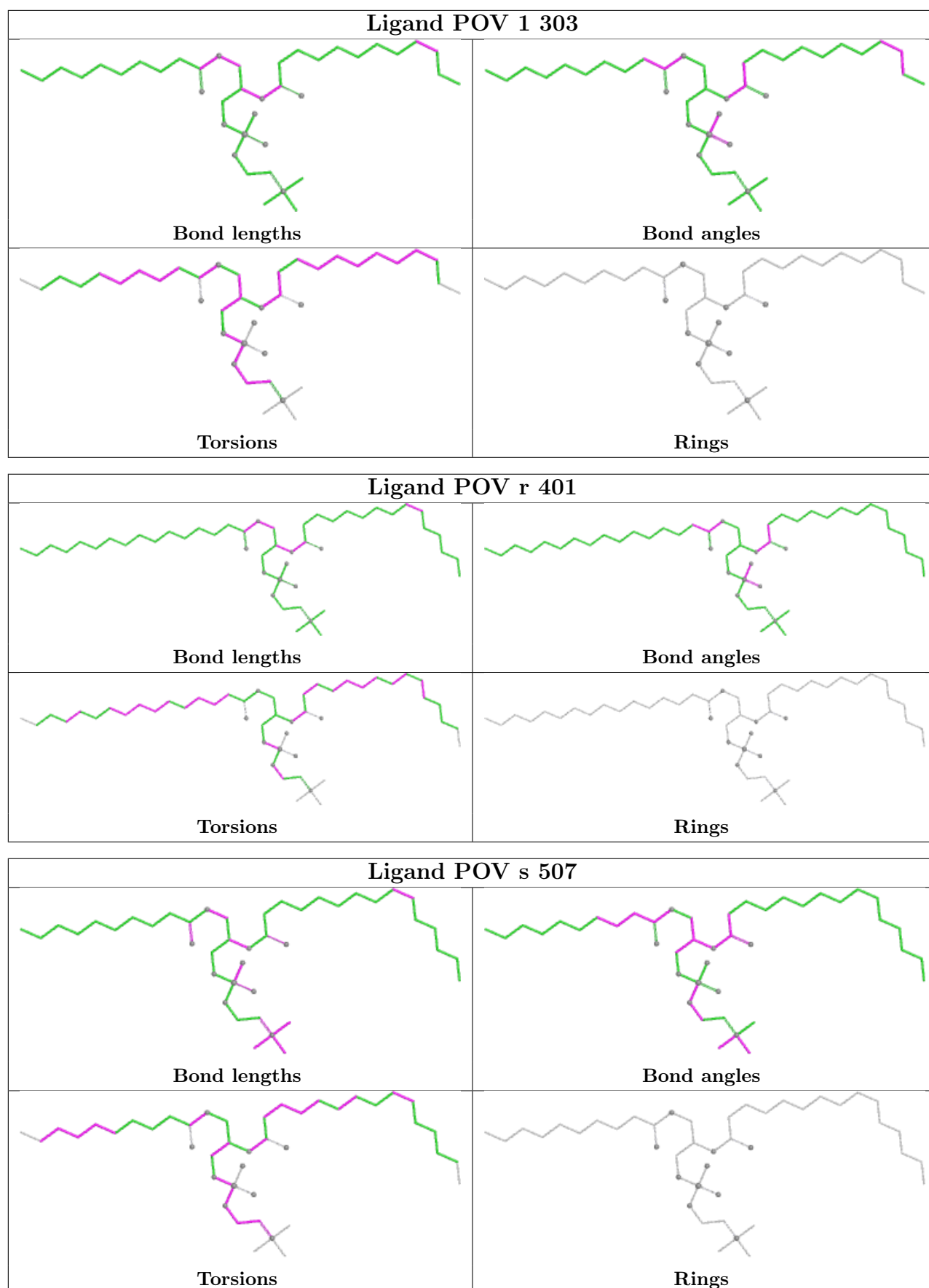
10 monomers are involved in 47 short contacts:

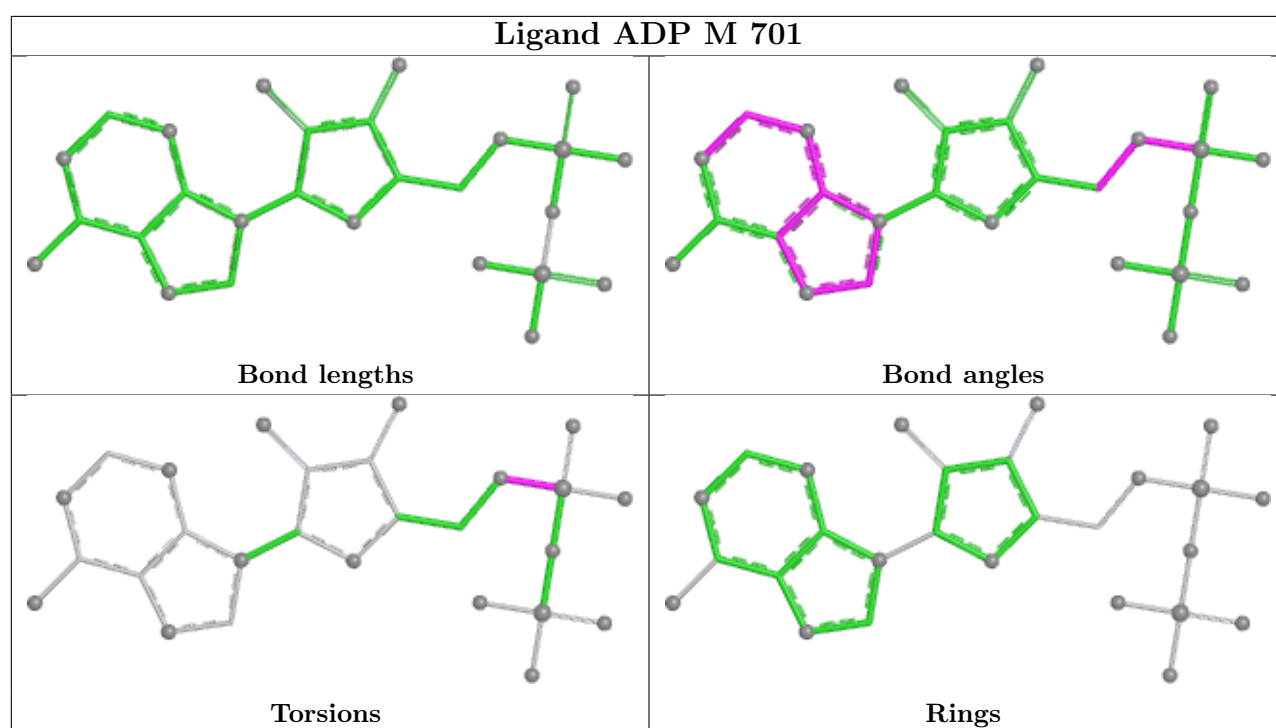
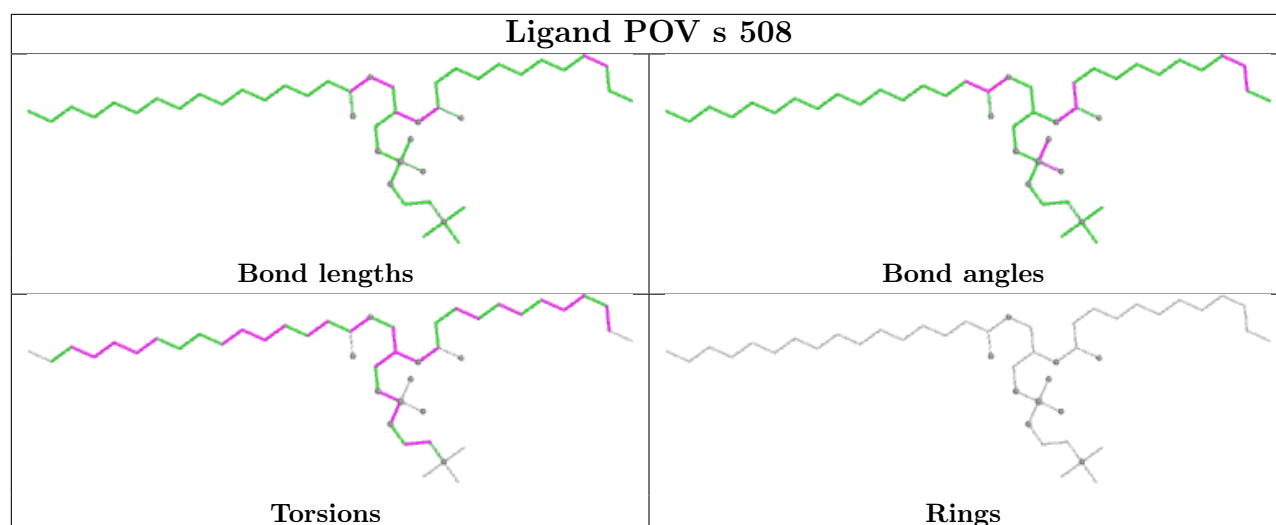
Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	8	201	POV	8	0
22	1	301	POV	1	0
22	1	303	POV	3	0
22	r	401	POV	2	0
22	s	507	POV	6	0
22	s	508	POV	4	0
20	M	701	ADP	12	0
22	r	402	POV	1	0
22	r	403	POV	10	0
22	1	302	POV	2	0

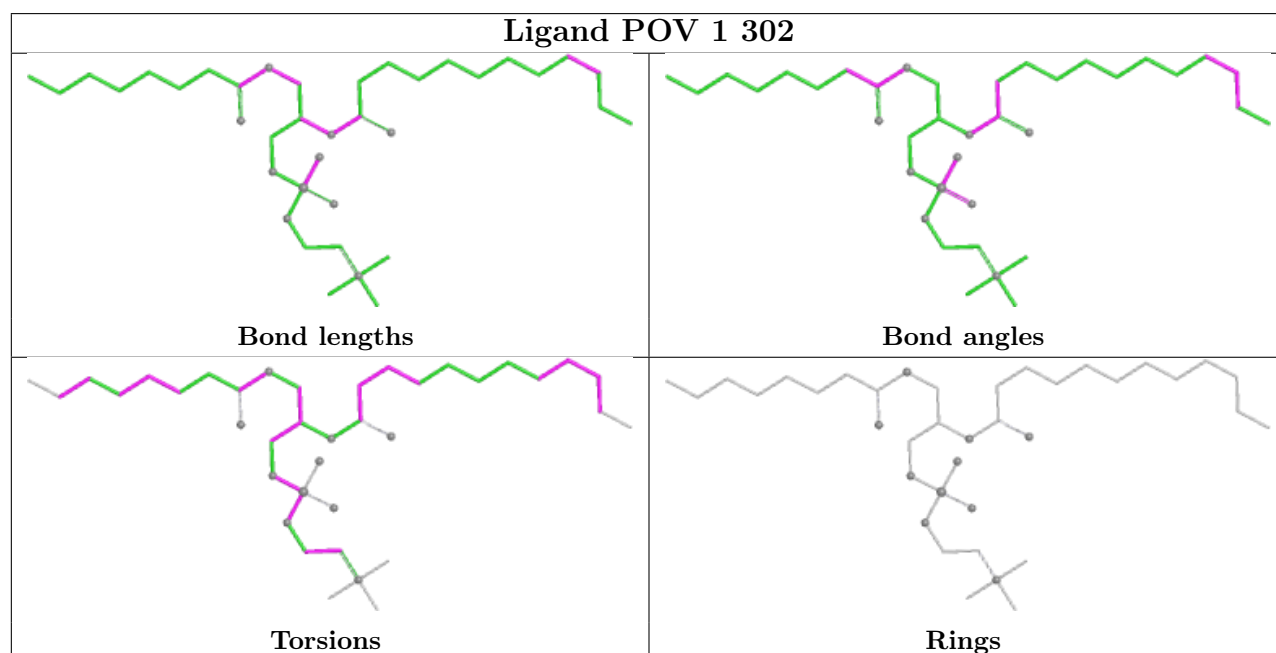
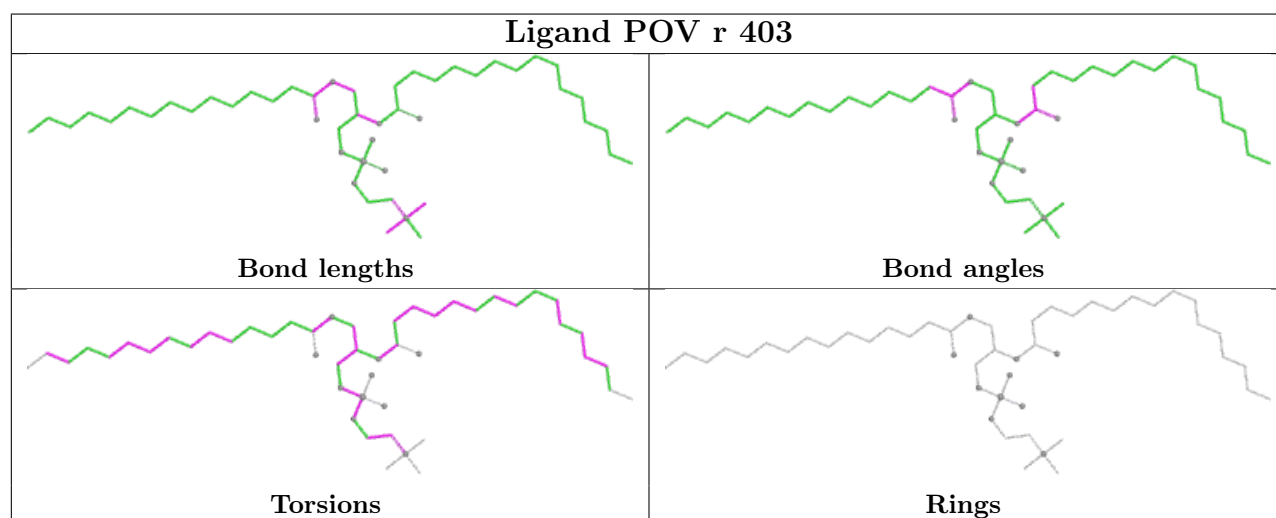
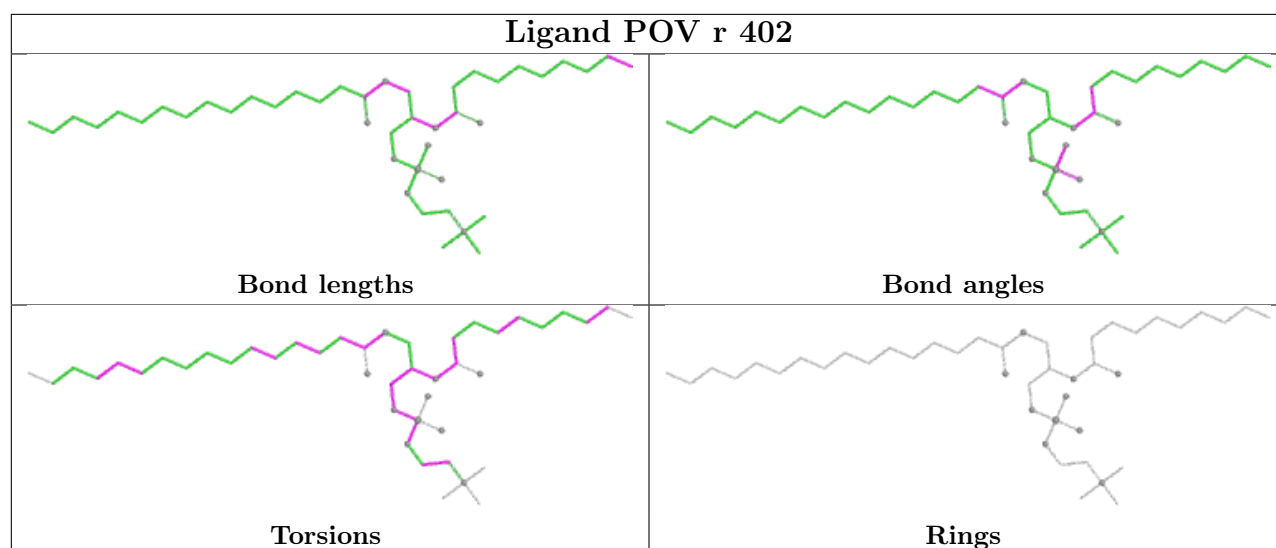
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

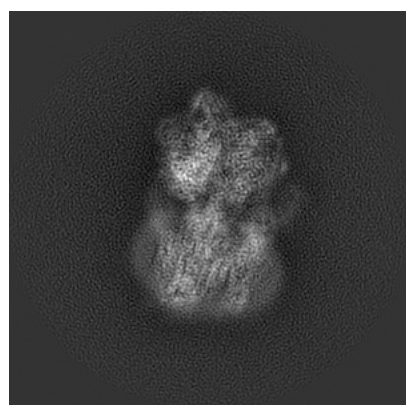
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26623. These allow visual inspection of the internal detail of the map and identification of artifacts.

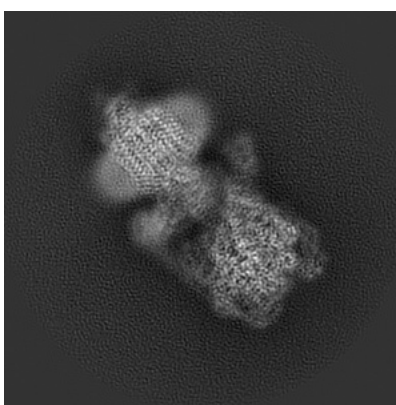
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

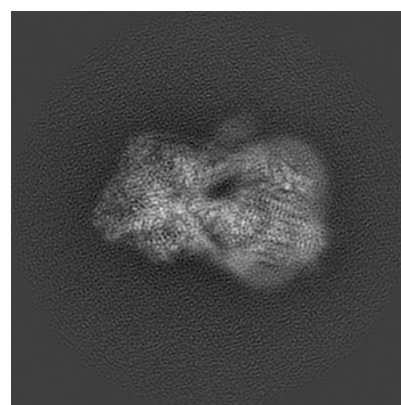
6.1.1 Primary map



X



Y

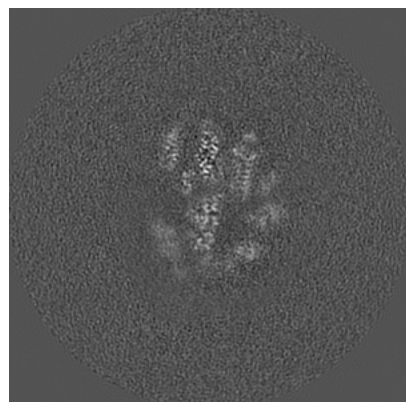


Z

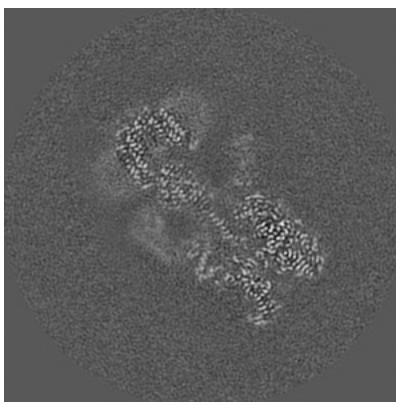
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

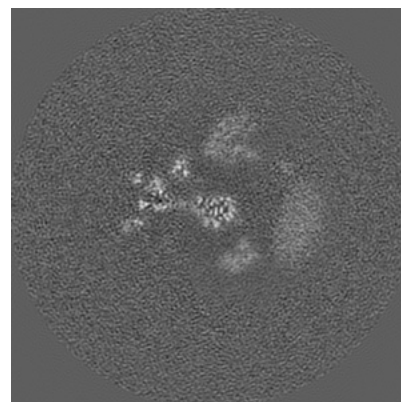
6.2.1 Primary map



X Index: 240



Y Index: 240

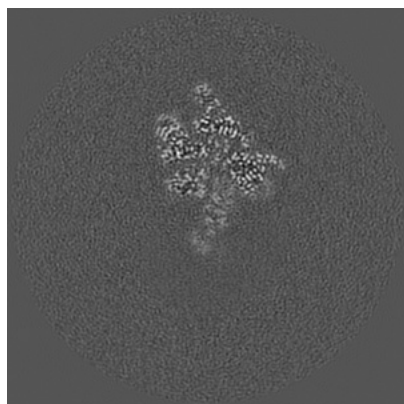


Z Index: 240

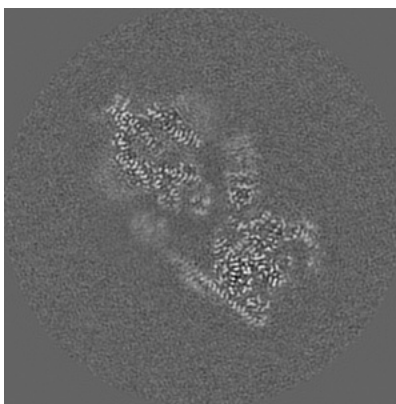
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

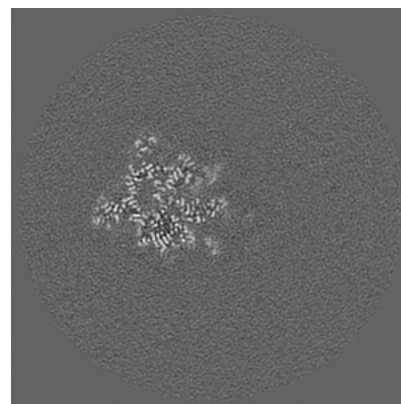
6.3.1 Primary map



X Index: 182



Y Index: 222

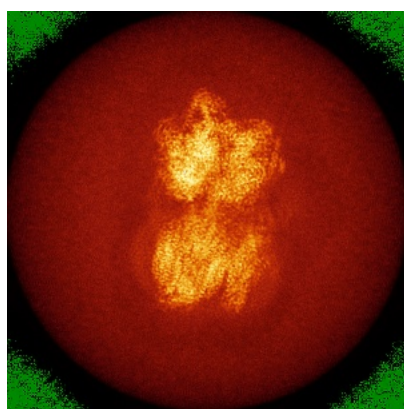


Z Index: 308

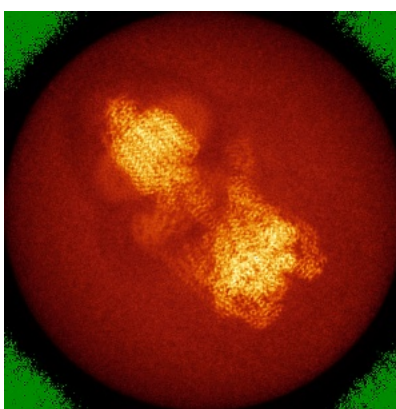
The images above show the largest variance slices of the map in three orthogonal directions.

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

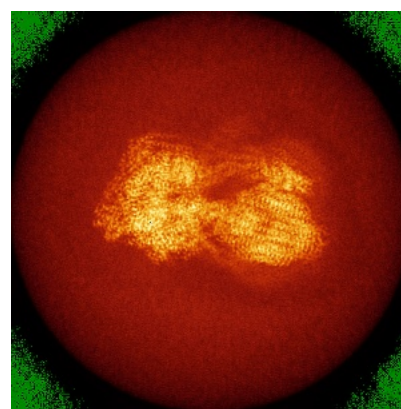
6.4.1 Primary map



X



Y

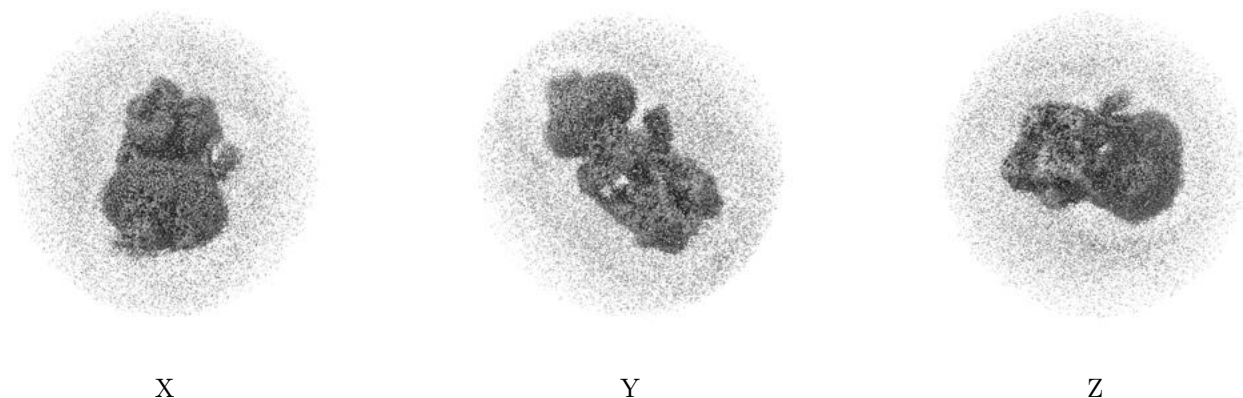


Z

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 2.95. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

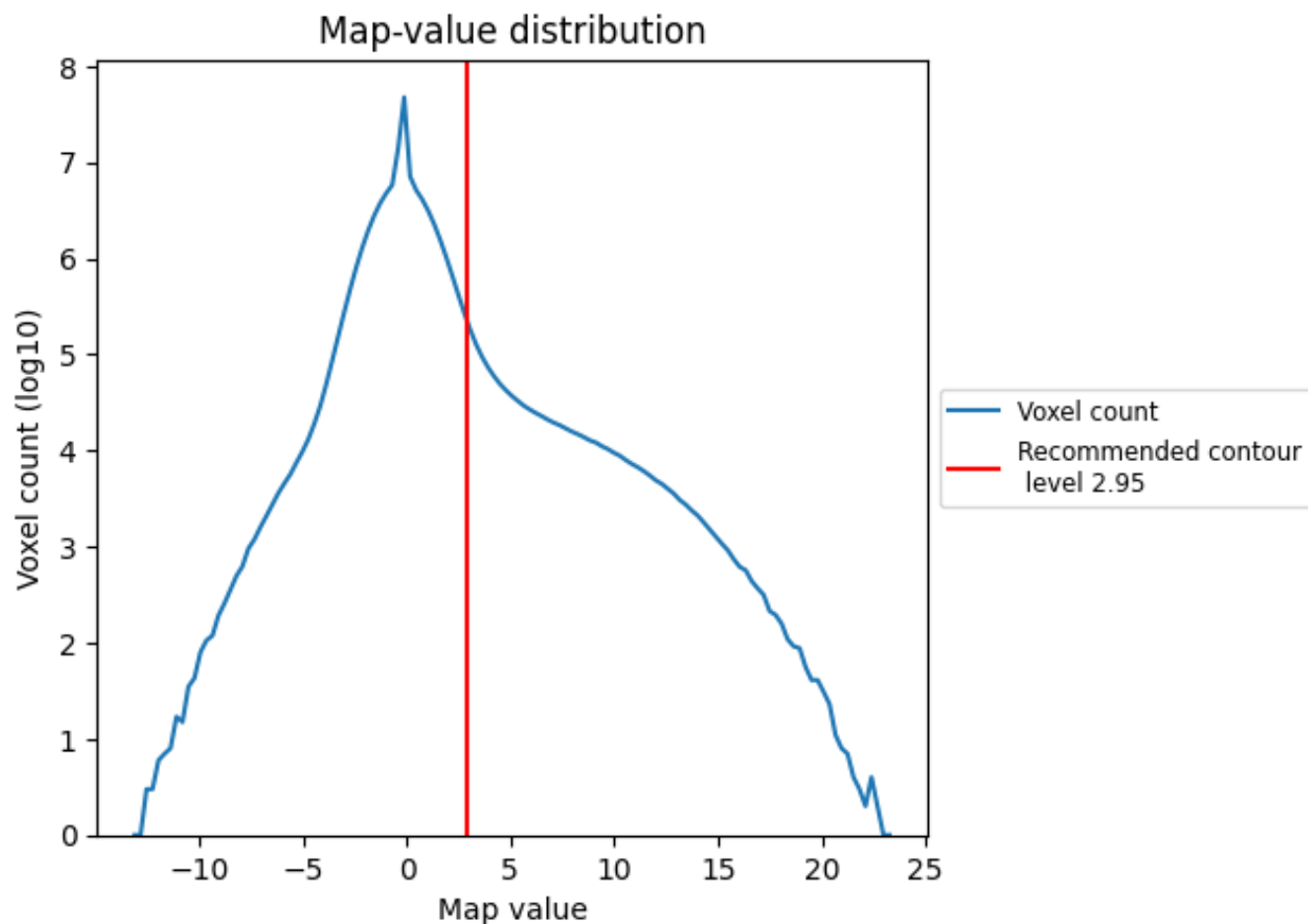
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

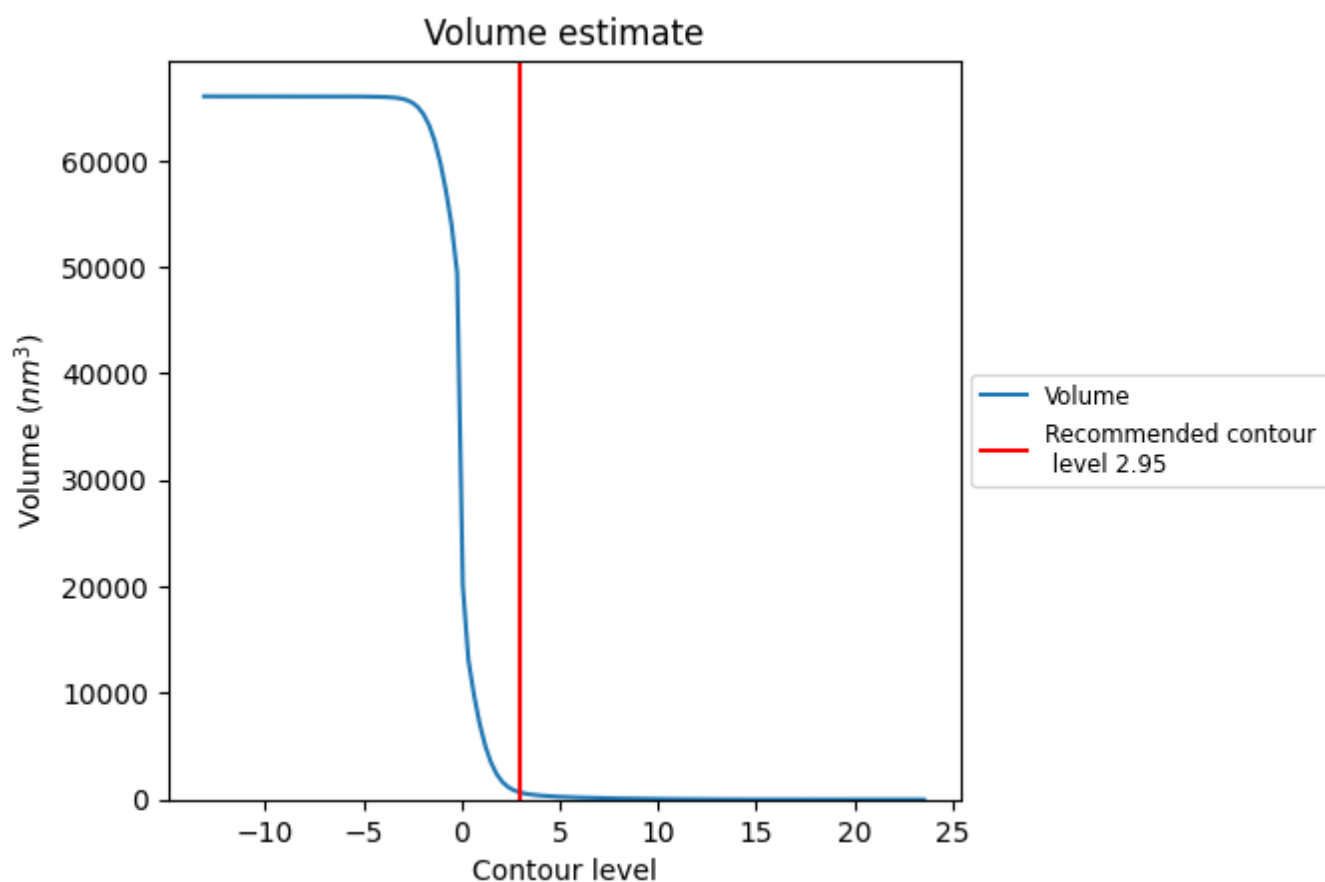
This section contains the results of statistical analysis of the map.

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.

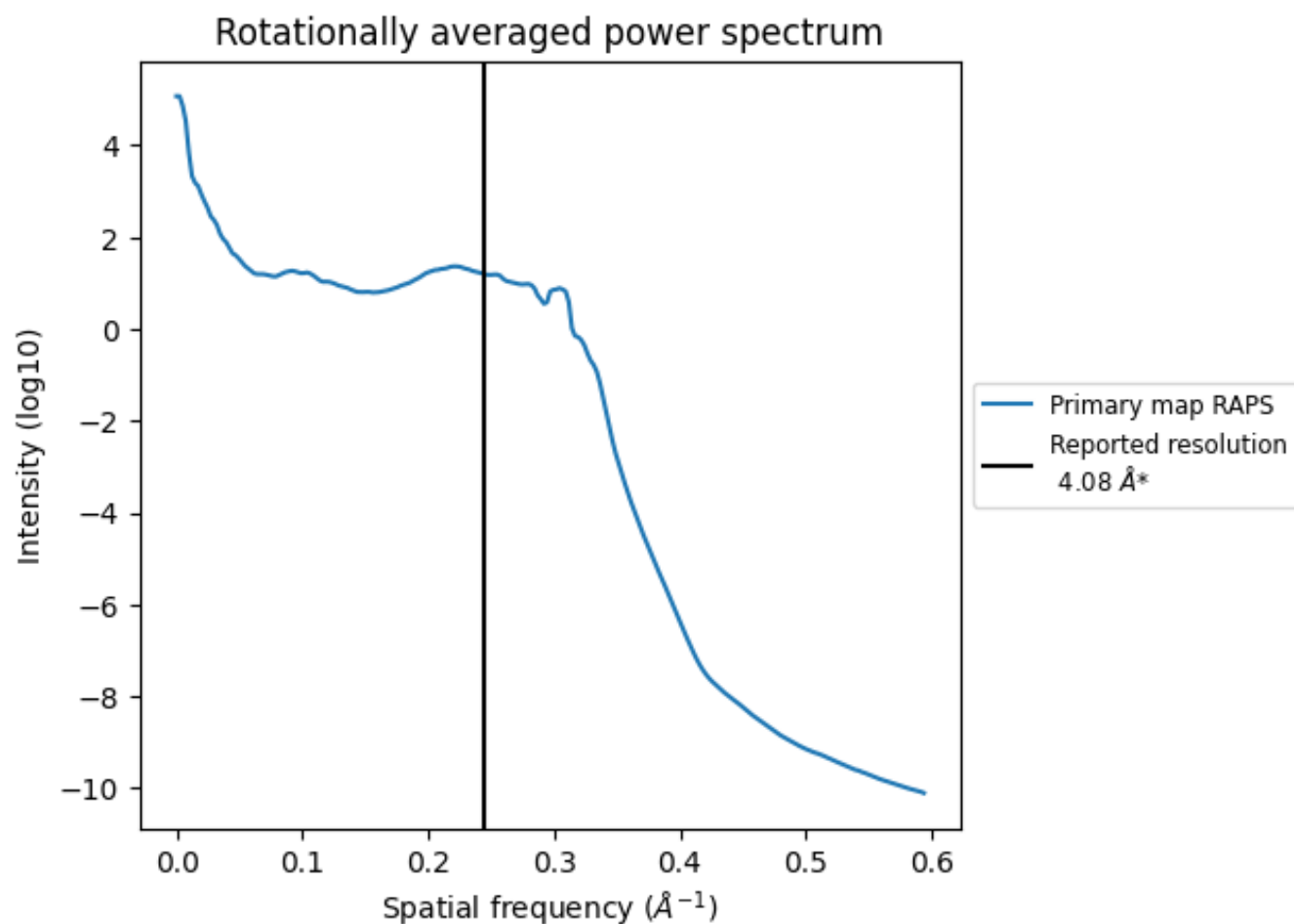
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 688 nm³; this corresponds to an approximate mass of 622 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 0.245 Å⁻¹

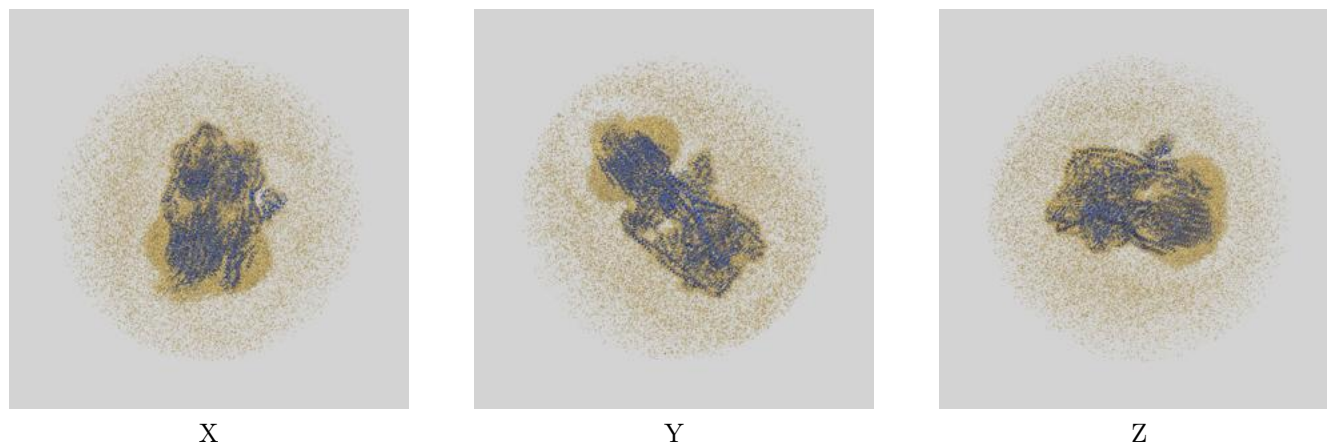
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

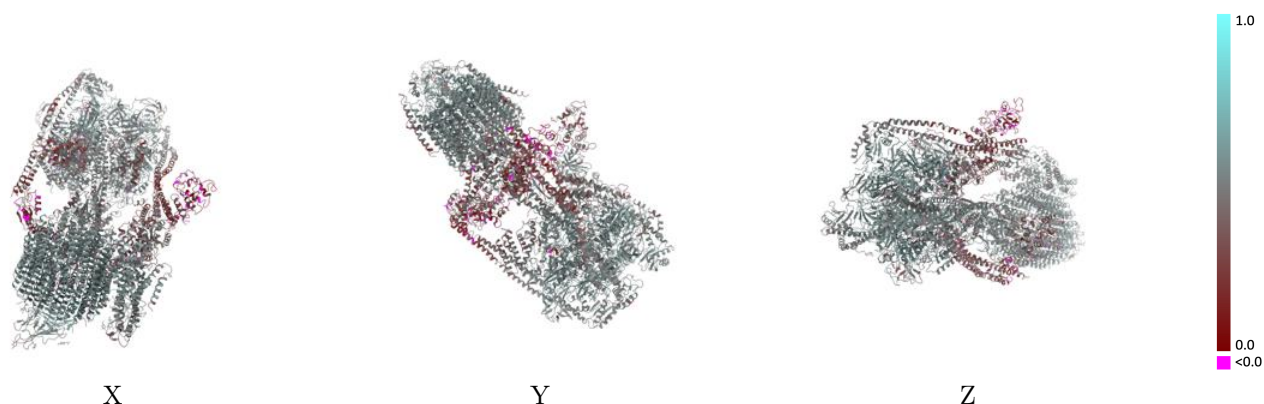
This section contains information regarding the fit between EMDB map EMD-26623 and PDB model 7UNF. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



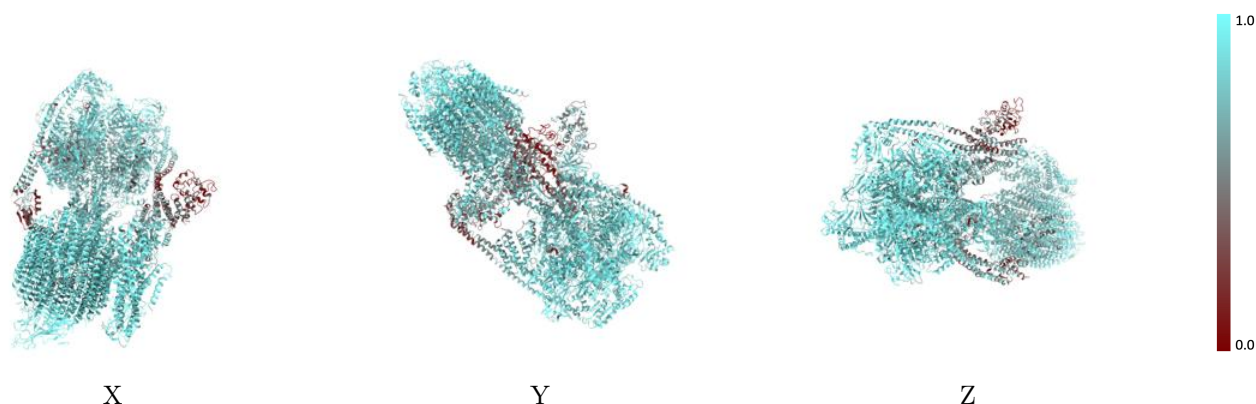
The images above show the 3D surface view of the map at the recommended contour level 2.95 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



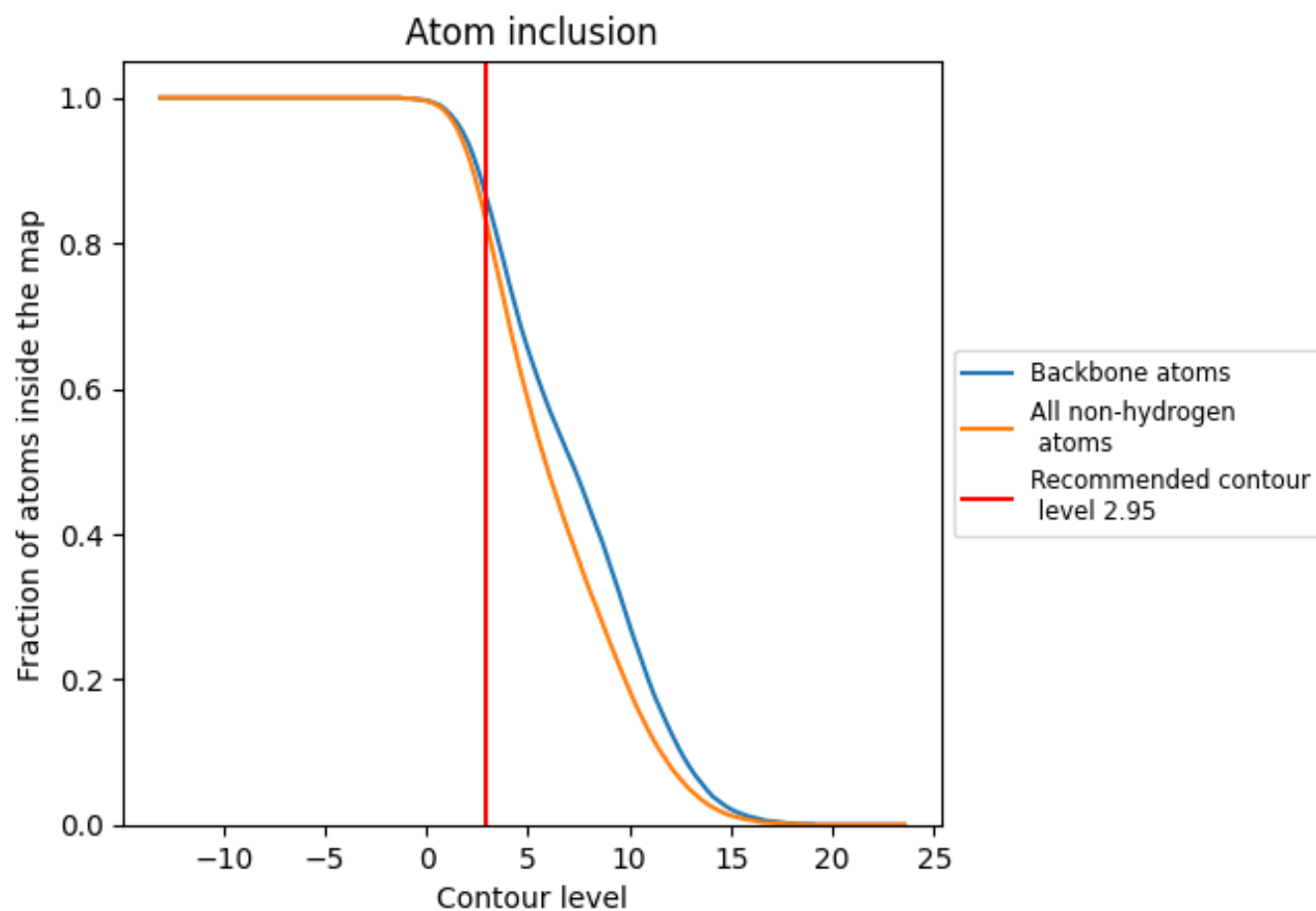
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.95).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 83% 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 (2.95) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8280	 0.4790
0	 0.9290	 0.5470
1	 0.9230	 0.5530
2	 0.9260	 0.5430
3	 0.9200	 0.5410
4	 0.9110	 0.5350
5	 0.9020	 0.5330
6	 0.9170	 0.5310
7	 0.9120	 0.5350
8	 0.9060	 0.5360
9	 0.9160	 0.5420
C	 0.4590	 0.2100
D	 0.8250	 0.4910
F	 0.7760	 0.4620
H	 0.4550	 0.2370
L	 0.8590	 0.4970
M	 0.8900	 0.5200
N	 0.8300	 0.4760
O	 0.8880	 0.5350
P	 0.9030	 0.5400
Q	 0.8990	 0.5380
U	 0.7120	 0.4090
a	 0.8150	 0.4390
b	 0.7450	 0.4440
c	 0.8240	 0.4590
d	 0.8080	 0.4660
e	 0.6130	 0.3810
f	 0.7050	 0.3810
g	 0.7690	 0.4000
k	 0.8660	 0.5200
m	 0.8870	 0.5030
n	 0.8310	 0.4410
r	 0.9020	 0.5450
s	 0.9200	 0.5280
t	 0.8830	 0.5000
w	 0.7730	 0.4010

